Agilent
Genomic Workbench 6.5

eArray$_{XD}$

User Guide

Agilent Technologies

Notices

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In This Guide...

This guide describes how to use the eArray$_{XD}$ program to create and submit custom microarray designs and SureSelect Target Enrichment libraries. eArray$_{XD}$ is part of the Agilent Genomic Workbench suite.

1 Getting Started

This chapter describes how to set up and navigate eArray$_{XD}$. It also gives an overview of the Agilent eArray system, and the main tasks that are available in the program.

2 Working with Probes

This chapter describes how to use the extensive set of probe tools in eArray$_{XD}$ to search for, create, upload, download, organize, and manage oligonucleotide probes for custom microarray designs.

3 Working with Probe Groups

This chapter describes how to create, search for, upload, download, and manage probe groups, which are the building blocks of microarray designs.

4 Working with Microarray Designs

This chapter describes how to search for, create, upload, download, manage, and submit microarray designs. It also gives instructions on how to use the many available Design Wizards, which guide you through the entire microarray creation process.

5 Working with SureSelect Target Enrichment Libraries

This chapter describes how to use oligonucleotide baits and bait groups to create bait libraries for target enrichment experiments.

6 eArray$_{XD}$ Reference

This chapter describes the elements of the eArray$_{XD}$ tab of Agilent Genomic Workbench, including the commands, menus, panes, and dialog boxes that can appear as you use the program. It also contains information about the many kinds of files that you can upload or download from the program, as well as microarray design guidance and answers from Agilent.

Contents

1 Getting Started

Welcome to eArray$_{XD}$, the desktop version of Agilent's eArray custom microarray design application. As illustrated in Figure 1, eArray$_{XD}$ is an integral part of the microarray research workflow, and it is a component of the Agilent Genomic Workbench 6.5 suite.

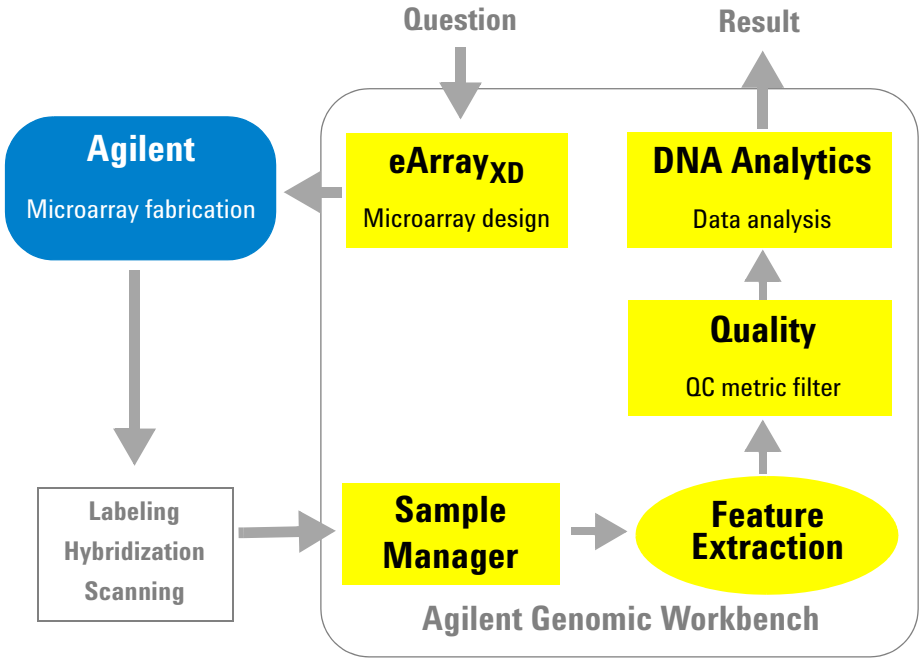


Figure 1 Microarray research pathway with Agilent Genomic Workbench 6.5

You use eArray at the beginning of the microarray research workflow to create custom microarray designs, which you then submit to Agilent for fabrication. After you hybridize the microarrays with labeled materials of interest, and scan them, you use the rest of Agilent Genomic Workbench to analyze the data.

The eArray System

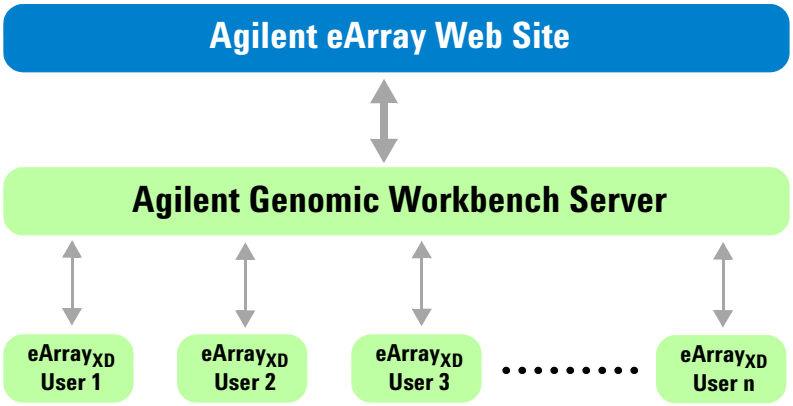


Figure 2 Components of eArray

The eArray system, illustrated in Figure 2, contains several main components:

- **Agilent eArray Web site** – The Web-based version of the eArray application that hosts several databases, including the Agilent Catalog Probe Database, the Agilent HD Probe Database, and a database of content that your workgroup may have previously created in the Web-based application. For you to use eArray$_{XD}$, your workgroup must be registered on the eArray Web site, and you must have a user account with a valid login name and password. See "eArray$_{XD}$ and the eArray Web site" on page 25 and the online help on the eArray Web site.
- **Agilent Genomic Workbench server** – The user-installed data repository and associated utilities that support the microarray-related and SureSelect Target Enrichment library-related content of your workgroup. This server is installed in a local environment (desktop computer, or another network-accessible machine). It stores workgroup content locally, and also communicates with the eArray Web site to download content as needed. In addition, this server submits probe design and other processing jobs to the eArray Web site and monitors their progress.

- **eArray$_{XD}$** – A component of the Agilent Genomic Workbench client software. This client software is installed on your own computer. eArray$_{XD}$ lets you create and manage custom microarray content for CGH, ChIP-on-chip, methylation, gene expression, and microRNA applications. It also lets you create and manage oligonucleotide bait libraries for target enrichment experiments.

  eArray$_{XD}$ communicates with your server to upload or retrieve data as needed. In general, it stores all content on your server, but you can also download specific types of files to your computer. It also lets you submit microarray designs and retrieve data from the eArray Web site through your server. If your workgroup has multiple users, they can all run eArray$_{XD}$ on their own computers and access the server through a standard network connection. eArray$_{XD}$ requires no license.

Once you are connected to your server and the eArray Web site, you can do all of your design work on your own computer in eArray$_{XD}$.

NOTE For a comparison of the features that are available in eArray$_{XD}$ and on the eArray Web site, see "Comparison of eArray$_{XD}$ and the eArray Web site" on page 31.

Probes, probe groups, and microarray designs

When you use eArray$_{XD}$ to create custom microarray designs, you use content on several levels of organization. Figure 3 illustrates these levels.

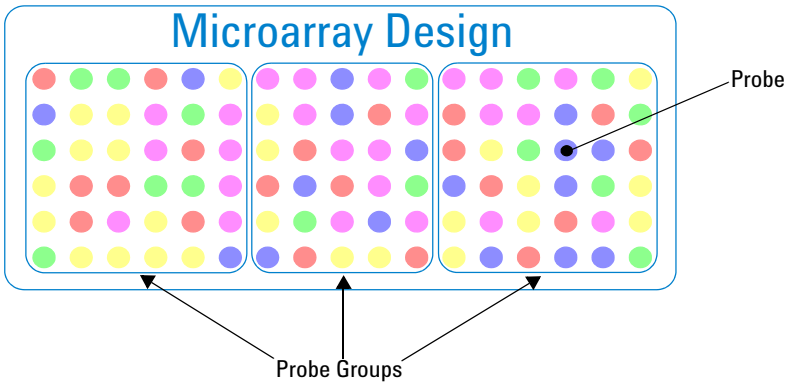


Figure 3 Levels of organization in eArray – Probes, Probe Groups, and Microarray Designs

- **Probes** are single-stranded oligonucleotide molecules that are represented as sequences of A, C, G, and T characters. Each character represents a single nucleotide base. eArray$_{XD}$ stores both the nucleotide sequence as well as annotation and accession information for each probe. You can use the extensive set of tools available in the program to search for, create, view, manage, and analyze probes. See Chapter 2, "Working with Probes."
- **Probe Groups** are collections of probes that are associated by one or more criteria, and are a means to organize probes. They are required organizational units that you use as the building blocks of microarray designs. See Chapter 3, "Working with Probe Groups."
- **Microarray designs** contain one or more probe groups. A given design is a set of files that contains all of the information necessary to manufacture a specific microarray slide, and to supply relevant information for downstream analysis. See Chapter 4, "Working with Microarray Designs."

NOTE For the SureSelect Target Enrichment application type, content is organized in a similar manner, with baits, bait groups, and libraries. See "Working with SureSelect Target Enrichment Libraries" on page 351.

Probes, probe groups, and microarray designs are integral to the microarray creation process, shown in Figure 4.

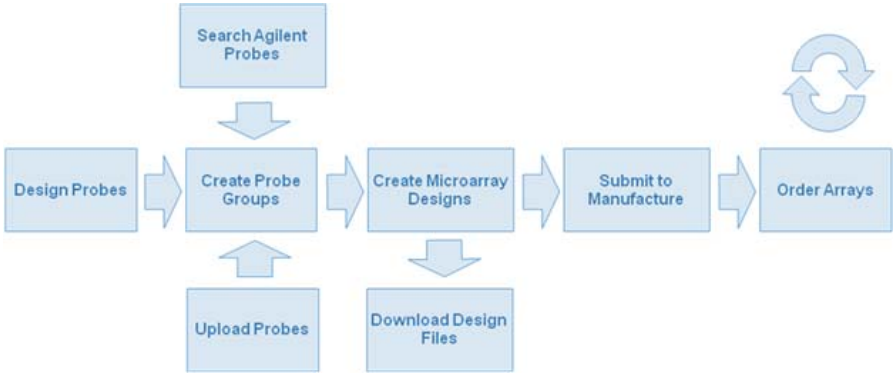


Figure 4 Microarray creation process with eArray

To create a custom microarray, you use the probe tools in eArray to search for existing probes, to design new probes, or to upload probes. You create one or more probe groups with the desired probes, and create a microarray design that contains these probe groups. After you create the microarray design, you submit it, which transfers the information that is needed to make the physical microarray slides to Agilent Manufacturing. You can then request a price quote through the eArray system, and subsequently place an order for microarrays through your Agilent sales representative.

For overviews of several available workflows, see these topics:

- "To create a microarray design with Agilent probes" on page 55
- "To create a microarray design with your own probes" on page 56
- "To use a wizard to create a microarray design" on page 58

eArray$_{XD}$ and the eArray Web site

eArray$_{XD}$ is designed to work seamlessly with the eArray Web site. Thus, to use eArray$_{XD}$, you must also be a registered user on the eArray Web site. In addition, your workgroup must be registered on the site. See "To become a registered user on the eArray Web site" on page 39.

Your Agilent Genomic Workbench server is the main link between the Agilent Genomic Workbench client program that runs on your desktop and the eArray Web site. For all features in eArray$_{XD}$ to be available, up to four different kinds of data may need to be transferred to the server from the eArray Web site:

- **Required "core" data** – This includes administrative data, control grids, and the **names** (only) of Catalog and workgroup probe groups, bait groups, microarray designs, and libraries. These data are transferred automatically when you install the server software. See below, "Transfer of data from the eArray Web site when you install the server."
- **Probes, baits, and exon boundary data** – This includes the nucleotide sequences of probes and baits, and annotation such as chromosomal locations and associated gene names. It also includes the genomic coordinates of exonic regions in the genomes of supported species, for use with certain search and design tools in the program. You can transfer desired subsets of these data after you install the client program. See "Transfer of probes, baits, and exon data from the eArray Web site after client installation" on page 26.
- **Microarrays, libraries, probe groups, and bait groups** – This "mapping" information defines the probe or bait content of specific probe groups, bait groups, microarray designs, and libraries. You use the client program to transfer these data as needed on a per-item basis. See "Transfer of probe groups, bait groups, microarray designs, and libraries from the eArray Web site" on page 27.
- **Agilent updates** – Agilent regularly updates probe and bait annotation, as well as other content. You use the client program to transfer some of these updates as needed on a per-item basis. The server retrieves other items automatically. See "Transfer of probe groups, bait groups, microarray designs, and libraries from the eArray Web site" on page 27.

Transfer of data from the eArray Web site when you install the server

When you install your Agilent Genomic Workbench server software, the server automatically retrieves certain required items from the eArray Web site:

- Items whose transfer must be complete before you can open the client program. These items are retrieved first, and require a total of approximately 30 minutes for transfer.
  - Administrative information about your workgroup, such as login names, passwords, and folder structure.
  - The names and certain other information (metadata) about the probe groups, bait groups, microarray designs, and SureSelect Target Enrichment bait libraries from the folders of your workgroup and from the Agilent Catalog. The names of these items appear in the Design Data pane of the Navigator. The server only retrieves these data for microarray designs and libraries with a status of Complete or Submitted.

    To use any of these items in eArray$_{XD}$, you must also download additional data. See below, "Transfer of probes, baits, and exon data from the eArray Web site after client installation" and "Transfer of probe groups, bait groups, microarray designs, and libraries from the eArray Web site" on page 27.
  - New microarray and library control grids, if required.
- Items that are transferred as download jobs that run in the background. While this information is transferred to your server, you can open the client program.
  - Default normalization and replicate probe groups.
  - Default filler probe group.

  These data transfer jobs can be viewed in the Job Queue Management Console. See "To monitor tasks" on page 59 and "Job Queue Management Console" on page 791. These jobs require a total of approximately 2 hours to finish. If you try to view or use one of these items before this transfer is complete, you get an error message.

Transfer of probes, baits, and exon data from the eArray Web site after client installation

After you install the Agilent Genomic Workbench client program, you can transfer probe and bait sequences and annotation, as well as the genomic coordinates of exon boundaries, from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. Although you

can transfer this data at any time after you install the client program, you must transfer it before you can do certain tasks in eArray$_{XD}$ that require it. For example, to search for expression probes from the Agilent Catalog, you must first transfer the Catalog expression probe data from the eArray Web site to your server.

The sets of data are transferred to your sever in the background, so you can use eArray$_{XD}$ during the transfer process. A given set of probe, bait, or exon data can only be transferred once. Also, if one person in your workgroup transfers a particular set of data, it becomes available to all members of the workgroup.

Tasks in eArray$_{XD}$ that do *not* require the kinds of transfers that are described above, can be done at any time after you open the client program. Examples of these tasks include High Density (HD) probe searches, Gene Expression Probe Design, and Probe Uploads. Note that if you upload probes or baits to your server through eArray$_{XD}$ *before* you transfer your workgroup data from the eArray Web site, eArray$_{XD}$ prefixes "XD_" to the IDs of all uploaded probes and baits. This avoids potential conflicts in names between the probes or baits that you upload and those that you may later transfer to your server from the folders of your workgroup on the eArray Web site.

The transfer of all probe data from the Agilent Catalog and from your workgroup can take up to several days or more, depending on network traffic and the amount of workgroup data. Agilent recommends that you transfer only the specific probes, baits, and exon data that you need.

Transfer of probe groups, bait groups, microarray designs, and libraries from the eArray Web site

You can use the client program to transfer a probe group, bait group, microarray design, or library from the eArray Web site to your server. When you retrieve such an item, you transfer only its probe or bait mapping information. Mapping information defines the probes or baits that are contained in a given item. Because this information refers to probe or bait data on your server, you must have already transferred the relevant probes or baits from the eArray Web site before you can transfer mapping information. See above, "Transfer of probes, baits, and exon data from the eArray Web site after client installation."

In the Design Data pane of the Navigator, a special icon appears next to the name of each item that needs to be retrieved. In search results, the only action that is available for these items is (Download from eArray Web site). See

"To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. After you transfer the mapping information for a given probe group, bait group, microarray design, or library, you can work with the given item in eArray$_{XD}$.

As a general rule, *after* you transfer a given workgroup probe group, bait group, microarray design, or library to your server for the first time, workgroup content that is subsequently added or changed on the eArray Web site is *not* automatically synchronized with the database on your server. Agilent recommends that you manage all of your workgroup design content on your local system through Agilent Genomic Workbench/eArray$_{XD}$. However, note these exceptions:

- If Agilent subsequently adds or makes changes to an Agilent Catalog probe group or bait group on the eArray Web site, your server automatically detects the change. The changed or added item can then be downloaded from the eArray Web site.  appears next to the name of the item. In search results, the only action that is available for these items is (Download from eArray Web site). These are the same icons that appear for any probe group or bait group that can be transferred to your server from the eArray Web site. When you transfer such items, the applicable probes or baits on your server are updated accordingly.
- If Agilent subsequently changes an Agilent Catalog library or microarray design, your server automatically detects the changed item. If you have already downloaded the design files from the eArray Web site, you can download them again. The program adds a **Download from eArray.com** option to the shortcut menu that appears when you right-click the name of the design in the Design Data pane of the Navigator.
- The server keeps all versions of the annotation files that have been transferred from the eArray Web site. When you download these design files from your server, you can select any desired version. See "To download microarray design files" on page 341 and "To download library design files" on page 461.
- If you subsequently save a SureSelect Target Enrichment library or a microarray design on the eArray Web site with a status of Complete or Submitted, your server automatically retrieves a GEML file (for microarray designs) or a BED file (for libraries). You can download these files to your computer from the **Custom Designs** folder in the Design Data pane of the Navigator. You can use these files for data analysis in the Feature Extraction and DNA Analytics programs. However, you cannot use eArray$_{XD}$ to edit these items, or to access their probes or baits.

- When certain items change on the eArray Web site, such as when Agilent changes the available species and microarray and library control grids and formats, these items are transferred to your server automatically.
- If you change your password on the eArray Web site, or new users are added to the workgroup, this information is detected and retrieved automatically by the server within approximately one day.

NOTE

Feature Extraction (FE) and the DNA Analytics data analysis applications in Agilent Genomic Workbench can also use the microarray designs that you download from the eArray Web site. For details, see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Submission of libraries and microarrays to Agilent

When you use eArray$_{XD}$ to submit a library or microarray design to Agilent, your server transfers the design files to the eArray Web site, which in turn sends them to Agilent Manufacturing. You can then request a quote for the library or microarray design, and subsequently place an order. Agilent manufactures the microarray or SureSelect Target Enrichment kit after you place an order.

See these topics:

- "Submitting Microarray Designs to Agilent" on page 346
- "To submit a library to Agilent" on page 458

The libraries and microarray designs that you submit to Agilent through eArray$_{XD}$ also become available in your user account on the eArray Web site, where you can search for, view, download, and request quotes for them. However, you cannot access their probes, copy them, or publish them to OpenGenomics.com. See the online help on the site.

Remote execution of jobs on the eArray Web site

The program submits certain jobs to the eArray Web site for completion, such as High Density (HD) Probe Searches, Gene Expression Probe Design, and Genomic (and Bait) Tiling of Agilent genomes. You can monitor these tasks and use their results from within eArray$_{XD}$. See "Managing Tasks" on page 70.

Role of the workgroup administrator on the eArray Web site

One or more users in the workgroup must have the role of **workgroup administrator** on the eArray Web site. It is the responsibility of the workgroup administrator to set up the workgroup on the site, and to do these ongoing administrative tasks:

- Create and approve new user accounts
- Reset user passwords
- Set up folders and access privileges for users in the workgroup

The workgroup assigns a workgroup administrator when it first registers on the eArray Web site. Subsequently, the workgroup administrator can assign this role to additional users. See the online help on the site.

Comparison of eArray$_{XD}$ and the eArray Web site

The table below compares the main features that are available in eArray$_{XD}$ with those available on the eArray Web site.

Feature	eArray$_{XD}$	eArray Web site
Application types supported		
CGH – Comparative Genomic Hybridization	✓	✓
CGH+SNP Arrays (In CGH application type)	✓	✓
ChIP-on-chip – Chromatin Immunoprecipitation	✓	✓
CH3 – Methylation	✓	✓
Expression – Gene Expression	✓	✓
microRNA	✓	✓
OLS – Oligonucleotide Library Synthesis		✓
SureSelect Capture Array		✓
SureSelect Target Enrichment	✓	✓
Probe tools		
Probe Search (workgroup and Agilent Catalog probes)	✓	✓
HD Probe Search (CGH, ChIP-on-chip, CH3)	✓[1]	✓
SNP Probe Search (CGH)	✓	✓
Gene Ontology (GO) Search (Expression)		✓
Biological network-based searches	✓	
Use Literature Search to create a network	✓	
Simple Tiling (Expression)	✓	✓
Genomic Tiling of Agilent Genomes	✓[1]	✓
Genomic Tiling of User Genomes	✓	
Gene Expression Probe Design	✓[1]	✓
Probe Performance Score (CGH, ChIP-on-chip, CH3)	✓	✓
Gene Expression probe quality check	✓[1]	✓

Feature	eArray$_{XD}$	eArray Web site
Upload probes	✓	✓
Download probes	✓	✓
Probe filters		✓
Custom probe annotation		✓
Delete probes	✓	✓
Probe Group tools		
Search probe groups	✓	✓
Browse probe groups by folder	✓	✓
Browse probe group by category		✓
Create probe group	✓	✓
Copy probe group	✓	✓
Edit probe group	✓	✓
Upload probe group	✓	✓
Download probe group	✓	✓
Move probe group	✓	✓
Display a probe group as a genomic plot	✓	
Add attachments to probe groups	✓	✓
Share probe group in a collaboration		✓
Compare probe groups		✓
Microarray design tools		
Search microarray designs	✓	✓
Browse microarray designs by folder	✓	✓
Browse microarray designs by category		✓
Create microarrays from existing probe groups	✓	✓
Create microarrays from probe uploads	✓	✓
Create microarrays using Genomic Tiling	✓[1]	✓

Feature	eArray$_{XD}$	eArray Web site
Create microarrays using Gene Expression Probe Design	✓[1]	✓
Create microarrays using other designs as templates	✓	✓
Create microarrays from HD probe searches	✓[1]	✓
Create CGH+SNP microarrays	✓	✓
Use wizards to conveniently create microarray designs	✓	✓
Submit microarray designs to Agilent	✓[1]	✓
Request quotes for microarrays	✓[1]	✓
Subscribe to content updates by e-mail		✓
Download microarray design files	✓	✓
Multiple GEML version support	✓	
Copy microarray designs	✓	✓
Edit microarray designs	✓	✓
Review of microarray designs by other users	✓	✓
Move microarray designs	✓	✓
Share microarray designs in a collaboration		✓
Add attachments to microarray designs	✓	✓
Randomized probe layout on microarray slides	✓	✓
Customer-specified probe layout on microarray slides		✓
Create microarray sets		✓
Express Array (Direct upload to Agilent Manufacturing)		✓
Visualize microarray design layouts	✓	
Publish designs on OpenGenomics.com		✓
Tools for SureSelect Target Enrichment libraries		
Search baits	✓	✓
Upload baits	✓	✓
Download baits	✓	✓

Feature	eArray$_{XD}$	eArray Web site
Bait Tiling of Agilent genomes	✓[1]	✓
Bait Tiling of user genomes	✓	
Search bait groups	✓	✓
Browse bait groups by folder	✓	✓
Browse bait groups by category		✓
Upload bait groups	✓	✓
Download bait groups	✓	✓
Create bait groups	✓	✓
Edit bait groups	✓	✓
Copy bait groups	✓	✓
Move bait groups	✓	✓
Share bait groups in a collaboration		✓
Add attachments to bait groups	✓	✓
Search bait libraries	✓	✓
Browse bait libraries by folder	✓	✓
Browse bait libraries by category		✓
Create libraries from existing bait groups	✓	✓
Create libraries from bait uploads	✓	✓
Create libraries using Bait Tiling	✓[1]	✓
Create libraries using other libraries as templates	✓	✓
Create “combined” libraries that include an Agilent Catalog library and additional baits that you design		✓
Use wizards to conveniently create bait libraries	✓	✓
Edit libraries	✓	✓
Review of bait libraries by other users	✓	✓
Share libraries in a collaboration		✓

Feature	eArray$_{XD}$	eArray Web site
Move libraries	✓	✓
Copy libraries	✓	✓
Add attachments to libraries	✓	✓
Submit libraries to Agilent	✓[1]	✓
Request quotes for libraries	✓[1]	✓
Miscellaneous features		
Local storage of workgroup content	✓	
Time-limited storage of content on the eArray Web site		✓
Manage pending jobs	✓	
Create and participate in collaborations		✓
Download supplemental files for Agilent Genomic Workbench		✓
Download supplemental files for Agilent GeneSpring		✓
Create and manage users		✓
Customize search criteria and results		✓
Languages supported		
English	✓	✓
Chinese		✓

[1]Uses eArray Web site

Setting up eArray$_{XD}$

To start eArray$_{XD}$

eArray$_{XD}$ is part of the Agilent Genomic Workbench suite. Before you start eArray$_{XD}$, you must be a registered user on the Agilent eArray Web site. Also, your workgroup must be registered on the site. See "To become a registered user on the eArray Web site" on page 39.

1 Start Agilent Genomic Workbench. For instructions, see the *Product Overview Guide*.

A Select Application Type dialog box appears. If this dialog box does not appear, an application type has already been selected.

2 Select the desired application type, such as **CGH** or **Expression**, then click **OK.**

You can select a different application type later, if needed. See "To set the application type" on page 48.

Several additional dialog boxes can appear before the main program window appears. For more information, see the *Product Overview Guide*.

eArray$_{XD}$ is available free of charge, and you do not need to enter any license information to use it. If a dialog box asks you for license information, you can click **Skip.**

However, if you have purchased a license for one or more of the microarray data analysis applications, you must enter your license information before those parts of the Agilent Genomic Workbench software become available to you. Alternatively, you can enter license information at any time in the User Preferences. To open the User Preferences dialog box, click **Home > User Preferences.** You can also use the User Preferences to change both the Agilent Genomic Workbench server and the eArray Web site account to which your Agilent Genomic Workbench client program is linked.

3 Click the **eArray$_{XD}$** tab.

A command ribbon appears. The commands let you use the main functionality of eArray$_{XD}$.

To display or change the location of your Agilent Genomic Workbench server

To start the program, you must have already specified the location of a valid server. However, within the program, you can view the current settings, or enter settings for a different server. This can be useful if you have installed the Agilent Genomic Workbench Server software on multiple machines, and you want to connect your Agilent Genomic Workbench client program to a different server.

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

   The Preferences dialog box appears.

2 Click the **Miscellaneous** tab.

   The database host name and port for your server appear under Configuration Parameters. See "User Preferences – Miscellaneous tab" on page 864.

3 To change the host name or port, click **Change.**

   A dialog box asks if you are sure that you want to change the database configuration parameters.

4 Click **Yes.**

   The Database Configuration Parameters become available.

5 Type the desired database host name and port, then click **OK.**

   The program makes a connection to the server that you entered. The entry in Common Storage Location changes accordingly. This location is set by the server software, and cannot be edited.

CAUTION eArray$_{XD}$ relies on the server for essential functions. For the program to work properly, you must enter configuration parameters for a location that contains a valid Agilent Genomic Workbench server program.

NOTE If you must use a proxy server for the client and/or server machines, you can set these from the Miscellaneous tab of the User Preferences dialog box. Ask your network administrator for the correct settings.

To link the Agilent Genomic Workbench client program to a different account on the eArray Web site

The Agilent Genomic Workbench client program on your computer is linked to a specific account on the eArray Web site. The identity of this account controls the content items that appear within eArray$_{XD}$, and what you can do with them. This information was entered the first time the program was started, but if you need to link the client program to a different account, you can do so from within the client program.

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

   The User Preferences dialog box appears.

2 In the dialog box, click the **Miscellaneous** tab. See "User Preferences – Miscellaneous tab" on page 864.

3 In **eArray User Details** type the following information:

   - **Username** – The desired existing login name on the eArray Web site.
   - **Password** – The current password for the account on the eArray Web site. For security, the actual characters of your password do not appear.

4 Click **OK.**

   You must close the program and restart it for your new login information to take effect.

NOTE

- The procedure above links the Agilent Genomic Workbench client program to a different user account that already exists on the eArray Web site. To create a new user account, or to change the login information of an existing account, see "To become a registered user on the eArray Web site" on page 39 and "To change your user information on the eArray Web site" on page 39.
- If you log in to the eArray Web site and change the password for your account, this information is automatically updated in eArray$_{XD}$ within approximately one day. You do not need to change this information in the User Preferences. After this update occurs, the program asks you to type your new password the next time you open it.

To become a registered user on the eArray Web site

To use eArray$_{XD}$, you must be a registered user on the eArray Web site. In addition, your workgroup must be registered on the site.

1 In Internet Explorer 7, go to https://earray.chem.agilent.com

The login page of the eArray Web site appears.

2 Click **Request for Registration.**

The eArray registration page appears. For more details about how to register, see the online help on the eArray Web site.

Login names and passwords of newly registered users in a workgroup are usually transferred to Agilent Genomic Workbench within one day.

To change your user information on the eArray Web site

You can change your login name, contact information, and password on the eArray Web site.

1 In Internet Explorer 7, go to https://earray.chem.agilent.com

The login page of the eArray Web site appears.

2 Type your current login name and password, then click **Log In.**

Your user workspace appears.

3 Click **My Account > Personal Info.**

The Personal Info page shows your current contact information. For security, your password does not appear.

4 Edit the information in the **User Details** and **Other Details** panes as desired. To restore all of your information to what it was before you edited it, click **Reset.** All items marked with a red asterisk "*" are required.

Note: If you change your e-mail address, your login name changes to your new e-mail address.

5 To change your password, follow these steps:

a Click **Change Password.**

The Change Password page appears.

b Type the following information. To start over at any time, click **Reset.** To go back to the Change Personal Information page without changing your password, click **Cancel.**

Setting	Instructions/Details
User ID	Displays your current e-mail address, which you cannot edit from this page.
Current Password	Type your current password. eArray asks for your current password for security reasons.
New Password	Type your new password. Your password is case-sensitive, and must be at least eight characters long. In the first eight characters, include at least two alphabetical characters, one non-alphabetical character, and at least four different characters.
Confirm New Password	Retype your new password.

c Click **Update.**

eArray enables the new password, and disables the old one.

6 Click **Update.**

eArray updates your personal information. A message tells you that your personal information was updated successfully.

7 Click **Close.**

8 On the eArray title bar, click **Log Out.**

A dialog box appears.

9 Click **OK.**

NOTE

If you change the password for your account on the eArray Web site, this information is automatically updated in eArray$_{XD}$ within approximately one day. You do not need to change your password in the User Preferences. After this update occurs, the program asks you to type your new password the next time you open it. Also, login names and passwords of newly registered users in a workgroup are usually transferred to Agilent Genomic Workbench within one day.

To reset your password on the eArray Web site

If you forget your password on the eArray Web site, your eArray workgroup administrator can reset it for you. You can also obtain a temporary password from Agilent:

1 In Internet Explorer 7, go to https://earray.chem.agilent.com

The eArray Login page appears.

2 In the User Login pane, click **Forgot Password.**

A password recovery page appears.

3 In **E-mail Address,** type your complete e-mail address for verification. Type the same e-mail address that you entered during registration or when you last updated your account. Without this information, Agilent cannot reset your password.

4 Click **Submit E-mail Address.**

If Agilent finds a match between the e-mail address that you entered and the eArray user records, you receive a new temporary password by e-mail. The next time you log in to eArray, use this password to log in. After you log in, you must change your password.

NOTE

Your password information is automatically updated in $eArray_{XD}$ within approximately one day. You do not need to change your password in the $eArray_{XD}$ User Preferences. After this update occurs, The program asks you to type your new password the next time you open it. Also, login names and passwords of newly registered users in a workgroup are usually transferred to Agilent Genomic Workbench within one day.

Using eArray$_{XD}$

This section describes the main parts of the eArray$_{XD}$ tab, and the main tasks that you can do with the program. All functionality is described more extensively in subsequent chapters.

When you start the program, the main window of Agilent Genomic Workbench appears. Almost all of the eArray$_{XD}$ functionality can be found in the eArray$_{XD}$ tab, shown in Figure 5. The other tabs give you access to the other programs that are part of the Agilent Genomic Workbench suite, as well as a few more eArray-related functions.

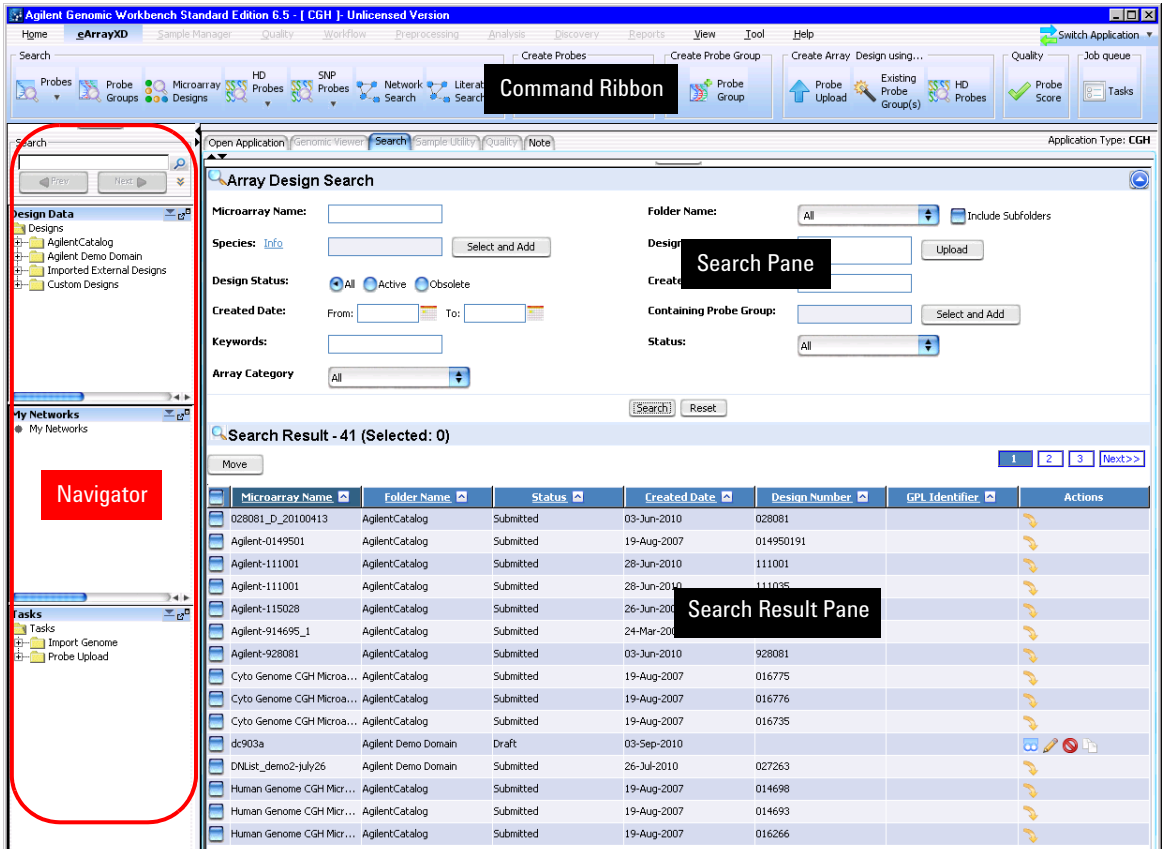


Figure 5 Agilent Genomic Workbench main window – eArray$_{XD}$ tab

The eArray$_{XD}$ tab contains several main elements, identified in Figure 5. These elements are described below. To see detailed descriptions of all of the elements of the eArray$_{XD}$ tab, and all of the menus, shortcut menus, panes, and dialog boxes that can appear, see "The eArray$_{XD}$ Tab" on page 468.

- **Command Ribbon** – Contains the commands that start the main processes that are available in the program, such as searching for, creating, and evaluating content. When you click a command on the command ribbon, a menu opens (or in some cases, a dialog box or a search pane), where you can start the process. See "Command ribbon (eArray$_{XD}$ tab)" on page 471.
- **Navigator** – In the eArray$_{XD}$ tab, the Navigator contains several panes:

Pane	Purpose
Navigator search pane	Lets you search within any pane of the Navigator for items that contain a specific string of characters. See "To search the Navigator" on page 51 and "Navigator – Search pane" on page 484.
Design Data	Shows content that is available to you, organized by folders. In general, you can: • Expand or collapse folders to show or hide content. • View the icon that appears with an item to monitor its status. • Right-click the name of a folder or item to open a shortcut menu that lets you take action on the item. The actions that are available for specific items depend on many factors. Each of the main folders in this pane lets you use specific types of content. See "Navigator – Design Data pane" on page 486.
Experiment	(SureSelect Target Enrichment application type) Shows the names and contents of sequence analysis experiments that you have created with the SureSelect Quality Analyzer. You do not use this pane when you use eArray$_{XD}$. For information, see the *SureSelect Quality Analyzer User Guide.*
My Networks	Shows the saved networks that you have created from literature searches. See "Using Biological Networks to Find or Create Probes or Baits" on page 184 and "Navigator – My Networks pane" on page 496.

Pane	Purpose
Tasks	Shows the jobs that you have submitted. Some jobs are completed locally by the server program. Others are sent to the eArray Web site for completion. In general, you can: • View the icon that appears with a job to monitor its status. • Right-click the name of a task to open a shortcut menu that lets you take further action on the job. See "To monitor tasks" on page 59 and "Managing Tasks" on page 70. For a detailed description of all icons, buttons, actions that are available, see "Navigator – Tasks pane" on page 498.

- **Search pane** – Lets you set the criteria for probe, probe group, and microarray design searches. When you select a search from the Command Ribbon, the search criteria appropriate to the specific type of search appear in the Search pane. In general, you type, select, and in some cases upload, search criteria, then click **Search.** The results of the search appear in the Search Result pane.

  See these topics:

  - "Searching for Probes" on page 92
  - "Searching for Agilent High Density (HD) Probes" on page 109
  - "To search for probe groups" on page 224
  - "Searching and Browsing Microarray Designs" on page 251
  - "To use a biological network to find or create probes" on page 193
  - "Search Panes" on page 525

- **Search Result pane** – Searches for probes, probe groups, or microarray designs are one of the main ways to take further action on existing content. When you submit a search from the search pane, the items that match your search criteria appear in the Search Result pane.

  To take action on a specific content item, you can click one of the buttons that appears in the **Actions** column. For example in Figure 6, which shows the results of a Probe Group Search, you can click  to delete the specific probe group from your server. For a complete list of buttons that can appear in the Actions column of search results, see "Search Result pane" on page 514.

You can also select items in a set of search results, then click a button above or below the search results to take action on them.

See these topics:

- "To take action on specific content item(s)" on page 52
- "To take action on probes in search results" on page 100
- "To search for probe groups" on page 224
- "To search for microarray designs" on page 251
- "Search Result pane" on page 514

NOTE

When you do a High Density (HD) probe search, or a SNP probe search, the program makes search results available as a options in the Tasks pane of the Navigator, rather than in the Search Result pane. See "To view HD probe search results" on page 134 and "To view the results of a SNP probe search job" on page 155.

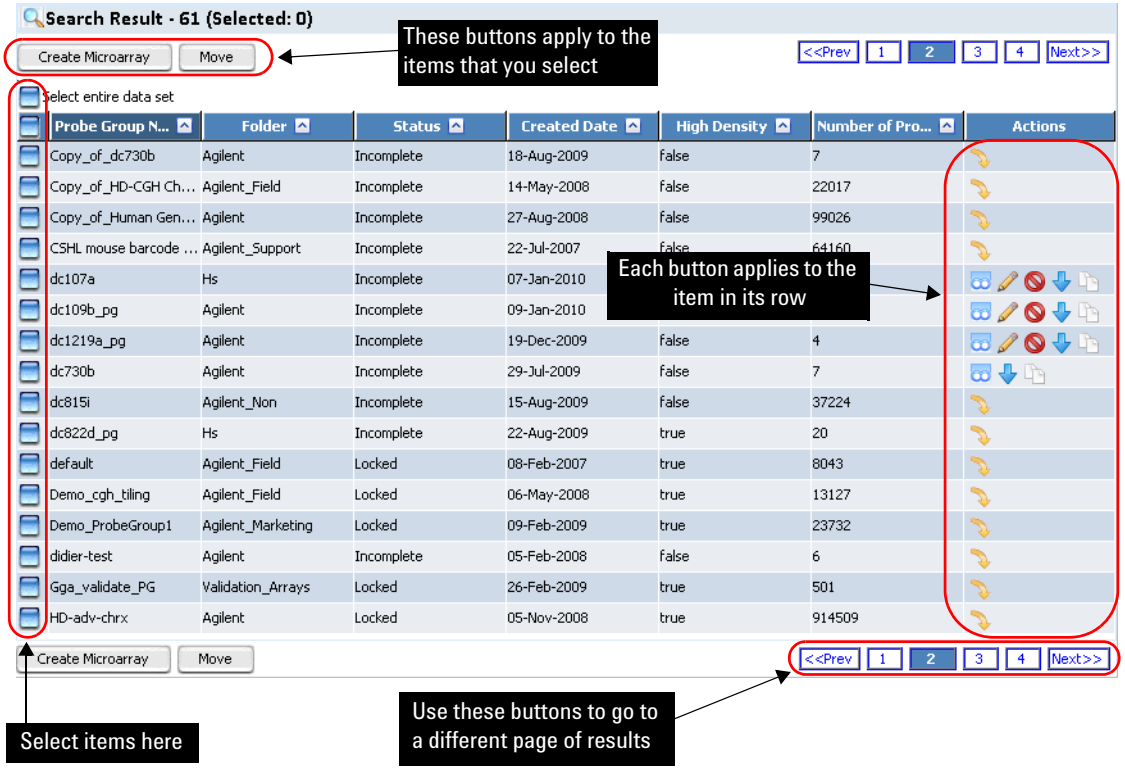


Figure 6 Search Result pane – Results from a Probe Group Search

To add a folder to the Navigator

The program stores all design-related content (probes, probe groups, and microarray designs, or (for the SureSelect Target Enrichment application type) baits, bait groups, and libraries, on your server. In the Design Data pane of the Navigator, you initially have a “main” folder (domain). You can add subfolders to this folder. You can also add additional subfolders to any subfolder that you create.

1 Expand the folders of the **Design Data** pane of the Navigator until you can see the folder to which you want to add the subfolder.

2 Right-click the name of the folder, then click **Create New Domain.**

The Create New Domain dialog box opens. See "Create New Domain" on page 677. The folder to which the new subfolder will be added appears in Parent Domain. To add the subfolder to a different folder, select another folder in **Parent Domain,** if one is available.

3 In **Domain Name,** type a name for the new folder. Use only letters, numbers, spaces, and underscores.

4 Click **Create.**

The new folder appears in the Design Data pane of the Navigator. A dialog box tells you that the domain has been created successfully.

5 Click **OK.**

NOTE

- Your main "default" folder has the same name as your main folder on the eArray Web site when your Agilent Genomic Workbench server software was installed. In many cases, the name of the folder is the name of your workgroup. You cannot change this name.
- You cannot add a subfolder to an Array Design or Probe Group folder.

To remove a folder

If you create a domain (folder) in the Design Data pane of the Navigator, you can remove it. The Array Design and Probe Group folders within it must be empty, and the folder must not contain any additional subfolders.

1 Expand the folders of the **Design Data** pane of the Navigator until you can see the folder that you want to delete.

2 Right-click the name of the desired folder, then click **Delete Domain.**

A dialog box asks if you really want to delete the selected domain.

3 Click **Yes.**

The program deletes the folder, and removes it from the Design Data pane of the Navigator. A dialog box tells you that the selected domain was successfully deleted.

4 Click **OK.**

To set the application type

You can use eArray$_{XD}$ to create microarrays or libraries for many experimental application types. The design requirements for these applications differ, and the available content and functionality within the program are partitioned by application type.

You select an application type before you start the program for the first time, but you can select a different application type at any time. eArray$_{XD}$ remembers your selection the next time you start the program.

1 In the eArray$_{XD}$ tab (or any other tab), click **Switch Application.**

These options appear:

Application type	Description
CGH	Array-based comparative genomics hybridization. You also select this application type to create CGH+SNP microarrays.
ChIP-on-chip	Array-based chromatin immunoprecipitation
CH3	Methylation microarray studies
Expression	Array-based gene expression studies.
microRNA	Array-based miRNA studies
SureSelect Target Enrichment	Creation of oligonucleotide bait libraries

2 In the menu that appears, mark the desired application type. These options appear:

In some cases, a dialog box asks you to supply license information. eArray$_{XD}$ is available free of charge, and does not require a license. If this dialog box appears, you can click **Skip.** However, if you have a license for one of the microarray data analysis applications, you can enter it at this point. See the *Installation Guide* for the Agilent Genomic Workbench software.

In the eArray$_{XD}$ tab, the commands in the ribbon, as well as the content in the Navigator, reflect the selected application type. Probe, probe group, and microarray design searches return only content that is associated with the selected application type. For example, if you select the **Expression**

application type, probe searches return only Expression type probes, and only the probe creation tools that are relevant to gene expression microarrays are available.

To search for probes, probe groups, or microarray designs

Several eArray$_{XD}$ tools let you search for existing microarray-related content, either from the workgroup folders to which you have access, or from the Agilent Catalog.

1 Set the application type to any type except SureSelect Target Enrichment. See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under **Search,** start the desired type of search. For additional information, see these topics:

- "Searching for Probes" on page 92
- "Searching for Agilent High Density (HD) Probes" on page 109
- "Searching for Agilent SNP Probes" on page 138
- "Using Biological Networks to Find or Create Probes or Baits" on page 184
- "To search for probe groups" on page 224
- "Searching and Browsing Microarray Designs" on page 251

You set parameters for the specific search in the Search pane. In the Search Result pane, the program shows a list of the names of the content items of the given application type that match your search criteria. For HD probe searches and SNP probe searches, the program lets you open the results from the Tasks pane of the Navigator, instead.

After you find the desired content, you can take action on it – see "To take action on specific content item(s)" on page 52. You can also search one or all of the panes of the Navigator for the occurrence of a search term – see "To search the Navigator" on page 51.

To search for baits, bait groups, and libraries

For the SureSelect Target Enrichment application type, you can search for bait library-related content.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under **Search,** start the desired type of search. For additional information, see these topics:

- "To search for baits" on page 358
- "To use a biological network or a literature search to find or create baits" on page 389
- "To search for bait groups" on page 396
- "To search for libraries" on page 416

In general, you set parameters for the specific search in the Search pane. In the Search Result pane, the program shows a list of the names of the content items that meet your search criteria.

After you find the desired content, you can take action on it – see "To take action on specific content item(s)" on page 52. You can also search one or all of the panes of the Navigator for the occurrence of a search term – see "To search the Navigator" on page 51.

To search the Navigator

You can search one or all of the panes of the Navigator for items that match a specific search term. Figure 7 shows the search pane of the Navigator, and identifies a couple of its elements. For a list of all of the parts of this pane, see "Navigator – Search pane" on page 484.

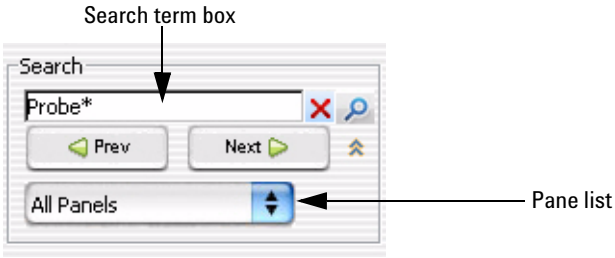


Figure 7 Search pane of the Navigator

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

   The program searches the selected pane(s) for items that match your search term. If it finds matching items, the program expands the appropriate folders, and displays the names of the matching items in red. The first matching item is highlighted in yellow.
4. Do any of the following:
   - To highlight the next matching item, if one is available, click Next.
   - To highlight the previous matching item, click Prev.
5. After you complete the search, click to clear the results of the search, as well as your search term.

To take action on specific content item(s)

After you start a search for specific content items, the program shows a list of matching items in the Search Result pane. You can use this pane to take action on the retrieved items. For example, you can delete a microarray design, or assign a set of returned probes to a new probe group. The actions that you can take depend on the ownership and status of the retrieved items.

1 Set the application type. See "To set the application type" on page 48.

2 Search for the desired content items. See "To search for probes, probe groups, or microarray designs" on page 49 and "To search for baits, bait groups, and libraries" on page 50.

   A list of items that match your search criteria appears in the Search Results pane. For example, Figure 8 on page 53 shows the results of a search for probe groups.

3 Do one of the following:

   - Mark the check boxes for the desired options, then click a button at the top or bottom of the search results to take action collectively on the selected items. For example, in the search results that appear in Figure 8, which shows the results of a probe group search, you can click **Create Microarray** to create a new microarray design that contains the selected probe group. If the search retrieves more than one page of results, the program remembers the items that you select as you go from page to page.
   - (Probe Group, Bait Group, Microarray Design, and Library searches only) In the **Actions** column, click the desired button. See Figure 8. For a description of the buttons that can appear, see "Search Result pane – Actions column" on page 516.

NOTE

As an alternative to the procedure described above, you can also right-click the name of an item in the Design Data pane of the Navigator, then select the desired action from the shortcut menu that appears. See "Design Data – Actions and shortcut menus (AgilentCatalog and workgroup folders)" on page 489.

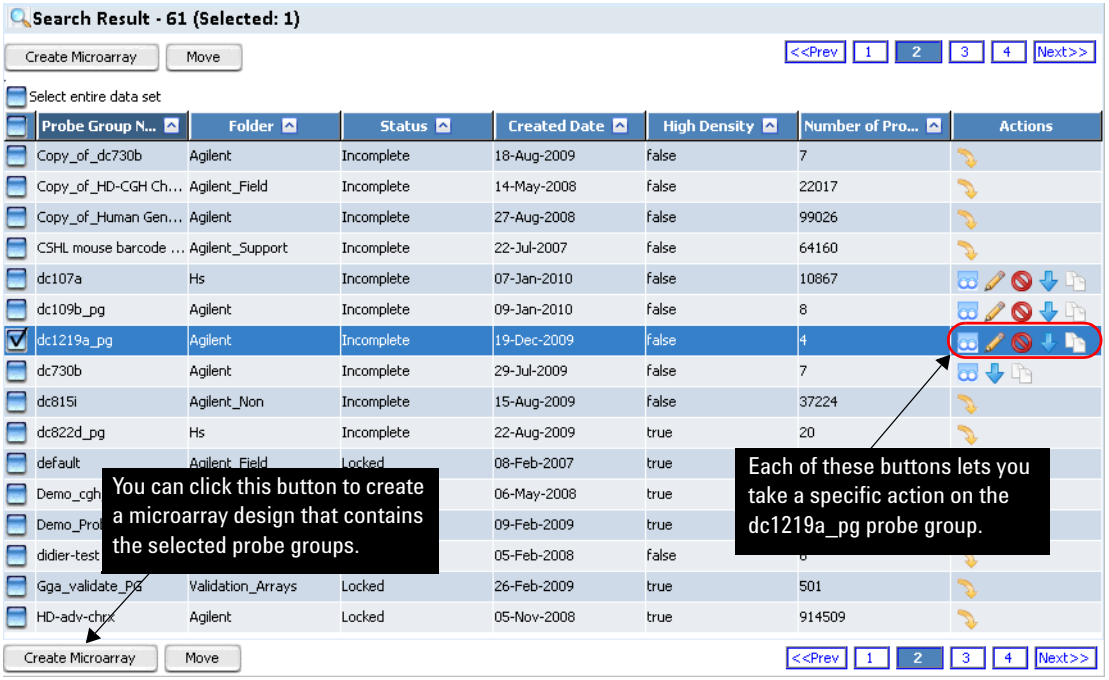


Figure 8 Search Result pane from a probe group search. The dc1219a_pg probe group is selected.

NOTE

You must follow a different procedure to take action on the results of an HD (High Density) probe search or a SNP probe search. See "To take action on an HD probe search job" on page 133 and "To monitor the status of a SNP probe search job" on page 153.

To create or upload probes

eArray$_{XD}$ gives you several ways to add new probe content to your Agilent Genomic Workbench server. You can upload probes for any available microarray-related application type except microRNA. The availability of other methods depends on the specific application type that you select.

1 Set the application type to any type except SureSelect Target Enrichment. See "To set the application type" on page 48.

2 Do one of the following:

- **To start a probe upload** – In the eArray$_{XD}$ tab, under Create Probes, click **Probe Upload.** See "Uploading Probes" on page 158.
- **To create new probes** – In the **eArray$_{XD}$ tab**, under **Create Probes,** select the desired method. See the following topics:

  "To set up a GE Probe Design job" on page 167

  "To set up a Simple Tiling job" on page 174

  "To set up a Genomic Tiling job" on page 176

In addition, you can use the results of several specialized types of searches to supply job parameters for certain probe creation jobs. See these topics:

- "To do a Simple Interval Finder Search" on page 127
- "To do an Advanced Interval Finder Search" on page 129
- "To use a biological network to find or create probes" on page 193

To create a probe group

Probe groups are a required intermediate level of probe organization that lets you handle large numbers of probes as a single unit.

1 Set the application type. See "To set the application type" on page 48.

2 Do one of the following:

- Search for probes. See "Searching for Probes" on page 92, "Searching for Agilent High Density (HD) Probes" on page 109, and "Searching for Agilent SNP Probes" on page 138.
- Upload probes. See "Uploading Probes" on page 158.
- Create new probes. See "Creating Probes" on page 166.

- Search for a probe group. See "To search for probe groups" on page 224.

After you complete one of these processes, you can create a probe group from the result. For probe group search results, you can make a copy of a desired probe group.

After you create a probe group, it is available for you to use in a microarray design.

To create a microarray design with Agilent probes

You can create microarray designs with probes from the Agilent Catalog, or the Agilent High Density (HD) probe database, which contains probes that cover the genomes of several species at very high densities. You can also use Agilent SNP probes. The use of Agilent probes is advantageous because the probes already exist within eArray and are easily accessed, and also because Agilent probes have already been validated to work on the Agilent platform. You find Agilent probes in the AgilentCatalog folder. They have probe IDs with the structure A_NN_PNNNNN, where N is any numeric value, for example: A_23_P23650.

Also, consider these additional points:

- Agilent Catalog probes are available for the Expression and microRNA application types. HD probes are available for the CGH, ChIP-on-chip, and CH3 application types.
- As you design your microarray, read the custom microarray design guidance from Agilent for your specific application type. See "Custom Design Guidance" on page 898.
- eArray$_{XD}$ has many wizards that can lead you through the microarray creation process. See "To use a wizard to create a microarray design" on page 58.
- A microarray design goes through several status changes during the design process. For an overview, see "Status of microarray designs" on page 248.

To create a microarray design with Agilent probes

1 Do one of the following:

- Search the main eArray probe database. For the **Folder** search criterion, select **AgilentCatalog** and mark **Include subfolders.** See "Searching for Probes" on page 92.
- Search the Agilent High Density (HD) probe database. See "Searching for Agilent High Density (HD) Probes" on page 109.
- Search for Agilent SNP probes. See "Searching for Agilent SNP Probes" on page 138.

2 Use the search results to create a new probe group. You can do multiple searches and create multiple probe groups. You can also edit the probe groups. See "To create a new probe group" on page 223 and "To edit a probe group" on page 234.

3 Create a new microarray design that uses the probe group(s). You can include Agilent Catalog probe groups, as well. To find Agilent Catalog probe groups, do a probe group search. In **Folder,** select **AgilentCatalog,** and mark **Include Subfolders.** See "To search for probe groups" on page 224 and "To create a microarray design from existing probe groups (Wizard)" on page 269.

4 Put the design into review, if desired, then wait for other users to make comments and changes. See "To place a microarray design in review" on page 324.

5 After enough review has occurred, complete the design, and submit it to Agilent Manufacturing. You can then request a quote. Agilent does not make the actual microarray slides until you subsequently order them through your Agilent representative. See "To prevent further edits or reviews of a design" on page 335 and "Submitting Microarray Designs to Agilent" on page 346.

To create a microarray design with your own probes

You can create microarray designs with your own probes for all application types, except microRNA. You can use eArray$_{XD}$ to search for or upload your own probes, or to create specialized probes.

Also, consider these additional points:

- As you design your microarray, read the Agilent custom microarray design guidance document for your specific application type. See "Custom Design Guidance" on page 898.
- eArray$_{XD}$ has several wizards that lead you through the microarray creation process. See the note at the end of this topic.
- A microarray design can go through several status changes during the design process. For an overview, see "Status of microarray designs" on page 248.

To create a microarray design with your own probes

1 Do one of the following:
   - Search for the desired probes. When you set the **Folder** search criterion, select the appropriate workgroup folder, then mark **Include subfolders,** if desired. See "Searching for Probes" on page 92.
   - Upload probes. See "Uploading Probes" on page 158.
   - Create probes based on uploaded target sequence data or GenBank accessions (GE probe design, available only for the Expression application type). See "To set up a GE Probe Design job" on page 167.
   - Create probes based on tiling of uploaded target sequences (Simple Tiling, available only for the Expression application type). See "To set up a Simple Tiling job" on page 174.
   - Create probes based on the tiling of specified genomic regions (Genomic Tiling, available only for the CGH, ChIP-on-chip, and CH3 application types). See "To set up a Genomic Tiling job" on page 176.

2 Create probe groups with the probes. "To create a new probe group" on page 223.

3 Create a microarray design that contains the probe groups, then edit the design as needed. See "To create a microarray design from existing probe groups (Wizard)" on page 269 and "To edit a microarray design" on page 310.

4 Place the design in review, if desired, then wait for other users to make comments and changes. "To place a microarray design in review" on page 324.

5 After enough review has occurred, complete the design, and submit it to Agilent Manufacturing. You can then request a quote for the array. Agilent does not fabricate the actual microarray slides until you subsequently order them through your Agilent representative. See "To prevent further edits or

reviews of a design" on page 335 and "Submitting Microarray Designs to Agilent" on page 346.

NOTE

As an alternative to this procedure, Agilent offers several wizards that lead you through the microarray design process. See these topics:

- "To create a microarray design from target transcripts" on page 289
- "To create a microarray design from uploaded probes" on page 282
- "To create a microarray design from existing probe groups (Wizard)" on page 269

To use a wizard to create a microarray design

eArray$_{XD}$ includes wizards that help you create microarray designs. When you use a wizard, it makes sure that you complete all of the necessary steps in the microarray design process. The wizards are flexible, and can accommodate most design needs within their particular scope.

1. Set the application type. See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, under Create Array Design (Wizard), click the name of the desired wizard.

   The selected wizard appears in a new window.
3. Complete the steps of the wizard.

   After specific steps of some wizards, the program submits a job to your server, or the eArray Web site. In some cases, these jobs can take up to one day or more to finish. During this wait, you can monitor the completion of the job in the Tasks pane of the Navigator. You can also close the program and turn off your computer. When the job is completed, you can continue the wizard.

These wizards are available:

Source of probes for microarray	Available for these application types	See these topics
Existing probe groups	CGH (including CGH+SNP arrays), ChIP-on-chip, CH3, Expression, microRNA	"To create a microarray design from existing probe groups (Wizard)" on page 269
Probe Upload	CGH, ChIP-on-chip, CH3, Expression	"To create a microarray design from uploaded probes" on page 282

Source of probes for microarray	Available for these application types	See these topics
GE Probe Design	Expression	"To create a microarray design from target transcripts" on page 289
HD Probes	CGH, ChIP-on-chip, CH3	"To create a microarray design with HD probes" on page 297

To monitor tasks

Some microarray design tasks take time for eArray to complete them. For most time-intensive tasks, the program creates a job and finishes it in the background. You can monitor the status of the job, and take action on it.

1 Expand the folders of the **Tasks** pane of the Navigator until you can see the name of the desired job.

2 Do any of the following:

- Look at the icon next to the name of the job. The icon shows the status of the job. For a description of the icons that can appear, see "Tasks – Icons, buttons, and special text" on page 498.
- Right-click the name of the job, then click the desired action. The availability of actions depends on the type of job and its status.
- In the command ribbon, under Job Queue, click **Tasks.**
  The Job Queue Management Console appears. You can use this console to search, view, delete, and troubleshoot tasks. See "Job Queue Management Console" on page 791 and "To troubleshoot a task" on page 74.

For more information about tasks, see "Managing Tasks" on page 70.

To transfer probe, bait, and exon data from the eArray Web site

eArray$_{XD}$ lets you transfer probes, baits, and exon boundary data from the eArray Web site to your server. These data include the nucleotide sequences of probes and baits, and available annotation and accession information. You can transfer this content by application type for Agilent Catalog content, and for content from the folders of your workgroup, as available. See "eArray$_{XD}$ and the eArray Web site" on page 25.

You must transfer probe, bait, or exon content before you can use certain program features that require it. For example, to search the Agilent Catalog for gene expression probes, you must first transfer the Agilent Catalog probes for the Expression application type. Agilent recommends that you transfer only the specific type(s) of data that you need. The transfer of all catalog and workgroup content can take up to several days or more.

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

   The Catalog and Workgroup Data dialog box appears. See "Catalog and Workgroup Data" on page 607.

2 For each set of data that you want to transfer to your server, do any of the following tasks:

   - To see more information about the given set of data, click **Learn More.**

     Information about the data set appears in a new window.

   - To see if a given data set has already been transferred, or to check the status of a transfer that you have requested, look at the message below the name of the data set. If the data set has already been transferred, the message reads **Downloaded and Available.**

   - To download the given data set to your server, click **Download.**

     A message tells you that the download job has been successfully submitted. An entry for the download job appears in the Tasks pane of the Navigator, in the Data Download folder. The transfer of a given data set can take one day or more.

NOTE If the Download button does not appear, the given data set has already been transferred to your server. Each set of data can only be transferred once from the eArray Web site to your server. Also, if you transfer a given data set to your server, that set is available to all members of the workgroup.

To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server

The names of probe groups, bait groups, libraries, and microarray designs from the eArray Web site, both from the Agilent Catalog and from the folders of your workgroup, appear in the Design Data pane of the Navigator. When you first install your Agilent Genomic Workbench server, it automatically retrieves these names. Be sure to read "eArray$_{XD}$ and the eArray Web site" on page 25. However, for the full use of these items, two additional types of data are needed from the eArray Web site:

- **Probe/Bait data** – The sequences, accessions, and annotation of probes and baits from the Agilent Catalog and from the folders of your workgroup. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.
- **Mapping Data for Probe Groups, Bait Groups, Microarray Designs, and Libraries** – Information that associates specific probes to probe groups or microarray designs, or that associates specific baits to bait groups or libraries. See the procedure below.

To transfer a probe/bait group, library, or microarray design

1 Set the desired application type. See "To set the application type" on page 48.

2 Do one of the following:

- In the Design Data pane of the Navigator, in the AgilentCataog folder or the folder that has the name of your workgroup, right-click the name of the desired item, then click **Download from eArray.com.** If this option does not appear, the item is already available on your server, and no transfer is needed.
- Search for the desired Agilent Catalog probe group or microarray design. See "To search for probe groups" on page 224 and "To search for microarray designs" on page 251. In the **Actions** column of the search results, next to the desired item, click  . If this button does not appear, the item is already available on your server.

In each case, a new task appears in the Tasks pane, in the appropriate Download folder. When the task has a status of Complete  , the content item is available. A different icon appears next to the name of the item in the Design Data pane of the Navigator. See "Design Data pane – Icons, buttons, and special text" on page 487.

NOTE

- For libraries and microarray designs, the program transfers design files to your server when you follow the procedure above. To download these files from your server, see "To download microarray design files" on page 341 and "To download library design files" on page 461.
- When Agilent updates Agilent Catalog probe, bait, and annotation content on the eArray Web site, you can update the database on your server with the new data. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.
- If you have not yet downloaded a probe group or bait group from the eArray Web site, but you can see its name in the Design Data pane of the Navigator, you can still include it in a library or microarray design. However, you must download the item from the eArray Web site before you can view its baits or probes, or save the library or microarray design with a status of Complete or Submitted.
- When Agilent updates Agilent Catalog libraries and microarray designs, you can retrieve this updated content. A **Download from eArray.com** option appears when you right-click the name of the item in the Design Data pane of the Navigator.
- The server keeps all versions of the annotation files that have been transferred from the eArray Web site. When you download these design files from your server, you can select any desired version. See "To download microarray design files" on page 341 and "To download library design files" on page 461.
- If you create libraries or microarray designs on the eArray Web site *after* you install your Agilent Genomic Workbench Server, these items appear in the **Custom Designs** folder in the Design Data pane of the Navigator, where you can download a design file for each of them. These design files are transferred automatically to your server, typically within 24 hours after you save them on the eArray Web site with a status of Complete or Submitted.

NOTE

Special notes for users of Feature Extraction (FE) and the DNA Analytics data analysis applications in Agilent Genomic Workbench:

- In FE and in the DNA Analytics data analysis applications, you can use the microarray designs that you transfer from the eArray Web site. After you start the transfer of a given design, as soon as a Genome Build node appears under the given design node in the Design Data pane of the Navigator, you can import microarrays for that design and run analyses. FE can also run the extraction for that design.
- To import design files for alternate genome builds for Agilent Catalog microarray designs, you must first transfer the design from the eArray Web site. The program then lets you import design files for that microarray design for additional genome builds.

To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site

Periodically, Agilent updates probe and bait content in the Agilent Catalog, and also updates probe and bait annotation. For background information on annotation changes, see "Frequently Asked Questions (FAQs)" on page 910. You can transfer updated probes, baits, and annotation from the eArray Web site to your server. To do this, you transfer the probe group, bait group, library, or microarray design that contains the content that you want to update.

1. Set the desired application type. See "To set the application type" on page 48.
2. In the Design Data pane of the Navigator, in the AgilentCatalog folder, right-click the name of an item that contains the probes or baits that you want to update, then click **Download from eArray.com.**

   If this option does not appear for an item in the AgilentCatalog folder, no update is available.

   An entry appears in the Tasks pane of the Navigator. When the task has a status of Complete  , the probes or baits that the item contains have been successfully updated in the database on your server.

To manually move custom probes or baits from the eArray Web site to your server

The first time that you want to transfer probe and bait data from the eArray Web site to your server, you typically use the Data command in the Home tab of Agilent Genomic Workbench. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. However, *after* this initial transfer, any probes or baits that you subsequently create on the eArray Web site are not automatically transferred to your server. See "eArray$_{XD}$ and the eArray Web site" on page 25.

Agilent recommends that you create and manage all of your custom probes and baits within Agilent Genomic Workbench/eArray$_{XD}$. However, if needed, you can manually transfer these items from the eArray Web site to your server.

CAUTION This procedure can produce undesirable results if the probes that you transfer from the eArray Web site have the same probe IDs as different probes that already exist on your server. For example, existing probes on your server can be overwritten, or only some of the desired probes might be transferred.

1. In Internet Explorer 7, go to https://earray.chem.agilent.com
2. Log in to your eArray user account.
3. Download the desired probes, baits, probe group, bait group, library, or microarray design. Download the content as a TDT file of probes/baits and annotation. See the online help on the eArray Web site.
4. Upload the probes to eArray$_{XD}$. See these topics for details:
   - "To upload probes and annotation" on page 161
   - "To upload baits" on page 370

NOTE If you create a microarray design on the eArray Web site after you install Agilent Genomic Workbench, and you only need to use Agilent Genomic Workbench to analyze microarray data in the Feature Extraction or DNA Analytics programs, you do not need to use eArray$_{XD}$. When you create the microarray design on the eArray Web site, and save it with a status of Complete or Submitted, the necessary GEML design file is automatically transferred to the **Custom Designs** folder in the Design Data pane of the Navigator in eArray$_{XD}$. This transfer typically occurs within one day. To download the GEML file, right-click the name of the desired microarray design, then click **Download.**

To import a new genome

You can import a user-defined genome for use with the Genomic Tiling or Bait Tiling tools. When you do, the genome becomes a permanent part of the database on your server, and is available to all of the users in your workgroup. For details on Genomic Tiling and Bait Tiling, see "To set up a Genomic Tiling job" on page 176 and "To set up a Bait Tiling job" on page 378.

1 Prepare a *.zip file that contains at least one FASTA format sequence file. For details about the requirements of this file, see "Genome" on page 886.

2 Set the application type to **CGH**, **ChIP-on-chip** or **SureSelect Target Enrichment.** See "To set the application type" on page 48.

3 In the **Home** tab, click **Import > Custom Genome for Tiling.**

The Import Genome dialog box appears. See "Import Genome" on page 789.

4 Under **Genome Details,** set these parameters:

Parameter	Instructions/Details
Species	Select the species of the user-defined genome that you wish to import. The species list contains all of the species currently available in the system. To upload a genome for a species that does not appear in this list, select **Na.** To select this genome for tiling, you select Na as the species.
Genome Name	Type a name for the genome import job. The program uses this name to identify the job in the Tasks pane of the Navigator.
Genome Build	Type the name of the specific build of the genome that is represented in your genome file. Use only letters, numbers, underscores, periods, and dashes.
Genome is soft-masked	Mark this check box if repeat sequences in your genome file are represented by lower-case letters. If you do not mark this option, the program changes any lower-case characters in your sequence(s) to capital characters.
Genome File	The genome file must be a *.zip archive that contains the FASTA format chromosomal sequence files. See "Genome" on page 886. **a** Click **Browse.** An Open dialog box appears. **b** Select the desired genome file, then click **Open.** The location of the file appears in Genome File.

5 Click **Save.**

The program starts your genome import, and adds the job to the Tasks pane of the Navigator. A dialog box tells you that the job has been submitted.

6 Click **OK.**

You can monitor the status of the genome import in the Tasks pane of the Navigator. The job appears in the Import Genome folder. One of these icons appears next to the name of the job:

Icon	Status
	Pending – The genome import job has been submitted.
	Processing – The task has been started, but it is not yet completed.
	Complete – The genome was successfully imported, and is now available for use by all members of your workgroup.
	Error – The system tried to upload the genome, but there is a problem. Errors are sometimes caused by improperly-formatted genome files. Refer to "Genome" on page 886, and double-check your genome files. Errors can also be caused by database connection or capacity issues.

When the genome import job has a status of Completed (or Error), information is available about each sequence in your imported *.zip file, including statistics and notes. To view this information, right-click the name of the genome import job, then click **View Genome Information.** The Genome Information dialog box appears. For details, see "Genome Information" on page 777.

NOTE

- You do not need to import the sequences of all of the chromosomes of an organism at the same time. To add additional chromosomes to the imported genome, see "To add more chromosomes to a custom genome" on page 68.
- Imported genomes become a permanent part of the database on your server. You cannot delete them.
- When the program imports your sequence files, it removes all tabs, spaces, and blank lines from each sequence, and changes other non-ACGT characters to N characters.

To add more chromosomes to a custom genome

After you import a custom genome, you can import additional chromosomes and add them to the custom genome.

1 Prepare a *.zip file that contains at least one FASTA format sequence file. For details about the requirements of this file, see "Genome" on page 886.

2 Set the application type to **CGH**, **ChIP-on-chip** or **SureSelect Target Enrichment.** See "To set the application type" on page 48.

3 In the **Home** tab, click **Import > Custom Genome for Tiling.**

The Import Genome dialog box appears. See "Import Genome" on page 789.

4 Under **Genome Details,** set these parameters:

Parameter	Instructions/Details
Species	Select the species of the custom genome to which you want to add chromosomes.
Genome Name	Type a name for the genome import job. The program uses this name to identify the job in the Tasks pane of the Navigator.
Genome Build	Type the name of the existing genome build to which you want to add chromosome(s). The program will add chromosome(s) to this specific genome build of the selected species.
Genome is soft-masked	Mark this option if repeat sequences in your genome file are represented by lower-case letters. If you do not mark this option, the program changes any lower-case characters in your sequence(s) to capital characters.
Genome File	The genome file must be a *.zip archive that contains the FASTA format chromosomal sequence files. See "Genome" on page 886. **a** Click **Browse.** An Open dialog box appears. **b** Select the desired genome file, then click **Open.** The location of the file appears in Genome File.

5 Click **Save.**

A dialog box tells you that the job has been submitted.

6 Click **OK.**

You can monitor the status of the job in the Tasks pane of the Navigator. The job appears in the Import Genome folder. One of these icons appears next to the name of the job:

Icon	Status
	**Pending** – The job has been submitted.
	**Processing** – The job has been started.
	**Complete** – The job has been completed.
	**Error** – The system tried to upload the sequences, but there is a problem. Errors are sometimes caused by improperly-formatted files. Refer to "Genome" on page 886, and double-check your genome files. Errors can also be caused by database connection or capacity issues.

When the job has a status of Complete (or Error), information is available about each sequence in your imported *.zip file, including statistics and notes. To display this information, right-click the name of the job, then click **View Genome Information.** The Genome Information dialog box appears. For details, see "Genome Information" on page 777.

Managing Tasks

For High Density (HD) probe searches, SNP probe searches, and other tasks such as probe uploads, Genomic Tiling of Agilent genomes, and probe design, eArray$_{XD}$ creates a task. A task is a job that runs in the background on your server or on the eArray Web site. While a task runs, you can use eArray$_{XD}$ for other purposes, and you can also close the program. If the Agilent Genomic Workbench server software is not also running on your computer, you can turn your computer off. For a list of the kinds of tasks that can be created in eArray$_{XD}$, see "Navigator – Tasks pane" on page 498. The program displays only the tasks that are associated with the currently selected application type.

You can view and take action on your tasks. See the following topics in this section:

To view the status of a task

After the program creates a task, you can monitor its status in the Tasks pane of the Navigator. The status of a task shows its progress.

1 Set the application type. See "To set the application type" on page 48.

2 Expand the folders of the Tasks pane of the Navigator until you can see the name of the desired job. A status icon appears next to the name of the task:

Status	Comments
	**Pending** – The task has been submitted to the job queue, but no action has been taken on it yet.
	**Processing** – The task has been started.

Status	Comments
	Complete – The task is finished. For many tasks, you can right-click the name of the task to view the results of the job, or to take further action.
	Error – An error occurred. You must re-submit the task. In some cases, you can right-click the name of the task to see additional details about the error(s) that occurred.

To take action on a task

The actions that you can take on tasks may be limited by the status of the task.

1 Set the application type. See "To set the application type" on page 48.

2 Expand the folders of the Tasks pane until you can see the desired task.

3 Right-click the name of the task, then click the desired command in the shortcut menu. If no shortcut menu appears, no actions are available for the task with its current status.

To view a list of your tasks

Although you can use the Tasks pane of the Navigator to see your tasks, you can also use the Job Queue Management Console. This dialog box displays all of your tasks as a list, and gives you additional information about them, such as their positions in the job queue and the dates and times when they were submitted. This dialog box also lets you view subsets of jobs, and sort jobs based on their properties.

1 Set the application type. "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Job Queue,** click **Tasks.**

The Job Queue Management Console appears. See "Job Queue Management Console" on page 791.

- Your jobs appear in the Search Result pane. If you have many jobs, the program separates the list into pages. To go to a different page, click a numbered page button above or below the list of jobs.

- Initially, the program shows your most recently submitted jobs first. To sort the list of jobs using the contents of any column, except Actions, click the desired column heading. To reverse the order of the items, click the same column heading again.
- To limit the list of jobs to those of a specific type or status, or to those that were submitted during a specific period of time, select the desired criteria in the Job Search pane, then click **Search.** The jobs that meet your criteria appear in the Search Result pane.

To search for tasks

You can search for a specific task by its job name. You can also use a different method to search for groups of tasks based on their job type, job status, or the time period in which they were submitted.

To search for a task based on its job name

This method uses the search capabilities of the Navigator. See "To search the Navigator" on page 51.

1. Set the desired application type. "To set the application type" on page 48.
2. In the top pane of the Navigator, under Search, click  to show the list of panes.
3. In the list, select **Tasks.**
4. Under Search, in the empty box, type the name of the desired job. The search term is not case sensitive, and you can use asterisk(s) (*) as "wildcards" to represent unspecified groups of characters.
5. Click  .

   The program searches the Tasks pane of the Navigator. The program opens the appropriate folders, and displays the job(s) that match your search term in red. The first matching job is highlighted in yellow.

   To take action on a job, right-click its name, then click the desired option.

To search for tasks based on type, status, or creation date

This method uses the Job Queue Management Console. You can use the results of this type of search to view, troubleshoot, and delete jobs.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Job Queue, click **Tasks.**

The Job Queue Management Console appears. See "Job Queue Management Console" on page 791. A list of all tasks appears in the Search Result pane.

3 In the Search pane, set any of the following criteria, as desired:

Search Criterion	Instructions/Details
Job Type	Select the desired type of task. By default, the program returns all types of jobs.
Job Status	Select one of these options: • **All** – Returns jobs with any status. • **COMPLETE** – Returns jobs that have been finished. • **ERROR** – Returns jobs that generated an error. • **PENDING** – Returns jobs that have been submitted, but which have not yet been started. • **PROCESSING** – Returns jobs that the system is currently processing.
Date Submitted	If you type or select dates, the program returns only the jobs that were submitted between the From and To dates, inclusively. Follow these guidelines: • To enter a date, type it in the format yyyy-mm-dd, for example `2009-07-28`. Alternatively, click  , then select the desired date from the calendar that appears. • To return all jobs that have been submitted up to and including a specific date, type or select a date in **To,** only. • To return all jobs that have been submitted since a given date, type or select a date in **From,** only.

4 Click **Search.**

In the Search Result pane, the program displays the jobs that match your search criteria. You can take action on the returned jobs. See "To troubleshoot a task" on page 74 and "To delete a task" on page 75.

To troubleshoot a task

You can use the Job Queue Management Console to troubleshoot a job. You can troubleshoot a job if  appears in the Actions column in its row in the Search Result pane. This icon appears for jobs that have had a status other than Complete for a significant length of time.

1. Set the application type. See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, under Job Queue, click **Tasks.**

   The list of tasks for your workgroup for the selected application type appears in the Search Result pane. Click a numbered page button to go to a different page of tasks, if available.
3. In the row of the desired task, in the **Actions** column, click  .

   The Troubleshoot Job dialog box appears. See "Troubleshoot Job" on page 863. Currently, the only option available is Notify support team.
4. Click **Next.**

   A dialog box tells you that your request to send the error log has been successfully submitted.
5. Click **OK.**

   You can contact Agilent Technical Support about the task. When you do, they will have your error log and will be able to help you resolve any issues. See "To contact Agilent Technical Support" on page 88.

   In the Job Queue Management Console, if a job has a status of Error, you can also click  . This button displays additional information, if available, about the job.

   If certain tasks are not complete, even after many hours or days, you might need to restart the AGW Backend Service on the server. See "To restart or stop server services" on page 76.

To delete a task

You can delete a task from the system if you are its owner and it has a status other than PROCESSING. When you delete a task, the program removes the task and any results from the system. However, the program does not remove any content that was already added or changed because of the task, such as a probe group, an imported genome, or a set of probe scores.

1 Set the desired application type. See "To set the application type" on page 48.

2 Search for the desired tasks. See "To search for tasks" on page 72.

3 Do one of the following:

- **From the Navigator** – In the Tasks pane, right-click the desired task, then click **Delete.**
- **From the Job Queue Management Console** – (To open the Job Queue Management Console, click **Tasks** on the command ribbon.) In the Search Result pane, in the Actions column, in the row of the task that you want to delete, click  . In the Job Queue Management Console, you can see the jobs of all of the members of your workgroup for the selected application type. However, you can only delete your own jobs.

If the Delete command does not appear, you cannot delete the task. You might need to wait for the task to finish. A dialog box asks if you really want to delete the job.

CAUTION When you delete a job, you remove the job and its results from the system. To restore a deleted job, you must submit a new job.

4 Click **Yes.**

A dialog box tells you that the job was successfully deleted.

5 Click **OK.**

To restart or stop server services

The Agilent Genomic Workbench server software runs an administrative service, the **AGW Backend Service,** on the machine on which it is installed. This service is essential for server communication with the eArray Web site. If your eArray$_{XD}$ tasks do not finish, even after many hours or days, this service might be stopped. If so, you can restart it. If desired, you can also stop the service.

CAUTION If you stop the AGW Backend Service, this affects all users of Agilent Genomic Workbench in your workgroup. Before you stop the service, make sure no one else is using the program.

1 In the Windows Start menu of the server machine, click **All Programs > Agilent Genomic Workbench Server > Administration.**

   The AGW Administration Panel appears. For more information about this panel, see the *Product Overview Guide*.

2 In **Manage AGW Backend Service,** do one of the following:

   - To restart it, click **Start.**
   - To stop it, click **Stop.**

Example Exercise

In this example exercise, you create a CGH microarray that contains probes for certain breast cancer loci in the human genome. The exercise is designed to familiarize you with some of the main parts of eArray$_{XD}$.

Before you begin this exercise

- Your workgroup must be registered on the eArray Web site, and you must have a user account with a valid login name and password.
- Familiarize yourself with the main elements of the Agilent Genomic Workbench user interface. See Figure 5 on page 42.

Creating a CGH microarray with High Density Probes

In the table that follows, the first column lists the main steps of the process. The second column gives detailed instructions for each main step. The third column gives additional information.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments

1 Start eArray$_{XD}$.	**a** Double-click the Agilent Genomic Workbench program icon. The program starts.
	b Click the **eArray$_{XD}$** tab. The eArray tab appears.
		• The location of the program icon can vary, depending on the options that you selected during installation. By default, it appears in the Start menu, but it can also appear on your desktop, or in a selected folder.
		• When you start the program, a dialog box can appear that asks you for the location of the Database server.
		  ◦ The location of the server is the network name of the computer that is running the Agilent Genomic Workbench server software. Type the full address.
		  ◦ In Port Number, type `3306`, unless you know that the server uses a different port number.
		• Another dialog box can appear that asks you to enter license information.
		  ◦ eArray$_{XD}$ is available free of charge, and you do not need a license to use it. Click **Skip** to close this dialog box.
		  ◦ If you have purchased licenses for one or more of the data analysis programs within Agilent Genomic Workbench, you can enter that information and gain access to this functionality.

2 Set the application type to CGH.	**a** Click **Switch Application** . **b** Mark **CGH.**	• You can use the Switch Application menu to switch to any available application type. • In eArray, content as well as functionality differs by application type.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
3 Create a new folder in the Navigator.	**a** In the Design Data pane of the Navigator, right-click the folder that bears the name of your workgroup, then click **Create New Domain.** The Create New Domain dialog box appears. **b** In **Domain Name,** type `Breast Cancer.` **c** Click **Create.** A dialog box tells you that the domain has been successfully created. **d** Click **OK.** A new folder appears within the workgroup folder.	• To see a labeled diagram of the main parts of the eArray tab, see Figure 2 on page 21.
4 Set up a High Density (HD) Probe Search.	**a** In the eArray$_{XD}$ tab, under Search, click **HD Probes > Simple Search.** The Simple HD Probe Search pane appears. **b** Under **Job Information,** type or select these values: • Search Name – Type `Breast Cancer Array` • Species – Select **H. sapiens.** **c** Under **Probe Options,** type or select these values: • Filters – Select **Total Probes.** • Filter Value – Type `500` **d** Under **Interval Options,** type or select these values: • Select HD Search by – Select **Gene Annotations.** • Gene Annotations – Type `BRCA1 | BRCA2 | ATM | P53 | P65`	• This type of probe search retrieves probes from the Agilent HD-CGH probe database, which contains probes that cover the genomes of several species at very high densities. • This specific search returns a total of 500 probes that cover the genomic regions that are associated with several breast cancer genes. • For more information on HD searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
5 Submit the HD Probe Search to the eArray Web site.	**a** At the bottom of the Simple HD Probe Search pane, click **Search.** A dialog box tells you that your HD search has been successfully submitted to the search queue. **b** Click **OK.** The search appears in the Tasks pane, in the HD Search folder. You now must wait for the eArray Web site to complete the HD probe search. The search can take up to one day or more. After the HD Search job has a status of Complete, you can continue with this example exercise.	• When you click Search, the program submits the search criteria to the eArray Web site, and creates a pending task. You can monitor the status of the job in the Tasks pane. One of these icons appears next to the job: ◦ – (Pending) The HD Search job has been submitted, but no action has been taken on it yet. ◦ – (Processing) The HD Search job is being processed. ◦ – (Complete) The HD Search job is finished. You can display the results and take action on them. • Once you submit a job, and it appears in the Tasks pane of the Navigator, the eArray $_{XD}$ server or the eArray Web site processes it even if you quit the program and turn off your computer.
6 Create a probe group from the High Density Probe Search results	**a** In the Tasks pane of the Navigator, in the HD Search folder, right-click the **Breast Cancer Array** job, then click **Create Probe Group.** A dialog box appears. See "Create Probe Group (from HD or SNP search results)" on page 681. **b** In Probe Group Name, type `Breast cancer probe group`. Leave all of the other properties in the dialog box as they are. **c** Click **Create Probe Group.** A dialog box tells you that the probe group was successfully created. **d** Click **OK.**	• Probe groups are required organizational units that contain one or more probes. Typically, you retrieve a set of related probes with a search, or create or upload probes, and assign these related probes to a probe group. • The program lets you create one probe group from the HD search results. • To display the probe group that you created, see "To view a probe group" on page 228.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
7 Search for the new probe group, and create a microarray design with it.	**a** In the eArray$_{XD}$ command ribbon, under Search, click **Probe Groups.** The Probe Group Search pane appears. **b** In Probe Group Name, type `Breast cancer` **c** Click **Search.** The program retrieves the probe groups that contain "Breast cancer" in their names, and displays them in the Search Result pane. **d** Mark the check box next to **Breast cancer probe group.** This selects the probe group. **e** Click **Create Microarray.** The Create Microarray Design dialog box appears. **f** Type or select these properties in the dialog box: • Microarray Name – Type `Breast Cancer Array` • Folder – Select **Breast Cancer** • Species – Select **H. sapiens** • Keywords – Type `breast, cancer` **g** Click **Create.** The program creates the microarray design, and saves it in the Breast Cancer folder that you created in step 2. A dialog box tells you that the microarray design has been successfully created. **h** Click **OK.**	• In this step, you create a new microarray design using the probe group that you created in the previous step. • The Create Microarray Design dialog box has three main panes: • **Top pane** – Lets you enter the general attributes of the microarray design, such as its name, format, and location. • **Microarray Statistics pane** – Shows statistics about the features of the microarray design, such as the number of features that are occupied and the number that are free. • **Layout Details pane** – Displays the probe group content of the microarray design and lets you change it. • For additional details, see "Create Microarray Design" on page 646.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
8 Search the Navigator for the new microarray design.	**a** In the Search pane of the Navigator, in the empty box, type `Breast*` **b** Click  . In the Design Data pane, the program expands and highlights the Breast Cancer folder. The program also highlights the other items in the Navigator that match your search term, including your new microarray design named **Breast cancer array.** In the next step, you use these search results to take action on the new microarray design	• In this step you use the search capabilities of the Navigator to find the new microarray design that you just created. • When you search the Navigator, the program looks for exact matches with the search term. You can also use asterisks (*) to represent unspecified groups of characters.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
9 Edit the microarray design.	**a** In the Design Data pane of the Navigator, right-click **Breast cancer array,** then click **Edit.** The Edit Microarray Design dialog box appears. **b** In the top pane of the dialog box, select the indicated options for these properties: • **Status** – Select **Review** • **Design Format** – Select **8 X 15K** **c** In the Layout Details pane, the Probe Groups tab is selected by default. In this tab, in the Replicate column, replace the **"1"** with the number `5`. **d** Click **Save.** A dialog box tells you that the microarray design has been successfully updated. **e** Click **OK.**	• In this step, you change the design format and status of the microarray design, and you also increase the number of copies of the probe group in the microarray design from one to five. • The status of microarray designs follows a one way order from **Draft** to **Review** to **Complete** to **Submitted.** Once you assign a particular status to a microarray design, you cannot subsequently go back to a previous status in the order. See "Status of microarray designs" on page 248. • The Review status lets anyone with access to the microarray design make changes and save new versions of it. See "To review a microarray design" on page 326. • Design formats specify the maximum number of features in an array, and the number and placement of replicate arrays on the glass microarray slide. **Example:** The 8 X 15K format has eight replicate arrays on the slide, and each array can accommodate a maximum of approximately 15,000 probes. All replicate arrays on a slide are identical. • When you save the edits to a microarray design, the program overwrites the previous version of the design, even if you change the folder location. • For more information, see "To edit a microarray design" on page 310.

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
10 Create another new folder.	**a** In the Design Data pane of the Navigator, right-click the **Breast Cancer** folder, then click **Create New Domain.** **b** In Domain Name, type `Trial V1A` **c** Click **Create.** The program adds a new folder to the Breast Cancer folder. A dialog box tells you that the domain was successfully created. **d** Click **OK.**	• In this step you create another folder in the Design Data pane of the Navigator. In the next step, you use the results of a microarray design search to move the new microarray design to this folder.
11 Move your microarray design to the new folder.	**a** In the eArray$_{XD}$ command ribbon, under Search, click **Microarray Designs.** The Array Design Search pane appears. **b** In Microarray Name, type `Bre` **c** Click **Search.** The program lists the microarray designs that have the search term in their names. **d** In the Search Result pane, mark the check box next to Breast Cancer Array. **e** Click **Move.** The Move Array Design dialog box appears. **f** In Move to Domain, select **Trial V1A.** **g** Click **Move.** A dialog box asks if you really want to move the array design. **h** Click **Yes.** The program moves the microarray design to the new location. A dialog box tells you that the array was successfully moved. **i** Click **OK.**	• Microarray design searches are not case sensitive. • You can also move a microarray design using the Design Data pane of the Navigator. To open the Move Array Design dialog box, right-click the name of the desired microarray design, then click **Move.**

Example Exercise – Creating an HD-CGH microarray design

Step	Detailed Instructions	Comments
12 If desired, delete the new microarray design.	**a** In the eArray$_{XD}$ command ribbon, under Search, click **Microarray Designs.** The Array Design Search pane appears. **b** In Microarray Name, type `Bre` **c** Click **Search.** The program lists the microarray designs that have the search term in their names. **d** In the Search Result pane, in the Actions column, in the row of **Breast cancer array,** click  . A dialog box asks if you are sure you want to delete the microarray design. **e** Click **Yes.**	• If you do not intend to do further work on this example microarray design, you can delete it. This reduces the number of unneeded files on your server. • The Actions column of search results lets you take action on a specific retrieved microarray design. For a list of actions that can appear, see "Search Result pane – Actions column" on page 516.
13 If desired, delete the probe group that you created.	**a** In the eArray$_{XD}$ command ribbon, under Search, click **Probe Groups.** The Probe Group Search pane appears. **b** In Probe Group Name, type `Bre` **c** Click **Search.** The program lists the probe groups that have the search term in their names. **d** In the Search Result pane, in the Actions column, in the row of **Breast_ cancer_probe_group,** click  . A dialog box asks if you want to delete the probe group. **e** Click **Yes.**	• Alternatively, you can use the Design Data pane of the Navigator to delete a microarray design or probe group. Right-click the name of the item, then click **Delete.** • The program lets you delete probe groups only if they are not in use in a microarray design.
14 Quit Agilent Genomic Workbench.	• Click the Close box on the title bar of the main program window.	• Typically, the program saves your content automatically as you create it, or after you edit it. You do not need to additionally save any files or documents as you quit the program. • You cannot quit the program if any dialog boxes are still open.

Administering eArray for Your Workgroup

One or more users in the workgroup must have the role of *workgroup administrator* in eArray. It is the responsibility of the workgroup administrator to set up the workgroup on eArray, and to do ongoing administrative tasks.

On the eArray Web site, workgroup administrators can do many tasks:

- Create and approve new user accounts
- Reset user passwords
- Set up folders and content browsing categories for users in the workgroup
- Assign user roles (privileges) that are specific to the eArray Web site

The workgroup assigns a workgroup administrator when it first registers on the eArray Web site. Subsequently, the workgroup administrator can assign this role to additional users.

If you are a workgroup administrator on the eArray Web site, you can quickly open the Create New User page on the site from within Agilent Genomic Workbench. In the **Tool** tab, under Create, click **New User.** The program opens your Web browser, logs you in to eArray, and opens the Create New User page.

See the online help on the site.

Getting Help

To get help within Agilent Genomic Workbench

The program has several built-in help resources:

Help Resource	Description/Instructions
Info links	Info links within the program display contextual help. • Next to a parameter or criterion, click Info , if it appears. A message appears with a description of the item and/or instructions that relate to it.
eArray$_{XD}$ User Guide	This user guide, which you are now reading, supplies comprehensive help on all available eArray$_{XD}$ tools.
Other User Guides	The Help tab in the program lets you view any of the available user guides that apply to the currently selected application type. **1** Set the desired application type. See "To set the application type" on page 48. **2** In the Agilent Genomic Workbench tab bar, click **Help.** Buttons for the available user guides appear in the command ribbon. For a description of all of the guides that can be available, see "Help tab" on page 521. **3** Click the button for desired user guide. The selected user guide opens in Adobe Reader.

To get help with the eArray Web site

The eArray Web site contains a comprehensive online help system that describes how to use the Web site and all of its available tools. You do not need to log in to the site, or to be a registered user on the site to view the online help.

1 In Internet Explorer 7, go to https://earray.chem.agilent.com

The login page of the eArray Web site appears.

2 At the top of the page, click **Help.**

The online help system for the eArray Web site opens in a new window.

In addition, Info links appear throughout the site that give additional details and instructions about selected parameters, criteria, and commands. Click Info where it appears.

To contact Agilent Technical Support

Technical support is available by phone and/or e-mail. Find the appropriate contact information for your region in the table below.

Region	Technical support contact information
North America	Telephone: (800) 227 9770 E-mail: pdl-earraysupport_afo@agilent.com
Europe	E-mail: pdl-earraysupport_efo@agilent.com
Asia Pacific	E-mail: pdl-earraysupport_apfo@agilent.com
Africa	E-mail: pdl-earraysupport_efo@agilent.com
Middle East	E-mail: pdl-earraysupport_efo@agilent.com

To learn about Agilent products and services

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

2
Working with Probes

This chapter describes how to use the extensive set of probe tools in eArray$_{XD}$. Probes are single-stranded oligonucleotides of defined sequence that are the fundamental components of microarrays. The program lets you work with probes in several ways:

- **Probe search** – Search probe content on your server. Several search methods are available. You can also search the High Density (HD) probe database on the eArray Web site.
- **Probe creation** – Create new probes based on target transcripts, or based on tiling selected genomic regions or uploaded sequences.
- **Probe upload** – Transfer files of probes to the probe database on your server.
- **Probe management** – Organize, view, download, evaluate, and delete probes.

When you use probes in eArray, you first assemble a desired set of probes within the program. You then assign the probes to a required organizational unit called a *probe group*. You use probe groups as the building blocks of microarray designs.

Before you work with probes, you must be a registered user on the Agilent eArray Web site, and have a valid login name and password. See "To become a registered user on the eArray Web site" on page 39.

Probe organization in eArray

In eArray, probes are partitioned by application type. When you select a specific application type (CGH, ChIP-on-chip, methylation (CH3), Expression, or microRNA), only probes designed for that application type are available. For example, if you select **Expression** as the application type, only probes designed for gene expression microarrays are available. Probe searches only return Expression type probes, and only the probe creation tools appropriate for Expression type microarrays are available (i.e. GE Probe Design and Simple Tiling).

Probes for application types other than microRNA are independently searchable entities that you associate together into one or more probe groups. A probe can be a member of any number of probe groups. You then select one or more probe groups for your microarray design.

For the microRNA application type, probes are grouped by the specific microRNA to which they bind. Up to four related probes are grouped under the name of each mature microRNA target. In general, for microRNA arrays, each mature microRNA is represented by 1-4 probes, which vary in length. These probes act in concert to measure the microRNA of interest, and the data are combined downstream in the Agilent Feature Extraction software.

For the CGH, ChIP and CH3 application types, an additional probe database is available that contains **High Density (HD) probes.** The probes in this database cover the genomes of several species at very high densities. You can retrieve these probes using a High Density (HD) Search. See "Searching for Agilent High Density (HD) Probes" on page 109.

Design decisions

What is the best way to generate probes for my particular experiments?

The best way to generate probes depends on the application type that you are investigating. Probes are application specific, and different application types require different criteria for the design and selection of probes. Because of this, eArray partitions probes separately for different application types—for example, when you create a CGH array, only CGH probes are available for inclusion on the array.

Because of the computational time needed to design probes for CGH, ChIP-on-chip, and methylation applications, Agilent suggests that you use the pre-designed probe sets in the High Density (HD) databases. These databases are located on the eArray Web site, and you can set up such a search from within eArray$_{XD}$. See "Searching for Agilent High Density (HD) Probes" on page 109.

For gene expression applications, successful probe design requires good quality data, but you can use the probe design tools in eArray to generate good quality probes. See "To set up a GE Probe Design job" on page 167.

For gene expression applications, should I use my own probes, or should I use Agilent Catalog probes?

Whether to design your own probes or to use Agilent catalog probes is a matter of personal choice. However, if your target sequence is well-represented by probes in the Agilent Catalog, you can save time and effort if you use those probes. To see the probes that are available, search the Agilent Catalog using GenBank identifiers, gene symbols, or other supported IDs. See "To use the Probe Search tool to find probes" on page 92.

The GE Probe Design tools that are available to you in eArray are the same tools that Agilent uses to create Expression type probes for the Agilent Catalog. However, Agilent also employs a rigorous target assembly process to define the targets for catalog probes.

How do I decide the best way to search for probes for my particular experiments?

For probes that are already designed, the best search method depends upon your level of familiarity with the target sequences. The Probe Search tool lets you retrieve probes in several ways. If you want to take a somewhat unstructured approach, you can type a search term, and Probe Search can return all probes that have an annotation value or accession that matches the search term. For a more specific, directed probe search, you can define multiple values for a specific probe property, such as Probe ID, sequence, or accession numbers, and use Probe Search to retrieve the probes that match each value. See "To use the Probe Search tool to find probes" on page 92.

For the CGH, ChIP-on-chip, and CH3 application types, you can also use a High Density Search, which retrieves probes that cover specific genomic intervals that you select. The probes in the HD Probe Database span the genomes of several species at extremely high densities. See "Searching for Agilent High Density (HD) Probes" on page 109.

Searching for Probes

You use the Probe Search tool to search the probe database on your server. This database contains your workgroup probes as well as Agilent Catalog probes. See the following topics in this section:

NOTE

- A separate section describes how to use the High Density (HD) Search tools to retrieve probes from the Agilent HD Probe Database. The HD database contains probes that cover the genomes of several species at extremely high density for CGH, ChIP-on-chip, and methylation applications. See "Searching for Agilent High Density (HD) Probes" on page 109.
- Another section describes how to search for Agilent SNP probes, which are designed specifically for CGH+SNP microarray designs. These designs combine both CGH and SNP probes on the same array. See "Searching for Agilent SNP Probes" on page 138.

To use the Probe Search tool to find probes

The Probe Search tool lets you retrieve and take action on both your custom probes and Agilent Catalog probes. With this tool, you search for probes based on the annotation, accession, or sequence information that is associated with them. The table below shows the type(s) of probe content that can be searched for each microarray-related application type.

Application type	Search Agilent Catalog	Search your custom probes
CGH		•
ChIP-on-chip		•
CH3		•
Expression	•	•
microRNA	•	

You can set up a search in which you enter a single search term, and retrieve all of the probes that have any accession or annotation value that matches the search term.

You can also set up a search that specifically searches one type of annotation or accession for exact matches with the search term. The specific criteria that are available vary by application type. You can also type or upload multiple search terms, and the program returns probes that match each of the terms. This is a powerful search methodology that can retrieve a set of well-defined probes, or a single probe based upon a specific set of criteria. However, it can take a lot of effort to effectively define the parameters necessary to create the desired results, and it may be too stringent for your purposes.

Two additional options are to use a search for biological networks, or a literature search, to define the search terms for a probe search. See "Using Biological Networks to Find or Create Probes or Baits" on page 184.

The Probe Search tool also lets you limit the probes that are returned to those associated with a particular species, probe group, or microarray, and/or that are located within a specific folder.

Before you use the Probe Search tool

- Before you can search for Agilent Catalog probes, or probes from the folders of your workgroup on the eArray Web site, you must make sure that the appropriate data set has been transferred from the site to your server. For example, to search for Agilent Catalog gene expression probes, the Agilent Catalog probe data set for the Expression application type must have previously been transferred to your server. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To search for probes

1 Set the application type. See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under **Search,** do one of the following:

   - For the Expression or microRNA application types, click **Probes.**
   - For the CGH, ChIP-on-chip, and CH3 application types, click **Probes > Simple Search.**

   The Probe Search pane appears. See "Probe Search" on page 560.

3 In **Search Type,** select one of these options:

Search Type	Description
ALL	In this type of search, you type a single search term. The program retrieves probes that have any annotation or accession value that matches the search term. Type the desired search term in the empty box. **Note:** • (Expression and microRNA application types) To return probes that have any type of annotation that exactly matches the search term, mark **Exact search.** Otherwise, the search returns probes that contain the search term *within* any annotation. • (CGH, ChIP-on-chip, and CH3 application types) The program always returns probes that have annotations that are an exact match with the search term.
Probe ID	Type a probe ID in the box. Separate multiple IDs with pipe "|" characters. Alternatively, to upload a file that contains the desired probe ID data, click **Upload,** then select the desired file.
Accessions	(Available for all application types except microRNA) Type a valid accession number, without its source, in the box. Separate multiple accessions with pipe "|" characters. Alternatively, to upload a file that contains the desired accession data, click **Upload,** then select the desired file. See "To upload data for probe searches" on page 101. **Note:** To search for microRNA probes based on miMAT accessions, select the **miMAT#** search type.
Gene Symbol	(Available for all application types except microRNA) Type a valid gene symbol in the box. Separate multiple gene symbols with pipe "|" characters. Alternatively, to upload a file that contains the desired gene symbol data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.

Search Type	Description
Chromosomal Location	Type a chromosomal location in the box, or multiple locations separated by pipe "|" characters. **Example:** `chr1:47995000-49867300|chr2:20078-90992` The search returns probes that are designed to genomic coordinates within the range that you enter. Alternatively, to upload a file that contains the desired chromosomal locations, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101. **Note:** You can also set up this type of search from the Genomic Viewer. Select the desired genomic region in Gene View, right-click the selected area, then click **Chromosomal Location Search.** The program opens the Probe Search pane and sets criteria for a search of the selected region. For information on the Genomic Viewer, see the *Data Viewing User Guide.*
Cytoband	(Available for all application types except microRNA) Type a cytoband identifier in the box. Separate multiple cytobands with pipe "|" characters. Alternatively, to upload a file that contains the desired cytoband data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.
Probe Sequence	Type a valid probe sequence in the box, or multiple sequences separated by pipe "|" characters. The search returns probes whose sequences are exact matches. To upload search sequences from a file, click **Upload.** See "To upload data for probe searches" on page 101.

Search Type	Description
miMAT#	(microRNA application type only) Type a miMAT accession in the box, or multiple miMAT accessions separated by pipe "|" characters. The search returns probes that are associated with the miMAT accession(s). Alternatively, to upload a file that contains the desired miMAT accession data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.
microRNA Name	(microRNA application type only) Type the name of a mature microRNA. Separate multiple names with pipe "|" characters. Alternatively, to upload a file that contains the desired microRNA names, click **Upload,** then select the desired file. See "To upload data for probe searches" on page 101. **Note:** For the microRNA application type, probes are grouped by the specific microRNA to which they bind. Up to four related probes are grouped under the name of each mature microRNA target. In general, for microRNA arrays, each mature microRNA is represented by one to four probes, which vary in length. These probes act in concert to measure the microRNA of interest, and the data are combined downstream in the Agilent Feature Extraction software.

NOTE You can use a biological network to supply search terms for a probe search. See "To use a biological network to find or create probes" on page 193.

4 Set the rest of the criteria for the search as described in the table below. These criteria are optional, except as noted. To clear all of the criteria at any point, click **Reset.**

Criterion	Instructions/Details
Folder	(Required) Select a folder from the list. The search returns probes only from the selected folder. To include the folder's subfolders in your search, mark **Include Subfolders.** The list of folders includes the ones to which you have access. **Note:** Agilent Catalog probes, which are located in the Agilent Catalog folder, are available for the Expression and microRNA application types. You can search for your own (non-Agilent) probes for all microarray applications except microRNA.
Species	(Required) Select the desired species. **Note:** For the microRNA application type, the Probe Search tool searches the primary species associated with probes.
Used in Probe Groups	If you set this criterion, the search returns probes only from the specified probe group(s). • To select probe groups, click **Select and Add.** See "To select probe groups for searches or microarrays" on page 106. **Note:** • The program does not return probes if you select a probe group that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. • The Probe Search tool cannot search High Density (HD) or SNP probe groups.

Criterion	Instructions/Details
Used in Microarray Designs	If you set this criterion, the search returns probes only from the specified microarray design(s). To select microarray design(s), follow these steps: **a** Click **Select and Add.** The Select and Add Microarray Name dialog box appears. See "Select and Add : Microarray Name" on page 841. **b** In Microarray Name, type all or part of the desired microarray name. To return a list of all available microarray names, leave Microarray Name blank. **c** Click **Search.** A list of matching microarray designs appears in the left box under Search Results. If there are many microarray designs that match, the program paginates the list. To go to a different pages of results, click the buttons in **Result Pages.** **d** Select the desired microarray design, then click **Add.** The program transfers the selected microarray design from the left box to the right box. You can add as many microarray designs as you want. To start over, click **Remove All.** **e** Click **Done.** The microarray designs that you selected appear in the Probe Search pane, in Used in Microarray Designs. **Note:** The program does not return probes if you select a microarray design that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Criterion	Instructions/Details
miRBase Version	(microRNA probe searches only) (Required) From the list, select the desired microRNA database version to search. To search all available versions, select **All.** miRBase is a comprehensive database that contains all published microRNAs, including their sequences, genomic locations, and related annotation. For more information, go to microrna.sanger.ac.uk **Note:** • It can be especially useful to search a previous version of miRBase if you have legacy data, for example from the Agilent V1 miRNA array, for a miRNA that has changed in subsequent versions of miRBase. • Probes are annotated to microRNAs from previous versions of miRBase only when the microRNA sequences change (and then only if that change requires new probes), or if the microRNA has been removed from subsequent versions of miRBase. • Probes that are annotated to previous versions of miRBase have the database version appended to the microRNA name. For example: miR-hsa-###_v9.1
Include * Sequence	(microRNA probe searches only) Mark this option to return probes for both star and non-star miRNAs. Star "*" sequences are an alternate class of miRNAs derived from the same precursor miRNAs as corresponding "non-star" miRNAs. A star sequence is generally the less predominant mature miRNA species. For example, miR-56 (the predominant species) and miR-56* (the less-predominant "star" sequence) are both thought to be derived from the same predicted precursor.

5 Click **Search.**

Your requested search begins. The search can take some time.

The probes that match your search criteria appear in the Search Result pane. From this pane, you can take action on the retrieved probes. See "To take action on probes in search results" on page 100.

For the microRNA application type, probes are grouped by the specific microRNA to which they bind. Up to four related probes are grouped under the name of each mature microRNA target. In general, for microRNA arrays, each mature microRNA is represented by one to four probes, which vary in

length. These probes act in concert to measure the microRNA of interest, and the data are combined downstream in the Agilent Feature Extraction software.

To take action on probes in search results

After you submit a probe search, and probe(s) appear in the Search Results pane, you can take action on them.

1 Search for probes. See "To use the Probe Search tool to find probes" on page 92.

2 Do any of these tasks:

Task	Instructions/Comments
View probe annotation	Available probe annotation appears in the table of probe search results. Additional columns of annotation may be available if you download the probes as a *.tdt file. See "To download probes" on page 206.
Re-sort the search results	If  or  appears in the heading of a column, you can sort the search results based on the contents of the column. Click the column heading. To reverse the order of the sort, click the same column heading again. **Note:** The heading of the column upon which the search results re sorted appears in a darker color than the other column headings.
View probe sequences and statistics	See "To view probe sequences and statistics" on page 202.
Create a probe group with the probes in the search results	See "To create a new probe group" on page 204.
Download probes	See "To download probes" on page 206.
Delete probes	See "To delete probes" on page 218.
Change the width of columns in the search results	In the column heading row, drag the border between columns right or left, as needed.

NOTE

- The availability of actions varies by application type and by probe. See the specific topics indicated above.
- For the microRNA application type, probes are grouped by the specific microRNA to which they bind. Up to four related probes are grouped under the name of each mature microRNA target. In general, for microRNA arrays, each mature microRNA is represented by one to four probes, which vary in length. These probes act in concert to measure the microRNA of interest, and the data are combined downstream in Agilent's Feature Extraction software.
- A separate topic describes how to take action on High Density (HD) Search results. See "To take action on an HD probe search job" on page 133. For information about HD searches, see "Searching for Agilent High Density (HD) Probes" on page 109.
- Another section describes how to take action on Agilent SNP probe search results. See "To monitor the status of a SNP probe search job" on page 153. For information about SNP probe searches, see "Searching for Agilent SNP Probes" on page 138.

To upload data for probe searches

When you do certain types of probe searches, you can upload files that contain search terms for specific probe search criteria. For example, when you use the Probe Search tool, you can upload a file of desired probe sequences. This feature is especially useful if you have many items to enter, or need to do several related searches that use the same list of items. The instructions below apply to both high density and non-high density probe searches.

1 Create a plain text file with an extension of `.txt` that contains the items that you want to upload. Do not save the files in a format that includes extra formatting information, such as RTF or the default file formats for most word processing and spreadsheet programs. Separate multiple entries

with **new line** characters—press **ENTER** to move the insertion point to the beginning of a new line, then type the next entry.

The table below contains specific instructions for different types of uploaded search terms.

Uploaded Search Term	Format Details
Accessions (Probe Search)	List one accession per line. Enter accession values **without** sources, as the sources are already supplied by eArray. So **sgd | Q0055** will be only **Q0055.**

Advanced Search Interval (Advanced Genomic Interval HD Search)	List one interval per line. You can include column headings in the first line of the file, but eArray does not interpret them. Each line must contain the following entries, separated by tabs, in this order:
	1 Genomic Interval – A cytoband (for example, 1p36.33) or a chromosomal location, for example:
	• chr1:1-500001
	• chr1 (all of chromosome 1)
	• chrX:2000500 (X chromosome from 2000500 to the end)
	For a given search, all the intervals must be of the same type (for example, all chromosomal locations or all cytobands).
	2 Average Spacing – Average number of base pairs between each of the retrieved probes within the interval.
	3 TM Filtered – **Yes** or **No.** For this interval, removes probes with T_Ms that lead to poor performance on the Agilent platform.
	4 HM Filtered – **Yes** or **No.** Removes probes that map to more than one location in the genome. (Homology filtering)
	
	Example:
	`chr1:1-1000000 500 Yes Yes`
	`chr2:500-5000000 1000 Yes No`
	`chr2:5000000-8000000 1000 Yes Yes`

Chromosomal Location (Probe Search)	List one chromosomal location per line. Use the format illustrated in the following examples. `chr1:1-500001` (Chromosome 1, base pairs 1 to 500001) `chr1` (all of chromosome 1) `chrX:2000500` (X chromosome from 2000500 to the end)

Uploaded Search Term	Format Details
Cytoband (Probe Search)	List one cytoband per line. **Examples:** • `1p12.123` (Chromosome 1, p arm, band 1, sub band 2, sub sub band 1, micro band 2, sub micro band 3) • `1p1` (Chromosome 1, p arm, band 1) • `1p1-1p2` (Gene interval range from the beginning of 1p1 to the end of 1p2)

Exclusion Intervals
(HD probe search and SNP probe search by gene intervals)
	List one interval per line.
	Example:
	`chr1:1192920-2000000`
	`chr2:2993891-3929322`
	`chr2:1129102-2238293`

Gene Annotations (HD-CGH Gene Annotations Search)	List one annotation per line. Annotations can be either accession numbers (for example, `NM_016660` or `AY884282`) or gene symbols (for example, `H3N2` or `CTSB`), but for a given search the annotations must all be of the same type.

Gene Symbol
(Probe Search)
	List one gene symbol per line.
	Example:
	`ACOX2`
	`BRCA1`
	`HRH4`
	`TXNDC1`

Uploaded Search Term	Format Details
Genomic Intervals (Simple HD Probe Searches and SNP probe searches by gene interval)	List one genomic interval per line. You can enter cytobands or chromosomal locations, but all intervals must be of the same type. **Examples:** Chromosomal locations: • `chr1:1-500001` (Chromosome 1, base pairs 1 to 500001) • `chr1` (all of chromosome 1) • `chrX:2000500` (X chromosome from 2000500 to the end) Cytobands: • `1p12.123` (Chromosome 1, p arm, band 1, sub band 2, sub sub band 1, micro band 2, sub micro band 3) • `1p1` (Chromosome 1, p arm, band 1) • `1p1-1p2` (Gene interval range from the beginning of 1p1 to the end of 1p2)

microRNA Name
(Probe Search)
	List one mature microRNA name per line.
	Example:
	`ptr-let-7a`
	`ptr-let-7b`
	`ptr-miR-1`

miMAT#
(Probe Search)
	List one miMAT number (mature miRNA sequence accession) per line.
	Example:
	`MIMAT0007946`
	`MIMAT0007937`
	`MIMAT0007936`

Probe ID
(Probe Search, HD Probe ID Search, and SNP probe search by probe ID)
	List one probe ID per line.
	Example:
	`A_14_P100053`
	`A_14_P100055`
	`A_14_P100056`
	`A_14_P100057`
	`A_14_P100059`
	`A_14_P100227`

Uploaded Search Term	Format Details
Probe Sequence (Probe Search)	List one sequence per line. Use only the capital characters A, C, G, and T. **Example:** ACGTAGCTAGAGCTAGCTGAGCTGAGCTGAGATCGATGCT ATTATGGATGATTGATGAGTAGTAGAGAGGCGCGCTAGCA ACGTACGATAGCGCGCAGCTAATGATGACGCAGATCAGAG CCTACCGATGTCTGCTACAGACGGCGGGGATGACGATACG
SNP Reference Cluster IDs (SNP probe search by reference cluster IDs)	List one reference cluster per line. Do not include database sources. **Example:** rs6662299 rs6661954 rs6663221

2 Select a probe search that lets you upload a file of search terms.

3 Next to the desired search criterion, click **Upload.**

A dialog box appears.

4 Do one of the following:

Type of search	Instructions
Non-HD and non-SNP probe searches	• Select the desired file, then click **Open.**
HD and SNP Probe searches	**a** In File Name, click **Browse.** An Open dialog box appears. **b** Select the desired file, then click **Open.** The name of the selected file appears in the File Upload dialog box. **c** Click **Upload.**

In either case, the program uploads the file. The search terms from the file appear in pipe-separated format in the appropriate box in the search pane.

To select probe groups for searches or microarrays

You can select one or more probe groups when you use several eArray$_{XD}$ tools:

- When you use the Probe Search tool to retrieve probes, you can limit the probes that are returned to those within specific probe group(s).
- When you search for microarray designs, you can limit the designs that are returned to those that contain selected probe group(s).
- When you create, edit, or review a microarray design, you can select probe groups to include in the design that serve one of several purposes.

In all of these contexts, the Select and Add Probe Group dialog box, or a pane that functions identically to it, appears. See "Select and Add : Probe Group" on page 843.

1 Set these probe group search criteria as needed:

Search criterion	Instructions/Details
Probe Group	Type all or part of the name of the desired probe group. To retrieve all available probe groups, leave this criterion blank.
Folder	To limit the search to a specific folder, select the desired folder. Otherwise, select **All.** The folders to which you have access appear in the list. To include the subfolders of the selected folder in your search, mark **Include Subfolders.**

2 Click **Search.**

The probe groups that match your search criteria appear in the dialog box under Search Results, in the left pane. See Figure 9. For each probe group, the pane also displays its availability. One of these statuses appears next to the name of the probe group:

- **Local** – The probe group is available on your server.

- **Not Downloaded** – The probe group must be downloaded from the eArray Web site before you have full access to it. You can create microarray designs with this type of probe group, but you can only save them with a status of Draft. To save them with a status of Review, Complete, or Submitted, you must first download them from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. Also, you cannot view the probes that are contained in probe groups of this type, or use them as search criteria in a probe search.

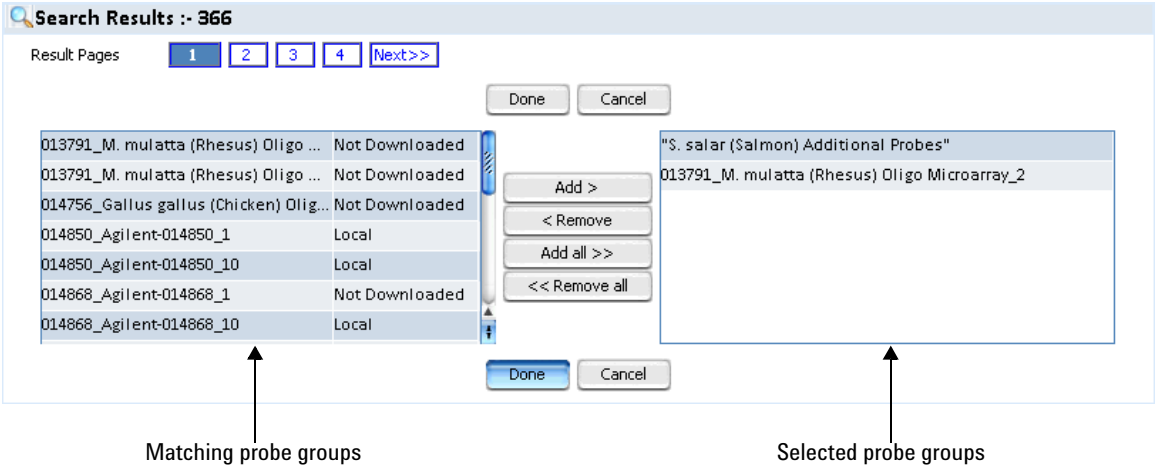


Figure 9 Select and Add Probe Groups – Search Results. The probe groups in the left pane are the ones that match your search term, and they are available for you to select. The left pane displays the probe groups that you have selected.

3 Under **Search Results,** in the left pane of the dialog box, do any of the following to select the desired probe groups:

- To select an individual probe group, click its name.
- To select additional probe groups, control-click their names.
- To select a contiguous block of probe groups, click the name of the first probe group, then shift-click the name of the last one.
- To go to another page of results, if available, click a button in Result Pages. The program keeps all of your selections as you go from page to page.

4 Move probe groups to the right pane of the dialog box. This creates a list of probe groups to be added to your search criteria. Do any of the following:

- To move the selected probe groups to the right pane, click **Add.**
- To move all of the probe groups in the left pane to the right pane, click **Add All.**
- To start over, click **Remove All.**
- To remove a probe group from the right pane, select the desired probe group, then click **Remove.**

You can do as many probe group searches as you want. The program accumulates all of the probe groups that you move to the right pane of the dialog box.

5 Click **Done.**

The selected probe groups appear as search criteria or as added probe groups, as appropriate. Multiple entries are separated by pipe "|" characters. The selected probe group(s) replace any existing entries.

Searching for Agilent High Density (HD) Probes

A High Density (HD) Search, also known as a *zoom-in* search, retrieves probes that cover specific regions of the genome of a given species. The eArray Web site has a separate database that contains HD probes for CGH, ChIP-on-chip, and methylation microarrays. The probes in this database cover several genomes at extremely high density.

To search for HD probes, you enter the chromosomal region(s) or cytoband(s) that are associated with the desired probes. For HD-CGH probes you can also enter gene annotations (such as accessions or gene symbols) to retrieve a subset of probes from all of the probes in the database. You can also retrieve HD probes based on a list of Probe IDs.

You can use an Interval Finder search to supply genomic intervals for HD Probe Searches. See "To do a Simple Interval Finder Search" on page 127 and "To do an Advanced Interval Finder Search" on page 129. You can also use a search for biological networks to supply search terms for an Advanced Interval Finder Search, and then use the search results for an HD Probe Search. See "To use a biological network to find or create probes" on page 193.

In a **Simple HD Search,** you set the overall density of retrieved probes. In an **Advanced HD Search,** you can set the density and certain filtering characteristics for each genomic interval independently. You can create HD probe groups from probes found in these searches.

When you start an HD probe search in eArray$_{XD}$, the program submits a search job to the eArray Web site through your server. When the eArray Web site finishes your search, your server automatically retrieves the results from the Web site, and makes them available to you. You can then view and take action on the search results. See "To take action on an HD probe search job" on page 133.

These types of HD Probe Searches are available:

Type of HD Search	Description	See these topics
Simple Genomic Intervals HD Search	Available for CGH, ChIP-on-chip and methylation HD probe searches. In this kind of search, you enter the chromosomal locations of genomic regions to search.	"To do a Simple Genomic Intervals HD Search for probes" on page 111
Advanced Genomic Intervals HD Search	Available for CGH, ChIP-on-chip, and methylation HD probe searches. In this kind of search, as in the Simple Genomic Intervals Search, you enter the chromosomal locations of the genomic regions to search. However, in this advanced search, you set the desired density and Hm and T_M filtering for each interval individually.	"To do an Advanced Genomic Intervals HD Search for probes" on page 117
Probe ID HD Search	Available for CGH, ChIP-on-chip, and methylation HD probe searches. In this kind of search, you enter the names of the desired probes.	"To do a Probe ID HD Search for probes" on page 125
Simple Gene Annotations HD Search	Available only for HD-CGH searches. In this kind of search, you enter annotations such as GenBank accession numbers or gene symbols. The search returns HD probes that cover the regions that correspond with the annotations.	• "To do a Simple Gene Annotations HD Search for probes" on page 120 • "Example Exercise" on page 77

To do a Simple Genomic Intervals HD Search for probes

This type of search retrieves HD probes for CGH, ChIP-on-chip, or methylation applications for a given species from the Agilent HD probe database based on chromosomal locations that you enter. For general information about HD probe searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

1 Set the application type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under **Search,** click **HD Probes > Simple Search.**

The Simple HD Probe Search pane appears. Under Interval Options, in Select HD Search By, Genomic Intervals is selected by default.

3 Set search parameters as described in the table below. You **must** set the **Search Name,** the **Species,** and one or more **Genomic Intervals.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	(Required) Type a name that will help you to identify this search job and its results.
Species	(Required) Select the desired species. Only the species represented in the HD database appear in the list of species.
Build Number	(Read-only) The name of the applicable genome build for the selected species appears. The HD probe database only contains probes designed to the most current genome build for each species.

Parameter	Instructions/Details
Probe Options	
Filters	Select one of the options below. If relevant, type a value for the filter in **FIlter Value.** Filters restrict the list of returned probes, based on specific criteria. • **None** – The search does not apply any of the filters in the list. • **Average Spacing** – In **Filter Value,** type the desired number of base pairs. This defines the average number of base pairs between the centers of the retrieved probes in each genomic interval. • **Probes Per Interval** – In **Filter Value,** type the desired number of probes. This defines the maximum number of probes that HD Search retrieves for each genomic interval. • **Total Probes** – In **Filter Value,** type the desired number of probes. This defines the total number of probes HD Search collectively retrieves for all specified genomic intervals.
Filter Value	(Available if you select a filter) Type the desired value for your selected filter.
Prefer Catalog Probes	(Available for HD-CGH probe searches) To give preference to Agilent Catalog probes in the probe selection process, mark this check box. If two probes are close to each other for a given probe interval, the search selects the Agilent Catalog probe.
Use TM Filter	Removes probes with T_Ms that produce unsatisfactory results on the Agilent platform. The search always applies this filter.
Similarity Filter	These options are available for most Genomic Intervals HD searches. Not all options are available for all species. • **No Filter** – The program does not apply a similarity filter. If you select this option, the Use Non-Unique Probe Filter check box becomes available (see below). Non-unique probes map to more than one location in the target genome. • **Perfect Match Filter** – Removes a probe from the search results if it has more than one perfect match in the genome of the selected species. • **Similarity Score Filter** – Removes a probe from the search results if it is designed to a given genomic region, but it also has significant similarity to other parts of the target genome. Probes such as this can cause cross-hybridization problems.

Parameter	Instructions/Details
Use Non-Unique Probe Filter	(Available if you select no similarity filter) Mark this check box to remove a probe if it maps to multiple locations in the target genome. You can set the stringency of this filter. See below, "Max Perfect Genomic Hits."
Max Perfect Genomic Hits	(Available if you select no similarity filter, and mark **Use Non-Unique Probe Filter**) Sets the maximum number of locations to which a probe can map in the target genome, and still pass the non-unique probe filter. Type the desired number of locations. **Example:** Probe A maps to two locations in the target genome, and Probe B maps to three locations. You select **No Filter** in Similarity Filter, mark **Use Non-Unique Probe Filter,** and type `2` in Max Perfect Genomic Hits. The filter removes Probe B, but does not remove Probe A.
Interval Options	
Select HD Search by	**Genomic Intervals** is selected by default.
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined genomic intervals. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.

Parameter	Instructions/Details

Genomic Intervals	Type either a chromosomal location range or a cytoband in the box. Separate multiple intervals with pipe "|" characters. All of the intervals must be of the same type.
	To upload a file of chromosomal locations or cytobands, click **Upload.** See "To upload data for probe searches" on page 101.
	You can also use an Interval Finder search to define the genomic intervals for this search parameter. See "To do a Simple Interval Finder Search" on page 127 and "To do an Advanced Interval Finder Search" on page 129.
	Examples of genomic interval formats
	• Cytoband:
	  ◦ `1p36.33`
	  ◦ `1p` (Chromosome 1, p arm)
	  ◦ `1p1-1p2` (Chromosome 1, p arm, beginning of band 1 to end of band 2)
	• Chromosomal location range:
	  ◦ `chr1:1-500001`
	  ◦ `chr1` (all of chromosome 1)
	  ◦ `chrX:2000500` (X chromosome from 2000500 to the end)
	For a given search, all the intervals must be of the same type (for example, all chromosomal locations or all cytobands).

Include Regions	(Available only for HD-CGH searches) Select one of the options below. You can use this parameter to limit your HD-CGH probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence." • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence."

Parameter	Instructions/Details
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.
Exclude Options	
Standard Exclusion Interval(s)	eArray lets you select from among many different sets of standard exclusion intervals, based on annotation tracks. To ignore genomic regions defined in one or more of these sets, mark this option, then select the desired set(s) from the list. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option, then click **Upload.** See "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

4 Click **Search.**

eArray$_{XD}$ submits your HD Probe Search job to the eArray Web site, through your server. A dialog box tells you that your search has been submitted.

5 Click **OK.**

The search job appears in the Tasks pane of the Navigator, in the HD Search folder. It can take one day or more for eArray to finish the job. For information about how to check the status of a job, and what you can do with the job and any returned search results, see "To check the status of an HD probe search" on page 132 and "To take action on an HD probe search job" on page 133.

NOTE

You can also pre-set the Genomic Intervals and Species search parameters from within the Genomic Viewer:

1. Click **Home.**
   The Genomic Viewer appears in the main pane.
2. In Gene View, within the data plotting area, select the desired chromosomal interval. For instructions on how to use the Genomic Viewer, see the *Data Viewing User Guide.*
3. Right-click within the data plotting area of Gene View, then click **Simple HD Search.**
   The eArray$_{XD}$ tab opens with the Simple HD Probe Search pane. The Genomic Intervals and Species search criteria reflect the selected region in the Genomic Viewer.

To do an Advanced Genomic Intervals HD Search for probes

This type of search retrieves HD probes for CGH, ChIP, and methylation applications for a given species from the Agilent HD probe database based on chromosomal locations that you enter. For this advanced search, you also prepare and upload a file that contains a list of the desired genomic intervals along with the desired tiling density and homology (Hm) and T_M filtering status for each interval. For details, refer to "Advanced Search Interval" on page 876. For general information about HD probe searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

1 Set the application type to **CGH, ChIP, or CH3.** See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under **Search,** click **HD Probes > Advanced Search.**

The Advanced HD Probe Search pane appears. See "Advanced HD Probe Search" on page 527. By default, **Genomic Intervals** appears in Select HD Search by.

3 Set search parameters as described in the table below. You **must** set the **Search Name** and the **Species,** and you must also upload a file of **Advanced Search Intervals.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	(Required) Type a name that will help you identify this search job and its results.
Species	(Required) Select the desired species. Only the species represented in the HD database appear in the list of species.
Build Number	(Read-only) The name of the applicable genome build for the selected species appears. The HD probe database only contains probes designed to the most current genome build for each species.
Prefer Catalog Probes	(Available for HD-CGH probe searches) To give preference to Agilent catalog probes in the probe selection process, mark this option. If two probes are close to each other for a given probe interval, the HD search selects the Agilent Catalog probe.

Parameter	Instructions/Details
Advanced Search Interval	Select and upload a file that contains the desired genomic intervals, along with the desired tiling density, and homology and T_M filtering status for each interval. For details about the requirements for this file, refer to "Advanced Search Interval" on page 876. **a** In **Advanced Search Interval,** click **Browse.** A dialog box appears. **b** Select the desired file of advanced search intervals, then click **Open.** The location of the file appears in Advanced Search Interval. **c** Click **Preview.** The program uploads the selected file. The Preview of Search Intervals pane appears, with the first few lines of your uploaded file. **d** Do any of the following: • If the first line of your file is actually a row of column headings, mark **My uploaded file contains column headings.** This prevents the program from interpreting the first line of your file as a search interval. The program does not interpret any column headings in the uploaded file. • To see all of the intervals in the uploaded file, click **Show All.** A dialog box displays all of the advanced search interval data in your file.
Interval Options	
Select HD Search by	The program sets this parameter to **Genomic Intervals.**
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined regions. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.

Parameter	Instructions/Details
Include Regions	(Available only for HD-CGH searches) Select one of the options below. You can use this parameter to restrict your HD-CGH probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence." • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence."
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.
Exclude Options	
Standard Exclusion Interval(s)	eArray lets you select from among many different sets of standard exclusion intervals, based on annotation tracks. To ignore the genomic regions that are defined in one or more of these sets, mark this option, then select the desired set(s) from the list that appears. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals that are defined in a file of genomic intervals, mark this option, then click **Upload.** See "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

4 Click **Search.**

eArray$_{XD}$ submits your HD probe search job to the eArray Web site, through your server. A dialog box tells you that your search has been submitted.

5 Click **OK.**

The search job appears in the Tasks pane of the Navigator. It can take one day or more for eArray to finish the job. For information about how to check the status of a job, and what you can do with the job and any returned search results, see "To check the status of an HD probe search" on page 132 and "To take action on an HD probe search job" on page 133.

To do a Simple Gene Annotations HD Search for probes

This type of search retrieves HD-CGH probes for a given species from the Agilent HD probe database based on gene annotations that you enter. For general information about HD probe searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

NOTE The example exercise in the first chapter guide includes this type of search. See "Example Exercise" on page 77.

1 Set the application type to **CGH.** See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under Search, click **HD Probes > Simple Search.**

The Simple HD Probe Search pane appears. See "Simple HD Probe Search" on page 565.

3 Under **Interval Options,** in **Select HD Search by,** select **Gene Annotations.**

4 Set search parameters as described in the table below. You must set the **Search Name** and the **Species,** and enter one or more **Gene Annotations.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	(Required) Type a name that will help you identify this search job and its results.

Parameter	Instructions/Details
Species	(Required) Select the desired species. Only the species represented in the HD database appear in the list of species.
Build Number	(Read-only) The name of the applicable genome build for the selected species appears. The HD probe database only contains probes designed to the most current genome build for each species.
Probe Options	
Filters	Select one of the options below. If relevant, type a value for the filter in **FIlter Value.** Filters limit the probes that are returned, based on specific criteria. • **None** – The search does not apply any of the filters in the list. • **Average Spacing** – In **Filter Value,** type the desired number of base pairs. This defines the average number of base pairs between the centers of the retrieved probes in each genomic interval. • **Probes Per Interval** – In **Filter Value,** type the desired number of probes. This defines the maximum number of probes that HD Search retrieves for each genomic interval. • **Total Probes** – In **Filter Value,** type the desired number of probes. This defines the total number of probes HD Search collectively retrieves for all specified genomic intervals.
Filter Value	(Available if you select a filter) Type the desired value.
Prefer Catalog Probes	To give preference to Agilent Catalog probes in the probe selection process, mark this check box. If two probes are close to each other for a given probe interval, HD search selects the Agilent Catalog probe.
Use TM Filter	Removes probes with T_Ms that produce unsatisfactory results on the Agilent platform. The search always applies this filter.

Parameter	Instructions/Details
Similarity Filter	The options below can appear. The availability of specific options depends on species and application type. • **No Filter** – The program does not apply a similarity filter. If you select this option, the Use Non-Unique Probe Filter check box becomes available (see below). Non-unique probes map to more than one location in the target genome. • **Perfect Match Filter** – Removes a probe from the search results if it has more than one perfect match in the genome of the selected species. • **Similarity Score Filter** – Removes a probe from the search results if it is designed to a given genomic region, but it also has significant similarity to other parts of the target genome. Probes such as this can cause cross-hybridization problems.
Use Non-Unique Probe Filter	(Available if you select no similarity filter) Mark this check box to remove a probe if it maps to multiple locations in the target genome. You can set the stringency of this filter. See below, "Max Perfect Genomic Hits."
Max Perfect Genomic Hits	(Available if you select no similarity filter, and mark **Use Non-Unique Probe Filter**) Sets the maximum number of locations to which a probe can map in the target genome, and still pass the non-unique probe filter. Type the desired number of locations. **Example:** Probe A maps to two locations in the target genome, and Probe B maps to three locations. You select **No Filter** in Similarity Filter, mark **Use Non-Unique Probe Filter,** and type 2 in Max Perfect Genomic Hits. The filter removes Probe B, but does not remove Probe A.

Parameter	Instructions/Details
Interval Options	
Select HD Search by	Select **Gene Annotations.**
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined genomic regions. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.
Gene Annotations	Type a gene annotation such as a GenBank accession number (for example, `NM_016660` or `AY884282`) or a gene symbol (for example, `H3N2` or `CTSB`) in the box. Use pipe "|" characters to separate multiple annotations. The program resolves annotations to genomic intervals before it starts your search. You can also upload a *.txt file of gene annotations. In the file, list one accession or gene symbol per line. In a given search, the annotations must all be of the same type. **a** Click **Upload.** A File Upload dialog box appears. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file, then click **Open.** The location of the file appears in the File Upload dialog box, in File Name. **d** Click **Upload.** The program uploads the gene annotations, and displays them in pipe-separated format in the HD search pane.

Parameter	Instructions/Details
Include Regions	Select one of the options below. You can use this parameter to limit your probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence." • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence."
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.
Exclude Options	
Standard Exclusion Interval(s)	eArray lets you select from among many different sets of standard exclusion intervals, based on annotation tracks. To ignore genomic regions defined in one or more of these sets, mark this option, then select the desired set(s) from the list. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option, then click **Upload.** See "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

5 Click **Search.**

eArray$_{XD}$ submits your HD probe search job to the eArray Web site, through your server. A dialog box tells you that your search has been submitted.

6 Click **OK.**

The search job appears in the Tasks pane of the Navigator. It can take one day or more for eArray to finish the job. For information about how to check the status of a job, and what you can do with the job and any returned search results, see "To check the status of an HD probe search" on page 132 and "To take action on an HD probe search job" on page 133.

To do a Probe ID HD Search for probes

This type of search retrieves HD probes for the CGH, ChIP, or methylation application type for a given species from the Agilent HD probe database based on probe IDs that you enter. If you have many probes to retrieve, you can prepare and upload a *.txt file that contains the desired probe IDs. For information about the required file format, refer to "To upload data for probe searches" on page 101. For general information about HD probe searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

1 Set the application type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under Search, click **HD Probes > Probe ID Search.**

The Probe ID Search pane appears. "Probe ID Search (HD probes)" on page 557.

3 Set search parameters as described in the table below. All are required.

Parameter	Instructions/Details
Job Information	
Search Name	Type a name that will help you identify this search job and its results.
Probe ID	Type at least one HD probe ID. Separate multiple probe IDs with pipe "|" characters. **Example:** `A_14_P100053|A_14_P100055|A_14_P100056` You can also upload a *.txt file that contains the desired probe IDs. Follow these steps: **a** Click **Upload.** A File Upload dialog box appears. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file of probe IDs, then click **Open.** **d** Click **Upload.** The names of the probes from the file appear in Probe ID.
HD Search by	This parameter is set to Probe ID, and cannot be changed.
Species	Select the desired species. Only the species represented in the HD database appear in the list of species.

4 Click **Search.**

eArray$_{XD}$ submits your HD probe search job to the eArray Web site, through your server. A dialog box tells you that your search has been submitted.

5 Click **OK.**

The search job appears in the Tasks pane of the Navigator. It can take one day or more for eArray to finish the job. For information about how to check the status of a job, and what you can do with the job and any returned search results, see "To check the status of an HD probe search" on page 132 and "To take action on an HD probe search job" on page 133.

To do a Simple Interval Finder Search

You use a Simple Interval Finder Search to retrieve the genomic intervals whose annotation contains a single search term. You can then download the retrieved intervals, or use them as the basis for a High Density (HD) probe search. You can also download the intervals and use them as the basis of a Genomic Tiling job.

1 Set the application type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Probes > Simple Interval Finder.**

The Simple Interval Finder pane appears.

3 Enter search criteria as described below. Both are required. To clear the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Search Term	Type a search term in the box. The program returns the genomic intervals whose annotation contains this term. The search term is not case-sensitive.
Species	Select a species from the list. This restricts your search to the intervals that are associated with the selected species.

4 Click **Search.**

The Search Results pane displays the intervals that are match your search term. For each interval, the pane lists the relevant annotation, and the number of probes available.

If there are many results, the program paginates them. Click a numbered page button to go to a different page.

Initially, the program sorts the results based on the contents of the Annotation column. To reverse the order of the sort, click this column heading again. To re-sort the results based on the contents of another column, click the heading of the desired column. The heading of the column by which the results are currently sorted appears in a darker color.

You can use the returned intervals in several ways:

Task	Instructions/Details
Use returned intervals in an HD probe search	You can use returned intervals as the basis of a Simple HD Search for probes. **a** In the Search Results pane, select the desired intervals. Use the following as a guide: • To select an interval, mark the check box in its row. • To select all of the intervals on the current page of results, mark the check box in the column heading row. • To select all of the intervals on all pages of results, mark **Select entire data set.** • To go to a different page of results, click the numbered page buttons above or below the results. The program remembers the intervals that you select as you go from page to page. **b** Click **Run HD Search.** The Simple HD Probe Search pane appears. The intervals that you selected appear in Genomic Intervals. **c** Set the other criteria for the HD search, then run the search. For details, see "To do a Simple Genomic Intervals HD Search for probes" on page 111.
Download returned intervals	**a** In the Search Results pane, select the desired intervals. Use the following as a guide: • To select an interval, mark the check box in its row. • To select all of the intervals on the current page of results, mark the check box in the column heading row. • To select all of the intervals on all pages of results, mark **Select entire data set.** • To go to a different page of results, click the numbered page buttons above or below the results. The program remembers the intervals that you select as you go from page to page. **a** Click **Download.** A Save dialog box appears. **b** Select a location for the downloaded file, then click **Save.** The program saves the file to the location that you selected. A dialog box tells you that the file was successfully downloaded. **c** Click **OK.**

Task	Instructions/Details
Use returned intervals in a Genomic Tiling job	**a** Download the intervals. (See above.) **b** Set up a Genomic Tiling job. In **Genomic Intervals,** upload the file of intervals that you just downloaded. For details about Genomic Tiling, see "To set up a Genomic Tiling job" on page 176.
View a list of chromosomes represented in returned intervals	**a** In the Search Results pane, select the desired intervals. Use the following as a guide: • To select an interval, mark the check box in its row. • To select all of the intervals on the current page of results, mark the check box in the column heading row. • To select all of the intervals on all pages of results, mark **Select entire data set.** • To go to a different page of results, click the numbered page buttons above or below the results. The program remembers the intervals that you select as you go from page to page. **b** Click **List Chromosome.** A dialog box appears. The chromosomes that are represented in the selected genomic intervals appear under List of Distinct Chromosomes.

To do an Advanced Interval Finder Search

You use an Advanced Interval Finder Search to retrieve the genomic intervals whose annotation exactly matches at least one of the search term(s) that you enter. You can use the returned intervals as the basis for an HD probe search. You can also download the intervals, and use them in a Genomic Tiling job.

1 Set the application type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Probes > Advanced Interval Finder.**

The Advanced Interval Finder pane appears.

3 Enter search criteria as described below. You must enter at least one annotation value, and the species. To clear all of the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Accessions	Type an accession number, without its source, or multiple accession numbers separated by pipe "|" characters. The search returns the intervals that correspond with each of the accessions. For the search to return intervals, accessions must match exactly. Use upper case (capital) letters in accessions. **Example:** `NM_012257|Q0055|NM_012298` You can also upload a file of accessions. Prepare a plain text file with an extension of .txt. List one accession per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Cytoband	Type a cytoband designation, without its source, or multiple cytobands separated by pipe "|" characters. The search returns the intervals that correspond with each of the cytobands. For the search to return intervals, cytobands must match exactly. Use lower case letters for the p or q chromosome arms. **Example:** `1p22.2|2q33.3` You can also upload a file of cytobands. Prepare a plain text file with an extension of .txt. List one cytoband per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.

Search Criterion	Instructions/Details
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns the intervals that correspond with each of the gene symbols. For the search to return intervals, gene symbols must match exactly. Use upper case (capital) letters in gene symbols. **Example:** `H3N2 | BRMS1 | BRCA1` You can also upload a file of gene symbols. Prepare a plain text file with an extension of .txt. List one gene symbol per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Species	Select a species from the list. This restricts your search to the intervals that are associated with the selected species.

4 Click **Search.**

The Search Results pane lists the intervals that are associated with your search term(s). For each search term that matches an existing annotation, the pane lists the associated genomic interval.

You can use selected intervals as the basis for an HD probe search or for a Genomic Tiling job. You can download selected intervals, and also get a list of the chromosomes that are represented in selected intervals. For specific instructions, see the end of the topic "To do a Simple Interval Finder Search" on page 127.

To check the status of an HD probe search

After you start an HD probe search, eArray$_{XD}$ submits an HD probe search job to the eArray Web site, through your server. You can monitor the status of the job.

1 Set the application type to **CGH, ChIP, or CH3.** See "To set the application type" on page 48.

2 In the **Tasks** pane of the Navigator, expand the **HD Search** folder.

The status of the job appears as an icon next to the name of the search job. The job has one of these status designations:

Status	Comments
	**Pending** – The job has been submitted to the eArray Web site.
	**Processing** – The eArray Web site is running the requested search.
	**Complete** – The search is finished. You can view and take action on the search results. See "To view HD probe search results" on page 134 and "To take action on an HD probe search job" on page 133.
	**Error** – An error occurred. You must re-submit the search.

To take action on an HD probe search job

After you submit an HD probe search job to the eArray Web site, and the job appears in the Tasks pane of the Navigator, you can take action on the job. The actions that you can take depend on the status of the job.

- In the Tasks pane of the Navigator, in the HD Search folder, right-click the name of the desired job, then click one of these options:

Option	Description
View Search Criteria	Opens the HD Search Criteria dialog box, where you can view the specific search criteria that were specified for the HD probe search job. See "To view the search criteria for an HD probe search" on page 134 and "HD Search Criteria" on page 782.
View Result	(Available for complete jobs) Opens the HD Search Results dialog box, where you can view the search criteria that were used in the search, as well as statistics about the search. See "To view HD probe search results" on page 134 and "HD Search Results" on page 783.
Create Probe Group	(Available for complete jobs) Opens the Probe Group dialog box, where you can create a new probe group that contains the probes that were returned by the search. See "To create a probe group from HD probe search results" on page 135 and "Create Probe Group (from HD or SNP search results)" on page 681.
Download	(Available for complete jobs) Opens a dialog box that lets you export a ZIP archive that contains a BED format file. This file contains the names and genomic locations of the returned probes. See "To download HD probes" on page 136.
Delete	(Available for pending or complete jobs) Removes the HD probe search job from the system, including any associated search results. See "To delete an HD probe search job" on page 137.

To view the search criteria for an HD probe search

After you submit an HD probe search job to the eArray Web site, and the job appears in the Tasks pane of the Navigator, you can view the search criteria specified for the job. This can help you to differentiate among different searches that you have requested, or to give you insight into how the probes in a given set of search results were retrieved.

1 In the Tasks pane of the Navigator, expand the **HD Search** folder.

2 Right-click the name of the desired job, then click **View Search Criteria.**

The HD Search Criteria dialog box lists the search criteria that are associated with the specific HD probe search job. See "HD Search Criteria" on page 782. For information about the search criteria that can appear in this dialog box, see the HD probe search topics referenced in "Searching for Agilent High Density (HD) Probes" on page 109.

3 When you are finished viewing the search criteria, click **Close.**

To view HD probe search results

After an HD probe search job has a status of Complete  , you can view statistics and other information about the search results.

1 In the **Tasks** pane of the Navigator, expand the **HD Search** folder.

2 Right-click the name of the job, then click **View Result.**

The HD Search Results dialog box appears. See "HD Search Results" on page 783.

To create a probe group from HD probe search results

If an HD probe search job has a status of Complete, you can create a new probe group that contains the probes from the search results. The program lets you create a single probe group from the results.

1 In the **Tasks** pane of the Navigator, expand the **HD Search** folder.

2 Right-click the name of the job, then click **Create Probe Group.** If this option does not appear, the HD Probe Search job may not be finished yet, or a probe group may already have been created from the results of this particular HD probe search.

The Probe Group dialog box appears. See "Create Probe Group (from HD or SNP search results)" on page 681.

3 Set the following probe group attributes. All are required, unless otherwise indicated. Attributes that do not appear below are set by the system and appear for your information, only.

Attribute	Instructions/Details
Probe Group Name	Type a name for the probe group. The program uses this name to reference the probe group in search results, probe group lists, and the like. The name can contain up to 100 characters. Use letters, numbers, spaces, and/or underscores, only.
Description	(Optional) Type a brief description, up to 4,000 characters in length.
Keyword	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. The program can use keywords as search criteria.
Folder	Select a folder. The program will save the new probe group to this location. Only the folders to which you have access appear in the list.

4 Click **Create Probe Group.**

The program creates the new probe group and saves it in the selected folder. A dialog box tells you that the probe group was successfully created.

5 Click **OK.**

You can now use the probe group in a microarray design. You can also view, copy, and download the probe group. The program saves the probe group with a status of Locked, which prevents editing.

To download HD probes

Once an HD probe search job has a status of Complete, you can download the names and locations of the probes that were retrieved in the search. eArray$_{XD}$ downloads a ZIP archive that contains a BED format file.

1. Expand the folders of the **Tasks** pane of the Navigator until you can see the desired HD probe search job.
2. Right-click the name of the job, then click **Download.**

   A dialog box appears.
3. Select a location for the file, then click **Open.**

   eArray$_{XD}$ downloads the file to the selected location. A dialog box tells you that the BED file was downloaded successfully.
4. Click **OK.**

NOTE

- You can view the downloaded BED format file with a compatible genome browser, including the Genomic Viewer within Agilent Genomic Workbench. See the *Data Viewing User Guide.* The BED file contains the Probe IDs and chromosomal locations of all of the returned HD probes.
- Once you create a probe group from the HD search results, you can download the probes in the probe group in several different formats. These formats can include sequence, accession, and annotation data for the probes. See "To download a probe group" on page 240.

To download the detailed results of an HD probe search

If an HD probe search job has a status of Complete, you can download the detailed results of the search. These results include statistics and other information about each genomic interval or gene annotation you specified in the HD probe search criteria.

1. In the Tasks pane of the Navigator, expand the **HD Search** folder.
2. Right-click the name of the desired job, then click **View Result.**

   The HD Search Results Dialog Box appears. See "HD Search Results" on page 783.
3. At the bottom of the Detail Result tab, click **Download Detail Results.**

   A Save dialog box appears.

4 Select a location for the downloaded file, then click **Save.**

The program downloads a TDT format file of the Detail Result information to the location that you selected. You can view this file in a word processing or spreadsheet program. A dialog box tells you that the file has been successfully downloaded.

5 Click **OK.**

6 Click **Close.**

NOTE The TDT file produced by this procedure contains statistics about each genomic interval that is represented in the HD search results. However, it does not contain information about individual probes. To download the list of probes, see "To download HD probes" on page 136.

To delete an HD probe search job

You can delete an HD probe search job with a status of Pending or Complete . When you delete an HD probe search job, the program cancels the job and removes the search criteria and any results from your server. However, it does not remove the probe group that you may have created from the results.

1 In the **Tasks** pane of the Navigator, expand the HD Search folder.

2 Right-click the name of the job, then click **Delete.**

A dialog box asks if you are sure you want to delete the search.

CAUTION When you delete an HD probe search job, you permanently remove the search criteria and any results associated with the search. To restore them, you must submit a new HD probe search.

3 Click **Yes.**

The program deletes the HD probe search job from your server. A dialog box tells you that the HD Search Details have been deleted successfully.

4 Click **OK.**

Searching for Agilent SNP Probes

Single nucleotide polymorphisms (SNPs) are sites in the genome where at least 1% of a population has a different base pair from the rest of the population at a given genomic location. You can access a collection of SNP probes that have been designed to interrogate specific SNP sites in the human genome. Agilent SNP probes are specifically designed for use in Agilent CGH+SNP microarrays, which combine CGH and SNP probes on the same microarray. For more information on CGH+SNP microarrays, see "To create a CGH+SNP microarray design" on page 301.

Agilent SNP Probes

Almost all SNP sites have two possible alleles. Agilent SNP probes differentiate the two alleles based on whether the SNP site is cleaved by the AluI/RsaI restriction enzyme mixture that is used in the target preparation process. One allele (the "cut" allele) is cleaved by the restriction enzymes, binds poorly to SNP probes, and produces a low signal level. The other allele (the "uncut" allele) is not cleaved by the restriction enzymes, binds well to SNP probes, and produces a high signal level. In analyses, a known genotyped reference is required, which can be one of five standard HapMap references, or a custom reference. SNP calls are made from the log ratios of the sample probes to those of the genotyped internal reference.

Although the platform is restricted to known SNP sites where at least one of the alleles is cut by the restriction enzyme mixture, tens of thousands of SNP sites can currently be resolved, and LOH (Loss or lack of heterozygosity) calls can be made for regions as small as approximately 5–10 Mb. For details, see the *CGH Interactive Analysis User Guide,* available in the Help tab of the CGH application of Agilent Genomic Workbench.

Agilent SNP probes, which vary in length from approximately 30 to 60 nucleotides, interrogate only those SNP sites whose alleles are differentiated by RsaI/AluI cleavage. Most sites are covered by two probes, one for each DNA strand. Some sites are covered by a single probe, because the other probe performs poorly.

NOTE

- SNP probes are distinct from other types of probes in eArray. They can only be included in SNP probe groups.
- SNP analysis on the Agilent CGH+SNP platform requires information from both CGH and SNP probes on the same microarray. Thus, CGH+SNP microarray designs must contain at least one CGH probe group and one SNP probe group.
- CGH and SNP probes cannot be included together in the same probe group.
- SNP probe groups cannot be used for other special-purpose probe groups such as normalization or filler probe groups.

SNP probe searches

To search for SNP probes, you set up a SNP probe search job and submit it to your Agilent Genomic Workbench server. When the server completes the search, you can take action on the results. The table below shows the main tasks that are related to SNP probe searches, and where to go in this user guide for more information.

Task	See this topic
Prerequisite – Required for all other tasks	
Download the Agilent SNP probe set from the eArray Web site	"To download the SNP probe set from the eArray Web site" on page 140
Search Tools	
Retrieve Agilent SNP probes from throughout the genome	"To do an Entire Agilent SNP Probe Set Search" on page 141
Retrieve Agilent SNP probes from specific genomic regions	"To do a SNP probe search by genomic intervals" on page 143
Retrieve Agilent SNP probes based on probe IDs	"To do a SNP probe search by probe ID" on page 148
Retrieve Agilent SNP probes based on SNP IDs	"To do a SNP probe search by SNP ID" on page 150
Working with SNP probe search results	
Monitor the status of a SNP probe search job	"To monitor the status of a SNP probe search job" on page 153
View the search criteria for a SNP probe search job that you have submitted	"To view the search criteria for a SNP probe search job" on page 154

Task	See this topic
View the results of a SNP probe search job	"To view the results of a SNP probe search job" on page 155
Download the results of a SNP probe search job	"To download the results of a SNP probe search job" on page 155
Create a probe group from the results of a SNP probe search job	"To create a probe group from SNP probe search results" on page 156
Delete a SNP probe search job	"To delete a SNP probe search job" on page 157

After you retrieve the desired SNP probes, and create a probe group, you can create a CGH+SNP microarray design. See "To create a CGH+SNP microarray design" on page 301.

To download the SNP probe set from the eArray Web site

Before you can do a SNP probe search of any type, you must first download the complete set of Agilent SNP probes from the eArray Web site. Once this data transfer is complete, the data are available to all members of your workgroup.

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

The Catalog and Workgroup Data dialog box appears. See "Catalog and Workgroup Data" on page 607.

In CGH+SNP, under **Catalog and SNP probe data,** if the message reads **Downloaded and Available,** the data have already been downloaded. You do not need to download it again.

2 Under CGH+SNP, next to Catalog SNP probe data, click **Download.**

A message tells you that the download job has been successfully submitted. An entry for the job appears in the Tasks pane of the Navigator, in the Data Download folder. The transfer of a given data set can take one day or more.

3 Click **OK.**

To do an Entire Agilent SNP Probe Set Search

This type of search lets you retrieve Agilent SNP probes from throughout the genome. It is best used when you want to retrieve all of the available Agilent SNP probes, and include them in an Agilent CGH+SNP microarray design. In addition, if desired, you can filter the returned probes based on several criteria. For general information about Agilent SNP probes and CGH+SNP microarrays, see "Searching for Agilent SNP Probes" on page 138.

Before you can do a SNP probe search in eArray$_{XD}$, one member of your workgroup must have transferred the Agilent SNP probe set from the eArray Web site to your Agilent Genomic Workbench server. See "To download the SNP probe set from the eArray Web site" on page 140.

1 In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Entire Agilent SNP Probe Set Search.**

The Entire SNP Search by Agilent Probe Set pane appears. See "Entire Agilent SNP Probe Set Search" on page 542.

2 Enter the following search criteria. The items in the pane that do not appear in the table below are set by the system, and are read-only.

Option	Instructions/Description
Job Information	
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The program returns Agilent SNP probes from throughout the genome of the selected species. Currently, the program supports human SNP probes.
Probe Options	
Use Only One Probe per SNP	(Optional) Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.

Option	Instructions/Description
Minimum MAF Value (%)	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.
Reference Samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. Agilent recommends that you select all five references. However, you can select fewer references: **a** Keep **Remove Doubly Cut SNPs** marked. **b** Click the name of one reference that you want to use, then control-click the names of any additional desired references. **Note:** If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove Doubly Cut SNPs.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.

3 Click **Search.**

A dialog box tells you that your SNP search query has been submitted. You can monitor the status of the search job from the Tasks pane, and take further action on the job. See "To monitor the status of a SNP probe search job" on page 153.

4 Click **OK.**

To do a SNP probe search by genomic intervals

This type of search lets you retrieve Agilent SNP probes that are associated with specific genomic intervals that you enter or upload. It is best used when you want to investigate SNP sites in specific regions of the genome, especially if you already have CGH probes that are designed to those same regions. In addition, if desired, you can filter the returned probes based on several criteria. For general information about Agilent SNP probes and CGH+SNP microarrays, see "Searching for Agilent SNP Probes" on page 138.

Before you search

- One member of your workgroup must have transferred the Agilent SNP probe set from the eArray Web site to your Agilent Genomic Workbench server. See "To download the SNP probe set from the eArray Web site" on page 140.
- (Optional) Prepare a *.txt file that contains the genomic intervals that you want to include in the search. Put one interval on each line. For format information on genomic intervals, see "Genomic Intervals (Simple HD and SNP Probe Searches)" on page 888.
- (Optional) You can also prepare another *.txt file that contains genomic intervals that want to explicitly *exclude* from the search. Put one interval on each line.

To search for SNP probes by genomic intervals

1 In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Genomic Interval Search.**

The SNP Search by Gene Interval pane appears. See "Genomic Interval Search (SNP Probe Search)" on page 546.

2 Enter the following search parameters. Parameters are optional unless otherwise indicated.

Parameter	Instructions/Description
Job Information	
Search Name	(Required) Type a brief name to identify the search job.
Species	(Required) Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Build Number	(Read-only) The build of the genome of the selected species to which the returned SNP probes are designed.
SNP Version	(Read only) The build of the SNP database of the selected species to which the returned SNP probes are designed.

Parameter	Instructions/Description
Probe Options	
Filters	Select one of these options: • **Total Probes** – This limits the total number of probes that the SNP probe search collectively returns for all specified genomic intervals. In **Filter Value,** type the desired number of probes. **Example:** If you type `2000` in Filter Value, the search returns the 2,000 best SNP probes that match the other search criteria. To find the best probes, the search considers empirically-determined probe scores. These scores reflect the likelihood that each given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. SNP probe scores are not available for download. • **Total SNPs** – This limits the total number of SNP sites that the search considers. In **Filter Value,** type the desired number of SNP sites. **Example:** If you type `2000` in Filter Value, the search considers only the 2,000 best SNP sites, and returns the SNP probes that are associated with those sites. To find the best SNP sites, the search considers the empirically-determined scores for the corresponding SNP probes. A probe score reflects the likelihood that a probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. SNP probe scores are not available for download. • **No Filter** – No limit is applied, either to the total number of returned SNP probes or to the number of SNP sites that are considered by the search.
Filter Value	Enter values for the **Total Probes** or **Total SNPs** filter. See above.
Prefer Catalog Probes	Currently, all of the SNP probes that are available in eArray$_{XD}$ are Agilent Catalog probes.

Parameter	Instructions/Description
Use Only One Probe per SNP	Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.
Minimum MAF Value	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.

Parameter	Instructions/Description
Reference Samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. Agilent recommends that you select all five references. However, you can select fewer references: **a** Keep **Remove Doubly Cut SNPs** marked. **b** Click the name of one reference that you want to use, then control-click the names of any additional desired references. **Note:** If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove Doubly Cut SNPs.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.
Interval Options	
Genomic Intervals	(Required) Type either chromosomal location(s) or cytoband(s) in the box. Separate multiple intervals with pipe "|" characters. All of the intervals must be of the same type. For information about how to enter genomic intervals, see "Genomic Intervals (Simple HD and SNP Probe Searches)" on page 888. To upload a file of chromosomal regions or cytobands, click **Upload.** The file must be a *.txt file that has one genomic interval on each line. See "To upload data for probe searches" on page 101.

Parameter	Instructions/Description
Extended Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined genomic intervals. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. the program extends an original interval of 9000–10000 to 8500–10300.
Exclude Options	
Standard Exclusion Interval(s)	You can exclude regions of known copy number variation from the SNP probe search. The program uses the CNV track in Agilent Genomic Workbench to define the intervals to exclude. To ignore these genomic regions, mark this option, then in the box, select **CNV.**
Custom Exclusion Interval(s)	To ignore the genomic intervals that are defined in a file of genomic intervals, mark this option. To upload a file of genomic intervals, click **Upload.** The file must be a *.txt format file with one genomic interval on each line. See "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

3 Click **Search.**

A dialog box tells you that your SNP search query has been submitted. You can monitor the status of the search job from the Tasks pane, and take further action on the job. See "To monitor the status of a SNP probe search job" on page 153.

4 Click **OK.**

To do a SNP probe search by probe ID

This type of search lets you retrieve the Agilent SNP probes that have the exact probe IDs that you enter or upload. For general information about Agilent SNP probes and CGH+SNP microarrays, see "Searching for Agilent SNP Probes" on page 138.

Before you search

- One member of your workgroup must have transferred the Agilent SNP probe set from the eArray Web site to your Agilent Genomic Workbench server. See "To download the SNP probe set from the eArray Web site" on page 140.
- (Optional) Prepare a *.txt file that contains the SNP probe IDs that you want to include in the search. Put one probe ID on each line.

To search for SNP probes by probe ID

1 In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Probe ID Search.**

The SNP Search by Probe ID pane appears. See "Probe ID Search (SNP probes)" on page 558.

2 Enter the following search parameters. All are required.

Parameter	Instructions/Description
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Probe ID	Type the desired SNP probe IDs. Separate multiple probe IDs with pipe "|" characters. The search returns any existing Agilent SNP probes that have the probe IDs that you enter. **Example:** `A_20_P00170194|A_20_P00182084` To upload a file of SNP probe IDs, click **Upload.** See "To upload data for probe searches" on page 101.

3 Click **Search.**

A dialog box tells you that your SNP search query has been submitted. You can monitor the status of the search job from the Tasks pane, and take further action on the job. See "To monitor the status of a SNP probe search job" on page 153.

4 Click **OK.**

To do a SNP probe search by SNP ID

This type of search lets you retrieve Agilent SNP probes that cover specific SNP sites. To define the desired SNP sites, you enter or upload SNP database accession values. This search is best used when you want to study a well-defined subset of SNP sites, and you know their accessions. For general information about Agilent SNP probes and CGH+SNP microarrays, see "Searching for Agilent SNP Probes" on page 138.

Before you search

- One member of your workgroup must have transferred the Agilent SNP probe set from the eArray Web site to your Agilent Genomic Workbench server. See "To download the SNP probe set from the eArray Web site" on page 140.
- (Optional) Prepare a *.txt file that contains the SNP reference cluster IDs that you want to include in the search. Put one reference cluster ID on each line.

To search for SNP probes by SNP ID

1 In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Reference Cluster IDs Search.**

The SNP Search by Reference Cluster IDs pane appears. See "SNP ID Search (SNP probe search)" on page 572.

2 Enter the following search parameters. Parameters are required, except as indicated.

Parameter	Instructions/Description
Job Information	
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Build Number	(Read-only) The build of the genome of the selected species to which the returned SNP probes are designed.
SNP Version	(Read only) The build of the SNP database of the selected species to which the returned SNP probes are designed.

Parameter	Instructions/Description
Reference Cluster Options	
SNP Reference Cluster IDs	Type the desired SNP database accession values. Separate multiple values with pipe "|" characters. **Example:** `rs2825825|rs12329873|rs4818586` Do not include the database identifier (*i.e.* type `rs2825825`, **not** `dbsnp|rs2825825`). To upload a file of SNP reference cluster IDs, click **Upload.** The file must be a *.txt file that has one SNP reference cluster ID on each line. See "To upload data for probe searches" on page 101.
Probe Options	
Use Only One Probe per SNP	(Optional) Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.
Minimum MAF Value	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.

Parameter	Instructions/Description
Reference Samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. Agilent recommends that you select all five references. However, you can select fewer references: **a** Keep **Remove Doubly Cut SNPs** marked. **b** Click the name of one reference that you want to use, then control-click the names of any additional desired references. **Note:** If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove Doubly Cut SNPs.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.

3 Click **Search.**

A dialog box tells you that your SNP search query has been submitted. You can monitor the status of the search job from the Tasks pane, and take further action on the job. See "To monitor the status of a SNP probe search job" on page 153.

4 Click **OK.**

To monitor the status of a SNP probe search job

After you submit a SNP probe search job to the server, you can monitor its status in the Tasks pane of the Navigator. You can also take further action on the job.

- In the Tasks pane of the Navigator, in the SNP Search folder, note the icon next to the name of the desired SNP probe search job. This icon indicates the status of the job. These icons can appear:

Status	Comments
	Pending – The SNP probe search job has been submitted to the server, but the search has not yet started.
	Processing – The SNP probe search is in progress.
	Complete – The SNP probe search is finished. You can now take

If the status of the job is Complete , you can take further action on the job:

Task	Comments
View Search Criteria	(Available for jobs with any status) See "To view the search criteria for a SNP probe search job" on page 154.
Re-use SNP probe search criteria	(Available for jobs with any status) You can use the criteria from an existing SNP probe search job as the basis for a new search. See "To use existing SNP probe search criteria to set up a new search" on page 154
View Result	View overall statistics about the search. For certain searches, other details can be available. See "To view the results of a SNP probe search job" on page 155.
Create Probe Group	Create a SNP probe group from the probes that were returned by the SNP probe search. See "To create a probe group from SNP probe search results" on page 156

Task	Comments
Download	Download a BED format file that contains the locations of the returned SNP probes. See "To download the results of a SNP probe search job" on page 155.
Delete	(Also available for jobs with a status of Pending.) Remove the SNP probe search job from the system. See "To delete a SNP probe search job" on page 157

NOTE You can also monitor the status of jobs in the Job Queue Management Console. This dialog box lets you see additional information about jobs, and take additional action. See "To view a list of your tasks" on page 71.

To view the search criteria for a SNP probe search job

You can view a list of all of the search criteria that were submitted for a SNP probe search job. The job can have any status.

- In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired SNP probe search job, then click **View Search Criteria.**

  The SNP Search Criteria dialog box appears. See "SNP Search Criteria" on page 854.

To use existing SNP probe search criteria to set up a new search

The search criteria for an existing SNP probe search job can serve as the basis for a new SNP probe search. This can be useful when you want to redo a search, but with small modifications.

1. In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired SNP probe search job, then click **View Search Criteria.**

   The SNP Search Criteria dialog box appears. See "SNP Search Criteria" on page 854.
2. Click **Execute.**

The appropriate SNP probe search pane appears, with the search criteria from the old search. You must type a new name for the search, and you can change any of the search criteria as desired, and submit a new SNP search job to the server.

To view the results of a SNP probe search job

When the status of a SNP probe search job is Complete, you can view the results of the job. These results always include the total number of probes that the search returned. For SNP searches by genomic interval, more detailed results are available.

- In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired job, then click **View Result.**

  The SNP Search Results dialog box appears.

  - For details on the available search results for SNP probe searches by gene interval, see "SNP Search Results (Genomic Interval Search)" on page 857.
  - For all other types of SNP probe searches, see "SNP Search Results (Except Gene Interval searches)" on page 856.

To download the results of a SNP probe search job

When the status of a SNP probe search job is Complete, you can download a BED format file that contains the IDs of the probes that were returned by the search, and the genomic location of the corresponding SNP site that each probe covers.

1 In the Tasks pane of the Navigator, in the SNP Search folder, right click the name of the desired job, then click **Download.**

  A Save dialog box appears.

2 Select a location for the file, the click **Save.**

  The program saves the file as a *.zip format archive. A dialog box tells you that the BED file was successfully downloaded.

  You can extract the BED format file from the *.zip archive. For file format information, see "BED" on page 878.

To create a probe group from SNP probe search results

When the status of a SNP probe search job is Complete, you can create a SNP probe group that contains all of the SNP probes that were returned by the search. You then use the SNP probe group in a custom CGH+SNP microarray design. The program lets you create one SNP probe group from the results of a given SNP probe search job.

1 In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired job, then click Create Probe Group.

A Create Probe Group dialog box appears. See "Create Probe Group (from HD or SNP search results)" on page 681.

2 Enter the following information:

Item	Instructions/Details
Probe Group Name	Type a name to identify the new probe group.
Status	Select one of these statuses: • **Incomplete** – This status lets you edit the probe group, if desired. • **Locked** - This status prevents further edits to the probe group. Locked probe groups cannot be unlocked.
Description	(Optional) Type a brief description to be saved with the probe group.
Keyword	(Optional) Type relevant keyword(s). Separate multiple keywords with commas. Keywords can make it easier to find the probe group in a probe group search. See "To search for probe groups" on page 224.
Folder	Select a destination folder for the new probe group. All of the folders to which you can save the probe group appear in the list.

3 Click **Create Probe Group.**

A dialog box tells you that the new probe group was successfully created. The probe group appears in the folder that you selected, in the Probe Group subfolder.

4 Click **OK.**

To delete a SNP probe search job

You can delete a SNP probe search job with a status of Pending or Complete . When you delete a SNP probe search job, the program cancels the job and removes the search criteria and any results from your server. However, it does not remove the probe group that you may have created from the results.

1 In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the job, then click **Delete.**

   A dialog box asks if you are sure you want to delete the search.

CAUTION When you delete a SNP probe search job, you permanently remove the search criteria and any results associated with the search. To restore them, you must submit a new SNP probe search.

2 Click **Yes.**

   The program deletes the SNP probe search job from your server. A dialog box tells you that the SNP search details have been deleted successfully.

3 Click **OK.**

Uploading Probes

One way to add new probe content to your server is to upload a file that contains probe sequences and annotation. When you upload probes, the program transfers the sequences and annotation from your probe file to your server. You can then use the uploaded probes to create new probe group(s). Later, you can use the probe groups to create microarray designs. See "To create a microarray design from existing probe groups (Wizard)" on page 269. You can upload probes for most application types. However, you cannot upload microRNA, HD, or SNP probes.

See these topics in this section:

To prepare a file of probes and annotation for upload

- Follow the guidelines below to prepare a probe data file.

Probe types

You can upload probes for most application types. However, you cannot upload microRNA, HD, or SNP probes.

File types

eArray$_{XD}$ supports these file types for probe uploads:

File Type	Notes
Microsoft Excel files (*.xls)	If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.
Tab-delimited text files (*.tdt or *.txt)	Place tabs between fields (columns) in a record (row). Use **new line** characters at the ends of records.

File formats

eArray$_{XD}$ supports the file formats in the table below. Your file can have columns in addition to those that are listed–if it does, be sure to label them as **Ignore** when you upload the file. See "To upload probes and annotation" on page 161.

File Format	Columns included in format
Complete	ProbeID
	Sequence
	TargetID
	Accessions
	GeneSymbols
	Description
	ChromosomalLocation
Minimal	ProbeID
	Sequence

NOTE The file formats are different for bait uploads for the SureSelect Target Enrichment application type. See "To upload baits" on page 370.

General format of data within a file

In uploaded files, eArray$_{XD}$:

- Accepts columns in any order – You label columns as part of the upload process.
- Accepts extra columns – When you label columns during the upload process, be sure to label any extra columns as **Ignore.**
- Accepts, but does not interpret column headings – Be sure to mark **My uploaded file contains column headings** when you label columns during the upload process.
- Does not accept double or single quotation marks, angle brackets, or forward or backward slashes.
- Ignores blank lines.
- Expects all entries within a row to be separated by tabs, even if the actual entry is blank.

NOTE eArray$_{XD}$ can upload fairly large probe files. Agilent has tested the 64-bit version of the program, and has successfully uploaded 150,000 probes in the Complete file format, which corresponds to a file size of approximately 32 MB.

Specific requirements for individual types of data

Type of data	Requirements
ProbeID	A unique identifier for the probe sequence, containing up to 15 characters. Probe ID cannot be blank.
Sequence	The base sequence of the probe, in 5' to 3' orientation. The sequence must be from 20 to 60 nucleotides in length, and must only contain the capital characters A, C, G, and T. Sequence cannot be blank.
TargetID	Also referred to as the primary accession, TargetID uniquely identifies the sequence that most exemplifies the target transcript. Only one annotation value is allowed, and it can include or omit the source designation. For example, both `ref|AK075564` and `AK075564` are acceptable. TargetID can be blank.
Accessions	Unique identifier(s) that refer to a nucleotide sequence that is a target for the associated probe and/or a protein sequence that is a product of the target. Accessions are represented in a <source>|<ID> pair format. <source> is the symbol of the database from which the accession was derived and <ID> is the unique identifier accession. For example, `ref|NM_015752` is a <source>|<ID> pair where `ref` (NCBI Refseq) is the source and `NM_015752` is the unique identifier for that source. The Accessions field can contain multiple <source>|<ID> pairs, delimited by pipe "|" characters. For example, `gi|7657630|ref|NM_015752` is an allowable accession that gives both an NCBI gene identifier (`gi`), and a Refseq identifier (`ref`) for the same probe sequence. Accessions can be blank.
GeneSymbols	A unique abbreviation for a gene name. GeneSymbols can be blank.

Type of data	Requirements
Description	A description of a phenotype, gene product, or its function. Description can be blank.
ChromosomalLocation	The chromosome number and the location of the sequence on the chromosome, expressed in the following example notation: `chr19:11392326-11391822` Enter only one chromosomal location. It can include or omit the source, and it can be blank.

Possible causes of upload errors

- Your file contains two probes with the same Probe ID, but different sequences, and you select **Remove replicate probes from upload.**
- Your file contains two probes with the same Probe ID and the same sequence, and you have not selected **Remove replicate probes from upload.**
- You are not the owner of an existing probe whose annotation would be overwritten by a probe in your uploaded file.
- A probe from your uploaded file has the same Probe ID as one that already exists in the system, but it does not have the same sequence, species, or application type as the one it is overwriting.
- One or more entries in your uploaded file do not have the correct format.

To upload probes and annotation

You can transfer the probes and annotation from a file to your server. Before you upload, you must first create a file that contains the desired probe sequences and annotation values. See "To prepare a file of probes and annotation for upload" on page 158. You can upload probes for most application types. However, you cannot upload microRNA, HD, or SNP probes.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Create Probes, click **Probe Upload.**

The Probe Upload dialog box appears. See "Probe Upload" on page 831.

3 Enter the following details. All are required.

Detail	Instructions/Comments
Probe Parameter Details	
Job Name	Type a name that will help you to identify this job.
Species	Select the desired species. The program associates all probes from the uploaded file with this species.
Remove replicate probes from upload	Mark this option to upload the first probe in each set of replicate probes in your file, and ignore the others. A replicate probe has the same Probe ID as another probe in the file. If your probe file contains replicate probes, and you do **not** mark **Remove replicate probes from upload,** the program does not upload your file.
Probe Precedence	These options define what the program does if it finds probes in your uploaded file that have the same Probe ID as probes that already exist in the system. Select one of these options: • **Overwrite matching probes** – The annotation of the matching uploaded probes replaces the annotation of the existing probes. You can use this option to reannotate existing probes. • **Skip matching probes** – The program ignores matching uploaded probes, but does upload other probes. • **Cancel upload if any probes already exist** – The program cancels the entire upload process if it finds a matching uploaded probe.
Upload Probe File Details	
Upload Type	Select one of these options: • **Upload Probes only** – Creates probes from the data in the uploaded file, and makes them available to you in the program as individual probes. • **Create New Probe Group** – In the box, type a name for the probe group. The probe group name can contain up to 100 characters. The program creates probes from the data in the uploaded file, and creates a probe group that contains the uploaded probes. The program saves the new probe group to your main "default" folder, and the probes are also available to you as individual probes.

Detail	Instructions/Comments
Upload File	Follow these steps to select the file of probe sequences and annotation for upload: **a** Click **Browse.** An Open dialog box appears. **b** Select the desired file, then click **Open.** The location of the file appears in Upload File.
File Format	Select **MINIMAL** or **COMPLETE.** The file format defines the specific types of data available in the uploaded file. See "To prepare a file of probes and annotation for upload" on page 158.
File Type	The file type defines how the data items in the file are specified and separated. Select one of these file types: • **TDT** – Tab-delimited text (*.tdt or *.txt) file. • **MS-EXCEL** – Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

CAUTION If you select **Overwrite Matching Probes** in Probe Precedence, the program reannotates matching probes upon upload. The original annotation of these probes cannot be recovered.

4 Click **Preview.**

The Define Uploaded File Columns pane appears in the lower part of the dialog box. The table contains a row of labels, and the first few rows of data from your file.

5 At the top of each column, select the most appropriate label for the data beneath it. Use each label exactly once, except for *Ignore,* which you can use any number of times. You must label all columns.

6 If the first row of your probe data file contains column headings, mark **My uploaded file contains column headings.** If you mark this option, the program ignores the first line of the file, and does not interpret it as actual probe data.

7 Click **Upload.**

If you have not yet transferred your workgroup's probe and annotation data for the given application type from the eArray Web site to your server, a warning message tells you that the system will add a prefix of **XD_** to the IDs of all new probes in your file. This differentiates your uploaded probes from any probes that you subsequently transfer from the eArray Web site that have the same names. To continue with the upload process, click **OK.**

A dialog box tells you that your file has been successfully submitted to the upload queue. The upload job appears in the Tasks pane of the Navigator, and in the Job Queue Management Console. The program imports the file, and transfers the probes and annotation to your server.

When you upload probes, the probes become part of the probe database on your server, but they are not uploaded to your user account on the eArray Web site. This is an important consideration if you do microarray design work both in eArray$_{XD}$ and on the eArray Web site.

8 Click **OK.**

You can monitor the status of the upload in the Tasks pane of the Navigator. In the Probe Upload folder, an icon appears next to the name of the probe upload job:

Status	Comments
	**Pending** – The probe upload job has been submitted to the upload queue.
	**Processing** – Your server is in the process of uploading the probes to the probe database.
	**Complete** – The probe upload is finished. You can now search for probes, and use them in probe groups and microarray designs.
	**Error** – An error occurred. You must re-submit the probe upload job. Errors are usually caused by problems in the uploaded probe file. To see any errors that the program detected in the uploaded probe file, follow these steps: **a** Right-click the name of the probe upload job, then click **Download Error File.** A dialog box appears. **b** Select a location for the downloaded error file, then click **Save.** The program saves a ZIP format archive to the location that you selected. The ZIP archive contains an HTML file that you can view with your Internet browser. The HTML file lists the lines in your original probe upload file that contain errors. Place the pointer over a highlighted item to see a ToolTip that describes the error.

To delete a probe upload job with any status except Processing, right-click the name of the job, then click **Delete.**

To create a probe group with uploaded probes

The program lets you create a probe group with uploaded probes either when you set up the upload, or after the upload.

To create a probe group during the upload process

If you create a probe group during the upload process, the resulting probe group contains all of the probes in the uploaded file.

- Upload probes as described in "To upload probes and annotation" on page 161. As you define the upload, under **Upload File Details,** in **Upload Type,** select **Create New Probe Group,** then type a name for the probe group.

To create a probe group after you upload a file of probes

If you create a probe group after you upload your probe file, the probe group can contain all of the uploaded probes, a subset of them, and/or additional probes.

1. Search for the desired probes. See "Searching for Probes" on page 92.
2. Select the desired probes, then create a probe group as described in "To create a new probe group" on page 204.

Creating Probes

You can create new probes in several ways:

Probe Creation Method	Description
Gene Expression (GE) Probe Design	Creates probes for the Expression application type based on specific target sequences. The design process can favor the creation of probes with optimal base composition, or probes that have melting temperatures close to a specific value. In addition, the process compares probes with a species transcriptome database to eliminate ones that can cross-hybridize with sequences other than the desired target. See "To set up a GE Probe Design job" on page 167.
Simple Tiling	Creates probes for the Expression application type that span uploaded target sequences at even intervals. You can set the density of tiling in one of several ways. See "To set up a Simple Tiling job" on page 174.
Genomic Tiling	Creates probes for the CGH, ChIP-on-chip, and CH3 application types that span specified regions of a selected genome at even intervals. The genome can be one that is available on the eArray Web site, or a custom genome that you upload. You can set the density of tiling in one of several ways, ignore repeat regions, and trim probes to conform better to a specific T_M. See "To set up a Genomic Tiling job" on page 176.
Network and Literature Searches	Although they are not actual probe creation methods, biological network searches and literature searches can supply relevant annotations or genomic intervals as input for the probe creation methods that are available in the program. See "Using Biological Networks to Find or Create Probes or Baits" on page 184.

To create probes, you set up a probe design or tiling job, upload any necessary file(s), then submit the job. For GE Probe Design and Simple Tiling, the program submits the job to the eArray Web site, through your server. For Genomic Tiling, the program either submits the job to the eArray Web site (for tiling of genomes available on the site) or locally in $eArray_{XD}$ and your server (for uploaded custom genomes).

You can monitor the progress of the probe design or tiling job, and take action on it. See the following topics for details:

- "To check the status of a probe design or tiling job" on page 180

- "To view the results of a probe design or tiling job" on page 181
- "To download probe design or tiling results" on page 182
- "To delete a probe design or tiling job" on page 183

To set up a GE Probe Design job

Gene Expression (GE) Probe Design creates probes for the Expression application type based on specific target sequences. To define the target sequences, you either upload a sequence data file in FASTA format, or a file that contains GenBank accessions. See "FASTA" on page 884 and "Accessions" on page 876. You set up the GE Probe Design job within eArray$_{XD}$. Your server then sends the job parameters to the eArray Web site. When the GE Probe Design job is completed, your server retrieves the results.

The program can guide you through the creation of a microarray design using GE Probe Design. See "To create a microarray design from target transcripts" on page 289.

Design methodologies

You can use one of two general GE Probe Design methodologies:

- **Base composition methodology** – The resulting probes adhere as closely as possible to the base composition profile that gives optimal performance on the Agilent platform, and they are all of equal length. This is the standard method, and it works best with Agilent protocols, and most eukaryotic organisms.
- **T_M matching methodology** – The resulting probes have melting temperatures (T_M) as similar as possible to a value that you enter. Probes can be all of equal length, or probes can be trimmed to increase compliance with the desired T_M. This methodology can work well when you design probes for prokaryotic organisms.

Transcriptome similarity database

GE Probe Design uses transcriptome data as a similarity database to eliminate potential probe sequences that would have significant cross-hybridization with targets other than the one of interest. In general, the better characterized

the transcriptome, the better eArray can design probes that are specific for each of the transcripts in your targets. You have several options for this transcriptome similarity database:

- **Agilent-provided transcriptome** – Uses an available Agilent species transcriptome database. Select this option if it is available for your species of interest, as these databases have been specifically constructed for use in GE Probe Design.
- **Uploaded target file** – Uses your file of uploaded target sequences as the transcriptome similarity database. Select this option if you are designing a "whole transcriptome" array for an organism that is not represented within the Agilent transcriptome set, and the target file represents most or all transcripts within the target transcriptome. This option works for uploaded target files that contain either actual sequence data, or GenBank accessions.
- **Uploaded transcriptome file** – Uses a FASTA format file of transcriptome sequence data. See "FASTA" on page 884.

Before you set up a GE Probe Design job

- Prepare either a FASTA format file that contains target sequence data, or a *.txt file that contains a list of GenBank accessions. For GenBank accessions, the file must contain the accession numbers separated by **new line** (return) characters. For information about FASTA format files, see "FASTA" on page 884.

  You can also use a search for biological networks to supply GenBank accessions for the job. See "To use a biological network to find or create probes" on page 193.
- If an Agilent-constructed species transcriptome database is not available for your species of interest, prepare a FASTA format file that contains custom transcriptome data to use as a similarity database in the probe design process. To see a list of available Agilent transcriptomes, set parameters for the job as described below. In Step 2, under Transcriptome File Details, the list of available transcriptomes appears in **Species of Transcriptome.**

To set parameters and upload file(s) for a GE Probe Design job

1 Set the application type to **Expression.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Probes,** do one of the following:

- To set up a GE Probe Design job using T_M Matching methodology, click **Probe Design (TM).**
- To set up a GE Probe Design job using Base Composition methodology, click **Probe Design (BC).**

In either case, the Create Probes dialog box appears. See "Create Probes (TM Matching or Base Composition Methods)" on page 683.

3 Set the desired design job parameters as described in the table below. All are required unless otherwise noted.

Parameter	Instructions/Comments
Design Options	
Design Job Name	Type a name that will help you to later identify this specific GE Probe Design job.
Probe Length	Type the maximum length for the generated probes. The allowable length is from 25 to 60 bases. Agilent has found that a probe length of 60 bases provides the optimal balance between sensitivity and specificity for most applications on the Agilent microarray platform.
Probes per Target	Select from 1 to 10 probes per target. This is the maximum number of probes the probe design process returns for each uploaded target sequence. If the target sequences are of poor quality (for example, if they contain repetitive and/or vector sequences), the probe design process can return fewer probes than the value you enter. Because of the length and high quality of the generated probes, Agilent recommends that you create one probe per target sequence. However, if you design multiple probes per target sequence, you can select the best of those probes after a validation process.

Parameter	Instructions/Comments
Probe Orientation	Select one of these options: • **Sense** – Produces probes in the sense or "coding strand" orientation, similar in sequence to the mRNA targets. Use this option if the sample preparation methodology yields cDNA or cRNA molecules. • **Antisense** – Select this option if you want probes in antisense or "template" orientation, complementary in sequence to the mRNA targets. This is the best option if your samples are directly labeled RNA.
Design Options	Select one of these options: • **Best Probe Methodology** – The probe design process favors production of the highest quality probes, rather than even coverage of each target sequence. The selection process favors empirically validated probes, and probes that are closer to the 3' end of a given primary accession. • **Best Distribution Methodology** – The probe design process favors even coverage of each target sequence, rather than production of the highest quality probes.
Design with 3' bias	Mark this option if you want probes derived mainly from the first 1,000 bp from the 3' end of each of your target sequences. If you use an Agilent (or other) labeling protocol that uses linear amplification, it is important to select probes from the 3' end of the sequence. Linear amplification generates sequences that are shorter than the initial template due to the attenuation of the polymerase reaction. Because of this, most of the labeled product represents only the first 1,000 bp from the 3' end of each target sequence. It is important to design probes that represent this region.

Parameter	Instructions/Comments
Masking	eArray always uses both of these options in the probe design process, and they cannot be disabled. • **Apply Vector Masking** – Identifies and ignores contaminant segments during probe design. Target sequences can contain contaminant segments not actually found in the sample under study. These segments are often artifacts from cloning vectors (e.g. plasmid, phage, BAC, YAC) used in cloning and amplification processes. • **Apply Repeat Masking** – Identifies and ignores repetitive sequences within your target sequences during probe design. The genome of any given organism contains interspersed repeats and low complexity DNA sequences. These sequences, which are unique at a species level, are replicated many times throughout the genome, and are found in the transcriptome as well. Replicate regions are poor candidates for unique probes.
Allow Probes to be Trimmed	(Available only for T_M-Matching GE Probe Design jobs) This option lets the program remove bases from candidate probes to increase compliance with the Preferred Probe T_M. eArray will not trim probes to shorter than 45 bases. In concept, a shorter probe has less complementary sequence available, which can reduce its specificity, or infringe on its ability to form a stable duplex with the desired target. However, the risk of this occurring to a significant extent is very low.
Preferred probe Tm	(Available only for T_M-Matching GE Probe Design jobs) Type the target T_M for the probe design process (in °C). The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms. Select a probe T_M based on these factors: • The mean and standard deviation of the T_M of all potential probes that could be generated for the target transcriptome. • The hybridization temperature identified in the hybridization protocol. In practice, the target T_M should be ~20°C higher than the hybridization temperature. For example, if the hybridization temperature is 60°C, then the target probe T_M should be 80°C.

Parameter	Instructions/Comments
Target File Details	
Species	Select the species associated with your target sequences.
Target File Format	Select one of these options • **FASTA format** – Select this option if you have a FASTA format file of target sequences that you want to use as the basis for the GE Probe Design process. • **GenBank Accessions** – Select this option if you have a *.txt file that contains GenBank accessions that you want to use as the basis for the GE Probe Design process. In either case, you must set the location of the file. See below, "Select Target File."
Select Target File	To select a target file for the GE Probe Design Process, follow these steps: **a** Click **Browse.** An Open dialog box appears. **b** Select the desired target file, then click **Open.** The location of the file appears in Select Target FIle. eArray resolves GenBank Accessions to actual sequence data before it starts the GE Probe Design process.

Parameter	Instructions/Comments
Transcriptome Details	
Species of Transcriptome	Select the desired species. In general, select the same species as you did for the target file. Alternatively, you can select a different species to eliminate certain cross-species hybridizations.
Select Transcriptome	Select the source of the transcriptome data that you want the probe design process to use. The process uses transcriptome data as a similarity database to eliminate potential probe sequences that would have significant cross-hybridization with targets other than the one of interest. • **Agilent-provided Transcriptome** – Uses one of Agilent's available species transcriptome databases. If a transcriptome is available for your species of interest, select this option. These databases have been specifically constructed for use in GE Probe Design. • **Use Target File as Transcriptome** – Uses the file you specified in Upload Target File as the transcriptome similarity database. Select this option if you are designing a "whole transcriptome" array for an organism that is not represented within the Agilent transcriptome set, and the target file represents most or all transcripts within the target transcriptome. This option works for uploaded target files containing either actual sequence data, or GenBank accessions. • **Upload Transcriptome File** – Uses a FASTA format transcriptome file that you upload as the similarity database. See below, "Upload Transcriptome File."
Upload Transcriptome File	(Available if you select Upload Transcriptome File in Select Transcriptome) **a** Click **Browse.** An Open dialog box appears. **b** Select the desired transcriptome file, then click **Open.** The location of the file appears in Upload Transcriptome File.

4 Click **Submit.**

The program submits your GE Probe Design job to the eArray Web site, through your server. A message tells you that your job has been submitted.

5 Click **OK.**

In the Tasks pane of the Navigator, your GE Probe Design Job appears in the Probe Design folder. You can monitor the status of the job, and take action on it. See "To check the status of a probe design or tiling job" on page 180.

NOTE The program handles highly homologous sequences in a specific way. See "How eArray handles highly homologous sequences" on page 899.

To set up a Simple Tiling job

Simple Tiling creates probes for gene expression microarrays that span uploaded target sequences at even intervals. To define the target sequences, you upload a FASTA format file that contains the sequence data. For guidelines on this file format, see "FASTA" on page 884.

1 Set the application type to **Expression.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Probes,** click **Simple Tiling.**

The Simple Tiling dialog box appears. See "Simple Tiling" on page 852.

3 Set the Simple Tiling job parameters as described in the table below. All parameters are required.

Parameter	Instructions/Details
Design Options	
Design Job Name	Type a name to identify this Simple Tiling job.
Probe Length	Type the desired length (from 45 to 60 bases) for the generated probes. Type the number of bases, without units. Agilent has found that a probe length of 60 bp provides the optimal balance between sensitivity and specificity for most applications on the Agilent microarray platform.

Parameter	Instructions/Details
Probe Density Option	Select one of these options, then type the appropriate value in **Probe Density Value.** • **Average Probe Spacing** – Defines the average distance (in bp) between the centers of the sequences to which probes are designed. • **Number of Probes per Sequence** – Defines the average number of probes designed for each target sequence. eArray uses this value to calculate average probe spacing on a per-sequence basis. The actual number of probes designed for each sequence may deviate from the specified value because of repeat regions and rounding, but this deviation is typically not large unless sequence length limits the design process. • **Total Number of Probes** – Defines the total number of probes generated, to be spaced evenly over all of the target sequences. eArray calculates the number of probes to be generated for each sequence, then uses these numbers to calculate average probe spacing.
Probe Density Value	Type the desired number of probes, or probe spacing (in bp), that applies to your selection in **Probe Density Option.** In all cases, type an integer that is greater than 0.
Target File Details	
Species	Select the species that applies to the data in your uploaded target sequence file. The program uses the selected species name to properly classify the new probes in the probe database on your server.
Select Target File	**a** Click **Browse.** An Open dialog box appears. **b** Select the desired FASTA format target sequence file, then click **Open.** The location of the file appears in Select Target File.

4 Click **Submit.**

A message tells you that your job has been submitted.

5 Click **OK.**

You can monitor your Simple Tiling job and take action on it. See "To check the status of a probe design or tiling job" on page 180.

To set up a Genomic Tiling job

Genomic Tiling creates probes for the CGH, ChIP-on-chip, and CH3 application types that span specified regions of a genome at even intervals. You can tile a genome that is available on the eArray Web site, or a user-defined genome that you have uploaded to your server. To define the desired genomic intervals to tile, you either type them directly in the program, or upload a file of chromosomal locations or cytobands.

Before you set up a Genomic Tiling job

- If you intend to tile a user-defined genome, first make sure that the genome has been imported to your server. To import a genome, see "To import a new genome" on page 66.
- If you do not intend to tile a user-defined genome, a genome build of your species of interest must be available on the eArray Web site. A list of the available species appears in the Genomic Tiling dialog box, in Species. To open this dialog box, see the beginning of the procedure in "To set up a Genomic Tiling job" below.
- (Optional) Prepare a *.txt file that contains a list of the chromosomal locations or cytobands to be tiled, one interval per line. See "Genomic Intervals (Genomic Tiling)" on page 888.

  You can use a search for biological networks to supply genomic intervals for the job. See "To use a biological network to find or create probes" on page 193.

To set up a Genomic Tiling job

1. Set the application type to **CGH, ChIP-on-chip,** or **CH3.** See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, under **Create Probes,** click **Genomic Tiling.**

   The Genomic Tiling dialog box appears. See "Genomic Tiling" on page 779.
3. Set the following Genomic Tiling job parameters. All are required.

Parameter	Instructions/Details
Design Options	
Design Job Name	Type a name to identify this Genomic Tiling job.

Parameter	Instructions/Details
Probe Length	Type the desired length (from 45 to 60 bp) for the generated probes. If you intend to T_M trim probes, keep the length set to its default value of 60 bp.
Probe Density Option	Select one of the following options, then type an appropriate number in **Probe Density Value.** • **Average Probe Spacing** – Defines the average distance (in bp) between the center points of the probes. Because of repeat regions, the actual spacing between probes may deviate from the ideal average probe spacing. • **Number of Probes per Sequence** – Defines the average number of probes designed for each target sequence. eArray uses this value to calculate average probe spacing on a per-sequence basis. The actual number of probes designed for each sequence may deviate from the specified value, because of repeat regions and rounding, but this deviation should not be large unless sequence length limits the design process. • **Total Number of Probes** – Defines the total probes generated, to be spaced evenly over all of the target sequences. eArray first calculates the number of probes to be generated for each sequence, and then uses these numbers to calculate average probe spacing.
Probe Density Value	Type the desired number of probes, or the desired probe spacing that applies to your selection in **Probe Density Option.**
Genome Details	
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Select this option to use a genome build that is available on the eArray Web site. • **User Defined Genome** – Select this option to use a genome build that has been previously uploaded to your server. To upload a genome build, see "To import a new genome" on page 66. In either case, the available genomes of the selected type appear in Species.
Species	Select the desired species. Only the species with genomes of the type that you selected in Type of Genome appear in the list.
Genome Build	Select the desired genome build. The genome build(s) that are available for your selected species appear in the list.

Parameter	Instructions/Details
Genomic Intervals	Type the genomic intervals to be tiled. Separate multiple intervals with pipe " | " characters. You can enter genomic intervals in several ways, illustrated in the following examples: • `chr1` (all of chromosome 1) • `chr1:1000` (chromosome 1, from base 1000 to the end) • `chr1:1000-5000` (chromosome 1, bases 1000 to 5000) Alternatively, you can upload a file that contains genomic intervals. The file must be a plain text file that contains one genomic interval per line. Follow these steps: **a** Click **Upload.** A File Upload dialog box appears. **b** Click **Browse.** An Open dialog box appears. **c** Select the file that contains the desired genomic intervals, then click **Open.** The name of the file appears in the File Upload dialog box, in File Name. **d** Click **Upload.** The genomic intervals from the file appear in Genomic Intervals, separated by pipe " | " characters. The intervals from the file replace any existing intervals. **Note**: You can use an Interval Finder search to define the genomic intervals that are associated with specific annotations. See "To do a Simple Interval Finder Search" on page 127 and "To do an Advanced Interval Finder Search" on page 129.
Skip repeat masked regions	Mark this option to ignore repeat regions within the selected genomic intervals during the tiling process.
Allow Probes to be Trimmed	This option lets the program trim probes to shorter than the size in Probe Length. This can yield tighter compliance with the desired T_M. The program will not trim probes to shorter than 45 bases.

Parameter	Instructions/Details
Preferred Probe Tm	(Available if you select Allow Probes to be Trimmed) Type the preferred probe T_M (in °C). The probe design algorithm trims probes so that they have a T_M close to the requested one. Set the Preferred Probe T_M to a temperature that is approximately 20°C higher than your intended hybridization temperature. The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms.
Avoid Restriction Sites	(Available for the CGH application type) Mark this option if you use the Agilent CGH enzymatic labeling protocol. This option avoids RsaI and AluI restriction enzyme recognition sites within the selected genomic intervals during the Genomic Tiling process. The CGH enzymatic labeling protocol uses these two enzymes. Because the target DNA is always cut at these sequences, probes that contain these sequences may not be able to hybridize effectively with the labeled DNA.

4 Click **Submit.**

One of the following occurs:

- For tiling of a user-defined genome, the program begins the Genomic Tiling job on your server.
- For tiling of an Agilent-provided genome, the program submits the Genomic Tiling job to the eArray Web site, through your server.

A dialog box tells you that your Genomic Tiling job has been submitted.

5 Click **OK.**

The Genomic Tiling job can take up to one day or more to finish, especially if you have selected to tile an Agilent-provided genome on the eArray Web site. You can monitor the status of the job in the Tasks pane of the Navigator. See "To check the status of a probe design or tiling job" on page 180.

To check the status of a probe design or tiling job

After you submit a GE Probe Design, Simple Tiling, or Genomic Tiling job, you can monitor its status and take action on it.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the **Tasks** pane of the Navigator, expand folders until you can see the name of the desired job.

Next to the name of the desired job, one of these status icons appears:

Status	Comments
	**Pending** – The job has been submitted, but no action has been taken on it yet.
	**Processing** – The job is being processed.
	**Complete** – The job is finished. You can now view, download, or delete the results of the job. You can also create a new probe group based on these results.
	**Error** – An error occurred. You must re-submit the job. Some possible causes for errors include: • No valid genomic intervals were specified for a tiling job • Uploaded sequence files contain errors

You can take action on a probe design or tiling job with a status of Completed  :

- You can delete the results of a job. See "To delete a probe design or tiling job" on page 183.
- You can also view and download the design or tiling results, and create a probe group from them. See these topics:

  "To view the results of a probe design or tiling job" on page 181

  "To create a probe group from probe design or tiling results" on page 181

  "To download probe design or tiling results" on page 182.

To view the results of a probe design or tiling job

After a GE Probe Design, Simple Tiling, or Genomic Tiling job has a status of Complete, you can view the results.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Design** folder.

3 Right-click the name of the desired job, then click **View Result.**

The Design Results dialog box appears. Several different results are available in separate tabs. See "Design Results (Gene Expression Probe Design)" on page 700 or "Design Results (Genomic Tiling)" on page 706.

To create a probe group from probe design or tiling results

After a GE Probe Design, Simple Tiling, or Genomic Tiling job has a status of Complete, you can create *one* new probe group from the results. If you need to create more than one copy or version of this probe group, see "To copy a probe group" on page 230.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Design** folder.

3 Right-click the name of the desired job, then click **Create Probe Group.**

The program creates a probe group with the same name as the GE Probe Design or Tiling job, and saves it in your main folder. A dialog box tells you that your Probe Group Creation job has been submitted.

4 Click **OK.**

To download probe design or tiling results

After a GE Probe Design, Simple Tiling, or Genomic Tiling job has a status of Complete, you can download the results.

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Design** or the appropriate **Tiling** folder.

3 Right-click the name of the desired job, then click **Download.**

The program downloads a *.zip file that contains the file(s) indicated in the table below. In general, you can open these files with a spreadsheet program.

File	Comments
Simple Tiling	
Tiling_fate	General information about each of the input intervals, including the number of probes created from each.
Tiling_sum	General statistics about the number of input targets, the number of probes generated, and the length of the generated probes.
Tiling_tdt	For each probe generated, lists the target from which the probe was derived, the position of the probe within the target, and the nucleotide sequence of the probe.
Genomic Tiling	
Tiling_bed	A BED format track file that you can use to view the tiling results in a compatible genome browser.
Tiling_fate	General information about each of the input intervals, including the number of probes created from each.
Tiling_sum	General statistics about the number of input targets, the number of probes generated, and the length of the generated probes.
Tiling_tdt	For each probe generated, lists the target from which the probe was derived, the position of the probe within the target, and the nucleotide sequence of the probe.

File	Comments
GE Probe Design	
MOST_cluster	Names of the target and transcriptome sequences used in the GE Probe Design process, and the cluster to which each belongs.
MOST_fate	List of the target sequences used in the GE Probe Design process, with information on which ones produced probes, and which did not.
MOST_sum	Information of an overall nature about the set of probes produced by the GE Probe Design process, including statistics on length, base composition, melting temperatures, and hybridization.
MOST_tdt	List of the probes generated by the GE Probe Design process, with specific information about each probe.

To delete a probe design or tiling job

You can delete a GE Probe Design, Simple Tiling, or Genomic Tiling job with a status of Complete .

1 Set the application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Design** folder.

3 Right-click the name of the desired job, then click **Delete.**

A dialog box asks if you are sure that you want to delete the job.

CAUTION When you delete a job, the program removes the job details and any results and uploaded files from the system. To restore the job, you must submit a new one.

The program does not delete the probe group that you may have created from the job results.

4 Click **Yes.**

Using Biological Networks to Find or Create Probes or Baits

Biological networks, also called **pathways,** document the relationships among the diverse components that are part of specific biological processes. These components include genes, gene products, metabolites, and cellular structures such as organelles and membranes.

eArray$_{XD}$ lets you use a biological network as the basis for a probe search, or for the design of new probes. For the SureSelect Target Enrichment application type, you can use a biological network as the basis for a bait search, or for the design of new baits. To define the network of interest, you can search for existing networks, and you can also use the results of a literature search to construct a custom network. See these topics:

- "To search for biological networks" on page 185
- "To use a literature search to create a custom network" on page 186

Once you define the network of interest, you can view a diagram of it and get more information about specific components, or **nodes,** in the network. After you select a set of nodes, you can use the names of the nodes, or the genomic intervals that are associated with them, to search for or to design new probes or baits. See these topics:

- "To view a biological network" on page 191
- "To use a biological network to find or create probes" on page 193

The program also lets you save networks. You can save the networks that you retrieve in a Network Search in **My Favorites**. My Favorites is an internal list of networks that you can search with a Network Search. You can also save literature searches, including the custom network that the program creates from the analysis of the search results. Saved literature searches appear in the **My Networks** pane of the Navigator. See these topics:

- "To add a network to My Favorites" on page 197
- "To remove a network from My Favorites" on page 198
- "To save a literature search" on page 199
- "To load a saved literature search" on page 199
- "To delete a saved literature search" on page 200

To search for biological networks

A network search, also called a pathway search, returns a list of biological networks that match search criteria that you enter.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under Search, click **Network Search.**

A search pane appears. See "Network Search" on page 553.

3 Enter the following search criteria:

Criterion	Instructions/Details
Source	Select one of these options: • **My Favorites** – Searches for biological networks from those that you have previously selected as "My Favorites." See "To add a network to My Favorites" **on page 197**. • **WikiPathways** – Searches for biological networks from the WikiPathways Web site. This site contains a database of biological networks that relies on the biological community for content and peer review. For more information, go to wikipathways.org.
Species	Select the desired species. The list contains the species that are represented in the WikiPathways database. To search for biological networks without regard to species, select **All Organisms.**
Search Terms	The program supports text string searches. Type one or more search terms in the box, separated by spaces. To return a network, the search term must exactly match a complete word in the given WikiPathways page. You can use an asterisk (*) as a "wild card" to represent an unspecified group of characters. If you enter multiple search terms, the program searches each term independently, and returns the networks that match each individual term.

4 Click **Search.**

The networks that meet your search criteria appear in the Search Result pane. You can view any of the returned networks and use it as the basis for a probe or bait search, or for probe or bait design. See "To use a biological network to find or create probes" on page 193.

If specific networks will be useful to you in the future, you can mark them as "favorites." See "To add a network to My Favorites" on page 197.

To use a literature search to create a custom network

A literature search uses one or more Web-based search engines to retrieve abstracts from the biomedical literature that meet the criteria that you enter. The program then examines each sentence in the retrieved abstracts for known terms. It uses these terms to create **associations** among the terms in a given sentence, and converts the associations into **interactions** that define the **nodes** (components) and **edges** (connections) of a custom network. Later, you can use the custom network to search for or design probes (or baits for SureSelect Target Enrichment libraries).

The program uses two collections of known terms, called **lexicons,** to identify meaningful terms in the sentences. The **concept lexicon** contains terms that are associated with entities such as genes and gene products. Concept lexicons are available for many different species. The **interaction lexicon** contains terms that define relationships between molecules, such as protein-protein interactions. Examples of these terms include *enhances, binds, increases, requires, up-regulates,* and the like.

1 Set the desired application type. Literature Search is available for all application types in eArray$_{XD}$. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Literature Search.**

   The Literature Search dialog box appears. See "Literature Search" on page 803.

   By default, the program uses the PubMed Web site as the search engine for the literature search. You can use other search engines instead of or in addition to the PubMed Web site. To change the search engine setting, follow these steps:

   a In the Literature Search dialog box, click **View > Engine Selection(s).**

      A dialog box appears with a list of available search engines.

b Mark one or more of these options:

Search engine	Description
PubMed	(This option is selected by default) Index of life sciences citations maintained by the U.S. National Library of Medicine at the National Institutes of Health. For more information, go to ncbi.nlm.nih.gov/pubmed/.
OMIM	**Online Mendelian Inheritance in Man** – Database of human genes and genetic phenotypes maintained by the McKusick-Nathans Institute of Genetic Medicine at the Johns Hopkins Universtiy School of Medicine. For more information, go to ncbi.nlm.nih.gov/omim.
USPTO	**United States Patent and Trademark Office** – Database of patents and published patent applications. For more information, go to uspto.gov.

c Close the Search Engine Selection dialog box.

3 In the Literature Search dialog box, enter these search parameters:

Parameter	Instructions/Details
Terms	In a typical literature search, these terms are biomolecules such as genes and gene products. Also, you can automatically include alternate names for each term that you enter. See *Use Aliases,* below. • Type the desired search terms. Press **return** after you type each term, so each term appears on a separate line.
Context	Context terms are terms that must appear in an abstract, in addition to the entries under Terms, for the program to return the given abstract. Context terms include, for example, names of diseases or therapeutic drugs. You can add the current species of interest to the list of context terms. See *Concept Lexicon Restricts Search,* below. • Type the desired context terms. Press **return** after you type each term, so each term appears on a separate line. **Note:** To use context term(s) in the literature search, be sure to mark **Use Context,** under Search Controls.

Parameter	Instructions/Details
Search Controls	
Max Engine Matches	This value defines the maximum number of abstracts that can be returned by each selected search engine for each query line. • Enter the desired value. The default value for this parameter is 10 abstracts, which is a good starting point for literature searches that balances comprehensive coverage of interactions with the creation of a custom network of manageable size. **Note:** The program also limits the total number of abstracts that can be returned for all queries from a given search engine during a literature search. For PubMed searches, this limit is 1,000 abstracts. For OMIM and USPTO searches, this limit is 100 abstracts.
Use Aliases	Aliases are alternate names for terms that you enter under Terms. The program uses the concept lexicon for the selected species to find aliases. • To automatically include aliases (if any) for the terms that you enter under Terms, mark this option.
Use Context	• To ignore any terms under Context in the literature search, clear this option.
Concept Lexicon Restricts Search	By default, literature searches include as a context term the name of the species that is selected for the concept lexicon. • To remove the species name of the concept lexicon as a context term in the literature search, clear this option.

Parameter	Instructions/Details
Extraction Controls	
Concept Lexicon	By default, literature searches use the human concept lexicon to identify meaningful terms for biomolecules such as genes and gene products. • To select the concept lexicon for a different species for the literature search, select the desired species from the list.
Interaction Lexicon	This parameter lets you set the stringency with which interactions are created from the sentences of retrieved abstracts. Interaction lexicons are lists of terms (verbs) that describe molecular interactions. Select one of these options: • **empty** – The interaction lexicon contains no terms. The program returns interactions without regard to the presence of terms that describe interactions. This is the least stringent setting, and returns interaction(s) for every sentence that contains at least two terms from the concept lexicon. • **limited** – (This is the default, most stringent setting) This interaction lexicon contains a subset of the terms found in the relaxed interaction lexicon. The program returns interaction(s) for a sentence if it contains at least one term from this lexicon, and two terms from the concept lexicon. • **relaxed** – This interaction lexicon contains a larger number of terms than does the limited interaction lexicon. The program returns interaction(s) for a sentence if it contains at least one term from this lexicon, and two terms from the concept lexicon.

4 Under **Query Editor,** edit each query line as desired. Each line is the exact text that the program submits to the selected search engine(s).

5 Click  .

The search starts. You can monitor and control the search as it occurs, and take further action. Use the following as a guide:

Task	Instructions
Temporarily pause the search	• Click  . To resume the search, click  .
Stop the search	• Click  . After you stop a search, any retrieved results remain available. However, you cannot resume or complete the search.

Task	Instructions
Monitor the progress of the search	• View the status messages and the progress bar that can appear at the bottom of the Literature Search dialog box.
View the search results	• Under Query Matches, view the list of results. Each result includes a citation and a URL for the returned literature reference, and can also include the first sentence of the abstract. To go to a different page of results, use the **Page** buttons at the bottom of the pane. All tabs of the Query Matches pane can contain citations: ◦ **Completed** – Citations for abstracts that were retrieved and analyzed for interactions. ◦ **Unanalyzed** – (Can be available if you pause or stop a search) Citations for abstracts that were retrieved, but were not analyzed for interactions. ◦ **Unread** – (Can be available if you pause or stop a search) Citations for abstracts that were have yet to be retrieved.
View the abstract associated with a citation	• Under Query Matches, click the desired citation. The abstract opens in your Web browser.
Remove a citation from the Query Matches pane	• Right-click the citation, then click **Delete Match.** **Note:** To restore a deleted citation, you must do a new literature search.
Reanalyze retrieved abstracts	Once a literature search is complete, you can change analysis settings, such as the interaction lexicon setting, or search terms. The program can then reanalyze the previously retrieved abstracts and build a network based on the new settings. This process takes much less time than a new literature search. • (Available after a literature search is complete) Click **Reanalyze.**

When the search is complete, and the program has analyzed the sentences in all returned abstracts and constructed the custom network, the Literature Network Inspector appears. You can use the Literature Network Inspector to view the network, get further information, and use the network to search for probes or to design new probes. See these topics:

• "To view a biological network" on page 191
• "To use a biological network to find or create probes" on page 193
• "To save a literature search" on page 199

- "Literature Network Inspector" on page 794
- "Literature Search" on page 803

To view a biological network

After you search for biological networks, or use a literature search to create a custom network, you can view the desired network in the Network Inspector.

1 Do one of the following:

- Do a search for biological networks. In the Search Result pane, in the Actions column, in the row of the desired network, click  . See "To search for biological networks" on page 185. The network of interest appears in the Network Inspector. See "Network Inspector" on page 815.
- Use a literature search to create a custom network. See "To use a literature search to create a custom network" on page 186. The network appears in the Literature Network Inspector. See "Literature Network Inspector" on page 794.
- Load a saved literature search. See "To load a saved literature search" on page 199.

2 In the Network Inspector or the Literature Network Inspector, do any of these tasks:

Task	Instructions/Details
Pan the network	In the Bird's Eye View pane, drag the purple rectangle to the desired location. If your mouse has three buttons, you can also pan the network in Network View. Hold down the middle mouse button, and drag the pointer in the desired direction.
Zoom in or zoom out the network	In Network View, hold down the right mouse button, and drag the pointer up (to zoom in) or down (to zoom out).
Get more information about a specific node	**a** Right-click the node, then click **LinkOut.** A list of databases appears. **b** Select the desired database. The program passes the node to the selected database as a search term. The search results appear in your Web browser.

Task	Instructions/Details
Find the most highly connected nodes in the network ("hubs")	Hubs are nodes in the network that have at least a minimum number of neighbors. The minimum number of neighbors is set so that less than 25% of nodes in the network are hubs. This number varies for different networks. • Right-click a node in the network, then click **Show Hubs.** The program displays the hubs in the Selected Nodes pane, and highlights them in Network View.
View and save the sentences that are related to a node	(Literature Network Search pane only) You can view the sentences from the literature from which the interaction(s) with a given node were derived. You can also save a file that contains the sentences, and view the entire abstract that is the source of each sentence. **a** Right-click the desired node, then click **Show Sentences.** The Agilent Literature Search Sentences dialog box appears, with a list of the sentences from the literature from which interactions with the node were derived. See "Agilent Literature Search Sentences" on page 581. **b** Do any of the following: ◦ To view the sentence in the context of its source abstract, click the sentence. In your Web browser, the associated citation opens in the appropriate search engine. ◦ To save a file that contains the sentences, click **Save.** In the dialog box that appears, select a location for the file, then click **Save.** The program saves an HTML file to the selected location. If you open the file in your Web browser, each sentence appears as a link that opens the associated citation in the appropriate search engine. **Note:** When you use the procedure above, the program also displays the sentences that are related to any nodes that are selected nodes. Selected nodes appear in yellow. For information on how to select nodes, see "To use a biological network to find or create probes" on page 193.

To use a biological network to find or create probes

After you do a search for a biological network, or use a literature search to create a custom network, you can use the network to supply terms for a probe search or to supply design parameters for a probe design job.

1 Do one of the following:

- Do a search for biological networks. In the Search Result pane, in the Actions column, in the row of the desired network, click  . See "To search for biological networks" on page 185. The network of interest appears in the Network Inspector. See "Network Inspector" on page 815.
- Use a literature search to create a custom network. See "To use a literature search to create a custom network" on page 186. The network appears in the Literature Network Inspector. See "Literature Network Inspector" on page 794.
- Load a saved literature search. See "To load a saved literature search" on page 199.

2 Select the desired nodes. Use the following as a guide:

Task	Instructions/Details
Select a specific node	In Network View, click the node. Only the network elements that appear in a box can be selected.
Select additional nodes	In Network View, shift-click each of the additional nodes. You can also drag-enclose a group of nodes to select them.
Select all nodes	In Network View, right-click any node, then click **Select All.**
Deselect a node	Shift-click the node. To clear all of your selections, click a blank area of Network View.
Pan the network	In the Bird's Eye View pane, drag the purple rectangle to the desired location. If your mouse has three buttons, you can also pan the network in Network View. Hold down the middle mouse button, and drag the pointer in the desired direction.
Select nodes from the network based on a search	In the Search Network pane, in Search Term, type a search term in the box, then click **Search Network.** Type a single search term. You can use asterisks (*) as "wildcards" to represent unspecified characters.

Task	Instructions/Details
Zoom in or zoom out the network	In network view, hold down the right mouse button, and drag the pointer up (to zoom in) or down (to zoom out).
Get more information about a specific node	**a** Right-click the node, then click **LinkOut.** A list of databases appears. **b** Select the desired database. The program passes the node to the selected database as a search term. The search results appear in your Web browser.
Select the neighbors of specific nodes	A neighbor node is one that is directly connected to your node(s) of interest in the network. **a** Select the desired node(s). **b** Right-click one of the selected nodes, then click **Show Neighbors.** The program adds the neighbors to the list of selected nodes, and highlights them in Network View. You can use neighbor nodes to define the probes for your next microarray design in a series of experiments. For example, in the context of drug discovery or disease, a network can form the basis of an hypothesis about a disease process: • If one microarray study shows a subset of genes to be differentially regulated, you can further study the behavior of other genes that are known to be connected, in networks, to the first set of regulated genes. • If the expression levels of these other genes increases and decreases in concert with the first set of genes, they might be part of the same process.
Select the most highly connected nodes in the network ("hubs")	Hubs are nodes in the network that have at least a minimum number of neighbors. The minimum number of neighbors is set so that less than 25% of nodes in the network are hubs. This number varies for different networks. • Right-click a node in the network, then click **Show Hubs.** The program displays the hubs in the Selected Nodes pane, and highlights them in Network View.
Select the node(s) that have names that match one of your original search terms	• In Network View, right-click a node, then click **Show Query.** The program selects and highlights the nodes that have a name that matches one of your original search terms.

Task	Instructions/Details
Select the node(s) that were derived form a specific abstract	(Literature Network Search pane only) **a** Click the title bar of the Literature Search dialog box. The dialog box becomes active. **b** In the Query Matches pane, next to the desired abstract, click  . This icon appears next to a reference only if the reference produced interaction(s). In the Literature Network Search pane, the program selects and highlights the nodes that were derived from the abstract.
View the specific sentence(s) that contained the name of a specific node	(Literature Network Search pane only) • In Network View, right-click the desired node, then click Show Sentences. The Agilent Literature Search Sentences dialog box appears. See "Agilent Literature Search Sentences" on page 581.

The selected nodes appear in the Selected Nodes pane. Also, when you select a node, it turns yellow.

3 In the Selected Nodes pane, do one of the following tasks:

Task	Instructions/Details
Download the list of nodes	• Click **Download Gene List.** The program downloads a text file that contains one node per line. **Note:** All nodes appear in the file, even if they are not genes.
Search for probes	(CGH, ChIP, CH3, and Expression application types) • Click **Search Probes.** The program transfers the names of all selected nodes to the Probe Search pane. It also sets the species. See "To use the Probe Search tool to find probes" on page 92.

Task	Instructions/Details
Set up a Gene Expression Probe Design Job	(Expression application type) **a** Click **Design Probes.** The Design Probes dialog box appears. **b** Select **Base Composition Methodology** or **Tm Matching Methodology.** For information about these options, and about Gene Expression probe design, see "To set up a GE Probe Design job" on page 167. The appropriate Create Probes dialog box appears. The program saves the names of all of the selected nodes as a file. In Target File Format, the program selects GenBank Accessions. It also displays the location of the file in Select Target File, and selects the appropriate species in both Species and in Species of Transcriptome. **c** Enter the other parameters for a Gene Expression Probe Design job, then click **Submit.**
Use Genomic Tiling to create probes, or use an HD Probe Search to retrieve probes	(CGH, ChIP-on-chip, and CH3 application types) **a** Click **Tile Probes from Interval Finder.** The Advanced Interval Finder pane appears. See "Advanced Interval Finder" on page 531 and "To do an Advanced Interval Finder Search" on page 129. The program enters the names of the selected nodes as search terms in Gene Symbol. The program also selects the relevant species. **b** Click **Search.** In the Search Result pane, the program displays the genomic intervals that match the search terms. **c** Do one of the following • To use Genomic Tiling to create probes – Download the intervals, then use the downloaded file to set up a Genomic Tiling job. See "To set up a Genomic Tiling job" on page 176. • To use an HD Probe Search to retrieve probes – Click **Run HD Search.** See "To do a Simple Genomic Intervals HD Search for probes" on page 111.
Search for baits	(SureSelect Target Enrichment application type) • Click **Search Baits.** The program transfers the names of all selected nodes to the Bait Search pane. It also sets the species. See "To search for baits" on page 358.

Task	Instructions/Details
Set up a Bait Tiling job through the Advanced Interval Finder	(SureSelect Target Enrichment application type) **a** Click **Tile Baits from Interval Finder.** The Advanced Interval Finder pane appears. See "Advanced Interval Finder" on page 531 and "To do an Advanced Interval Finder Search" on page 364. The program enters the names of the selected nodes as search terms in Gene Symbol. The program also selects the relevant species. **b** Click **Search.** In the Search Result pane, the program displays the genomic intervals that match the search terms. **c** Select the desired intervals, then click **Run Bait Tiling.**
Set up a Bait Tiling job through the Advanced Exon Interval Finder	(SureSelect Target Enrichment application type) **a** Click **Tile Baits from Exon Finder.** The Advanced Exon Interval Finder pane appears. See "To do an Advanced Interval Finder Search" on page 364 and "Advanced Exon Interval Finder" on page 525. The program enters the names of the selected nodes as search terms in Gene Symbol. The program also selects the relevant species. **b** Click **Search.** In the Search Result pane, the program displays the exons genomic intervals that match the search terms. **c** Select the desired intervals, then click **Run Bait Tiling.**
Get more information about a specific selected node	(Network Search only) • In the Database Reference column, click a link, if one is available.

To add a network to My Favorites

When you use a Network Search to retrieve biological networks, you can add any of them to My Favorites. My Favorites is a list of networks that you select for later action. It is kept internally by the program, and is not application type-specific.

1 Do a Network Search. In Source, select **WikiPathways.** See "To use a biological network to find or create probes" on page 193.

2 In the Search Result pane, select the items that you want to add to My Favorites. Use the following as a guide:

- To select an item, mark the check box next to its name.
- To select all of the networks on the current page of results, mark the check box in the column heading row.
- To go to a different page of search results, if available, click a numbered page button. The program remembers your selections as you go from page to page.

3 Click **Add to My Favorites.**

A dialog box tells you that the selected network(s) were successfully added to My Favorites.

4 Click **OK.**

NOTE

- You can also add a network to My Favorites when you view it. This lets you inspect the network before you add it to My Favorites. When you view the network in the Network Inspector, click **Add to My Favorites.**
- You use a different method to save a network that you create through a literature search. See "To save a literature search" on page 199.

To remove a network from My Favorites

My Favorites is a list of biological networks that you select for later action. It is kept internally by the program, and is not application type-specific. See "To add a network to My Favorites" on page 197. You can remove a network from My Favorites.

1 Do a Network Search. In Source, select **My Favorites.** See "To use a biological network to find or create probes" on page 193.

2 In the Search Result pane, select the items that you want to remove from My Favorites. Use the following as a guide:

- To select an item, mark the check box next to its name.
- To select all of the networks on the current page of results, mark the check box in the column heading row.
- To go to a different page of search results, if available, click a numbered page button. The program remembers your selections as you go from page to page.

3 Click **Remove from My Favorites.**

A dialog box tells you that the selected network(s) were successfully removed from My Favorites.

4 Click **OK.**

To save a literature search

You can save the search terms, settings, and returned citations from a literature search. When you save a literature search, you also save the network that the program created from the analysis of the text in the returned abstracts. Saved literature searches appear in the My Networks pane of the Navigator. See "Navigator – My Networks pane" on page 496.

1 Do a literature search. See "To use a literature search to create a custom network" on page 186.

2 In the Literature Network Search dialog box, click **Save.**

A dialog box appears.

3 In the box, type a name for the search, then click **OK.**

The search appears in the My Networks pane of the Navigator. A dialog box tells you that the search result was successfully saved.

4 Click **OK.**

NOTE The saved literature searches in the My Networks pane are all available in every application type that is supported in Agilent Genomic Workbench.

To load a saved literature search

After you save a literature search (see "To save a literature search" on page 199), you can load the search at any time. This lets you view the literature search settings, the citations for the returned abstracts, and the custom network that the program created from the analysis of the returned abstracts.

You can make changes to the search, and either resubmit the search or reanalyze the retrieved abstracts. You can also use the custom network to find or create probes for a microarray design.

- In the My Networks pane of the Navigator, right-click the name of desired literature search, then click **Load.**

The Literature Search dialog box and the Literature Network Inspector appear with the saved literature search and the custom network that the program created from the analysis of the search results. See "Literature Search" on page 803 and "Literature Network Inspector" on page 794.

To resubmit the search, or to reanalyze the abstracts that were retrieved by the search, see "To use a literature search to create a custom network" on page 186.

To use the custom network to find or create probes, see "To use a biological network to find or create probes" on page 193.

To delete a saved literature search

You can delete any saved literature search from the My Networks pane.

CAUTION When you delete a literature search from the My Networks pane, the program permanently removes all of the associated search settings and retrieved abstracts. It also removes the custom network that was created from the analysis of the retrieved abstracts. To restore these items, you must set up and submit the search again.

- In the My Networks pane of the Navigator, right-click the name of the desired saved literature search, then click **Delete.**

  A dialog box tells you that the selected network was successfully removed from the list.

Viewing, Managing, and Evaluating Probes

After you retrieve probes with a probe search, create probes, or upload them, you can take action on them. See the table below.

Action	Details
View probes	Lets you view probes in two general ways: • **As a list** – You can view a list of probes, and get details about the them, including their sequences, names, and annotation. See "To view probe sequences and statistics" on page 202. • **Graphically** – You can view the locations of specific probes within the context of the genome of your species of interest. This option uses the genomic viewer that is built into Agilent Genomic Workbench. See "To plot the genomic locations of probes" on page 203.
Create a probe group	Lets you create a new probe group based on the results of a search, upload, probe design job, or tiling job. See "To create a new probe group" on page 204.
Download probes	Lets you save probe sequences, IDs, and annotation to a location that you select. Several file formats are available. See "To download probes" on page 206.
Check GE probe quality	(Available for the Expression application type) Lets you evaluate the quality of gene expression probes, to see if they will work on the Agilent platform. See "To check GE probe quality" on page 208.
Calculate Probe Performance Scores	(Available for the CGH, ChIP-on-chip, and CH3 application types) Calculates performance scores for non-Agilent probes in a probe group that you select. These scores indicate how likely it is that a probe will produce a good log ratio response on the Agilent microarray platform. See "To calculate probe performance scores" on page 214.
Delete probes	Lets you permanently remove specific probes from the probe database on your server. See "To delete probes" on page 218.

NOTE

To work with the probes of your workgroup that are stored on the eArray Web site, you must first transfer the probe and annotation data. Some limitations apply. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To view probe sequences and statistics

When you search for probes, the search results list the probes that match your search criteria, along with their associated accession and annotation data. You can also view the sequences of the returned probes. If you have retrieved Expression type probes, you can also view the results of statistical calculations based on the base composition of the probes.

1 Search for probes. See "Searching for Probes" on page 92.

2 In the Search Results pane, select the probes of interest. Follow these guidelines:

- To select an individual probe, mark the check box next to its Probe ID.
- To select all of the probes in the search results, mark **Select entire data set.**
- To select all of the probes on the current page, mark the check box in the column heading row.
- To select probes on more than one page, just select the probes on the desired pages. The program remembers your selections as you go from page to page.

3 Click **Show Statistics.**

The Probe Statistics dialog box opens. It lists the Probe ID and sequence of each selected probe. For Expression type probes, additional calculated statistics appear. See "Probe Statistics" on page 829.

You can change the width of individual columns, or the width of the entire dialog box. Drag the desired border between columns, or the side or bottom edges of the dialog box.

NOTE

- A separate topic describes how to view the probes in the search results of a high density (HD) search. See "To view HD probe search results" on page 134.
- This feature is not available for the microRNA application type. To view the sequences of microRNA probes, download the probes in TDT, COMPLETE, or MINIMAL format, then use a spreadsheet program to view the downloaded file. See "To download probes" on page 206.
- You can view the annotation of SNP probes, but you cannot view their sequences or statistics.
- To work with the probes of your workgroup that are stored on the eArray Web site, you must first transfer the probe and annotation data. Some limitations apply. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To plot the genomic locations of probes

You can view the locations of probes in the context of their associated genome. This feature is available for the CGH, ChIP-on-chip, and CH3 application types. To plot the locations of HD or SNP probes, see "To view the probes in a probe group graphically" on page 229.

1. Search for probes. See "Searching for Probes" on page 92.
2. In the Search Results pane, select the probes of interest. Use the following as a guide:
   - To select an individual probe, mark the check box next to its Probe ID.
   - To select all of the probes in the search results, mark **Select entire data set.**
   - To select all of the probes on the current page, mark the check box in the column heading row.
   - To select probes on more than one page, just select the probes on the desired pages. The program remembers your selections as you go from page to page.
3. Click the **Genomic Viewer** button.

   The probes appear in red in Genome, Chromosome, and Gene views. See Figure 10 on page 204. For more information on how to use the Genomic Viewer, see the *Data Viewing User Guide*.

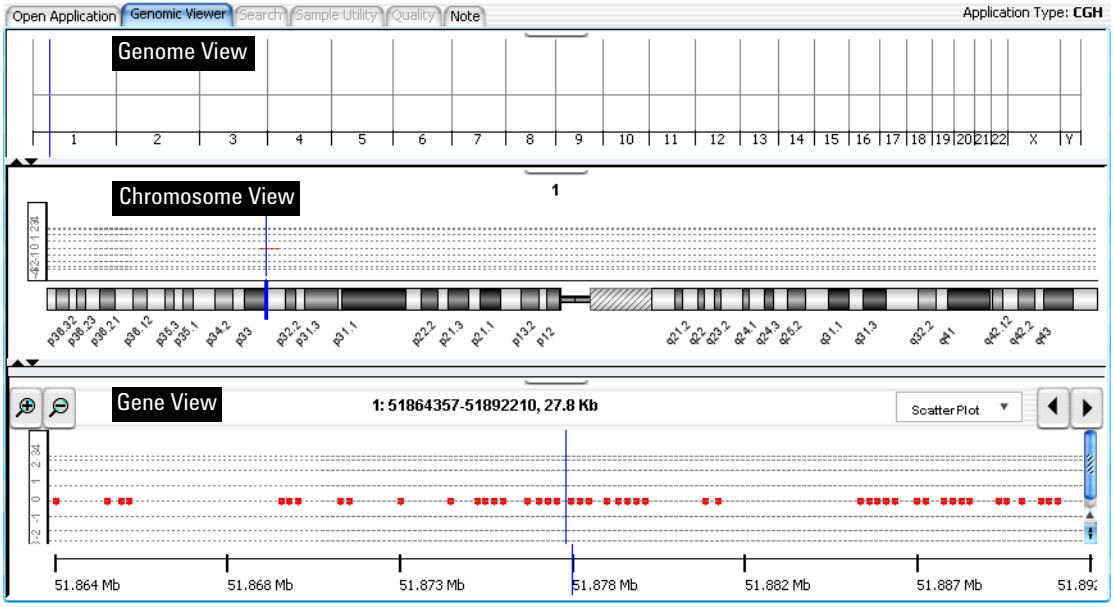


Figure 10 Genomic Viewer, with probes (in red) associated with human chromosome 1. The vertical blue bar in each view is the **cursor,** whose genomic location is the same in all three views.

To create a new probe group

A probe group is an organizational unit that contains links to one or more probes. You use probe groups as the building blocks of microarray designs. This topic describes how to use the results of a probe search to create a new probe group.

1 Search for the desired probes. See "Searching for Probes" on page 92.

2 In the Search Result pane, select the probes of interest. Follow these guidelines:

- To select an individual probe, mark the check box next to its Probe ID.
- To select all of the probes in the search results, mark **Select Entire Data.**
- To select all of the probes on the current page, mark the check box in the column heading row.

- To go to a different page of the search results, click the numbered page buttons above or below the list of probes. The program remembers your selections as you go from page to page.
- For the microRNA application type, probes are grouped by the microRNA to which they bind. You select these groups of probes by microRNA name, instead of selecting individual probes.

3 Click **Create Probe Group.**

The Probe Group dialog box appears. See "Create Probe Group" on page 678. The selected probes appear in the Search Result pane. For the microRNA application type, probes are grouped by the microRNA to which they bind.

4 At the top of the dialog box, set the following properties. All properties are required unless otherwise indicated. The properties that do not appear below are set by the system, and are read-only.

Property	Instructions/Details
Probe Group Name	Type a name for the probe group. eArray uses this name to reference the probe group in search results, probe group lists, view pages, and the like. Use only letters, numbers, underscores, and spaces.
Folder	Select the desired location for the new probe group. Only the folders to which you have access appear in the list.
Status	Select either **Incomplete** or **Locked.** By default, eArray creates the new probe group with a status of Incomplete. If you set the status to Locked, you will not be able to further edit the probe group.
Description	(Optional) Type a brief description of up to 4,000 characters.
Keywords	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. You can type up to 4,000 characters.

5 Do any of the following:

- To add additional probes to the probe group, click **Add New Probes.** For details, see "To add probes to a probe group" on page 236.
- To remove probes from the probe group, select the probes that you want to remove, then click **Remove Probes.** For details, see "To remove probes from a probe group" on page 237.

6 Click **Save Probe Group.**

A dialog box tells you that the probe group has been successfully created.

7 Click **OK.**

You can now use the probe group in a microarray design. See "To create a microarray design from existing probe groups (Wizard)" on page 269.

You can also create a new probe group in several other ways — see these topics:

- "To create a probe group from HD probe search results" on page 135
- "To create a probe group from SNP probe search results" on page 156
- "To create a probe group with uploaded probes" on page 165
- "To create a probe group from probe design or tiling results" on page 181

NOTE

- For the microRNA application type, probes are grouped by the microRNA to which they bind. When you add or remove probes from a probe group for this application type, you add or remove all of the probes that are associated with a given microRNA.
- To work with the probes of your workgroup that are stored on the eArray Web site, you must first transfer the probe and annotation data. Some limitations apply. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To download probes

After you do a search for probes, you can download selected probes in the search results in one of several different file formats.

1 Search for the desired probes. See "To use the Probe Search tool to find probes" on page 92.

2 In the Search Result pane, select the probes of interest. Follow these guidelines:

- To select an individual probe, mark the check box next to its Probe ID.
- To select all of the probes in the search results, mark **Select entire data set.**
- To select all of the probes on the current page, mark the check box in the column heading row.

- To select probes on more than one page, just select the probes on the desired pages. The program remembers your selections as you go from page to page.

3 Click **Download.**

The Download Probes dialog box appears.

4 Select one these types of files to download:

- **TDT** – Tab-delimited text file that contains the probe attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the probe attributes indicated in the table below.
- **COMPLETE** – Tab-delimited text file that contains the probe attributes indicated in the table below.
- **MINIMAL** – Tab-delimited text file that contains the probe attributes indicated in the table below.

Attribute	TDT	FASTA	COMPLETE	MINIMAL
ProbeID	•	•	•	•
Sequence	•	•	•	•
TargetID	•		•	
Species	•			
GeneName	•			
GeneSymbol	•		•	
Description	•		•	
ControlType	•			
Accessions	•		•	
ProbeGroups	•			
Status	•			
ValidationMethod	•			
Chromosomal Locations	•		•	

Attribute	TDT	FASTA	COMPLETE	MINIMAL
Cytoband	•			
GOID	•			

• – Attribute included in file format

5 Click **Download.**

A dialog box appears.

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

The program downloads the probe file. A dialog box tells you that the probes have been downloaded successfully.

7 Click **OK.**

NOTE

- For microRNA microarrays, probes are grouped by the microRNA to which they are designed. One to four probes act in concert to measure a given microRNA. In downloaded files, each probe appears on a separate line, but the file lists the probes for a given microRNA on consecutive lines. The name of the microRNA to which each probe binds appears explicitly in the downloaded TDT and COMPLETE format files, in the TargetID column.
- The program also offers several other ways to download probes. See these topics:
  - "To download HD probes" on page 136
  - "To download the results of a SNP probe search job" on page 155
  - "To download probe design or tiling results" on page 182
  - "To download a probe group" on page 240
  - "To download microarray design files" on page 341
- To work with the probes of your workgroup that are stored on the eArray Web site, you must first transfer the probe and annotation data. Some limitations apply. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To check GE probe quality

If you have Expression type probes, especially ones that have been designed outside of eArray, you can use eArray$_{XD}$ to evaluate them to see if they will work on the Agilent platform, with Agilent protocols. The Probe Quality tool analyzes the probes in a probe group, or in an uploaded file. You can compare probes to a given transcriptome, and get an analysis of potential probe targets

and possible cross-hybridization problems. The tool also calculates statistics based on the base composition of the probes, and assigns a base composition score to each probe.

Before you check GE probe quality

- You must have a TDT or FASTA format file of probe sequences, or have a probe group stored on your server that contains the probes of interest. See "TDT files" on page 892 and "FASTA" on page 884. If you prepare a TDT file, use the Minimal format, *without* column headings. See "Minimal (for probes)" on page 890.
- (Optional) Prepare a FASTA format transcriptome file for eArray to use to evaluate potential targets and cross-hybridization problems. Note: Transcriptomes for many species are already available within eArray.

To check GE probe quality

1 Set the application type to **Expression.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Quality,** click **Probe.**

The Probe Quality dialog box appears.

3 Set the following parameters. All are required.

Parameter	Instructions/Details
Probe Details	
Job Name	Type a name that will help you to identify this job.
Species	Select a species. This is the species that is associated with the probes to be checked.

Parameter	Instructions/Details
Source of Probes (Select one of these options)	**Upload File** – Select this option to check the quality of the probes in a file that you upload. **a** In Select Probe File, click **Browse.** An Open dialog box appears. **b** Select the desired TDT or FASTA format probe file, then click **Open.** The location of the file appears in Select Probe File
	Select Probe Group – Select this option to check the quality of the probes in an existing probe group. This option is useful if you want to check the quality of probes that you have already uploaded. The program can check one probe group at a time. **a** In Select a Probe Group, click **Select and Add.** The Select and Add dialog box appears. See "Select and Add : Probe Group" on page 843. **b** In Probe Group, type a search term in the box, then click **Search.** To retrieve all probe groups available to you, leave the search term blank. **c** Select the desired probe group from the left pane of the dialog box. To select a probe group, click its name. **d** Click **Add.** The program transfers the selected probe group to the right pane. **e** Click **Done.** The name of the selected probe group appears in the Probe Quality dialog box, in Select a Probe Group. **Note:** To work with the probes of your workgroup that are stored on the eArray Web site, you must first transfer the probe and annotation data. Some limitations apply. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Parameter	Instructions/Details
Transcriptome Details	
Select Transcriptome (Select one of these options)	**None** – Select this option if you do not want to select a transcriptome. If you select this option, eArray checks only the base composition of your probes, and does not identify potential probe targets or cross-hybridizations.
	Agilent-provided Transcriptome – Select this option to use a pre-defined species transcriptome as a similarity database. Select this option if your target species is represented by one of the available transcriptomes. • Select the desired species from the list.
	Upload Transcriptome File – Select this option to use an uploaded transcriptome data file as a similarity database. **a** In Upload Transcriptome File, click **Browse.** A dialog box appears. **b** Select the desired FASTA format transcriptome file, then click **Open.** The name of the file appears in the Probe Quality dialog box, in Upload Transcriptome File.

4 Click **Submit.**

The program submits the Probe Quality job to the eArray Web site, through your server. A dialog box tells you that your job has been submitted.

5 Click **OK.**

In the Tasks pane of the Navigator, you can monitor the status of the job in the Probe Check folder. The icon next to the name of the job indicates its status:

Status	Comments
	Pending – The job has been submitted, but no action has been taken on it.
	Processing – The job is being processed.
	Complete – The job is finished. You can now view, download, or delete the results of the job. You can also create a new probe group based on these results.
	Error – An error occurred. You must re-submit the job.

To view the results of a GE Probe Check job

Once a GE Probe Check job has a status of Complete, you can view the results.

1. Set the application type to **Expression**. See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Check** folder.
3. Right-click the name of the desired job, then click **View Result.**

   The Design Results dialog box appears, with the analysis of your probes. For details about the metrics and statistics that appear in this dialog box, see "Design Results (Gene Expression Probe Check)" on page 696.

To download the results of a GE Probe Check job

Once a GE Probe Check job has a status of Complete, you can download the results.

1. Set the application type to **Expression**. See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Check** folder.
3. Right-click the name of the job, then click **Download.**

   A Save dialog box appears.
4. Select a location for the downloaded file, then click **Save.**

   The program downloads the probe check results as a *.zip file. A dialog box tells you that your file was downloaded successfully.
5. Click **OK.**

The downloaded *.zip file contains two TDT format files that you can view with a word processing or spreadsheet program:

File	Description
MOST_sum	Contains overall statistics on the set of probes that was submitted for analysis.
MOST_tdt	Lists the name and sequence of each probe that was submitted for analysis, and gives calculated statistics and metrics for each probe based on base composition.

The results that are available in these downloaded files are the same as the results that are described in "Design Results (Gene Expression Probe Design)" on page 700.

To create a probe group from a GE Probe Check job

Once a GE Probe Check job has a status of Complete, you can create a new probe group that contains the probes that were evaluated.

1 Set the application type to **Expression.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand the **Probe Check** folder.

3 Right-click the name of the job, then click **Create Probe Group.**

A dialog box tells you that your probe group creation job has been submitted.

4 Click **OK.**

You can monitor the status of the probe group creation job in the Tasks pane of the navigator, in the Probe Upload folder. These status icons can appear beside the name of the job:

Status	Comments
	Pending – The job has been submitted, but no action has been taken on it.
	Complete – The job is finished. The new probe group is now available in the Probe Group node of your main folder. The new probe group bears the name of the probe quality job.

To delete a GE Probe Quality job

Once a GE Probe Quality job has a status of Complete, and you no longer need the results, you can delete the job from the system.

1. In the eArray$_{XD}$ tab, in the Tasks pane of the Navigator, expand folders until you can see the name of the desired job. Probe Quality jobs are located in the **Probe Design** folder.
2. Right-click the name of the job, then click **Delete.**

   A dialog box asks if you are sure that you want to delete the job.

CAUTION When you delete the job, the system removes all associated results and uploaded data from the system. To restore the results, you must re-submit the job.

The program does not delete the probe group that you may have created from the job results.

3. Click **Yes.**

   A dialog box tells you that the job results were successfully deleted.
4. Click **OK.**

To calculate probe performance scores

If you have non-Agilent CGH, ChIP-on-chip, or CH3 probes, eArray$_{XD}$ can calculate probe performance scores for them. A probe performance score is a value between 0 and 1. The higher the score, the more likely it is that a probe will produce a good log ratio response when it is used in a CGH or ChIP microarray on the Agilent platform. In addition, the program supplies other analyses based on sequence.

The program stores probe performance scores with probes in the main probe database on your server. These scores are also included in the GEML file that you can download after you complete a microarray design. This lets you import the scores into DNA Analytics, and use them in downstream analyses to color-code or filter data values.

Before you set up a Probe Score job, you must be the owner of a probe group in eArray that contains the probes to be scored. The probe group must contain at least one non-Agilent probe.

Alternatively, prepare and upload a file that contains the probes to be scored. See "To upload probes and annotation" on page 161. Be sure to select the Create New Probe Group option when you set up the upload. The program must finish the upload of the file, and the creation of the probe group, before you can score the probes.

1 Set the application type to **CGH, ChIP-on-chip,** or **CH3.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Quality, click **Probe Score.**

The Score Custom Probes dialog box appears. See "Score Custom Probes" on page 835.

3 In the Job Detail pane, set these items:

Item	Details/Instructions
Job Name	Type a name for the Probe Score job. The program uses this name to refer to the job in job lists, notifications, and the like.
Species	Select the species associated with the probes that you want to score. Probe Score is available only for the species that appear in the list.
Probe Group	Select the probe group that contains the probes to be scored. To select a probe group, click **Select and Add.** For instructions on how to use the dialog box that appears, see "To select probe groups for searches or microarrays" on page 106.

4 Click **Submit.**

A dialog box tells you that the job was successfully submitted.

5 Click **OK.**

A new job appears in the Probe Score folder in the Tasks pane of the Navigator. To monitor the status of the job, observe the icon next to the name of the job. One of these icons appears:

Status	Comments
	**Pending** – The Probe Score job has been submitted to the upload queue.
	**Processing** – Your program is in the process of scoring the probes.

Status	Comments
	Complete – The Probe Score job is finished.
	Error – An error occurred. You must re-submit the Probe Score job. Make sure that the probe group that you submitted contains at least one non-Agilent probe.

After the job has a status of Completed, you can download and view the results. See "To download Probe Score results" on page 217.

NOTE

- Probe scores have already been calculated for Agilent CGH and ChIP-on-chip probes. To view these scores, view a probe group that contains the desired probes. See "To view a probe group" on page 228. Agilent probes have probe IDs with the format A_NN_PNNNNNNNN, where N is a digit. **Example: A_16_P35466372.**
- You cannot submit a SNP probe group to be scored. Also, although probe scores for SNP probes are used internally by the program, you cannot view or download these probe scores.

To view Probe Score results

After a Probe Score job has a status of Complete , you can view the probe scores that were calculated for the probes that you submitted.

1. In the eArray$_{XD}$ tab, set the Application Type to **CGH, ChIP-on-chip,** or **CH3.** See "To set the application type" on page 48.
2. In the Tasks pane of the Navigator, in the **Probe Score** folder, right-click the name of the desired job, then click **View Probe Group.**

   The View Probe Group dialog box appears. See "View Probe Group" on page 873. In the Search Result pane, the calculated probe score for each probe appears in the Probe Score column.

To download Probe Score results

After a Probe Score job has a status of Complete, you can download the results of the job.

1 In the eArray$_{XD}$ tab, set the Application Type to **CGH, ChIP-on-chip,** or **CH3.** See "To set the application type" on page 48.

2 In the Tasks pane of the Navigator, in the **Probe Score** folder, right-click the name of the desired job, then click **Download.**

A Save dialog box appears.

3 Select the desired location for the downloaded file, then click **Save.**

The program downloads a *.zip file and saves it to the location that you specified. A dialog box tells you that the file was successfully downloaded.

4 Click **OK.**

The downloaded *.zip file contains these files:

File	Description
fit	Tab-delimited text file that lists the Probe IDs of the probes that were scored, and the calculated T_M, GC percentage, and probe score for each probe.
ProbeScoreCuration_fate	Tab-delimited text file that lists the Probe IDs of the probes that were scored, and the length and status of each probe. Valid probes that could be reannotated to include calculated probe scores have a status of **Pass.**
ProbeScoreCuration_sum	Tab-delimited text file that contains the Probe Annotation Summary Report. This report includes header information that identifies the Probe Score job. It also lists the overall statistics of the job, including the number of probes that were submitted and the number of probes that passed validation. In addition, it details the number of probes that were removed for each of several specific reasons.

To delete a Probe Score job

You can delete a Probe Score job with any status except Processing .

1. In the eArray$_{XD}$ tab, set the Application Type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.
2. In the Tasks pane of the Navigator, in the Probe Score folder, right-click the name of the desired job, then click **Delete.**

   A dialog box asks if you are sure you want to delete the job.
3. Click **Yes.**

   The program deletes the job. However, if the program has already calculated probe scores, the scores remain associated with probes. A dialog box tells you that the job has been successfully deleted.
4. Click **OK.**

To delete probes

You can permanently remove probes from your server. This gives you a way to remove "orphan" probes that are not in use, or probes that you have uploaded or created in error. You must be the owner of the probes. In addition, you cannot delete probes in the AgilentCatalog folder, HD probes, SNP probes, or probes that are in use in probe groups or in microarray designs. Also, probe deletion has no effect on the probes that are available to your workgroup on the eArray Web site.

1. Search for the desired probes. See "Searching for Probes" on page 92.
2. In the Search Results pane, select the probes that you want to delete. Follow these guidelines:
   - To select an individual probe, mark the check box next to its Probe ID.
   - To select all of the probes in the search results, mark **Select Entire Data.**
   - To select all of the probes on the current page, mark the check box in the column heading row.
   - To select probes on more than one page, just select the probes on the desired pages. The program remembers your selections as you go from page to page.
3. Click **Delete.**

A dialog box asks if you really want to delete the selected probes.

CAUTION When you delete probes, you permanently remove them from your server. To restore deleted probes, you must upload or create them again.

4 Click **Yes.**

A dialog box tells you that the Delete Probes job will appear in the Tasks pane. The job appears in the Tasks pane of the Navigator, in the Delete Probes folder.

5 Click **OK.**

The icon next to the name of the job indicates its status:

Status	Comments
	Pending – The job has been submitted, but it is not yet finished.
	Processing – The job is being processed.
	Complete – The job is finished.
	Error – An error occurred. You must re-submit the job.

After a Delete Probes job has a status of Complete , you can download a report that lists the probes that were deleted, and those that were not. For probes that were not deleted, the report lists the reasons. To download and view this report, follow these steps:

a Right-click the name of the desired Delete Probes job, then click **Download Report.**

A dialog box appears.

b Select a location for the downloaded report, then click **Save.**

The program downloads the report as a *.tdt file to your computer. A dialog box tells you that the file was successfully downloaded.

c Click **OK.**

To view the report, open the downloaded file in a spreadsheet program.

3
Working with Probe Groups

Probe Groups are collections of probes that are associated by one or more criteria, and give you a way to organize probes. Probe groups are required organizational units that you use as the building blocks of microarray designs. eArray$_{XD}$ gives you a variety of ways to create and manage probe groups, summarized in the following table:

Task	Purpose
Create probe group	Associate specific probes with each other. You can use probe searches, uploads, or other probe creation methods as the basis. See "To create a new probe group" on page 223.
Search probe groups	Find probe groups in the Agilent Catalog, or in your folders on your server, that match specified search criteria. See "To search for probe groups" on page 224.
Browse probe groups	View lists of available probe groups in the Agilent Catalog, or in the folders of your workgroup to which you have access. See "To browse available probe groups" on page 227.
View probe group	View information about a probe group, including its list of probes. See "To view a probe group" on page 228.
View probe group graphically	View probes in the context of the genome of the applicable organism. "To view the probes in a probe group graphically" on page 229.
Copy probe group	Create a new probe group that uses an existing one as a template. See "To copy a probe group" on page 230.
Edit probe group	Change the attributes of a probe group. You can also add and remove probes from the probe group. See "To edit a probe group" on page 234.
Add probes to probe group	Add additional probes to a probe group when you create, edit, or copy it. See "To add probes to a probe group" on page 236.
Remove probes from probe group	Remove selected probes from a probe group when you create, edit, or copy it. See "To remove probes from a probe group" on page 237.
Move probe group	Move probe groups that you own to a different folder. See "To move probe groups" on page 239.
Download probe group	Save probe group files to a location that you select. See "To download a probe group" on page 240.

Task	Purpose
Delete probe group	Permanently remove a probe group that you own from your server. See "To delete a probe group" on page 242.
Add/view attachment	View or attach a note, file, or URL to a probe group. See "To add an attachment to a probe group" on page 243 and "To view the attachments to a probe group" on page 244.

NOTE The names of available probe groups appear in the Design Data pane of the Navigator. However, before you can take certain actions on probe groups, you may need to transfer probes and annotation or download the probe group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To create a new probe group

To create a new probe group, you first search for probes, upload a file of probes, or submit a Probe Design, Tiling, or Probe Quality job. You create the new probe group from the results of the process, or as part of the process. You can also create a probe group based on another probe group. The table below summarizes the ways you can create probe groups in eArray$_{XD}$, and the topics to which you can refer for more details.

Source of Probes	See this topic to create a new probe group
Probe search	"To create a new probe group" on page 204
HD probe search	"To create a probe group from HD probe search results" on page 135
SNP probe search	"To create a probe group from SNP probe search results" on page 156
Probe upload	"To create a probe group with uploaded probes" on page 165
GE Probe Design	"To create a probe group from probe design or tiling results" on page 181
Simple Tiling or Genomic Tiling	"To create a probe group from probe design or tiling results" on page 181

Source of Probes	See this topic to create a new probe group
Existing probe group	"To copy a probe group" on page 230
GE Probe Quality job	"To create a probe group from a GE Probe Check job" on page 213

CAUTION If you make changes to your custom content within Agilent Genomic Workbench, these changes are not automatically synchronized with your user account on the eArray Web site. Similarly, after you install eArray$_{XD}$ and your server, if you use the eArray Web site to create or change custom content, this content is not automatically synchronized with Agilent Genomic Workbench.

NOTE Before you can create a probe group, you may need to transfer probe and annotation data from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To search for probe groups

You can search for existing probe groups, either your own probe groups or probe groups from the Agilent Catalog. Alternatively, it can be easier to browse probe groups, rather than doing a search – see "To browse available probe groups" on page 227.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Search,** click **Probe Groups.**

The Probe Group Search pane appears.

3 Set any of the following search criteria, as desired. To return all available probe groups, set no search criteria. You can click **Reset** at any time to start over.

Search criterion	Instructions/Details
Probe Group Name	Type all or part of the name of a desired probe group. This search criterion is not case-sensitive.
Folder	Select a specific folder to search. The list contains the names of the folders to which you have access. Select **All** to search in all folders available to you. To search the subfolders of folders as well, mark **Include Subfolders.**
Keywords	Type all or part of a keyword. This search criterion is not case sensitive.
Probe Group Category	(CGH Application type only) This criterion lets you limit the probe group search to standard CGH probe groups, or to CGH+SNP probe groups. Select one of these options: • **All** – Returns both CGH and CGH+SNP probe groups. • **CGH** – Limits the search to standard CGH probe groups. • **CGH+SNP** – Limits the search to CGH+SNP probe groups.
Created by	Type all or part of a name of the desired probe group creator.
Date Created	Type dates in **From** and **To.** For dates, use the format yyyy-mm-dd. This limits the returned probe groups to those created within the specified range of dates. Alternatively, click the calendar  buttons to select dates.
Status	Select one of these options: • **All** – Returns probe groups of any status. • **Incomplete** – Limits probe groups that are returned to those with Incomplete status. Incomplete probe groups can be edited. • **Locked** – Limits the probe groups that are returned to those with Locked status. Locked probe groups cannot be edited, and they cannot be unlocked.

4 Click **Search.**

The program begins the requested search. Search results appear in the Search Result pane. Do any of the following to navigate the search results:

- To sort the search results, click the name of any column heading, except Actions. The program sorts the search results based on the entries in that column. To reverse the order of the sort, click the same column heading again. The column on which the results are sorted appears in a darker color than the others.
- To go to a different page of results, click a numbered page button above or below the list of probe groups.

You can take action on the probe group(s) in the search results. In general, you click a button in the Actions column, or you select one or more probe groups and click a button at the top of the Search Result pane. See these topics:

- "Search Result pane" on page 514
- "To view a probe group" on page 228
- "To view the probes in a probe group graphically" on page 229
- "To copy a probe group" on page 230
- "To edit a probe group" on page 234
- "To download a probe group from the eArray Web site" on page 232
- "To move probe groups" on page 239
- "To download a probe group" on page 240
- "To delete a probe group" on page 242
- "To add an attachment to a probe group" on page 243
- "To create a microarray design from a probe group search" on page 259

NOTE

- When you search for your own custom probe groups, the program searches the content on your server, not on the eArray Web site.
- Probe group searches return the names of all available probe groups that match your search criteria. However, before you can take certain actions on probe groups, you may need to transfer probe and annotation data or download the probe group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To browse available probe groups

You can use the Design Data pane of the Navigator to view and take action on probe groups in the Agilent Catalog folder and in the workgroup folders to which you have access. In addition to the procedure described below, you can also search the Design Data pane for items that match a search term – see "To search the Navigator" on page 51.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the **Design Data** pane of the Navigator, expand the **Designs** folder.

   The main folders to which you have access appear. Within each main folder, you can view available probe groups in the **Probe Group** node.

3 To take action on a probe group, right-click its name, then click the desired action. The actions that are available depend on the specific probe group. See the following topics:

   - "To view a probe group" on page 228
   - "To copy a probe group" on page 230
   - "To edit a probe group" on page 234
   - "To download a probe group from the eArray Web site" on page 232
   - "To move probe groups" on page 239
   - "To download a probe group" on page 240
   - "To delete a probe group" on page 242
   - "To add an attachment to a probe group" on page 243

NOTE The names of all available probe groups appear in the Design Data pane of the Navigator. However, before you can take certain actions on probe groups, you may need to transfer probe and annotation data or download the probe group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To view a probe group

You can view information about a specific probe group of any status, including the list of probes in the probe group and their sequences, annotation, accessions, and statistical information.

1 Search or browse for the probe group that you want to view. See "To search for probe groups" on page 224 and "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **View.**

The View Probe Group dialog box appears. The dialog box contains the properties of the probe group. For details, see "View Probe Group" on page 873.

Below these properties, the Search Result pane displays a list of the probes in the probe group. Several additional columns of probe annotation can appear.

From the Search Result pane, you can take several actions:

Task	Instructions/Details
Download the probes in the probe group	For details, see "To download a probe group" on page 240.
View probe sequences and statistics	(Available for all application types except microRNA) • Click **Show Statistics.** The Probe Statistics dialog box appears. See "Probe Statistics" on page 829. The dialog box contains probe ID and sequence information for each probe in the probe group. For the Expression application type, the dialog box also contains calculated statistics based on the base composition of each probe.
View the probes graphically in the Genomic Viewer	(Available for all application types except Expression) • Click **Genomic Viewer** or **Genomic Plot.** The probes in the probe group appear as a scatter plot in Gene View of the Genomic Viewer. See "To view the probes in a probe group graphically" on page 229.

3 Click **Close.**

NOTE

- For the microRNA application type, probes are grouped by the microRNA to which they are designed. Up to four probes of varying lengths act in concert to measure a given microRNA species.
- Before you can view a probe group, you may need to transfer probe and annotation data or download the probe group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.
- The properties that you can view vary by probe group.

To view the probes in a probe group graphically

You can view the probes in a probe group within the context of the applicable genome. This feature is available for the CGH, ChIP-on-chip, and CH3 application types.

1 Search or browse for the desired probe group See "To search for probe groups" on page 224 or "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **View.**

The View Probe Group dialog box appears. See "View Probe Group" on page 873.

3 Click the **Genomic Viewer** button.

The Genomic Viewer opens in the Home tab of Agilent Genomic Workbench. The probes in the probe group appear as a scatter plot in Gene View of the Genomic Viewer. To view an example of probes in the Genomic Viewer, see Figure 10 on page 204. For information on how to use the Genomic Viewer, see the *Data Viewing User Guide*.

NOTE

Before you can view a probe group graphically, you may need to transfer probe and annotation data or download the probe group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To copy a probe group

When you copy a probe group, you create a new probe group that contains the same probes as the original one. You can copy any probe group that you can access on your server. The original probe group can be located in any folder to which you have access.

1 Search or Browse for the desired probe group. See "To search for probe groups" on page 224 or "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **Copy.**

The Copy Probe Group dialog box appears. See "Copy Probe Group" on page 618.

3 Define the properties of the new probe group as described in the table below. You can change properties from their default values, as desired. The properties that are not listed in the table are read-only, and cannot be changed. For details, see "Copy Probe Group" on page 618.

Property	Instructions/Details
Probe Group Name	The program displays a default name that contains the name of the original probe group, preceded by "Copy_Of_." Edit this name, if desired. Do not include special characters.
Folder	Select a location for the new probe group. Only the folders to which you have access appear in the list.
Status	Select one of these options: **Incomplete** – This option lets you make edits to the new probe group after you save it. This is the default option. **Locked** – This option prevents edits to the probe group after you save it. Locked probe groups cannot be unlocked.
Description	Type brief descriptive information, if desired, up to 4,000 characters in length.
Keywords	Type search keyword(s), if desired, up to a total length of 4,000 characters. Separate multiple keywords with pipe "|" characters, commas, or semicolons.

4 If desired, add or remove probes from the probe group. See "To add probes to a probe group" on page 236 and "To remove probes from a probe group" on page 237.

5 Click **Save Probe Group.**

A dialog box tells you that the probe group has been successfully created.

6 Click **OK.**

NOTE

It can be useful to copy a probe group for several reasons:

- To create a probe group that has most or all of its probes in common with an existing probe group.
- To make changes to an Agilent Catalog probe group, or another probe group that you do not own. Normally, you cannot edit these kinds of probe groups, but when you copy a probe group, you become the owner of the copy, and you can make changes to it.
- To make changes to a probe group that has a status of Locked (and thus cannot be edited) – You can create the copy with a status of Incomplete, which lets you edit it.
- To move a probe group that is in use in a microarray design (and thus cannot be moved) – You can create a copy, then move the copy.

Also, before you can copy a probe group, you may need to transfer probe and annotation data or update the probe group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To download a probe group from the eArray Web site

When you download a probe group from the eArray Web site, you transfer the information that maps specific probes to the probe group. Also, if Agilent updates the probe content of a probe group, the program also updates the probe and annotation data on your server when you download the probe group.

The names of probe groups from the eArray Web site, both from the Agilent Catalog and from the folders of your workgroup, appear in the Design Data pane of the Navigator. When you first install your Agilent Genomic Workbench server, the program automatically retrieves the *names* of these probe groups. However, you must download these types of probe groups to take most actions on them.

You must download a probe group from the eArray Web site if:

- It is an Agilent Catalog probe group or a probe group from the folders of your workgroup on the eArray Web site that has never been downloaded.
- It was previously downloaded from the eArray Web site, but Agilent has subsequently updated its probe content.

Also, the program lets you create microarray designs with probe groups that have not yet been downloaded from the eArray Web site. However, you must download these probe groups before you can save the microarray design with a status of Complete or Submitted.

NOTE

Before you download a probe group from the eArray Web site, you may first need to transfer probe and annotation data for the given application type. See "eArray$_{XD}$ and the eArray Web site" on page 25 and "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1. Set the desired application type. See "To set the application type" on page 48.
2. Expand the folders of the **Design Data** pane of the Navigator until you can see the desired probe group.

3 Observe the icon next to the name of the desired probe group.

Icon	Comments
	The probe group must be downloaded from the eArray Web site. To transfer the probe group to your server, follow the rest of the steps of this procedure.
	The probe group is available on your server. Stop here. (Also, the probe group has a status of Locked, and cannot be edited.)
	The probe group is available on your server. Stop here. (Also, the probe group has a status of Incomplete. If desired, you can edit it.)

4 Right-click the name of the desired probe group, then click **Download From eArray.com.**

A dialog box tells you that your update request has been submitted successfully.

Alternatively, instead of doing steps 2–4, search for the desired probe group, then in the Actions column of the Search Result pane, in the row of the desired probe group, click  .

5 Click **OK.**

You can monitor the status of the probe group update job in the Tasks pane of the Navigator. In the Probe Group Update folder, your update request appears with a status icon:

Icon	Comments
	**Pending** – Your request has been submitted, but the probes and annotation are not yet available. To cancel the download, right-click the name of the job, then click Delete.
	**Processing** – The eArray Web site is downloading the requested probes and annotation to your server.
	**Complete** – The download of the probes and annotation of the requested probe group is finished.
	**Error** – An error occurred. You must re-submit the download request.

To edit a probe group

You can change the information that is associated with a probe group, such as its name or search keywords, and you can also add or remove probes from it. You must be the owner of the probe group, and it must have a status of Incomplete.

Before you can edit a probe group, you may need to download it from the eArray Web site. See "To download a probe group" on page 240.

1 Search or Browse for the desired probe group. See "To search for probe groups" on page 224 or "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **Edit.**

The Edit Probe Group dialog box appears.

3 Change the properties of the probe group, as desired. See the table below. The properties that are not listed in the table are read-only, and cannot be changed. For details, see "Edit Probe Group" on page 771.

Property	Instructions/Details
Probe Group Name	Type a new name, if desired. Do not use special characters such as $, #, @, &, and the like.
Folder	Select a new location for the probe group. Only the folders to which you have access appear in the list.
Status	Select one of these options: **Incomplete** – This option lets you make additional edits to the probe group after you save it. This is the default option. **Locked** – This option prevents edits to the probe group after you save it. Locked probe groups cannot be unlocked.
Description	Type brief descriptive information, if desired, up to 4,000 characters in length.
Keywords	Type search keyword(s), if desired, up to a total length of 4,000 characters. Separate multiple keywords with pipe "|" characters, commas, or semicolons.

4 If desired, add or remove probes from the probe group. See "To add probes to a probe group" on page 236 and "To remove probes from a probe group" on page 237.

5 Click **Save Probe Group.**

A dialog box tells you that the probe group was successfully updated.

6 Click **OK.**

To add probes to a probe group

When you create, edit, or copy a probe group, you can add additional probes to it. To add probes to a probe group, you must be the owner of the probe group.

1 Start to create, edit, or copy a probe group as described in one of these topics:

- "To create a new probe group" on page 223.
- "To edit a probe group" on page 234.
- "To copy a probe group" on page 230.

Part way through the process, a dialog box appears that contains a list of probe group properties, and a Search Result pane that lists the probes in the probe group.

2 In the Search Result pane, click **Add New Probes.**
The Add Probes to Probe Group dialog box appears. See "Add Probes to Probe Group" on page 578. This dialog box functions identically to the Probe Search pane.

3 Set parameters for a probe search. See "To use the Probe Search tool to find probes" on page 92.

4 Click **Search.**
The Search Result pane displays the probes that match your search criteria.

5 Select the probes that you want to add to the probe group. Use the following instructions as a guide:

Task	Instructions
Select a probe	• Mark the check box next to the name of the probe.
Select all of the probes on the current page of results	• Mark the check box in the column heading row.
Select all of the probes on all of the pages of results	• Mark **Select entire data set.**
Go to a different page of results (when available)	• Click one of the numbered page buttons at the top or bottom of the dialog box. The program remembers your selections as you go from page to page.

6 Click **Add Probes to Probe Group.**

A dialog box asks if you really want to add the selected probes to the probe group.

7 Click **Yes.**

The program adds the selected probes to the probe group. A dialog box tells you that the new probes were added to the probe group.

8 Click **OK.**

If desired, you can add additional probes.

NOTE

- The program adds only new, unique probes to the probe group. Selected probes that already exist in the probe group are not duplicated.
- You cannot add probes to Agilent Catalog, HD, or SNP probe groups.

To remove probes from a probe group

When you create, edit, or copy a probe group, you can remove probes from the initial list of probes.

1 Start to create, edit, or copy a probe group as described in one of these topics:

- "To create a new probe group" on page 223.
- "To edit a probe group" on page 234.
- "To copy a probe group" on page 230.

Part way through the process, a dialog box appears that contains a list of probe group properties, and a Search Result pane that lists the probes in the probe group.

2 In the **Search Result** pane, select the probe(s) that you want to remove. Use the following instructions as a guide:

Task	Instructions
Select a probe	• Mark the check box next to the name of the probe.
Select all of the probes on the current page of results	• Mark the check box in the column heading row.

Task	Instructions
Select all of the probes on all of the pages of results	• Mark **Select entire data set.**
Go to a different page of results (when available)	• Click one of the numbered page buttons at the bottom of the dialog box. The program remembers your selections as you go from page to page.

3 Click **Remove Probes.**

A dialog box asks if you really want to remove the probes from the probe group.

4 Click **Yes.**

The program removes the probes from the probe group. A dialog box tells you that the probes were removed.

5 Click **OK.**

NOTE

- When you remove a probe from a probe group, you only remove the link between the probe and the probe group. To completely remove the probe from the probe database on your server, see "To delete probes" on page 218.
- You cannot remove probes from Agilent Catalog, HD, or SNP probe groups, or from probe groups that you do not own.

To move probe groups

You can move one or more probe groups to another folder.

Before you move probe groups

- You must be the owner of the probe group(s).
- You must have access to the desired destination folder.
- The probe group must not be in use in an existing microarray design.
- The probe group must not be located in the Agilent Catalog folder, but it **can** contain Agilent Catalog probes.

To move a probe group

1 Search for the desired probe group. See "To search for probe groups" on page 224.

2 In the Search Result pane, mark the check box next to each probe group that you want to move. The program remembers your selections as you go from page to page.

3 Click **Move.**

The Move Probe Group dialog box lists the name(s) and location(s) of the probe groups that you selected. See "Move Probe Group" on page 813.

4 In **Move to Domain,** select the desired destination folder.

5 Click **Move.**

A dialog box asks if you really want to move the probe group(s).

6 Click **Yes.**

A dialog box lists each probe group, and whether or not the move was successful. If a probe group could not be moved, the reason appears next to its name.

7 Click **OK.**

NOTE

- You can also use the Navigator to move probe groups. In the **Design Data** pane, right-click the name of the probe group, then click **Move.**
- You cannot move probe groups if someone else owns them, or if they are in use in a microarray design. However, you can achieve the equivalent. Make a copy of the desired probe group, then move the copy. See "To copy a probe group" on page 230.

To download a probe group

When you download a probe group, the program retrieves the probe group from your server, and saves it in a file format and location that you select. To download a probe group from your server, you may first need to download the probe group from the eArray Web site to your server. See "To download a probe group from the eArray Web site" on page 232.

1 Search or Browse for the desired probe group. See "To search for probe groups" on page 224 or "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **Download.**

The Download Probe Group dialog box appears. See "Download Probe Group" on page 732.

3 In Download Type, select the desired file type. The list and table below describe the available file types.

- **TDT** – Tab delimited text file that contains the attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the attributes indicated in the table below.
- **COMPLETE** – Tab delimited text file that contains the attributes indicated in the table below.
- **MINIMAL** – Tab delimited text file that contains the attributes indicated in the table below.
- **BED** – Tab delimited text file that contains the attributes indicated in the table below. This file is A BED format track file that you can view in a compatible genome browser.

Attribute	TDT	FASTA	COMPLETE	MINIMAL	BED
ProbeID	•	•	•	•	•
Sequence	•	•	•	•	
TargetID	•		•		
Species	•				

Attribute	TDT	FASTA	COMPLETE	MINIMAL	BED
GeneName	•				
GeneSymbol	•		•		
Description	•		•		
ControlType	•				
Accessions	•		•		
ProbeGroups	•				
Status	•				
ValidationMethod	•				
Chromosomal Locations	•		•		•
Cytoband	•				
GOID	•				

• – Attribute included in file format

4 Click **Download.**

A Save dialog box appears.

5 Select a location for the downloaded file, then click **Save.**

The program downloads the probe group to the selected location. A dialog box tells you that the download was successful.

6 Click **OK.**

NOTE

For microRNA microarrays, probes are grouped by the microRNA to which they are designed. One to four probes act in concert to measure a given microRNA. In downloaded files, each probe appears on a separate line, but the file lists the probes for a given microRNA on consecutive lines. The name of the microRNA to which each probe binds appears explicitly in the downloaded TDT and COMPLETE format files, in the TargetID column.

To delete a probe group

When you delete a probe group, you remove the associations that bind a particular set of probes together, not the actual probes and annotation. A separate topic describes how to delete probes — see "To delete probes" on page 218.

To delete a probe group, you must be the owner of the probe group, and the probe group must not be in use in a microarray design. In addition, you may need to download the probe group from the eArray Web site before you can delete it from your server. See "To download a probe group from the eArray Web site" on page 232.

1 Search or Browse for the desired probe group. See "To search for probe groups" on page 224 or "To browse available probe groups" on page 227.

2 Do one of the following:

- If you retrieved the probe group of interest in a probe group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the probe group of interest, right-click its name, then click **Delete.**

In either case, a dialog box asks if you really want to delete the selected probe group.

CAUTION When you delete a probe group, the program permanently removes it from the system. To restore a deleted probe group, you must create it again.

3 Click **Yes.**

A message tells you that the probe group was successfully deleted.

4 Click **OK.**

To add an attachment to a probe group

You can attach a note, file, or URL to any probe group to which you have access, except Agilent Catalog probe groups. The probe group can have a status of Incomplete or Locked. Also, you may need to download the probe group from the eArray Web site before you can add an attachment to it. See "To download a probe group from the eArray Web site" on page 232.

1 In the Design Data pane of the Navigator, right-click the name of the desired probe group.

2 Click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593.

3 Add the desired attachment(s) as described in the table below.

Type of Attachment	Instructions/Details
Note	You can attach text to a probe group. **a** In **Attachment Type,** select **Notes.** The box in Note becomes available. **b** In **Note,** type the desired text. **c** Click **Add.** In the Total Attachments pane, the note appears in the list of attachments. The beginning of the note appears in Attachment Name.
File	You can attach a file to a probe group. When users view the attachments to the probe group, they can open the attached file. **a** In **Attachment Type,** select **File.** **b** In **Name,** type a name for the attachment. This becomes the display name for the file in the Total Attachments pane. **c** In **File,** click **Browse.** An Open dialog box appears. **d** Select the desired file, then click **Open.** The location of the file appears in File. **e** Click **Add.**In the Total Attachments pane, the newly attached file appears in the list of attachments.

Type of Attachment	Instructions/Details
URL	You can attach a URL to a probe group. The URL can point to a Web site or other resource. When users view the attachments to the probe group, they can open the URL in their Web browser. **a** In Attachment Type, select **URL.** **b** In **Name,** type a name for the attachment. This becomes the display name for the URL in the Total Attachments pane. **c** In **URL,** type the complete URL — for example, `http://www.agilent.com` **d** Click **Add.** In the Total Attachments pane, the new URL appears in the list of attachments.

To view the attachments to a probe group

You can view the notes, files or URLs that are attached to a probe group. You may need to download the probe group from the eArray Web site before you can view its attachment(s). See "To download a probe group from the eArray Web site" on page 232.

1 In the Design Data pane of the Navigator, right-click the name of the desired probe group, then click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. The notes, files and URLs that are attached to the probe group appear in the Total Attachments pane. If there are many attachments, the program paginates the list. To go to a different page, click one of the numbered page buttons above or below the list.

2 In the **Actions** column, in the row of the desired attachment, click  . You can view the attachment as described in the table below:

Type of attachment	Details/Instructions
Note	Notes appear in the Note dialog box. See "Note" on page 825. **Note:** The program also displays the notes that you have created in the Note tab in the main pane of the program. Each note appears as a note icon with the name of the note. To open a note, double-click its icon. To delete a note in this tab, as well as from the probe group, right-click the desired note icon, then click **Delete.**
File	Files open in an appropriate program, if one exists on your computer.
URL	URLs open in your Web browser.

To remove attachments from a probe group

You can remove attached notes, files and URLs from a probe group. You may need to download a probe group from the eArray Web site before you can remove its attachment(s). See "To download a probe group from the eArray Web site" on page 232.

1 In the Design Data pane of the Navigator, right-click the name of the desired probe group, then click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. If there are many attachments, the program paginates the list. To go to a different page of attachments, click a numbered page button above or below the list.

2 In the Total Attachments pane, select the URL(s) and/or file(s) that you want to remove. To select a file or URL, mark the check box next to its name. To select all of the files and URLs on the current page of attachments, mark the check box in the column heading row. The program remembers your selections as you go from page to page.

3 Click **Delete.**

A dialog box asks if you are sure you want to delete the attachments.

CAUTION When you remove an attached note, file or a URL, the program permanently removes the item from the probe group. To restore an attachment, you must re-attach the item.

4 Click **Yes.**

A dialog box tells you that the attachment(s) were successfully deleted.

5 Click **OK.**

4 Working with Microarray Designs

eArray$_{XD}$ gives you a full set of tools that you can use to search, create, and manage microarray designs. A **microarray design** is the layout of probes on a single glass slide with a particular format. Each design contains the biological and control probe groups that you select, as well as a required Agilent quality control grid. In eArray$_{XD}$, you do not have to decide on a format ahead of time – you can select the probes that you want, then try out many potential configurations.

You can work with microarray designs in several general ways:

- **Search for microarray designs** – You can use many different criteria to search for existing microarray designs. You can also browse available microarray designs in the Agilent Catalog, or in your own folders. See "Searching and Browsing Microarray Designs" on page 251.
- **Create microarray designs** – The program gives you many specific ways to create new microarray designs.
  - All microarray application types let you create a new microarray design from existing probe groups. You can also create a new microarray design from an existing one.
  - All microarray application types except microRNA let you create a new microarray design from a file of uploaded probes.
  - The Expression application type lets you create a new microarray design based on an uploaded file of target transcripts or other target sequences.

- The CGH, ChIP-on-chip, and methylation application types let you create a new microarray design based on a search of the Agilent high density (HD) probe database. This is a special database on the eArray Web site that contains probes that cover the genomes of several species at extremely high densities. In addition, you can create a new microarray design based on custom genomic tiling of either an Agilent genome, or a user-defined genome.
- The CGH application type lets you design CGH+SNP microarrays, which combine CGH probes and probes for SNP sites on the same microarray. These microarrays let you do SNP copy number analysis as well as loss (or lack) of heterozygosity (LOH) analysis.

In many cases, the program can lead you through the microarray creation process one step at a time. See "Creating Microarray Designs" on page 258.

- **View and change microarray designs** – Once you find or create a microarray design, you can view its details. If you are its owner, you can make changes to the design, and also let others make changes to it. See "Viewing and Changing Microarray Designs" on page 304.
- **Manage microarray designs** – The program lets you move, delete, and download microarray designs. See "Managing Microarray Designs" on page 338.
- **Submit microarray designs to Agilent** – Once you are satisfied with a microarray design, you can use eArray$_{XD}$ to submit it to Agilent Manufacturing. After you submit the design, you can request a price quote through the program. Your local Agilent sales representative can then help you place an order for your custom arrays. Agilent manufactures the arrays after you order them. See "Submitting Microarray Designs to Agilent" on page 346.

Status of microarray designs

The status of a microarray design reflects its progress through the microarray creation process. Status designations follow a defined order:

Draft >>> **Review** (optional) >>> **Complete** >>> **Submitted**

In some cases, the program assigns the status, and in others, the owner of the microarray design selects the status. This is a one-way process—once a microarray design has a particular status, you cannot subsequently assign it a status that comes earlier in the order.

The following table summarizes the status designations that a microarray design can have in eArray.

Status	Description
Draft 	The design is in its early stages of development. **Additional details** • The owner of the design can edit or delete it, or change its status to Review or Complete. • The design cannot be submitted.
Review 	This is an optional status that the owner of the design can select. It lets others make changes to the design. See "To place a microarray design in review" on page 324. **Additional Details** • Users who can access the design can review the design, make changes to it, save a new version of it, and download it as a *.tdt file. • The program saves each new version of the design, and keeps a version history. • The owner can delete the design. • The design cannot be submitted.
Complete 	You, as the owner of the design, can select this status when you and any reviewers have finished editing it. This prevents further changes. See "To prevent further edits or reviews of a design" on page 335. **Additional Details** • An AMADID number is assigned to the design. • The program generates all design files. • No one can edit the design, not even its owner. • The owner can submit the design. • Anyone who has access to the design can download the design files and the tab-delimited text (*.tdt) file. • The design can be deleted by its owner. • The owner can change the control types of the probe groups in the design.
Submitted 	eArray$_{XD}$ sets this status after you submit the design to Agilent Manufacturing. See "To submit a microarray design to Agilent as part of a wizard" on page 347. **Additional Details** • The design cannot be edited or deleted. • The owner can change the control types of the probe groups in the design. • Anyone with access to the design can request a quote for it. • The owner of the design can search, view, download, and request a quote for the design on the eArray Web site.

Available actions by status

The status of a microarray design affects the actions you can take on it. The table below summarizes available actions by status.

	Status			
Action	**Draft**	**Review**	**Complete**	**Submitted**
Edit design	•			
View design	•	•	•	•
Copy design	•	•	•	•
Delete design	•	•	•	
Review design		•		
Move design	•	•	•	•
Download design		•	•	•
Submit design			•	
Change control type of probe groups	•	•	•	•
Request quote for design				•
Add or display attachments	•	•	•	•
View probe layout with ArrayVisualizer			•	•

NOTE

- To take most actions on a microarray design, you must be its owner. However, anyone who has access to a design can copy, review, download, or request a quote for it, or add or view attachments. Fewer options are available for items in the AgilentCatalog folder.
- To work with a microarray design, you may need to first download it from the eArray Web site. You may also need to transfer probe and annotation data from the eArray Web site for the given application type. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61 and "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Searching and Browsing Microarray Designs

This section describes how to access existing microarray designs, including Agilent Catalog designs, and your own custom designs. Two methods are available:

Method	Details
Search	Retrieves microarray designs based on search criteria that you enter. You can then view or take action on the retrieved designs. See "To search for microarray designs" on page 251.
Browse	Lets you view a list of the available microarray designs on your server by folder. You can then take action on a specific design. See "To browse available microarray designs" on page 256.

To search for microarray designs

You can search for microarray designs based on many different criteria. Once you retrieve the design of interest, you can take action on it.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the command ribbon of the eArray$_{XD}$ tab, under Search, click **Microarray Designs.**

The Array Design Search pane appears.

3 Set as many or as few of the following search criteria as you like. To start over, click **Reset.**

Search Criterion	Instructions/Details
Microarray Name	Type all or part of a name of a microarray design.
Folder name	To limit the search to a specific folder, select a folder from the list. Only the folders to which you have access appear in the list. To search all available folders, select **All.** To include the subfolders within the selected folder, mark **Include Subfolders.**

Search Criterion	Instructions/Details
Species	To select one or more species, follow these steps: **a** Click **Select and Add.** A dialog box appears. See "Select and Add : Species" on page 845. **b** In **Species,** type some or all of a desired species name, then click **Search.** To return a list of all available species, leave Name blank. **Note:** Use abbreviated binomial nomenclature for species names, for example `H. sapiens` Matching species name(s) appear at the bottom of the dialog box, in the left pane. If the search returns many species, eArray$_{XD}$ paginates the list, and a set of page links appears. **c** In the left pane of the dialog box, click the name of the desired species to select it. You can select more than one species: • To select additional species, control-click the names of individual species. • To select a contiguous block of species, click the name of the first species, then shift-click the name of the last one. **d** Click **Add.** eArray transfers the selected species to the right pane of the dialog box. You can add as many species as you want. The program remembers all of the species that you select on all pages. You can also do the following: • To transfer all of the species from the left pane to the right pane, click **Add All.** • To start over, click **Remove All.** • To remove one or more species from the right pane of the dialog box, select their names, then click **Remove.** **e** Click **Done.** The selected species appear(s) in the Array Design Search pane in Species. Multiple species appear in pipe-separated format. **Note:** When eArray searches for microarray designs based on species, it searches only the primary species associated with them. This is true even if you select multiple species as search criteria. Also, to retrieve designs for which no species are assigned, do not set the Species search criterion.

Search Criterion	Instructions/Details
Design ID	Type a design ID number, or multiple design ID numbers separated by pipe "|" characters. Design ID numbers are also called **AMADIDs.**
Design Status	Select one of these options: • **All** – Returns microarray designs without regard to their design status. • **Active** – Returns microarray designs that use design formats that are currently available. • **Obsolete** – Returns microarray designs that use design formats that are no longer available.
Created by	Type all or part of the name of the microarray design owner whose designs you want to find. This criterion is not case sensitive.
Date Created	Type or select a range of dates. Use yyyy-mm-dd as the date format, for example `2009-03-20`. To select the desired dates from calendars, click  next to **From** and **To.** To return all designs that were created before a given date, select the desired date in **To,** but do not select a date in **From.**
Containing Probe Group	Set this parameter to find array designs that contain specific probe group(s). To select the probe group(s) to use as search criteria, click **Select and Add.** A dialog box appears. See "To select probe groups for searches or microarrays" on page 106. The selected probe groups appear in pipe-separated format in the search pane.
Keywords	Type all or part of a keyword, or multiple keywords separated by commas. This search criterion is not case-sensitive.

Search Criterion	Instructions/Details
Status	Select the desired status. The status of a microarray design reflects its progress through the design process. See "Status of microarray designs" on page 248. To return microarray designs without regard to status, select **All.**
Array Category	(CGH application type only) Select one of these options: • **All** – Returns both standard CGH and CGH+SNP microarray designs. • **CGH** – Limits returned microarrays to only standard CGH microarrays. • **CGH+SNP** – Limits returned microarrays to only CGH+SNP microarrays. For more information on CGH+SNP microarrays, see "To create a CGH+SNP microarray design" on page 301.

4 Click **Search.**

The program searches for microarray designs that match your search criteria. A Search Result pane appears. To sort the search results based on the contents of a column, click the name of any column heading except Actions. To reverse the order of the sort, click the name of the column heading again. The heading of the column whose contents are used for the sort appears in a darker color.

You can take action on the microarray designs in the search results. In the Actions column, the following buttons can appear:

Icon	Details
	**Copy** – Lets you make a copy of a microarray design. See "To copy a microarray design" on page 340.
	**Edit** – (Available only to the owner of a design. The design must have a status of Draft.) Lets you make changes to the microarray design. See "To edit a microarray design" on page 310.
	**Review** – (Available only for designs with a status of Review) Lets the owner, and others with access to the design make changes to it. See "To review a microarray design" on page 326. To place a design in review, see "To place a microarray design in review" on page 324.
	**View** – Lets you view the probes, statistics, and other details of a microarray design. See "To view a microarray design" on page 305.

Icon	Details
	**Download from eArray.com** – (Available for microarray designs that have updated Agilent content, or that have never been downloaded from the eArray Web site) Downloads the microarray design from the eArray Web site. If this button appears, you must download the microarray design before you can use it. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
	**Delete** – (Available only to the owner of a design, and only if it has a status other than Submitted.) Lets you remove a design from your server. See "To delete a microarray design" on page 345.
	**Submit** – (Available only to the owner of a design, and only if it has a status of Complete.) Lets you submit a design to Agilent Manufacturing. See "To submit a microarray design to Agilent" on page 346.
	**Request Quote** – (Available only for designs with a status of Complete.) Lets you request a price quote for a design. See "To request a quote" on page 348.
	**Change control type of probe group(s)** – (Available only for designs with a status of Complete or Submitted) Lets you change the control type designation assigned to each of the probe groups in the design. See "To change the control type of probe groups" on page 336. **Note:** • To change the control type of probe groups in a microarray design with a status of Draft, edit the design. See "To edit a microarray design" on page 310. • To change the control type of probe groups in a microarray design with a status of Review, review the design. See "To review a microarray design" on page 326.
	**Download** – (Available for designs with a status other than Draft) Lets you download files associated with the design to a location that you select. See "To download microarray design files" on page 341 and "To download microarray design files" on page 341.

In addition, if you are the owner of a microarray design, you can move it to another folder. See "To move a microarray design" on page 338.

NOTE

Before you take action on a retrieved microarray design, you may need to download the design from the eArray Web site. You may also need to transfer probe and annotation data from the eArray Web site for the given application type. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61 and "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To browse available microarray designs

The Design Data pane of the Navigator can display the microarray designs in the folders of your server to which you have access, and let you take action on them.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the **Design Data** pane of the Navigator, expand folders until you can see the name of the desired design.

3 Right-click the name of the desired microarray design.

A shortcut menu appears. These options can appear:

Option	Details
Download from eArray.com	(Appears for a microarray design if it contains new Agilent content that was made available since the content was last downloaded from the eArray Web site, or if the design has never been downloaded from the eArray Web site.) Sends an update request for the microarray design to the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Move	(Available for microarray designs that you own) Opens a dialog box that lets you move the microarray design to a different folder. See "To move a microarray design" on page 338.
Copy	Lets you make a copy of a microarray design. See "To copy a microarray design" on page 340.
Edit	(Available only to the owner of a design. The design must have a status of Draft.) Lets you make changes to the microarray design. See "To edit a microarray design" on page 310 and "Edit Microarray Design" on page 751.
Review	(Available for designs with a status of Review) Lets the owner, and others with access to the design to make changes to it. See "To review a microarray design" on page 326. To place a design in review, see "To place a microarray design in review" on page 324.
View	Displays the probes, statistics, and other details of a microarray design. See "To view a microarray design" on page 305.
Delete	(Available only to the owner of a design, and only if it has a status other than Submitted.) Lets you remove a design from your server. See "To delete a microarray design" on page 345.

Option	Details
Submit	(Available only to the owner of a design, and only if it has a status of Complete.) Lets you submit a design to Agilent Manufacturing. See "To submit a microarray design to Agilent" on page 346.
Request Quote	(Available only for designs with a status of Submitted.) Lets you request a price quote for a design from Agilent. See "To request a quote" on page 348.
Download	(Available for designs with a status other than Draft) Lets you download files that are associated with the design to a location that you select. See "To download microarray design files" on page 341.
Change Control Type	(Available only for designs with a status of Complete or Submitted) Lets you change the control type assigned to each of the probe groups in the design. See "To change the control type of probe groups" on page 336.
Attach	Opens another menu that lets you attach a note, file, or URL to the design. See "To add an attachment to a microarray design" on page 320.
ArrayVisualizer	(Available for microarray designs with a status of Complete or Submitted, after the design files have been created by the system.) Opens the Array Layout dialog box, where you can view the layout of probes on the microarray design graphically. See "To view the layout of probes on a microarray graphically" on page 306 and "Array Layout" on page 583.

NOTE

- In addition to the procedure described above, you can also search the Design Data pane of the Navigator for items that match a specific search term – see "To search the Navigator" on page 51.
- Before you take action on a microarray design, you may need to download the design from the eArray Web site. You may also need to transfer probe and annotation data from the eArray Web site for the given application type. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61 and "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Creating Microarray Designs

eArray$_{XD}$ lets you create microarray designs in many ways. This section describes the methods that are available. The methods, summarized in the table below, each use probes from a different source. Some methods are only available for specific application types.

Source of probes	See these topics
Existing probe group(s)	• "To create a microarray design from a probe group search" on page 259 • "To create a microarray design from existing probe groups (Wizard)" on page 269.
File of uploaded probes	(Available for all microarray application types except microRNA) • "To create a microarray design from uploaded probes" on page 282.
Existing microarray design	• "To create a new microarray design from an existing one" on page 288
Uploaded target transcripts	(Available for the Expression application type) • "To create a microarray design from target transcripts" on page 289.
Agilent HD probe database	(Available for the CGH, ChIP-on-chip, and methylation application types) • "To create a microarray design with HD probes" on page 297.
CGH probes and Agilent SNP probes	(Available for the CGH application type) • "To create a CGH+SNP microarray design" on page 301

To create a microarray design from a probe group search

You can use the results of a probe group search to create a new microarray design. This method is available for the CGH, ChIP-on-chip, CH3, Expression, and microRNA application types. It is an effective way to construct a microarray that uses probe groups that you have previously created in the program.

1 Set the desired application type. See "To set the application type" on page 48.

2 Search for the desired probe groups. See "To search for probe groups" on page 224.

3 In the Search Result pane of the probe group search, select the probe group(s) that you want to include in your new microarray design. Use these instructions as a guide:

- To select a probe group, mark the check box next to its name.
- To select all of the probe groups on the current page of results, mark the check box in the column heading.
- To go to a different page of probe group search results, click a numbered page button above or below the list of returned probe groups. The program remembers your selections as you go from page to page.

4 Click **Create Microarray.**

- For the CGH application type only, the Select Array Type dialog box appears. See "Select Array Type" on page 847. Select one of these options, then click **Next.**
  - **Standard** – Creates a standard CGH microarray design.
  - **SNP** – Creates a CGH+SNP microarray design, which combines both CGH and SNP probes on the same array. For details about this type of array, see "To create a CGH+SNP microarray design" on page 301.

  The Create Microarray Design dialog box appears. See "Create Microarray Design" on page 646. Continue to step 5.
- For all other application types, the Create Microarray Design dialog box appears. Continue to step 5.

5 Enter the following parameters. Parameters are required unless otherwise indicated. All of the other parameters in the top pane of the dialog box are set by the program, and cannot be changed.

Parameter	Instructions/Details
Microarray Name	Type a name for the microarray design. eArray$_{XD}$ uses this name as one of the search keys for microarray designs, and as a way to refer to the design in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder Name	Select a location for your new microarray design. The folders to which you have access appear in the list.
Species	Select the desired species. Species is optional for Expression type arrays, and required for CGH, ChIP-on-chip, CH3, and microRNA type arrays. For microRNA microarrays, the species that you select is the primary species for the array. However, for this application type, you can create a multi-species array. For details on how eArray handles microRNAs from multiple species, see "Custom Design Guidance" on page 898.
Design Format	Select a design format from the list. Only the design formats that are available for your chosen application type and species appear in the list. When you select or change the design format, an appropriate control grid appears in Control Grid. The design format defines the number and location of features on a microarray slide. It also defines the number of replicate arrays that appear on the slide. **Example:** The 4x44K design format places four identical arrays on the slide. Each array contains approximately 44,000 features.
Control Grid	The program automatically selects a control grid that is appropriate for your application type and design format. For CGH, ChIP-on-chip, and methylation applications, the control grid is also species-specific. You can select an alternate control grid from the list, if one is available. For microRNA microarrays, the program always applies a standard human control grid.
Description	(Optional) Type a brief description for the design.

Parameter	Instructions/Details
Keywords	(Optional) Type search keywords to associate with the design, separated by commas. Keywords can help you search for the microarray design later.
Comments	(Optional) Type comments to include with the microarray design.

NOTE

- You can use a probe group in a microarray design if it appears in the results of a Probe Group Search. However, if you use a probe group from the eArray Web site that has not yet been downloaded to your server, or that requires an update, you can only save the new microarray design with a status of Draft. After you download the probe group from the eArray Web site, you can save the microarray design with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.
- The program always creates new microarray designs with an initial status of Draft, which lets the owner edit the design.
- The program always creates a design with Randomized feature layout, which assigns probes randomly to feature positions. To create a microarray design in which probes are assigned to specific feature positions that you select, you must create the design on the eArray Web site. For details, see the *Provide Feature Order* topic in the online help on the eArray Web site.

6 In the Layout Details pane of the dialog box, do any of the tasks in the table below to refine the content of the microarray design.

Task	Instructions/Details
Add or remove biological or user control probe group(s)	You can add or remove biological or user control probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe groups appear in the list. **c** In the Control Type column, select the desired control type for each probe group. For details, see "Change the control type of a probe group" on page 263. **To remove biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Note:** • Separate tasks below describe how to add or remove SNP, normalization, or replicate probe groups. • For microRNA microarrays, you can only add *biological* type probe groups.

Task	Instructions/Details
Change the control type of a probe group	The control type of a probe group influences how the program handles the data from the probe group in downstream analysis. **a** Click **Probe Groups.** **b** Next to the name of the desired probe group, in the **Control Type** column, select an option from the list. Positive and negative control probe groups cannot collectively occupy more than 50% of the features in your design. • **biological** – Identifies the probe group as a non-control probe group (condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample. **Note:** The control type of user probe groups on microRNA microarrays is always **biological,** and cannot be changed.

Task	Instructions/Details
Add or remove SNP probe group(s)	(CGH+SNP microarrays only) SNP probe groups contain probes that interrogate specific SNP sites, and are designed for use in CGH+SNP microarray designs. See "To create a CGH+SNP microarray design" on page 301. You can add or remove SNP probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add SNP probe group(s)** **a** Click **SNP Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the SNP Probe Groups pane. **To remove a SNP probe group** **a** Click **SNP Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**
Change the number of copies of a probe group	You can include multiple copies of most types of probe groups in a microarray design. **a** Click the desired **Probe Groups** tab. **b** In the **Replicate** column (if available), next to the desired probe group, type the number of copies of the probe group that you want to include in the microarray design. The default is 1. **Example:** You have selected a design format of 4x44K, and for a given probe group you type 2 in **Replicate.** The probe group appears eight times on the microarray slide, twice in each of the four individual arrays on the slide. **Note:** For the microRNA application type, the **Replicate** parameter is always set to 1.

Task	Instructions/Details
Add or remove a normalization probe group	(CGH application type only) A normalization probe group is a special control probe group that supplies data that can be used to normalize the two dye channel data generated from the array. **To add a normalization probe group** **a** Click **Normalization Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Normalization Probe Groups pane. **To remove a normalization probe group** **a** Click **Normalization Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Notes:** When you create an array for certain species and design formats, eArray automatically adds a default Agilent normalization probe group. If normalization probe group(s) appear in your design, you can download a list of unique probes to use in the Agilent Feature Extraction program. The name of this file is *NormalizedProbeTDT*. See "To download microarray design files" on page 341. You can also create your own normalization probe group. See "CGH Normalization Probes" on page 900.

Task	Instructions/Details
Add or remove a replicate probe group	(CGH and Expression application type only) **To add a replicate probe group** **a** Click **Replicate Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Replicate Probe Groups pane. **c** In the **Replicate** column, type the number of copies of the probe group to be included in the design. Agilent recommends a value of 5. **To remove a replicate probe group** **a** Click **Replicate Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Notes:** These replicate probe groups are distinct from the user probe groups that you can include in designs in multiple copies. A replicate probe group is a special control probe group that the Feature Extraction and DNA Analytics programs can use to calculate the Reproducibility QC Metric. For each channel, this metric is the median %CV of background-subtracted signal for the replicate probes after outlier rejection. When you create an microarray design for certain species and design formats, eArray automatically adds a default Agilent replicate probe group. You can also create your own replicate probe group. Agilent offers these guidelines: • Use a minimum of 1,000 probes for each design. For lower-density design formats, such as 8x15K, use a minimum of 300 probes. • Replicate the probe group 5 times.

Task	Instructions/Details
Add or edit linkers	**a** Click **Linker Options.** **b** Mark **Append Linker to 3' End.** The options in Linker Length and Linker Sequence become available. **c** In **Linker Length,** select one of these options: • **Append linker to make total probe length of** – Adds nucleotides to the 3' ends of probes so that the resulting probes have the length specified. In the box, type a number of nucleotides from 20 to 60. If there are probes in your microarray design longer than the length that you set, the program leaves them alone. They are not trimmed, and no linkers are added to them. • **Add linker of fixed length** – Adds the specified number of nucleotides to the 3' ends of probes. In the box, type a number of nucleotides from 1 to 49. The program truncates the linker on a probe, as necessary, to keep the total length of the probe from exceeding 60 nucleotides. If the linker sequence is shorter than the length that you set, eArray replicates the linker sequence to fill the length. **d** In **Linker Sequence,** select one of these options: • **Use Agilent Linker Sequence** – You cannot edit the Agilent-provided linker sequence. • **Use Customer Linker Sequence** – Type a DNA base sequence for the linker. Use a random sequence, or derive it from a sequence not found in nature. **Notes:** • For Agilent probes, the program adds the Agilent linker sequence, even if you select Use Customer Linker Sequence. • For the microRNA application type, the program adds 5′ and 3′ linkers to probes automatically. No linker options are available.
Remove linkers from probes	**a** Click **Linker Details.** **b** Clear **Append linker to 3' end.** **Note:** You cannot remove the linkers from probes in a microRNA microarray design.

Task	Instructions/Details
Fill unused features or change filler probe group.	You can fill the unused "empty" features of your design with probes from the probe group of your choice. The program applies probes from the selected probe group, multiple times if needed, until all features are filled. You can also use this procedure to select a different filler probe group. **a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Mark **Fill Microarrays.** A button appears. **c** In **Probe Group to Fill Microarray,** click **Select.** The Select Probe Group to Fill Microarray pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **d** Search for, select, and add one probe group, then click **Done.** The selected probe group appears in the Fill Microarray pane, in Probe Group to Fill Microarray. **Note:** For microRNA microarrays, the program always uses a default structural filler probe group.
Remove filler probes	**a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Clear **Fill Microarrays.** **Note:** The structural filler probe group used in microRNA microarrays cannot be removed.

7 Click **Create.**

The program creates the new microarray design, and saves it to the selected folder with a status of Draft. A dialog box tells you that the microarray design has been successfully created.

8 Click **OK.**

To create a microarray design from existing probe groups (Wizard)

You can create a microarray design that contains probe groups that are accessible to you on your server. This includes probe groups that you have previously uploaded or created in the program, or downloaded from the eArray Web site. This wizard leads you step-by-step through the microarray design creation process. It is available for the CGH, ChIP-on-chip, CH3, Expression, and microRNA application types.

1 Set the desired application type. "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Array Design using,** click **Existing Probe Group(s).**

A dialog box appears with the main steps of the process. See "Create Microarray Design from Existing Probe Groups (Wizard)" on page 648. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the process. At any time, click **Cancel** to discard your settings and close the dialog box.

Separate sections in this topic cover each of the steps of the process:

- Step 1 – Select Species and Define Design. See "Step 1 – Select Species and Define Design" on page 270.
- Step 2 – Layout Probes. See "Step 2 – Layout Probes" on page 272.
- Step 3 – Create Microarray Design. See "Step 3 – Create Microarray Design" on page 281.

Step 1 – Select Species and Define Design

1 Enter the following parameters. Parameters are required unless otherwise indicated.

Parameter	Instructions/Details
Select Array Type	(CGH application type only) Select one of these options: • **Standard** – Creates a standard CGH microarray design. • **SNP** – Creates a CGH+SNP microarray design that combines CGH and SNP probes on the same array. For details, see "To create a CGH+SNP microarray design" on page 301.
Microarray Name	Type a name for the microarray design. eArray$_{XD}$ uses this name as one of the search keys for microarray designs, and as a way to refer to the design in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Description	(Optional) Type a brief description for the design.
Species	Select the desired species. Species is optional for Expression arrays, and required for CGH, ChIP-on-chip, CH3, and microRNA arrays. For microRNA microarrays, the species that you select is the primary species for the array. However, for this application type, you can create a multi-species array. For details on how eArray handles microRNAs from multiple species, see "Custom Design Guidance" on page 898.
Folder	Select a location for your new microarray design. The folders to which you have access appear in the list.
Design Format	Select a design format from the list. Only the design formats that are available for your chosen application type and species appear in the list. When you select or change the design format, an appropriate control grid appears in Control Grid. The design format defines the number and location of features on a microarray slide. It also defines the number of replicate arrays that appear on the slide. **Example:** The 4x44K design format places four identical arrays on the slide. Each array contains approximately 44,000 features.

Parameter	Instructions/Details
Control Grid	The program automatically selects a control grid that is appropriate for your application type, design format, and for CGH, ChIP-on-chip, and methylation applications, species. You can select an alternate control grid from the list, if one is available. For the microRNA application type, the program always applies a standard human control grid.
Keywords	(Optional) Type search keywords that are related to the design, separated by commas. Keywords can help you search for the microarray design later.
Comments	Type comments to include with the microarray design. If you will create the microarray design with a status of Complete, which prevents further editing of the design, comments are required. Otherwise, comments are optional.
Feature Layout	(Read-only) The process always produces a design with **Randomized** feature layout, which assigns probes randomly to feature positions. **Note:** To create a microarray design in which probes are assigned to specific feature positions that you select, you must create the design on the eArray Web site. For details, see the *Provide Feature Order* topic in the online help system on the eArray Web site.

2 Click **Next.**

The next step of the process appears in the dialog box.

Step 2 – Layout Probes

In this step, you select the probes for your new microarray design:

- You add the desired probe groups to the microarray design.
- (Optional) You can add linkers to probes, which "stilt" the active hybridizing probe sequences away from the glass microarray substrate. This reduces steric hindrance, and makes the sequence more available for hybridization.
- (Optional) You can select a probe group to fill any unused feature positions in the design.

As you add (or remove) probe groups, you can monitor the values in the Microarray Statistics pane to see how many features have been filled in the design.

NOTE

When you select probe groups for a microarray design, the program tells you if a probe group is *Local* or if it is *Not Downloaded.* If you select one or more probe groups that are *Not Downloaded,* you can only save the new microarray design with a status of Draft. After you download the given probe group(s) from the eArray Web site, you can save the microarray design with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

1 At the bottom of the dialog box, make changes to the probe content of the design. Use the tasks described in the table below.

Task	Instructions/Details
Add or remove biological or user control probe group(s)	You can add or remove biological or user control probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe groups appear in the list. **c** In the Control Type column, select the desired control type for each probe group. For details, see "Change the control type of a probe group" on page 274. **To remove biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Note:** • Separate tasks below describe how to add or remove SNP, normalization, or replicate probe groups. • For microRNA microarrays, you can only add *biological* type probe groups.

Task	Instructions/Details
Change the control type of a probe group	The control type of a probe group influences how the data from the probe group are handled in downstream analysis. **a** Click **Probe Groups.** **b** Next to the name of the desired probe group, in the **Control Type** column, select an option from the list. Positive and negative control probe groups cannot collectively occupy more than 50% of the available features in your design. • **biological** – Identifies the probe group as a non-control probe group (condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of a positive control is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following the addition of spike-in controls to the sample. **Note:** The control type of user probe groups on microRNA microarrays is always **biological,** and cannot be changed.

Task	Instructions/Details
Add or remove SNP probe group(s)	(CGH+SNP microarrays only) SNP probe groups contain probes that interrogate specific SNP sites, and are designed for use in CGH+SNP microarray designs. See "To create a CGH+SNP microarray design" on page 301. You can add or remove SNP probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add SNP probe group(s)** **a** Click **SNP Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the SNP Probe Groups pane. **To remove a SNP probe group** **a** Click **SNP Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**
Change the number of copies of a probe group	You can include multiple copies of most probe groups in a microarray design. **a** Click the desired **Probe Groups** tab. **b** In the **Replicate** column (if available), next to the desired probe group, type the number of copies of the probe group that you want to include in the microarray design. The default is 1. **Example:** You have selected a design format of 4x44K, and for a given probe group you type 2 in **Replicate.** The probe group appears eight times on the microarray slide, twice in each of the four individual arrays on the slide. **Note:** For the microRNA application type, the **Replicate** parameter is always set to 1.

Task	Instructions/Details
Add or remove a normalization probe group	(CGH arrays only) A normalization probe group is a special control probe group that supplies data that can be used to normalize the two dye channel data generated from the array. For more information on normalization probes, see "CGH array design guidance" on page 900. **To add a normalization probe group** **a** Click **Normalization Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Use the pane to search for and select one or more probe groups, then click **Done.** The selected probe group(s) appear in the Normalization Probe Groups pane. **To remove a normalization probe group** **a** Click **Normalization Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add pr remove a replicate probe group	(CGH and Expression arrays only) A replicate probe group is a special control probe group that is used in downstream analysis by the Feature Extraction and DNA Analytics programs. These probe groups are distinct from the user probe groups that you select in the Probe Groups pane. See "Expression array design guidance" on page 898 and "CGH array design guidance" on page 900. **To add a replicate probe group** **a** Click **Replicate Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Replicate Probe Groups pane. **c** In the **Replicate** column, type the number of copies of the probe group to be included in the design. Agilent recommends a value of 5. **To remove a replicate probe group** **a** Click **Replicate Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add or edit linkers	Linkers are nucleic acid molecules that are synthesized to the 3′ end of the "active" (hybridizing) sequences of probes. In principle, linker sequences do not hybridize to any sequences in the target sample. They move the active sequences farther off of the array surface, which reduces steric hindrance. This makes the active probe sequence more available for a hybridization event. **a** Click **Linker Options.** **b** Mark **Append Linker to 3' End.** The options in Linker Length and Linker Sequence become available. **c** In **Linker Length,** select one of these options: • **Append linker to make total probe length of** – Adds nucleotides to the 3' ends of probes so that the resulting probes have the length specified. In the box, type a number of nucleotides from 20 to 60. If there are probes in your microarray design longer than the length that you enter, the program leaves them alone. They are not trimmed, and no linkers are added to them. • **Append linker of fixed length** – Adds the specified number of nucleotides to the 3' ends of probes. In the box, type a number of nucleotides from 1 to 49. The program truncates the linker on a probe, as necessary, to keep the total length of the probe from exceeding 60 nucleotides. If the linker sequence is shorter than the length that you enter, eArray replicates the linker sequence to fill in the length. **d** In **Linker Sequence,** select one of these options: • **Use Agilent Linker Sequence** – You cannot edit the Agilent-provided linker sequence. • **Use Customer Linker Sequence** – Type a DNA base sequence for the linker. Use a random sequence, or derive it from a sequence not found in nature. **Note:** • For Agilent probes, the program adds the Agilent linker sequence, even if you select Use Customer linker sequence. • For the microRNA application type, 5′ and 3′ linkers are added to probes automatically by the program. No linker options are available.

Task	Instructions/Details
Remove linkers from probes	**a** Click **Linker Options.** **b** Clear **Append Linker to 3' End.** **Note:** You cannot remove the linkers from probes in a microRNA microarray design.
Fill unused features or change filler probe group.	You can fill the unused "empty" features of your design with probes from the probe group of your choice. The program applies probes from the selected probe group, multiple times if needed, until all features are filled. You can also use this procedure to select a different filler probe group. **a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Mark **Fill Microarrays.** In Probe Group to Fill Microarray, a Select button appears. **c** In **Probe Group to Fill Microarray,** click **Select.** The Select Probe Group to Fill Microarray pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **d** Search for and add one probe group, then click **Done.** The selected probe group appears in the Fill Microarray pane, in Probe Group to Fill Microarray. **Note:** For microRNA microarrays, the program always uses a default structural filler probe group.
Remove filler probes	**a** Click **Fill Microarray.** **b** Clear **Fill Microarrays.** **Note:** The structural filler probe group used in microRNA microarrays cannot be removed.

Task	Instructions/Details
Select the number of features assigned to each microRNA	(microRNA application type only) In **Features per microRNA,** select the desired number of features from the list. This setting reflects the total number of features on the array assigned to each microRNA. Each microRNA has from one to four different probes associated with it. eArray adjusts the number of replicates of each of these probes to achieve the specified number of features per target (microRNA). A higher number generates slightly more robust data, while a lower setting lets you measure more microRNAs per array. The default value is 16 features per microRNA target. Agilent Catalog arrays use 16 features per microRNA target for human arrays, and 20 features per microRNA target for mouse and rat arrays.

2 Click **Next.**

The next step of the process appears in the dialog box.

Step 3 – Create Microarray Design

In this step, you select a status for the new microarray design. The status that you select affects the actions that you can take on the design. See "Status of microarray designs" on page 248.

1 In **How do you want to save and create your design,** select one of these options:

Option	Details
Draft	The program saves the design with a status of Draft. This status lets only you edit the design. This is the default option. For details, see "To edit a microarray design" on page 310.
Review	The program saves the design with a status of Review. This status lets other users who have access to the design make changes and save versions of it. For details, see "To review a microarray design" on page 326.
Complete	The program saves the design with a status of Complete, and retrieves a unique design ID (AMADID) number for it from the eArray Web site. You can subsequently submit the design to Agilent Manufacturing. No one can edit or review a design with this status.
Submitted	The program saves the design with a status of Submitted, and submits the design to Agilent Manufacturing. No one can edit or review a design with this status. If you select this option, you must also click **Show Checklist,** read and mark all of the items that appear, then click **Done.** To preview this checklist, see "Design Checklists" on page 894. You can subsequently request a quote for the design. See "To request a quote" on page 348. When you submit a design, it also becomes available on the eArray Web site. On the eArray Web site, you can search for the design, view it, request a quote for it, and download its design files. However, you cannot copy it, or publish it on OpenGeonimcs.com.

2 Click **Finish.**

A dialog box tells you that the microarray design has been successfully created.

3 Click **OK.**

To create a microarray design from uploaded probes

To use this method to create a microarray design, you must have a file that contains the probes that you want to include. The file must be a Microsoft Excel (*.xls) file, or a tab-delimited text file (*.tdt or *.txt). The file can contain probe data in either the COMPLETE or MINIMAL file formats. See "Complete (for probes)" on page 881 and "Minimal (for probes)" on page 890.

The program leads you step-by-step through the microarray design creation process. This method is available for the CGH, ChIP-on-chip, CH3, and Expression application types.

NOTE

If you want to create a CGH+SNP microarray design that includes uploaded CGH probes, do not use the procedure below. Instead, upload the CGH probes and create a probe group as described in "Uploading Probes" on page 158. You can then create the design from this probe group and a SNP probe group. See "To create a CGH+SNP microarray design" on page 301.

1. Set the desired application type. "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, under **Create Array Design using,** click **Probe Upload.**

   A dialog box appears with the main steps of the process. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the process. At any time, click **Cancel** to discard your settings and close the dialog box.

   Separate sections in this topic cover each of the steps of the process:

   - Step 1 – Probe Parameter and File Details. See "Step 1 – Probe Parameter and File Details" on page 283.
   - Step 2 – Preview of Uploaded Probes. See "Step 2 – Preview of Uploaded Probes" on page 285.
   - Step 3 – Define Design. See "Step 3 – Define Design" on page 286.
   - Step 4 – Layout Probes. See "Step 4 – Layout Probes" on page 288.
   - Step 5 – Create Microarray Design. See "Step 5 – Create Microarray Design" on page 288.

Step 1 – Probe Parameter and File Details

In this step, you enter details about how the program handles the probes in your uploaded file, as well as details about the probe data file itself.

1 Under **Probe Parameter Details,** enter the following parameters:

Parameter	Instructions/Details
Job Name	Type a name for the microarray design. As the program creates the design, this name identifies the job in the Tasks pane of the Navigator. After the program creates the design, the name identifies the design in search results and the Design Data pane of the Navigator.
Species	Select the species associated with your probes. You can use this information later to search for the probes.
Remove replicate probes from upload	A replicate probe has the same Probe ID as another probe in the file. To ignore all but the first probe in each set of replicate probes in your file, mark this option. If your probe file contains replicate probes, and you do *not* mark **Remove replicate probes from upload,** the program displays an error message after you begin the upload, and does not upload your file.
Probe precedence	These options define what you want the program to do if it finds probes in your uploaded file that have the same Probe ID as probes that already exist in the system. Select one of these options: • **Overwrite matching probes** – The annotation of the matching uploaded probe replaces the annotation of the existing probe. This option is useful for reannotating probes. • **Skip matching probes** – The program ignores the matching uploaded probes, and only uploads new ones. • **Cancel upload if any probes already exist** – The program cancels the entire upload process if it finds a matching uploaded probe.

2 Under **Upload Probe File Details,** enter the following parameters:

Parameter	Instructions/Details
Probe Group Name	After the program uploads your probe data file, it creates a probe group that contains all the probes from the file. Type a name for this probe group.
Upload File	To select your probe sequence file, follow these steps. Your file must meet the requirements described in "Complete (for probes)" on page 881 or "Minimal (for probes)" on page 890. **a** Click **Browse.** An Open dialog box appears. **b** Select the desired probe data file, then click **Open.** The location of the selected file appears in Upload File.
File Format	Select either **MINIMAL** or **COMPLETE.** For details about these file formats, see "Complete (for probes)" on page 881 and "Minimal (for probes)" on page 890.
File Type	Select the appropriate file type from the list. eArray accepts Microsoft Excel (*.xls) files, and tab-delimited text (TDT) files with file extensions of .txt and .tdt. **Note:** If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

3 Click **Next.**

The next step of the wizard appears in the dialog box.

NOTE

eArray$_{XD}$ can upload fairly large probe files. Agilent has tested the 64-bit version of the program, and has successfully uploaded 150,000 probes in the Complete file format, which corresponds to a file size of approximately 32 MB.

Step 2 – Preview of Uploaded Probes

In this step, you identify the contents of each column of your probe data file. The first few rows of data from your probe data file appear under Define Uploaded File Columns.

1 At the top of each column of data, select the label that best describes the contents of the column. ProbeID and Sequence are required. If you want the upload process to ignore a specific column, select **Ignore.** Use each label exactly once, except Ignore, which you can use any number of times.

2 If the first row of your probe data file is actually a row of column headings, mark **My uploaded file contains column headings.** Otherwise, the program interprets the first line of the file as a set of probe data. The program does not interpret any column headings in your uploaded file.

3 Click **Next.**

If you have not yet transferred your workgroup's probe and annotation data for the given application type from the eArray Web site, a warning message tells you that to avoid probe name conflicts, the system will add a prefix of **XD_** to all of the new probes in your file. This differentiates your uploaded probes from any probes that you transfer from the eArray Web site that have the same names. To continue with the upload process, click **OK.**

The program uploads the file and submits a job to your server. The job appears in the Tasks pane of the Navigator, where you can monitor its status. A dialog box tells you that the file was successfully submitted to the upload queue.

4 Click **OK.**

You can monitor the status of the job in the Probe Upload (Wizard) folder of the Tasks pane in the Navigator. These icons can appear next to the name of the probe upload job:

Icon	Status/Comments
	**Pending** – The job has been submitted to the upload queue.
	**Processing** – The job is being processed.

Icon	Status/Comments
	**Complete** – Your server has successfully uploaded the probes in your file. You can now continue with the wizard.
	**Error** – An error occurred. You must re-start the wizard. Errors are usually caused by irregularities in the uploaded probe file. To see any errors that the program detected in the uploaded probe file, follow these steps: **a** Right-click the name of the probe upload job, then click **Download Error File.** A dialog box appears. **b** Select a location for the downloaded error file, then click **Save.** The program saves a ZIP format archive to the location that you selected. The ZIP archive contains an HTML file that you can view with your Internet browser. The HTML file lists the errors that the program detected in your original probe upload file.

Step 3 – Define Design

When the program has successfully uploaded the probes from your file, a  icon appears next to the name of the job. You can now continue with the wizard.

1 In the Tasks pane of the Navigator, in the Probe Upload (Wizard) folder, right-click the name of the probe upload job, then click **Create Microarray.**

A dialog box appears with the next step of the wizard.

2 Enter the following parameters. Parameters are required unless otherwise indicated.

Parameter	Instructions/Details
Microarray Name	Type a name for the microarray design. eArray$_{XD}$ uses this name as one of the search keys for microarray designs, and as a way to refer to the design in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Description	(Optional) Type a brief description for the design.
Species	(Read-only) Displays the species that you selected in Step 1 of the wizard.
Folder	Select a location for your new microarray design. The folders to which you have access appear in the list.

Parameter	Instructions/Details
Design Format	Select a design format from the list. Only the design formats that are available for your chosen application type and species appear in the list. When you select or change the design format, an appropriate control grid appears in Control Grid. The design format defines the number and location of features on a microarray slide. It also defines the number of replicate arrays that appear on the slide. **Example:** The 4x44K design format places four identical arrays on the slide. Each array contains approximately 44,000 features.
Control Grid	The program automatically selects a control grid that is appropriate for your application type, design format, and for CGH, ChIP-on-chip, and methylation applications, species. You can select an alternate control grid from the list, if one is available.
Keywords	(Optional) Type search keywords to associate with the design, separated by commas. Keywords can help you search for the microarray design later.
Comments	Type comments to include with the microarray design. If you intend to create the microarray design with a status of Complete, which prevents further editing of the design, comments are required. Otherwise, comments are optional.
Feature Layout	(Read-only) The process always produces a design with **Randomized** feature layout, which assigns probes randomly to feature positions. **Note:** To create a microarray design in which probes are assigned to specific feature positions that you assign, you must create the design on the eArray Web site. For details, see the *Provide Feature Order* topic in the online help system on the eArray Web site.

3 Click **Next.**

The next step of the process appears in the dialog box.

Step 4 – Layout Probes

The Layout Probes step is identical for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 2 – Layout Probes" on page 272.

Step 5 – Create Microarray Design

The Create Microarray Design step is identical for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 3 – Create Microarray Design" on page 281.

To create a new microarray design from an existing one

In this method of microarray design creation, you make a copy of an existing design, then make any desired changes to the copy. This method is available for the CGH, ChIP-on-chip, CH3, Expression, and microRNA application types. It can be useful in several circumstances:

- To create a microarray design that has all or most of its probes in common with an existing one. You can make a copy of the existing design, then edit the copy.
- To make changes to a microarray design that has a status of Complete or Submitted (and thus cannot be edited). You can make a copy of the Complete or Submitted microarray design, then edit the copy.
- To move a microarray design that you do not own to a different location. You can make a copy of the existing design, then move the copy.

1 Search or browse for the desired existing microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you retrieved the microarray design with a search, click  next to the desired design in the **Actions** column of the search results.
- In the **Design Data** pane of the Navigator, right-click the name of the desired microarray design, then click **Copy.**

In either case, the program creates a copy of the microarray design, with a status of Draft. A dialog box asks if you are sure that you want to copy the microarray design.

3 Click **Yes.**

A dialog box tells you that the microarray design has been successfully copied.

4 Click **OK.**

The Edit Microarray Design dialog box appears. See "Edit Microarray Design" on page 751. The new microarray design has the name of the original design, with "Copy_of_" added to the beginning of the name.

5 Edit the design as desired. See "To edit a microarray design" on page 310.

6 Click **Save.**

A dialog box tells you that the microarray design has been successfully updated.

7 Click **OK.**

To create a microarray design from target transcripts

This method is available for the Expression application type. It is based on the Gene Expression Probe Design process. See "To set up a GE Probe Design job" on page 167. It creates a microarray design that contains probes that are designed to specific transcripts. You define these transcripts in an uploaded file of sequence data, or as an uploaded file of GenBank accessions.

Before you begin

- Prepare either a FASTA format file that contains target sequence data, or a *.txt file that contains a list of GenBank accessions. For GenBank accessions, the file must contain the accession numbers separated by **new line** (return) characters. For information about FASTA format files, see "FASTA" on page 884.
- If an Agilent-constructed species transcriptome database is not available for your species of interest, prepare a FASTA format file that contains custom transcriptome data to use as a similarity database in the probe design process.

To start the microarray creation process

1 Set the application type to **Expression.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Array Design using,** click **Probe Design.**

A dialog box appears with the main steps of the wizard. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the process. At any time, click **Cancel** to discard your settings and close the dialog box.

Separate sections in this topic cover each of the steps of the process:

- Step 1 – Select Method. See "Step 1 – Select Method" on page 290.
- Step 2 – Select Parameters. See "Step 2 – Select Parameters" on page 291.
- Step 3 – Upload Target and Transcriptome. "Step 3 – Upload Target and Transcriptome" on page 294.
- Step 4 – Select Species and Define Design. See "Step 4 – Select Species and Define Design" on page 296.
- Step 5 – Layout Probes. See "Step 5 – Layout Probes" on page 296.
- Step 6 – Create Microarray Design. See "Step 6 – Create Microarray Design" on page 296.

Step 1 – Select Method

1 In **Design Method,** select one of these options:

- **Base Composition Methodology** – The resulting probes adhere as closely as possible to the base composition profile that provides optimal performance on the Agilent platform, and they are all of equal length. This is the standard method, and it works best with Agilent protocols, and most eukaryotic organisms.
- **Tm Matching Methodology** – The resulting probes have melting temperatures (T_M) as similar as possible to a value that you set. Probes can be all of equal length, or probes can be trimmed to increase compliance with the desired T_M. This methodology can work well when you design probes for prokaryotic organisms.

2 Click **Next.**

The next step of the wizard appears.

Step 2 – Select Parameters

In this step, you enter the name and design parameters for a Gene Expression Probe Design job.

1 Set the following parameters:

Parameter	Instructions/Comments
Design Job Name	Type a name that will help you to later identify this specific GE Probe Design job. The job name can be from 1 to 50 characters in length, and can contain letters, numbers, underscores, periods, and dashes. Do not include spaces or special characters.
Probe Length	Type the maximum length for the generated probes. The allowable length is from 25 to 60 bases. Agilent has found that a probe length of 60 bases provides the optimal balance between sensitivity and specificity for most applications on the Agilent *in situ* microarray platform.
Probes per Target	Select from 1 to 10 probes per target. This is the maximum number of probes that the probe design process returns for each uploaded target sequence. If the target sequences are of poor quality (for example, if they contain repetitive and/or vector sequences), the probe design process can return fewer probes than you enter. Because of the length and high quality of the generated probes, Agilent recommends that you create one probe per target sequence. However, if you design multiple probes per target sequence, you can select the best of those probes after a validation process.
Probe Orientation	Select one of these options: • **Sense** – Produces probes in the sense or "coding strand" orientation, similar in sequence to the mRNA targets. Use this option if the sample preparation methodology yields cDNA or cRNA molecules. • **Antisense** – Select this option if you want probes in the antisense or "template" orientation, complementary in sequence to the mRNA targets. This is the best option if your samples are directly labeled RNA.

Parameter	Instructions/Comments
Design Options	Select one of these options: • **Best Probe Methodology** – The probe design process favors production of the highest quality probes, rather than even coverage of each target sequence. The selection process favors empirically validated probes, and probes that are closer to the 3' end of a given primary accession. • **Best Distribution Methodology** – The probe design process favors even coverage of each target sequence, rather than production of the highest quality probes.
Design with 3' bias	Mark this option if you want to design probes that are derived mainly from the first 1,000 bp from the 3' end of each of your target sequences. If you use an Agilent (or other) labeling protocol that uses linear amplification, it is important to design probes to the 3' ends of the sequences. Linear amplification generates sequences that are shorter than the initial template due to the attenuation of the polymerase reaction. Because of this, most of the labeled product represents only the first 1,000 bp from the 3' end of each target sequence. It is important to design probes that represent this region.
Masking	eArray always uses both of these options in the probe design process: • **Apply Vector Masking** – Identifies and ignores contaminant segments during probe design. Target sequences can contain contaminant segments not actually found in the sample under study. These segments are often artifacts from cloning vectors (e.g. plasmid, phage, BAC, YAC) used in cloning and amplification processes. • **Apply Repeat Masking** – Identifies and ignores repetitive sequences within your target sequences during probe design. The genome of any given organism contains interspersed repeats and low complexity DNA sequences. These sequences, which are unique at a species level, are replicated many times throughout the genome, and are found in the transcriptome as well. Replicate regions are poor candidates for unique probes.

Parameter	Instructions/Comments
Allow Probes to be Trimmed	(Available only for T_M-Matching methodology) This option lets the program remove bases from candidate probes to increase compliance with the Preferred Probe T_M. eArray will not trim probes to shorter than 45 bases. In concept, a shorter probe has less complementary sequence available, which can reduce its specificity, or infringe on its ability to form a stable duplex with the desired target. However, the risk of this occurring to a significant extent is very low.
Preferred probe Tm	(Available only for T_M-Matching methodology) Type the target T_M for the probe design process (in °C). Do not include units. The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms. Select a probe T_M based on these factors: • The mean and standard deviation of the T_M of all potential probes that could be generated for the target transcriptome. • The hybridization temperature identified in the hybridization protocol. In practice, the target T_M should be ~20°C higher than the hybridization temperature. For example, if the hybridization temperature is 60°C, then the target probe T_M should be 80°C.

2 Click **Next.**

The next step of the wizard appears in the dialog box.

Step 3 – Upload Target and Transcriptome

In this step, you define the transcripts to which probes will be designed, and the transcriptome data that the program uses as a similarity database to evaluate potential cross-hybridization problems.

1 Enter the following parameters:

Parameter	Instructions/Comments
Species	Select the species that is associated with your target sequences.
Target File Format	Select one of these options: • **FASTA format** – Select this option if you have a FASTA format file of target sequences that you want to use as the basis for the GE Probe Design process. • **GenBank Accessions** – Select this option if you have a *.txt file that contains GenBank accessions that you want to use as the basis for the GE Probe Design process. In either case, you must select the location of the file. See below, "Select Target File."
Select Target File	To select a target file for the GE Probe Design Process, follow these steps: **a** Click **Browse.** A dialog box appears. **b** Select the desired target file, then click **Open.** The location of the file appears in Select Target FIle. eArray resolves GenBank Accessions to actual sequence data before it starts the GE Probe Design process.
Species of Transcriptome	Select the desired species for the transcriptome data that the program uses to evaluate potential cross-hybridization problems. In general, select the same option that you did in Species, above. If desired, you can select a different species to eliminate certain potential cross-species hybridization problems.

Parameter	Instructions/Comments
Select Transcriptome	Select the source of the transcriptome data for the probe design process. The process uses transcriptome data as a similarity database to eliminate potential probe sequences that would have significant cross-hybridization with targets other than the one of interest. • **Agilent-provided Transcriptome** – Uses one of Agilent's available species transcriptome databases. If a transcriptome is available for your species of interest, select this option. These databases have been specifically constructed for use in GE Probe Design. • **Use Target File as Transcriptome** – Uses the file you specified in Upload Target File as the transcriptome similarity database. Select this option if you are designing a "whole transcriptome" array for an organism that is not represented within the Agilent transcriptome set, and the target file represents most or all transcripts within the target transcriptome. This option works for uploaded target files containing either actual sequence data, or GenBank accessions. • **Upload Transcriptome File** – Uses a FASTA format transcriptome file that you upload as the similarity database. See below, "Upload Transcriptome File."
Upload Transcriptome File	(Available if you select **Upload Transcriptome File** in Select Transcriptome) **a** Click **Browse.** A dialog box appears. **b** Select the desired transcriptome file, then click **Open.** The location of the file appears in Upload Transcriptome File.

2 Click **Next.**

The program submits the GE probe design job to the eArray Web site, through your server. The job appears in the Probe Design (Wizard) folder in the Tasks pane of the Navigator. A dialog box tells you that your job has been successfully submitted.

3 Click **OK.**

The probe design job can take up to one day or more to finish. An icon next to the name of the job indicates its status:

Icon	Status/Comments
	Pending – The probe design job has been submitted to the eArray Web site, but no action has been taken on it yet.
	Processing – The probe design job is being processed.
	Complete – The eArray Web site has finished the probe design job, and the results have been transferred to your server. You can now return to the wizard.
	Error – An error occurred. You must re-start the wizard. Errors are usually caused by irregularities in the uploaded sequence file(s).

Step 4 – Select Species and Define Design

When the probe design job from the previous step has a status of Complete, you can continue with the wizard.

- In the **Tasks** pane of the Navigator, in the Probe Design (Wizard) folder, right-click the name of your job, then click **Create Microarray.**

  A dialog box appears, with the next step of the wizard.

  The Select Species and Define Design step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 1 – Select Species and Define Design" on page 270.

Step 5 – Layout Probes

The Layout Probes step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 2 – Layout Probes" on page 272.

Step 6 – Create Microarray Design

The Create Microarray Design step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 3 – Create Microarray Design" on page 281.

To create a microarray design with HD probes

You can create a CGH, ChIP-on-chip, or CH3 microarray design based on one of several different types of searches of the Agilent High Density (HD) Probe Database. This topic describes the wizard that you can use for this purpose. For details about HD searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

After you enter search parameters for the desired type of HD probe search, the wizard submits a search job to the eArray Web site. When eArray finishes the job, it transfers the results to your server. The wizard then leads you through the rest of the microarray creation process.

NOTE

If you want to create a CGH+SNP microarray design that includes HD probes, do not use the procedure below. Instead, do a HD probe search and create a probe group as described in "Searching for Agilent High Density (HD) Probes" on page 109. You can then create the design from this probe group and a SNP probe group. See "To create a CGH+SNP microarray design" on page 301.

1. Set the application type to **CGH, ChIP-on-chip, or CH3.** See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, under **Create Array Design using,** click **HD Probes.**

   A dialog box appears with the main steps of the wizard. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the process. At any time, click **Cancel** to discard your settings and close the dialog box.

   Separate sections in this topic cover each of the steps of the process:

   - **Step 1 – Search Parameters.** See "Step 1 – Search Parameters" on page 298.
   - **Step 2 – Create Probe Group**. See "Step 2 – Create Probe Group" on page 299.
   - **Step 3 – Define Design.** See "Step 3 – Define Design" on page 301.
   - **Step 4 – Layout Probes.** See "Step 4 – Layout Probes" on page 301.
   - **Step 5 – Create Microarray Design.** See "Step 5 – Create Microarray Design" on page 301.

Step 1 – Search Parameters

In this step, you set up an HD probe search job and submit it to the eArray Web site.

1 In the Create Microarray Design dialog box, enter parameters for one of these types of HD searches:

Type of HD Search	Instructions/Details
Simple Genomic Intervals	This type of search retrieves probes from the Agilent HD Probe Database based on genomic intervals that you enter. **a** In **Search,** select **Simple.** **b** Under **Interval Options,** in **Select HD Search by,** select **Genomic Intervals.** **c** Enter parameters for the search as described in "To do a Simple Genomic Intervals HD Search for probes" on page 111.
Advanced Genomic Intervals	This type of search retrieves probes from the Agilent HD Probe Database based on genomic intervals that you upload. You set the density of returned probes, and T_M and homology filtering characteristics on a per-interval basis. **a** In **Search,** select **Advanced.** **b** Under Interval Options, in **Select HD Search by,** select **Genomic Intervals.** **c** Set parameters for the search as described in "To do an Advanced Genomic Intervals HD Search for probes" on page 117.
Probe ID	This type of search retrieves probes from the Agilent HD Probe Database based on Probe IDs that you enter. **a** In **Search,** select **ProbeID.** **b** Set parameters for the search as described in "To do a Probe ID HD Search for probes" on page 125.
Simple Gene Annotations	(Available for CGH microarrays only) This type of search retrieves probes from the Agilent HD-CGH Probe Database based on their association with specific gene annotations that you enter. **a** In **Search,** select **Simple.** **b** In **Select HD Search by,** select **Gene Annotations.** **c** Set parameters for the search as described in "To do a Simple Gene Annotations HD Search for probes" on page 120.

2 Click **Next.**

The program submits an HD probe search job to the eArray Web site, though your server. A dialog box tells you that your job has been submitted.

3 Click **OK.**

Your job appears in the Tasks pane of the Navigator, in the HD Search (Wizard) folder. The icon that appears next to the name of the job indicates its status. The following icons can appear:

Icon	Status/Comments
	Pending – The HD probe search job has been submitted to the eArray Web site, but no action has been taken on it yet.
	Processing – The eArray Web site has started the requested HD probe search.
	Complete – The eArray Web site has finished your HD probe search job, and its results have been transferred to your server. You can now return to the wizard.
	Error – An error occurred. You must re-start the wizard.

Step 2 – Create Probe Group

When the status of the HD probe search job is Complete , you can continue with the wizard. In this step, you submit a job to your server, which creates a new HD probe group based on your HD probe search results.

1 In the Tasks pane, in the **HD Search (Wizard)** folder, right-click the name of the applicable search job, then click **Create Probe Group.**

A dialog box appears, with the steps of the microarray design process. The second step of the process is visible.

2 Set the following parameters. All other parameters are read-only. For descriptions of all parameters, see "Step 2 – Create Probe Group" on page 660.

Parameter	Instructions/Details
Probe Group Name	Type a name for the probe group.
Description	(Optional) Type a brief description.
Folder	Select a location for the probe group. Only the folders to which you have access appear in the list.

Parameter	Instructions/Details
Status	Select one of these options: • **Incomplete** – Lets you subsequently make changes to the probe group. • **Locked** – Prevents further changes to the probe group. Locked probe groups cannot be unlocked.
Keywords	(Optional) Type search keywords separated by commas.

3 Click **Next.**

The program submits your probe group creation job to your server. A dialog box tells you that your probe group creation job has been successfully submitted.

4 Click **OK.**

The program closes the dialog box. You can monitor the progress of the job in the HD Search (Wizard) folder in the Tasks pane of the Navigator. These icons can appear:

Status	Comments
	**Pending** – The HD probe group creation job has been submitted.
	**Complete** – Your new HD probe group is available for your use. You can now return to the wizard.
	**Error** – An error occurred. You must re-start the wizard.

Step 3 – Define Design

When the status of the probe group creation job is Complete, you can continue with the wizard. In this step, you define the properties of your new microarray design.

- In the Tasks pane, in the **HD Search (Wizard)** folder, right-click the name of the applicable search job, then click **Create Microarray.**

  A dialog box appears, with the steps of the microarray design process. The third step of the process is visible.

  This step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)" on page 269. See specifically "Step 1 – Select Species and Define Design" on page 270.

Step 4 – Layout Probes

The Layout Probes step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 2 – Layout Probes" on page 272.

Step 5 – Create Microarray Design

The Create Microarray Design step is the same for all microarray-related wizards. Detailed instructions appear in the topic "To create a microarray design from existing probe groups (Wizard)." See specifically "Step 3 – Create Microarray Design" on page 281.

To create a CGH+SNP microarray design

Agilent CGH+SNP microarrays combine CGH and SNP (single nucleotide polymorphism) probes on the same microarray. With the CGH probes on these microarrays, you can do all of the high resolution CGH aberration analyses that are available for standard Agilent CGH microarrays. However, combined with information from the CGH probes on the microarray, the additional SNP probes let you detect copy-neutral variations such as UPD (uniparental disomy) and cnLOH (copy-neutral loss or lack of heterozygosity). The results can be useful for constitutional cytogenetic studies and studies of

tumorigenesis. To do these types of copy-neutral variation analyses, you use the CGH application of Agilent Genomic Workbench (separate license required).

Single nucleotide polymorphisms are sites in the genome where at least 1% of a population has a different base pair from the rest of the population at a given genomic location. Almost all SNP sites have two possible alleles. The Agilent CGH+SNP platform differentiates the two alleles based on whether the SNP site is cleaved by the AluI/RsaI restriction enzyme mixture that is used in the target preparation process. One allele (the "cut" allele) is cleaved by the restriction enzymes, binds poorly to SNP probes, and produces a low signal level. The other allele (the "uncut" allele) is not cleaved by the restriction enzymes, binds well to SNP probes, and produces a high signal level. In analyses, a known genotyped reference is required, which can be one of five standard HapMap references, or a custom reference. SNP calls are made from the log ratios of the sample probes to those of the genotyped internal reference. For more information on Agilent SNP probes, see "Searching for Agilent SNP Probes" on page 138.

Although the platform is restricted to known SNP sites where one of the alleles is cut by the restriction enzyme mixture, tens of thousands of SNP sites can currently be resolved, and LOH calls can be made for regions as small as approximately 5–10 Mb. For details, see the *CGH Interactive Analysis User Guide,* available in the Help tab of the CGH application of Agilent Genomic Workbench.

General design procedure for CGH+SNP microarrays

Design methods for CGH+SNP microarrays are extensions of the CGH microarray design workflow. To create a CGH+SNP microarray design, follow this general procedure:

1 Search for SNP probes and create a probe group from the search results. Alternatively, use a probe group search to identify an Agilent Catalog SNP probe group of interest. See these topics:

- "Searching for Agilent SNP Probes" on page 138
- "To create a probe group from SNP probe search results" on page 156
- "To search for probe groups" on page 224

2 Identify or create a CGH probe group that contains the CGH probes that you want to include in the design. eArray gives you many options, including HD

Probe Search, Genomic Tiling, probe upload, and searches for existing probe groups. See these topics:

- "Searching for Agilent High Density (HD) Probes" on page 109
- "To set up a Genomic Tiling job" on page 176
- "To upload probes and annotation" on page 161
- "To search for probe groups" on page 224

If you use one of the design wizards that are described in the next step, this probe group creation or selection process is included in the wizard. See these topics

3 Use the **Create Array Design Using Existing Probe Group(s)** wizard to create the CGH+SNP microarray design. In this wizard, you select the desired CGH and SNP probe groups to include in the design. The desired probe groups must already exist in a folder to which you have access. See "To create a microarray design from existing probe groups (Wizard)" on page 269.

After you save a new CGH+SNP microarray design, you can take additional actions that vary by the status with which it was saved. For example, if you save the design with a status of Draft, you can edit the design, place it in review so that others can make changes to the design and save new versions of it, or complete the design and prevent additional changes. If the status of the design is Complete, you can submit the design to Agilent Manufacturing, after which you can request a quote for, or purchase the microarrays, either online or through your Agilent representative. See "Status of microarray designs" on page 248.

NOTE

H. sapiens is the only species option for CGH+SNP designs. However, if you want to include CGH probes for another species, upload these CGH probes with a species setting of **Na.** See "Uploading Probes" on page 158.

Also, to promote high quality analyses, eArray enforces several numerical guidelines on the probes in a CGH+SNP microarray design:

- The array must contain a minimum of 2,000 distinct SNP probes.
- At least 5% of the total features on the array must be filled by biological CGH probes.
- No more than 50% of the total features on the array can be occupied by control probes.

Viewing and Changing Microarray Designs

This section describes how to do the following tasks:

Task	See these topics
View the probes, statistics, and other details of a design	"To view a microarray design" on page 305
View the layout of probes on an array graphically	"To view the layout of probes on a microarray graphically" on page 306
Edit a design that you own	"To edit a microarray design" on page 310
Attach a note, file, or URL to a microarray design	"To add an attachment to a microarray design" on page 320
View, change, or remove the attachments to a microarray design	"To view the attachments to a microarray design" on page 322 "To remove attachments from a microarray design" on page 323
Let others edit a design that you own	"To place a microarray design in review" on page 324 "To place a different version of a design in review" on page 325
Edit a design that is owned by someone else	"To review a microarray design" on page 326
Prevent further changes to a design	"To prevent further edits or reviews of a design" on page 335
Change the control type assigned to probe groups in a microarray design	"To change the control type of probe groups" on page 336.

To view a microarray design

You can view the probes, statistics and other details of a microarray design. Before you can view a microarray design, you may need to download it from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer probe and annotation data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **View.**

In either case, the View Microarray Design dialog box appears. For information on the content of this dialog box, see "View Microarray Design" on page 871.

If the View button or command is not available for a microarray design, you may need to download the design from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

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

To view the layout of probes on a microarray graphically

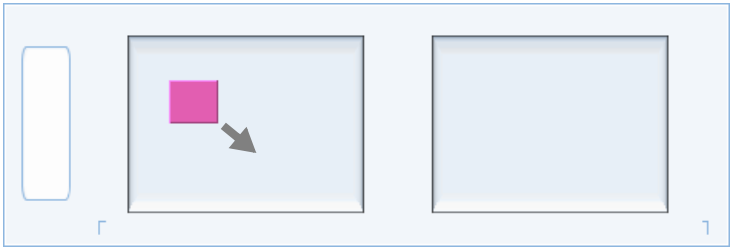
If a microarray design has a status of Complete or Submitted, you can view the layout of its probes graphically. This feature lets you view probes in several ways, but it does not let you edit the probes or their locations.

1 In the Design Data pane of the Navigator, right-click the name of the desired microarray design, then click **Array Visualizer.**

The Array Layout dialog box opens. A diagram of the microarray slide appears, probe side up, with its barcode on the left. Each replicate array on the slide appears as a raised rectangle. See "Array Layout" on page 583.

2 Under **Slide View,** in the diagram of the microarray slide, do one of the following to select the region to view:

- Within the diagram of the left-most array, drag the pointer diagonally through the desired area.

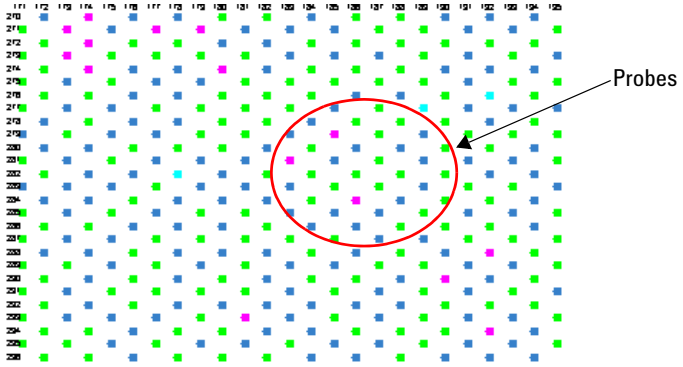


- Click **Find Area.** In the dialog box that appears, type the coordinates of the desired region (described in the table below), then click **Done.**

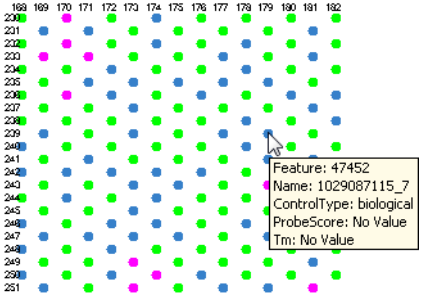
Coordinate	Description
X Start	The first column of features in the desired region.
Y Start	The first row of features in the desired region.
X End	The last column of features in the desired region.
Y End	The last row of features in the desired region.
Periodicity X	Currently, this parameter is always set to 1, which displays all columns in the selected area.
Periodicity Y	Currently, this parameter is always set to 1, which displays all rows in the selected area.

- To view the entire array, click **Select entire array.**

An expanded version of the selected region appears in the bottom pane of Slide View. Individual features appear as circles in the relative positions in which they are laid out on the array. Feature colors correspond with the definitions in Color Legend. For large regions, especially when you display the entire array, no distinct features are visible.



3 Do any of the following to get information about the probes in the array.

Task	Instructions/Details
View information about a specific probe	• Place the pointer over one of the features in the bottom pane of Slide View. A ToolTip appears with the feature number and ID of the probe, as well as control type, probe score, and T_M information, if it is available. 
View the coordinates of the currently selected region in Slide View	• Look under **Selected Area Details.**

Task	Instructions/Details
View the list of probes for the entire array	In the left pane of the dialog box, do either of the following: • Click **Probe List.** The probe groups that comprise the microarray design appear. To view the probes in a given probe group, click ⊞ beside its name. To hide the list of the probes in a probe group, click ⊟ • Click **Probes on Slide.** Lists the name and sequence of each probe on the array, sorted by the feature number from the GEML design file.
Color-code the probes in the microarray design in Slide View.	• In **Color Legend,** select the desired probe property. The program color codes the probes at the bottom of Slide View based on their values for the selected property. The colors that can appear, and the information that they represent depend on the option that you select. These options can appear: ◦ **Control Type** – Color codes probes based on their control types. ◦ **Probe Score** – Color codes probes based on their calculated probe performance scores. See "To calculate probe performance scores" on page 214. ◦ **Tm** – Color codes probes based on their predicted dissociation temperatures from their respective targets.
Change the color that is assigned to a specific value or range.	**a** Under **Color Legend,** click the color swatch that you want to change. The Choose Color Background dialog box appears. See "Select Background Color" on page 848. **b** In the Swatches tab, select the desired color, then click **OK.** You can also use the HSB or RGB tabs of this dialog box to more precisely set the desired color. For details, see "HSB tab" on page 849 and "RGB tab" on page 850.

Task	Instructions/Details
Change the probe score or the Tm that the program uses as the basis to color-code probes	**a** In Color Legend, select either **Probe Score** or **Tm.** **b** Click **Change Cutoff.** An Input dialog box appears. **c** In Please Type the Cutoff Value for Probe Score (or Tm), type the desired cutoff value, without units, then click **OK.** The new cutoff value is reflected in the color schema in Color Legend. **Note:** Type T_Ms in °C, but leave out the unit. For information on probe scores, see "To calculate probe performance scores" on page 214.
Restore the colors in the color legend to their default values	• Click **Restore Default.**

To edit a microarray design

You can edit the content and properties of a microarray design. You must own the design, and it must have a status of Draft.

1 If you are creating a new microarray design from an existing one, skip to step 3. Otherwise, search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **Edit.**

In either case, the Edit Microarray Design dialog box appears. See "Edit Microarray Design" on page 751.

NOTE

If the Edit button or command is not available, you may not be the owner of the design, or the design may not have a status of Draft — see the note at the end of this topic. Also, the design may need to be downloaded from the eArray Web site — see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

3 At the top of the dialog box, make changes to any of the following properties, as desired. The properties that do not appear in the table below are calculated by the program, or are informational only, and cannot be edited. For details on all of the items in this dialog box, see "Edit Microarray Design" on page 751.

Property	Instructions/Details
Microarray Name	Type a new name for the microarray design. The name can be from 1 to 100 characters long. Use only letters, numbers, spaces, hyphens, underscores, and periods.

Property	Instructions/Details
Status	Select one of these options: • **Draft** – The design will continue to have a status of Draft, which lets only the owner edit it. • **Review** – Places the design in review, which lets anyone with access to the design make changes to it. See "To review a microarray design" on page 326. • **Complete** – Assigns a status of Complete to the design. The design can subsequently be submitted to Agilent. It cannot be edited. **Caution:** Design status follows a one-way order from Draft to Review to Complete. Once you save a design with a given status, you cannot change the status to a previous one in the order.
Folder	Select a new location for the design. Only the folders to which you have access appear in the list.
Design Format	Select a different design format, if one is available. The design format reflects the number of replicate arrays and the approximate total number of features in each array on a slide. **Example:** The 4x44K format contains four replicate arrays on a single glass slide. Each of these arrays contains approximately 44,000 features.
Control Grid	Select an alternate control grid, if one is available. The name of the currently selected Agilent control grid appears in the list. This is a required group of probes that is included in each design for quality control, background subtraction, and the like. The control grid can vary based on the application type, species, design format, and user choice. It occupies a portion of the features in each design.
Description	Edit the description, as desired.
Keywords	Edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Edit comments. If you intend to save the design with a status of Complete, which prevents further editing of the design, comments are required. Otherwise, comments are optional.

Property	Instructions/Details
Features pre microRNA	(microRNA application type only) Select the desired number of features. This property reflects the total number of features on the array assigned to each microRNA. Each microRNA has from one to four different probes associated with it. eArray adjusts the number of replicates of each of these probes to achieve the specified number of features per target (microRNA). A higher number generates slightly more robust data, while a lower setting lets you measure more microRNAs per array. The default value is 16 features per microRNA target. Agilent Catalog arrays use 16 features per microRNA target for human arrays, and 20 features per microRNA target for mouse and rat arrays.

4 Under **Layout Details,** make changes to the probe content of the microarray design. Use the tasks described in the table below. As you change the probe

content of the microarray design, the program updates the values in the Microarray Statistics pane.

Task	Instructions/Details
Add or remove biological or user control probe group(s)	You can add or remove biological or user control probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe groups appear in the list. **c** In the Control Type column, select the desired control type for each probe group. For details, see "Change the control type of a probe group" on page 314 **To remove biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Note:** • Separate tasks below describe how to add or remove SNP, normalization, or replicate probe groups. • For microRNA microarrays, you can only add *biological* type probe groups.

Task	Instructions/Details
Change the control type of a probe group	The control type of a probe group influences how the data from the probe group are handled in downstream analysis. **a** Click **Probe Groups.** **b** Next to the name of the desired probe group, in the **Control Type** column, select an option from the list. Positive and negative control probe groups cannot collectively occupy more than 50% of the available features in your design. • **biological** – Identifies the probe group as a non-control probe group (condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample. **Note:** The control type of user probe groups on microRNA microarrays is always **biological,** and cannot be changed.

Task	Instructions/Details
Add or remove SNP probe group(s)	(CGH+SNP microarrays only) SNP probe groups contain probes that interrogate specific SNP sites, and are designed for use in CGH+SNP microarray designs. See "To create a CGH+SNP microarray design" on page 301. You can add or remove SNP probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add SNP probe group(s)** **a** Click **SNP Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the SNP Probe Groups pane. **To remove a SNP probe group** **a** Click **SNP Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**
Change the number of copies of a probe group	You can include multiple copies of biological probe groups in a microarray design. **a** Click the desired **Probe Groups** tab. **b** In the **Replicate** column, next to the desired probe group, type the number of copies of the probe group that you want to include in the microarray design. The default is 1. **Example:** You have selected a design format of 4x44K, and for a given probe group you type 2 in **Replicate.** The probe group appears eight times on the microarray slide, twice in each of the four individual arrays on the slide. **Note:** For the microRNA application type, the **Replicate** parameter is always set to 1.

Task	Instructions/Details
Add or remove a normalization probe group	(CGH arrays only) A normalization probe group is a special control probe group that supplies data that can be used to normalize the two dye channel data generated from the array. For more information on normalization probes, see "CGH array design guidance" on page 900. **To add a normalization probe group** **a** Click **Normalization Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Normalization Probe Groups pane. **To remove a normalization probe group** **a** Click **Normalization Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add or remove a replicate probe group	(CGH and Expression arrays only) A replicate probe group is a special control probe group that is used in downstream analysis by the Feature Extraction and DNA Analytics programs. These probe groups are distinct from the user probe groups that you select in the Probe Groups pane. See "Expression array design guidance" on page 898 and "CGH array design guidance" on page 900. **To add a replicate probe group** **a** Click **Replicate Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Replicate Probe Groups pane. **c** In the **Replicate** column, type the number of copies of the probe group to be included in the design. Agilent recommends a value of 5. **To remove a replicate probe group** **a** Click **Replicate Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add or edit linkers	Linkers are nucleic acid molecules that are synthesized to the 3′ end of the "active" (hybridizing) sequences of probes. In principle, linker sequences do not hybridize to any sequences in the target sample. They move the active sequences farther off of the array surface, which reduces steric hindrance. This makes the active probe sequence more available for a hybridization event. **a** Click **Linker Options.** **b** Mark **Append linker to 3' end.** The options in Linker Length and Linker Sequence become available. **c** In **Linker Length,** select one of these options: • **Append linker to make total probe length of** – Adds nucleotides to the 3' ends of probes so that the resulting probes have the length specified. In the box, type a number of nucleotides from 20 to 60. If there are probes in your microarray design that are longer than the length that you set, the program leaves them alone. They are not trimmed, and no linkers are added to them. • **Append linker of fixed length** – Adds the specified number of nucleotides to the 3' ends of probes. In the box, type a number of nucleotides from 1 to 49. The program truncates the linker on a probe, as necessary, to keep the total length of the probe from exceeding 60 nucleotides. If the linker sequence is shorter than length you set, eArray replicates the linker sequence to fill in the length. **d** In **Linker Sequence,** select one of these options: • **Use Agilent Linker Sequence** – You cannot edit the Agilent-provided linker sequence. • **Use Customer Linker Sequence** – Type a DNA base sequence for the linker. Use a random sequence, or derive it from a sequence not found in nature. **Note:** • For Agilent probes, the program adds the Agilent linker sequence, even if you select Use Customer Linker Sequence. • For the microRNA application type, 5′ and 3′ linkers are added to probes automatically by the program. No linker options are available.

Task	Instructions/Details
Remove linkers from probes	**a** Click **Linker Options.** **b** Clear **Append linker to 3' end.** **Note:** You cannot remove the linkers from probes in a microRNA microarray design.
Fill unused features or change filler probe group.	You can fill the unused "empty" features of a microarray design with probes from the probe group of your choice. The program applies probes from the selected probe group, multiple times if needed, until all features are filled. You can also use this procedure to select a different filler probe group. **a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Mark **Fill Microarrays.** In Probe Group to Fill Microarray, a Select button appears. **c** Click **Select.** The Select Probe Group to Fill Microarray pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **d** Search for and add one probe group, then click **Done.** The selected probe group appears in the Fill Microarray pane, in Probe Group to Fill Microarray. **Note:** For microRNA microarrays, the program always uses a default structural filler probe group.
Remove filler probes	**a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Clear **Fill Microarrays.** **Note:** The structural filler probe group used in microRNA microarrays cannot be removed.

NOTE

- When you select probe groups for a microarray design, the program tells you if a probe group is *Local* or if it is *Not Downloaded.* If you select one or more probe groups that are *Not Downloaded,* you can only save the new microarray design with a status of Draft. After you download the given probe group(s) from the eArray Web site, you can save the microarray design with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.
- In the Microarray Statistics pane, the Percentage Filled (%) statistic must not exceed 100%. If it does, select a design format with a higher feature capacity, or remove probe groups from the design.

5 At the bottom of the dialog box, click **Save.**

The program saves your edited design to your server. The new version replaces the previous version, even if you selected a different location for the design. A dialog box tells you that the microarray design has been updated successfully.

6 Click **OK.**

NOTE

To edit a design, you must own it, and it must have a status of Draft. To make changes to designs that you do not own, or that have a status other than Draft, use either of these methods:

- Make a copy of the design, then make changes to the copy. See "To copy a microarray design" on page 340.
- Ask the owner of a microarray design to place it in review, which lets other users who can access the design make changes to it. See "To place a microarray design in review" on page 324 and "To review a microarray design" on page 326.

To add an attachment to a microarray design

You can attach notes, files or URLs to any microarray design to which you have access, except Agilent Catalog designs. Attachments let you include background material, protocols, and other related information with the design.

1 In the Design Data pane of the Navigator, expand folders until you can see the microarray design to which you want to add an attachment.

2 Right-click the name of the desired microarray design, then click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593.

3 Add the desired attachment as described in the table below.

Type of Attachment	Instructions/Details
Note	You can attach text to a microarray design. **a** In **Attachment Type,** select **Notes.** The box in Note becomes available. **b** In **Note,** type the desired text. **c** Click **Add.** In the Total Attachments pane, the note appears in the list of attachments. The beginning of the note appears in Attachment Name.
File	You can attach a file to a microarray design. When users view the attachments to the microarray design, they can open the attached file. **a** In **Attachment Type,** select **File.** **b** In **Name,** type a name for the attachment. This becomes the display name for the file in the Total Attachments pane. **c** In **File,** click **Browse.** An Open dialog box appears. **d** Select the desired file, then click **Open.** The location of the file appears in File. **e** Click **Add.**In the Total Attachments pane, the newly attached file appears in the list of attachments.
URL	You can attach a URL to a microarray design. The URL can point to a Web site or other resource. When users view the attachments to the microarray design, they can open the URL in their Web browser. **a** In Attachment Type, select **URL.** **b** In **Name,** type a name for the attachment. This becomes the display name for the URL in the Total Attachments pane. **c** In **URL,** type the complete URL — for example, `http://www.agilent.com` **d** Click **Add.** In the Total Attachments pane, the new URL appears in the list of attachments.

To view the attachments to a microarray design

You can view the notes, files and URLs that are attached to a microarray design.

1 Browse for the desired microarray design. See "To browse available microarray designs" on page 256.

2 Right-click the name of the desired design, then click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. The notes, files and URLs that are attached to the microarray design appear in the Total Attachments pane. If there are many attachments, the program paginates the list. To go to a different page, click one of the numbered page buttons above or below the list.

3 In the **Actions** column, in the row of the desired attachment, click  . You can view the attachment as described in the table below:

Type of attachment	Details/Instructions
Note	Notes appear in the Note dialog box. See "Note" on page 825. **Note:** The program also displays the notes that you have created in the Note tab in the main pane of the program. Each note appears as a note icon with the name of the note. To open a note, double-click its icon. To delete a note in this tab, as well as from the microarray design, right-click the desired note icon, then click **Delete.**
File	Files open in an appropriate program, if one exists on your computer.
URL	URLs open in your Web browser.

To remove attachments from a microarray design

You can remove attached notes, files and URLs from a microarray design.

1 In the Design Data pane of the Navigator, right-click the name of the desired microarray design, then click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. If there are many attachments, the program paginates the list. To go to a different page of attachments, click a numbered page button above or below the list.

2 In the Total Attachments pane, select the URL(s) and/or file(s) that you want to remove. To select a file or URL, mark the check box next to its name. To select all of the files and URLs on the current page of attachments, mark the check box in the column heading row. The program remembers your selections as you go from page to page.

3 Click **Delete.**

A dialog box asks if you are sure you want to delete the attachments.

CAUTION When you remove an attached note, file or a URL, the program permanently removes the item from the microarray design. To restore an attachment, you must re-attach the item.

4 Click **Yes.**

A dialog box tells you that the attachment(s) were successfully deleted.

5 Click **OK.**

To place a microarray design in review

If you are the owner of a microarray design with a status of Draft, you can place it in review. This lets any user who has access to the design make changes and save new versions of it.

NOTE

If your microarray design contains any Agilent Catalog probe groups, or probe groups from the folders of your workgroup on the eArray Web site, you must transfer them from the eArray Web site to your server before you can place the microarray design in review. If Agilent has updated the content of a probe group since you transferred it to your server, you must transfer it again. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

In addition, you may also need to transfer probe and annotation data from the eArray Web site to your server for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1. Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.
2. Do one of the following:
   - If you searched for the design – In the **Actions** column of the search results, next to the desired design, click .
   - If you browsed for the design – Right-click the name of the desired design, then click **Edit.**

   In either case, the Edit Microarray Design dialog box appears. For details about this dialog box, see "Edit Microarray Design" on page 751.
3. In **Status,** select **Review.**
4. At the bottom of the dialog box, click **Save.**

   The program places the design in review. In the Design Data pane of the Navigator, the icon next to the microarray design changes to . Other users with access to the design can now make changes and save new versions of it. See "To review a microarray design" on page 326.

   A dialog box tells you that the design was updated successfully.
5. Click **OK.**

To place a different version of a design in review

When a microarray design is in review, the program keeps all saved versions of the design, each with a unique version number. By default, all reviews use the original version of the design as a starting point. However, the owner of the design can select any version as the starting point for subsequent reviews.

To place a different version of a design in review, you must be the owner of the design. Also, the design must have a status of Review. See "To place a microarray design in review" on page 324.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **Review.**

In either case, the Edit Microarray Design dialog box appears. For details about this dialog box, see "Edit Microarray Design" on page 751.

3 In the Layout Details pane, click **List of Versions.**

4 In the **Select Version** column, select the desired version.

A dialog box asks if you are sure you want to change the current version.

5 Click **Yes.**

The selected version becomes the current version. A dialog box tells you that the microarray design version has been successfully updated.

6 Click **OK.**

7 Click **Save.**

A dialog box tells you that the microarray design has been successfully updated.

8 Click **OK.**

To review a microarray design

If a microarray design has a status of Review, any user with access to it can make changes and save new versions of it.

For you to review a design, its owner must place it in review. See "To place a microarray design in review" on page 324. By default, all reviews use the original version of the design as a starting point. However, the owner of the design can select any version as the starting point for subsequent reviews. See "To place a different version of a design in review" on page 325.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **Review.**

In either case, the Edit Microarray Design dialog box appears. See "Edit Microarray Design" on page 751.

3 At the top of the dialog box, make changes to any of the following properties, as desired. The properties that do not appear in the table below are calculated by the program, or are informational only, and cannot be edited.

Property	Instructions/Details
Microarray Name	Type a new name for the microarray design. The name can contain from 1 to 100 characters. Use only letters, numbers, spaces, dashes, underscores, and hyphens.
Status	(Available only to the owner of the design) Do one of the following: • To let the review process continue, keep Status set to **Review.** • To end the review process, and prevent further changes to the design, select **Complete.** After you save the design, you can subsequently submit it to Agilent. **Caution:** If you save the design with a status of Complete, this prevents all further changes to it. You cannot subsequently change the status of the design back to Review or Draft.

Property	Instructions/Details
Folder	Select a new location for the design. Only the folders to which you have access appear in the list.
Design Format	Select a different design format, if one is available. The design format reflects the number of replicate arrays and the approximate total number of features in each array on the slide. **Example:** The 4x44K format contains four replicate arrays on a single glass slide. Each of these arrays contains approximately 44,000 features.
Control Grid	Select an alternate control grid, if one is available. The name of the currently selected Agilent control grid appears in the list. This is a required group of probes that is included in each design for quality control, background subtraction, and the like. The control grid can vary based on the application type, species, design format, and user choice. It occupies a portion of the features in each design. For microRNA microarrays, the program always applies a standard human control grid.
Description	Edit the description, as desired.
Keywords	Edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Edit comments, as desired. The comments appear during further reviews of the design. They also appear in the Comments column for the current version of the design when you click Version History.

4 At the bottom of the dialog box, make changes to the probe content of the design. Use the tasks described in the table below. As you change the probe

content of the design, the program updates the statistics in the Microarray Statistics pane.

Task	Instructions/Details
Add or remove probe group(s)	You can add or remove biological or user control probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe groups appear in the list. **c** In the Control Type column, select the desired control type for each probe group. For details, see "Change the control type of a probe group" on page 329. **To remove biological or user control probe group(s)** **a** Click **Biological <type> Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.** **Note:** • Separate tasks below describe how to add or remove SNP, normalization, or replicate probe groups. • For microRNA microarrays, you can only add *biological* type probe groups.

Task	Instructions/Details
Change the control type of a probe group	The control type of a probe group influences how the data from the probe group are handled in downstream analysis. **a** Click **Probe Groups.** **b** Next to the name of the desired probe group, in the **Control Type** column, select an option from the list. Positive and negative control probe groups cannot collectively occupy more than 50% of the available features in your design. • **biological** – Identifies the probe group as a non-control probe group condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample. **Note:** The control type of user probe groups on microRNA microarrays is always **biological,** and cannot be changed.

Task	Instructions/Details
Add or remove SNP probe group(s)	(CGH+SNP microarrays only) SNP probe groups contain probes that interrogate specific SNP sites, and are designed for use in CGH+SNP microarray designs. See "To create a CGH+SNP microarray design" on page 301. You can add or remove SNP probe group(s) from your microarray design. As you add or remove probe groups, the program displays statistics about feature utilization in the Microarray Statistics pane. See "Edit Microarray Design" on page 751. **To add SNP probe group(s)** **a** Click **SNP Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more probe groups, then click **Done.** The selected probe group(s) appear in the SNP Probe Groups pane. **To remove a SNP probe group** **a** Click **SNP Probe Groups.** A list of the biological and user control probe groups appears. **b** In the **Select** column, mark the check box next to the probe group that you want to remove. Click **Remove.**
Change the number of copies of a probe group	You can include multiple copies of most types of probe groups in a microarray design. **a** Click the desired **Probe Groups** tab. **b** In the **Replicate** column, next to the desired probe group, type the number of copies of the probe group that you want to include in the microarray design. The default is 1. **Example:** You have selected a design format of 4x44K, and for a given probe group you type 2 in **Replicate.** The probe group appears eight times on the microarray slide, twice in each of the four individual arrays on the slide. **Note:** For the microRNA application type, the **Replicate** parameter is always set to 1.

Task	Instructions/Details
View a list of the current and previous versions of the design	• In the Layout Details pane, click **List of Versions.** The List of Versions pane appears. All saved versions of the design appear by version number, along with the person who saved each one. The date the version was saved, and any comments from each reviewer, also appear. Reviewers can only make changes to the current version of a microarray design. However, if you are the owner of the design, you can use this pane to select a different version of the design as the "current" one. See "To place a different version of a design in review" on page 325.
Add or remove a normalization probe group	(CGH arrays only) A normalization probe group is a special control probe group that supplies data that can be used to normalize the two dye channel data generated from the array. For more information on normalization probes, see "CGH array design guidance" on page 900. **To add a normalization probe group** **a** Click **Normalization Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Select one or more probe groups, then click **Done.** The selected probe group(s) appear in the Normalization Probe Groups pane. **To remove a normalization probe group** **a** Click **Normalization Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add pr remove a replicate probe group	(CGH and Expression arrays only) A replicate probe group is a special control probe group that is used in downstream analysis by the Feature Extraction and DNA Analytics programs. These probe groups are distinct from the user probe groups that you select in the Probe Groups pane. See "Expression array design guidance" on page 898 and "CGH array design guidance" on page 900. **To add a replicate probe group** **a** Click **Replicate Probe Groups,** then click **Add.** The Add Probe Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Add one or more probe groups, then click **Done.** The selected probe group(s) appear in the Replicate Probe Groups pane. **c** In the **Replicate** column, type the number of copies of the probe group to be included in the design. Agilent recommends a value of 5. **To remove a replicate probe group** **a** Click **Replicate Probe Groups.** **b** In the **Select** column, mark the check box next to the probe group that you want to remove. **c** Click **Remove.**

Task	Instructions/Details
Add or edit linkers	**a** Click **Linker Options.** The Linker Options pane appears. **b** Mark **Append linker to 3' end.** The options in Linker Length and Linker Sequence become available. **c** In **Linker Length,** select one of these options: • **Append linker to make total probe length of** – Adds nucleotides to the 3' ends of probes so that the resulting probes have the length specified. In the box, type a number of nucleotides from 20 to 60. If there are probes in your microarray design longer than the length you set, the program leaves them alone. They are not trimmed, and no linkers are added to them. • **Add linker of fixed length** – Adds the specified number of nucleotides to the 3' ends of probes. In the box, type a number of nucleotides from 1 to 49. The program truncates the linker on a probe, as necessary, to keep the total length of the probe from exceeding 60 nucleotides. If the linker sequence is shorter than length that you set, eArray replicates the linker sequence to fill in the length. **d** In **Linker Sequence,** select one of these options: • **Use Agilent Linker Sequence** – You cannot edit the Agilent-provided linker sequence. • **Use Customer Linker Sequence** – Type a DNA base sequence for the linker. Use a random sequence, or derive it from a sequence not found in nature. **Notes:** • For Agilent probes, the program adds the Agilent linker sequence, even if you select Use Customer Linker Sequence. • For the microRNA application type, 5′ and 3′ linkers are added to probes automatically by the program. No linker options are available.
Remove linkers from probes	**a** Click **Linker Options.** **b** Clear **Append linker to 3' end.** **Note:** You cannot remove the linkers from probes in a microRNA microarray design.

Task	Instructions/Details
Fill unused features or change filler probe group.	You can fill the unused "empty" features of your design with probes from the probe group of your choice. The program applies probes from the selected probe group, multiple times if needed, until all features are filled. You can also use this procedure to select a different filler probe group. **a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Mark **Fill Microarrays.** A select button appears. **c** Click **Select.** The Select Probe Group to Fill Microarray pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **d** Search for, select, and add one probe group, then click **Done.** The selected probe group appears in the Fill Microarray pane, in Probe Group to Fill Microarray. **Note:** For microRNA microarrays, the program always uses a default structural filler probe group.
Remove filler probes	**a** Click **Fill Microarray.** The Fill Microarray pane appears. **b** Clear **Fill Microarrays.** **Note:** The structural filler probe group used in microRNA microarrays cannot be removed.

5 At the bottom of the dialog box, click **Save.**

The program saves the design to your server with a new, unique version number. A dialog box tells you that the microarray design has been successfully updated.

6 Click **OK.**

To prevent further edits or reviews of a design

If you are the owner of a microarray design, and it has a status of Draft or Review, you can change the status to Complete. When a microarray design has this status, no further changes can be made to it. This status also lets you subsequently submit the design to Agilent. See "To submit a microarray design to Agilent as part of a wizard" on page 347.

NOTE

If your microarray design contains any Agilent Catalog probe groups, or probe groups from the folders of your workgroup on the eArray Web site, you must transfer them from the eArray Web site to your server before you can change the status of the microarray design to Complete. If Agilent has updated the content of a probe group since you transferred it to your server, you must transfer it again. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

In addition, you may also need to transfer probe and annotation data from the eArray Web site to your server for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1. Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.
2. Do one of the following:
   - If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  if its status is Draft, or  if its status is Review.
   - If you browsed for the design – Right-click the name of the desired design, then click **Edit** if its status is Draft  , or **Review** if its status is Review  .

   The Edit Microarray Design dialog box appears. See "Edit Microarray Design" on page 751.
3. In **Status,** select **Complete.**
4. In **Comments,** type comments. Comments are required.

CAUTION

When you save the design with a status of Complete, this prevents further edits or reviews to it. You cannot subsequently change the status of the design back to Review or Draft.

5 Click **Save.**

A dialog box tells you that you are about to complete the design, and that once you save it, no additional changes can be made.

6 Click **OK.**

The program saves the design with a status of Complete. A dialog box tells you that your microarray design has been successfully updated.

7 Click **OK.**

To change the control type of probe groups

When a microarray has a status of Complete or Submitted, you cannot edit most of its properties, even if you are its owner. However, if you are the owner of the design, you can change the control type that is associated with each of the biological or user control probe groups in it. This can influence how data from the probe groups is handled in downstream analysis.

1 Search or Browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click .
- If you browsed for the design – Right-click the name of the desired design, then click **Change Control Type.**

In either case, the Change Control Type of Microarray Design dialog box appears. See "Change Control Type of Microarray Design" on page 612.

3 In the Layout Details pane, in the Probe Groups pane, under **Control Type,** select new options as needed. The following options are available:

Control type	Description
biological	Identifies the probe group as a non-control probe group (condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design.
ignore	Omits the probe group from the Feature Extraction analyses and output.

Control type	Description
neg	Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal.
pos	Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample.

All of the other options in this dialog box are read-only.

4 Click **Save.**

A dialog box tells you that the control types of the microarray design have been successfully updated.

5 Click **OK.**

NOTE

- A microarray design must contain at least one biological probe group.
- The control type of all user probe groups for microRNA microarrays is **biological.** This cannot be changed.
- You cannot change the control type of a normalization, replicate, or SNP probe group.
- Control probe groups cannot collectively occupy more than 50% of the features of a microarray design.

Managing Microarray Designs

This section describes how to move, copy, delete, and download microarray designs. Refer to these topics:

Task	See these topics
Move a microarray design that you own to another folder	"To move a microarray design" on page 338
Copy an existing microarray design	"To copy a microarray design" on page 340
Download microarray design file(s) from your server	"To download microarray design files" on page 341
Make additional design files available, so you can download them	"To select the types of design files that the program creates" on page 343
Remove a microarray design from your server	"To delete a microarray design" on page 345

To move a microarray design

You can move a microarray design that is stored on your server to a new folder. The program gives you several ways to do this.

Before you move a microarray design

- You must be the owner of the design. (However, see the note at the end of this topic.)
- You must have access to the destination folder.

To move a microarray design, do one of the following:

- Expand the folders of the **Design Data** pane of the Navigator until you can see the desired design, then follow these steps:

  1 Right-click the name of the design, then click **Move.**

  The Move Array Design dialog box appears. See "Move Array Design" on page 810.

  2 In **Move to Domain,** select the desired destination folder. Only the folders to which you have access appear in the list.

3 Click **Move.**

A dialog box asks if you really want to move the design.

4 Click **Yes.**

The program moves your design to the selected location. A dialog box tells you that your design was successfully moved.

5 Click **OK.**

- (This method lets you move more than one design at a time.) Search for one or more microarray designs. (See "To search for microarray designs" on page 251.) Then follow these steps:

1 In the search results, mark the check boxes next to the designs that you want to move.

2 Click **Move.**

The Move Array Design dialog box lists the selected designs. See "Move Array Design" on page 810.

3 In **Move to Domain,** select the desired destination folder for the designs. Only the folders to which you have access appear in the list.

4 Click **Move.**

A dialog box asks if you really want to move the design.

5 Click **Yes.**

A dialog box lists the selected designs, and indicates which ones were successfully moved. If any designs were not moved, the reason appears in the dialog box

6 Click **OK.**

NOTE To move a design that you do not own, create a copy of the desired design, then move the copy. See "To copy a microarray design" on page 340.

To copy a microarray design

You can make a copy of an existing microarray design. This can be useful in several situations:

- You want to create a microarray design that has all or most of its probes in common with an existing one. You can make a copy of the existing design, then edit the copy.
- You want to make changes to a microarray design that has a status of Complete or Submitted (and thus cannot be edited). You can make a copy of the Complete or Submitted array design, then edit the copy.
- You want to move a microarray design that you do not own to a different location. You can make a copy of the existing design, then move the copy.
- You want to edit a microarray design that you do not own. You can make a copy of a design that is owned by someone else, then edit the copy.

To copy a design with a status of Complete or Submitted, you must have access to it. To copy a design with a status of Draft or Review, you must either be the owner of the design, or all of the probe groups in the design must have a status of Locked.

1 Search or browse for the desired existing microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you retrieved the microarray design with a search, click next to the desired design in the **Actions** column of the search results.
- In the **Design Data** pane, right-click the name of the desired microarray design, then click **Copy.**

A dialog box asks if you are sure that you want to copy the design.

3 Click **Yes.**

In either case, the program creates a copy of the microarray design, with a status of Draft. A dialog box tells you that the design has been copied successfully.

4 Click **OK.**

The Edit Microarray Design dialog box appears. See "Edit Microarray Design" on page 751. The new microarray design has the name of the original design, with "Copy_of_" added to the beginning of the name.

5 Edit the design, as desired. You can change many properties of the design, including its name, status, format, and probe content. See "To edit a microarray design" on page 310.

6 Click **Save.**

The program saves your edits. A dialog box tells you that the design has been successfully updated.

7 Click **OK.**

NOTE For microarray designs from the eArray Web site, if the copy command is not available, you must first update the design from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

To download microarray design files

You can download the design files for a microarray design that is stored on your server. Certain essential design files contain the information that is required to manufacture microarray slides, and to successfully analyze array sample data. Other design files supply additional array-specific information.

Your server keeps every version of the design files for a given microarray design that is transferred from the eArray Web site, or that is created in eArray$_{XD}$. When you download design files from your server, you can select any available version. Each available set of design files is associated with a specific design ID and timestamp, which you select in **Build Number.** Each set of files also maps to a specific genome build. More than one version (set) of files can map to a given genome build or design ID.

Follow the steps below to download design files for microarrays from the AgilentCatalog folder, and from the folder that has the name of your workgroup. For microarray designs that are contained in the Custom Designs folder, see the last note at the end of this topic.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **Download.**

If these options do not appear, you may first need to download the design from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

The Download Microarray Design dialog box appears. See "Download Microarray Design" on page 726. In Build Number, a list of design IDs/timestamps appears.

Example: In Build Number, **015068_20091214** is one of the options. This refers to the microarray design with a design ID of 015068, specifically the version of the design files that has a timestamp of 20091214.

3 In **Build Number,** select the design ID/timestamp of the set of design files that you want to download.

All of the design files that are associated with the selected design ID and timestamp appear.

4 Mark the name(s) of the desired file(s), then click **Download.**
To select all of the file types that appear in the dialog box, mark **Select All,** if it appears.

A Save dialog box appears.

5 Select a location for the downloaded files, then click **Save.**

The program downloads all of the requested files as a single *.zip file. A dialog box tells you that your files were successfully downloaded.

6 Click **OK.**

NOTE

- For microarray designs with a status of Draft, no design files can be downloaded.
- For microarray designs with a status of Review that you have created in eArray$_{XD}$, you can download a TDT (tab-delimited text) file that gives the feature location of each of the probes in the design.
- For microarray designs with a status of Complete or Submitted, many files can be available. For a complete list, see "Download Microarray Design" on page 726. The availability of particular design files depends on the application type, whether the design was created locally or on the eArray Web site, and other factors. See "Availability of design files" on page 728.
- You can customize which types of files the program creates. See "To select the types of design files that the program creates" on page 343.
- For design files that have been transferred from the eArray Web site, the timestamp that is associated with the transferred files is the same as the timestamp of this set of files on the eArray Web site, without regard to when the files were transferred to your server.
- When the program downloads microarray design files, it does not download any files that have been added as attachments to the design. For information about attached files, see "To add an attachment to a microarray design" on page 320.
- If you save a microarray design on the eArray Web site with a status of Complete or Submitted *after* you install your Agilent Genomic Workbench server, you can only download a GEML file. You download this file from the **Custom Designs** folder in the Design Data pane of the Navigator. It is typically available within 24 hours after you save the design on the eArray Web site. No other actions are available for these types of designs. To download this GEML file, right-click the name of the design, then click **Download.**

To select the types of design files that the program creates

This procedure lets you set your preferences for which design files the program creates for microarray designs and SureSelect Target Enrichment libraries.

1 Set the desired application type. See "To set the application type" on page 48.

2 In the **Home** tab, click **User Preferences > Miscellaneous.**

The Miscellaneous tab of the User Preferences dialog box appears. See "User Preferences – Miscellaneous tab" on page 864.

3 At the bottom of the tab, click **Change Writer Preferences.**

The File Writer Preferences dialog box appears. See "File Writer Preferences" on page 774.

4 Mark the check boxes next to the types of files that you want the program to create, then click **Apply.**

A dialog box tells you that your preferences were successfully created. When you set your writer preferences for one application type, this sets your preferences for all application types.

5 Click **OK.**

6 In the User Preferences dialog box, click **OK.**

NOTE

- By default, the program only creates the design files that are required for data analysis in Agilent Genomic Workbench, or in GeneSpring. You cannot clear these options.
- The files that the program can create vary by application type. See "Download Microarray Design" on page 726.
- The program creates the files that you select for microarray designs that you *subsequently* create in eArray$_{XD}$ or transfer from the eArray Web site.

To delete a microarray design

When you delete a microarray design, you remove its design files and parameters from your server. You do not remove its component probes and probe groups. Also, the Delete command has no effect on your content on the eArray Web site.

Before you delete a microarray design

- You must be the owner of the design.
- The design must have a status of Draft, Review, or Complete. You cannot delete designs with a status of Submitted.

To delete a microarray design

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the **Actions** column of the search results, next to the desired design, click  .
- If you browsed for the design – Right-click the name of the desired design, then click **Delete.**

A dialog box asks if you are sure that you want to delete the design.

CAUTION When you delete a microarray design, the program permanently removes it from your server. To restore a deleted design, you must create or upload it again.

3 Click **Yes.**

Submitting Microarray Designs to Agilent

You submit designs through eArray$_{XD}$ and your server to Agilent Manufacturing. After you submit a design, you can request a price quote. Your Agilent sales representative can then help you place an order for your custom microarray. Agilent fabricates the arrays after you order them. Refer to the following topics:

Task	See these topics
Submit a microarray design to Agilent Manufacturing	"To submit a microarray design to Agilent" on page 346.
Submit a microarray design to Agilent Manufacturing as part of a wizard	"To submit a microarray design to Agilent as part of a wizard" on page 347
Request a price quote for a microarray that you have submitted	"To request a quote" on page 348
Order microarrays from Agilent	"To order microarrays" on page 350

To submit a microarray design to Agilent

You can submit a microarray design to Agilent Manufacturing from the Design Data pane of the Navigator, or from the results of a microarray design search. The design must have a status of Complete. Once you submit a design, the program does not let you change or delete it.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the microarray design – In the search results, in the **Actions** column, next to the desired design, click .
- If you browsed for the design – In the Design Data pane of the Navigator, right-click the name of the design, then click **Submit.**

In either case, the Submit Microarray Design dialog box appears. See "Submit Microarray Design" on page 862.

3 In **Comments,** type brief comments to be saved with the design. Comments are required as a means to minimize accidental submission of designs.

4 Click **Show Checklist.**

A design checklist appropriate to your application type appears. To see a copy of this checklist, see "Design Checklists" on page 894.

5 Read and mark all of the items in the checklist, then click **Done.**

CAUTION If you submit a microarray design to Agilent Manufacturing, you cannot subsequently "un-submit" it. You also cannot delete a submitted design.

6 In the Submit Microarray Design dialog box, click **Save.**

The program submits the design to Agilent Manufacturing, and gives it a status of Submitted. A dialog box tells you that the design has been successfully submitted.

7 Click **OK.**

Later, you can request a price quote through the program, and place an order for microarrays through your Agilent sales representative. See "To request a quote" on page 348.

NOTE When you submit a design from eArray$_{XD}$, the design becomes available in your user account on the eArray Web site, where you can retrieve the design in an eArray$_{XD}$ design search, view or download the design, and request a quote for it. However, on the eArray Web site, you cannot copy the design, access its probes, or publish it on OpenGenomics.com.

To submit a microarray design to Agilent as part of a wizard

You can submit a microarray design to Agilent Manufacturing as the final step in each of the design creation wizards that are available in eArray$_{XD}$. This can be convenient, especially if you are sure that you will not need to make subsequent changes to a design before you order it. Once you submit a design, the program does not let you make further changes to it.

1 Start creating a microarray design. Use a method that is described in one of these topics:

- "To create a microarray design from existing probe groups (Wizard)" on page 269
- "To create a microarray design from uploaded probes" on page 282

- "To create a microarray design from target transcripts" on page 289
- "To create a microarray design with HD probes" on page 297

2 In the final step of the wizard, when you select a status for the design, select **Submitted,** then finish the design creation process.

The program submits the design to Agilent Manufacturing, and gives it a status of Submitted. Later, you can request a price quote through the program, and place an order for microarrays through your Agilent sales representative. See "To request a quote" on page 348.

CAUTION If you submit a microarray design to Agilent Manufacturing, you cannot subsequently "un-submit" it. You also cannot delete a submitted design.

NOTE When you submit a design, the program uploads the design files to Agilent Manufacturing. The design also becomes available in your user account on the eArray Web site, where you can retrieve the design in an eArray$_{XD}$ design search, view or download the design, and request a quote for it. However, on the eArray Web site, you cannot copy the design, access its probes, or publish it on OpenGenomics.com.

To request a quote

You can request a price quote for a microarray design through the program. The design must have a status of Submitted, and you must have access to it. You can also request a quote from your Agilent sales representative.

1 Search or browse for the desired microarray design. See "Searching and Browsing Microarray Designs" on page 251.

2 Do one of the following:

- If you searched for the design – In the search results, next to the desired microarray design, click 
- If you browsed for the design – In the **Design Data** pane of the Navigator, right-click the name of the desired design, then click **Request Quote.**

In either case, the eArray Web site opens in your Web browser.

The Request Quote page appears. The name of the design, its design format, and associated design number(s) appear under Microarray Details.

3 Under Quote Details, in **Quantity,** type the number of microarray slides that you want.

The corresponding total number of microarrays appears in Array Quantity. **Example:** If you type 5 in Quantity, and your design format is 8x15K, **40** appears in Array Quantity.

4 Click **Next.**

A confirmation page appears, with the details of your quote request.

5 Do any of the following:

- To change the quote request, click **Edit Quote Request.** You can edit the Quantity of arrays.
- To print the page, click the **Print** button.
- To delete the quote request, click **Cancel.**

6 Click **Submit.** This submits your quote to Agilent.

A success message appears.

7 Click **Close.**

A message tells you that your quote request has been submitted, and that you will receive a confirmation e-mail from Agilent. An Agilent sales representative will contact you to follow up on the quote.

8 Click **Log Out.**

A dialog box asks if you are sure you want to log out.

9 Click **OK.**

NOTE If you have purchased products from Agilent in the past, you can also place an order for microarrays at the Agilent Online Store through the eArray Web site. You do not need to obtain a price quote to place an order. See the online help on the site.

To order microarrays

You can place an order for custom or Agilent Catalog microarrays through your Agilent sales representative or the Agilent Online Store.

Before you place an order

- The microarray design must have a status of Submitted.

To place an order

Do one of the following:

- Contact your Agilent sales representative.

  To obtain the contact information for your Agilent sales representative, contact Agilent Technical Support. See "To contact Agilent Technical Support" on page 88.

- Order online at the Agilent Online Store.

  If you have purchased items from Agilent in the past, you can place an order for microarrays at the Agilent Online Store. You start the online ordering process on the eArray Web site on the quote request page for a specific microarray design. See "To request a quote" on page 348 and the online help on the eArray Web site. You do not need to obtain a price quote to place an order.

5 Working with SureSelect Target Enrichment Libraries

Target enrichment, also known as *genome partitioning,* is a method that isolates specific fragments of genomic DNA for sequencing. You use a library of complementary oligonucleotide **baits** to harvest fragments of interest (target DNA). The target DNA hybridizes well with the baits, but other DNA does not, which forms the basis of a powerful selection method that lets you focus your sequencing efforts.

When you order a SureSelect Target Enrichment library from Agilent, the product that you receive is a kit that contains a set of biotinylated RNA oligonucleotides. However, as part of the library manufacturing process, Agilent first creates DNA oligonucleotides, and then later transcribes them into RNA. Thus, when you create a library in eArray$_{XD}$, bait sequences are defined in terms of DNA bases (A, C, G, T).

With eArray$_{XD}$, you can access existing baits and bait libraries or create custom libraries of baits. A bait library is a collection of oligonucleotides in a tube, not a microarray, but you can leverage the well-developed eArray microarray creation infrastructure to design and obtain the libraries that you need for your research. To use eArray$_{XD}$ to create bait libraries, you set the application type to SureSelect Target Enrichment, and the relevant commands appear.

After you use a SureSelect Target Enrichment kit to prepare enriched samples, and you sequence those samples, you can use SureSelect Quality Analyzer to assess the quality of target fragment pull-down. This program is available free of charge within Agilent Genomic Workbench. See the *SureSelect Quality Analyzer User Guide.*

Libraries, bait groups, and baits

In eArray, bait libraries contain one or more bait groups, and each bait group contains individual baits. See Figure 11.

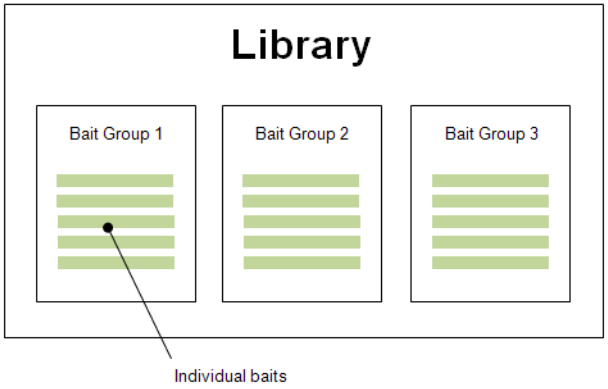


Figure 11 Baits, bait groups and libraries

For individual baits, you can use both existing baits in the Agilent Catalog and your own baits on your server. To put your own baits on your server, you can upload them, and you can also use Bait Tiling, a method that creates baits that cover selected regions of a genome of interest at even intervals.

To organize baits into bait groups, you can select baits based on a search for baits that already exist in the system. You can also create a bait group that contains baits that you upload or those that you create with Bait Tiling. Baits and bait groups are separate entities—you can use an individual bait in any number of bait groups.

Agilent currently supports a bait length of 120 nucleotides. In search panes or dialog boxes where you can set the bait length, select a value of 120.

Transfer of data from the eArray Web site

In eArray$_{XD}$ you can work with baits, bait groups, and libraries from the Agilent Catalog, and also from the folders of your workgroup on the eArray Web site. To do so, you may need to transfer several kinds of data:

- **Bait data and exon boundary data** – This kind of data includes the bait IDs, sequences, accessions and annotation of Agilent Catalog baits, and baits from your workgroup on the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.
- **Bait group and library mapping information** – This kind of data defines the baits that are found in a given bait group, and which bait group(s) are found in a given library. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
- **Agilent updates of bait content** – When Agilent updates the bait content of a bait group or library, you must download the updated content before you regain full use to these items. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

Creating libraries

One of the easiest ways to design a bait library is to use one of the wizards that are available in the program for the SureSelect Target Enrichment application type. Each leads you step-by-step through the library creation process. As you complete a wizard, you can submit your newly-designed library to Agilent Manufacturing. To obtain the library, you request a quote online through the program, and then place an order through your Agilent representative. These wizards are available for the creation of libraries:

- **Create Library using Bait Tiling** – Use this wizard to design a library from oligonucleotides that cover specific regions of the genome of interest at even intervals. See "To create a library using Bait Tiling (wizard)" on page 433.
- **Create Library using Existing Bait Groups** – Use this wizard to design a library that uses existing collection(s) (groups) of baits. You can include your own bait groups if they are on your server, and you can also include bait groups from the Agilent Catalog. See "To create a library from existing bait groups (wizard)" on page 428.
- **Create Library using Bait Upload** – Use this wizard to create a library based on a file of bait sequences that you upload. See "To create a library from a bait upload (wizard)" on page 422.

If you require greater flexibility, or want to focus your attention on one level of organization at a time, eArray lets you do this, as well. See these topics for more details:

- "Working with Baits" on page 355

- "Working with Bait Groups" on page 394
- "Working with Bait Libraries" on page 414

Working with Baits

Baits are oligonucleotides that retrieve specific genomic DNA fragments of interest for sequencing. The desired DNA hybridizes with the baits, and other DNA does not. This forms the basis of a powerful selection method that lets you focus your sequencing efforts. The baits manufactured by Agilent are biotinylated RNA oligonucleotides. Currently, Agilent supports a bait length of 120 nucleotides.

In eArray$_{XD}$, a single bait is a nucleotide sequence that is linked to a unique BaitID and species. Although the final product supplied by Agilent is a kit of RNA oligonucleotides, Agilent first creates DNA oligonucleotides, and later transcribes these into RNA. Thus, bait sequences in eArray are specified in terms of DNA bases (A, C, G, T). Additional annotation can also be included, such as the applicable genomic interval, chromosomal location, gene symbols, and accession numbers. The table below shows a list of what you can do with baits.

Bait tool	Description	See these topics
Search tools		
Bait Search	Returns all baits that have any accession or annotation value that is an exact match with the search term. Alternatively, you can enter values for a specific type of annotation, such as a list of accession numbers, and the program retrieves the baits that exactly match each one. You can also upload the list as a text file.	"To search for baits" on page 358
Simple Interval Finder	Returns a list of the genomic intervals whose annotation contains a given search term. You can use the returned list of intervals to set up a Bait Tiling job.	• "To do a Simple Interval Finder Search" on page 363 • "To take action on interval search results" on page 369

Bait tool	Description	See these topics
Advanced Interval Finder	Returns a list of the genomic intervals whose annotation exactly matches a given search term. You can enter multiple terms. You can use the returned list of intervals to set up a Bait Tiling job.	• "To do an Advanced Interval Finder Search" on page 364 • "To take action on interval search results" on page 369
Simple Exon Finder	Returns a list of the exonic genomic intervals whose annotation contains a given search term. You can use the returned list of intervals to set up a Bait Tiling job.	• "To do a Simple Exon Interval Finder Search" on page 366 • "To take action on interval search results" on page 369
Advanced Exon Finder	Returns a list of the exonic genomic intervals whose annotation exactly matches a given search term. You can enter multiple terms. You can use the returned list of intervals to set up a Bait Tiling job.	• "To do an Advanced Exon Interval Finder Search" on page 367 • "To take action on interval search results" on page 369
Network or Literature Search	You can search for existing biological networks, and you can also use a literature search to create a custom network. The given network can supply relevant annotations or genomic intervals as input for bait searches, certain Interval Finder and Exon Interval Finder searches, and Bait Tiling.	• "To use a biological network or a literature search to find or create baits" on page 389
Other tools		
Upload baits	Lets you upload a file that contains bait IDs, sequences, and annotation to your server. You can also create a new bait group based on the baits in the uploaded file.	• "To upload baits" on page 370 • "To prepare a file of baits and annotation for upload" on page 371 • "To upload baits and annotation" on page 374 • "To create a bait group with uploaded baits" on page 378

Bait tool	Description	See these topics
Bait Tiling	Creates baits that cover specified genomic regions of a given species at even intervals. You can customize the tiling process for specific sequencing technologies and protocols, as well as adjust the density of tiling.	• "To set up a Bait Tiling job" on page 378 • "To view Bait Tiling results" on page 385 • "To download Bait Tiling results" on page 387 • "To create a bait group from Bait Tiling results" on page 387 • "To delete a Bait Tiling job" on page 388
View bait details and statistics	Displays the IDs and sequences of baits, bait annotation and accessions, and calculated statistics based on sequence and base composition.	"To view bait details and statistics" on page 362
Download baits	Lets you download baits in a variety of different file formats.	"To download baits" on page 389
Delete baits	Lets you permanently remove baits from your server.	"To delete baits" on page 392

To search for baits

This type of search can retrieve baits from any folder to which you have access, including the AgilentCatalog folder. You can enter a single search term that is related to any property of baits, except sequence. The program retrieves all baits that have an annotation or accession value that exactly matches the search term.

Alternatively, you can select a specific type of annotation, and enter one or more search terms. The program returns the baits that exactly match each of the terms.

You can also limit your search to baits in a specific folder, and/or those in specific bait group(s) or librar(ies). For a general discussion of baits, see "Working with Baits" on page 355.

Before you search for baits, you may need to transfer bait and annotation data to your server from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Baits.**

The Bait Search pane appears.

3 In **Search Type,** select one of these options:

Option	Details/Instructions
ALL	In this type of search, you enter a single search term. eArray retrieves baits that have any annotation or accession value that exactly matches the search term. In **Search Type,** type the desired search term in the empty box.
Bait ID	Type a bait ID, or multiple bait IDs separated by pipe "|" characters. The search returns baits whose bait IDs match exactly. A bait ID is a unique identifier for a bait. Alternatively, to upload a file that contains the desired bait ID data, click **Upload,** then select the desired file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.

Option	Details/Instructions
Accessions	Type an accession, or multiple accessions separated by pipe "|" characters. The search returns baits whose associated accessions are an exact match. An accession is a unique identifier that refers to a specific nucleotide sequence that is a target for the associated bait, or a protein sequence that is a product of the target. Enter accessions without sources. For example, list **ref|NM_015752** as `NM_015752`. Alternatively, to upload a file that contains the desired accession data, click **Upload,** then select the desired file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns baits with associated gene names that are an exact match. A gene symbol is a unique abbreviation that represents a gene, for example **H3N1,** or **CTSB.** Alternatively, to upload a file that contains the desired gene symbol data, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Chromosomal Location	Type a chromosomal location in the box, or multiple locations separated by pipe "|" characters. The search returns baits that are designed to genomic coordinates within the ones that you enter. **Example:** `chr1:47995000-49867300|chr2:20078-90992` Alternatively, to upload a file that contains the desired chromosomal locations, click **Upload,** then select the desired file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101. **Note:** You can also set up this type of search from the Genomic Viewer. Select the desired genomic region in Gene View, right-click the selected area, then click **Chromosomal Location Search.** The program opens the Bait Search pane and sets criteria for a search of the selected region. For information on the Genomic Viewer, see the *Data Viewing User Guide*.

Option	Details/Instructions
Cytoband	Type a cytoband identifier in the box, or multiple cytobands separated by pipe "|" characters. The search returns baits that are found in the listed cytobands. Follow this example format: `11p15.4` Alternatively, to upload a file that contains the desired cytoband data, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Bait Sequence	Type a valid bait sequence in the box, or multiple sequences separated by pipe "|" characters. The search returns baits whose sequences are exact matches. Alternatively, to upload a file that contains the desired bait sequences, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.

NOTE You can use a search for biological networks to supply search terms for a bait search. You can also use a literature search to create a custom network for this purpose. See "To use a biological network or a literature search to find or create baits" on page 389.

4 Enter additional search criteria as described below. **Folder, Species,** and **Length** are required. To clear all of the search criteria at any point, click **Reset.**

Search criterion	Instructions/Details
Folder	(Required) Select a folder from the list. The search returns baits only from the selected folder. To include the subfolders of the folder in your search, mark **Include Subfolders.** The list of folders contains only the ones to which you have access.
Species	(Required) Select the species associated with the baits that you want to retrieve.

Search criterion	Instructions/Details
Used in Bait Groups	If you set this criterion, the search returns baits only from selected bait group(s). To select bait groups, click **Select and Add.** The process is the same as the one described for selecting probe groups in "To select probe groups for searches or microarrays" on page 106. **Note:** The program does not return baits if you select a bait group that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Used in Libraries	If you set this criterion, the search returns baits only from selected librar(ies). To select libraries, click **Select and Add.** The process is the same as the one described for selecting probe groups in "To select probe groups for searches or microarrays" on page 106. **Note:** The program does not return baits if you select a library that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Length	(Required) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. **Note:** All baits in a bait library have the same length.

5 Click **Search.**

When the program completes the search, the returned baits appear in the Search Result pane. These results are a gateway to actions that you can take on baits. See these topics:

- "To view bait details and statistics" on page 362
- "To download baits" on page 389
- "To create a bait group from existing baits" on page 401
- "To delete baits" on page 392

To view bait details and statistics

After you do a search for baits, you can view bait sequences, accessions and annotation, as well as calculated statistics based on the sequences of the returned baits.

1 Do a Bait Search. See "To search for baits" on page 358.

The Search Result pane displays the baits that match your search criteria. To go to a different page of results, click a numbered page button.

The accessions associated with each bait appear in the Accessions column in the Search Result pane. Additional annotation, when available, can also appear in the other columns of the search results.

2 In the Search Result pane, select the bait(s) of interest. Use the following as a guide:

- To select an individual bait, mark the check box next to its Bait ID.
- To select all of the baits on the current page, mark the check box in the heading row of the Search Result table.
- eArray remembers the baits that you select as you go from page to page.
- To select all of the baits on every page of the search results, mark **Select entire data set.**

3 Click **Show Statistics.**

The Bait Statistics dialog box lists the Bait ID and sequence of each bait, along with results of statistical calculations based on the bait's sequence. For information about these statistics, see "Bait Statistics" on page 596.

You can download the bait sequences and statistics. Follow these steps:

a In the Bait Statistics dialog box, click **Download.**

A Save dialog box appears.

b Select a location for the downloaded file, then click **Save.**

The program downloads a *.tdt format file that contains the bait sequences and statistics. You can use a word processing or spreadsheet program to view the file. A dialog box tells you that the file was downloaded successfully.

c Click **OK.**

To do a Simple Interval Finder Search

You use a Simple Interval Finder Search to return genomic intervals whose annotation contains a single search term that you enter. You can then download the retrieved intervals, or use them as the basis for a Bait Tiling job.

1 Set the application type to **SureSelect Target Enrichment**. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Tools, click **Interval Finder > Simple Interval Finder.**

The Simple Interval Finder Search pane appears.

3 Enter search criteria as described below. Both are required. To clear the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Search Term	Type a search term in the box. The program returns the genomic intervals whose annotation contains this term. The search term is not case-sensitive.
Species	Select the desired species from the list.

4 Click **Search.**

The Search Results pane displays the returned intervals and the annotations that are associated with them.

You can use the intervals as the basis of a Bait Tiling job, and you can also download the intervals, or view a list of the distinct chromosomes represented in them. See "To take action on interval search results" on page 369.

To do an Advanced Interval Finder Search

You use an Advanced Interval Finder Search to retrieve the genomic intervals whose annotation exactly matches at least one of the search term(s) that you enter. You can then download the retrieved intervals, or use them as the basis for a Bait Tiling job.

1 Set the application type to **SureSelect Target Enrichment**. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Tools, click **Interval Finder > Advanced Interval Finder.**

The Advanced Interval Finder pane appears.

3 Enter search criteria as described below. You must enter at least one annotation value, and the species. To clear all of the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Accessions	Type an accession number, without its source, or multiple accession numbers separated by pipe "|" characters. The search returns the intervals that correspond with each of the accessions. For the search to return intervals, accessions must match exactly. Use upper case (capital) letters in accessions. **Example:** `NM_012257|Q0055|NM_012298` You can also upload a file of accessions. Prepare a plain text file with an extension of .txt. List one accession per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.

Search Criterion	Instructions/Details
Cytoband	Type a cytoband designation, without its source, or multiple cytobands separated by pipe "|" characters. The search returns the intervals that correspond with each of the cytobands. For the search to return intervals, cytobands must match exactly. Use lower case letters for the p or q chromosome arms. **Example:** `1p22.2|2q33.3` You can also upload a file of cytobands. Prepare a plain text file with an extension of .txt. List one cytoband per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns the intervals that are associated with each of the gene symbols. For the search to return intervals, gene symbols must match exactly. Use upper case (capital) letters in gene symbols. **Example:** `H3N2|BRMS1|BRCA1` You can also upload a file of gene symbols. Prepare a plain text file with an extension of .txt. List one gene symbol per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101. In addition, you can use a biological network search or a literature search to supply gene symbols. See "To use a biological network or a literature search to find or create baits" on page 389.
Species	(Required) Select the desired species from the list.

4 Click **Search.**

The Search Results pane lists the intervals that are associated with your search term(s).

You can use the intervals as the basis of a Bait Tiling job, and you can also download the intervals, or view a list of the distinct chromosomes that are represented in them. See "To take action on interval search results" on page 369.

To do a Simple Exon Interval Finder Search

A Simple Exon Interval Finder Search returns a list of the exonic genomic intervals whose annotation contains a single search term. You can then download the returned intervals, or use them as the basis for a Bait Tiling job.

To use this search tool, you may first need to transfer exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Set the application type to **SureSelect Target Enrichment**. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Tools, click **Exon Finder > Simple Exon Interval Finder.**

The Exon Interval Finder pane appears.

3 Enter search criteria as described below. Both are required. To clear the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Search Term	Type a search term in the box. The program returns the exons whose annotation contains this term. The search term is not case-sensitive.
Species	Select the desired species from the list.

4 Click **Search**

The Search Results pane displays the exonic intervals that are associated with your search term(s). For each interval, the pane lists the associated annotation and whether the exon is found on the + strand or the – strand of the DNA. For annotations that are associated with multiple exons, the pane lists each exon on a separate line.

You can use the intervals as the basis of a Bait Tiling job, and you can also download the intervals, or view a list of the distinct chromosomes represented in them. See "To take action on interval search results" on page 369.

To do an Advanced Exon Interval Finder Search

An Advanced Exon Interval Finder Search returns a list of the exonic genomic intervals whose annotation exactly matches at least one of the search term(s) that you enter.

To use this search tool, you may first need to transfer exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Set the application type to **SureSelect Target Enrichment**. See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Tools, click **Exon Finder > Advanced Exon Interval Finder.**

The Advanced Exon Interval Finder pane appears.

3 Enter search criteria as described below. You must enter at least one annotation value, and the species. To clear all of the search criteria at any point, click **Reset.**

Search Criterion	Instructions/Details
Accessions	Type an accession number, without its source, or multiple accession numbers separated by pipe "|" characters. The search returns the exonic intervals that correspond with each of the accessions. For the search to return intervals, accessions must match exactly. Use upper case (capital) letters in accessions. **Example:** `NM_012257|Q0055|NM_012298` You can also upload a file of accessions. Prepare a plain text file with an extension of .txt. List one accession per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.

Search Criterion	Instructions/Details
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns the exonic intervals that correspond with each of the gene symbols. For the search to return intervals, gene symbols must match exactly. Use upper case (capital) letters in gene symbols. **Example:** `H3N2 | BRMS1 | BRCA1` You can also upload a file of gene symbols. Prepare a plain text file with an extension of .txt. List one gene symbol per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101. In addition, you can use a biological network search or a literature search to supply gene symbols. See "To use a biological network or a literature search to find or create baits" on page 389.
Species	Select a species from the list. This limits your search to exonic intervals that are associated with the selected species. To return relevant intervals for all available species, select **All.**

4 Click **Search.**

The Search Result pane lists the exonic intervals that are associated with your search term(s). For each interval, the pane lists the associated annotation and whether the exon is found on the + strand or the – strand of the DNA. For annotations that are associated with multiple exons, the pane lists each exon on a separate line.

You can use the intervals as the basis of a Bait Tiling job, and you can also download the intervals, or view a list of the distinct chromosomes represented in them. See "To take action on interval search results" on page 369.

To take action on interval search results

You can select one or more intervals in the results of an Interval Finder or Exon Interval Finder search, and download them, set up a Bait Tiling job based on them, and list the chromosomes that are associated with them.

1 In the **Search Results** pane, select the desired intervals. Use the following as a guide:

- To select an interval, mark the check box in its row.
- To select additional intervals, mark their check boxes.
- To select all of the intervals on a page of results, mark the check box in the column heading row.
- To go to a different page of results, if available, click a numbered page button. The program remembers your selections as you go from page to page.
- To re-sort the search results, click a column heading. To reverse the order of the sort, click the same column heading again.
- To select all of the intervals on all pages of the search results, mark **Select entire data set.**

2 Do any of the following tasks:

Task	Instructions/Details
Download a file that contains a list of the selected intervals	**a** Click **Download.** A dialog box appears. **b** Select a location for the downloaded file, then click **Save.** The program downloads a *.tdt file. The file contains each selected interval on a separate line. You can open the file in a word processing or spreadsheet program.

Task	Instructions/Details
Set up a Bait Tiling job based on the selected intervals	**a** Click **Run Bait Tiling.** The Bait Tiling dialog box appears. See "Bait Tiling" on page 599. The selected intervals from your interval search appear in Genomic Target Intervals. The program also sets the relevant species and genome build in the dialog box, as well as default design options and target details. **b** Type a name for the Bait Tiling job and make any desired changes to the design options and target details, then submit the job. For details, see "To set up a Bait Tiling job" on page 378.
View a list of chromosomes that are represented by the selected intervals	• Click **List Chromosome.** A list of the distinct chromosomes that are represented by the selected intervals appears in a new window.

To upload baits

To add new bait content to your server, you can upload a file that contains the desired bait sequences and annotation. When you upload baits, the program transfers the sequences and annotation from your bait file to a location that you select on your server. You can then use the uploaded baits to create new bait group(s). Later, you can use the bait groups to create a library. See "To create a library from existing bait groups (wizard)" on page 428.

See these topics:

- "To prepare a file of baits and annotation for upload" on page 371
- "To upload baits and annotation" on page 374
- "To create a bait group with uploaded baits" on page 378

To prepare a file of baits and annotation for upload

Follow the guidelines below to prepare a bait data file.

File types

eArray$_{XD}$ supports these file types for bait uploads:

File Type	Notes
Microsoft Excel files (*.xls)	If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.
Tab-delimited text files (*.tdt or *.txt)	Place tabs between fields (columns) in a record (row). Use **new line** characters at the ends of records.

File formats

eArray$_{XD}$ supports the file formats in the table below. Your file can have columns in addition to those that are listed—if it does, be sure to label them **Ignore** when you upload the file. See "To upload baits and annotation" on page 374.

File Format	Columns included in format
Complete	BaitID Bait Sequence Genomic Interval Bait Genomic Location Accessions GeneSymbols Description Strand
Minimal	BaitID Bait Sequence

General format of data within a file

In uploaded files, eArray$_{XD}$:

- Accepts columns in any order – You label columns as part of the upload process.
- Accepts extra columns – When you label columns during the upload process, be sure to label any extra columns **Ignore.**
- Accepts, but does not interpret column headings – Be sure to mark **My uploaded file contains column headings** when you label columns during the upload process.
- Does not accept double or single quotation marks, angle brackets, or forward or backward slashes.
- Ignores blank lines.
- Expects all entries within a row to be separated by tabs, even if the actual entry is blank.

NOTE eArray$_{XD}$ can upload fairly large files. Agilent has tested the 64-bit version of the program, and has successfully uploaded 150,000 probes in the Complete file format, which corresponds to a file size of approximately 32 MB.

Specific requirements for individual types of data

Type of data	Requirements
BaitID	A unique identifier for the bait sequence, containing up to 15 characters. Bait ID cannot be blank.
Bait Sequence	The base sequence of the bait, in 5' to 3' orientation. The sequence must be 120 nucleotides in length, and must only contain the capital characters A, C, G, and T. All baits in the file must have the same length. Sequence cannot be blank.
Genomic Interval	The segment of the genome associated with the bait, for example chr1:1-10000. This column can be blank.
Bait genomic location	The exact position of the bait in the genome, for example chr1:1-169. This column can be blank.

Type of data	Requirements
Accessions	Unique identifier(s) that refer to a nucleotide sequence that is a target for the associated probe and/or a protein sequence that is a product of the target. Accessions are represented in a <source>|<ID> pair format. <source> is the symbol of the database from which the accession was derived and <ID> is the unique identifier accession. For example, `ref|NM_015752` is a <source>|<ID> pair where `ref` (NCBI Refseq) is the source and `NM_015752` is the unique identifier for that source. The Accessions field can contain multiple <source>|<ID> pairs, delimited by pipe "|" characters. For example, `gi|7657630|ref|NM_015752` is an allowable accession that gives both an NCBI gene identifier (`gi`), and a Refseq identifier (`ref`) for the same probe sequence. Accessions can be blank.
GeneSymbols	A unique abbreviation for a gene name. GeneSymbols can be blank.
Description	A description of a phenotype, gene product, or its function. Description can be blank.
Strand	The orientation of the bait, which can be + (sense) or – (antisense). The program interprets blank entries as **sense.**

Some possible causes of upload errors

- Your file contains two baits with the same Bait ID, but different sequences, and you select **Remove replicate baits from upload.**
- Your file contains two baits with the same Bait ID and the same sequence, and you have not selected **Remove replicate baits from upload.**
- You are not the owner of an existing bait whose annotation would be overwritten by a bait in your uploaded file.
- A bait from your uploaded file has the same Bait ID as one that already exists in the system, but it does not have the same sequence, species, or application type as the one it is overwriting.
- One or more entries in your uploaded file do not have the correct format.

To upload baits and annotation

You can upload baits and annotation to your server.

1 Create a file that contains the desired bait sequences and annotation values. See "To prepare a file of baits and annotation for upload" on page 371.

2 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

3 In the **eArray$_{XD}$** tab, under Create Bait, click **Bait Upload.**

The Bait Upload dialog box appears.

4 Enter the following details. All are required.

Detail	Instructions/Comments
Bait Parameter Details	
Job Name	Type a name that will help you to identify this job.
Species	Select the desired species. The program associates all baits in the uploaded file with this species.

Detail	Instructions/Comments
Remove replicate baits from upload	Mark this option to upload the first bait in each set of replicate baits in your file, and ignore the others. A replicate bait has the same Bait ID as another bait in the file. If your bait file contains replicate baits, and you do **not** mark **Remove replicate baits from upload,** the program does not upload your file.
Bait Precedence	These options define what the program does if it finds baits in your uploaded file that have the same Bait ID as baits that already exist in the system. Select one of these options: • **Overwrite matching baits** – The annotation of the matching uploaded baits replaces the annotation of the existing baits. You can use this option to reannotate existing baits. • **Skip matching baits** – The program ignores matching uploaded baits, but does upload other baits. • **Cancel upload if any baits already exist** – The program cancels the entire upload process if it finds a matching uploaded bait.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. The program uploads your file only if the length of every bait in your file matches this number.
Upload Bait File Details	
Upload Type	Select one of these options: • **Upload Baits Only** – Creates baits from the data in the uploaded file, and makes them available to you in the program as individual baits. • **Create New Bait Group** – In the box, type a name for the bait group. The bait group name can contain up to 100 characters. The program creates baits from the data in the uploaded file, and creates a bait group that contains the uploaded baits. The program saves the new bait group to your main "default" folder, and the baits are also available to you as individual baits.

Detail	Instructions/Comments
Upload File	Follow these steps to select the file of bait sequences and annotation to be uploaded: **a** Click **Browse.** An Open dialog box appears. **b** Select the desired file, then click **Open.** The location of the file appears in Upload File.
File Format	Select **MINIMAL** or **COMPLETE.** The file format defines the specific types of data available in the uploaded file. See "To prepare a file of baits and annotation for upload" on page 371.
File Type	Select the appropriate file type from the list. The file type defines how the data items in the file are specified and separated. The program accepts tab-delimited text (*.tdt and *.txt) and Microsoft Excel (*.xls) files. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

CAUTION If you select **Overwrite Matching Baits** in Bait Precedence, the program reannotates matching baits when it uploads your file. The original annotation of these baits cannot be recovered.

5 Click **Preview.**

The Define Uploaded File Columns pane appears in the lower part of the dialog box. The table contains a row of lists, and the first few rows of data from your file.

6 From the list at the top of each column, select the most appropriate label for the data beneath it. Use each label exactly once, except for *Ignore,* which you can use any number of times. You must label all columns.

7 If the first row of your bait data file contains column headings, mark **My uploaded file contains column headings.** If you mark this option, the program ignores the first line of the file, and does not interpret it as actual bait data.

8 Click **Upload.**

If you have not yet transferred your workgroup's bait and annotation data for the SureSelect Target Enrichment application type from the eArray Web site, a warning message tells you that the system will add a prefix of **XD_** to all of the new baits in your file. This differentiates your uploaded baits from any baits that you subsequently transfer from the eArray Web site that have the same names. To continue with the upload process, click **OK.**

A dialog box tells you that your file has been successfully submitted to the upload queue. A job appears in the Tasks pane of the Navigator, in the Bait Upload folder.

When you upload baits, the baits become part of the bait database on your server, but they are not uploaded to your user account on the eArray Web site. This is an important consideration if you do library design work both in eArray$_{XD}$ and on the eArray Web site.

9 Click **OK.**

You can monitor the status of the job in the Tasks pane of the Navigator. In the Bait Upload folder, an icon appears next to the name of the job:

Icon	Status/Comments
	**Pending** – The job has been submitted to the upload queue.
	**Processing** – Your server is in the process of uploading the baits to the bait database.
	**Complete** – The job is finished. You can now search for the baits, and use them in bait groups and libraries.
	**Error** – An error occurred. You must re-submit the job. Errors are usually caused by problems in the uploaded bait file. To see any errors that the program detected in the uploaded bait file, follow these steps: **a** Right-click the name of the job, then click **Download Error File.** A dialog box appears. **b** Select a location for the error file, then click **Save.** The program saves a ZIP format archive to the location that you selected. The ZIP archive contains an HTML file that you can open with your Internet browser. The HTML file lists the lines in your original bait file that contain errors. Place the pointer over a highlighted item to see a ToolTip that describes the error.

To delete a bait upload job with any status, right-click the name of the job, then click **Delete.**

To create a bait group with uploaded baits

The program lets you create a bait group with uploaded baits either when you set up the upload, or after the upload. If you create a bait group during the upload process, the resulting bait group contains all of the baits in the uploaded file. If you create a bait group after you upload your bait file, the bait group can contain all of the uploaded baits, a subset of them, and/or additional baits.

To create a bait group during the upload process

- Upload baits as described in "To upload baits and annotation" on page 374. As you define the upload, under **Upload Bait File Details,** in **Upload Type,** select **Create New Bait Group,** then type a name for the bait group.

To create a bait group after you upload a file of baits

1. Search for the desired baits. See "To search for baits" on page 358.
2. Select the desired baits, then create a bait group as described in "To create a bait group from existing baits" on page 401.

To set up a Bait Tiling job

Bait Tiling creates baits that evenly cover selected genomic regions of a given species. You can customize the tiling process for specific sequencing technologies and protocols, as well as select the length of baits and the density of tiling. If you like, you can use a wizard to design and submit a bait library that contains baits created by the Bait Tiling process. See "To create a library using Bait Tiling (wizard)" on page 433. Additional details about bait tiling appear at the end of this topic.

You can tile baits to regions of any genome that is present on your server. If the genome of interest is not present, you can import it. See "To import a new genome" on page 66. You can also tile baits to regions of Agilent-provided genomes. To tile Agilent-provided genomes, the program submits a job to the eArray Web site, through your server.

To supply the necessary genomic intervals for tiling, you can type them directly in the program, or you can upload a file of genomic intervals. You can also use an Interval Finder search to retrieve the necessary intervals. See these topics:

- "To do a Simple Interval Finder Search" on page 363
- "To do an Advanced Interval Finder Search" on page 364
- "To do a Simple Exon Interval Finder Search" on page 366
- "To do an Advanced Exon Interval Finder Search" on page 367

In addition, you can use a search for biological networks or a literature search to supply search terms for an Advanced Interval Finder or Advanced Exon Interval Finder search. You then use the retrieved intervals in a Bait Tiling job. See "To use a biological network or a literature search to find or create baits" on page 389.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Create Bait, click **Bait Tiling.**

The Bait Tiling dialog box appears. See "Bait Tiling" on page 599.

3 Enter the following parameters. All are required.

Parameter	Instructions/Details
Design Options	
Design Job Name	Type a name to identify this Bait Tiling job.
Sequencing Technology	Select the type of DNA sequencer that you will use to analyze your target DNA fragments.
Sequencing Protocol	Select the desired protocol. In the list, eArray displays the available protocols for the selected DNA sequencing technology.
Use Optimized Parameters	In general, mark **Use Optimized Parameters.** With this option, based on your selected sequencing technology and protocol, the program automatically sets the best values for Design Strategy, Bait Length, Bait Tiling Frequency, and Allowed Overlap. To set all of these options manually, clear **Use Optimized Parameters.** The options all become available.

Parameter	Instructions/Details
Design Strategy	(Available if you clear **Use Optimized Parameters.**) Select one of these options: • **Centered** – eArray centers sets of tiled baits over their respective target intervals. That is, each set of baits hangs over both ends of its target interval by equal amounts. This option exactly respects the value that you select in Bait Tiling frequency. • **Justified** – eArray designs sets of tiled baits to exactly cover their respective target intervals. This option adjusts the overlap of baits to achieve the precise and even tiling of only the target intervals, without any overhang into non-target regions. With this option, the actual tiling frequency can deviate from the value that you select in Bait Tiling Frequency.
Bait Length	(Available if you clear **Use Optimized Parameters.**) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in a library must have this length.
Bait Tiling Frequency	(Available if you clear **Use Optimized Parameters.**) Select the desired tiling frequency. This setting controls the density of tiling. The density can also be affected by the option that you select in Design Strategy. • **2x** – eArray overlaps baits by 50% as it tiles each interval. Two baits cover each base in each interval. • **3x** – eArray overlaps baits as it tiles each interval so that three baits cover each base in each interval. • **4x** – eArray overlaps baits as it tiles each interval so that four baits cover each base in each interval. • **5x** – eArray overlaps baits as it tiles each interval so that five baits cover each base in each interval. **Note:** The exact density of tiling can be somewhat less than that indicated above at the extreme 5' and 3' ends of each interval.
Allowed Overlap	(Available if you clear **Use Optimized Parameters.**) To change the value, select it, then type the desired distance in base pairs. eArray generates baits that may extend by this distance into the regions specified in Genomic Avoid Intervals (see below). For best results, set this distance to a maximum of 20 bp.

Parameter	Instructions/Details
Strand	Select one of these options: • **Sense** – Produces baits that are similar in sequence to the sense strand of the target genomic DNA. • **Antisense** – Produces baits that are complementary to the sense strand of the target genomic DNA. • **Both** – Produces both a sense bait and an antisense bait for each target location.
Target Details	
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Lets you tile one of the standard genomes available in eArray. The available species appear in Species. Once you select a species, the genome build that is available for the species appears in Genome Build. • **User Defined Genome** – Lets you tile a genome that you have uploaded to your server. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. To upload a custom genome, see "To import a new genome" on page 66.
Species	Select the desired species.
Genome Build	Select the desired genome build. For Agilent-provided genomes, only the most recent build of the genome for the selected species is available.

Parameter	Instructions/Details
Genomic Target Intervals	Type the desired target intervals. Use the format chrX:<start>-<end> . **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. Alternatively, you can upload a list of intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—that is, in a word processor, press **Enter** at the end of each line. Then follow these steps: **a** Next to the box in Genomic Target Intervals, click **Upload.** A File Upload dialog box appears. See "File Upload" on page 773. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file, then click **Open.** The name of the file appears in the File Upload dialog box, in File Name. **d** Click **Upload.** eArray uploads the list of intervals, and displays them in pipe-separated format in the Genomic Target Intervals box. **Note:** To use the results of an Interval Finder Search or an Exon Interval Finder Search to supply genomic target intervals, select the desired intervals, then click **Run Bait Tiling.** See the topics that are referenced in the introduction to this topic.

Parameter	Instructions/Details
Genomic Avoid Intervals	Mark any of these options: • **Avoid Standard Repeat Masked Regions** – The program excludes a standard set of repetitive genomic regions from the Bait Tiling process. These are regions of the genome that generally produce poor quality baits. This option is marked by default. When you tile a user-imported genome, these repeat regions are the sequences represented by lower case letters in your sequence files, if you marked Genome is Soft Masked when you imported it. • **Custom Avoid Intervals** – In the Bait Tiling process, eArray excludes the genomic intervals that you enter in the box. Type intervals using the format chrX:<start>-<end> **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. Alternatively, you can upload a list of intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—that is, in a word processor, press **Enter** at the end of each line. Then follow these steps: **a** Next to the Custom Avoid Intervals box, click **Upload.** A File Upload dialog box appears. See "File Upload" on page 773. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file, then click **Open.** The name of the file appears in the File Upload dialog box, in File Name. **d** Click **Upload.** eArray uploads the list of intervals, and displays them in pipe-separated format in the Custom Avoid Intervals box.

4 Click **Submit.**

The program begins the tiling job, and adds this job to the Tasks pane of the Navigator, in a Bait Tiling folder. A dialog box tells you that your job was successfully submitted.

5 Click **OK.**

You can monitor the status of the job in the Tasks pane. An icon appears next to the name of the job, indicating its status:

Icon	Status/Description
	Pending – The job has been submitted to your server, but no action has been taken on it yet.
	Processing – The job is being processed.
	Complete – The job is finished. You can view and use the results. See "To view Bait Tiling results" on page 385.
	Error – An error occurred. You must re-submit the job.

Additional Bait Tiling details

What design guidance can Agilent offer regarding target enrichment libraries?

When you generate custom SureSelect Target Enrichment Bait Libraries:

- Avoid repeat regions in the bait design with fairly high stringency (at most 20 bp overlap).
- Follow the "Optimized" bait design strategy (Mark the **Use Optimized Parameters** option). These parameters have been found to work well under standard conditions and are optimized for a given sequencing technology.

How much genomic space can be targeted?

Agilent can create libraries with up to 55,000 baits per kit. The currently available bait length for all users is 120 nucleotides, and the default tiling frequency is 2X. Given these parameters, you can target up to 3.3 Mb. As you increase the tiling frequency, this limit decreases.

What is the largest region that can be targeted?

Assuming 120-mer baits and 2X tiling, the longest single region that can be captured is 3.3 Mb. However, you can identify regions for eArray to avoid in the tiling process as **Genomic Avoid Intervals.** These regions can include the default standard set of repeat regions, as well as custom regions that you identify. This can increase the size of the region that can be captured.

Why is 2X tiling helpful?

Baits tiled at a density of 2X cover target regions in a staggered manner. A target sequence that is represented at the end of a given bait is represented toward the middle of the alternate bait that covers the same region. For sequencing technologies that use end-sequencing, such as the Illumina technology, 2X tiling can help you sequence regions in the middle of a DNA segment more effectively.

If I have not reached the capacity of the library, should I increase my tiling?

Yes. In general, the more tiling the better.

At a bait length setting of 120 nucleotides, what is the active capture size?

120 nucleotides.

What happens if a target region is shorter than the bait length?

eArray centers the resulting bait on the target region. The bait sequence includes enough of the immediately adjacent genomic regions to fill the bait to its full, specified length.

Is DNA sequencing potential driven by bait length or by shear size?

Shear size. If a 120-mer bait pulls down a 500 bp DNA segment, the entire 500 bp segment is available for sequencing, without regard to the part that aligns with the 120-mer bait.

To view Bait Tiling results

When your Bait Tiling job has a status of Complete, you can view its results.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right-click the name of the desired Bait Tiling job, then click **View Design Details.**

The Design Results dialog box appears.

3 To view any of the available types of results, click the desired tab at the top of the dialog box. The available results are described in the table below. For

descriptions of the individual statistics and other items in each of these results, see "Design Results (Bait Tiling)" on page 690.

Result	Description
Summary Result	Information of an overall nature about the set of baits that was produced by the Bait Tiling process, including the criteria that were used to tile the baits, and statistics on the length and number of baits.
Target Fate	List of the target intervals that were used in the Bait Tiling process, with information on which ones produced baits, and which did not.
Detail Result	List of the first 100 baits designed by the Bait Tiling process, with specific information about each bait, including its length and sequence. It also details the target interval from which each bait was derived, and its location within the target interval. To view the complete set of baits, download the Bait Tiling results, then use a word processing or spreadsheet program to view the BaitTiling_tdt file. See "To download Bait Tiling results" on page 387.
BED File	Preview of the first 100 data lines of the BED track file produced by the Bait Tiling process. You can download this file and view it in a genome browser that accepts BED format files.

4 After you have viewed the results of your Bait Tiling job, click **Close.**

You can also download the results, create a bait group from them, and delete the job. See these topics:

- "To download Bait Tiling results" on page 387
- "To create a bait group from Bait Tiling results" on page 387
- "To delete a Bait Tiling job" on page 388

To download Bait Tiling results

When your bait tiling job has a status of Complete, you can download its results.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right click the name of the desired Bait Tiling job, then click **Download.**

A Save dialog box appears.

3 Select a location for the downloaded file, then click **Save.**

The program downloads the file in *.zip format to the location that you selected. A dialog box tells you that the file was downloaded successfully.

4 Click **OK.**

The downloaded ZIP archive contains four files, corresponding with the four types of available results. See "To view Bait Tiling results" on page 385. You can use a word processing or spreadsheet program to view most of these files. To view the BaitTiling_bed file, upload it to a compatible genome browser.

To create a bait group from Bait Tiling results

When your bait tiling job has a status of Complete, you can create a new bait group based on its results. Later, you can use the bait group to create a SureSelect Target Enrichment library. You can create one bait group from the results.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right-click the name of the desired bait tiling job, then click **Create Bait Group.**

A dialog box tells you that your bait group creation job has been submitted.

3 Click **OK.**

The job appears in the Tasks pane, in the Bait Upload folder. The icon next to the name of the job indicates its status:

Icon	Description
	Pending – The job has been submitted to your server, but no action has been taken on it yet.
	Processing – The job has started.
	Complete – The job is finished.
	Error – An error occurred. You must re-submit the job.

When the job has a status of Complete, the bait group appears in your main "default" folder in the Design Data pane of the Navigator, and you can work with the bait group and use it in a library. See "Working with Bait Groups" on page 394 and "To create a library from existing bait groups (wizard)" on page 428.

To delete a Bait Tiling job

You can delete a Bait Tiling job from the Tasks pane. The job can have any status except Processing. When you delete a job, its results are removed from the system. However, the bait group that you may have created with the results is not removed.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right-click the name of the desired Bait Tiling job, then click **Delete.**

A dialog box asks if you are sure you want to delete the job.

CAUTION If you delete a Bait Tiling job, the program permanently removes the job and its results from the system. To restore a deleted job, you must submit a new one.

3 Click **OK**.

To use a biological network or a literature search to find or create baits

Biological networks, also called **pathways,** document the interactions among the diverse components of specific biological processes. Components include genes, gene products, metabolites, and cellular structures such as organelles and membranes.

eArray$_{XD}$ lets you use a biological network as the basis for a bait search, or for the design of new baits. Once you define the network of interest, you can also view a diagram of it and get more information about specific nodes in the network. You can define the network of interest in two ways:

- **Network Search** – A network search returns a list of biological networks that meet the search criteria that you enter. You can view each returned network as a diagram that displays a set of connected elements or *nodes*. You can then select one or more nodes in the network, and use them to search for or create baits.
- **Literature Search** – A literature search uses one or more Web-based search engines to retrieve text from the biomedical literature that meets the criteria that you enter. The program then examines each sentence in the retrieved text for known terms. It uses these terms to create **associations** among the terms in a given sentence, and converts the associations into **interactions** that define the **nodes** (components) and **edges** (connections) of a custom network. You can then select one or more nodes in the network, and use them to search for or create baits.

For details, see the topics in "Using Biological Networks to Find or Create Probes or Baits" on page 184.

To download baits

You can download files that contain selected baits from bait search results in TDT, FASTA, COMPLETE, or MINIMAL file formats.

1 Search for the desired baits. See "To search for baits" on page 358.

The baits that match your search criteria appear in the Search Result pane.

2 In the Search Result pane, select one or more baits to include in your downloaded file. Use the following as a guide:

- To select an individual bait, mark the check box in its row.
- To navigate among multiple pages of results, use the numbered page buttons. The program remembers the baits that you select as you navigate from page to page.
- To select all of the baits on the current page, mark the check box in the heading row of the search results.
- To select all of the baits on every page of the search results, mark **Select entire data set.**

3 Click **Download.**

The Download Baits dialog box lists the available file types that you can download.

4 Select the desired file type:

- **TDT** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892.
- **FASTA** – FASTA format text file that contains the bait attributes indicated in the table below. See "FASTA" on page 884.
- **COMPLETE** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892.
- **MINIMAL** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892.

Attribute	TDT	FASTA	COMPLETE	MINIMAL
BaitID	•	•	•	•
Sequence	•	•	•	•
TargetID	•		•	
Species	•			
GeneName	•			
GeneSymbol	•		•	
Description	•		•	
ControlType	•			
Accessions	•		•	
BaitGroups	•			
Status	•			
ValidationMethod	•			
ChromosomalLocation	•		•	
CytoBand	•			
GoIDs	•			
Strand			•	

• – Attribute included in file format

5 Click **Download.**

A Save dialog box appears.

6 Select a location for the downloaded file, then click **Save.**

eArray downloads the bait file as a *.tdt file. You can view the file with a word processing or spreadsheet program.

A dialog box tells you that your file has been downloaded successfully.

7 Click **OK.**

To delete baits

You can permanently remove baits from your server. You must be the owner of the baits, and the baits cannot be in use in any bait group. This function gives you a way to remove “orphan” baits that are not being used, or baits that you have uploaded or created in error. Bait deletion has no effect on the baits that are available to your workgroup on the eArray Web site.

1 Search for the desired baits. You can prepare a file of the bait IDs of the baits that you want to delete, and upload the terms in this file as search criteria for the bait search.

2 In the Search Result pane, select the baits that you want to delete. Use the following as a guide:

- To select an individual bait, mark the check box in its row.
- To go to a different page of results, click a numbered page button. The program remembers the baits that you select as you go from page to page.
- To select all of the baits on the current page, mark the check box in the heading row of the search results.
- To select all of the baits on every page of the search results, mark **Select entire data set.**

3 Click **Delete.**

A dialog box asks if you really want to delete the selected baits.

CAUTION When you delete baits, you permanently remove them from the system. To restore deleted baits, you must upload them or create them again

4 Click **Yes.**

A message tells you that your Delete Baits job has been submitted.

5 Click **OK.**

You can monitor the progress of the job in the Tasks pane of the Navigator in the Delete Baits folder. These icons can appear next to the name of the job:

Icon	Description
	Pending – The job has been submitted to your server, but no action has been taken on it yet.
	Processing – The job is being processed.
	Complete – The job is finished.
	Error – An error occurred. You must re-submit the job.

Sometimes, the program can only delete some of the baits that you select. If so, the program deletes the baits that it can.

After the job has a status of Complete , you can download and view a report that lists the baits that you selected for deletion. The report indicates whether or not each bait was deleted. If a particular bait was not deleted, the report gives the reason. To download this report, follow these steps:

a In the Tasks pane, in the Delete Baits folder, right-click the name of the desired bait deletion job, then click **Download Report.**

A Save dialog box appears.

b Select a location for the downloaded file, then click **Save.**

The program downloads the file to the selected location. A dialog box tells you that the file was successfully downloaded.

c Click **OK.**

You can view the file with a word processing or spreadsheet program.

Working with Bait Groups

A bait group is a collection of baits that are linked by a set of logical criteria. Bait groups are a required intermediate level of organization for baits that makes it easier to create libraries. Instead of having to enter hundreds or thousands of baits at once, you first create bait groups, and then select the bait groups to include in a library. You can also create copies of bait groups and use them as building blocks for many different libraries.

The program lets you create and manage bait groups in many ways, summarized in the table below.

Task	Description	See these topics
Search for bait groups	Find bait groups on your server that match specific search criteria.	"To search for bait groups" on page 396
Browse bait groups	View available bait groups by folder.	"To browse available bait groups" on page 398
Update bait group or other Agilent content from the eArray Web site	Transfer Agilent Catalog content from the eArray Web site.	"To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61
View bait group	View information about a bait group, including its list of baits.	"To view a bait group" on page 399
Create bait group	Use baits from a bait search in a bait group.	"To create a bait group from existing baits" on page 401
	Use baits from a bait upload in a bait group.	"To create a bait group from uploaded baits" on page 403
	Use baits created by a Bait Tiling job in a bait group	"To create a bait group using Bait Tiling" on page 404
	Use an existing bait group as the basis for a new bait group.	"To create a bait group from an existing bait group" on page 405
Copy bait group	Create a new bait group using an existing one as a template.	"To copy a bait group" on page 405

Task	Description	See these topics
Edit bait group	Change the attributes of a bait group. You can also add and remove baits.	"To edit a bait group" on page 406
Move bait group	Move bait group(s) to a different folder.	"To move bait group(s)" on page 408
Download bait group	Save bait group files to your computer.	"To download a bait group" on page 409
Delete bait group	Permanently remove a bait group from your server.	"To delete a bait group" on page 413
Add an attachment to a bait group	Attach a note, file, or URL	"To attach a file, note, or URL to a bait group or library" on page 444
Remove an attachment from a bait group	Remove a note, file or URL.	"To remove attachments from a bait group or library" on page 446
Open an attachment to a bait group	Open an attached file in an appropriate program, open an attached URL in your browser, or view an attached note.	"To view the attachments to a bait group or library" on page 445

NOTE

The names of available bait groups appear in the Design Data pane of the Navigator. However, before you can take certain actions on bait groups, you may need to transfer baits and annotation or download the bait group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To search for bait groups

A bait group search returns bait groups that match specific search criteria. Each search criterion can take a single value, and can represent all or part of a term. For example, if you type `genome` as a bait group name to be searched, the search returns, potentially, bait groups with names of **Human genome, Rat genome, genome Q55,** and the like. Bait group searches are not case-sensitive.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Bait Groups.**

The Bait Group Search pane appears.

3 Set the desired search criteria. All parameters are optional, except **Length.** You can click **Reset** at any time to start over.

Search criterion	Instructions/Details
Bait Group Name	Type all or part of a bait group name. This search criterion is not case-sensitive.
Folder	Select a specific folder to search. The list only contains the names of folders that you can access. To include the subfolders of the selected folder in your search, mark **Include Subfolders.** Select **All** to search all of the folders that are available to you.
Keywords	Type all or part of a keyword.
Length	(Required) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in a bait group must have this length.
Created by	Type all or part of a person's name. The search returns bait groups created by people whose names contain the search string.

Search criterion	Instructions/Details
Date Created	Click  next to the **From** and **To** boxes. For each, select the desired dates from the calendars that appear. The search returns bait groups created between the From and To dates.
Status	Select one of these options: • **All** – Returns bait groups without regard to their status. • **Incomplete** – Limits the bait groups that are returned to those with a status of Incomplete. A bait group with this status can be edited by its owner. • **Locked** – Limits the bait groups that are returned to those with a status of Locked. A bait group with this status cannot be edited. Locked bait groups cannot be unlocked.

4 Click **Search.**

The search starts. A Search Result pane lists the bait groups that match your search criteria.

To go to another page of results, click a numbered page button below the list of returned baits.

From the Search Result pane, depending on the status and ownership of the bait group(s), you can take action on the retrieved bait groups. In general, you click a link in the **Actions** column of the search results, or you mark the check boxes next to the desired bait groups, then click one of the buttons above or below the list of bait groups. See the following topics for details:

- "To view a bait group" on page 399
- "To copy a bait group" on page 405
- "To edit a bait group" on page 406
- "To move bait group(s)" on page 408
- "To download a bait group" on page 409
- "To delete a bait group" on page 413
- "To create a library from bait group search results" on page 439

NOTE

- When you search for your own custom bait groups, the program searches the content on your server, not on the eArray Web site.
- Bait group searches return the names of all available bait groups that match your search criteria. However, before you can take certain actions on bait groups, you may need to transfer bait and annotation data or download the bait group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To browse available bait groups

You can use the Design Data pane of the Navigator to view lists of available bait groups by folder. From this pane, you can get information about bait groups, and also take further action on them.

1. Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.
2. In the eArray$_{XD}$ tab, expand the folders of the **Design Data** pane. Note the following details:
   - Bait groups, if any, can be found in the Bait Group node within each folder in the pane. If bait groups are present, you can click ⊞ to expand the node and view them.
   - Agilent Catalog content can be found in the AgilentCatalog folder.
   - Only the folders to which you have access appear in the Design Data pane.
   - The icon next to each bait group shows its status. For a description of the status icons that can appear, see "Navigator – Design Data pane" on page 486.
   - If  appears next to a bait group, it contains content that must be downloaded from the eArray Web site. You can immediately include such a bait group in a library, but you must download bait group from the eArray Web site before you view it, or save the library with a status of Complete. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
   - To take further action on a bait group, right-click its name, then select the desired option from the shortcut menu. For a description of the options that can appear, see "Navigator – Design Data pane" on page 486.

NOTE The Design Data pane of the Navigator contains the names of all available bait groups. However, before you can take certain actions on bait groups, you may need to transfer bait and annotation data or download the bait group(s) from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To view a bait group

You can view information about a specific bait group, including the list of baits in the bait group and their sequences, associated keywords, accessions, and statistical information.

Before you can view a bait group, you may need to transfer bait and annotation data or download the bait group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

1 Search or browse for the desired bait group. See "To search for bait groups" on page 396 and "To browse available bait groups" on page 398.

2 Do one of the following:

- If you searched for the bait group – In the Search Result pane, in the **Actions** column, click  .
- If you browsed for the bait group, right-click the name of the bait group, then click **View.**

The View Bait Group dialog box appears. The dialog box lists the properties of the bait group. Below these properties, the Search Result pane displays a list of the baits in the bait group. Several additional columns of annotation can appear. For details about this dialog box, see "View Bait Group" on page 867.

3 Do any of the following tasks, as desired:

Task	Instructions
Go to a different page of baits	Click a numbered page button above or below the list of baits.
View or download additional bait statistics	You can view calculated statistics that are based on the sequences of the baits in the bait group. Follow these steps: **a** In the Search Result pane, click **Show Statistics.** The Bait Statistics dialog box appears. See "Bait Statistics" on page 596. To view the complete contents of some of the entries in the table of bait statistics, you may need to download the statistics, and view the table with a spreadsheet program. See the next step. **b** Take any of these actions, as desired: • To sort the table of bait statistics by Bait ID or Internal ID, click the desired column heading. To reverse the order, click the same column heading again. • To go to another page of baits, click a numbered page button above or below the table of bait statistics. • To download the bait statistics, click **Download.** In the Save dialog box that appears, select a location for the downloaded file, then click **Save.** The program downloads a tab-delimited text file to the location that you selected. You can use a spreadsheet program to view the file.
Download bait group	You can use the View Bait Group dialog box to download the baits in the bait group. Follow these steps: **a** Click **Download.** The Download Bait Group dialog box appears. See "Download Bait Group" on page 717. **b** In Download type, select the desired type of file, then click **Download.** For details about the contents of each of the available file types, see "To download a bait group" on page 409. A Save dialog box appears. **c** Select a location for the downloaded file, then click **Save.** A dialog box tells you that the file was downloaded successfully. **d** Click **OK.**

4 Click **Close.**

To create a bait group from existing baits

You can create a bait group from the results of a bait search. This is an effective way to construct a bait group from baits to which you have access that are already on your server.

1 Search for the desired baits. See "To search for baits" on page 358.

2 In the Search Result pane, select the desired baits. Follow these guidelines:

- To select individual baits, mark the check boxes next to their names.
- To select all of the baits on the current page, mark the check box in the heading row of the search results.
- To go to a different page of results, click a numbered page button. The program remembers the baits that you select as you go from page to page.
- To select all of the baits on every page of the search results, mark **Select entire data set.**

3 Click **Create Bait Group.**

The Create Bait Group dialog box appears. See "Create Bait Group" on page 621. Bait group attributes appear in the Create Bait Group pane. The selected baits appear in the Search Result pane.

4 Enter the following bait group attributes. All attributes are required unless otherwise indicated. The attributes that do not appear below are set by the system, and are read-only.

Attribute	Instructions/Details
Bait Group Name	Type a name for the bait group. The program uses this to refer to the bait group in search results, bait group lists, and the like.
Folder	Select the folder where you want the program to save the new bait group. Only the folders to which you have access appear in the list.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Status	Select either **Incomplete** or **Locked.** By default, the program creates your new bait group with a status of Incomplete. If you set the status to **Locked,** you will not be able to further edit the bait group. Locked bait groups cannot be unlocked.

Attribute	Instructions/Details
Description	(Optional) Type a brief description.
Keyword	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. Keywords can make it easier to find the bait group when you search for it.

5 To add or remove baits from the bait list in the Search Result pane, do one of these tasks:

Task	Instructions
Add baits	**a** In the Search Result pane, click **Add New Baits.** The Add Baits to Bait Group dialog box appears. See "Add Baits to Bait Group" on page 576. **b** Under Bait Search, set the desired search criteria. See "To search for baits" on page 358. **c** Click **Search.** A Search Result pane lists the baits that meet your search criteria. **d** Select the baits that you want to add to your bait group. Follow these guidelines: • To select a bait, mark the check box in its row. The program remembers your selections as you go from page to page. • To select all baits on the current page, mark the check box in the column heading row. • To select all baits in the search results, mark **Select entire data set.** **e** Click **Add Baits to Bait Group.** A dialog box asks if you are sure that you want to add the selected baits to your bait group. **f** Click **Yes.** A dialog box tells you of the number of baits that have been added to the bait group. **g** Click **OK.**

Task	Instructions
Remove baits	**a** In the Search Result pane, select the baits that you want to remove. **b** Click **Remove Baits.** A dialog box asks if you are sure you want to remove the baits from the bait group. **c** Click **Yes.** A dialog box tells you the number of baits that have been removed from the bait group. **d** Click **OK.** **Note:** This procedure removes the links between the selected baits and the given bait group. It does not delete the actual bait sequences and annotation from your server. To delete baits, see "To delete baits" on page 392.

6 Click **Save Bait Group.**

The program creates and saves the bait group. A dialog box tells you that your bait group has been successfully created.

7 Click **OK.**

To create a bait group from uploaded baits

You can upload new baits to your server. As part of the upload process, you can create a new bait group that contains the uploaded baits.

- Upload baits as described in "To upload baits" on page 370. When you select the **Upload Type** in the Upload Bait File Details pane, select **Create New Bait Group,** then type a name for the bait group.

  After the program uploads the baits. it creates the requested bait group. You can then search for the bait group, edit it, and use it to create a library.

To create a bait group using Bait Tiling

Bait Tiling creates baits that evenly cover specified genomic regions. See "To set up a Bait Tiling job" on page 378. You can use the baits that Bait Tiling generates to create a new bait group. The new bait group has the same name as the Bait Tiling job.

The program lets you create a single bait group with the following procedure for each set of Bait Tiling results. If you need more than one copy or version of this bait group, use the Copy Bait Group command. See "To create a bait group from an existing bait group" on page 405.

1. Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.
2. Set up and submit a Bait Tiling job as described in "To set up a Bait Tiling job" on page 378.

   When the Bait Tiling job is completed, it appears in the Tasks pane of the Navigator with a status of Complete  .
3. In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right-click the name of the desired Bait Tiling job, then click **Create Bait Group.**

   The program creates the new bait group, and saves it in your main "default" folder. A dialog box tells you that your bait group has been successfully created.
4. Click **OK.**

To create a bait group from an existing bait group

When you create a new bait group from an existing one, you search for the existing bait group and make a copy of it. You then edit this copy. This method is useful if the existing bait group contains most or all of the baits that you want in your new bait group. Also, if you want to move a bait group, but it is already in use in a library, you can make an exact copy of the bait group, then move the copy.

Before you can copy a bait group, you may need to transfer bait and annotation data or update the bait group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

1 Search or browse for the desired existing bait group. See "To search for bait groups" on page 396 and "To browse available bait groups" on page 398.

2 Do one of the following:

- If you searched for the bait group – In the Actions column of the Search Result pane, next to the desired bait group, click  .
- If you browsed for the bait group – In the Design Data pane of the Navigator, right-click the name of the desired bait group, then click **Copy.**

The Copy Bait Group dialog box appears. See "Copy Bait Group" on page 615.

3 Edit the properties and content of the bait group as needed. Be sure to select the desired destination folder. See "To edit a bait group" on page 406.

4 Click **Save Bait Group.**

A dialog box tells you that the bait group was successfully created.

5 Click **OK.**

To copy a bait group

You copy a bait group as the first step when you create a new bait group based on an existing one. This method of creating a bait group is especially useful if the new bait group has many baits in common with the existing one. Also, since you cannot move a bait group if it is part of an existing library, or if you are not its owner, you can create a copy of the bait group, and move the copy.

For further instructions, see "To create a bait group from an existing bait group" on page 405.

To edit a bait group

You can change the information that is associated with a bait group, such as its name or location, and you can also add or remove baits from a bait group.

Before you edit a bait group

- You must be the owner of the bait group. To edit a bait group that you do not own, first make a copy of the bait group, then edit the copy. See "To create a bait group from an existing bait group" on page 405.
- The status of the bait group must be Incomplete.
- You may need to transfer bait and annotation data or update the bait group from the eArray Web site. See "eArray$_{XD}$ and the eArray Web site" on page 25.

To edit a bait group

1 Search or Browse for the desired bait group. See "To search for bait groups" on page 396 and "To browse available bait groups" on page 398.

2 Do one of the following:

- If you searched for the bait group – In the **Actions** column of the search results, next to the desired bait group, click  .
- If you browsed for the bait group – In the Design Data pane of the Navigator, right-click the name of the desired bait group, then click **Edit.**

In either case, the Edit Bait Group dialog box appears. See "Edit Bait Group" on page 737.

3 Make changes to any of the following bait group attributes. The attributes that do not appear below are set by the system, and are read-only.

Attribute	Instructions/Details
Bait Group Name	Type a name for the bait group. The program uses this name to refer to the bait group in search results, bait group lists, and the like.
Folder	Select the folder where you want the program to save the new bait group. Only the folders to which you have access appear in the list.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.

Attribute	Instructions/Details
Status	Select either **Incomplete** or **Locked.** By default, the program creates your new bait group with a status of Incomplete, which lets you further edit the bait group. Bait groups with a status of Locked cannot be edited, and they also cannot be unlocked.
Description	(Optional) Type a brief description.
Keyword	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. Keywords can make it easier to find the bait group when you search for it.

4 If desired, add or remove baits from the bait group, as described below.

Task	Instructions
Add baits	**a** In the Search Result pane, click **Add New Baits.** A search page appears. **b** Set criteria for a Bait Search. See "To search for baits" on page 358. **c** Click **Search.** A Search Result pane lists the baits that match your search criteria. **d** Select the baits that you want to add to the bait group. Follow these guidelines: • To select a bait, mark the check box in its row. The program remembers your selections as you go from page to page. • To select all baits on the current page, mark the check box in the column heading row. • To select all of the baits in the search results, mark **Select entire data set.** **e** Click **Add Baits to Bait Group.** A dialog box asks if you are sure that you want to add the selected baits to the bait group. **f** Click **Yes.** A dialog box displays the number of baits that were successfully added to the bait group, and the resulting total number of baits in the bait group. **g** Click **OK.**

Task	Instructions
Remove baits	**a** In the Search Result pane, select the baits that you want to remove. **b** Click **Remove Baits.** A dialog box asks if you really want to remove the baits from the bait group. **c** Click **Yes.** A dialog box tells you that the baits have been successfully removed from the bait group. **d** Click **OK.** **Note:** This procedure removes the associations that link the selected baits to the given bait group. It does not delete the actual bait sequences and annotation from your server. To delete baits, see "To delete baits" on page 392.

5 Click **Save Bait Group.**

The program saves the bait group with the edits you made. A dialog box tells you that your bait group has been successfully updated.

6 Click **OK.**

To move bait group(s)

You can move one or more bait groups to another folder.

Before you move bait groups

- You must be the owner of the bait group(s).
- You must have access to the desired destination folder.
- The bait group must not be in use in an existing library.
- The bait group must not be located in the AgilentCatalog folder, but it *can* contain Agilent Catalog baits.

To move bait group(s)

1 Search for the desired bait group(s). See "To search for bait groups" on page 396.

2 In the Search Result pane, mark the check box next to each bait group that you want to move. For multiple pages of results, the program remembers your selections as you go from page to page. To select all of the bait groups on a page of results, mark the check box in the column heading row. To select all of the bait groups on all pages of results, mark **Select entire data set.**

3 Click **Move.**

The Move Bait Group dialog box lists the name(s) and location(s) of the bait groups that you selected. See "Move Bait Group" on page 811.

4 In **Move to Domain,** select the desired destination folder.

5 Click **Move.**

A dialog box asks if you really want to move the bait group(s).

6 Click **Yes.**

A dialog box lists each bait group, and whether or not the move was successful. If a bait group could not be moved, the reason appears next to its name.

7 Click **OK.**

NOTE

- You can also use the Navigator to move bait groups one at a time. In the **Design Data** pane, right-click the name of the bait group, then click **Move.**
- Although you cannot move bait groups that you do not own, or that are in use in a library, you can achieve the equivalent. Make a copy of the desired bait group, then move the copy. See "To create a bait group from an existing bait group" on page 405.

To download a bait group

When you download a bait group, the program retrieves the bait group from your server, and saves it in a file format and location that you select. To download a bait group from the Agilent Catalog folder, you must first retrieve its baits and annotation from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation

data for the SureSelect Target Enrichment application type from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Search or Browse for the desired bait group. See "To search for bait groups" on page 396 and "To browse available bait groups" on page 398.

2 Do one of the following:

- If you retrieved the bait group of interest in a bait group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the bait group of interest, right-click its name, then click **Download.**

The Download Bait Group dialog box appears. See "Download Bait Group" on page 717.

3 In **Download Type,** select the desired file type. The list and table below describe the available file types.

- **TDT** – Tab delimited text file that contains the attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the attributes indicated in the table below.
- **COMPLETE** – Tab delimited text file that contains the attributes indicated in the table below.
- **MINIMAL** – Tab delimited text file that contains the attributes indicated in the table below.
- **BED** – Tab delimited text file that contains the attributes indicated in the table below. This file is A BED format track file that you can view in a compatible genome browser

Attribute	TDT	FASTA	COMPLETE	MINIMAL	BED
BaitID	•	•	•	•	•
Sequence	•	•	•	•	
TargetID	•		•		
Species	•				
GeneName	•				
GeneSymbol	•		•		
Description	•		•		
ControlType	•				
Accessions	•		•		
BaitGroups	•				
Status	•				
ValidationMethod	•				
Chromosomal Location	•		•		•
Cytoband	•				
GOID	•				
Strand			•		

• – Attribute included in file format

4 Click **Download.**

A Save dialog box appears.

5 Select a location for the downloaded file, then click **Save.**

The program downloads the bait group to the selected location. A dialog box tells you that the baits were successfully downloaded.

For large files, the program submits a job to the download queue. You can view the job in the Tasks pane of the Navigator, in the Download Bait Group Folder. A status icon appears next to the name of the job:

Icon	Description
	**Pending** – The job has been submitted to the server, but no action has been taken on it yet.
	**Processing** – The job is being processed.
	**Complete** – The job is finished. To download the file, right click the name of the job, then click **Download.** Select a location for the file, then click **Save.**
	**Error** – An error occurred. You must re-submit the job.

6 Click **OK.**

To delete a bait group

When you delete a bait group, you remove the links that bind a particular set of baits together, not the actual baits and annotation. A separate topic describes how to delete baits — see "To delete baits" on page 392.

To delete a bait group, you must be the owner of the bait group, and the bait group must not be in use in a library. Before you can delete a bait group, you may need to update it from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

1 Search or Browse for the desired bait group. See "To search for bait groups" on page 396 and "To browse available bait groups" on page 398.

2 Do one of the following:

- If you retrieved the bait group of interest in a bait group search, click  in the **Actions** column of the Search Result pane.
- If you browsed for the bait group of interest, right-click its name, then click **Delete.**

In either case, a dialog box asks if you really want to delete the selected bait group.

CAUTION When you delete a bait group, the program permanently removes it from the system. To restore a deleted bait group, you must create it again.

3 Click **Yes.**

A message tells you that the bait group was successfully deleted.

4 Click **OK.**

Working with Bait Libraries

In the Agilent SureSelect Target Enrichment protocol, a library is a collection of biotinylated RNA oligonucleotide baits that you use to isolate specific genomic DNA fragments for sequencing. You can use eArray$_{XD}$ to find, upload, create, and organize the nucleotide sequences that are represented in custom libraries. Once you create a library, you can submit it to Agilent Manufacturing. You request a quote for the library from within eArray$_{XD}$, and later place an order through your Agilent representative.

Libraries contain one or more bait groups, and each bait group contains individual baits. See "Working with Baits" on page 355 and "Working with Bait Groups" on page 394.

One of the easiest ways to create a library is to use one of the wizards in eArray$_{XD}$. Wizards take you step-by-step through a specific library creation process. Each wizard lets you submit the library to Agilent Manufacturing. These wizards are available under **Create Library Using** in the eArray$_{XD}$ tab:

- **Bait Upload** – Creates a library from baits in a file that you upload. See "To create a library from a bait upload (wizard)" on page 422.
- **Existing Bait Group(s)** – Creates a library from bait group(s) from a bait group search. The bait groups can be from any folder on your eArray server to which you have access. See "To create a library from existing bait groups (wizard)" on page 428.
- **Bait Tiling** – Creates a library of baits that evenly cover specified genomic regions of your species of interest. You can optimize the bait creation process for your specific sequencer and sequencing protocol, and also customize the tiling density and the length of baits. In addition, you can identify genomic regions to avoid. See "To create a library using Bait Tiling (wizard)" on page 433.

You can also create a custom library without the use of a wizard from bait group search results. See "To create a library from bait group search results" on page 439

If your desired library already exists in a folder to which you have access, you can search or browse for it. You can then submit it to Agilent Manufacturing and request a quote for it. Search results, as well as the list of libraries in the Design Data pane of the Navigator, let you use several other commands to manage libraries. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

As you create libraries, they go through several status changes. The status designations for libraries parallel those for microarray designs. For a description of these designations, see "Status of microarray designs" on page 248.

The table below lists the library-related tasks that you can do in eArray$_{XD}$, and the topics in this section that describe them.

Task	See these topics
Search or browse existing libraries	• "To search for libraries" on page 416 • "To browse available libraries" on page 420
Create a library	• "To create a library from a bait upload (wizard)" on page 422 • "To create a library from existing bait groups (wizard)" on page 428 • "To create a library using Bait Tiling (wizard)" on page 433 • "To create a library from bait group search results" on page 439
View a library	"To view a library" on page 443
Add an attachment to a library	"To attach a file, note, or URL to a bait group or library" on page 444
View the attachments to a library	"To view the attachments to a bait group or library" on page 445
Remove attachments from a library	"To remove attachments from a bait group or library" on page 446
Edit a library	"To edit a library" on page 447
Review a library	• "To place a library in review" on page 451 • "To place a different version of a library in review" on page 452 • "To review a library" on page 453
Move librar(ies)	"To move libraries" on page 456
Complete a library	"To complete a library" on page 457
Submit a library	"To submit a library to Agilent" on page 458
Request a quote for a library	"To request a quote for a library" on page 460

Task	See these topics
Download a library	"To download library design files" on page 461
Delete a library	"To delete a library" on page 465

NOTE To work with a library, you may need to first download it from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To search for libraries

You can use many different criteria to search for libraries. Once you retrieve the library of interest, you can take action on it.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Search, click **Libraries.**

The Library Search pane appears. See "Library Search" on page 551.

3 Enter any of the following search criteria, as desired. You can click **Reset** at any time to clear all search criteria.

Search Criterion	Instructions/Details
Library Name	Type all or part of a name of a library.
Folder Name	To limit the search to a specific folder, select a folder from the list. Only the folders to which you have access appear in the list. To search all available folders, select **All.** To include the subfolders within the selected folder, mark **Include Subfolders.**

Search Criterion	Instructions/Details
Species	To select one or more species, follow these steps: **a** Click **Select and Add.** A dialog box appears. See "Select and Add : Species" on page 845. **b** In **Species,** type some or all of a desired species name, then click **Search.** To return a list of all available species, leave Species blank. The program uses abbreviated binomial nomenclature to identify species, for example **H. sapiens.** Matching species name(s) appear at the bottom of the dialog box, in the left pane. If the search returns many species, eArray$_{XD}$ paginates the list, and a set of page links appears in Result Pages. **c** In the left pane of the dialog box, select the desired species. To select a species, click its name. To select additional species, control-click their names. **d** Click **Add.** eArray transfers the selected species to the right pane of the dialog box. You can add as many species as you want. The program remembers all of the species that you select on all pages. **e** Click **Done.** The selected species appear(s) in the Library Search pane in Species. Multiple species appear in pipe-separated format.
ELID	Type an ELID, or multiple ELIDs separated by pipe "|" characters. An ELID is a unique Agilent ID number that identifies a bait library.
Design Status	Select one of these options: • **All** – Returns libraries without regard to their status. • **Active** – Returns libraries that use library formats that are currently available. • **Obsolete** – Returns libraries that use library formats that are no longer available.
Created by	Type all or part of the name of the library owner whose libraries you want to find. This criterion is not case sensitive.

Search Criterion	Instructions/Details
Date Created	Enter a range of dates. Use yyyy-mm-dd as the date format, for example 2009-03-20. Alternatively, to select the desired dates from calendars, click  next to **From** and **To.** To return all libraries that were created before a given date, select the desired date in **To,** but do not select a date in **From.**
Containing Bait Group	Set this criterion to find libraries that contain specific bait group(s). To select the bait group(s) to use as search criteria: • Click **Select and Add.** A dialog box appears. This dialog box functions similarly to the one described in "To select probe groups for searches or microarrays" on page 106. The selected bait groups appear in pipe-separated format in the search pane.
Keywords	Type all or part of a keyword, or multiple keywords separated by commas. This search term is not case-sensitive.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in a library have the same length.
Status	Select a status from the list. To return libraries without regard to status, select **All.** Status designations for libraries parallel those for microarray designs. For more information, see "Status of microarray designs" on page 248.

4 Click **Search.**

The program searches for libraries that meet your search criteria. A Search Result pane appears. To sort the search results based on the contents of a column, click any column heading except **Actions.** To reverse the order, click the name of the column heading again.

You can take action on the libraries in the search results. In the Actions column, these icons can appear:

Icon	Details
	**Edit** – (Available only to the owner of a library. The library must have a status of Draft.) Lets you make changes to the library. See "To edit a library" on page 447.
	**Review** – (Available only for libraries with a status of Review) Lets the owner, and others with access, make changes to the library. See "To review a library" on page 453. To place a library in review, see "To place a library in review" on page 451.

Icon	Details
	**View** – Lets you view the baits, statistics, and other details of a library. See "To view a library" on page 443.
	**Delete** – (Available only to the owner of a library, and only if it has a status other than Submitted.) Removes a library from your server. See "To delete a library" on page 465.
	**Submit** – (Available only to the owner of a library, and only if it has a status of Complete.) Submits a library to Agilent Manufacturing. See "To submit a library to Agilent" on page 458.
	**Request Quote** – (Available only for libraries with a status of Submitted.) Lets you request a price quote for a library. See "To request a quote for a library" on page 460.
	**Change control type of bait group(s)** – (Available only for libraries with a status of Complete or Submitted) Lets you change the control type designation assigned to each of the bait groups in the library. See "To change the control type assigned to a bait group" on page 464.
	**Download** – (Available for libraries with a status other than Draft) Lets you download files associated with the library to a location that you select. See "To download library design files" on page 461.
	**Download from eArray Web site** – (Available for libraries from the eArray Web site that have not yet been transferred to your server, or that contain Agilent content that requires an update) Downloads the specific item from the eArray Web site. If this icon appears, you *must* download the library from the eArray Web site before you can take action on it.

In addition, if you are the owner of a library, you can move it to another folder. See "To move libraries" on page 456.

NOTE

Before you take action on a retrieved library, you may need to download the library from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To browse available libraries

You can use the Design Data pane of the Navigator to view and take action on the libraries in the folders of your server to which you have access.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, in the **Design Data** pane of the Navigator, expand folders until you can see the name of the desired library. In each folder in the Design Data pane, libraries can be found in the Library folder.

3 Right-click the name of the desired library.

A shortcut menu appears. These options can appear:

Option	Details
Download from eArray.com	(Appears for libraries from the eArray Web site that have not yet been transferred to your server, or that contain Agilent content that requires an update) Downloads the library from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Move	(Available for libraries that you own) Lets you move the library to a different folder. See "To move libraries" on page 456.
Edit	(Available only to the owner of a library. The library must have a status of Draft.) Lets you make changes to the library. See "To edit a library" on page 447.
Review	(Available for libraries with a status of Review) Lets anyone with access to the library make changes to it. See "To review a library" on page 453. To place a library in review, see "To place a library in review" on page 451.
View	Lets you view the baits, statistics, and other details of a library. See "To view a library" on page 443.
Delete	(Available to the owner of a library, if the library has a status other than Submitted.) Removes a library from your server. See "To delete a library" on page 465.
Submit	(Available to the owner of a library, if the library has a status of Complete.) Submits the library to Agilent Manufacturing. See "To submit a library to Agilent" on page 458.
Request Quote	(Available for libraries with a status of Submitted.) Lets you request a price quote for a library from Agilent. See "To request a quote for a library" on page 460.

Option	Details
Download	(Available for libraries with a status other than Draft, if design files are available) Lets you download library design files. See "To download library design files" on page 461.
Change Control Type	(Available for libraries with a status of Complete or Submitted) Lets you change the control type that is assigned to each of the bait groups in the library. See "To change the control type assigned to a bait group" on page 464.
Attach	Lets you attach a note, file, or URL to the library. You can also use this command to view existing attachments. See "To attach a file, note, or URL to a bait group or library" on page 444.

NOTE

- You can also search the Design Data pane of the Navigator for items that match a specific search term – see "To search the Navigator" on page 51.
- Before you take action on a retrieved library, you may need to download the library from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To create a library from a bait upload (wizard)

To use this wizard to create a library, you must have a file that contains the baits that you want to include. The file must be a Microsoft Excel (*.xls) file, or a tab-delimited text file (*.tdt or *.txt). The file can contain bait data in either the COMPLETE or MINIMAL file formats. See "To prepare a file of baits and annotation for upload" on page 371. The wizard leads you through the library creation process. It is available for the SureSelect Target Enrichment application type.

1 Set the application type to **SureSelect Target Enrichment.** "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Library Using,** click **Bait Upload.**

A dialog box appears with the main steps of the process. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the process. At any time, click **Cancel** to discard your settings and close the dialog box.

Separate sections in this topic cover each of the steps of the process:

- Step 1 – Bait Parameter and File Details. See"Step 1 – Bait Parameter and File Details" on page 423.
- Step 2 – Preview of Uploaded Baits. See "Step 2 – Preview of Uploaded Baits" on page 425.
- Step 3 – Define Library. See "Step 3 – Define Library" on page 426.
- Step 4 – Layout Baits. See "Step 4 – Layout Baits" on page 427.
- Step 5 – Create Library. See "Step 5 – Create Library" on page 427.

Step 1 – Bait Parameter and File Details

In this step, you enter details about how the program handles the baits in your uploaded file, as well as details about the bait data file itself.

1 Under **Bait Parameter Details,** enter the following parameters.

Parameter	Instructions/Details
Job Name	Type a name for the library. As the program creates the library, this name identifies the job in the Tasks pane of the Navigator. After the program creates the library, the name identifies the library in search results and in the Design Data pane of the Navigator.
Species	Select the species that is associated with your baits. You can use this information later to search for the baits.
Remove replicate baits from upload	A replicate bait has the same Bait ID as another bait in the file. To ignore all but the first bait in each set of replicate baits in your file, mark this option. If your bait file contains replicate baits, and you do **not** mark **Remove replicate baits from upload,** the program displays an error message after you begin the upload, and does not upload your file.
Bait Precedence	These options define what you want the program to do if it finds baits in your uploaded file that have the same Bait IDs as other baits that already exist in the system. Select one of these options: • **Overwrite matching baits** – The annotation of the matching uploaded bait replaces the annotation of the existing bait. This option is useful for reannotating baits. • **Skip matching baits** – The program ignores the matching uploaded baits, and only uploads new ones. • **Cancel upload if any baits already exist** – The program cancels the entire upload process if it finds a matching uploaded bait.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in the file must have this length.

2 Under **Upload Bait File Details,** enter the following parameters:

Parameter	Instructions/Details
Bait Group Name	After the program uploads your bait data file, it creates a bait group that contains all of the baits from the file. Type a name for this bait group.
Upload File	To identify your bait file, follow these steps. Your file must meet the requirements described in "To prepare a file of baits and annotation for upload" on page 371. **a** Click **Browse.** An Open dialog box appears. **b** Select the desired bait file, then click **Open.** The location of the selected file appears in Upload File.
File Format	Select either **MINIMAL** or **COMPLETE.** For details about these file formats, see "To prepare a file of baits and annotation for upload" on page 371.
File Type	Select the appropriate file type from the list. The program accepts Microsoft Excel (*.xls) files, and tab-delimited text (TDT) files with file extensions of .txt and .tdt **Note:** If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

3 Click **Next.**

The next step of the wizard appears in the dialog box.

NOTE

eArray$_{XD}$ can upload fairly large files. Agilent has tested the 64-bit version of the program, and has successfully uploaded 150,000 probes in the Complete file format, which corresponds to a file size of approximately 32 MB.

Step 2 – Preview of Uploaded Baits

In this step, you identify the contents of each column of your bait file. The first few rows of data from your bait data file appear under Define Uploaded File Columns.

1 At the top of each column of data, select the label that best describes the contents of the column. BaitID and BaitSequence cannot be blank. If you want the upload process to ignore a specific column, select **Ignore.** You must use each label exactly once, except Ignore, which you can use any number of times.

2 If the first row of your bait data file is actually a row of column headings, mark **My uploaded file contains column headings.** Otherwise, the program interprets the first line of the file as a set of bait data. The program does not interpret any column headings in your uploaded file.

3 Click **Next.**

If you have not yet transferred your workgroup's bait and annotation data for the SureSelect Target Enrichment application type from the eArray Web site, a warning message tells you that to avoid bait ID conflicts, the system will add a prefix of **XD_** to all of the new baits in your file. This differentiates your uploaded baits from any baits that you transfer from the eArray Web site that have the same names. To continue with the upload process, click **OK.**

The program uploads the file and submits a job to your server. The job appears in the Tasks pane of the Navigator, where you can monitor its status. A dialog box tells you that the file was successfully submitted to the upload queue.

4 Click **OK.**

You can monitor the status of the job in the Bait Upload (Wizard) folder of the Tasks pane of the Navigator. These icons can appear next to the name of the bait upload job:

Icon	Status/Comments
	**Pending** – The bait upload job has been submitted to the upload queue.
	**Complete** – Your server has successfully uploaded the baits in your file. You can now continue with the wizard.

Icon	Status/Comments
	Error – An error occurred. You must re-start the wizard. Errors are usually caused by irregularities in the uploaded bait file. To see any errors that the program detected in the uploaded bait file, follow these steps: **a** Right-click the name of the bait upload job, then click **Download Error File.** A dialog box appears. **b** Select a location for the error file, then click **Save.** The program saves a ZIP format file to the location that you selected. The ZIP file contains an HTML file that you can open with your Internet browser. The HTML file lists the errors that the program detected in your original bait file.

Step 3 – Define Library

When the program has successfully uploaded the baits from your file, a icon appears next to the name of the job. You can now continue with the wizard.

1 In the Tasks pane of the Navigator, in the Bait Upload (Wizard) folder, right-click the name of the bait upload job, then click **Create Library.**

The Create Library dialog box appears with the next step of the wizard.

2 Enter the following parameters. Parameters are required unless otherwise indicated.

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.
Species	(Read-only) The species that you selected in Step 1 of the wizard.
Length	(Read-only) The length of the baits in your uploaded file.
Library Size	(Read-only) The capacity of the library. The program selects an appropriate library size. **Example:** A library size of 1 X 55K can accommodate up to 57,750 baits.

Parameter	Instructions/Details
Control Grid	The program automatically selects an appropriate control grid for your library. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process. You can select a different control grid, if one is available.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to create the library with a status of Complete, which prevents further edits to the library, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

3 Click **Next.**

The next step of the wizard appears in the dialog box.

Step 4 – Layout Baits

The Layout Baits step is identical for all library creation wizards. Detailed instructions appear in the topic "To create a library from existing bait groups (wizard)" on page 428. See specifically "Step 2 – Layout Baits" on page 430.

Step 5 – Create Library

The Create Library step is identical for all library creation wizards. Detailed instructions appear in the topic "To create a library from existing bait groups (wizard)" on page 428. See specifically "Step 3 – Create Library" on page 432.

To create a library from existing bait groups (wizard)

This wizard creates a library that contains bait groups that you have previously uploaded or created in the program.

1 Set the application type to **SureSelect Target Enrichment.** "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under **Create Library using,** click **Existing Bait Group(s).**

The Create Library dialog box appears with the main steps of the wizard. Initially, the first step is visible. In general, you enter all of the parameters in a given step, then click **Next** to go to the next step. You can click **Previous,** when available, to go back to the previous step in the wizard. At any time, click **Cancel** to discard your settings and close the dialog box.

Separate sections in this topic cover each of the steps of the process:

- Step 1 – Select Species and Define Library. See "Step 1 – Select Species and Define Library" on page 429.
- Step 2 – Layout Baits. See "Step 2 – Layout Baits" on page 430.
- Step 3 – Create Library. See "Step 3 – Create Library" on page 432.

Step 1 – Select Species and Define Library

1 Set the following parameters. Parameters are required unless otherwise indicated.

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.
Species	Select the desired species.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Library Size	(Read-only) Select the desired library size. For example, the 1X55K library size can accommodate up to 57,750 baits.
Control Grid	This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process. If desired, select an alternate control grid if one is available.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to create the library with a status of Complete, which prevents further edits to the library, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

2 Click **Next.**

The next step of the process appears in the dialog box.

Step 2 – Layout Baits

In this step, you define the baits in your new library. As you add (or remove) bait groups, you can monitor the values in the Library Statistics pane to see how many baits the library contains, and how many more it can accommodate. See "Step 2 – Layout Baits" on page 627.

1 In the Layout Details pane, make changes to the bait content of the library, as described in the tasks in the table below.

Task	Instructions/Details
Add bait group(s)	**a** Click **List of Bait Groups,** then click **Add.** The Add Bait Groups pane appears. This pane functions identically to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Use the pane to search for, select, and add one or more bait groups, then click **Done.** The selected bait groups appear in the List of Bait Groups pane.
Remove bait group(s)	**a** Click **List of Bait Groups.** **b** In the **Select** column, mark the check box next to the bait group that you want to remove. **c** Click **Remove.**
View details about a bait group	(Available after the library contains bait groups) • In the List of Bait Groups tab within the dialog box, click  The View Bait Group dialog box appears. See "View Bait Group" on page 867. **Note:** To view the details of a bait group, you may need to transfer the given bait group from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data for the SureSelect Target Enrichment application type from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Task	Instructions/Details
Change the control type of a bait group	Next to the desired bait group, in the Control Type column, select an option from the list. The option that you select has no effect on the composition of the library. The program attaches the designation to the bait group for user reference. These options are available: • **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications. • **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.
Change the number of copies of a bait group	In the **Replicate** column, next to the desired bait group, type the number of copies of the bait group that you want to include in the library. **Note:** • The program also copies the required Agilent control bait group the same number of times as your least-replicated bait group. • The program automatically includes as many complete sets of baits as will fit in the available space in the library. **Example:** Your library contains 12,000 baits, including the required Agilent control baits. The capacity of the 1 X 55K library format is 57,750 baits. eArray includes four complete sets of baits in your library (12,000 x 4 = 48,000 baits). Five complete sets would be too large for the library format (12,000 x 5 = 60,000 baits).

NOTE

When you select bait groups for a library, the program tells you if a bait group is *Local* or if it is *Not Downloaded.* If you select one or more bait groups that are *Not Downloaded,* you can only save the new library with a status of Draft. After you download the given bait group(s) from the eArray Web site, you can save the library with a status of Complete or Submitted. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to download bait and annotation data for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

2 Click **Next.**

The next step of the wizard appears in the dialog box.

Step 3 – Create Library

In this step, you select the status to assign to the new library. The status that you select affects the actions that you can take on the library. The status designations for libraries parallel those for microarray designs. For more information, see "Status of microarray designs" on page 248.

1 In **How do you want to save and create your library,** select one of these options:

Option	Details
Draft	The program saves the library with a status of Draft. This status lets only you edit the library. This is the default option. For details, see "To edit a library" on page 447.
Review	The program saves the library with a status of Review. This status lets you and other users who have access to the library make changes and save versions of it. For details, see "To review a library" on page 453.
Complete	The program saves the library with a status of Complete, and retrieves a unique library ID (ELID) number for it from the eArray Web site. You can subsequently submit the library to Agilent Manufacturing. No one can edit or review a library with this status.
Submitted	The program saves the library with a status of Submitted, and submits the library to Agilent Manufacturing. No one can edit or review a library with this status. If you select this option, you must also click **Show Checklist,** read and mark all of the items that appear, then click **Done.** To preview this checklist, see "Design Checklists" on page 894. You can subsequently request a quote for the library. See "To request a quote for a library" on page 460. When you submit a library, it also becomes available on the eArray Web site. You can search, view , and request a quote for it, and download its design file. However, you cannot copy it, access its baits, or publish it on OpenGenomics.com.

2 Click **Finish.**

A dialog box tells you that the library has been successfully created.

3 Click **OK.**

To create a library using Bait Tiling (wizard)

Bait Tiling creates baits that evenly cover specified genomic regions of a given species. This wizard helps you use this method to design a library and submit it to Agilent. You can customize the tiling process for specific sequencing technologies and protocols. You can also select the and the density of tiling. For additional details about bait tiling, see "To set up a Bait Tiling job" on page 378.

The genome to be tiled must either be an Agilent-provided genome that is available on the eArray web site, or a user-defined genome that is present on your server. If desired, you can import a custom genome to your server before you use this wizard. See "To import a new genome" on page 66.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the eArray$_{XD}$ tab, under Create Library Using, click **Bait Tiling.**

The first step of the wizard appears.

Separate sections in this topic describe each of the steps of the wizard:

- Step 1 – Library Options and Target Details. See "Step 1 – Library Options and Target Details" on page 434.
- Step 2 – Define Library. See "Step 2 – Define Library" on page 438.
- Step 3 – Layout Baits. See "Step 3 – Layout Baits" on page 439.
- Step 4 – Create Library. See "Step 4 – Create Library" on page 439.

Step 1 – Library Options and Target Details

1 Set the following parameters. All are required.

Parameter	Instructions/Details
Design Options	
Design Job Name	Type a name that will later enable you to identify this Bait Tiling job.
Sequencing Technology	From the list, select the type of DNA sequencer that you will use to analyze your target DNA fragments.
Sequencing Protocol	Select the desired protocol. In the list, the program displays the available protocols for your chosen DNA sequencing technology.
Use Optimized Parameters	In general, mark this option. With this option, based on your selected sequencing technology and protocol, the program automatically sets the best values for Design Strategy, Bait Length, Bait Tiling Frequency, and Avoid Overlap. To set parameters manually, clear this option. The design parameters all become available.
Design Strategy	(Available if you clear **Use Optimized Parameters**) Select one of these options: • **Centered** – eArray centers sets of tiled baits over their respective target intervals. Each set of baits hangs over both ends of its target interval by equal amounts. This option exactly respects the value that you select in Bait Tiling Frequency. • **Justified** – eArray designs sets of tiled baits to exactly cover their respective target intervals. This option adjusts the overlap of baits to achieve the precise and even tiling of only the target intervals, without any overhang into non-target regions. With this option, the actual tiling frequency can deviate from the value that you select in Bait Tiling Frequency.
Bait Length	(Available if you clear **Use Optimized Parameters.**) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.

Parameter	Instructions/Details
Bait Tiling Frequency	(Available if you clear **Use Optimized Parameters**) Select the desired tiling frequency. This setting controls the density of tiling. The density can also be affected by your choice of Design Strategy. • **2x** – eArray overlaps baits by 50% as it tiles each interval. Two baits cover each base in each interval. • **3x** – eArray overlaps baits as it tiles each interval so that three baits cover each base in each interval. • **4x** – eArray overlaps baits as it tiles each interval so that four baits cover each base in each interval. • **5x** – eArray overlaps baits as it tiles each interval so that five baits cover each base in each interval. **Note:** Depending on your other settings, the exact density of tiling may be somewhat less than that indicated above at the extreme 5' and 3' ends of each interval.
Avoid Overlap	(Available if you clear **Use Optimized Parameters**) To change the value, select it, then type the desired distance in base pairs. The program generates baits that may extend by this distance into the regions that are specified in Genomic Avoid Intervals (see below). For best results, set this distance to a maximum of 20 bp.
Strand	Select one of these options: • **Sense** – Produces baits that are similar in sequence to the sense strand of the target DNA. • **Antisense** – Produces baits that are complementary to the sense strand of the target DNA. • **Both** – Produces both a sense bait and an antisense bait for each target location. **Note:** If you are going to use the library to enrich genomic targets, either sense or antisense baits typically work. For the enrichment of cDNA targets, the selection of sense vs. antisense baits is important, since genes can appear on either strand.

Parameter	Instructions/Details
Target Details	
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Lets you select one of the standard genomes available on the eArray Web site for the Bait Tiling job. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. • **User Defined Genome** – Lets you select a genome that you have uploaded to your server. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build.
Species	Select the desired species.
Genome Build	If desired, select a different genome build, if one is available. The program uses the selected genome build to generate baits.
Genomic Target Intervals	Type target intervals using the format chrX:<start>-<end>. **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. Alternatively, you can upload a list of intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—in a word processor, press **Enter** at the end of each line. Then follow these steps: **a** Next to the Genomic Target Intervals box, click **Upload.** A File Upload dialog box appears. See "File Upload" on page 773. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file, then click **Open.** The location of the file appears in the File Upload dialog box, in File Name. **d** Click **Upload.** The intervals from the uploaded file appear in pipe-separated format in the Genomic Target Intervals box.

Parameter	Instructions/Details
Avoid Standard Repeat Masked Regions	This option excludes a standard set of repetitive genomic regions from the Bait Tiling process. These regions generally produce poor quality baits. This option is marked by default. If you are tiling a user-defined genome, these repeat regions are the sequences that are represented by lower case letters in your sequence files, if you marked Genome is Soft Masked when you imported it.
Avoid Custom Intervals	This option excludes the genomic intervals that you enter in the Genomic Avoid Intervals box from the Bait Tiling process. If you mark this option, the Genomic Avoid Intervals box becomes available (see below).
Genomic Avoid Intervals	(Available if you mark Avoid Custom Intervals) The program excludes the genomic intervals that you enter in the box from the Bait Tiling process. Use this format to enter intervals: chrX:<start>-<end>. **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. **Note:** You can upload a list of custom intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—in a word processor, press **Enter** at the end of each line. Then follow these steps: **a** In Genomic Avoid Intervals, click **Upload.** A File Upload dialog box appears. **b** Click **Browse.** An Open dialog box appears. **c** Select the desired file, then click **Open.** In the File Upload dialog box, the location of the file appears in File Name. **d** Click **Upload.** eArray uploads the list of intervals, and displays them in pipe-separated format in the Genomic Avoid Intervals box

2 Click **Next.**

The program adds a job to the Tasks pane of the **Navigator,** in a Bait Tiling folder. A dialog box tells you that your job has been submitted.

3 Click **OK.**

The wizard pauses here. Before you can continue, you must wait for the program to finish the tiling job. When the job is finished, and its status icon changes to (Complete), you can continue with the rest of the steps of the wizard.

Step 2 – Define Library

When the program has successfully completed the Bait Tiling job that you submitted in the first step, a icon appears next to the name of the job. You can now continue with the wizard.

1 In the Tasks pane of the Navigator, in the appropriate Wizard Bait Tiling folder, right-click the name of the Bait Tiling job, then click **Create Library.**

A dialog box appears with the next step of the wizard.

2 Set the following parameters. Parameters are required unless otherwise indicated.

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.
Species	(Read-only) Displays the species that you selected in Step 1 of the wizard.
Length	(Read-only) Displays the bait length that you selected in Step 1 of the wizard.
Library Size	(Read-only) Displays the capacity of the library. The program selects an appropriate available library size. **Example:** If 1 X 55K appears, the library supports 55K baits (57,750 baits).
Control Grid	The program automatically selects an appropriate control grid for your library. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process. You can select a different control grid, if one is available.

Parameter	Instructions/Details
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to create the library with a status of Complete, which prevents further edits to the library, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

3 Click **Next.**

The next step of the wizard appears in the dialog box.

Step 3 – Layout Baits

The Layout Baits step is identical for all library creation wizards. Detailed instructions appear in the topic "To create a library from existing bait groups (wizard)" on page 428. See specifically "Step 2 – Layout Baits" on page 430.

Step 4 – Create Library

The Create Library step is identical for all library creation wizards. Detailed instructions appear in the topic "To create a library from existing bait groups (wizard)" on page 428. See specifically "Step 3 – Create Library" on page 432.

To create a library from bait group search results

After you do a search for bait groups, you can create a library that contains one or more of the bait groups in the search results. In addition to the procedure described in this topic, the program also has a Library Wizard that leads you through this process. See "To create a library from existing bait groups (wizard)" on page 428.

1 Search for the desired bait group(s). See "To search for bait groups" on page 396. If you intend to include multiple bait groups in your library, you

do not have to retrieve all of them at once—you can add additional bait groups later in the process.

The Search Result pane lists the bait groups that match your search criteria.

2 Select the desired bait groups. Use the following as a guide:

- To select a bait group, mark the check box next to its name.
- To go to a different page of results, if available, click a numbered page button.
- You can select more than one bait group. The program remembers your selections as you go from page to page.
- To select all of the bait groups on a page, mark the check box in the column heading row.
- To select all of the bait groups on all pages of the search results, mark **Select entire data set.**

3 Click **Create Library.**

The Create Library dialog box appears. See "Create Library" on page 622.

4 Set the following parameters. Parameters are required unless otherwise indicated. The parameters indicated as *read-only* are set by the program, and cannot be changed.

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Species	Select the species that best represents the bait groups that you have selected for the library.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. This value must match the length of baits in all of the bait groups that you use in the library. All baits in a library must have the same length. When you select a length, the program automatically selects the library size and the appropriate control grid.
Status	(Read-only) The program always creates new libraries with an initial status of **Draft,** which lets the owner edit the design.

Parameter	Instructions/Details
Library Size	(Available after you select a species and bait length) Select the desired library capacity. **Example:** A library with a size of 1 X 55K can accommodate up to 57,750 baits.
Control Grid	(Available after you select a species and bait length) A control grid that is appropriate for your species, bait length, and library size appears. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process.
Folder	Select a location for the new library. The folders to which you have access appear in the list.
ELID	This property is blank for new libraries. An ELID is a unique ID that Agilent assigns to a library. This ID is assigned when a library is saved with a status of Complete or Submitted.
Description	(Optional) Type a brief description for the library.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	(Optional) Type comments to include with the library.

5 Under Layout Details, do any of the tasks in the table below to refine the content of the library. As you add (or remove) bait groups, you can monitor the available spade in the library using the Library Statistics pane.,

Task	Instructions/Details
Add bait group(s)	**a** Click **List of Bait Groups**, then click **Add.** The Add Bait Groups pane appears. This pane functions similarly to the dialog box described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one ore more bait groups, then click **Done.** The selected bait groups appear in the List of Bait Groups pane.

Task	Instructions/Details
Remove bait group(s)	**a** Click **List of Bait Groups.** **b** In the **Select** column, mark the check box next to the bait group that you want to remove. **c** Click **Remove.**
View details about a bait group	(Available after the library contains bait groups) • In the List of Bait Groups pane, click  The View Bait Group dialog box appears. See "View Bait Group" on page 867.
Change the control type of a bait group	Next to the desired bait group, in the Control Type column, select an option from the list. The option that you select has no effect on the composition of the library. The program attaches the designation to the bait group for user reference. These options are available: • **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications. • **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.
Change the number of copies of a bait group	In the **Replicate** column, next to the desired bait group, type the number of copies that you want to include in the library. **Note:** • The program also copies the required Agilent control bait group the same number of times as your least-replicated bait group. • The program automatically includes as many complete sets of baits as will fit in the available space in the library. **Example:** Your library contains 12,000 baits, including the required Agilent control baits. The capacity of the 1 X 55K library format is 57,750 baits. eArray includes four complete sets of baits in your library (12,000 x 4 = 48,000 baits). Five complete sets would be too large for the library format (12,000 x 5 = 60,000 baits).
Monitor the number of features available	As you add, remove, and/or replicate bait groups, the program updates the values in the Library Statistics pane. For information about the available values, see "Create Library" on page 622

NOTE

You can use a bait group in a library if it appears in the results of a Bait Group Search. However, if you use a bait group from the eArray Web site that has not yet been downloaded to your server, or that requires an update, you can only save the new library with a status of Draft. After you download the bait group from the eArray Web site, you can save the library with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

6 Click **Save.**

The program creates the new library, and saves it to the selected folder with a status of Draft. A dialog box tells you that the library has been created successfully.

7 Click **OK.**

To view a library

You can view the baits, statistics and other details of a library. Before you can view a library, you may need to download it from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **View.**

In either case, the View Library dialog box appears. For information on the content of this dialog box, see "View Library" on page 869.

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

To attach a file, note, or URL to a bait group or library

You include background material, protocols, and other related information with a library or bait group. You can add an attachment to any bait group or library to which you have access, except Agilent Catalog bait groups and libraries.

If you want to add an attachment to a bait group or library that came from the folders of your workgroup on the eArray Web site, you may first need to transfer the item to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Design Data pane of the Navigator, expand folders until you can see the library or bait group to which you want to add an attachment.

3 Right-click the name of the desired library. Click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593.

4 Add the desired attachment as described in the table below.

Type of Attachment	Instructions/Details
Note	You can attach text to a bait group or a library. **a** Under Add Attachment, in Attachment Type, select **Notes.** **b** In **Note,** type the desired text. **c** Click **Add.** The program attaches your note to the library. An entry for the note appears in the Total Attachments pane.
File	You can attach a file to a bait group or a library. **a** Under Add Attachment, in Attachment Type, select **File.** **b** In **Name,** type a display name for the file. This name identifies the attachment in the Total Attachments pane. **c** In File, click **Browse.** An Open dialog box appears. **d** Select the desired file, then click **Open.** The location of the file appears in File. **e** Click **Add.** An entry for the file appears in the Total Attachments pane.

Type of Attachment	Instructions/Details
URL	**a** Under Add Attachment, in Attachment Type, select **URL.** **b** In **Name,** type a display name for the URL. This name identifies the attachment in the Total Attachments pane. **c** In **URL,** type the complete URL. **Example:** `http://www.agilent.com` **d** Click **Add.** An entry for the URL appears in the Total Attachments pane.

5 Click **Close.**

To view the attachments to a bait group or library

You can view a file, note, or URL that is attached to a bait group or library. If you want to view an attachment to a bait group or library that came from the folders of your workgroup on the eArray Web site, you may first need to transfer the item to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

1 Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.

2 In the Design Data pane of the Navigator, expand folders until you can see the bait group or library whose attachment(s) you want to view.

3 Right-click the name of the desired library. Click **Attach.**

The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. The files and URLs that are attached to the library or probe group appear in the Total Attachments pane. To go to a different page of attachments, if available, click one of the numbered page buttons above or below the list.

4 In the **Actions** column, in the row of the attachment that you want to view, click  .

The program opens files in the appropriate program, if available, and opens URLs in your Web browser. The program opens notes in separate windows, and lets you view and make changes to them.

To remove attachments from a bait group or library

1. Set the application type to **SureSelect Target Enrichment.** See "To set the application type" on page 48.
2. Right-click the name of the bait group or library, then click **Attach.**

   The Add/Remove Attachments dialog box appears. See "Add/Remove Attachments" on page 593. To go to a different page of attachments, if available, click a numbered page button above or below the list.
3. In the Total Attachments pane, select the URL(s) and/or file(s) that you want to remove. To select a file or URL, mark the check box next to its name. To select all of the files and URLs on the current page of attachments, mark the check box in the column heading row. The program remembers your selections as you go from page to page.

CAUTION When you remove an attached file or a URL, the program permanently removes the file, note, or URL from the bait group or library. To restore a file, you must have a copy of the file, and re-attach it. To restore a URL or a note, you must re-enter it.

4. Click **Delete.**

   A dialog box ask you if you are sure you want to delete the attachments.
5. Click **Yes.**

   A dialog box tells you that the selected attachments were deleted.

NOTE If you want to remove an attachment from a bait group or library that came from the folders of your workgroup on the eArray Web site, you may first need to transfer the item to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. Also, if you remove an attachment within eArray$_{XD}$, this does not affect any attachments to the item on the eArray Web site.

To edit a library

You can edit the content and properties of a library. You must own the library, and it must have a status of Draft.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **Edit.**

In either case, the Edit Library dialog box appears. See "Edit Library" on page 740. If the Edit button or command is not available, you are either not the owner of the library, or the library does not have a status of Draft – see the note at the end of this topic.

3 At the top of the dialog box, make changes to any of the following properties, as desired. The properties that do not appear in the table below are calculated by the program or are informational only, and cannot be edited. For details on all of the items in this dialog box, see "Edit Library" on page 740.

Property	Instructions/Details
Library Name	Type a new name for the library. The name can be from 1 to 100 characters long. Use only letters, numbers, spaces, hyphens, underscores, and periods.
Status	Select one of these options: • **Draft** – The library will continue to have a status of Draft, which lets only the owner edit it. • **Review** – Places the library in review, which lets anyone with access to the library make changes and save new versions of it. See "To review a library" on page 453. • **Complete** – Assigns a status of Complete to the library. The library can subsequently be submitted to Agilent. It cannot be edited. **Caution:** Library status follows a one-way order from Draft to Review to Complete. Once you save a library with a given status, you cannot change the status to a previous one in the order.

Property	Instructions/Details
Folder	Select a new location for the library. Only the folders to which you have access appear in the list.
Library Size	Select the desired library size. **Example:** A library size of 1 X 55K can accommodate up to 57,750 baits.
Control Grid	Select a different control grid, if one is available. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process.
Description	Edit the description, as desired.
Keywords	Edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Add or edit comments. If you intend to save the library with a status of Complete, comments are required. Otherwise, comments are optional.

4 At the bottom of the dialog box, make changes to the bait content of the library. Use the tasks described in the table below. As you change the bait content, use the Library Statistics pane to monitor the number of remaining features that are available in the library.

Task	Instructions/Details
Add bait group(s)	**a** Click **List of Bait Groups,** then click **Add.** The Add Bait Groups tab appears. This tab functions similarly to the dialog box for probe groups described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one ore more bait groups, then click **Done.** You may need to scroll down to see this button. The selected bait groups appear in the List of Bait Groups tab.
Remove bait group(s)	**a** In the **List of Bait Groups** tab, in the **Select** column, mark the check box next to the bait group that you want to remove. **b** Click **Remove.**

Task	Instructions/Details
Change the control type of a bait group	Next to the desired bait group, in the Control Type column, select an option from the list. The option that you select has no effect on the composition of the library. The program attaches the designation to the bait group for user reference. These options are available: • **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications. • **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.
Change the number of copies of a bait group	In the **Replicate** column, next to the desired bait group, type the desired number of copies. **Note:** • The program also copies the required Agilent control bait group the same number of times as your least-replicated bait group. • The program automatically includes as many complete sets of baits as will fit in the available space in the library. **Example:** Your library contains 12,000 baits, including the required Agilent control baits. The capacity of the 1 X 55K library format is 57,750 baits. eArray includes four complete sets of baits in your library (12,000 x 4 = 48,000 baits). Five complete sets would be too large for the library format (12,000 x 5 = 60,000 baits).

5 At the bottom of the dialog box, click **Save.**

The program saves your edited library to your server. The new version replaces the previous version. A dialog box tells you that the library has been updated successfully.

6 Click **OK.**

NOTE

- To edit a library, you must own it, and it must have a status of Draft. To make changes to a library that you do not own, ask its owner to place it in review. This lets other users who can access the library make changes to it. See "To place a library in review" on page 451 and "To review a library" on page 453.
- To edit a library that came from the folders of your workgroup on the eArray Web site, you may first need to transfer the library to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

To place a library in review

If you are the owner of a library with a status of Draft, you can place it in review. This lets any user who has access to the library make changes and save new versions of it.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **Edit.**

In either case, the Edit Library dialog box appears. For details about this dialog box, see "Edit Library" on page 740.

3 In **Status,** select **Review.**

4 At the bottom of the dialog box, click **Save.**

The program places the library in review. In the Design Data pane of the Navigator, the icon next to the name of the library changes to  .Other users with access to it can now make changes and save new versions of it. See "To review a library" on page 453.

A dialog box tells you that the library has been successfully updated.

5 Click **OK.**

NOTE

To place a library in review, you may first need to download (or update) one or more bait groups from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait and annotation data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

To place a different version of a library in review

When a library is in review, the program retains all versions of the library, each with a unique version number. By default, all reviews use the original version of the library as a starting point. However, the owner of the library can select any version as the starting point for subsequent reviews.

To place a different version of a library in review, you must be the owner of the library. Also, the library must have a status of Review. See "To place a library in review" on page 451.

1. Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.
2. Do one of the following:
   - If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
   - If you browsed for the library – Right-click the name of the desired library, then click **Review.**

   In either case, the Edit Library dialog box appears. See "Edit Library" on page 740.
3. In the Layout Details pane, click **List of Versions.**

   A list of the available versions of the library appears.
4. In the **Select Version** column, select the desired version.

   A dialog box asks if you are sure you want to change the current version.
5. Click **Yes.**

   The selected version becomes the current version. A dialog box tells you that the library version has been successfully updated.
6. Click **OK.**
7. Click **Save.**

   A dialog box tells you that the library has been successfully updated.
8. Click **OK.**

To review a library

If a library has a status of Review, any user with access to it can make changes and save new versions of it.

For you to review a library, its owner must place it in review. See "To place a library in review" on page 451. By default, all reviews use the original version of the library as a starting point. However, the owner of the library can select any version as the starting point for subsequent reviews. See "To place a different version of a library in review" on page 452.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **Review.**

In either case, the Edit Library dialog box appears. See "Edit Library" on page 740.

3 At the top of the dialog box, make changes to any of the following properties, as desired. The properties that do not appear in the table below are calculated by the program or are informational only, and cannot be edited.

Property	Instructions/Details
Library Name	Type a new name for the library. The name can contain from 1 to 100 characters. Use only letters, numbers, spaces, dashes, underscores, and hyphens.
Status	(Available only to the owner of the library) Do one of the following: • To let the review process continue, keep Status set to **Review.** • To end the review process, and prevent further changes to the library, select **Complete.** After you save the library, you can subsequently submit it to Agilent. **Caution:** If you save the library with a status of Complete, this prevents all further changes to it. You cannot subsequently change the status of the library back to Review or Draft.

Property	Instructions/Details
Folder	Select a new location for the library. Only the folders to which you have access appear in the list.
Library Size	Select the desired library size. **Example:** A library size of 1 X 55K can accommodate up to 57,750 baits.
Control Grid	Select another control grid, if one is available. This required Agilent control grid contains baits that are used for quality control purposes in the bait manufacturing process.
Description	Edit the description, as desired.
Keywords	Add or edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Add or edit comments. The comments appear during further reviews of the library. They also appear in the Comments column for the current version of the library when you click Version History. If you intend to save the library with a status of Complete, comments are required. Otherwise, comments are optional.

4 At the bottom of the dialog box, make changes to the bait content of the library. Use the tasks described in the table below. As you change the bait content of the library, use the Library Statistics pane to monitor the number of remaining available features.

Task	Instructions/Details
Add bait group(s)	**a** Click **List of Bait Groups,** then click **Add.** The Add Bait Groups pane appears. This pane functions similarly to the dialog box for probe groups described in "To select probe groups for searches or microarrays" on page 106. **b** Search for, select, and add one or more bait groups, then click **Done.** The selected bait groups appear in the List of Bait Groups pane.

Task	Instructions/Details
Remove bait group(s)	**a** In the **List of Bait Groups** pane, in the **Select** column, mark the check box(es) next to the bait group(s) that you want to remove. **b** Click **Remove.**
Change the control type of a bait group	Next to the desired bait group, in the Control Type column, select an option from the list. The option that you select has no effect on the composition of the library. The program attaches the designation to the bait group for user reference. These options are available: • **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications. • **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.
Change the number of copies of a bait group	In the **Replicate** column, next to the desired bait group, type the number of copies of the bait group you want to include in the library. **Note:** • The program also copies the required Agilent control bait group the same number of times as your least-replicated bait group. • The program automatically includes as many complete sets of baits as will fit in the available space in the library. **Example:** Your library contains 12,000 baits, including the required Agilent control baits. The capacity of the 1 X 55K library format is 57,750 baits. eArray includes four complete sets of baits in your library (12,000 x 4 = 48,000 baits). Five complete sets would be too large for the library format (12,000 x 5 = 60,000 baits).

Task	Instructions/Details
View a list of the current and previous versions of the library	(Available for libraries with a status of Review) • In the Layout Details pane, click **List of Versions.** The List of Versions pane appears. All saved versions of the library appear by version number, along with the person who saved each one. The date the version was saved, and any comments from each reviewer, also appear. By default, the program uses the original version of a library as the starting point for all reviews. However, if you are the owner of the library, you can use this pane to select a different version of the library as the starting point. See "To place a different version of a library in review" on page 452.

5 At the bottom of the dialog box, click **Save.**

The program saves the library to your server with a new, unique version number. A dialog box tells you that the library has been successfully updated.

6 Click **OK.**

To move libraries

You can move one or more libraries that are stored on your server to a new folder.

Before you move a library

- You must be the owner of the library.
- You must have access to the destination folder.

To move a library

1 Search for one or more libraries. See "To search for libraries" on page 416.

2 In the search results, mark the check boxes next to the libraries that you want to move.

3 Click **Move.**

The Move Library dialog box lists the selected libraries. The dialog box lists the current location of each library.

4 In **Move to Domain,** select the desired destination folder for the libraries. Only the folders to which you have access appear in the list.

5 Click **Move.**

A dialog box asks if you really want to move the library.

6 Click **Yes.**

A dialog box lists the selected libraries, and indicates which ones were successfully moved. If any libraries were not moved, the reason appears in the dialog box

7 Click **OK.**

NOTE You can also move certain libraries that appear in the Design Data pane of the Navigator. Right-click the name of the desired library, then click **Move.** If you use this method, you can only move one library at a time. In addition, you may need to download the library from the eArray Web site.

To complete a library

If you are the owner of a library, and it has a status of Draft or Review, you can change the status to Complete. With this status, no further changes can be made to the library. This status also lets you subsequently submit the library to Agilent. See "To submit a library to Agilent" on page 458.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  if its status is Draft, or  if its status is Review.
- If you browsed for the library – Right-click the name of the desired library, then click **Edit** if its status is Draft, or **Review** if its status is Review.

The Edit Library dialog box appears. See "Edit Library" on page 740.

3 In **Status,** select **Complete.**

4 In **Comments,** type comments. Comments are required.

5 Click **Save.**

A dialog box asks if are sure you want to complete the library.

CAUTION When you save the library with a status of Complete, this prevents further edits or reviews to it. You cannot subsequently change the status of the library back to Review or Draft.

6 Click **Yes.**

The program saves the library with a status of Complete. The library cannot be further edited or reviewed. In the Design Data pane of the Navigator, the icon next to the name of the library changes to .

The program also downloads a unique ELID number from the eArray Web site and assigns it to the library. The ELID appears with the name of the library in the Design Data pane of the Navigator, and it also appears in the ELID column in the Search Result pane when you search for the library.

A dialog box tells you that your library has been successfully completed.

7 Click **OK.**

To submit a library to Agilent

You can submit a library to Agilent Manufacturing from the Design Data pane of the Navigator, or from the results of a library search. The library must have a status of Complete . Once you submit a library, you cannot further edit it.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the search results, in the **Actions** column, next to the desired library, click .
- If you browsed for the library – In the Design Data pane of the Navigator, right-click the name of the library, then click **Submit.**

In either case, the Submit Library dialog box appears. See "Submit Library" on page 861.

3 In **Comments,** type brief comments to be saved with the library. Comments are required as a means to minimize accidental submission of libraries.

4 Click **Show Checklist.**

A checklist appears. To see a copy of this checklist, see "Design Checklists" on page 894.

5 Read and mark all of the items in the checklist, then click **Done.**

6 In the Submit Library dialog box, click **Save.**

The program submits the library to Agilent Manufacturing, and assigns it a status of Submitted. In the Design Data pane of the Navigator, the icon next to the name of the library changes to ➡. A dialog box tells you that the library has been successfully submitted.

7 Click **OK.**

Later, you can request a price quote through the program, and place an order for the library through your Agilent sales representative. See "To request a quote for a library" on page 460.

CAUTION If you submit a library to Agilent Manufacturing, you cannot subsequently "un-submit" it. You also cannot delete a submitted design.

NOTE When you use a wizard to create a library, you can submit the library to Agilent in the final step. See these topics:

- "To create a library from a bait upload (wizard)" on page 422
- "To create a library from existing bait groups (wizard)" on page 428
- "To create a library using Bait Tiling (wizard)" on page 433

When you submit a library, the program uploads the design file for the library to Agilent Manufacturing. The library becomes available in your user account, and you can use the eArray Web site to retrieve the library in a search, view or download it, and to request a quote for it. However, on the eArray Web site, you cannot copy the library, access its baits, or publish it on OpenGenomics.com.

To request a quote for a library

You can request a price quote for a library through the program. The library must have a status of Submitted, and you must have access to it. You can also request a quote from your Agilent sales representative.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the search results, next to the desired library, click 
- If you browsed for the library – In the **Design Data** pane of the Navigator, right-click the name of the desired library, then click **Request Quote.**

In either case, the eArray Web site opens in your Web browser. The Request Quote page appears. The Library Details Pane displays information that identifies the library.

3 Under Quote Details, enter the following information:

Detail	Instructions
Quantity	Type the desired number of custom library kits.
Reaction Size	Select the desired reaction size. The numbers in the list indicate the total number of captures that you can do with each custom library kit.
Sequencing Technology	Select the type of sequencing instrument that you will use to sequence the DNA fragments that are retrieved by your bait library.
Sequencing Protocol	Select the desired sequencing protocol. The option(s) that are available depend on your selected Sequencing Technology.

4 Click **Next.**

A confirmation page appears, with the details of your quote request.

5 Do any of the following:

- To change the quote request, click **Edit Quote Request.** You can change your entries under Quote Details.
- To print the page, click the **Print** button.
- To delete the quote request, click **Cancel.**

6 Click **Submit.** This submits the quote request to Agilent.

A success message appears.

7 Click **Close.**

A message tells you that your quote request has been submitted, and that you will receive an e-mail confirmation from Agilent. An Agilent sales representative will contact you to follow up on the quote.

8 Click **Log out.**

A dialog box asks if you are sure that you want to log out.

9 Click **OK.**

NOTE To purchase libraries, you can place an order through your Agilent sales representative. If you have previously purchased products from Agilent, you can also use the eArray Web site to set up an order for Catalog or custom libraries from the Agilent Online Store. See the online help on the eArray Web site. You do not need to request a quote before you purchase libraries.

To download library design files

You can download two types of design files for a library:

- **TDT** – Tab-delimited text file that contains the bait ID, sequence, and replicate count of each bait, and the strand (sense or antisense) to which each bait was designed. This file can be available for libraries with statuses of Review, Complete, or Submitted.
- **BED** – Browser Extensible Data (BED) format text file that you can use with a compatible genome browser to view the genomic locations of baits in the library. You can also use this file as the target intervals file when you use the SureSelect Quality Analyzer—see the *User Guide* for the SureSelect Quality Analyzer. This file can be available for libraries with a status of Complete or Submitted.

Your server keeps every version of the design files for a given library that is transferred from the eArray Web site, or that is created in eArray$_{XD}$. When you download design files from your server, you can select any available version. Each available set of design files is associated with a specific library ID and timestamp, which you select in **Build Number.** Each set of files also maps to a specific genome build. More than one version (set) of files can map to a given genome build or library ID.

Use the procedure below to download design files for libraries from the AgilentCatalog folder, and from the folder that has the name of your workgroup. For libraries from the Custom Designs folder, see the last note at the end of this topic.

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **Download.**

If these options do not appear, you may first need to download the library from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

The Download Library dialog box appears. See "Download Library" on page 721. In Build Number, a list of library IDs/timestamps appears.

Example: In Build Number, **015068_20091214** is one of the options. This refers to the library with a library ID of 015068, specifically the version of the design files that has a timestamp of 20091214.

3 In **Build Number,** select the library ID/timestamp of the set of library files that you want to download.

All of the design files that are associated with the selected library ID and timestamp appear.

4 Mark the desired file types. To download all available file types, mark **Select All,** if it is available.

5 Click **Download.**

A Save dialog box appears.

6 Select a location for the downloaded file(s), then click **Save.**

A dialog box tells you that the file(s) were successfully downloaded.

7 Click **OK.**

NOTE

- The availability of design files depends on whether the library was created locally or on the eArray Web site, and other factors. See "Availability of design files" on page 723.
- You can customize which types of files the program creates. See "To select the types of design files that the program creates" on page 343.
- For design files that have been transferred from the eArray Web site, the timestamp that is associated with the transferred files is the same as the timestamp of this set of files on the eArray Web site, without regard to when the files were transferred to your server.
- When the program downloads library design files, it does not download any files that are attached to the library. For information about attachments, see "To attach a file, note, or URL to a bait group or library" on page 444.
- If you save a library on the eArray Web site with a status of Complete or Submitted *after* you install your Agilent Genomic Workbench server, you can only download a BED file. You download this file from the **Custom Designs** folder in the Design Data pane of the Navigator. It is typically available within 24 hours after you save the library on the eArray Web site. No other actions are available for these types of libraries. To download this BED file, right-click the name of the library, then click **Download.**

To change the control type assigned to a bait group

When a library has a status of Complete or Submitted, you cannot edit it, even if you are its owner. However, you can change the control type that is assigned to each of the bait groups in the library. Although the control types that are assigned to bait groups have no effect on the composition of a library, these designations may be useful to you later.

To change the control type of a library, you may first need to download the library from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

1 Search or Browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click  .
- If you browsed for the library – Right-click the name of the desired library, then click **Change Control Type.**

In either case, the Change Control Type of Library dialog box appears. See "Change Control Type of Library" on page 610.

3 Under Layout Details, in the List of Bait Groups pane**,** under **Control Type,** select new options as needed.

These control types are available:

- **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications.
- **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.

All other options in this dialog box are read-only.

4 Click **Save.**

A dialog box tells you that the library has been updated.

5 Click **OK.**

NOTE

- A library must contain at least one biological bait group.
- Control bait groups cannot collectively occupy more than 50% of the features of a library.

To delete a library

When you delete a library, you remove its design files and parameters from your server. You do not remove its component baits and bait groups. Also, the Delete command has no effect on your content on the eArray Web site.

Before you delete a library

- You must be the owner of the library.
- The library must have a status of Draft, Review, or Complete. You cannot delete libraries with a status of Submitted.

To delete a library

1 Search or browse for the desired library. See "To search for libraries" on page 416 and "To browse available libraries" on page 420.

2 Do one of the following:

- If you searched for the library – In the **Actions** column of the search results, next to the desired library, click .
- If you browsed for the library – Right-click the name of the desired library, then click **Delete.**

A dialog box asks if you are sure you want to delete the library.

CAUTION When you delete a library, the program permanently removes it from your server. To restore a deleted library, you must create it again. However, the program does not delete the individual probes and probe groups that comprise the library.

3 Click **Yes.**

A dialog box tells you that the library was successfully deleted.

4 Click **OK.**

6
eArray$_{XD}$ Reference

This chapter describes the elements of the eArray$_{XD}$ tab of the Agilent Genomic Workbench suite, and the menus, shortcut menus, search panes, and dialog boxes that can appear. It also contains additional reference information, including details about the files that are used by the program, and design guidance from Agilent.

For descriptions of the other tabs in Agilent Genomic Workbench, see the appropriate User Guides. For general information about all of the applications that are available in the program, see the *Product Overview Guide*. See "Help tab" on page 521.

The eArray$_{XD}$ Tab

The eArray$_{XD}$ tab (Figure 12) opens when you click **eArray$_{XD}$** on the Agilent Genomic Workbench tab bar.

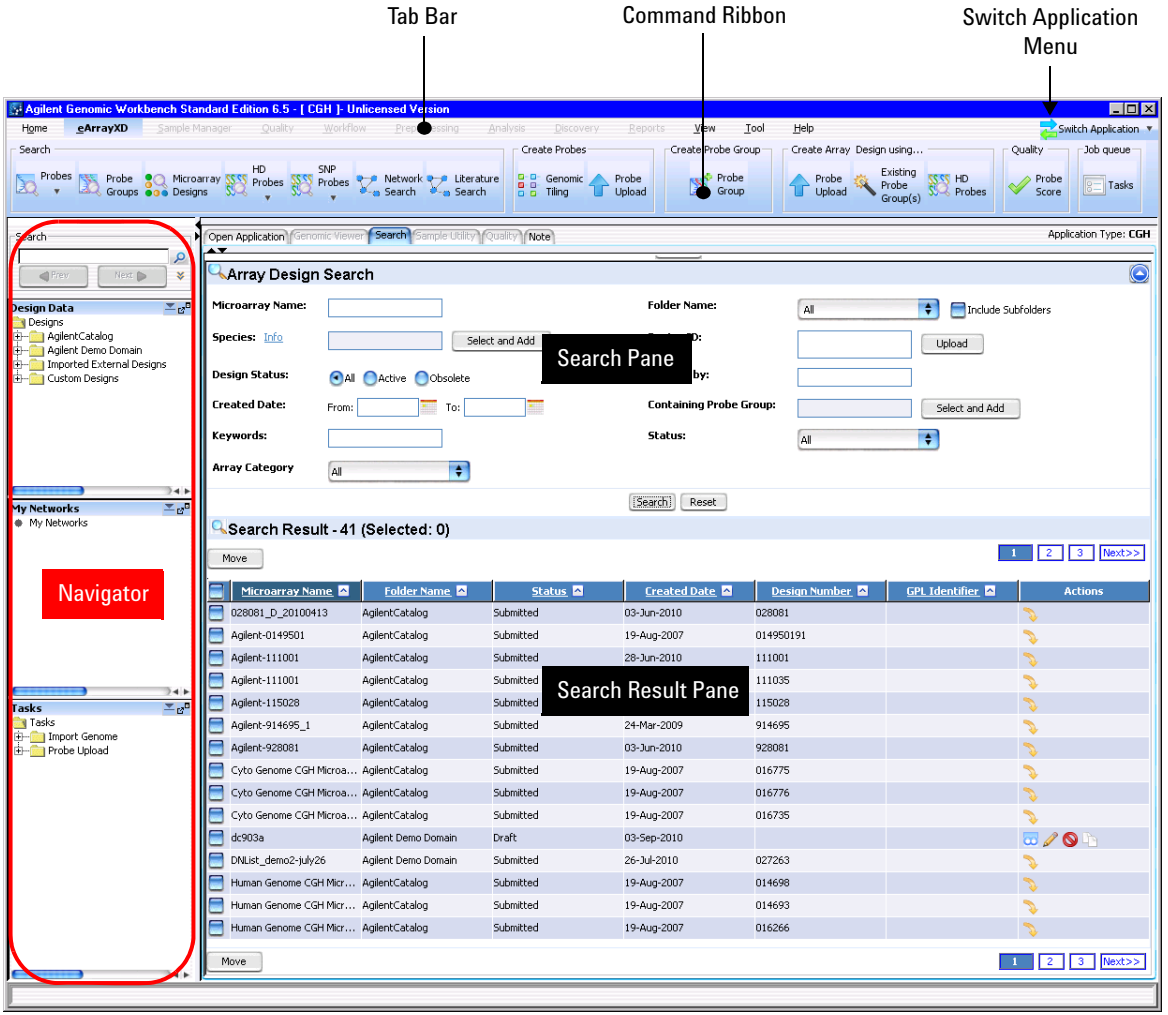


Figure 12 Agilent Genomic Workbench main window — eArray$_{XD}$ tab

The table below describes the elements of the eArray$_{XD}$ tab.

Element	Description
Switch Application menu	Content and functionality in eArray$_{XD}$ is partitioned by application type. This menu is available on all tabs in Agilent Genomic Workbench, and it lets you switch the current application type. See "Switch Application menu" on page 470.
Command Ribbon	Contains the main commands that you can use to search and create custom microarray content. See "Command ribbon (eArray$_{XD}$ tab)" on page 471.
Navigator	Contains several panes: • **Navigator Search pane** – Lets you find all occurrences of a search string within any of the panes of the Navigator. See "Navigator – Search pane" on page 484. • **Design Data pane** – Lets you view and take action on available content. See "Navigator – Design Data pane" on page 486. • **Experiment pane** – (SureSelect Target Enrichment application type) Lets you see the experiments that you have set up with the SureSelect Quality Analyzer. The items in this pane are not used by eArray$_{XD}$. For more information, see the *SureSelect Quality Analyzer User Guide*. • **My Networks pane** – Lets you view and take action on custom biological networks that you have created and saved from the results of a literature search. See "Navigator – My Networks pane" on page 496. • **Tasks pane** – Lets you monitor and take action on the jobs that you have submitted to your server and the eArray Web site. See "Navigator – Tasks pane" on page 498.
Search pane	Lets you set search criteria for content searches in eArray$_{XD}$. See "Search pane" on page 512.
Search Result pane	Lets you view and take action on the results of content searches. See "Search Result pane" on page 514.

Switch Application menu

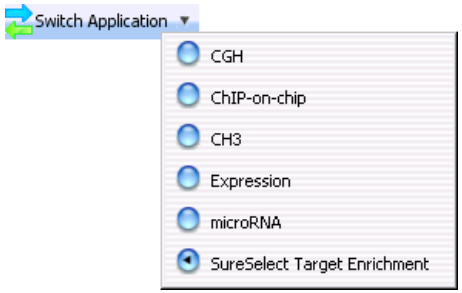


Figure 13 Switch Application menu

Purpose: The Switch Application menu lets you select the application type for your microarray or bait library design work. Application types are the general types of experimental approaches in which you use microarrays and oligonucleotide libraries. The program partitions content and functionality by application type. This menu sets the application type for all parts of Agilent Genomic Workbench, including the DNA Analytics data analysis applications. See "To set the application type" on page 48.

To open: At the top of the Agilent Genomic Workbench main window, click **Switch Application.**

Switch Application

Opens a menu with these options:

Option	Application Type
CGH	Array-based comparative genomics hybridization. You also select this application type to work with CGH+SNP microarray designs.
ChIP-on-chip	Array-based chromatin immunoprecipitation
CH3	Methylation microarray studies
Expression	Array-based gene expression studies
microRNA	Array-based miRNA studies
SureSelect Target Enrichment	Creation of oligonucleotide bait libraries

Command ribbon (eArray$_{XD}$ tab)

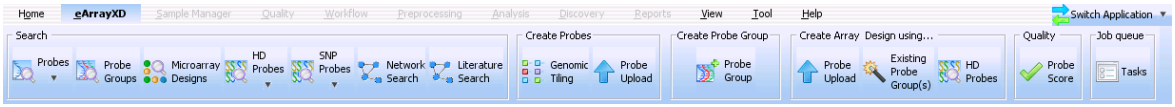


Figure 14 eArray$_{XD}$ command ribbon, as it appears for the CGH application type

In the eArray$_{XD}$ tab, the command ribbon lets you work with content. The available commands and options vary by application type. These groups of commands can appear:

Group	Description
Search	Search for many different types of content. See "Search commands" on page 473.
Create Probes	(Available for all application types except SureSelect Target Enrichment) Create or upload new probes for use in custom microarray designs. See "Create Probes commands" on page 477.
Create Probe Group	(Available for all application types except SureSelect Target Enrichment) Use a probe search to create a new probe group. See "Create Probe Group command" on page 479.
Create Array Design using	(Available for all application types except SureSelect Target Enrichment) Use one of the built-in wizards in eArray$_{XD}$ to create a microarray design. Wizards lead you through all aspects of the design process, and let you submit a microarray design to Agilent Manufacturing. See "Create Array Design commands" on page 480.
Create Baits	(SureSelect Target Enrichment Application Type) Create or upload new baits for use in bait libraries. See "Create Bait commands" on page 478.
Create Bait Group	(SureSelect Target Enrichment Application Type) Use a bait search to create a new bait group. See "Create Bait Group command" on page 479.
Create Library using	(SureSelect Target Enrichment Application Type) Use one of the built-in wizards in eArray$_{XD}$ to create a bait library. Wizards lead you through all aspects of the design process, and let you submit a library to Agilent Manufacturing. See "Create Library commands" on page 481.

Group	Description
Quality	• (CGH, ChIP-on-chip, and CH3 application types) Calculate probe performance scores for non-Agilent probes. A probe performance score indicates how likely it is that a probe will produce a good log ratio response on the Agilent platform. • (Expression application type) Evaluate the base composition of probes to see if they will work on the Agilent platform. See "Quality commands" on page 482.
Job Queue	Lets you view, search, troubleshoot, and delete the tasks that have been submitted to your server or to the eArray Web site. See "Job Queue command" on page 482.
Tools	(SureSelect Target Enrichment application type) Retrieve a list of intervals (or exonic intervals) whose annotation or accessions match search terms that you enter. See "Tools commands" on page 483.

Search commands

Figure 15 Search commands (as they appear for the CGH application type)

These commands let you use many different methods to retrieve existing content of interest.

Probes

- **For the Expression and microRNA application types** – Opens the Probe Search pane. See "Probe Search" on page 560 and "To use the Probe Search tool to find probes" on page 92.
- **For the CGH, ChIP-on-chip, and CH3 application types** – Opens a menu with these options:

Option	Description
Simple Search	Opens the Probe Search pane. See "Probe Search" on page 560. This type of search returns probes based on matches with annotation, accession, or sequence information. See "To use the Probe Search tool to find probes" on page 92.
Simple Interval Finder	Opens the Simple Interval Finder pane. See "Simple Interval Finder" on page 570. This type of search returns genomic intervals that contain the search term within any available annotation or accession. See "To do a Simple Interval Finder Search" on page 127.
Advanced Interval Finder	Opens the Advanced Interval Finder pane. See "Advanced Interval Finder" on page 531. This type of search returns genomic intervals with an accession or annotation that exactly matches one or more search term(s). See "To do an Advanced Interval Finder Search" on page 129.

- **For the SureSelect Target Enrichment application type** – Not available.

Probe Groups

(All application types except SureSelect Target enrichment) Opens the Probe Group Search pane, where you can start a search for probe groups of interest based on several criteria. See "Probe Group Search" on page 555 and "To search for probe groups" on page 224.

Microarray Designs (All application types except SureSelect Target Enrichment) Opens the Array Design Search pane, where you can start a search for microarray designs of interest based on several criteria. See "Array Design Search" on page 533 and "To search for microarray designs" on page 251.

HD Probes (CGH, ChIP-on-chip, and CH3 application types) Opens a menu with the following options that let you to search the High Density (HD) probe database on the eArray Web site. This database contains probes that cover the genomes of many species at extremely high density.

Option	Description
Simple Search	Opens the Simple HD Probe Search pane, where you can start these types of searches: • **Simple Genomic Intervals HD probe search** – (Available for CGH, ChIP-on-chip, and CH3 HD probe searches.) In this kind of search, you enter the chromosomal locations of genomic regions to search. See "Simple HD Probe Search" on page 565 and "To do a Simple Genomic Intervals HD Search for probes" on page 111. • **Simple Gene Annotations HD probe search** – (Available only for CGH HD probe searches.) In this kind of search, you enter annotations such as GenBank accession numbers or gene symbols. The search returns HD probes that tile the regions that correspond with the annotations. See "Simple HD Probe Search" on page 565 and "To do a Simple Gene Annotations HD Search for probes" on page 120.

Option	Description
Advanced Search	Opens the Advanced HD Probe Search pane, where you can start an Advanced Genomic Intervals HD probe search. See "Advanced HD Probe Search" on page 527. This type of search is available for CGH, ChIP-on-chip, and CH3 HD probe searches. In this kind of search, as in a Simple Genomic Intervals Search, you supply the chromosomal locations of the genomic regions to search. However, in this advanced search, you upload a file of intervals that also includes individual settings for the probe density and Hm and T_M filtering for each interval. See "To do an Advanced Genomic Intervals HD Search for probes" on page 117.
Probe ID Search	Opens the Probe ID Search pane, where you can start a search for HD probes based on Probe IDs. See "Probe ID Search (HD probes)" on page 557. This type of search is available for CGH, ChIP-on-chip, and CH3 HD probe searches. In this kind of search, you enter the names (Probe IDs) of the desired probes. See "To do a Probe ID HD Search for probes" on page 125.

SNP Probes (CGH application type) Opens a menu that lets you search for Agilent SNP probes. Agilent SNP probes are designed specifically for use in Agilent CGH+SNP microarray designs. See "Searching for Agilent SNP Probes" on page 138. These options are available:

Option	Description
Entire Agilent SNP Probe Set Search	Opens the SNP Search by Agilent Probe Set search pane, where you can set up a search that returns SNP probes from throughout the genome. See "Entire Agilent SNP Probe Set Search" on page 542 and "To do an Entire Agilent SNP Probe Set Search" on page 141.
Genomic Interval Search	Opens the SNP Search by Gene Interval search pane, where you can set up a search that returns SNP probes that are designed to specific genomic intervals that you enter. See "Genomic Interval Search (SNP Probe Search)" on page 546 and "To do a SNP probe search by genomic intervals" on page 143.

Option	Description
SNP ID Search	Opens the SNP Search by Reference Cluster IDs search pane, where you can set up a search that returns SNP probes that are designed to the specific SNP sites with the IDs that you enter. See "SNP ID Search (SNP probe search)" on page 572 and "To do a SNP probe search by SNP ID" on page 150.
Probe ID Search	Opens the SNP Search by Probe ID search pane, where you can set up a search that returns the SNP probes that have the specific probe IDs that you enter. See "Probe ID Search (SNP probes)" on page 558 and "To do a SNP probe search by probe ID" on page 148

Baits (SureSelect Target Enrichment application type) Opens the Bait Search pane. This type of search retrieves baits based on matches between the search term(s) and annotation or accession values. See "Bait Search" on page 538 and "To search for baits" on page 358.

Bait Groups (SureSelect Target Enrichment application type) Opens the Bait Group Search pane, where you can start a search for bait groups of interest based on several criteria. See"Bait Group Search" on page 536 and "To search for bait groups" on page 396.

Libraries (SureSelect Target Enrichment application type) Opens the Library Search pane, where you can start a search for bait libraries of interest based on several criteria. See "Library Search" on page 551 and "To search for libraries" on page 416.

Network Search Opens a search pane where you can start a search for biological networks. You can use retrieved networks to search for or create probes for microarray designs (or baits for libraries). See "Network Search" on page 553 and "To search for biological networks" on page 185.

Literature Search Opens the Literature Search dialog box, where you can start a search of the biomedical literature. The program analyzes the sentences in retrieved abstracts to construct a custom biological network. You can use this network to search for or create probes for microarray designs (or baits for libraries). See "Literature Search" on page 803 and "To use a literature search to create a custom network" on page 186.

Create Probes commands

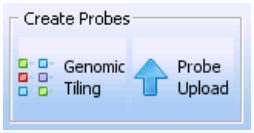


Figure 16 Create Probes commands, as they appear for the CGH application type

These commands let you create or upload new probes.

Simple Tiling (Expression application type) Opens the Simple Tiling dialog box, where you can set up a Simple Tiling Job. See "Simple Tiling" on page 852.

Simple Tiling creates probes for gene expression applications that span uploaded target sequences at even intervals. You can set the density of tiling in one of several ways. See "To set up a Simple Tiling job" on page 174

Genomic Tiling (CGH, ChIP-on-chip, and CH3 application types) Opens the Genomic Tiling dialog box, where you can set up a Genomic Tiling job. See "Genomic Tiling" on page 779.

Genomic Tiling creates probes for CGH, ChIP-on-chip, or CH3 microarrays that span specified regions of a selected genome at even intervals. The genome can be one that is available on the eArray Web site, or a custom genome that you upload. You can set the density of tiling in one of several ways, ignore repeat regions, and trim probes to conform better to a specific T_M. See "To set up a Genomic Tiling job" on page 176.

Probe Design (TM) (Expression application type) Opens the Create Probes (TM Matching Method) dialog box, where you can set up a Gene Expression Probe Design job that uses T_M-matching methodology. See "Create Probes (TM Matching or Base Composition Methods)" on page 683.

This type of probe design creates probes for gene expression microarrays based on target sequences that you enter. The design process favors the creation of probes that have melting temperatures close to a specific value. In addition, the process compares probes with a species transcriptome database to eliminate candidate probes that can cross-hybridize with sequences other than the desired target. See "To set up a GE Probe Design job" on page 167.

Probe Design (BC) (Expression application type) Opens the Create Probes (Base Composition Method) dialog box, where you can set up a Gene Expression Probe Design job that uses Base Composition methodology. See "Create Probes (TM Matching or Base Composition Methods)" on page 683.

This type of probe design creates probes for gene expression applications based on target sequences that you enter. The design process favors the creation of probes with a base composition that gives optimum performance on the Agilent microarray platform. In addition, the process compares probes with a species transcriptome database to eliminate candidate probes that can cross-hybridize with sequences other than the desired target. See "To set up a GE Probe Design job" on page 167.

Probe Upload (All application types except SureSelect Target Enrichment) Opens the Probe Upload dialog box, where you can define and submit a probe upload job. See "Probe Upload" on page 831 and "To upload probes and annotation" on page 161

Create Bait commands

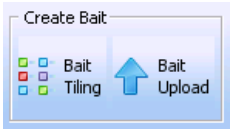


Figure 17 Create Bait commands (SureSelect Target Enrichment application type)

Bait Tiling Opens the Bait Tiling dialog box, where you can set up and submit a Bait Tiling job. Bait Tiling generates baits that evenly cover specific genomic regions. See "Bait Tiling" on page 599 and "To set up a Bait Tiling job" on page 378.

Bait Upload Opens the Bait Upload dialog box, where you can define and submit a bait upload job. See "Bait Upload" on page 603 and "To upload baits and annotation" on page 374.

Create Probe Group command

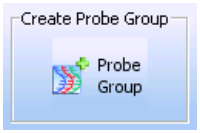


Figure 18 Create Probe Group command

Probe Group (All application types except SureSelect Target Enrichment) Opens the Probe Search pane. See "Probe Search" on page 560. After you set parameters for the search, and submit them, you can create a probe group from the results. See "To create a new probe group" on page 223.

Create Bait Group command

Figure 19 Create Bait Group command

Bait Group (SureSelect Target Enrichment application type) Opens the Bait Search pane. See "Bait Search" on page 538. After you set parameters for the search, and submit them, you can create a bait group from the results. See "To create a bait group from existing baits" on page 401.

Create Array Design commands

Figure 20 Create Array Design commands, as they appear for the CGH application type

These commands let you start one of the wizards that are available for your selected microarray application type. Wizards lead you through the microarray creation process. Each wizard uses a specific source of content.

Probe Upload (All application types except microRNA and SureSelect Target Enrichment) Opens the Create Microarray Design from Probe Upload dialog box. See "Create Microarray Design (Probe Upload wizard)" on page 671.

Existing Probe Group(s) (All application types except SureSelect Target Enrichment) Opens the Create Microarray Design from Existing Probe Group(s) dialog box. See "Create Microarray Design from Existing Probe Groups (Wizard)" on page 648.

Probe Design (Expression application type) Opens the Create Microarray from Target Sequences dialog box, where you can create a microarray design based on transcript sequences that you upload. See "Create Microarray from Target Sequences (wizard)" on page 662.

HD Probes (CGH, ChIP-on-chip, and CH3 application types) Opens the Create Microarray Design Using HD Search dialog box, where you can create a microarray design based on a search of the high density (HD) CGH probe database on the eArray Web site. See "Create Microarray Design (HD Probes wizard)" on page 656.

Create Library commands

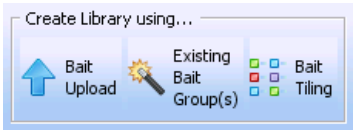


Figure 21 Create Library commands (SureSelect Target Enrichment application type)

These commands let you start one of the wizards that are available for the SureSelect Target Enrichment application type. These wizards lead you through the process of creating a bait library. Each wizard uses a specific source of baits.

Existing Bait Group(s) (SureSelect Target Enrichment application type) Opens the Create a Library from Existing Bait Group(s) dialog box, where you can create a bait library based on bait groups that are stored on your server. See "Create Library from Existing Bait Groups (wizard)" on page 624 and "To create a library from existing bait groups (wizard)" on page 428.

Bait Upload (SureSelect Target Enrichment application type) Opens the Create Library from Bait Upload dialog box, where you can create a bait library based on the baits in an uploaded file. See "Create Library (Bait Upload wizard)" on page 638and "To create a library from a bait upload (wizard)" on page 422.

Bait Tiling (SureSelect Target Enrichment application type) Opens the Create Library from Bait Tiling dialog box, where you can create a bait library based on the even coverage of selected genomic regions. See "Create Library (Bait Tiling wizard)" on page 630 and "To create a library using Bait Tiling (wizard)" on page 433.

Quality commands

Figure 22 Quality command (CGH application type)

Probe (Expression application type) Opens the Probe Quality dialog box, where you can set up a Probe Check job. This type of job evaluates the base composition of probes and potential cross-hybridization problems. See "Probe Quality" on page 826 and "To check GE probe quality" on page 208.

Probe Score (CGH, ChIP-on-chip, and CH3 application types) Opens the Score Custom Probes dialog box, where you can set up a Probe Score job. This type of job calculates probe performance scores for non-Agilent probes in a probe group that you select. A probe performance score indicates how likely it is that a given probe will produce a good log ratio response when it is used on the Agilent microarray platform. See "Score Custom Probes" on page 835 and "To calculate probe performance scores" on page 214.

Job Queue command

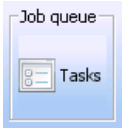


Figure 23 Job Queue command

Tasks Opens the Job Queue Management Console, where you can view, search, troubleshoot, and delete jobs that you have submitted to your server, or to the eArray Web site. See "Job Queue Management Console" on page 791 and "Managing Tasks" on page 70.

Tools commands

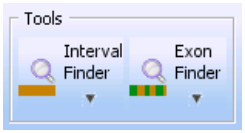


Figure 24 Tools commands (SureSelect Target Enrichment application type_

This set of commands appears only for the SureSelect Target Enrichment application type.

Interval Finder Opens a menu with these options:

Option	Description
Simple Interval Finder	Opens the Simple Interval Finder pane. See "Simple Interval Finder" on page 570. This type of search returns genomic intervals that contain the search term within any available annotation or accession. See "To do a Simple Interval Finder Search" on page 127.
Advanced Interval Finder	Opens the Advanced Interval Finder pane. See "Advanced Interval Finder" on page 531. This type of search returns genomic intervals with an accession or annotation that exactly matches one or more search term(s). See "To do an Advanced Interval Finder Search" on page 129.

Exon Finder Opens a menu with these options:

Option	Description
Simple Exon Interval Finder	Opens the Exon Interval Finder pane. See "Exon Interval Finder" on page 545. This type of search returns the genomic coordinates of exons whose annotation contains the search term. See "To do a Simple Exon Interval Finder Search" on page 366.
Advanced Exon Interval Finder	Opens the Advanced Exon Interval Finder pane. "Advanced Exon Interval Finder" on page 525. This type of search returns the genomic coordinates of exons that have specific annotations that are an exact match with the search terms. See "To do an Advanced Exon Interval Finder Search" on page 367.

Navigator – Search pane

The search pane of the Navigator lets you find all occurrences of a specific search term in any pane of the Navigator. See Figure 25. It also contains several buttons that you can use to detach, hide, show or resize the Navigator.

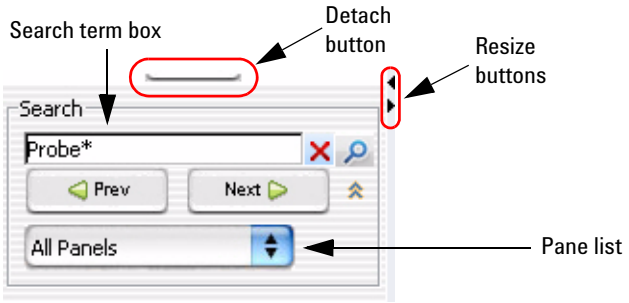


Figure 25 Navigator – Search pane

Detach button Detaches the entire Navigator from the main window of the program and opens it in a new, separate window. To re-attach the Navigator to the main program window, click its Close button .

Resize buttons Hides, shows, or expands the Navigator. For more information, see the *Data Viewing User Guide*.

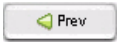
Search term box Lets you type your desired search term. Search terms are not case-sensitive, but they must reflect the entire name of an array or other content item that you want to find. You can use asterisks (*) as wildcards to represent groups of unspecified characters.

(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.

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

(Hide 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, and highlights each of them in red.



(For multiple results, when available) Makes the previous matching result visible, and highlights it.

(For multiple results, when available) Makes the next matching result visible, and highlights it.

Pane list Lets you limit a search to a specific pane. Select the name of the desired pane from the list. To select all panes, select **All Panels.** By default, the program searches all panes.

Navigator – Design Data pane

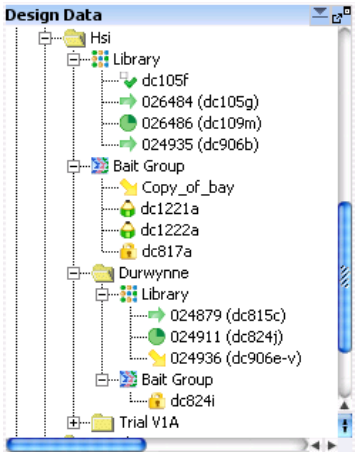


Figure 26 Design Data pane of the Navigator

The Design Data pane of the Navigator shows content items that are available for the selected application type.

Main Folders

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

Folder	Contents
AgilentCatalog	Microarray designs, libraries, bait groups, and probe groups from the Agilent Catalog that are available for the selected application type. You can use these items in eArray$_{XD}$. Microarray sample data that are associated with Agilent Catalog designs also appear in this folder, but eArray$_{XD}$ does not use these data.
<Workgroup Name>	Custom workgroup microarray designs, libraries, bait groups, and probe groups that are available for the selected application type. You can use these items in eArray$_{XD}$. This folder has the name of your workgroup. Microarray sample data that are associated with your custom workgroup designs also appear in this folder, but eArray$_{XD}$ does not use these data.

Folder	Contents
Imported External Designs	Design information and array data that you have imported into Agilent Genomic Workbench, but that is not available in Array$_{XD}$. eArray$_{XD}$ does not use any of the items in these folders. For more information, see the applicable user guide for each data analysis application.
Custom Designs	Libraries and microarray designs that you have created in your account on the eArray Web site *after* you install your Agilent Genomic Workbench server. The program lets you download a GEML design file (for microarrays) or a BED file (for libraries).

Design Data pane – Icons, buttons, and special text

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

Item	Details
	An unexpanded folder (domain) that contains subfolders or other items
	An expanded folder. The items that it contains are visible in the Navigator.
	Expands a folder to show its contents.
	Collapses a folder to hide its contents.
	A folder that can contain microarray design(s) or bait librar(ies).
	A folder that can contain probe group(s) or bait group(s).
	An item that you must download from the eArray Web site before you can take most actions on it. In addition, designs with this icon are not available for use in analyses in the DNA Analytics applications of Agilent Genomic Workbench.
	An available microarray design with a status of Draft, or an available probe or bait group with a status of Incomplete.
	An available library or microarray design with a status of Review.
	An available library or microarray design with a status of Complete.
	An available library or microarray design with a status of Submitted.
	An available probe or bait group with a status of Locked.

Item	Details
Build	A folder that contains sample data for a design. The design is read-only to the user who is currently logged in. The data within this folder apply to the indicated genome build, and are not used by eArray$_{XD}$. See the note at the bottom of this table.
	Data from an individual microarray sample. The design that is associated with the sample data is read-only to the user who is currently logged in. Sample data are not used by eArray$_{XD}$.
Build	A folder that contains sample data for a design. The design can be edited by the user who is currently logged in. The data within this folder apply to the indicated genome build, and are not used by eArray$_{XD}$. See the note at the bottom of this table.
	Data from an individual microarray sample. The design that is associated with the sample data can be edited by the user who is currently logged in. Sample data are not used by eArray$_{XD}$.
red text	An item that matches your search term in a search of the Navigator.
highlighted text	The current result when you search the Navigator. Click **Next** to highlight the next result, and **Previous** to highlight the previous one.

NOTE

In FE and in the DNA Analytics data analysis applications in Agilent Genomic Workbench, you can use the microarray designs that you transfer from the eArray Web site. After you start the transfer of a given design, as soon as a Genome Build node appears under the given design node in the Design Data pane of the Navigator, you can import microarrays for that design and run analyses. FE can also run the extraction for that design. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Design Data – Actions and shortcut menus (AgilentCatalog and workgroup folders)

- Double-click the name of a folder to expand or collapse it.
- Right-click the name of a workgroup folder to open a shortcut menu. The shortcut menu can contain these options:

Option	Details
Create New Domain	Opens the Create New Domain dialog box, where you can create a new folder in the Design Data pane. See "Create New Domain" on page 677 and "To add a folder to the Navigator" on page 46.
Delete Domain	Lets you remove the specific folder from the Design Data pane. See "To remove a folder" on page 47. **Note:** You cannot delete the main workgroup folder.

NOTE

Different options are available for the Imported External Designs folder, and the folders within it. These folders contain design information and array data for downstream processing by the data analysis applications in Agilent Genomic Workbench. eArray$_{XD}$ does not use any of the items in these folders. For more information, see the applicable user guide for each data analysis application.

- Right-click the name of a probe group or bait group to open a shortcut menu with these options:

Option	Details
Move	(Available to the owner of a probe group or bait group) Opens a dialog box, where you can move the specific probe group or bait group to a new location. See these topics: • "Move Probe Group" on page 813 • "Move Bait Group" on page 811 • "To move probe groups" on page 239 • "To move bait group(s)" on page 408
Copy	Opens a dialog box, where you can create a new probe group or bait group that uses an existing one as a template. See these topics: • "Copy Probe Group" on page 618 • "Create Bait Group" on page 621 • "To copy a probe group" on page 230 • "To copy a bait group" on page 405
Edit	(Available if you are the owner of the bait group or probe group, and it has a status of Incomplete.) Opens a dialog box, where you can change the attributes and content of the bait group or probe group. See these topics: • "Edit Probe Group" on page 771 • "Edit Bait Group" on page 737 • "To edit a probe group" on page 234 • "To edit a bait group" on page 406
View	Opens a dialog box, where you can view information about a probe group or bait group, including its list of probes/baits, and their sequences, associated keywords, accessions, and statistical information. See these topics: • "View Probe Group" on page 873 • "View Bait Group" on page 867 • "To view a probe group" on page 228 • "To view a bait group" on page 399
Delete	(Available if you are the owner of the probe group or bait group, and it is not in use in a library or microarray design.) Lets you permanently remove a probe group from your server. See "To delete a probe group" on page 242 and "To delete a bait group" on page 413.

Option	Details
Download	Opens the Download Probe Group dialog box, where you can save the probe group in one of several file formats to a location that you select. See "Download Probe Group" on page 732 and "To download a probe group" on page 240.
Attach	Opens the Add/Remove Attachments dialog box, where you can attach a note, file, or URL to the probe group or bait group. See these topics: • "Add/Remove Attachments" on page 593 • "To add an attachment to a probe group" on page 243 • "To view the attachments to a probe group" on page 244 • "To attach a file, note, or URL to a bait group or library" on page 444

NOTE

If appears next to the name of the probe group or bait group, the only option available is Download from eArray.com. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

- Right-click the name of a microarray design or bait library to open a shortcut menu with these options: (Note – The availability of these options varies by design status and ownership. See "Status of microarray designs" on page 248.)

Option	Details
Move	(Available to the owner of a library or microarray design) Opens a dialog box, where the owner of a library or microarray design can move it to a different folder on your server. See these topics: • "Move Array Design" on page 810 • "Move Library" on page 812 • "To move a microarray design" on page 338 • "To move libraries" on page 456
Copy	(Available for microarray designs) Opens the Edit Microarray Design dialog box, where you can create a new microarray design based on an existing one. See "Edit Microarray Design" on page 751. Your ability to copy a microarray design depends on its design status and other factors. See "To copy a microarray design" on page 340.
Edit	(Available to the owner of a library or microarray design. The item must have a status of Draft.) Opens an Edit dialog box, where the owner of the library or microarray design can make changes to its properties and content. See these topics: • "Edit Microarray Design" on page 751 • "Edit Library" on page 740 • "To edit a microarray design" on page 310 • "To edit a library" on page 447
Review	(Available for libraries or microarray designs with a status of Review.) Opens an Edit dialog box, where any user with access to the library or microarray design can make changes to its properties and content, and save a new version of it. See these topics: • "Edit Microarray Design" on page 751 • "Edit Library" on page 740 • "To review a microarray design" on page 326 • "To review a library" on page 453

Option	Details
View	Opens a View dialog box, where you can view the properties and content of a library or microarray design. See these topics: • "View Microarray Design" on page 871 • "View Library" on page 869 • "To view a microarray design" on page 305 • "To view a library" on page 443
Delete	(Available to the owner of a library or microarray design, and only if it has a status other than Submitted.) Lets the owner of the item remove it from the server. See "To delete a microarray design" on page 345 and "To delete a library" on page 465.
Download	(Available for libraries and microarray designs with a status of Review, Complete, or Submitted.) Opens a Download dialog box, where you can download library or design files that are available on your server to a location that you select. See these topics: • "Download Microarray Design" on page 726 • "Download Library" on page 721 • "To download microarray design files" on page 341 • "To download library design files" on page 461 **Note:** To download files from the eArray Web site, you use a different command. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Submit	(Available to the owner of a library or microarray design. The item must have a status of Complete.) Opens a Submit dialog box, where the owner of the item can submit it to Agilent Manufacturing. See these topics: • "Submit Microarray Design" on page 862 • "Submit Library" on page 861 • "To submit a microarray design to Agilent" on page 346 • "To submit a library to Agilent" on page 458
Attach	Opens the Add/Remove Attachments dialog box, where you can attach notes, files, and URLs to the microarray or library. See these topics: • "To add an attachment to a microarray design" on page 320 • "To attach a file, note, or URL to a bait group or library" on page 444 • "Add/Remove Attachments" on page 593

Option	Details
Change Control Type	(Available to the owner of a library or microarray design. The item must have a status of Complete or Submitted.) Opens the Change Control Type dialog box, where the owner of an item can change the control type of each of its probe groups or bait groups. See these topics: • "Change Control Type of Microarray Design" on page 612 • "Change Control Type of Library" on page 610 • "To change the control type of probe groups" on page 336 • "To change the control type assigned to a bait group" on page 464
Request Quote	(Available for libraries and microarray designs with a status of Submitted.) Opens the Request Quote page on the eArray Web site in your Web browser, where you can request a price quote for the design from Agilent. See "To request a quote" on page 348.
ArrayVisualizer	(Available for all application types except SureSelect Target Enrichment.) Opens the Array Layout dialog box. You can use this dialog box to view the layout of probes from your design on the fabricated microarray slide. You can also color-code the resulting diagram of features by Tm, probe score, or control type. See "Array Layout" on page 583 and "To view the layout of probes on a microarray graphically" on page 306. **Note:** The microarray design must have a status of Complete or Submitted, and the program must have created the appropriate design files.

Design Data – Actions and shortcut menus (Custom Designs folder)

The designs and libraries that can appear in this folder are those that you create on the eArray Web site *after* you install your Agilent Genomic Workbench Server. These items are typically transferred from the eArray Web site to your server automatically within 24 hours after you save them with a status of Complete or Submitted.

- Double-click the Custom Designs folder, or the folders within it, to show or hide the contents of the folder.
- Right-click the name of a library or microarray design to open a shortcut menu with a Download command. This command lets you download a GEML design file (for microarray designs) or a BED file (for libraries) to your computer. No other options are available for these items.

Navigator – Experiment pane

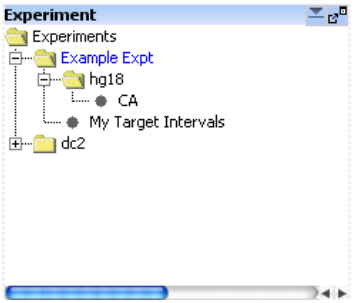


Figure 27 Experiment pane of the Navigator

In eArray$_{XD}$, this pane is available only for the SureSelect Target Enrichment application type. It lets you see the experiments that you have set up with SureSelect Quality Analyzer. The items in this pane are not used by eArray$_{XD}$. For more information, see the *SureSelect Quality Analyzer User Guide*.

Navigator – My Networks pane

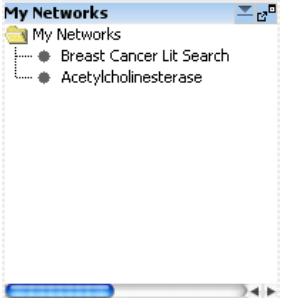


Figure 28 My Networks pane of the Navigator

This pane shows biological networks that you save after you create them with the Literature Search tool. All saved networks appear in this pane, without regard to the selected application type. See "To use a literature search to create a custom network" on page 186.

My Networks – Icons and buttons

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

Item	Details
	Unexpanded My Networks folder (domain) that contains saved networks
	Expanded My Networks folder. The items that it contains are visible in the Navigator.
	A saved network.
	(Available when the My Networks pane is not collapsed.) Collapses the My Networks pane. When you collapse the pane, its title bar appears at the bottom of the Navigator.
	(Available when the My Networks pane is collapsed.) Expands the My Networks pane.
	If the My Networks pane appears within the Navigator, this button detaches the pane and opens it in a new window. If the My Networks pane appears in its own window, this button re-attaches the pane to the Navigator.

My Networks – Actions and shortcut menus

- Double-click the My Networks folder to expand or collapse it.
- Right-click the name of a network to open a shortcut menu. The following options appear:

Option	Description
Load	Opens the Literature Search dialog box and the Literature Network Inspector for the given saved network. See "Literature Search" on page 803 and "Literature Network Inspector" on page 794.
Delete	Lets you remove a saved literature search and its associated network from your server.

Navigator – Tasks pane

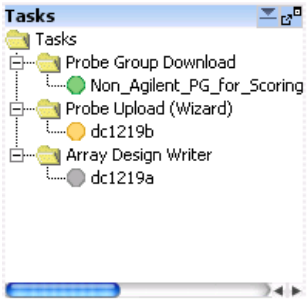


Figure 29 Tasks pane of the Navigator

Many tasks that you do in eArray$_{XD}$ create jobs that are completed in the background on your server or on the eArray Web site. You use the Tasks pane to keep track of the status of these jobs, and to take action on them when their results become available.

Tasks – Icons, buttons, and special text

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

Item	Details
	An unexpanded folder (domain) that contains subfolders or other items
	An expanded folder. The items that it contains are visible in the Navigator.
	Expands a folder to show its contents.
	Collapses a folder to hide its contents.
	A task with a status of **Pending.** The task has been submitted to the job queue, but no action has been taken on it yet.
	A task with a status of **Processing.** The task has been submitted to the job queue, and the program (or the eArray Web site) is processing the job.
	A task with a status of **Complete.** The results of the job are now available for your use.
	A task with a status of **Error.** An error has occurred, and you must re-submit the job. For probe or bait uploads, an error file is available that lists the errors in your input file.

Item	Details
	A task in the Data Download folder, which can appear when you request a transfer of probe, bait, or exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. You do not need to take action on these types of jobs. When the transfer of data is complete, the program removes the task from the Tasks pane.
	(Available when the Tasks pane is not collapsed.) Collapses the Tasks pane. When you collapse the pane, its title bar appears at the bottom of the Navigator.
	(Available when the Tasks pane is collapsed.) Expands the Tasks pane.
	If the Tasks pane appears within the Navigator, this button detaches the pane and opens it in a new window. If the Tasks pane appears in its own window, this button re-attaches the pane to the Navigator.

Tasks – Actions and shortcut menus

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

Type of Task	Shortcut menu options
Array Design Submission	• **Delete** – (Available for jobs with a status of Complete) Removes the job from the Tasks pane. To create this type of pending task, see "To submit a library to Agilent" on page 458.
Array Design Update	• **Delete** – For pending jobs, this option cancels the update request. For completed jobs, this option removes the job from the Tasks pane, but retains the updated content on your server. To set up this kind of Pending Task, see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Array Design Writer	When you save a microarray design with a status that generates one or more design files (Review, Complete, or Submitted), the program creates a pending task and places it this folder. You can monitor the status of these tasks. In general, you cannot download a microarray design until the design files have been written. No additional options are available.
Bait Group Download	• **Delete** – For pending jobs, this option cancels the update request. For completed jobs, this option removes the job from the Tasks pane, but retains the updated content on your server. To set up this kind of Pending Task, see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Type of Task	Shortcut menu options
Bait Tiling	These options are available in all of the different Bait Tiling folders (User Genomes, Agilent Genomes, Wizard) for Bait Tiling jobs with a status of Complete. The Delete option is also available when the status of the job is Pending. • **Create Bait Group** – Lets you create a probe group from the results of the Bait Tiling job. See "To create a bait group from Bait Tiling results" on page 387. • **View Design Details** – Opens the dialog box, where you can view the overall and detailed results of the Bait Tiling job. See "Design Results (Bait Tiling)" on page 690 and "To view Bait Tiling results" on page 385. • **Delete** – Lets you delete the results of a Bait Tiling job from your server. See "To delete a Bait Tiling job" on page 388. • **Download** – Opens a Save dialog box, where you can download the overall and detailed results of the Bait Tiling job. See "To download Bait Tiling results" on page 387. To set up a Bait Tiling job, see "To set up a Bait Tiling job" on page 378.
Bait Upload	These options are available in both the Bait Upload and Bait Upload (Wizard) folders. • **Delete** – Removes the job from the Tasks pane of the Navigator, but does not remove the bait group that you may have created with the uploaded baits. • **Download Error File** – (Available if the upload job has a status of Error) – Opens a Save dialog box, where you can select a location for the error file. The error file is an HTML file that you can open in a Web browser. When you view the file, place the pointer over any highlighted text to view a ToolTip that explains why the item generated an error. To set up a bait upload, see "To upload baits" on page 370.
Data Download	Tasks appear in the Data Download folder when you request a transfer of probe, bait, or exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. You do not need to take action on these types of jobs. When the transfer of data is complete, the program removes the task from the Tasks pane.

Type of Task	Shortcut menu options
Delete Baits	• **Download Report** – Opens a Save dialog box, where you can select a location for a report about which baits in the job were deleted, and which were not. • **Delete** – Removes the Delete Baits job from the Tasks pane of the Navigator. To set up a bait deletion job, see "To delete baits" on page 392.
Delete Probes	• **Download Report** – Opens a Save dialog box, where you can select a location for a report about which probes in the job were deleted, and which were not. • **Delete** – Removes the Delete Probes job from the Tasks pane of the Navigator. To set up a probe deletion job, see "To delete probes" on page 218.
Download Bait Group	The system creates this type of task when you request a download of a large bait group. See "To download a bait group" on page 409. • **Download** – Opens a Save dialog box, where you can select a location for the downloaded file. • **Delete** – Removes the job from the Tasks pane.
Download <content item> from eArray.com	The system creates this type of task when you download content items from the eArray Web site, including probe groups, bait groups, microarray designs, and libraries. • **Delete** – (Available when the status of the job is Pending.) Cancels the job.

Type of Task	Shortcut menu options
Genomic Tiling	These options can appear for Genomic Tiling jobs for user-defined genomes. These jobs are processed on your server. All options except Delete appear only after the job is finished. • **Create Probe Group** – Submits a probe group creation job to your server. This creates a probe group from the results of the genomic tiling process. You can create one probe group in this way for each set of results. • **View Result** – Opens the Design Results dialog box, where you can view the overall and detailed results of the Genomic Tiling job. See "Design Results (Genomic Tiling)" on page 706. • **Delete** – Deletes the Genomic Tiling job and any results, but does not delete the probe group that you may have created from the results. • **Download** – Opens a Save dialog box, where you can select a location for a downloaded ZIP-format file that contains files for all available results. To set up a Genomic Tiling job, see "To set up a Genomic Tiling job" on page 176. **Note:** Jobs that involve the tiling of Agilent genomes appear in the Probe Design folder. These types of jobs are processed on the eArray Web site.

Type of Task	Shortcut menu options
HD Search	• **View Search Criteria** – Opens the HD Search Criteria dialog box, where you can view the job information and search criteria associated with the HD probe search job. See "HD Search Criteria" on page 782. • **View Result** – (Available for completed jobs) Opens the HD Search Results dialog box, where you can view the HD search criteria, statistics about the returned probes, and statistics about each interval that was submitted for the HD search. See "HD Search Results" on page 783. • **Create Probe Group** – (Available for completed jobs) Opens a dialog box where you can save the returned probes as an HD probe group. You can create one probe group with a given set of HD probe search results. See "Create Probe Group (from HD or SNP search results)" on page 681. • **Download** – (Available for completed jobs) Opens an Open dialog box, where you can select a location for a downloaded file. The program downloads a BED format file that contains the Probe IDs of all returned probes and the chromosomal location of each. • **Delete** – For pending jobs, this option cancels the HD Search request. For completed jobs, this option removes the job and its results from the tasks pane. However, it does not delete the probe group that you may have created from the results. For information about HD probe searches, see "Searching for Agilent High Density (HD) Probes" on page 109.

Type of Task	Shortcut menu options
HD Search (Wizard)	• **View Search Criteria** – Opens the HD Search Criteria dialog box, where you can view the job information and search criteria associated with the HD probe search job. See "HD Search Criteria" on page 782. • **View Result** – (Available after eArray completes the HD probe search that you requested in Step 1 of the wizard) Opens the HD Search Results dialog box, where you can view the HD search criteria, statistics about the returned probes, and statistics about each interval that was submitted for the HD Search job. See "HD Search Results" on page 783. • **Create Probe Group** – (Available after eArray completes the HD probe search that you requested in Step 1 of the wizard.) Resumes the wizard at Step 2, where you can save the returned probes as an HD probe group. You can create one probe group with a given set of HD probe search results. See "Step 2 – Create Probe Group" on page 660. • **Create Microarray** – (Available after you create a probe group from the HD search results in Step 2 of the wizard) Resumes the wizard at Step 3, where you can enter the parameters of a microarray design. See "Step 3–5 – Define Design, Layout Probes, and Create Array Design" on page 661. • **Download** – (Available after eArray completes the HD probe search that you requested in Step 1 of the wizard) Opens an Open dialog box, where you can select a location for a downloaded file. The program downloads a BED format file that contains the Probe IDs of all returned probes and the chromosomal location of each. • **Delete** – Cancels the wizard and removes any results from the system. However, this does not remove the probe group or microarray design that you may have created from the HD search results. See "To create a microarray design with HD probes" on page 297 and "Create Microarray Design (HD Probes wizard)" on page 656

Type of Task	Shortcut menu options
Import Genome	• **Delete** – (Available for jobs with a status of Pending) Cancels the job and removes it from the Tasks pane. • **View Genome Information** – (Available after the job is finished.) Opens the Genome Information dialog box, where you can view information about each sequence in your imported genome file. See "Genome Information" on page 777. To set up this kind of pending task, see "To import a new genome" on page 66.
Library Submission	• **Delete** – If the status of the job is Pending, this command cancels the job. If the status of the job is COMplete, this command removes the job entry from the Tasks pane. To set up this type of pending task, see "To submit a library to Agilent" on page 458.
Library Download	• **Delete** – For pending jobs, this option cancels the update request. For completed jobs, this option removes the job from the Tasks pane, but retains the updated content on your server. To set up this type of pending task, see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Library Writer	When you save a library with a status that generates one or more design files (Review, Complete, or Submitted), the program creates a pending task and places it this folder. You can monitor the status of these tasks. You cannot download a library until the design files have been written. No options are available for this type of task.

Type of Task	Shortcut menu options

Probe Design	All of these options are available after eArray completes a Genomic Tiling (for Agilent genomes), GE Probe Design, or Probe Quality job.
	• **Create Probe Group** – Creates a probe group that contains all of the probes in the results of the job.
	• **View Result** – Opens a dialog box that contains statistics and other information about the job. The available results vary by job. See the following topics:
	  ◦ "Design Results (Gene Expression Probe Design)" on page 700
	  ◦ "Design Results (Genomic Tiling)" on page 706
	  ◦ "Design Results (Gene Expression Probe Check)" on page 696
	• **Delete** – Removes the job and its results from the system, but does not remove the probe group that you may have created with the results.
	• **Download** – Opens a Save dialog box, where you can select a location for the downloaded results. The downloaded files contain the contents of each of the tabs that are available when you view the results of the job.s
	To set up these kinds of tasks, see:
	• "To set up a Genomic Tiling job" on page 176
	• "To set up a GE Probe Design job" on page 167
	• "To check GE probe quality" on page 208

Type of Task	Shortcut menu options
Probe Design (Wizard)	All of these options are available after eArray completes the probe design job that you submit in Step 3 of the wizard. • **Create Microarray** – Resumes the wizard at Step 4, which lets you enter microarray design parameters. After you complete the wizard, this option is no longer available. • **View Result** – Opens the Probe Design Results dialog box. See "Design Results (Gene Expression Probe Design)" on page 700. • **Delete** – Cancels the wizard if it is in progress, removes the probe design job from the Tasks pane, and removes any results. However, this option does not remove the probe group that you may have created from the results. • **Download** – Opens a Save dialog box, where you can select a location for the downloaded results. The downloaded files contain the contents of each of the tabs that are available when you view the results of the job. To use this wizard, see "To create a microarray design from target transcripts" on page 289.
Probe Group Download	• **Delete** – For pending jobs, this command cancels the update request. For completed jobs, this option removes the job from the Tasks pane, but retains the updated content on your server. To set up this kind of Pending Task, see "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Probe Score	The program creates this task when you set up a Probe Score job. • **Delete** – For pending jobs, this command cancels the job. For completed jobs, this command removes the job from the Tasks pane, but does not remove any probe scores that have been added to the probe database on your server. To set up this type of job see "To calculate probe performance scores" on page 214.

Type of Task	Shortcut menu options
Probe Upload	• **Delete** – Cancels the upload. • **Download Error File** – (Available if the probe upload failed because of errors in the probe file) – Opens a Save dialog box, where you can select a location for the error file. The error file is an HTML file that you can open in your Web browser. When you view the file, place the pointer over any highlighted text to display a ToolTip that explains why the item caused an error. To set up this kind of task, see "To upload probes and annotation" on page 161.
Probe Upload (Wizard)	• **Delete** – Cancels the wizard, and removes any results from the system. However, if the system has already created a probe group from the uploaded probes, this probe group is not removed. • **Download Error File** – (Available if the probe upload failed because of errors in the probe file) – Opens a Save dialog box, where you can select a location for the error file. The error file is an HTML file that you can open in an Internet browser. When you view the file, place the pointer over any highlighted text to view a ToolTip that explains why the item generated an error. • **Create Microarray** – (Available only after the system uploads the probes in your file) Resumes the wizard at Step 3, where you can enter design parameters for the microarray. To use this wizard, see "To create a microarray design from uploaded probes" on page 282.

Type of Task	Shortcut menu options
SNP Search	• **View Search Criteria** – Opens the SNP Search Criteria dialog box, where you can view the search parameters for the SNP probe search job. See "SNP Search Criteria" on page 854. • **View Result** – (Available if the SNP search job has a status of Complete) Opens the SNP Search Results dialog box, where you can view summary and detailed statistics about the intervals and probes that were returned by the search. See "SNP Search Results (Genomic Interval Search)" on page 857 and "SNP Search Results (Except Gene Interval searches)" on page 856. • **Create Probe Group** – (Available if the SNP search job has a status of Complete) Opens a Create Probe Group dialog box, where you can create a probe group that contains the probes that were returned by the SNP search. See "Create Probe Group (from HD or SNP search results)" on page 681. • **Download** – (Available if the SNP search job has a status of Complete) Open a Save dialog box, where you can select a location for a ZIP file that contains the Summary and Detail results. See "To download the results of a SNP probe search job" on page 155. • **Delete** – (Available if the SNP search job has a status other than Processing) Removes the results of the SNP search job from the Tasks pane. However, this option does not remove the probe group that you may have created from the results.

Type of Task	Shortcut menu options
Tiling (Unmasked)	All of these options are available after the program completes a Simple Tiling job that you submit. • **Create Probe Group** – Creates a probe group that contains all of the probes in the job results. • **View Result** – Opens the dialog box, where you can view the overall and detailed results of the Simple Tiling job. See "Design Results (Genomic Tiling)" on page 706. • **Delete** – Removes the results of the Simple Tiling job from the Tasks pane. However, this option does not remove the probe group that you may have created from the results. • **Download** – Opens a Save dialog box, where you can select a location for a ZIP file that contains the Summary, Detail, and Target Fate results. See "To download probe design or tiling results" on page 182. To set up this kind of Pending task, see "To set up a Simple Tiling job" on page 174.

NOTE The Job Queue Management Console lets you search, delete, and troubleshoot all of your tasks for the selected application type. See "To search for tasks" on page 72.

Search pane

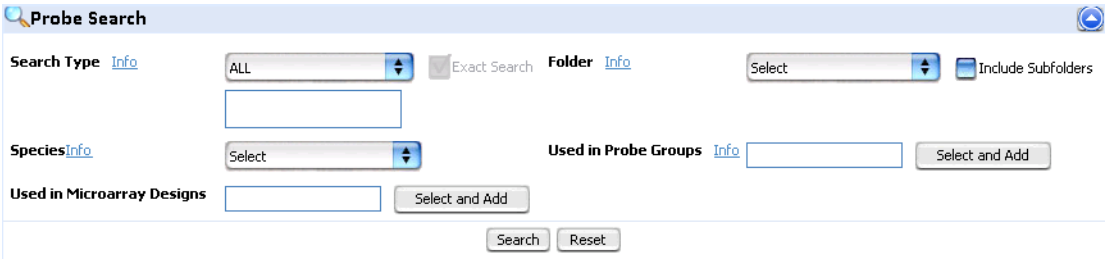


Figure 30 Example of a search pane. This pane shows criteria for a Probe Search.

When you begin a search for a particular type of content item, the available search parameters appear in the Search pane. The table below lists the search panes that can appear in eArray$_{XD}$. To see descriptions of each search pane. see "Search Panes" on page 525, which presents all available search panes in alphabetical order.

Type of Search	See these topics
Probe Searches	
Probe Search	"Probe Search" on page 560
Simple Genomic Intervals HD Search	"Simple HD Probe Search" on page 565
Advanced Genomic Intervals HD Search	"Advanced HD Probe Search" on page 527
Simple Gene Annotations HD Search	"Simple HD Probe Search" on page 565
Probe ID HD Search	"Probe ID Search (HD probes)" on page 557
Entire Agilent SNP Probe Set Search	"Entire Agilent SNP Probe Set Search" on page 542
Genomic Interval Search	"Genomic Interval Search (SNP Probe Search)" on page 546
Probe ID SNP Probe Search	"Probe ID Search (SNP probes)" on page 558
SNP ID Search	"SNP ID Search (SNP probe search)" on page 572

Type of Search	See these topics
Probe Group Search	"Probe Group Search" on page 555
Microarray Design Search	"Array Design Search" on page 533
Bait Search	"Bait Search" on page 538
Bait Group Search	"Bait Group Search" on page 536
Library Search	"Library Search" on page 551
Interval Finder Searches	
Simple Interval Finder	"Simple Interval Finder" on page 570
Advanced Interval Finder	"Advanced Interval Finder" on page 531
Exon Interval Finder	"Exon Interval Finder" on page 545
Advanced Exon Interval Finder	"Advanced Exon Interval Finder" on page 525
Biological Network Search	"Network Search" on page 553

NOTE You enter parameters for a Literature Search in the Literature Search dialog box, rather than in a search pane. See "Literature Search" on page 803.

Search Result pane

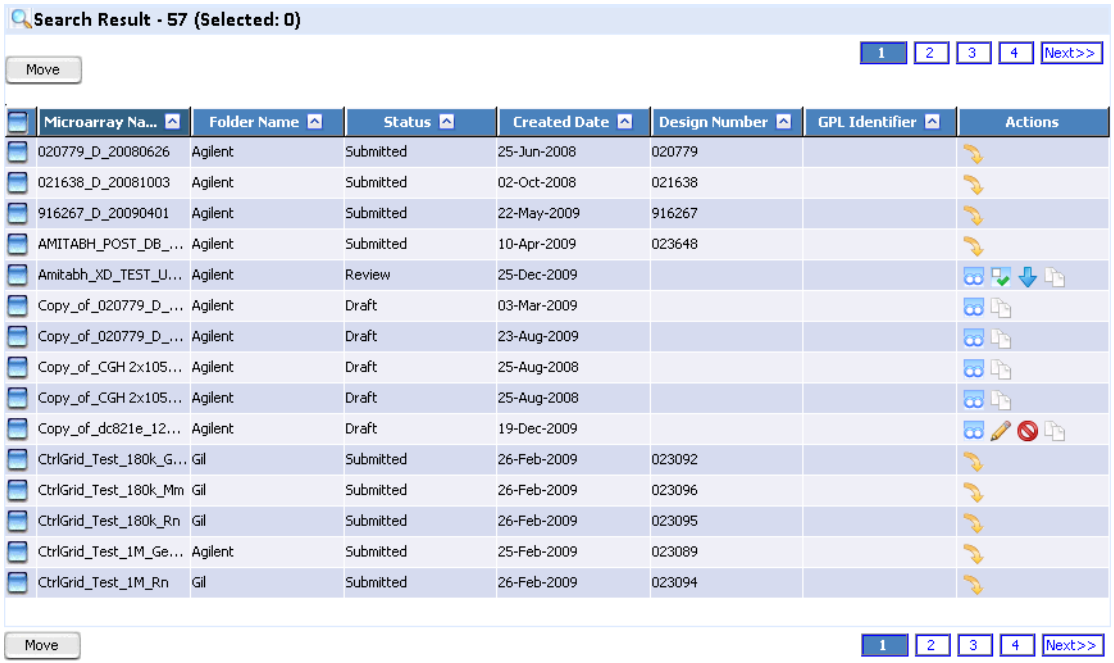


Figure 31 Example Search Result pane, with the results of a search for microarray designs

After you request a search for a particular type of content, the program lists matching items in the Search Result pane. Search results are one of the main ways that the program lets you take action on content items.

NOTE

When you submit a High Density (HD) Probe Search or a SNP Probe Search, the program starts a search job. When your search finishes, the results are available from the Tasks pane of the Navigator, not from the Search Result pane.

Search Result pane – Check boxes

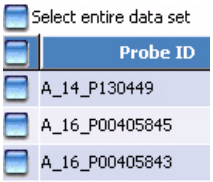


Figure 32 Check boxes in the Search Result pane

The check boxes in the first column of a set of search results let you select one or more of the returned items for further action. Use the following as a guide:

- To select an item, mark the check box next to its name.
- To select all of the items on the current page of results, mark the check box in the column heading row.
- To select items on more than one page, mark the desired check boxes on each page. The program remembers your selections as you go from page to page.
- To select all of the items in the search results, mark **Select entire data set.**

To take action on the items after you select them, click an appropriate button at the top or bottom of the Search Result pane. See "Search Result pane – Buttons" on page 517.

Search Result pane – Actions column

(Available for probe group, bait group, library, microarray design, and Network search results) The buttons in the Actions column of a Search Result pane let you take action on the specific item with which they are associated. These buttons can appear:

Button	Details
	**View** – Opens a dialog box, where you can view the properties and content of the item.
	**Edit** – (Available for libraries and microarray designs with a status of Draft, and probe groups and bait groups with a status of Incomplete. You must be the owner of the item.) Opens an Edit dialog box, where you can make changes to the properties and content of the item.
	**Delete** – (Available for items that you own, except libraries and microarray designs with a status of Submitted) Lets you remove the item from your server.
	**Download** – (Available for items with a status other than Draft, after the program has created the design files) Opens a dialog box, where you can begin a download of the item from your server to the location of your choice.
	**Copy** – Creates a copy of a microarray design, bait group, or probe group, and saves it to your primary domain (folder).
	**Review** – (Available for libraries and microarray designs with a status of Review) Opens a dialog box, where you can make changes to the item, and save a new version of it.
	**Change Control Type** – (Available for libraries and microarray designs with a status of Complete or Submitted. You must be the owner of the item.) Opens a dialog box where you can change the control types that are assigned to specific probe groups in a library or microarray design.
	**Download from eArray Web site**– (Available for items from the eArray Web site that have not yet been transferred to your server, or that contain Agilent content that requires an update) Downloads the specific item from the eArray Web site.
	**Submit** – (Available for libraries and microarray designs with a status of Complete. You must be the owner of the item.) Opens a dialog box, where you can submit the design to Agilent Manufacturing.
	**Request Quote** – (Available for microarray designs with a status of Submitted) Opens the Request Quote page of the eArray Web site in your Internet browser, where you can request a price quote for the microarray.

Search Result pane – Other columns

The other columns that appear in the search results pane vary by the type of search. They present information that identifies or characterizes the specific content item, such as its name, accessions, annotation, or location. If  appears next to a column heading, you can click the heading to re-sort the search results based on the contents of the column. Click such a column heading again to reverse the order.

Search Result pane – Buttons

The buttons that can appear at the top and bottom of the Search Result pane either let you navigate the program, or apply an action to all of the selected items in the search results. To select items, see "Search Result pane – Check boxes" on page 515.

Delete (Available for bait and probe search results) Opens a confirmation dialog box. If you click **Yes,** the program deletes the selected items from your server. See "To delete probes" on page 218 and "To delete baits" on page 392.

Show Statistics (Available for bait search and probe search results) Opens a dialog box, where you can view and download the sequences of the selected items, and calculated statistics based on their base composition. See these topics:

- "To view probe sequences and statistics" on page 202
- "Probe Statistics" on page 829
- "To view bait details and statistics" on page 362
- "Bait Statistics" on page 596

Download (Available for bait search and probe search results) Opens a dialog box, where you can start to download the selected items. See these topics:

- "To download probes" on page 206
- "Download Probes" on page 734
- "To download baits" on page 389
- "Download Baits" on page 719

Create Probe Group (Available for probe search results) Opens a dialog box, where you can enter the attributes of a new probe group and save it. The new probe group contains the probes that you select from the search results. See "Create Probe Group" on page 678 and "To create a new probe group" on page 223.

Create Bait Group (Available for bait search results) Opens the Create Bait Group dialog box, where you can enter the attributes of a new bait group and save it. The new bait group contains the baits that you select from the search results. See "Create Bait Group" on page 621 and "To create a bait group from existing baits" on page 401.

Create Microarray (Available for probe group search results) Opens the Create Microarray Design dialog box, where you can enter the properties of a new microarray design based on the selected probe groups. See "Create Microarray Design" on page 646 and "To create a microarray design from a probe group search" on page 259.

Create Library (Available for bait group search results) Opens the Create Library dialog box, where you can enter the properties of a new library based on the selected bait groups. See "Create Bait Group" on page 621 and "To create a library from bait group search results" on page 439.

Move (Available for Probe Group, Bait Group, Library, and Microarray Design search results) Opens a Move dialog box, where you can select a destination folder for the selected item(s). See these topics:

- "To move probe groups" on page 239
- "To move a microarray design" on page 338
- "To move bait group(s)" on page 408
- "To move libraries" on page 456

Genomic Viewer (Available for non-HD probe search results for the CGH, ChIP-on-chip, and CH3 application types) Opens the Genomic Viewer, and shows the locations of the selected probes graphically within the context of the genome of the organism. See "To plot the genomic locations of probes" on page 203.

Other Tabs in Agilent Genomic Workbench

In addition to the eArray$_{XD}$ tab, many other tabs can be available. These other tabs let you use the other programs in Agilent Genomic Workbench. However, several commands can be found in some of these other tabs that let you do certain eArray-related tasks. This section describes these eArray-related commands.

Home tab

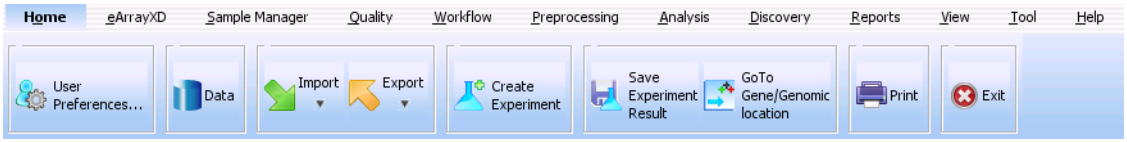


Figure 33 Home tab, as it appears for the CGH application type

This tab is available for all application types. Within this tab, these commands can help you use eArray$_{XD}$:

User Preferences Opens the User Preferences dialog box, where you can switch the account on the eArray Web site to which the client program is linked, and switch the Agilent Genomic Workbench server to which the client program connects. You can also select the file types that the program can make available for libraries and microarray designs. See these topics:

- "User Preferences – Miscellaneous tab" on page 864
- "To display or change the location of your Agilent Genomic Workbench server" on page 37
- "To link the Agilent Genomic Workbench client program to a different account on the eArray Web site" on page 38

Data Opens the Catalog and Workgroup Data dialog box, where you can start the transfer of probe, bait, and annotation data from the eArray Web site by application type. You can also transfer exon boundary data. See "Catalog and Workgroup Data" on page 607 and "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Import Opens a menu with many items that you can import into the program. These two are relevant to eArray$_{XD}$:

- **Probe Upload** – Opens the Probe Upload dialog box, which lets you upload a file of probes and annotation to your server. See "Probe Upload" on page 831 and "To upload probes and annotation" on page 161.
- **Custom Genome for Tiling** – Opens the Import Genome dialog box, which lets you upload the base sequence(s) of one or more chromosomes of your organism of interest. You can use a custom genome with the Genomic Tiling and Bait Tiling tools. See "Import Genome" on page 789 and "To import a new genome" on page 66.

Tool tab

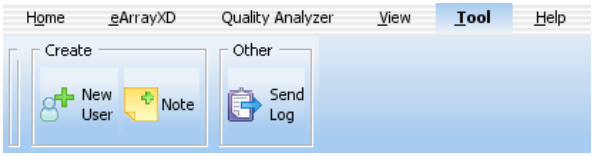


Figure 34 Tool tab, as it appears for the SureSelect Target Enrichment application type

In this tab, which is available for all application types, this command can help you use eArray$_{XD}$:

New User (Available if you are a workgroup administrator on the eArray Web site.) Opens the user management page of the eArray Web site in your Web browser, which lets you search, add, enable, and disable users. See "Administering eArray for Your Workgroup" on page 86 and the online help on the eArray Web site.

Help tab

Figure 35 Help tab, as it appears for the CGH application type

The Help tab contains commands that open the user guides that are available for Agilent Genomic Workbench. It also contains additional commands that let you display version and license information for the program, view information about the software updates that have been installed, and check the Agilent Web site for software updates that are available.

Help buttons

These buttons let you view the users guides that are available for Agilent Genomic Workbench. The guides that are available vary by application type. Each opens in Adobe Reader. These buttons can appear:

Button	Description
Application Guide	(Available for all application types except Expression and microRNA) For each of these application types, this button opens the indicated user guide: • **CGH** – Opens the *CGH Interactive Analysis User Guide*. This guide describes how to use the CGH application of Agilent Genomic Workbench to analyze comparative genomic hybridization data and create reports. It also describes how to analyze CGH+SNP microarrays. • **ChIP-on-chip** – Opens the *ChIP Interactive Analysis User Guide*. This guide describes how to use the ChIP application of Agilent Genomic Workbench to analyze chromatin immunoprecipitation data and create reports. • **CH3** – Opens the *Methylation (CH3) Analysis User Guide*. This guide describes how the use the Methylation (CH3) application of Agilent Genomic Workbench to apply algorithms that help identify methylated regions. • **SureSelect Target Enrichment** – Opens the *SureSelect Quality Analyzer User Guide*. This guide describes how to use the SureSelect Quality Analyzer application of Agilent Genomic Workbench to assess the effectiveness of fragment pull-down for target enrichment experiments
eArray$_{XD}$	(Available for all application types) Opens the *eArray$_{XD}$ User Guide*. This guide describes how to design and submit custom microarray designs and SureSelect Target Enrichment bait libraries.
Sample Manager	(Available for all application types except SureSelect Target Enrichment) Opens the *Sample Manager User Guide*. This guide describes how to use the Sample Manager module of Agilent Genomic Workbench to organize microarrays and edit their attributes. You can use Sample Manager for Feature Extraction without any of the analysis applications.

Button	Description
Feature Extraction	(Available for all application types except SureSelect Target Enrichment) Opens a menu with these options: • **Quick Start** – Opens the *Feature Extraction Quick Start Guide.* This guide gives an overview of how to use the Feature Extraction software to extract and generate QC reports for Agilent microarrays. • **User Guide** – Opens the *Feature Extraction User Guide.* This guide shows you how to set up and run Feature Extraction to automatically extract a batch of image files. It also describes how to extract image files in real time. • **Reference Guide** – Opens the *Feature Extraction Reference Guide.* This guide contains tables that list default parameter values and results for Feature Extraction analyses, and explanations of how Feature Extraction uses its algorithms to calculate results.
Quality Tools	(Available for the CGH, ChIP-on-chip, and CH3 application types) Opens the *Quality Tools User Guide.* This guide describes how to query, filter, and evaluate microarray extractions within Agilent Genomic Workbench. It also describes how to visualize current and historical batch microarray extraction processes.
Workflow	(Available for the CGH and ChIP-on-chip application types) Opens the *Workflow User Guide.* This guide describes how to use the workflow module of Agilent Genomic Workbench to extract image files with Agilent Feature Extraction software and/or analyze data using the CGH and ChIP analysis applications.
Data Viewing	(Available for all application types except Expression and microRNA) Opens the *Data Viewing User Guide.* This guide describes how to import, organize, manage, export, and display data and other content (experiments, gene lists, tracks) within Agilent Genomic Workbench. It is targeted for users who have no DNA Analytics application license(s).

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

Other commands

About Opens a dialog box that displays version and copyright information for your installation of Agilent Genomic Workbench. You can also use this dialog box to display the License Agreement for the Agilent Genomic Workbench software.

Installation History Opens a dialog box that lets you view information about the server and client updates that you have installed.

Check Updates Checks the Agilent Web site for software updates that are available for Agilent Genomic Workbench.

Search Panes

This section contains descriptions of the Search panes that can appear when you use the eArray$_{XD}$ tab of Agilent Genomic Workbench. The search panes appear in alphabetical order.

Advanced Exon Interval Finder

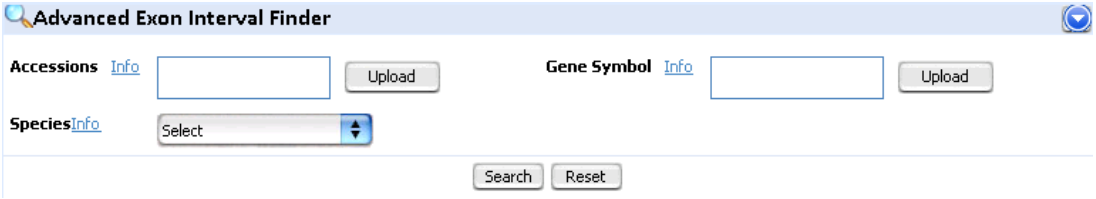


Figure 36 Advanced Exon Interval Finder pane

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you set up and submit a search for exonic genomic intervals whose annotation exactly matches one or more search terms that you enter. The program can use the returned intervals in a Bait Tiling job. See "To do an Advanced Exon Interval Finder Search" on page 367 and "To set up a Bait Tiling job" on page 378.

To open: In the eArray$_{XD}$ tab, under Tools, click **Exon Finder > Advanced Exon Interval Finder.**

NOTE

To do an Exon Finder search, you may first need to transfer exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Search Criteria You must enter the **Species** and at least one annotation value.

Search Criterion	Instructions/Details
Accessions	Type an accession number, without its source, or multiple accession numbers separated by pipe "|" characters. The search returns the exonic intervals that correspond with each of the accessions. For the search to return intervals, accessions must match exactly. Use upper case (capital) letters in accessions. **Example:** `NM_012257|Q0055|NM_012298` You can also upload a file of accessions. Prepare a plain text file with an extension of .txt. List one accession per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns the exonic intervals that match each of the gene symbols. For the search to return intervals, gene symbols must match exactly. Use upper case (capital) letters in gene symbols. **Example:** `H3N2|BRMS1|BRCA1` You can also upload a file of gene symbols. Prepare a plain text file with an extension of .txt. List one gene symbol per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Species	(Required) Select a species from the list. This limits your search to the exonic intervals that are associated with the selected species.

(Available if the search pane is not hidden) Hides the search pane. This can make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

Advanced HD Probe Search

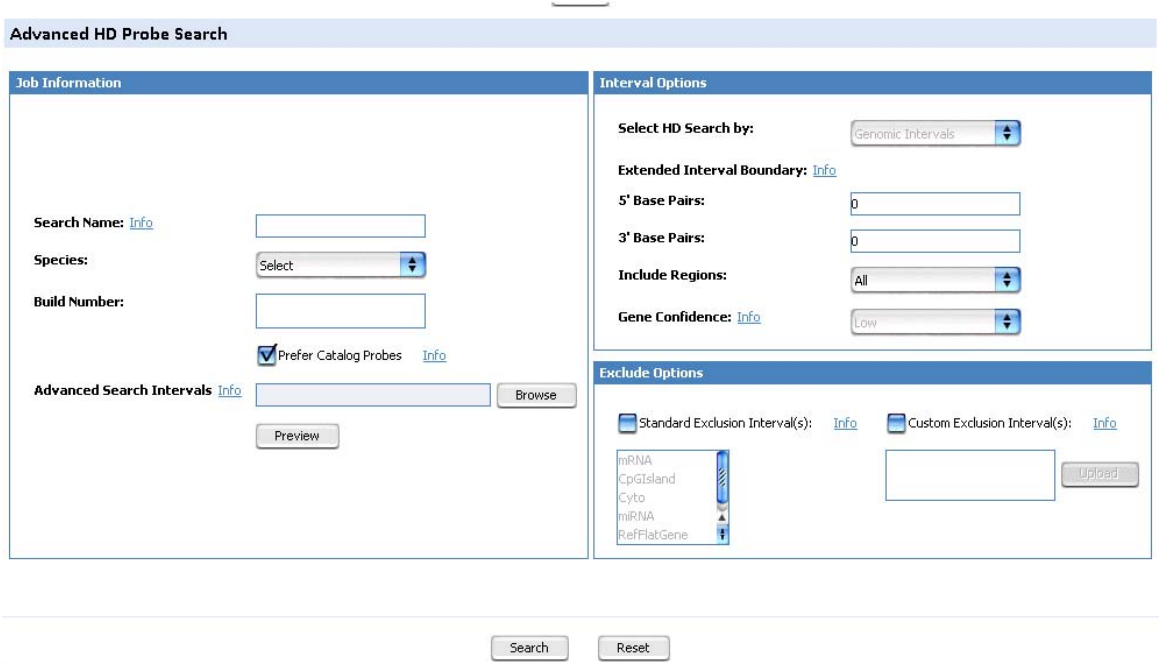


Figure 37 Advanced HD Probe Search pane

Purpose: Retrieves HD probes from the Agilent HD Probe Database that are designed to the genomic intervals that you upload. You set the tiling density, homology (Hm) filtering, and T_M filtering characteristics independently for each interval. This type of search is available for the CGH, ChIP-on-chip, and CH3 application types. See "To do an Advanced Genomic Intervals HD Search for probes" on page 117.

To open: In the eArray$_{XD}$ tab, under **Search,** click **HD Probes > Advanced Search.**

Search Parameters

The table below describes the search parameters that can appear. You **must** set the **Search Name** and the **Species,** and you must also upload a file of **Advanced Search Intervals.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	Type a name that will help you to identify this search job and its results.
Species	Select the desired species. The species that appear in the list are the ones that are available in the HD probe database for your selected application type.
Build Number	(Read-only) The name of the applicable genome build for the selected species. The HD probe database only contains probes designed to the most current genome build for each species.
Prefer Catalog Probes	(Available for HD-CGH probe searches) To give preference to Agilent catalog probes in the probe selection process, mark this check box. If two probes are close to each other for a given probe interval, HD search selects the Agilent catalog probe.
Advanced Search Interval	Select and upload a file that contains the desired genomic intervals, along with the desired tiling density, and homology and T_M filtering status for each interval. For details about the requirements for this file, refer to "Advanced Search Interval" on page 876. **Browse** – Opens an Open dialog box, where you can select a file that contains the desired search interval data. **Preview** – Opens the selected file, and displays its contents in the Preview of Search Intervals pane. See below, "Preview of Search Intervals."

Parameter	Instructions/Details
Preview of Search Intervals	(Appears after you upload a file of search intervals) Shows one or more lines of data from your uploaded search intervals file. See above, "Advanced Search Interval." **Show All** – Opens the Advanced Search Interval dialog box, where you can view all of the data from the search intervals file. See "Advanced Search Intervals" on page 580. **My uploaded file contains column headings** – Mark this option if the first line of your file is actually a row of column headings. This prevents the program from interpreting the first line of your file as a search interval. The program does not interpret any column headings in the uploaded file.
Interval Options	
Select HD Search by	For Advanced HD Probe Searches, **Genomic Intervals** is always the selected option, and cannot be changed.
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined regions of your genomic intervals. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.
Include Regions	(Available only for HD-CGH searches) Select one of the options below. You can use this parameter to limit your HD-CGH probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence." • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence."

Parameter	Instructions/Details
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.
Exclude Options	
Standard Exclusion Interval(s)	Lets you select from among many sets of standard exclusion intervals, based on annotation tracks. To ignore genomic regions defined in one or more of these sets, mark this option, then select the desired set(s) from the list that appears. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option. **Upload** – Opens a File Upload dialog box, where you can upload a file of the desired genomic intervals. See "File Upload" on page 773 and "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

Search Submits the search job through your server to the eArray Web site.

Reset Clears all parameters, or restores them to their default values.

Advanced Interval Finder

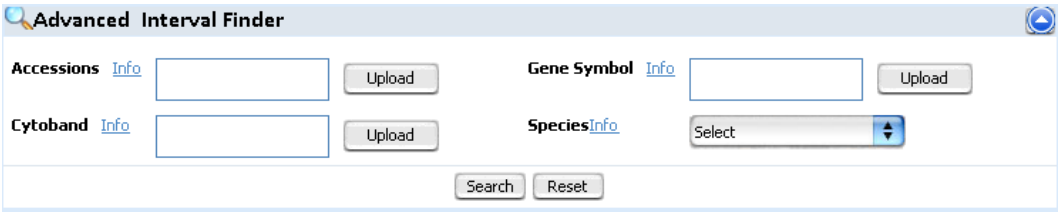


Figure 38 Advanced Interval Finder pane

Purpose: Lets you set up and submit a search for genomic intervals whose annotation exactly matches one or more of the search terms that you enter. This type of search is available for the CGH, ChIP, CH3, and SureSelect Target Enrichment application types. The program can use the returned intervals in a Bait Tiling or Genomic Tiling job, or in an HD Probe Search. See these topics:

- "To do an Advanced Interval Finder Search" on page 364
- "Searching for Agilent High Density (HD) Probes" on page 109
- "To set up a Genomic Tiling job" on page 176
- "To set up a Bait Tiling job" on page 378

To open:

- For the CGH, ChIP-on-chip, and CH3 application types – In the eArray$_{XD}$ tab, under Search, click **Probes > Advanced Interval Finder.**
- For the SureSelect Target Enrichment application type – In the eArray$_{XD}$ tab, under Tools, click **Interval Finder > Advanced Interval Finder.**

Search Criteria You must enter the **Species** and at least one annotation value.

Search Criterion	Instructions/Details
Accessions	Type an accession number, without its source, or multiple accession numbers separated by pipe "|" characters. The search returns the intervals that correspond with each of the accessions. For the search to return intervals, accessions must match exactly. Use upper case (capital) letters in accessions. **Example:** `NM_012257|Q0055|NM_012298` You can also upload a file of accessions. Prepare a plain text file with an extension of .txt. List one accession per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Cytoband	Type a cytoband designation, without its source, or multiple cytobands separated by pipe "|" characters. The search returns the intervals that correspond with each of the cytobands. For the search to return intervals, cytobands must match exactly. Use lower case letters for the p or q chromosome arms. **Example:** `1p22.2|2q33.3` You can also upload a file of cytobands. Prepare a plain text file with an extension of .txt. List one cytoband per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns the intervals that correspond with each of the gene symbols. For the search to return intervals, gene symbols must match exactly. Use upper case (capital) letters in gene symbols. **Example:** `H3N2|BRMS1|BRCA1` You can also upload a file of gene symbols. Prepare a plain text file with an extension of .txt. List one gene symbol per line, and end each line with a **new line** character (press **Enter**). To upload the file, click **Upload.** For details, see "To upload data for probe searches" on page 101.
Species	Select a species from the list. This limits your search to the intervals that are associated with the selected species.

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

Array Design Search

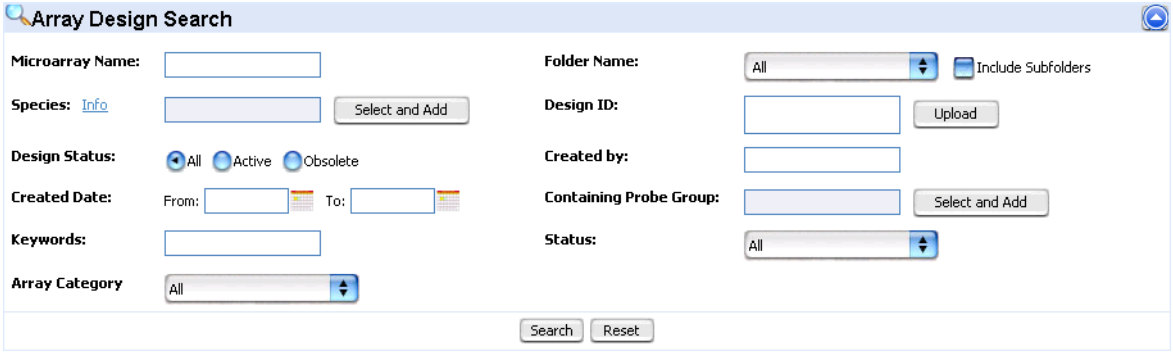


Figure 39 Microarray Design Search pane

Purpose: Lets you set up and submit a search for existing microarray designs. This type of search is available for all microarray-related application types, and it can retrieve microarray designs from the Agilent Catalog or from the folders of your workgroup. See "To search for microarray designs" on page 251.

To open: In the eArray$_{XD}$ tab, under **Search,** click **Microarray Designs.**

Search Criteria

The table below describes the search criteria that appear in the Array Design Search pane.

Search Criterion	Instructions/Details
Microarray Name	Type all or part of a name of a microarray design.
Folder Name	To limit the search to a specific folder, select a folder from the list. Only the folders to which you have access appear in the list. To search all available folders, select **All.** To include the subfolders within the selected one in the search, mark **Include Subfolders.**
Species	Lets you select one or more species as search criteria. **Select and Add** – Opens the Select and Add : Species dialog box, where you can select the desired species for the search. See "Select and Add : Species" on page 845. **Note:** For the microRNA application type, the search only retrieves a microarray design if its primary species matches one of the species that you select for this criterion.
Design ID	Type a design ID number, or multiple design ID numbers separated by pipe "|" characters. Design ID numbers are also called **AMADIDs.**
Design Status	When Agilent discontinues a particular design format, the microarray designs that use that format become obsolete. After you delete obsolete designs, you can delete them, or you can edit them to use an available design format. Select one of these options: • **All** – Returns microarray designs without regard to design status. • **Active** – Returns microarray designs that use design formats that are currently available. • **Obsolete** – Returns microarray designs that use design formats that are no longer available.
Created by	Type all or part of the name of the array design owner whose designs you want to find. This criterion is not case sensitive.
Date Created	Enter a range of dates. Use yyyy-mm-dd as the date format, for example `2009-03-20`. Alternatively, to select the desired dates from calendars, click  beside **From** and **To.** To return only designs that were created before a given date, select the desired date in **To**, and do not select a date in **From.**

Search Criterion	Instructions/Details
Containing Probe Group	Set this parameter to find microarray designs that contain specific probe group(s). **Select and Add** – Opens the Select and Add : Probe Group dialog box, where you can select probe group(s) to use as search criteria. See "Select and Add : Probe Group" on page 843 and "To select probe groups for searches or microarrays" on page 106.
Keywords	Type all or part of a keyword, or multiple keywords separated by commas. This search term is not case-sensitive.
Status	The status of a microarray design shows its progress through the design creation process. See "Status of microarray designs" on page 248. Select a status to limit your search to microarray designs that have a specific status. To return microarray designs without regard to status, select **All.**
Array Category	(CGH application type only) Lets you limit your search to one of the specific types of microarrays that can be available in the CGH application type. These options are available: • **All** – The program does not use array category as a search criterion. • **CGH** – Limits returned microarray designs to standard CGH microarray designs. • **CGH+SNP** – Limits returned microarray designs to CGH+SNP microarray designs. This category of microarray design includes both CGH and SNP probes on the same array. See "To create a CGH+SNP microarray design" on page 301.


(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.


(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

Bait Group Search

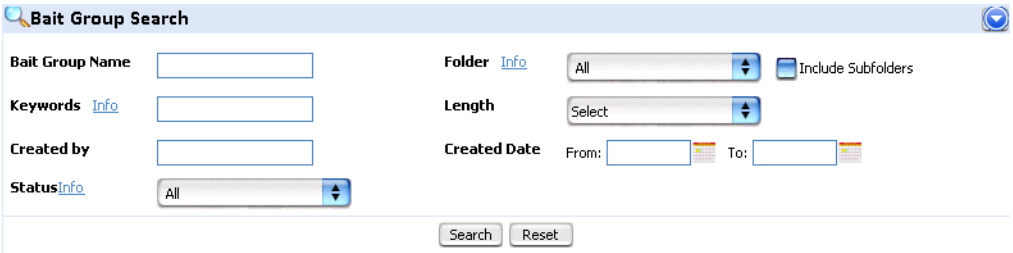


Figure 40 Bait Group Search pane

Purpose: Lets you set up and submit a search for existing bait groups. This type of search is available for the SureSelect Target Enrichment application type. See "To search for bait groups" on page 396.

To open: In the eArray$_{XD}$ tab, under **Search,** click **Bait Groups.**

Search Criteria

The table below describes the search criteria that appear in the Bait Group Search pane.

Search criterion	Instructions/Details
Bait Group Name	Type all or part of the name of a desired bait group. This search criterion is not case-sensitive.
Folder	Select a specific folder to search. The list contains the names of folders that you can access. Select **All** to search in all folders available to you. **Include Subfolders** – Includes the folder's subfolders in the search.
Keywords	Type all or part of a keyword. This search criterion is not case sensitive.
Length	(Required) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Created by	Type all or part of the name of the user who first saved the bait group.

Search criterion	Instructions/Details
Date Created	Type dates in **From** and **To.** For dates, use the format yyyy-mm-dd. (For example, type `2008-05-02`.) This limits the probe groups that are returned to those created within the specified range of dates. Alternatively, click the  buttons to select dates.
Status	Select one of these options: • **All** – Returns bait groups of any status. • **Incomplete** – Limits the bait groups that are returned to those with Incomplete status. Incomplete bait groups can be edited. • **Locked** – Limits the bait groups that are returned to those with Locked status. Locked bait groups cannot be edited, and they cannot be unlocked.

 (Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

 (Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears all parameters, or restores them to their default values.

Bait Search

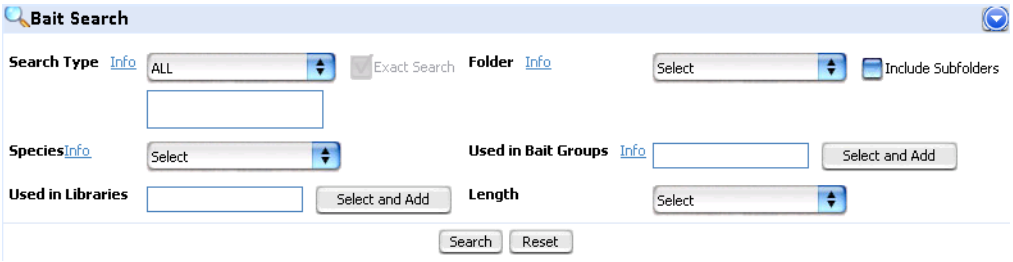


Figure 41 Bait Search pane

Purpose: Lets you set up and submit a Bait Search. This type of search is available for the SureSelect Target Enrichment application type. It retrieves baits that have annotations, accessions or sequences that match search term(s) that you enter. See "To search for baits" on page 358.

To open: In the eArray$_{XD}$ tab, under Search, click **Baits.**

Search Type This search criterion lets you select the specific type of annotation or accession to be searched. The table below summarizes the available options. Currently, the program supports only exact searches.

Option	Details/Instructions
ALL	In this type of search, you enter a single search term. eArray retrieves baits that have any annotation or accession value that exactly matches the search term. In **Search Type,** type the desired search term in the empty box.
Bait ID	Type a bait ID, or multiple bait IDs separated by pipe "|" characters. The search returns baits whose bait IDs match exactly. A bait ID is a unique identifier for a bait. Alternatively, to upload a file that contains the desired bait ID data, click **Upload,** then select the desired file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.

Option	Details/Instructions
Accessions	Type an accession, or multiple accessions separated by pipe "|" characters. The search returns baits whose associated accessions are an exact match. An accession is a unique identifier that refers to a specific nucleotide sequence that is a target for the associated bait, or a protein sequence that is a product of the target. Enter accessions without sources. For example, list **ref|NM_015752** as `NM_015752`. Alternatively, to upload a file that contains the desired accession data, click **Upload,** then select the desired file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Gene Symbol	Type a gene symbol, or multiple gene symbols separated by pipe "|" characters. The search returns baits with associated gene names that are an exact match. A gene symbol is a unique abbreviation that represents a gene, for example **H3N1,** or **CTSB.** Alternatively, to upload a file that contains the desired gene symbol data, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Chromosomal Location	Type a chromosomal location in the box, or multiple locations separated by pipe "|" characters. The search returns any baits that are designed to genomic coordinates within the range that you enter. **Example:** `chr1:47995000-49867300|chr2:20078-90992` Alternatively, to upload a file that contains the desired chromosomal locations, click Upload, then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101. **Note:** You can also set up this type of search from the Genomic Viewer. Select the desired genomic region in Gene View, right-click the selected area, then click **Chromosomal Location Search.** The program opens the Bait Search pane and sets criteria for a search of the selected region. For information on the Genomic Viewer, see the *Data Viewing User Guide.*

Option	Details/Instructions
Cytoband	Type a cytoband identifier in the box, or multiple cytobands separated by pipe "|" characters. The search returns baits that are found in the listed cytobands. Follow this example format: `11p15.4` Alternatively, to upload a file that contains the desired cytoband data, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.
Bait Sequence	Type a valid bait sequence in the box, or multiple sequences separated by pipe "|" characters. The search returns baits whose sequences are exact matches. Alternatively, to upload a file that contains the desired bait sequences, click **Upload,** then select the appropriate file. The process is the same as the one described for probe searches in "To upload data for probe searches" on page 101.

Other Search Criteria

The table below describes the remaining search criteria that appear in the pane.

Search criterion	Description
Folder	(Required) Limits the search to the selected folder. The list of folders contains only the ones to which you have access. **Include Subfolders** – Includes the folder's subfolders in the search.
Species	(Required) Select the species associated with the baits that you want to retrieve.
Used in Bait Groups	Limits the search to baits in the specified bait group(s). **Select and Add** – Opens the Select and Add Bait Group dialog box, where you can select the desired bait group(s) for the search. See "Select and Add : Bait Group" on page 837. **Note:** The program does not return baits if you select a bait group that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Search criterion	Description
Used in Libraries	Limits the search to baits in the specified librar(ies). **Select and Add** – Opens the Select and Add : Library Name dialog box that lets you select the desired librar(ies) for the search. See "Select and Add : Library Name" on page 839. **Note:** The program does not return baits if you select a library that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.
Length	(Required) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in a bait library must have this length.

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears the search criteria, or restores them to their default values.

NOTE To search for baits, you may need to transfer bait data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Entire Agilent SNP Probe Set Search

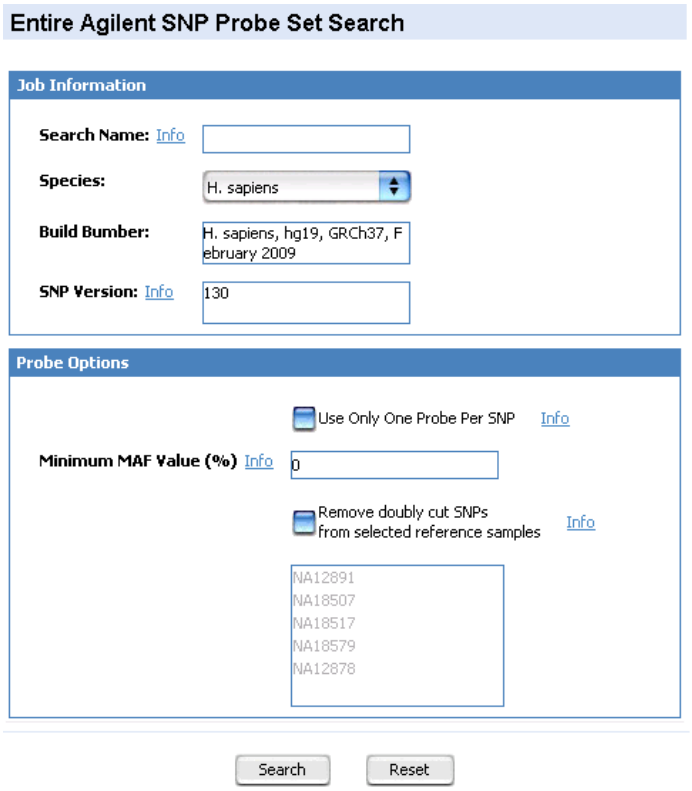


Figure 42 Search pane for a SNP Probe Search by Agilent Probe Set

Purpose: Lets you set up a SNP probe search job that returns Agilent SNP probes from throughout the genome of the selected species. You can use several criteria to filter the returned set of probes. Agilent SNP probes are designed specifically for use in Agilent SNP microarrays. See "To do an Entire Agilent SNP Probe Set Search" on page 141.

To open: In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Entire Agilent SNP Probe Set Search.**

Job Information These items appear. All are required, except as noted.

Item	Instructions/Description
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The program returns Agilent SNP probes from throughout the genome of the selected species. Currently, the program supports human SNP probes.
Build Number	(Read-only) The build of the genome of the selected species to which the returned SNP probes are designed.
SNP Version	(Read only) The build of the SNP database of the selected species to which the returned SNP probes are designed.

Probe Options These options appear. All are optional.

Option	Instructions/Description
Use Only One Probe per SNP	Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.
Minimum MAF Value (%)	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.

Option	Instructions/Description
Remove doubly cut SNPs from selected reference samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. • To exclude such probes, mark **Remove doubly cut SNPs from selected reference samples,** then click the name of the desired reference sample. To select additional reference samples, control-click their names. • If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove doubly cut SNPs from selected reference samples.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.

Search Submits the search job to your Agilent Genomic Workbench server.

Reset Clears the search pane.

NOTE To do a SNP probe search, you may first need to transfer SNP probe data to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Exon Interval Finder

Figure 43 Exon Interval Finder pane

Purpose: Lets you set up and submit a search for exonic genomic intervals whose annotation contains a specified search term. This type of search is available for the SureSelect Target Enrichment application type. The program can use the returned intervals in a Bait Tiling job. See "To do a Simple Exon Interval Finder Search" on page 366 and "To set up a Bait Tiling job" on page 378.

To open: In the eArray$_{XD}$ tab, under Tools, click **Exon Finder > Simple Exon Interval Finder.**

Search Criteria These search criteria appear in the pane:

Search Criterion	Instructions/Details
Search Term	Type a search term in the box. The program returns the exonic genomic intervals whose annotation contains this term. The search term is not case-sensitive, and it can be all or part of an annotation.
Species	Select the desired species from the list. To select all available species, select **All.**

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

NOTE To do an exon finder search, you may first need to transfer exon boundary data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60

Genomic Interval Search (SNP Probe Search)

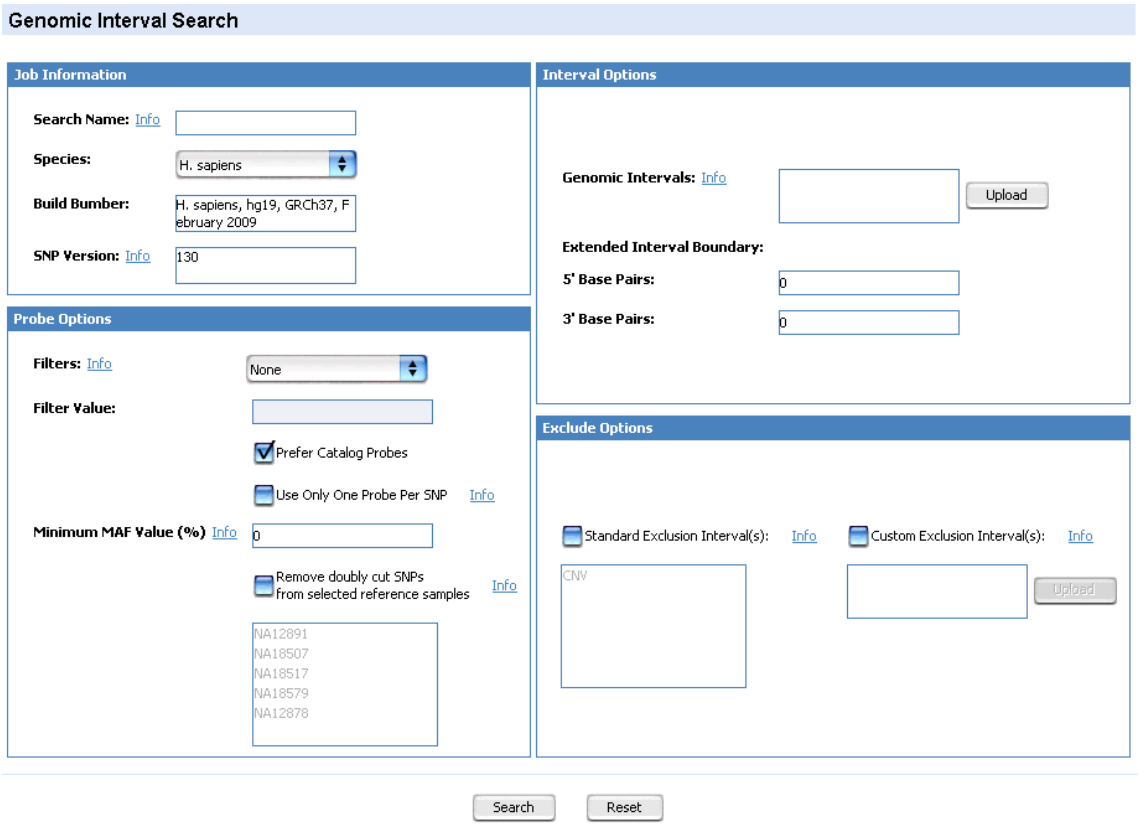


Figure 44 Search pane for a SNP probe search by genomic intervals

Purpose: Lets you set up and submit a SNP probe search job based on genomic intervals that you enter or upload. The job returns Agilent SNP probes for the selected species that are designed to the given genomic intervals. Agilent SNP probes are designed specifically for use in Agilent SNP microarrays. See "To do a SNP probe search by genomic intervals" on page 143.

To open: In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Genomic Interval Search.**

Job Information

These items set the general parameters for the SNP probe search job. All parameters are required, except as noted.

Item	Instructions/Description
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Build Number	(Read-only) The build of the genome of the selected species to which the returned SNP probes are designed.
SNP Version	(Read only) The build of the SNP database of the selected species to which the returned SNP probes are designed.

Probe Options These options let you filter the returned set of probes. All are optional.

Option	Instructions/Description
Filters	Select one of these options: • **None** – No limit is applied, either to the total number of returned SNP probes or to the number of SNP sites that are considered by the search. • **Total Probes** – This limits the total number of probes that the SNP probe search collectively returns for all specified genomic intervals. In **Filter Value,** type the desired number of probes. **Example:** If you type `2000` in Filter Value, the search returns the 2,000 best SNP probes that match the other search criteria. To find the best probes, the search considers empirically-determined probe scores. These scores reflect the likelihood that each given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. SNP probe scores are not available for download. • **Total SNPs** – This limits the total number of SNP sites that the search considers. In **Filter Value,** type the desired number of SNP sites. **Example:** If you type `2000` in Filter Value, the search considers only the 2,000 best SNP sites, and returns the SNP probes that are associated with those sites. To find the best SNP sites, the search considers the empirically-determined scores for the corresponding SNP probes. A probe score reflects the likelihood that a probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. SNP probe scores are not available for download.
Filter Value	Enter a value for the **Total Probes** or **Total SNPs** filter (see above).
Prefer Catalog Probes	Currently, all of the SNP probes that are available in eArray$_{XD}$ are Agilent Catalog Probes.
Use Only One Probe per SNP	Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.

Option	Instructions/Description
Minimum MAF Value (%)	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.
Remove doubly cut SNPs from selected reference samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. • To exclude such probes, mark **Remove doubly cut SNPs from selected reference samples,** then click the name of the desired reference sample. To select additional reference samples, control-click their names. • If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove doubly cut SNPs from selected reference samples.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.

Interval Options These options define the genomic intervals for which probes are returned. All are required.

Option	Instructions/Description
Genomic Intervals	Type either a chromosomal location or a cytoband in the box. Separate multiple intervals with pipe "|" characters. All of the intervals must be of the same type. For information about how to enter genomic intervals, see "Genomic Intervals (Simple HD and SNP Probe Searches)" on page 888. **Upload** – Opens a File Upload dialog box, where you can upload a file of chromosomal locations or cytobands. See "File Upload" on page 773 and "To upload data for probe searches" on page 101
Extended Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined genomic intervals. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. the program extends an original interval of 9000–10000 to 8500–10300.

Exclude Options These options let you ignore certain genomic intervals in the search. Both are optional.

Option	Instructions/Description
Standard Exclusion Interval(s)	You can exclude regions of known copy number variation from the SNP probe search. The program uses the CNV track in Agilent Genomic Workbench to define the intervals to exclude. To ignore these genomic regions, mark this option, then in the box, select **CNV.**
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option. **Upload** – Opens a File Upload dialog box, where you can upload a file of the desired genomic intervals. See "File Upload" on page 773 and "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

Search Submits the search job to your Agilent Genomic Workbench server.

Reset Clears the search pane.

NOTE To do a SNP probe search, you may first need to transfer SNP probe data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Library Search

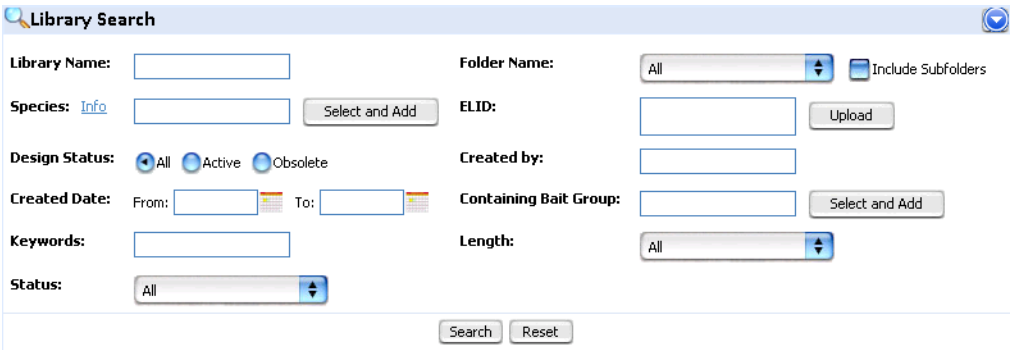


Figure 45 Library Search pane

Purpose: Lets you set up and submit a search for existing libraries. This type of search is available for the SureSelect Target Enrichment application type. See "To search for libraries" on page 416.

To open: In the eArray$_{XD}$ tab, under **Search,** click **Libraries.**

Search Criteria The table below describes the search criteria that appear in the Library Search pane.

Search Criterion	Instructions/Details
Library Name	Type all or part of a name of a library.
Folder Name	Limits the search to a specific folder. Select a folder from the list. Only the folders to which you have access appear in the list. To search all available folders, select **All.** **Include Subfolders** – Includes the subfolders within the selected folder in the search.

Search Criterion	Instructions/Details
Species	Lets you select one or more species as a search criterion. **Select and Add** – Opens the Select and Add : Species dialog box, where you can select the desired species for the search. See "Select and Add : Species" on page 845.
ELID	Type an ELID, or multiple ELIDs separated by pipe "|" characters. An ELID is a unique Agilent ID number that identifies a bait library. **Upload** – Opens an Open dialog box, where you can select and upload a file of ELIDs.
Design Status	Select one of these options: • **All** – Returns libraries without regard to their status. • **Active** – Returns libraries that use library sizes that are currently available. • **Obsolete** – Returns libraries that use library sizes that are no longer available. **Note:** Currently, eArray does not contain any libraries with obsolete formats.
Created by	Type all or part of the name of the library owner whose designs you want to find. This criterion is not case sensitive.
Date Created	Enter a range of dates. Use yyyy-mm-dd as the date format, for example 2009-03-20. Alternatively, to select the desired dates from calendars, click  next to **From** and **To.** To return only libraries that were created before a given date, select the desired date in **To**, and do not select a date in **From.**
Containing Bait Group	Set this parameter to find libraries that contain specific bait group(s). **Select and Add** – Opens the Select and Add : Bait Group dialog box, where you can select bait group(s) to use as search criteria. See "Select and Add : Bait Group" on page 837 and "To select probe groups for searches or microarrays" on page 106.
Keywords	Type all or part of a keyword, or multiple keywords separated by commas. This search term is not case-sensitive.

Search Criterion	Instructions/Details
Length	(Required) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Status	The status of a library shows its progress through the library creation process. The statuses of libraries parallel those of microarray designs. See "Status of microarray designs" on page 248. Select a status to limit your search to libraries that have a specific status. To return libraries without regard to status, select **All.**

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

Network Search

Figure 46 Search pane for Network searches

Purpose: Lets you set up and submit a search for biological networks. The program supports searches of the WikiPathways database. See "To use a biological network to find or create probes" on page 193.

To open: In the eArray$_{XD}$ tab, under Search, click **Network Search.**

Search Criteria The table below describes the search criteria that can appear in this pane.

Search criterion	Instructions/Details
Source	Select the source of the biological networks that you want to search. These options are available: • **My Favorites** – Networks that you have selected from previous searches to add to your collection of favorite networks. See "To add a network to My Favorites" on page 197. • **WikiPathways** – An open, Web-based repository of biological network data. For details, go to wikipathways.org.
Species	Select the desired species. To return biological networks without regard to species, select **All organisms.**
Search Terms	The program supports text string searches. Type one or more search terms in the box, separated by spaces. If you enter multiple search terms, the program searches each term independently, and returns the networks that match each individual term. To return a network, the search term must exactly match a complete word in the given WikiPathways page. You can use an asterisk (*) as a "wild card" to represent an unspecified group of characters.

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears all parameters, or restores them to their default values.

Probe Group Search

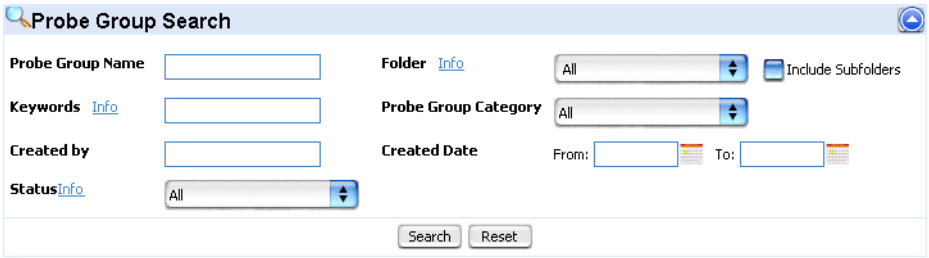


Figure 47 Probe Group Search pane (CGH application type)

Purpose: Lets you set up and submit a search for existing probe groups. This type of search is available for all microarray-related application types. See "To search for probe groups" on page 224.

To open: In the eArray$_{XD}$ tab, under **Search,** click **Probe Groups.**

Search Criteria

The table below describes the search criteria that can appear in the Probe Group Search pane.

Search criterion	Instructions/Details
Probe Group Name	Type all or part of the name of a desired probe group. This search criterion is not case-sensitive.
Folder	Select a specific folder to search. The list contains the names of folders that you can access. Select **All** to search in all folders available to you. **Include Subfolders** – Includes the folder's subfolders in the search.
Keywords	Type all or part of a keyword. This search criterion is not case sensitive.

Search criterion	Instructions/Details
Probe Group Category	(CGH application type only) Lets you limit your search to one of the specific types of probe groups that can be available in the CGH application type. These options are available: • **All** – The program does not use probe group category as a search criterion. • **CGH** – Limits returned probe groups to standard CGH probe groups. • **CGH+SNP** – Limits returned probe groups to probe groups that contain Agilent SNP probes. These probe groups are designed specifically for use in Agilent CGH+SNP microarray designs. See "To create a CGH+SNP microarray design" on page 301.
Created by	Type all or part of the name of the user who first saved the probe group.
Date Created	Type dates in **From** and **To.** For dates, use the format yyyy-mm-dd. (For example, type `2008-05-02`.) This limits the probe groups that are returned to those created within the specified range of dates. Alternatively, click the buttons to select dates.
Status	Select one of these options: • **All** – Returns probe groups of any status. • **Incomplete** – Limits the probe groups that are returned to those with Incomplete status. Incomplete probe groups can be edited. • **Locked** – Limits the probe groups that are returned to those with Locked status. Locked probe groups cannot be edited, and they cannot be unlocked.

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears all parameters, or restores them to their default values.

Probe ID Search (HD probes)

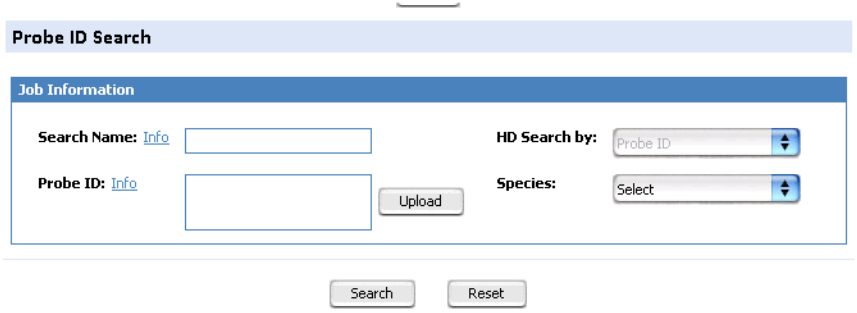


Figure 48 Probe ID HD Probe Search pane

Purpose: Retrieves HD probes for the CGH, ChIP-on-chip, or CH3 application types from the Agilent High Density Probe Database that have the probe IDs that you enter. See "To do a Probe ID HD Search for probes" on page 125.

To open: In the eArray$_{XD}$ tab, under **Search,** click **HD Probes > Probe ID Search.**

Search Parameters

The table below describes the search parameters that appear in the Probe ID HD Probe Search pane. All parameters are required.

Parameter	Instructions/Details
Job Information	
Search Name	Type a name that will help you to identify this search job and its results.
Probe ID	Type at least one HD probe ID. Separate multiple probe IDs with pipe "|" characters. **Example:** `A_14_P100053|A_14_P100055|A_14_P100056` **Upload** – Opens a File Upload dialog box, where you can upload a *.txt file that contains the desired probe IDs. See "File Upload" on page 773 and "To upload data for probe searches" on page 101. The file of probe IDs must contain one probe ID per line. See "ProbeID" on page 891.

Parameter	Instructions/Details
HD Search by	This parameter is set to Probe ID, and cannot be changed.
Species	Select the desired species. The species that appear in the list are those that are available in the HD probe database for the selected application type.

Search Submits the search job to the eArray Web site.

Reset Clears all parameters, or restores them to their default values.

Probe ID Search (SNP probes)

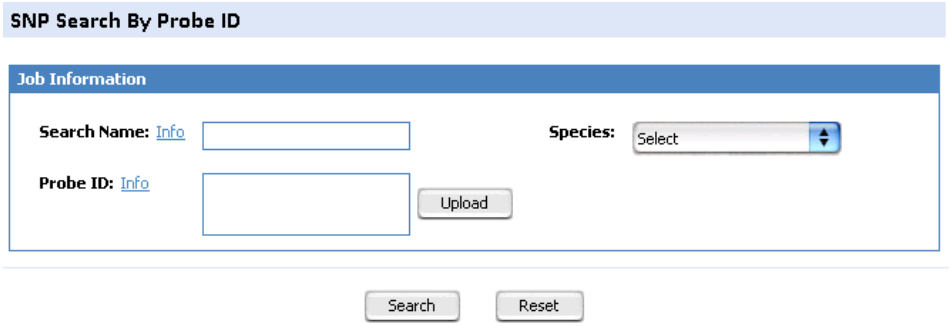


Figure 49 Search pane for a SNP probe search by probe ID

Purpose: This search pane lets you set up and submit a SNP probe search job that returns Agilent SNP probes for the selected species that have the specific probe IDs that you enter. Agilent SNP probes are designed specifically for use in Agilent CGH+SNP microarrays. See "To do a SNP probe search by probe ID" on page 148.

To open: In the eArray$_{XD}$ tab, under Search, click **SNP Probes > Probe ID Search.**

Job Information These search parameters are available. All are required.

Parameter	Instructions/Description
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Probe ID	Type the desired SNP probe IDs. Separate multiple probe IDs with pipe "|" characters. The search returns any existing Agilent SNP probes that have the probe IDs that you enter. **Example:** `A_20_P00170194|A_20_P00182084` **Upload** – Opens a File Upload dialog box, where you can select a file of SNP probe IDs to upload. See "File Upload" on page 773. The file must be a *.txt file that has one SNP probe ID on each line.

Search Submits the search job to your Agilent Genomic Workbench server.

Reset Clears the search pane.

NOTE To do a SNP probe search, you may first need to transfer SNP probe data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Probe Search

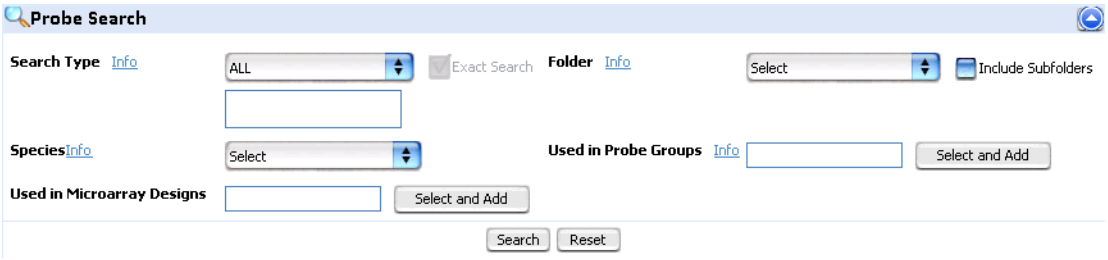


Figure 50 Probe Search pane

Purpose: Lets you set up and submit a Probe Search. This type of search is available for all microarray-related application types. It retrieves probes that match the search term(s) that you enter. See "To use the Probe Search tool to find probes" on page 92.

To open: The way that you open this pane varies by application type:

- For the Expression and microRNA application types – In the eArray$_{XD}$ tab, under **Search,** click **Probes.**
- For the CGH, ChIP-on-chip and CH3 application types – In the eArray$_{XD}$ tab, under **Search,** click **Probes > Simple Search.**

NOTE

- To search for probes, you may need to transfer Agilent Catalog or workgroup probe data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60
- To search for High Density (HD) probes or SNP probes, you use other commands. See "Searching for Agilent High Density (HD) Probes" on page 109 and "Searching for Agilent SNP Probes" on page 138.

Search Type This search criterion lets you select the specific type of annotation or accession to be searched. The table below summarizes the available options.

Search Type	Description
ALL	In this type of search, you enter a single search term. The program retrieves probes that have any annotation or accession value that matches the search term. Type the desired search term in the empty box. **Note:** • (Expression and microRNA application types) To return probes that have any type of annotation that exactly matches the search term, mark **Exact search.** Otherwise, the search returns probes that contain the search term *within* any annotation. • (CGH, ChIP-on-chip, and CH3 application types) The program always returns probes that have annotations that are an exact match with the search term.
Probe ID	Type a probe ID in the box. Separate multiple IDs with pipe "|" characters. Alternatively, to upload a file that contains the desired probe ID data, click **Upload,** then select the desired file. See "To upload data for probe searches" on page 101.
Accessions	(Available for all application types except microRNA) Type a valid accession number, without its source, in the box. Separate multiple accessions with pipe "|" characters. Alternatively, to upload a file that contains the desired accession data, click **Upload,** then select the desired file. See "To upload data for probe searches" on page 101. **Note:** To search for microRNA probes based on miMAT accessions, select the **miMAT#** search type.
Gene Symbol	(Available for all application types except microRNA) Type a valid gene symbol in the box. Separate multiple gene symbols with pipe "|" characters. Alternatively, to upload a file that contains the desired gene symbol data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.

Search Type	Description
Chromosomal Location	Type a chromosomal location in the box, or multiple locations separated by pipe "|" characters. **Example:** `chr1:47995000-49867300|chr2:20078-90992` The search returns probes that are designed to genomic coordinates within the range that you enter. Alternatively, to upload a file that contains the desired chromosomal locations, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101. **Note:** You can also set up this type of search from the Genomic Viewer. Select the desired genomic region in Gene View, right-click the selected area, then click **Chromosomal Location Search.** The program opens the Probe Search pane and sets criteria for a search of the selected region. For information on the Genomic Viewer, see the *Data Viewing User Guide*.
Cytoband	(Available for all application types except microRNA) Type a cytoband identifier in the box. Separate multiple cytobands with pipe "|" characters. Alternatively, to upload a file that contains the desired cytoband data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.
Probe Sequence	Type a valid probe sequence in the box, or multiple sequences separated by pipe "|" characters. The search returns probes whose sequences are exact matches. To upload search sequences from a file, click **Upload.** See "To upload data for probe searches" on page 101.

Search Type	Description
miMAT#	(microRNA application type only) Type a miMAT accession in the box, or multiple miMAT accessions separated by pipe " | " characters. The search returns probes that are associated with the miMAT accession(s). Alternatively, to upload a file that contains the desired miMAT accession data, click **Upload,** then select the appropriate file. See "To upload data for probe searches" on page 101.
microRNA Name	(microRNA application type only) Type the name of a mature microRNA. Separate multiple names with pipe " | " characters. Alternatively, to upload a file that contains the desired microRNA names, click **Upload,** then select the desired file. See "To upload data for probe searches" on page 101. **Note:** For the microRNA application type, probes are grouped by the specific microRNA to which they bind. Up to four related probes are grouped under the name of each mature microRNA target. In general, for microRNA arrays, each mature microRNA is represented by one to four probes, which vary in length. These probes act in concert to measure the microRNA of interest, and the data are combined downstream in the Agilent Feature Extraction software.

Other Search Parameters

These search parameters appear in the pane:

Search Parameter	Details
Folder	(Required) The search returns probes only from the selected folder. **Include Subfolders** – Includes the folder's subfolders in your search. The list of folders includes the ones to which you have access.
Species	(Required) Limits the search to probes that are associated with the selected species.

Search Parameter	Details
Used in Probe Groups	(Optional) Limits the search to probes that are found in the specified probe group(s). **Select and Add** – Opens the Select and Add : Probe Group dialog box, where you can select one or more probe groups for the search. See "Select and Add : Probe Group" on page 843 and "To select probe groups for searches or microarrays" on page 106. **Note:** • The program does not return probes if you select a probe group that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. • The Probe Search Tool cannot search High Density (HD) probe groups.
Used in Array Designs	(Optional) Limits the search to probes that are found in the specified microarray design(s). **Select and Add** – Opens the Select and Add : Microarray Name dialog box, where you can select one or more microarray designs for the search. See"Select and Add : Microarray Name" on page 841. **Note:** The program does not return probes if you select a microarray design that needs to be downloaded from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

(Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

(Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears all parameters, or restores them to their default values.

Search

See "Network Search" on page 553.

Simple Exon Interval Finder

See "Exon Interval Finder" on page 545.

Simple HD Probe Search

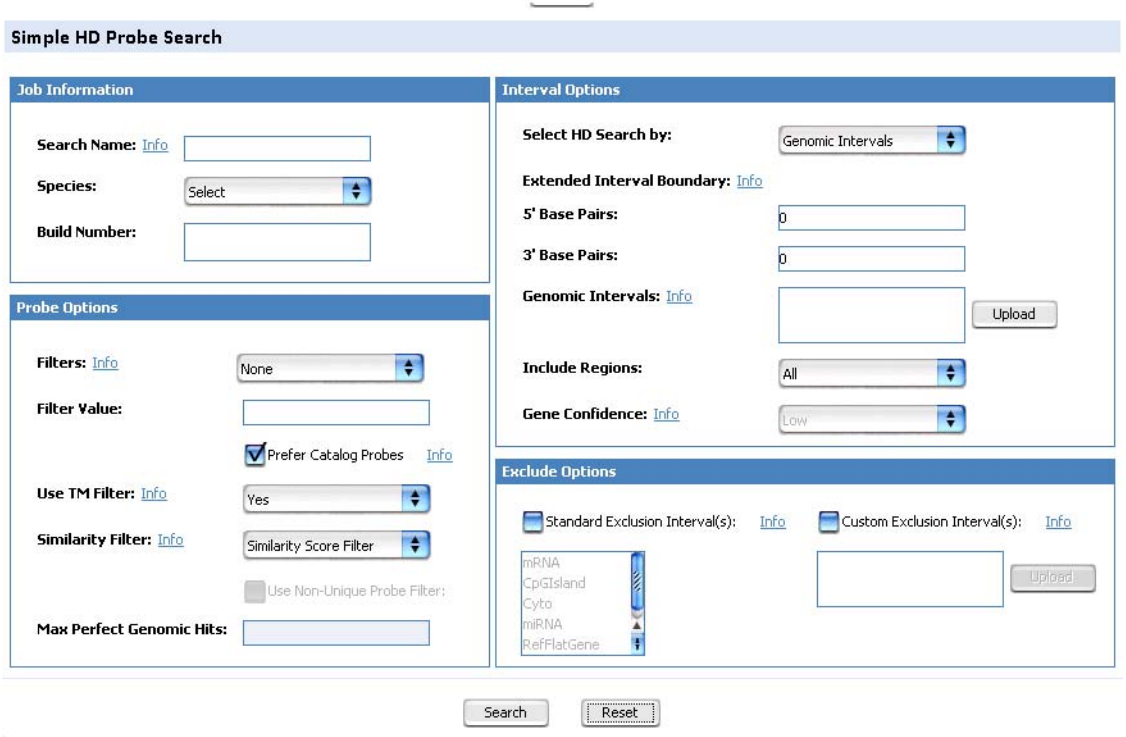


Figure 51 Simple HD Probe Search pane

Purpose: Lets you set up and submit a Simple HD Probe Search job to the eArray Web site. Two main options are available for this type of search:

- **Simple Genomic Intervals HD Searc**h – (Available for CGH, ChIP-on-chip, and methylation applications) Retrieves probes from the Agilent HD probe database on the eArray Web site based on genomic coordinates that you enter. See "To do a Simple Genomic Intervals HD Search for probes" on page 111.
- **Simple Gene Annotations HD Search** – (Available for the CGH application type) Retrieves probes from the Agilent HD probe database on the eArray Web site based on gene annotations that you enter, such as gene symbols or GenBank accession numbers. See "To do a Simple Gene Annotations HD Search for probes" on page 120.

To open: In the eArray$_{XD}$ tab, under **Search,** click **HD Probes > Simple Search.**

Search Parameters

The table below describes the search parameters that can appear. You **must** set the **Search Name,** the **Species,** the **Select HD Search by** setting, and one or more **Genomic Intervals** or **Gene Annotations.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	Type a name that will help you to identify this search job and its results.
Species	Select the desired species. The species that appear in the list reflect the species available in the HD probe database for your application type.
Build Number	(Read-only) The name of the applicable genome build for the selected species. The HD probe database only contains probes that are designed to the most current genome build for each species.

Parameter	Instructions/Details
Probe Options	
Filters	Select one of the options below. If relevant, type a value for the filter in **FIlter Value.** Filters restrict the list of returned probes, based on specific criteria. • **None** – The search does not apply any of the filters in the list. • **Average Spacing** – In **Filter Value,** type the desired number of base pairs. This defines the average number of base pairs between the centers of the retrieved probes in each genomic interval. • **Probes Per Interval** – In **Filter Value,** type the desired number of probes. This defines the maximum number of probes that HD Search retrieves for each genomic interval. • **Total Probes** – In **Filter Value,** type the desired number of probes. This defines the total number of probes HD Search collectively retrieves for all specified genomic intervals.
Filter Value	(Available if you select a filter) Type the desired value for your selected filter.
Prefer Catalog Probes	(Available for HD-CGH probe searches, if you select a filter) To give preference to Agilent catalog probes in the probe selection process, mark this check box. If two probes are close to each other for a given probe interval, HD search selects the Agilent catalog probe.
Use TM Filter	Removes probes with T_Ms that produce unsatisfactory results on the Agilent platform. The search always applies this filter.
Similarity Filter	The options below can appear. The availability of specific options depends on species and application type. • **No Filter** – The program does not apply a similarity filter. If you select this option, the Use Non-Unique Probe Filter check box becomes available (see below). Non-unique probes map to more than one location in the target genome. • **Perfect Match Filter** – Removes a probe from the search results if it has more than one perfect match in the genome of the selected species. • **Similarity Score Filter** – Removes a probe from the search results if it is designed to a given genomic region, but it also has significant similarity to other parts of the target genome. Probes such as this can cause cross-hybridization problems.

Parameter	Instructions/Details
Use Non-Unique Probe Filter	(Available if you select no similarity filter) Mark this check box to remove a probe if it maps to multiple locations in the target genome. You can set the stringency of this filter. See below, "Max Perfect Genomic Hits."
Max Perfect Genomic Hits	(Available if you select no similarity filter, and mark **Use Non-Unique Probe Filter**) Sets the maximum number of locations to which a probe can map in the target genome, and still pass the non-unique probes filter. Type the desired number of locations. **Example:** Probe A maps to two locations in the target genome, and Probe B maps to three locations. You select **No Filter** in Similarity Filter, mark **Use Non-Unique Probe Filter,** and type 2 in Max Perfect Genomic Hits. The filter removes Probe B, but does not remove Probe A.
Interval Options	
Select HD Search by	**Genomic Intervals** – Sets up the search to retrieve probes based on genomic intervals that you enter. **Gene Annotations** – Sets up the search to retrieve probes based on gene annotations that you enter, such as gene symbols or GenBank accession numbers.
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined regions of your genomic intervals. **Example:** You type 500 in 5' base pairs and 300 in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.
Genomic Intervals	(Available if you select **Genomic Intervals** in Select HD Search By) Type either a chromosomal location or a cytoband in the box. Separate multiple intervals with pipe "|" characters. All of the intervals must be of the same type. For information about how to enter genomic intervals, see "Genomic Intervals (Simple HD and SNP Probe Searches)" on page 888. **Upload** – Opens a File Upload dialog box, where you can upload a file of chromosomal locations or cytobands. See "File Upload" on page 773 and "To upload data for probe searches" on page 101.

Parameter	Instructions/Details
Gene Annotations	(Available if you select **Gene Annotations** in Select HD Search By) Type a gene annotation such as a GenBank accession number (for example, NM_016660 or AY884282) or a gene symbol (for example, H3N2 or CTSB) in the box. Use pipe "|" characters to separate multiple annotations. eArray resolves annotations to genomic intervals before it starts your search. **Upload** – Opens a File Upload dialog box, where you can upload a *.txt file of gene annotations. In the file, list one accession or gene symbol per line. In a given search, the annotations must all be of the same type. See "File Upload" on page 773 and "Gene Annotations" on page 885.
Include Regions	(Available only for HD-CGH searches) Select one of the options below. You can use this parameter to limit your HD-CGH probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence." • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below, "Gene Confidence."
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.

Parameter	Instructions/Details
Exclude Options	
Standard Exclusion Interval(s)	eArray lets you select from among many sets of standard exclusion intervals, based on annotation tracks. To ignore genomic regions defined in one or more of these sets, mark this option, then select the desired set(s) from the list that appears. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option. **Upload** – Opens a File Upload dialog box, where you can upload a file of the desired genomic intervals. See "File Upload" on page 773 and "To upload data for probe searches" on page 101. You can set both standard and custom exclusion intervals in the same search.

Search Submits the search job to the eArray Web site.

Reset Clears all parameters, or restores them to their default values.

Simple Interval Finder

Figure 52 Simple Interval Finder pane

Purpose: Lets you set up and submit a search for genomic intervals whose annotation contains a specified search term. This type of search is available for the CGH, ChIP, CH3, and SureSelect Target Enrichment application types. The program can use the returned intervals in a Bait Tiling or Genomic Tiling job, or in an HD Probe Search. See these topics:

- "To do a Simple Interval Finder Search" on page 363
- "Searching for Agilent High Density (HD) Probes" on page 109

- "To set up a Genomic Tiling job" on page 176
- "To set up a Bait Tiling job" on page 378

To open: In the eArray$_{XD}$ tab, do one of the following:

- For the SureSelect Target Enrichment application type – Under **Tools,** click **Interval Finder > Simple Interval Finder.**
- For the CGH, ChIP-on-chip, and CH3 application types – Under **Search,** click **Probes > Simple Interval Finder.**

Search Criteria These search criteria appear in the pane:

Search Criterion	Instructions/Details
Search Term	(Required) Type a search term in the box. The program returns the genomic intervals whose annotation contains this term. The search term is not case-sensitive.
Species	(Required) Select the desired species from the list.

 (Available if the search pane is not hidden) Hides the search pane. This can help make the Search Result pane more convenient to view.

 (Available if the search pane is hidden) Shows the search pane.

Search Submits the search.

Reset Clears parameters, or restores them to their default values.

SNP ID Search (SNP probe search)

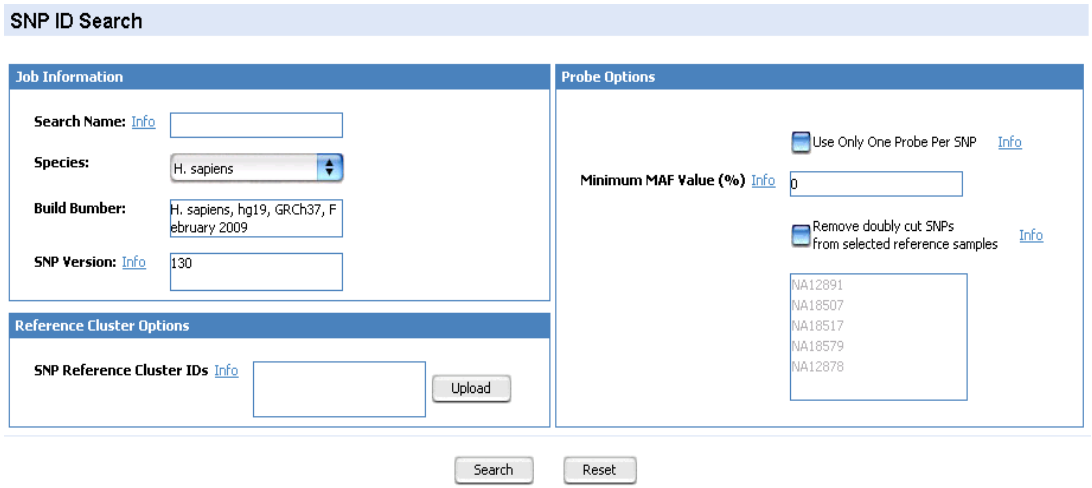


Figure 53 Search pane for a SNP Search by Reference Cluster IDs

Purpose: Lets you set up and submit a SNP Probe Search job, which returns Agilent SNP probes based on SNP database accession values that you enter. This type of search lets you retrieve probes that are associated with specific SNP sites in the genome. Agilent SNP probes are designed specifically for use in Agilent CGH+SNP microarrays. See "To do a SNP probe search by SNP ID" on page 150.

To open: In the eArray$_{XD}$ tab, under Search, click **SNP Probes > SNP ID Search.**

NOTE

To do a SNP probe search, you may first need to transfer SNP probe data from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Job Information

These items set the general parameters for the SNP probe search job. All parameters are required, except as noted.

Item	Instructions/Description
Search Name	Type a brief name to identify the search job.
Species	Select the desired species. The search returns Agilent SNP probes only for the selected species. Currently, the program supports human SNP probes.
Build Number	(Read-only) The build of the genome of the selected species to which the returned SNP probes are designed.
SNP Version	(Read only) The build of the SNP database of the selected species to which the returned SNP probes are designed.

Reference Cluster Options

In SNP Reference Cluster IDs, type the desired SNP database accession values. Separate multiple values with pipe "|" characters.

Example: `rs2825825|rs12329873|rs4818586`

Do not include the database identifier (i.e. type `rs2825825`, **not** `dbsnp|rs2825825`).

Upload – Opens a File Upload dialog box, where you can select a file of SNP reference cluster IDs to upload. See "File Upload" on page 773. The file must be a *.txt file that has one SNP reference cluster ID on each line.

Probe Options

These options let you filter the returned set of probes. All are optional, except as noted.

Option	Instructions/Description
Use Only One Probe per SNP	Most SNP sites are represented by two probes, one for each DNA strand. To return only the best probe for each SNP, mark this option. To select the best probe, the search selects the probe with the higher empirically-determined probe score. This probe score reflects the likelihood that a given probe will produce a good log ratio response when it is used on the Agilent CGH+SNP platform. **Note:** SNP probe scores are not available for download.

Option	Instructions/Description
Minimum MAF Value (%)	Type the desired value in the box. The minimum MAF can be a value from 0 to 50. The search returns probes for SNP sites whose MAFs are at least the entered value. To return probes without regard to MAF, enter a value of 0. The MAF (minor allele frequency) is the percentage of the total alleles in the population for a given SNP site that are the less common allele. Because the minor allele is present in the population, the MAF is always greater than 0%. Also, because the minor allele is the less common allele, the MAF is less than 50%.
Remove doubly cut SNPs from selected reference samples	When you use Agilent Genomic Workbench to analyze CGH+SNP array data, the program excludes data from SNP sites in which both of the alleles in the reference sample are cut by the AluI/RsaI enzyme mixture during the sample preparation process. These data are excluded because "cut" alleles generate essentially no signal, and the reported log ratio value [log (sample/reference)] would involve division by a very small number. This would cause an extremely high, spurious log ratio value to be reported. This option lets you exclude the SNP probes from your design that are associated with these "doubly cut" reference SNP sites. The data from these probes would be excluded from the analysis anyway. eArray currently supports five HapMap reference samples. By default, the program selects all five references, which excludes such probes that are found in any of the references. • To exclude such probes, mark **Remove doubly cut SNPs from selected reference samples,** then click the name of the desired reference sample. To select additional reference samples, control-click their names. • If you intend to use a custom, known genotyped reference when you analyze the data from your CGH+SNP array, clear **Remove doubly cut SNPs from selected reference samples.** This returns SNP probes without regard to whether or not they interrogate doubly cut SNP sites in any of the standard references.

Search Submits the search job to your Agilent Genomic Workbench server.

Reset Clears the search pane.

Dialog Boxes

This section describes the dialog boxes that can appear when you use eArray$_{XD}$ to design and submit custom microarray designs and SureSelect Target Enrichment libraries. Dialog boxes appear in alphabetical order.

Add Baits to Bait Group

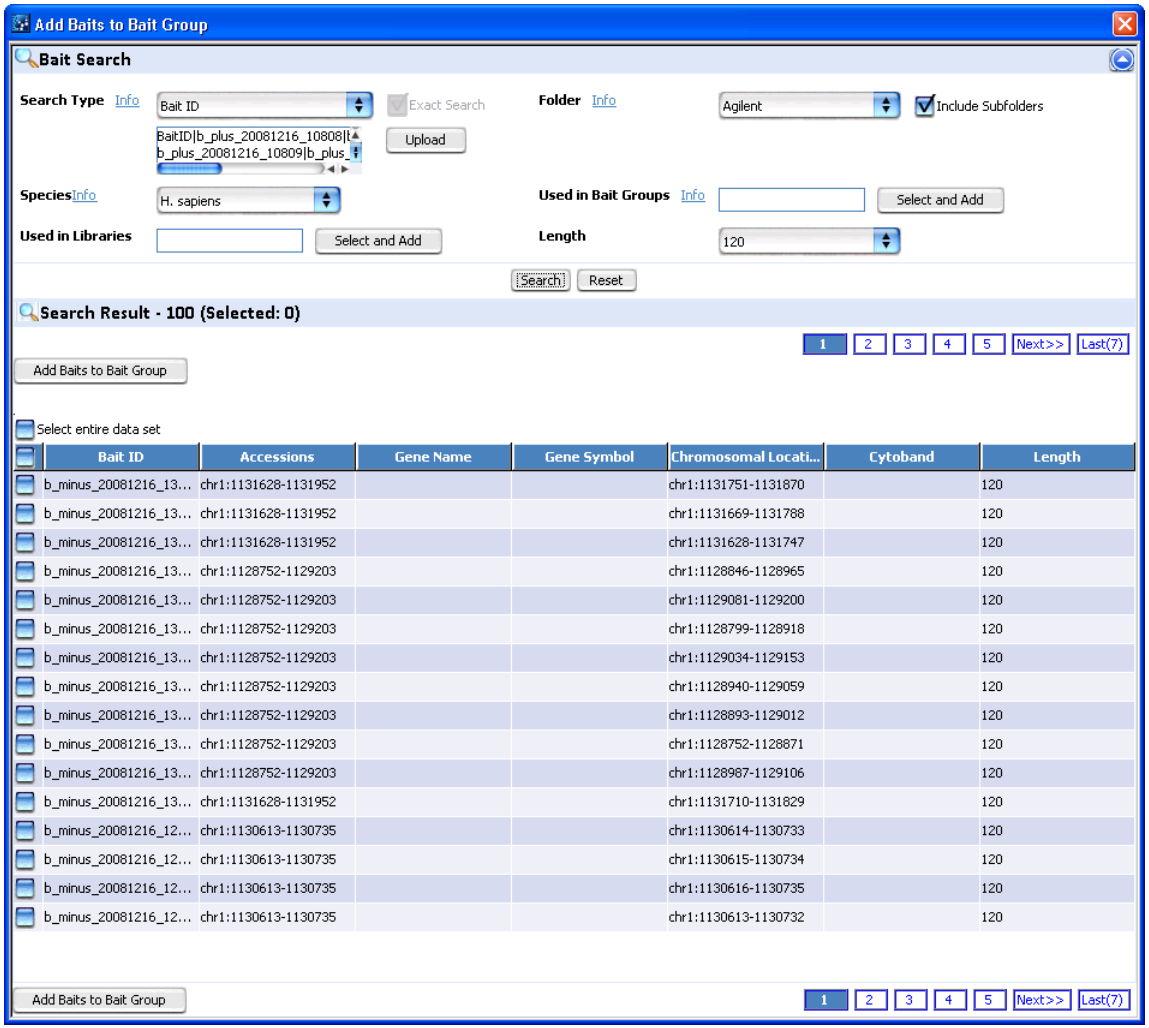


Figure 54 Add Baits to Bait Group dialog box

Purpose: Lets you add additional baits to a bait group as you create or edit it. You retrieve the additional baits with a Bait Search. See "To create a bait group from existing baits" on page 401 and "To edit a bait group" on page 406.

To open: In the Create Bait Group or Edit Bait Group dialog box, in the Search Result pane, click **Add New Baits.** See "Create Bait Group" on page 621 and "Edit Bait Group" on page 737.

Bait Search pane

Search criteria For details on the search criteria in this pane, see "Bait Search" on page 538.

Search Starts the search.

Reset Clears the search parameters.

Search Result pane

Table of search results Displays the baits that match your search criteria.

Columns:

- **Check boxes** – Let you select the specific baits to be added to the bait group. Mark the desired baits. To select all of the baits on the current page, mark the check box column heading. The program remembers your selections as you go from page to page.
- **Bait ID** – The unique name for each bait.
- The availability of data for the other annotation columns in the table varies by bait.

Select entire data set Selects all of the baits on all pages of the search results for inclusion in your bait group.

Add Baits to Bait Group Adds all of the selected baits to your bait group, and closes the dialog box.

Page Buttons – Go to specific pages of search results. The highlighted button shows the current page.

Add Probes to Probe Group

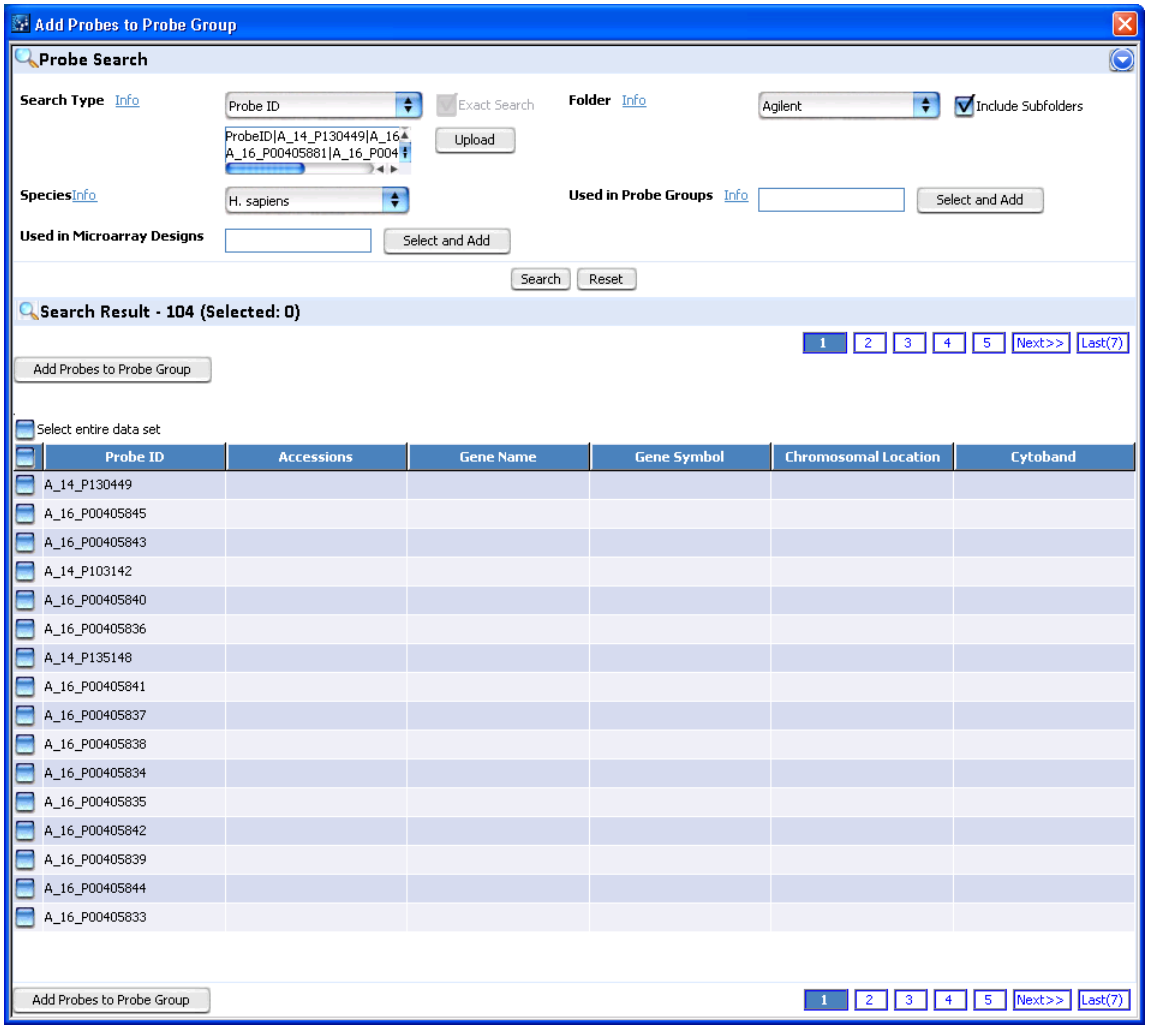


Figure 55 Add Probes to Probe Group dialog box

Purpose: Lets you search for and add additional probes as you create, copy, or edit a probe group. See these topics:

- "To create a new probe group" on page 223

- "To copy a probe group" on page 230
- "To edit a probe group" on page 234

To open: In the **Search Result** pane of the Create Probe Group, Copy Probe Group, or Edit Probe Group dialog box, click **Add New Probes.** See "Create Probe Group" on page 678, "Copy Probe Group" on page 618, and "Edit Probe Group" on page 771.

Probe Search pane

Search Criteria For information on the search criteria that appear in this pane, see "Probe Search" on page 560.

Search Starts the search.

Reset Clears the search parameters.

Search Result pane

Table of search results Displays the probes that match your search criteria.

Columns:

- **Check boxes** – Let you select the specific probes to be added to the probe group. Mark the desired probes. To select all of the probes on the current page, mark the check box column heading. The program remembers your selections as you navigate from page to page.
- **Probe ID** – The unique probe name for each probe.
- The availability of data for the other annotation columns in the table varies by probe.

Select entire data Selects all of the probes on all pages of the search results for inclusion in your probe group.

Add Probes to Probe Group Adds all of the selected probes to your probe group, and closes the dialog box.

1 2 3 **Page Buttons** – Go to specific pages of search results. The highlighted button shows the current page.

NOTE You cannot add HD probes or SNP probes to a probe group. Instead, create a new HD or SNP probe group. See "Searching for Agilent High Density (HD) Probes" on page 109 and "Searching for Agilent SNP Probes" on page 138.

Advanced Search Intervals

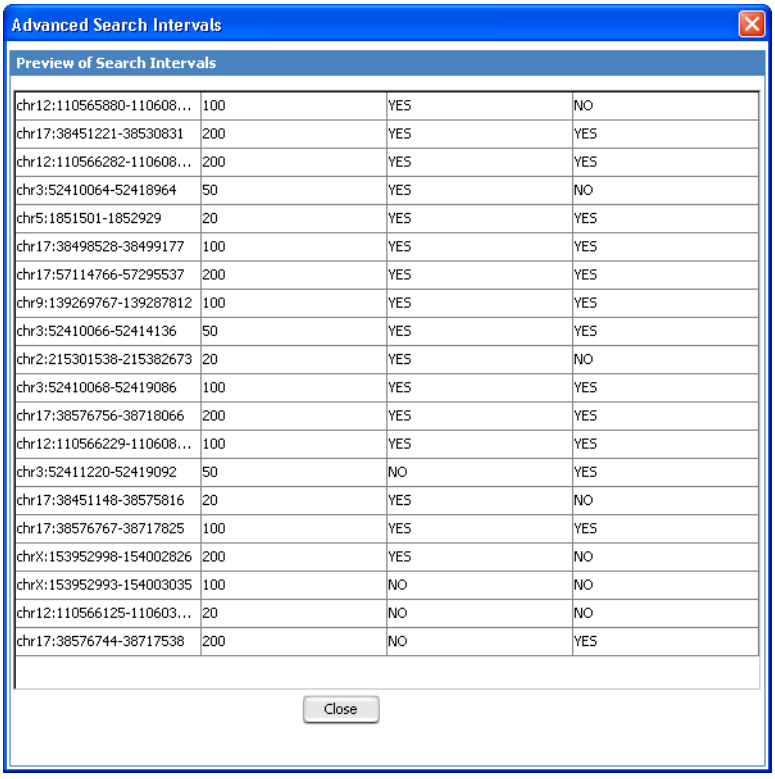


Figure 56 Advanced Search Intervals dialog box

Purpose: Lets you view all of the intervals in your uploaded file for an Advanced Genomic Intervals HD Probe Search. See "To do an Advanced Genomic Intervals HD Search for probes" on page 117. This dialog box also appears, for the same purpose, when you use a wizard to create a microarray design from HD database probes. See "To create a microarray design with HD probes" on page 297 and "Create Microarray Design (HD Probes wizard)" on page 656.

To open: When you set up an Advanced Genomic Intervals HD search for probes, in the **Preview of Search Intervals** pane, click **Show All.**

Table Columns

- **Column 1** – The genomic intervals in the uploaded file.

- **Column 2** – The number of probes to be returned for each interval.
- **Column 3** – **Yes** if T_M filtering will be applied to the returned probes for the interval, **No** if T_M filtering will not be applied.
- **Column 4** – **Yes** if homology filtering will be applied to the returned probes for the interval, **No** if homology filtering will not be applied.

Close Closes the dialog box.

Agilent Literature Search Sentences

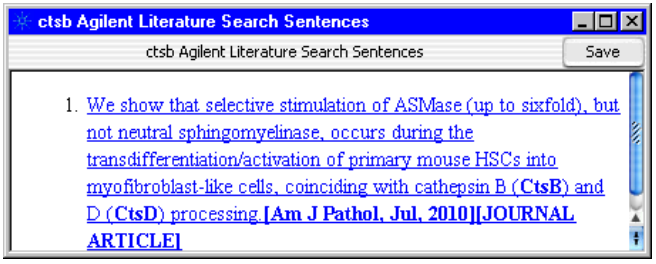


Figure 57 Agilent Literature Search Sentences dialog box

Purpose: After you do a literature search, and the program constructs a custom biological network based on an analysis of the returned abstracts, this dialog box lets you see the sentence(s) from the literature search that produced selected nodes. See "To use a literature search to create a custom network" on page 186.

To open: After you do a Literature Search, in the Literature Network Inspector, right-click a node, then click **Show Sentences.** Alternatively, in the Literature Network Inspector, select one or more nodes, right-click a node, then click **Show Sentences.** See "Literature Network Inspector" on page 794.

Save Opens a dialog box, where you can select a location to save an HTML file. This file contains all of the sentences in the Literature Search Sentences dialog box, and preserves the hyperlinks to the abstracts from which the sentences were derived.

Main pane The main pane of the dialog box contains a list of sentences from which nodes and interactions in the custom network were derived. The sentences that appear depend on how you opened the dialog box:

- If you right-clicked a selected node, sentences appear for all of the selected nodes.
- If you right-clicked an unselected node, sentence(s) appear for that node, plus any selected nodes.

Each sentence appears as a link. If you click the link, the relevant abstract opens in your Web browser, in the appropriate search engine.

Array Layout

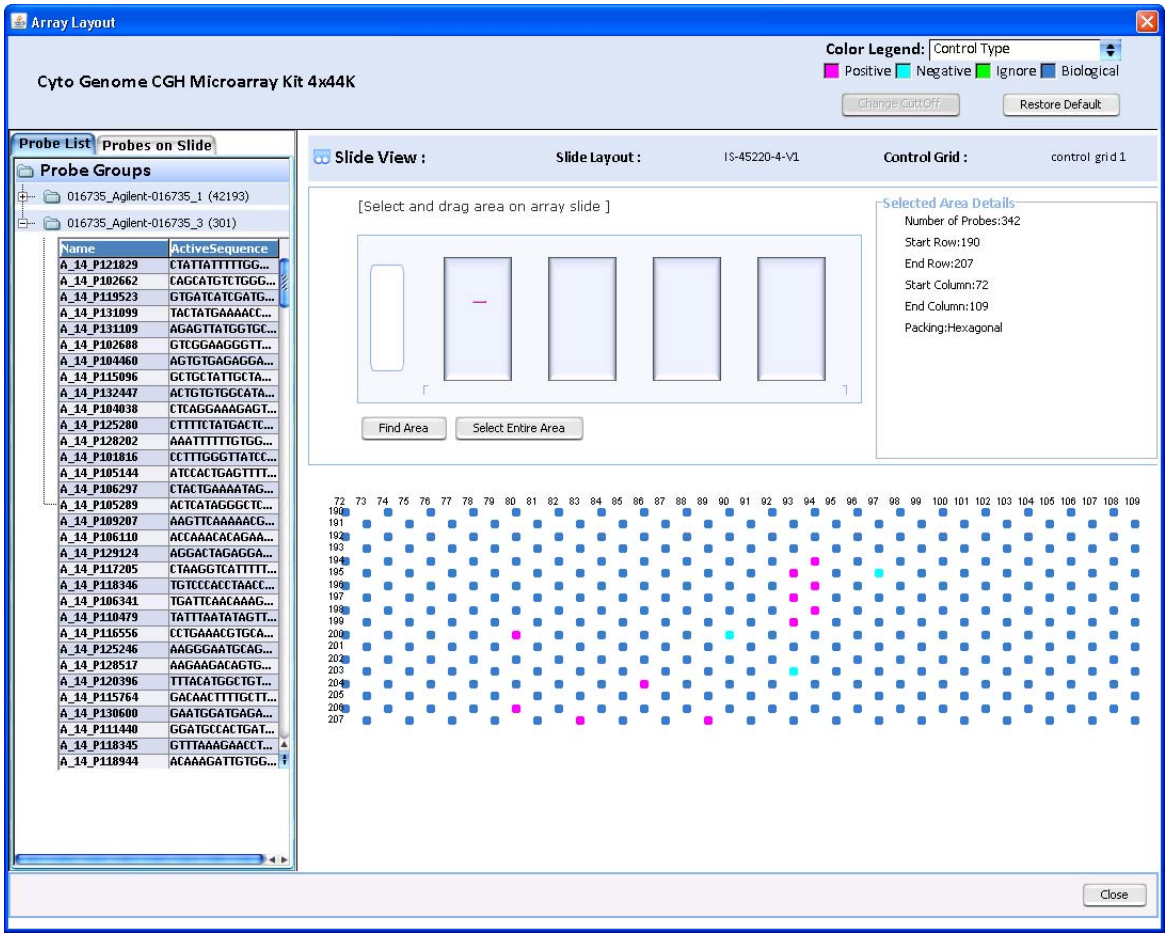


Figure 58 Array Layout dialog box

Purpose: (Available for all microarray application types) Lets you view the probes in a microarray design as they will be laid out on the glass microarray slide. You can color code probes based on their control types, probe scores, or T_Ms. The microarray design must have a status of Complete or Submitted. See "To view the layout of probes on a microarray graphically" on page 306.

To open: In the Design Data pane of the Navigator, right click the name of a microarray design, then click **ArrayVisualizer.** If this command does not appear, you must first update the Agilent content in the microarray design. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Name (Read-only) The name of the microarray design whose probe layout appears in the dialog box.

Color Legend The color-coding options for probes in Slide View, These options can appear:

Option	Description
Control Type	Color codes probes based on their control types, as indicated in the legend. These control types are available in eArray: • **biological** – Identifies the probe group as a non-control probe group (condition = **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. Once a microarray design is submitted, the control types of its probe groups cannot be changed, so the only way to "re-activate" these probe groups, if desired, would be to modify the ControlType field of the design file. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample.
Probe Score	(CGH and ChIP-on-chip application types) Color codes probes based on their probe performance scores, as indicated in the legend. A probe performance score indicates the likelihood that a probe will produce a good log ratio response when it is used on the Agilent microarray platform. See "To calculate probe performance scores" on page 214.
Tm	Color codes probes based on their predicted Tm with their targets, as indicated in the legend.

Color swatches Color swatches appear with labels that identify the meaning of each color. These labels depend on the options that you select in Color Legend.

To change the color that is assigned to a color swatch, click the color swatch. The Choose Color Background dialog box opens. From this dialog box, you can select the desired color in several different ways. See "Select Background Color" on page 848.

Change Cutoff (Available when you select Probe Score or Tm in Color Legend) Opens an Input dialog box, where you can type a cutoff value for the selected property. The program displays probes in different colors based on this value.

Restore Default Restores the colors in Color Legend to the original ones before you made any changes to them.

Probe List tab

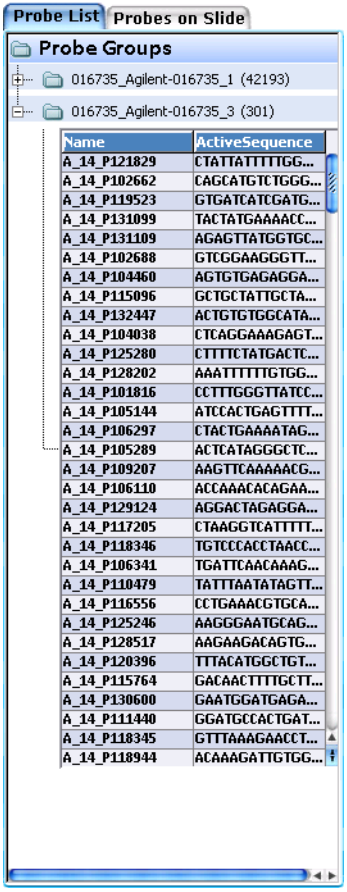
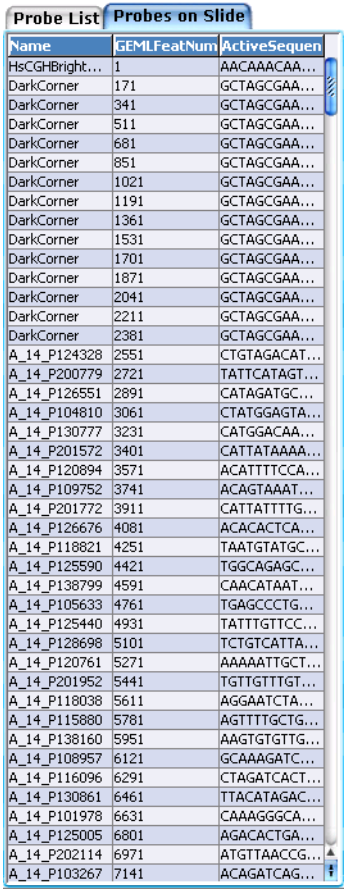


Figure 59 Array Layout dialog box – Probe List tab

Probe Groups This tab organizes the probes in the microarray design by probe group. These icons can appear:

Icon	Description
	A probe group folder that contains the names and sequences of the probes in a specific probe group.
	Expands a probe group folder to display the probe IDs and sequences of the probes in the probe group.
	Collapses a probe group folder to hide the probes in the probe group.

Probes on Slide tab



Name	GEMLFeatNum	ActiveSequen
HsCGHBright...	1	AACAAACAA...
DarkCorner	171	GCTAGCGAA...
DarkCorner	341	GCTAGCGAA...
DarkCorner	511	GCTAGCGAA...
DarkCorner	681	GCTAGCGAA...
DarkCorner	851	GCTAGCGAA...
DarkCorner	1021	GCTAGCGAA...
DarkCorner	1191	GCTAGCGAA...
DarkCorner	1361	GCTAGCGAA...
DarkCorner	1531	GCTAGCGAA...
DarkCorner	1701	GCTAGCGAA...
DarkCorner	1871	GCTAGCGAA...
DarkCorner	2041	GCTAGCGAA...
DarkCorner	2211	GCTAGCGAA...
DarkCorner	2381	GCTAGCGAA...
A_14_P124328	2551	CTGTAGACAT...
A_14_P200779	2721	TATTCATAGT...
A_14_P126551	2891	CATAGATGC...
A_14_P104810	3061	CTATGGAGTA...
A_14_P130777	3231	CATGGACAA...
A_14_P201572	3401	CATTATAAAA...
A_14_P120894	3571	ACATTTTCCA...
A_14_P109752	3741	ACAGTAAAT...
A_14_P201772	3911	CATTATTTTG...
A_14_P126676	4081	ACACACTCA...
A_14_P118821	4251	TAATGTATGC...
A_14_P125590	4421	TGGCAGAGC...
A_14_P138799	4591	CAACATAAT...
A_14_P105633	4761	TGAGCCCTG...
A_14_P125440	4931	TATTTGTTCC...
A_14_P128698	5101	TCTGTCATTA...
A_14_P120761	5271	AAAAATTGCT...
A_14_P201952	5441	TGTTGTTTGT...
A_14_P118038	5611	AGGAATCTA...
A_14_P115880	5781	AGTTTTGCTG...
A_14_P138160	5951	AAGTGTGTTG...
A_14_P108957	6121	GCAAAGATC...
A_14_P116096	6291	CTAGATCACT...
A_14_P130861	6461	TTACATAGAC...
A_14_P101978	6631	CAAAGGGCA...
A_14_P125005	6801	AGACACTGA...
A_14_P202114	6971	ATGTTAACCG...
A_14_P103267	7141	ACAGATCAG...

Figure 60 Array Layout dialog box – Probes on Slide tab

This tab lists all of the probes in the microarray design in the order in which they appear in the GEML design file. You can use the up and down arrows on your keyboard, as well as the scroll bar on the side of the tab, to go through the list of probes.

Name Displays the full name of each probe. To view the full name for any item in this column, double-click the entry, then press the right-arrow key on your keyboard.

GEML FeatNum The GEML Feature Number. Lists the order in which each probe appears in the GEML design file. The program lays out probes in order in rows from left to right in “book reading” fashion.

Active Sequence The nucleotide sequence of the active, hybridizing portion of each probe. To view the full sequence for any probe, double-click the entry, then press the right-arrow key on your keyboard. The sequences that appear in this column do not include any linker sequences.

Slide View

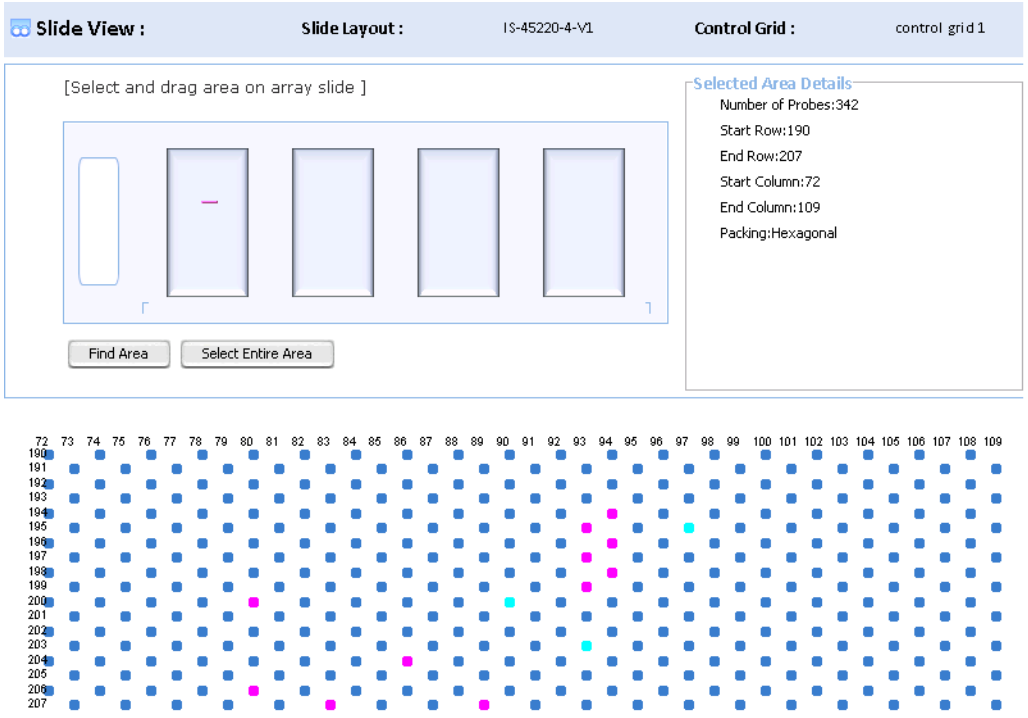


Figure 61 Array Layout dialog box – Slide View

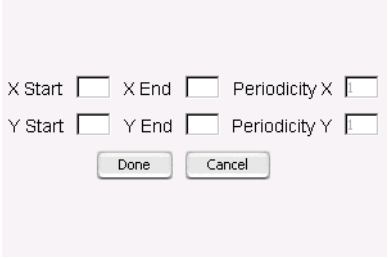
Slide Layout The name of the microarray design format. Design formats set the number of features in a microarray, and the number of replicate arrays that appear on one slide.

Control Grid The name of the required Agilent quality control grid that appears on each microarray on the slide.

Microarray Slide diagram Diagram of the entire microarray slide. The slide appears probe side up, with the barcode on the left. Each raised rectangle represents one array.

To select a region of an array to view, drag the pointer diagonally across the desired region in the left-most array. The program highlights the selected region in pink, and shows an expanded view of the region in the bottom pane of Slide View.

Find Area Opens a dialog box, where you can enter the coordinates of the desired region of the array.



Item	Description
X Start	The first column in the desired region
X End	The last column in the desired region
Periodicity X	Currently, this item is always set to 1, which displays all columns in the selected region.
Y Start	The first row in the desired region.
Y End	The last row in the desired region
Periodicity Y	Currently, this item is always set to 1, which displays all rows in the selected region.
Done	Selects the region that you defined, and closes the dialog box. The program highlights this region in the diagram of the microarray, and displays an expanded view of the region in Layout View
Cancel	Closes the dialog box without selecting a region.

Select Entire Area Selects all of the features in the microarray design. The program highlights the left-most array on the slide. An expanded view of the region appears in the bottom pane of Slide View.

Selected Area Details These details appear :

Detail	Description
Number of Probes	Total number of probes in the selected region.
Start Row	First row of probes in the selected region
End Row	Last row of probes in the selected region
Start Column	First column of probes in the selected region
End Column	Last column of probes in the selected region
Packing	Geometric orientation of each feature on the array with respect to other features. One of these packing arrangements appears: • **Hexagonal** – Features are laid out on the slide so that each successive row is staggered from the previous one. Each feature is surrounded by six other features, except at the edges of the array. • **Rectilinear** – Features are laid out on the array so that the features in each successive row line up exactly with those in the previous one.

Diagram of selected region Shows an expanded view of the probes in the selected region, using the color scheme shown in Color Legend. In addition, when you place the cursor over each feature, a ToolTip appears that lists the feature number, the ID of the probe (if any) that occupies the feature, and the control type, probe score, and T_M of the probe, if available.

The numbers across the top of the diagram are column numbers (X), and the numbers on the left edge of the diagram are row numbers (Y).

Add/Remove Attachments

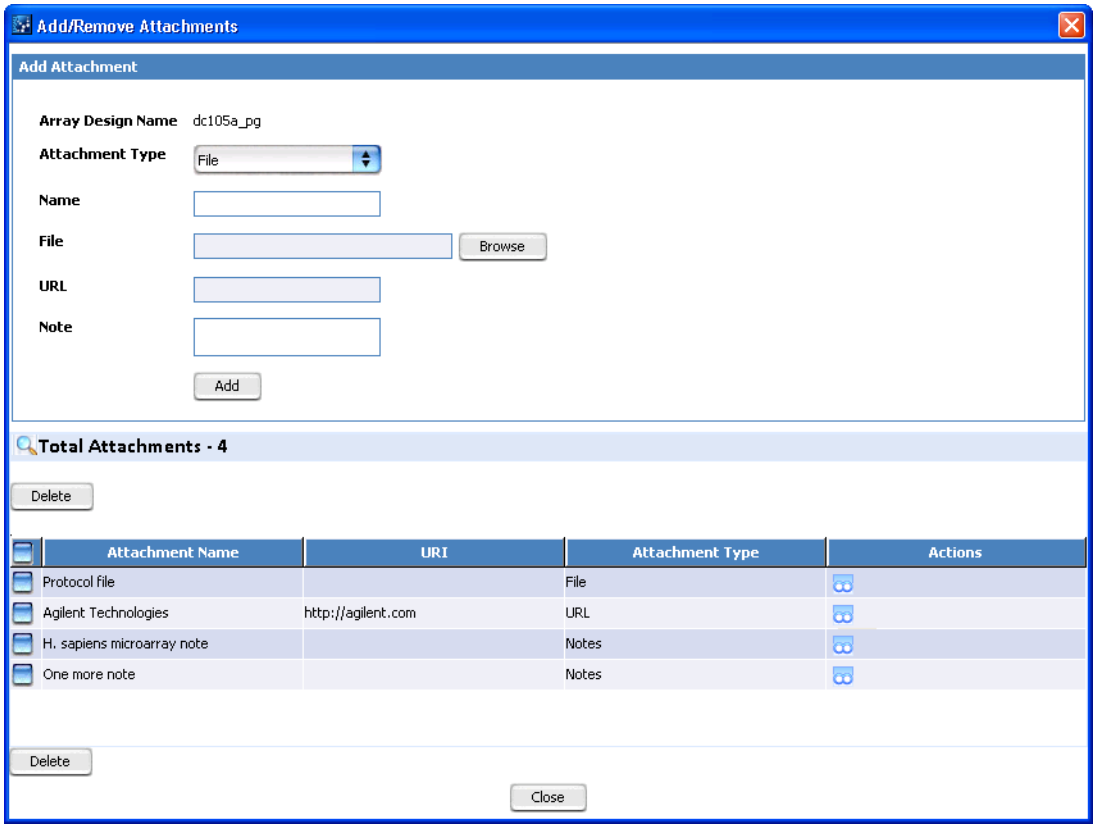


Figure 62 Add/Remove Attachments dialog box.

Purpose: Lets you attach, open, and remove notes, files, and URLs from a probe group, bait group, microarray design, or library. You can add an attachment to any item to which you have access, except those from the Agilent Catalog. See these topics:

"To add an attachment to a probe group" on page 243

"To add an attachment to a microarray design" on page 320

"To attach a file, note, or URL to a bait group or library" on page 444

To open: In the Design Data pane of the Navigator, right-click the name of a probe group, bait group, library or microarray design, then click **Attach.**

Top pane

Attachment Type Lets you select a type of attachment to add. These options are available:

- **File** – A file on your computer of any type.
- **URL** – The address of a Web page, or other external or internal resource.
- **Notes** – Text

Name The display name for the file or URL. The program uses this name to identify the item in the list of attachments to the microarray design or probe group.

File (Available when you select **File** in Attachment Type) The location of the file to be attached.

Choose – Opens an Open dialog box, where you can select a file to attach

URL (Available when you select **URL** in Attachment Type) The complete URL of the Web page or other resource—for example, `http://chem.agilent.com`

Note (Available when you select **Notes** in Attachment Type) The text that will be attached.

Add Attaches the note, file or URL, and displays an entry for it in the Total Attachments pane.

Total Attachments pane

This pane displays the files and URLs that are currently attached to the probe group or microarray design. The number in the title of this pane indicates the umber of files and URLs that are attached to the microarray design or probe group. If there are no attached notes, files, or URLs, the name of this pane is *Search Result.*

Columns These columns appear in the dialog box:

Column	Description
Check box column	Lets you select attachments to be opened or removed. • To select an attachment, mark the check box next to its name. • To select all of the attachments on the page, mark the check box in the column heading row. • The program remembers your selections as you go from page to page.
Attachment Name	The display name of the attachment, as specified by the person who attached the item.
URL	The complete URL of an attached Web page or other resource
Attachment Type	Shows the type of attachment, which can be Notes, File, or URL.
Actions	 – Lets you view the attachment. • Notes open in the Note pane. See "Note" on page 825. • URLs open in your Web browser. • Files open in the appropriate program, if it exists on your computer.

Open Opens the selected file(s) in the relevant program, if available. Opens the selected URL(s) in your Web browser.

Delete Removes selected URLs or file(s) from the probe group or microarray design.

Page Buttons – Go to specific pages of search results. The highlighted button shows the current page.

Close Closes the dialog box.

NOTE

To add an attachment to an item, you may first need to transfer it from the eArray Web site to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer probe or bait data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Bait Statistics

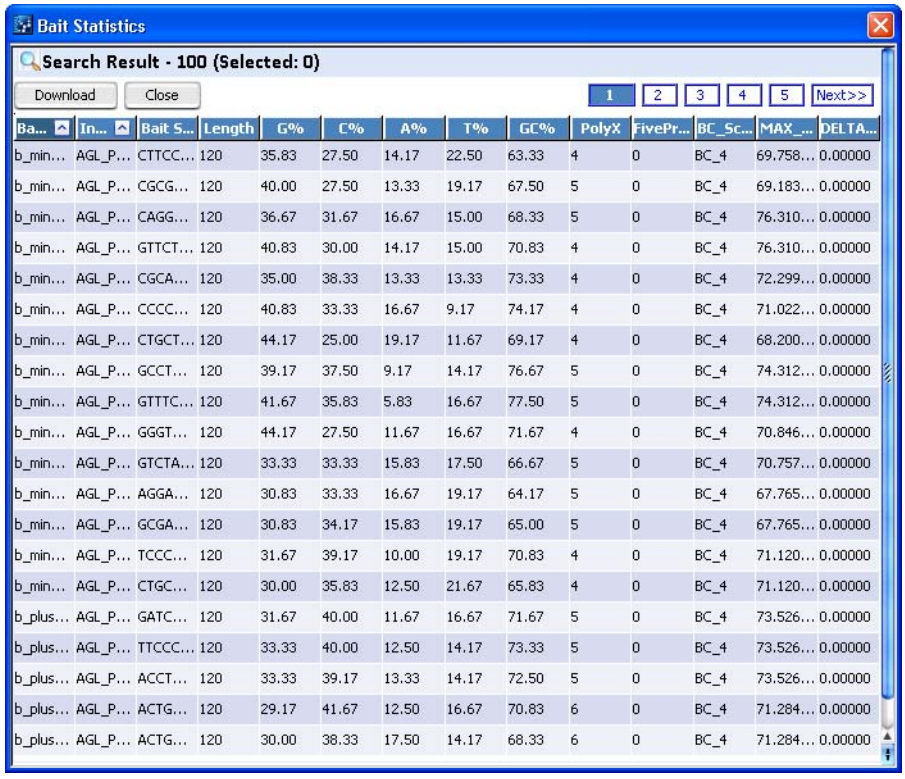


Figure 63 Bait Statistics dialog box

Purpose: (Available for the SureSelect Target Enrichment application type) Displays the names and sequences of baits, and calculated statistics based on their nucleotide sequences.

To open: In the Search Result pane of a bait search, select the desired baits, then click **Show Statistics.** See "To view bait details and statistics" on page 362.

Alternatively, view a bait group. From the View Bait Group dialog box, click **Show Statistics.** See "To view a bait group" on page 399.

Bait ID The name of each bait. For user baits, this is the user-provided name of each bait.

Internal ID The system-generated identification code of the bait within the database on your server.

Bait Sequence The nucleotide sequence of each bait in 5' to 3' orientation.

Additional Statistics These statistics are derived from the nucleotide sequence of each bait.

Statistic	Description	Example
Length	The number of nucleotides in the bait	A given bait has 120 nucleotides. Length = 120
G%	Percentage of bases in the bait sequence that are G bases	Same probe as above: 46 Gs; %G = 38.33%
C%	Percentage of bases in the bait sequence that are C bases	Same probe as above: 16 Cs; %C = 13.33%
A%	Percentage of bases in the bait sequence that are A bases	Same probe as above: 25 As; %A = 20.83%
T%	Percentage of bases in the bait sequence that are T bases	Same probe as above: 33Ts; %T = 27.50%
GC%	Percentage of bases in the bait sequence that are, collectively, G and C bases	Same probe as above: 46 Gs and 16 C's. %GC = 51.67%
PolyX	The longest homeomeric run (run of one type of base) in the bait sequence, represented as the number bases in the run.	CATTAGTTTATG has a PolyX of 3 because it contains a run of three Ts.
FivePrimeAs	The length of any poly A sequence on the 5' end of the bait	AAAAAATTGCATTA FivePrimeAs = 6
BC_Score	Base Composition Score – A numeric value that defines the quality of the bait, based upon its base composition and distribution	BC_1 is the best, and BC_Poor is the worst.

Statistic	Description	Example
MAX_SUBSEQ_TM	The highest calculated Tm of a moving window of 20 bp regions within the bait	
DELTA_G	The calculated ΔG of self-folding. This indicates how likely it is that the bait will fold in on itself, which can affect both the bait manufacturing process as well as the pull-down of the desired genomic fragments.	

Download Opens a Save dialog box, where you can download the information in the dialog box as a TDT format file. You can open this file in a word processing or spreadsheet program.

Close Closes the dialog box.

Page Buttons – Go to specific pages of search results. The highlighted button shows the current page.

Bait Tiling

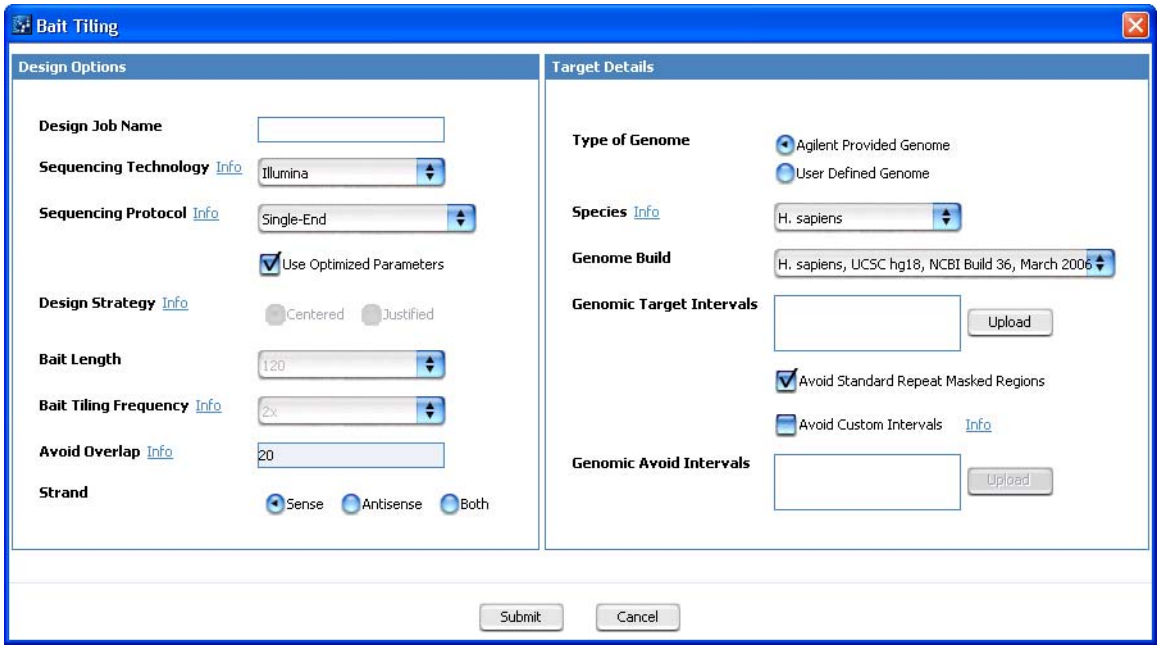


Figure 64 Bait Tiling dialog box

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you set parameters for a Bait Tiling job. Bait Tiling generates baits that evenly cover selected regions of a specified genome. See "To set up a Bait Tiling job" on page 378.

To open: In the eArray$_{XD}$ tab, under Create Bait, click **Bait Tiling.**

Design Options These job options appear:

Option	Instructions/Details
Design Job Name	Type a name that will later enable you to identify the Bait Tiling job.
Sequencing Technology	From the list, select the type of DNA sequencer you will use to analyze your target DNA fragments.

Option	Instructions/Details
Sequencing Protocol	Select the desired protocol. In the list, eArray displays the available protocols for your chosen DNA sequencing technology.
Use Optimized Parameters	In general, mark **Use Optimized Parameters.** With this option, based on your selected sequencing technology and protocol, the program automatically sets the best values for Design Strategy, Bait Length, Bait Tiling Frequency, and Avoid Overlap. To set all of these options manually, clear **Use Optimized Parameters.** The options all become available.
Design Strategy	(Available if you clear **Use Optimized Parameters.**) Select one of these options: • **Centered** – eArray centers sets of tiled baits over their respective target intervals. That is, each set of baits hangs over both ends of its target interval by equal amounts. This option exactly respects the value you select for Bait Tiling frequency. • **Justified** – eArray designs sets of tiled baits to exactly cover their respective target intervals. This option adjusts the overlap of baits to achieve the precise and even tiling of only the target intervals, without any overhang into non-target regions. With this option, the actual tiling frequency can deviate from the value you select in Bait Tiling Frequency.
Bait Length	(Available if you clear **Use Optimized Parameters.**) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Bait Tiling Frequency	(Available if you clear **Use Optimized Parameters.**) Select the desired tiling frequency. This setting controls the density of tiling. The density can also be affected by your choice of Design Strategy. • **2x** – eArray overlaps baits by 50% as it tiles each interval. Two baits cover each base in each interval. This is the default tiling frequency. • **3x** – eArray overlaps baits as it tiles each interval so that three baits cover each base in each interval. • **4x** – eArray overlaps baits as it tiles each interval so that four baits cover each base in each interval. • **5x** – eArray overlaps baits as it tiles each interval so that five baits cover each base in each interval. **Note:** The exact density of tiling depends on your other settings. It can be somewhat less than that indicated above at the extreme 5' and 3' ends of each interval.

Option	Instructions/Details
Avoid Overlap	(Available if you clear **Use Optimized Parameters.**) To change the value, select it, then type the desired distance in base pairs. The program creates baits that can extend by this distance into the regions that are specified in Genomic Avoid Intervals (see below). For best results, set this distance to a maximum of 20 bp. Do not include the unit.
Strand	Select one of these options: • **Sense** – Produces baits that are similar in sequence to the sense strand of the target genomic DNA. • **Antisense** – Produces baits that are complementary to the sense strand of the target genomic DNA. • **Both** – Produces both a sense bait and an antisense bait for each target location. **Note:** In general, if you use the library to enrich genomic targets, either sense or antisense baits will work. For the enrichment of cDNA targets, the selection of sense vs. antisense baits is important, since genes can appear on either strand.

Target Details These options appear:

Option	Instructions/Details
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Lets you select one of the standard genomes available in eArray for the Bait Tiling job. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. • **User Defined Genome** – Lets you select a genome that you have uploaded to your server for the Bait Tiling job. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. To import a user-defined genome, see "To import a new genome" on page 66.
Species	Select the desired species. This sets the species of the genome to which baits will be designed.
Genome Build	Select the desired genome build. For Agilent-provided genomes, only the most recent build of the genome for the selected species is available.

Option	Instructions/Details
Genomic Target Intervals	Target intervals are the genomic intervals to which baits will be designed. Use this format for target intervals: `chrN:<start>-<end>` **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. **Upload** – Opens a dialog box that lets you upload a file of genomic target intervals. The file must be a *.txt file with one interval per line. End each line with a **new line** character—in a word processor, press **Enter** at the end of each line.
Avoid Standard Repeat Masked Regions	If you mark this option, the program excludes a standard set of repetitive genomic regions from the Bait Tiling process. These are regions of the genome that generally produce poor quality baits. This option is marked by default. When you tile a user-imported genome, these repeat regions are the sequences that are represented by lower case letters in your sequence files, if you marked Genome is Soft Masked when you imported the genome.
Avoid Custom Intervals	If you mark this option, Genomic Avoid Intervals becomes available, where you can enter custom intervals to avoid during the Bait Tiling process. You can avoid both standard and custom intervals in the same Bait Tiling job.
Genomic Avoid Intervals	(Available if you mark **Avoid Custom Intervals**) During the Bait Tiling Process, the program avoids intervals that you define. Use this format to define each genomic interval: `chrX:<start>-<end>` **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. **Upload** – Opens a dialog box that lets you upload a file of custom avoid intervals. The file must be a *.txt file with one interval per line. End each line with a new line character—in a word processor, press **Enter** at the end of each line.

Submit Submits the Bait Tiling job, creates an entry in the Tasks pane of the Navigator, and closes the dialog box.

Cancel Closes the dialog box, and does not submit a Bait Tiling job.

Bait Upload

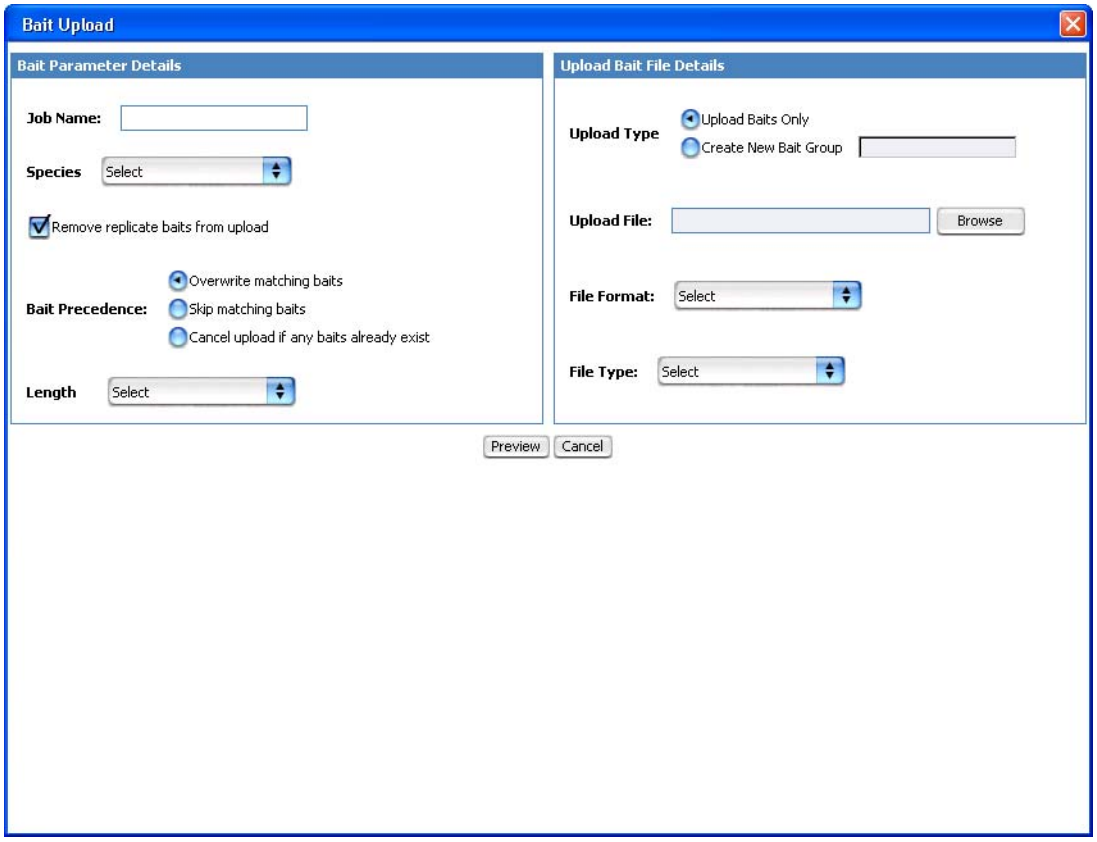


Figure 65 Bait Upload dialog box

Purpose: Lets you set up and submit a bait upload job. Bait uploads transfer bait sequences and annotation to your server. They are available for the SureSelect Target Enrichment application type. See "To upload baits and annotation" on page 374.

To open: In the eArray$_{XD}$ tab, under Create Bait, click **Bait Upload.**

Bait Parameter Details

Detail	Instructions/Comments
Job Name	Type a name that will help you to identify this job.
Species	Select the desired species. The program associates all baits in the uploaded file with this species.
Remove Replicate Baits from Upload	Mark this option to upload the first bait in each set of replicate baits in your file, and ignore the others. A replicate bait has the same Bait ID as another bait in the file. If your bait file contains replicate baits, and you do **not** mark **Remove replicate baits from upload,** the program does not upload your file.
Bait Precedence	These options define what the program does if it finds baits in your uploaded file that have the same Bait ID as baits that already exist in the system. Select one of these options: • **Overwrite matching baits** – The annotation of the matching uploaded baits replaces the annotation of the existing baits. You can use this option to reannotate existing baits. • **Skip matching baits** – The program ignores matching uploaded baits, but does upload other baits. • **Cancel upload if any baits already exist** – The program cancels the entire upload process if it finds a matching uploaded bait.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.

Upload Bait File Details

Detail	Instructions/Comments
Upload Type	Select one of these options: • **Upload baits only** – Creates baits from the data in the uploaded file, and makes them available to you in the program as individual baits. • **Create new bait group** – In the box, type a name for the bait group. The bait group name can contain up to 100 characters. The program creates baits from the data in the uploaded file, and creates a bait group that contains the uploaded baits. The program saves the new bait group to your main "default" folder, and the baits are also available to you as individual baits.
Upload File	Follow these steps to select the file of bait sequences and annotation for upload: **a** Click **Browse.** An Open dialog box appears. **b** Select the desired file, then click **Open.** The location of the file appears in Upload File.
File Format	Select **MINIMAL** or **COMPLETE.** The file format defines the specific types of data that are available in the uploaded file. See "To prepare a file of baits and annotation for upload" on page 371.
File Type	Select the appropriate file type from the list. The file type defines how the data items in the file are specified and separated. The program accepts tab-delimited text (*.tdt and *.txt) and Microsoft Excel (*.xls) files. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

Preview Temporarily uploads and displays the first few lines of your file in a new Define Uploaded File Columns pane of the dialog box. See Figure 66.

Cancel Closes the dialog box without uploading your file.

Define Uploaded File Columns

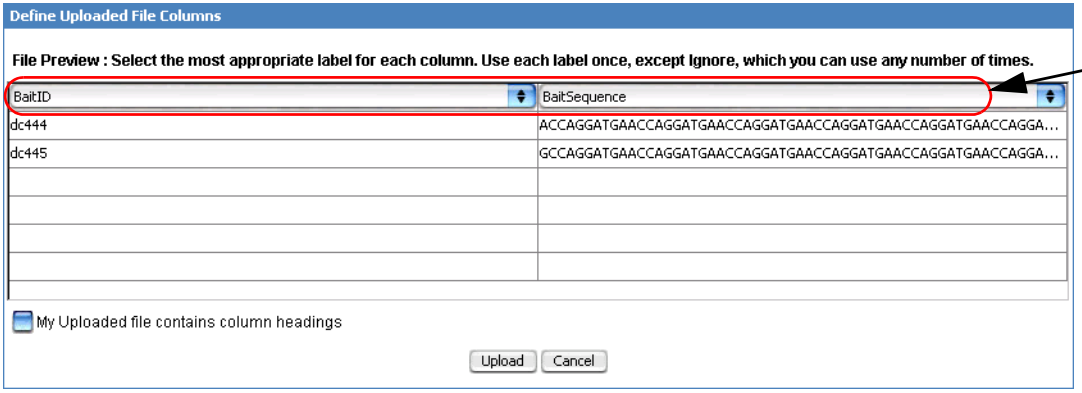


Figure 66 Bait Upload dialog box – Define Uploaded File Columns pane

The Define Uploaded File Columns pane (see Figure 66) lets you label the columns of data in your uploaded bait file. It displays the first few lines of your bait file. For each column, you select the column label that best identifies its contents.

Column Labels Select the most appropriate label for each column. Use every label exactly once, except Ignore, which you can use any number of times. Select **Ignore** for extra columns that do not apply to the selected upload format.

My uploaded file contains column headings If you mark this option, the program ignores the first line of your file. Otherwise, the program interprets all lines in your file as actual bait data. The program does not interpret column headings, even if you mark this option.

Upload Submits the job. The system checks the format and content of your file. If your file passes this validation, the program uploads the baits in the file to your server.

Cancel Closes the dialog box, and does not submit a job.

Catalog and Workgroup Data

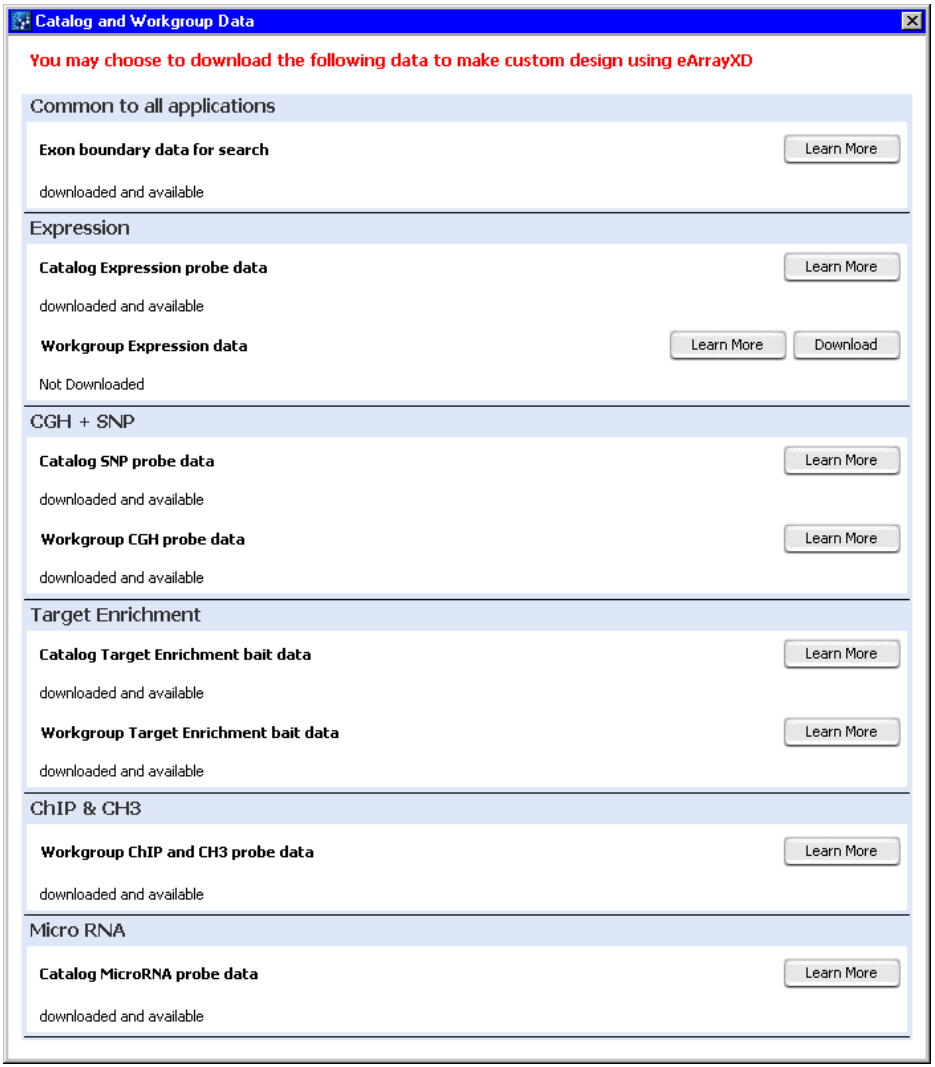


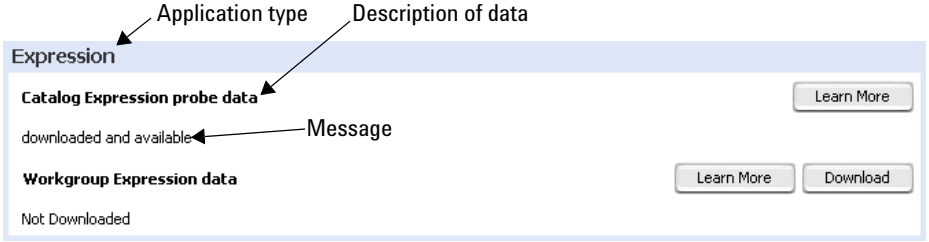
Figure 67 Catalog and Workgroup Data dialog box

Purpose: Lets you transfer probe data and exon boundary data from the eArray Web site to your Agilent Genomic Workbench server. You can transfer probe data from both the Agilent Catalog and from the folders of your workgroup. Probe data are available by application type (i.e. Expression, ChIP, and so on). Exon boundary data apply to all application types. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

The transfer of a specific type of data must be complete before you can perform tasks in eArray$_{XD}$ that require that data. For example, you must transfer Catalog expression probe data before you can use the probe search tool to search for Agilent Catalog expression probes. Also, to transfer other types of data from the eArray Web site, such as probe groups, bait groups, microarray designs, and libraries, you must use other commands. For an overview of data transfers, see "eArray$_{XD}$ and the eArray Web site" on page 25.

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

For each type of data, several items can appear. See the example below:



Application type The experimental application type to which the probe data apply.

Description of data The specific source and type of data to be transferred. In the example above, the source of the data is the folders of your workgroup on the eArray Web site, and the specific type of data is probe data for the chromatin immunoprecipitation (ChIP-on-chip) application type.

Message Shows the status of the given data transfer. Two messages can appear:

- **Not Downloaded** – The given data have not been transferred, or a download request has been made, but the transfer is not yet complete.
- **Downloaded and available** – The transfer of the given data is complete. You can use the data when you work in eArray$_{XD}$.

Learn More Opens a new window that gives details about the specific type of data.

Download Transfers the given type of data from the eArray Web site to your Agilent Genomic Workbench server. If this button does not appear, the given type of data has already been transferred. eArray$_{XD}$ lets you transfer a given type of data only once.

NOTE Any member of your workgroup can request the transfer of workgroup and catalog probe data from the eArray Web site. If one user transfers a given set of data, that set is available to all members of the workgroup.

Change Control Type of Library

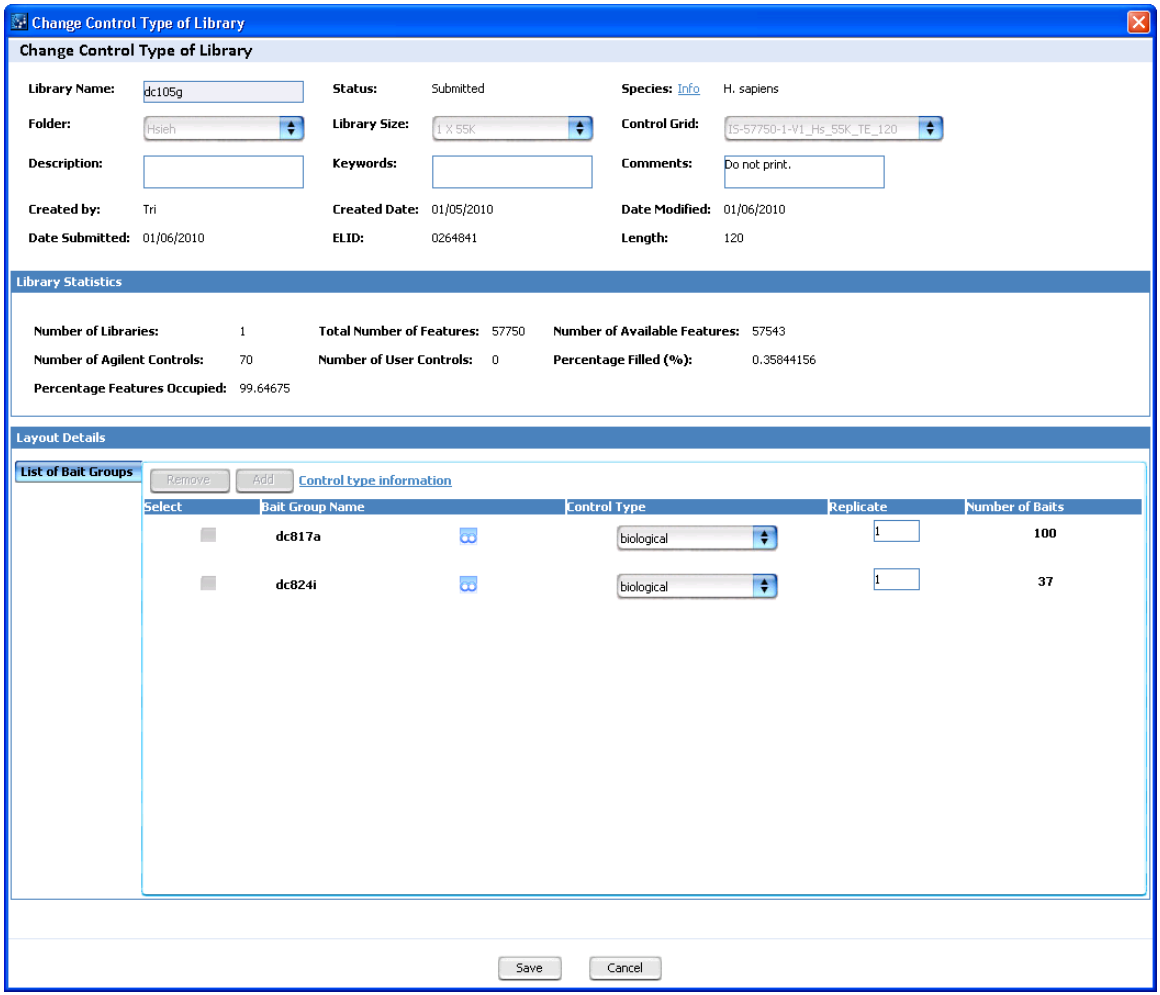


Figure 68 Change Control Type of Library dialog box

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you change the control type that is assigned to the user biological or control bait groups in a library. The library must have a status of Complete

or Submitted . Control types have no effect on the composition of a library. They are included in the library design files for user reference. See "To change the control type assigned to a bait group" on page 464.

NOTE

You can also change the control type of bait groups when you edit or review a library. See these topics:

- "To edit a library" on page 447
- "To review a library" on page 453

To open: In the Design data pane of the Navigator, right-click the name of the desired library, then click **Change Control Type.**

Alternatively, search for the desired library, then in the Actions column of the search results, click . See "To search for libraries" on page 416.

Control Type This is the only property that you can edit in this dialog box. The control types of bait groups do not have any effect on the composition of a library, and they are not used in the SureSelect Target Enrichment protocol or in downstream sequence analyses. They are included in the library design files for user reference. For each bait group, you can select one of these options:

- **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications.
- **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.

Other Properties All of the properties in the dialog box, except the control types of bait groups, are read-only, and cannot be edited. These properties are identical to the ones that appear in the Edit Library dialog box. For details, see "Edit Library" on page 740.

Save Saves the library with any changes that you made to the control types of its bait groups.

Cancel Closes the dialog box without making any changes.

Change Control Type of Microarray Design

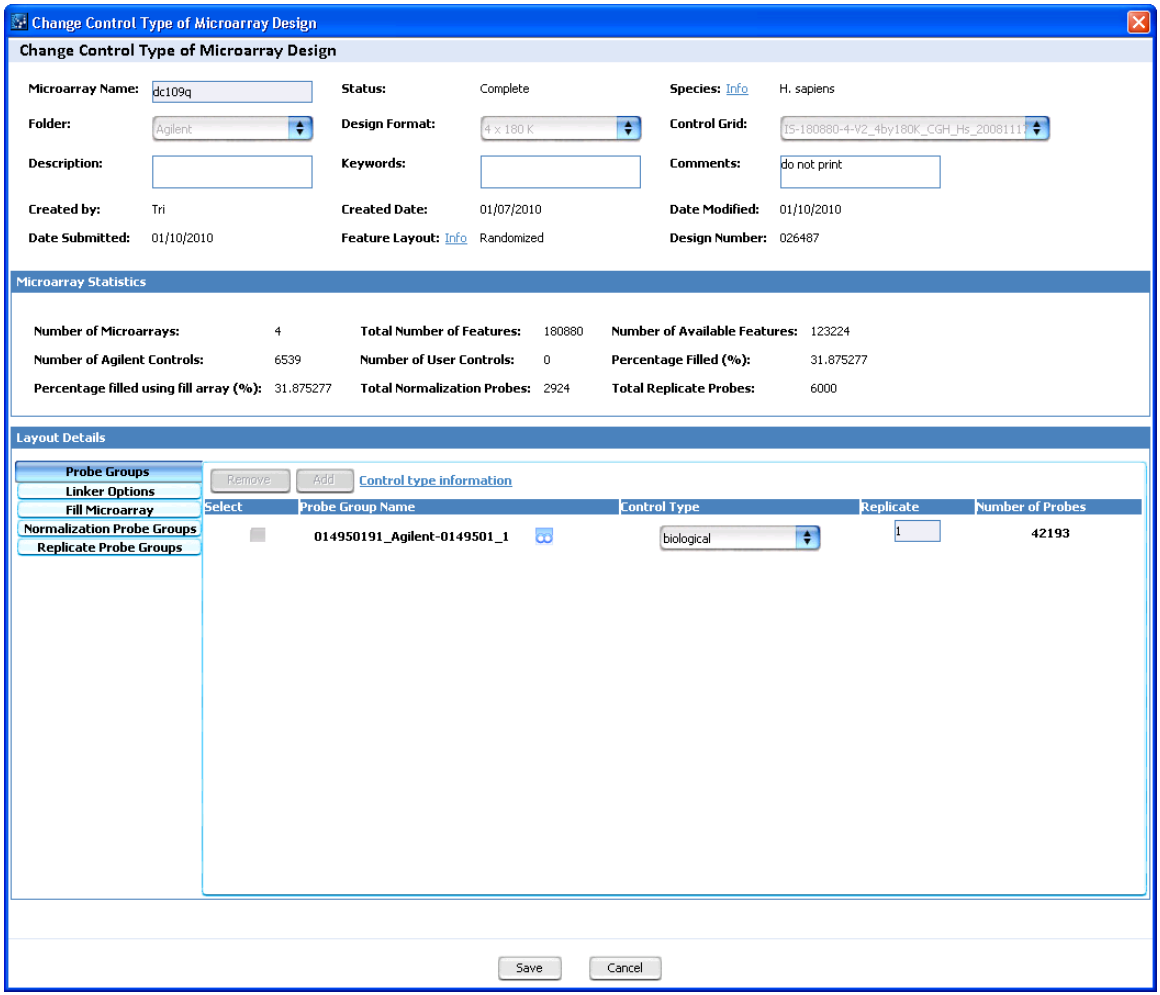


Figure 69 Change Control Type of Microarray Design dialog box

Purpose: Lets you change the control type(s) assigned to the biological and user control probe groups in a microarray design. The microarray design must have a status of Complete or Submitted. See "To change the control type of probe groups" on page 336.

NOTE

You can also change the control types of probe groups when you edit or review a microarray design. See these topics:

- "To edit a microarray design" on page 310
- "To review a microarray design" on page 326

To open: In the Design data pane of the Navigator, right-click the name of the desired microarray design, then click **Change Control Type.**

Alternatively, search for the desired microarray design, then in the Actions column of the search results, click  . See "To search for microarray designs" on page 251.

In either case, in the Layout Details pane, click **Biological <type> Probe Groups.**

Control Type

This is the only property that you can edit in this dialog box. For each biological or user control probe group, you can select one of these options:

Control type	Description
biological	Identifies the probe group as a non-control probe group (condition="FALSE"). It is the default option for biological probes, which should comprise at least 50% of your design.
ignore	Omits the probe group from the Feature Extraction analyses and output.
neg	Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal.
pos	Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample.

Other Properties All of the properties in the dialog box, except the control types of user-defined probe groups, are read-only, and cannot be edited. These properties are identical to the ones that appear in the Edit Microarray Design dialog box. For details, see "Edit Microarray Design" on page 751.

Save Saves the microarray design with any changes that you made to the control types of its probe groups.

Cancel Closes the dialog box without making any changes.

Copy Bait Group

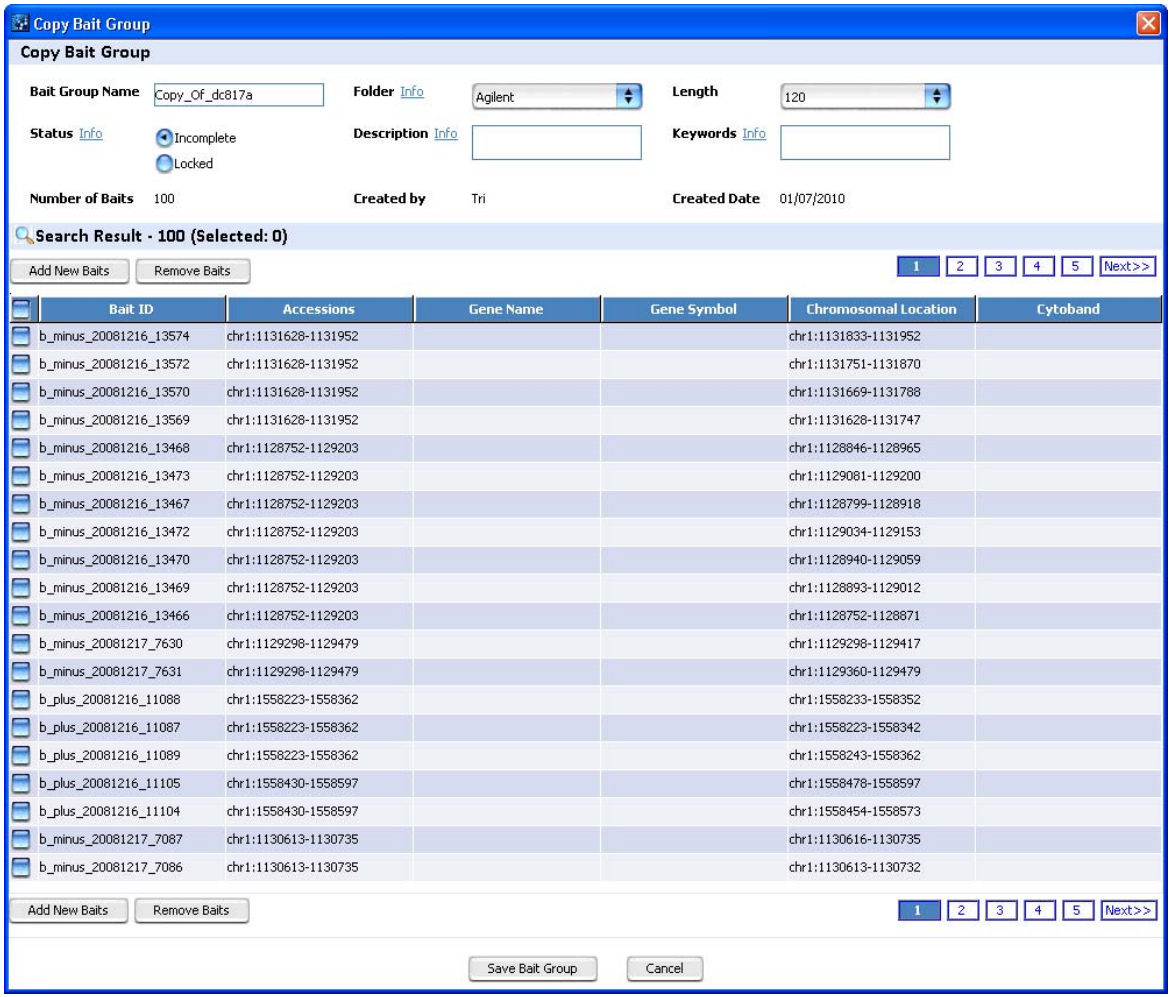


Figure 70 Copy Bait Group dialog box

Purpose: Lets you make a copy of an existing bait group. You become the owner of the newly-created bait group. See "To copy a bait group" on page 405.

To open: In the eArray$_{XD}$ tab, in the Design Data pane of the Navigator, right-click the name of the bait group that you want to copy, then click **Copy.**

Alternatively, search for bait groups. In the Search Result pane, in the **Actions** column, click  . See "To search for bait groups" on page 396.

Properties These bait group properties appear in the dialog box:

Property	Instructions/Details
Bait Group Name	The program displays a default name that contains the name of the original bait group, preceded by the words "Copy of." Edit this name, if desired. Do not include special characters.
Folder	Select a location for the new probe group. Only the folders to which you have access appear in the list.
Length	(Read-only) The length of the baits in the bait group, in nucleotides. Agilent currently supports a bait length of 120 nucleotides.
Status	Select one of these options: **Incomplete** – This option lets you make edits to the new bait group after you create it. This is the default option. **Locked** – This option prevents edits to the bait group after you create it. Locked bait groups cannot be unlocked.
Description	(Optional) Type brief descriptive information, if desired, up to 4,000 characters in length.
Keywords	(Optional) Type search keyword(s), if desired, up to a total length of 4,000 characters. Separate multiple keywords with pipe "|" characters, commas, or semicolons.
Number of Baits	(Read-only) The total number of baits in the bait group.
Created by	(Read-only) Your name.
Date Created	(Read-only) Today's date.

Add New Baits Opens the Add Baits to Bait Group dialog box, where you can search for, select, and add new baits to the bait group. See "Add Baits to Bait Group" on page 576.

Remove Baits Removes selected baits from the bait group. To select baits for removal, mark the check boxes next to their names.

Search Result table

Lists the Bait IDs of all of the baits in the bait group. Additional annotation can also be available. Use the numbered links at the top and bottom of the table to go to other pages.

The check boxes in the table let you select baits for removal. To select all of the baits on a given page, mark the check box in the column heading row.

Save Bait Group

Saves the copied/edited bait group in the selected location, and closes the dialog box.

Cancel

Closes the dialog box without creating a bait group.

NOTE

To copy a bait group, you may first need to transfer it from the eArray Web site to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Copy Probe Group

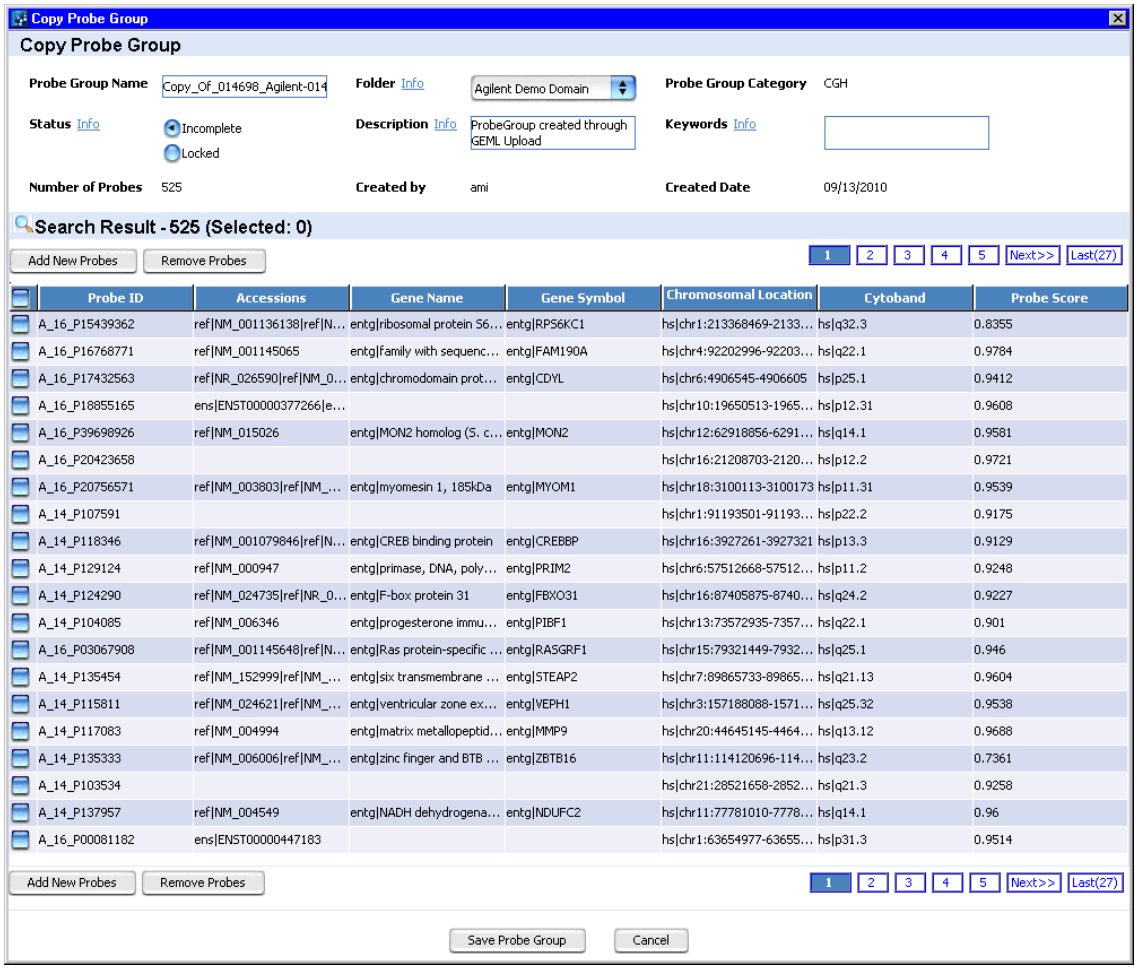


Figure 71 Copy Probe Group dialog box

Purpose: Lets you save a copy of a probe group, and make changes to the copy. See "To copy a probe group" on page 230.

To open: In the **Actions** column of the search results of a probe group search, next to the desired probe group, click  . See "To search for probe groups" on page 224. Alternatively, in the **Design Data** pane of the Navigator, right-click the name of the desired probe group, then click **Copy.**

Properties These probe group properties appear in the dialog box:

Property	Instructions/Details
Probe Group Name	The program displays a default name that contains the name of the original probe group, preceded by the words "Copy_of_." Edit this name, if desired. Do not include special characters.
Folder	Select a location for the new probe group. Only the folders to which you have access appear in the list.
Probe Group Category	(Read-only, available for the CGH application type) One of these types appears: • **CGH** – The probe group is a standard CGH probe group that can included on standard CGH microarrays and on CGH+SNP microarrays. • **CGH+SNP** – The probe group is a SNP probe group that contains only Agilent SNP probes, and can be only used in CGH+SNP microarrays. See "To create a CGH+SNP microarray design" on page 301.
Status	Select on of these options: **Incomplete** – This option lets you make edits to the new probe group after you create it. This is the default option. **Locked** – This option prevents edits to the probe group after you create it. Locked probe groups cannot be unlocked.
Description	Type brief descriptive information, if desired, up to 4,000 characters in length.
Keywords	Type search keyword(s), if desired, up to a total length of 4,000 characters. Separate multiple keywords with pipe " | " characters, commas, or semicolons
Number of Probes	(Read-only) The total number of probes in the probe group.
Created by	(Read-only) Your name.
Date Created	(Read-only) Today's date.

Add New Probes Opens the Add Probes to Probe Group dialog box, where you can search for, select, and add new probes to the probe group. See "Add Probes to Probe Group" on page 578.

Remove Probes Removes selected probes from the probe group. To select probes for removal, mark the check boxes next to their names.

Search Result table Lists the Probe IDs of all of the probes in the probe group. Additional annotation and probe performance scores can also be available.

The check boxes in the table let you select probes for removal. To select all of the probes on a given page, mark the check box in the column heading row.

Page Buttons – Go to specific pages of probes. The highlighted button shows the current page.

Save Probe Group Saves the copied/edited probe group in the selected location, and closes the dialog box.

Cancel Closes the dialog box without creating a probe group.

NOTE To copy a probe group, you may first need to transfer it from the eArray Web site to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer probe data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Create Bait Group

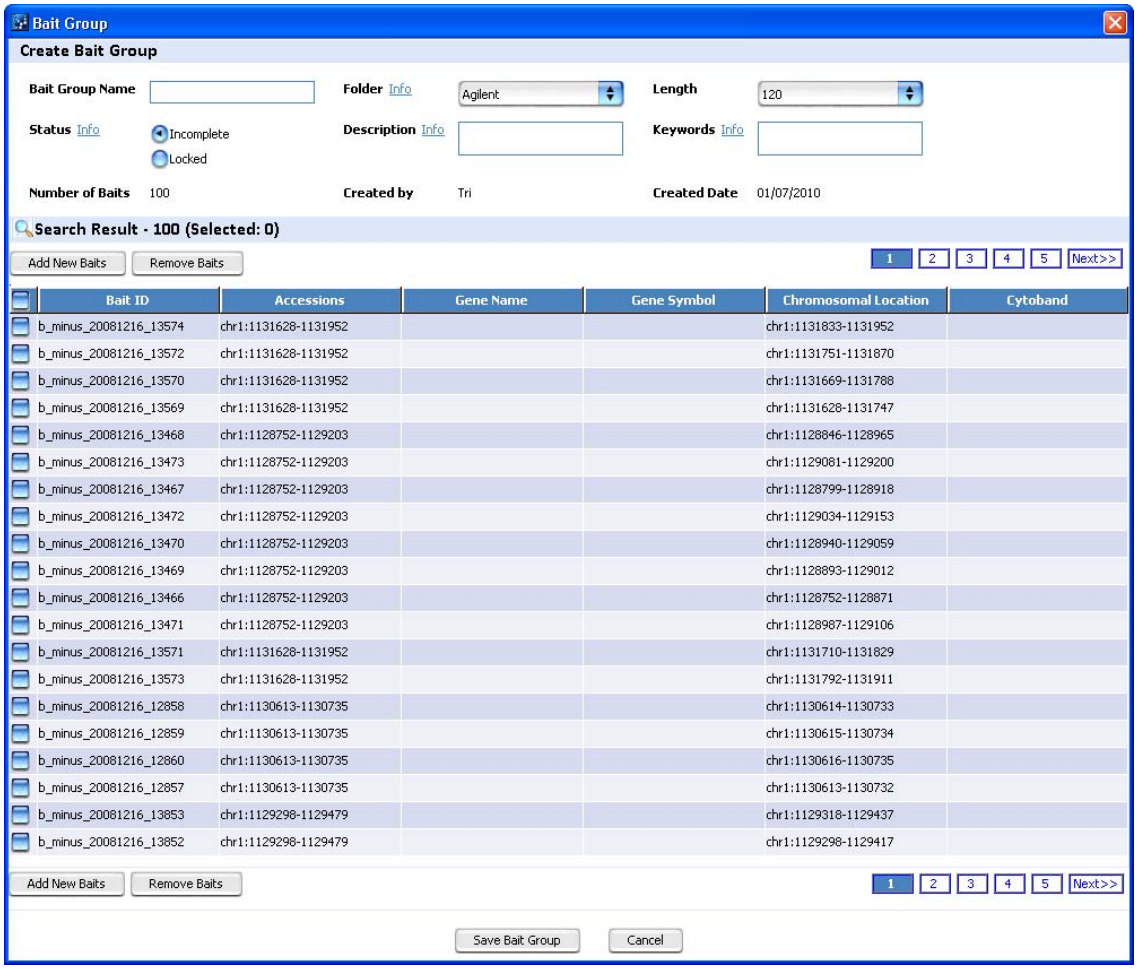


Figure 72 Create Bait Group dialog box

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you define the properties and content of a new bait group. The options in this dialog box are the same as the ones in the Copy Bait Group dialog box. See "Copy Bait Group" on page 615.

To open: In the Search Result pane of a bait search, select the desired baits, then click **Create Bait Group.** See "To create a bait group from existing baits" on page 401.

Create Library

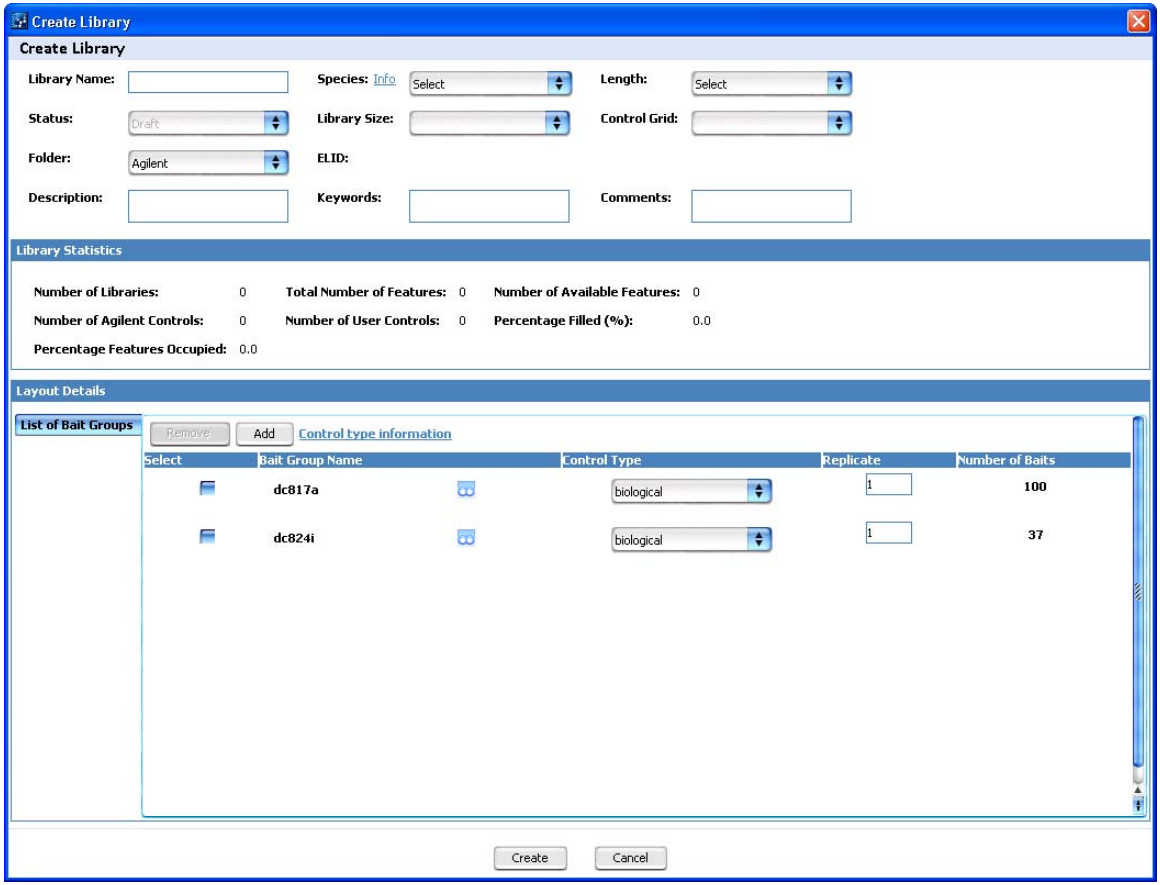


Figure 73 Create Library dialog box

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you define the properties and bait content of a bait library. See "To create a library from bait group search results" on page 439.

To open: In the Search Result pane of a bait group search, select one or more bait groups that you own, then click **Create Library.** See "To search for bait groups" on page 396.

Create Library, Library Statistics, and Layout Details panes

All options and commands that appear in the Create Library, Library Statistics, and Layout Details panes are identical to those in the Edit Library dialog box. See "Edit Library" on page 740.

Buttons

Save Creates the new library with the properties and content that you entered, and closes the dialog box.

Reset Clears the dialog box.

Cancel Closes the dialog box without creating a library.

Create Library from Existing Bait Groups (wizard)

Purpose: This wizard takes you through the steps that are required to design and submit a library using bait groups that are stored on your server. This wizard is available for the SureSelect Target Enrichment application type. See "To create a library from existing bait groups (wizard)" on page 428.

To open: In the eArray$_{XD}$ tab, under **Create Library using,** click **Existing Bait Group(s).**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step.

Finish (Available for the last step of the wizard) Creates a new library based on all of the settings that you entered in the wizard.

This wizard has three steps:

- **Step 1 – Select species and define library** – See "Step 1 – Select species and define library" on page 625.
- **Step 2 – Layout Baits** – See "Step 2 – Layout Baits" on page 627.
- **Step 3 – Create Library** – See "Step 3 – Create Library" on page 628.

Step 1 – Select species and define library

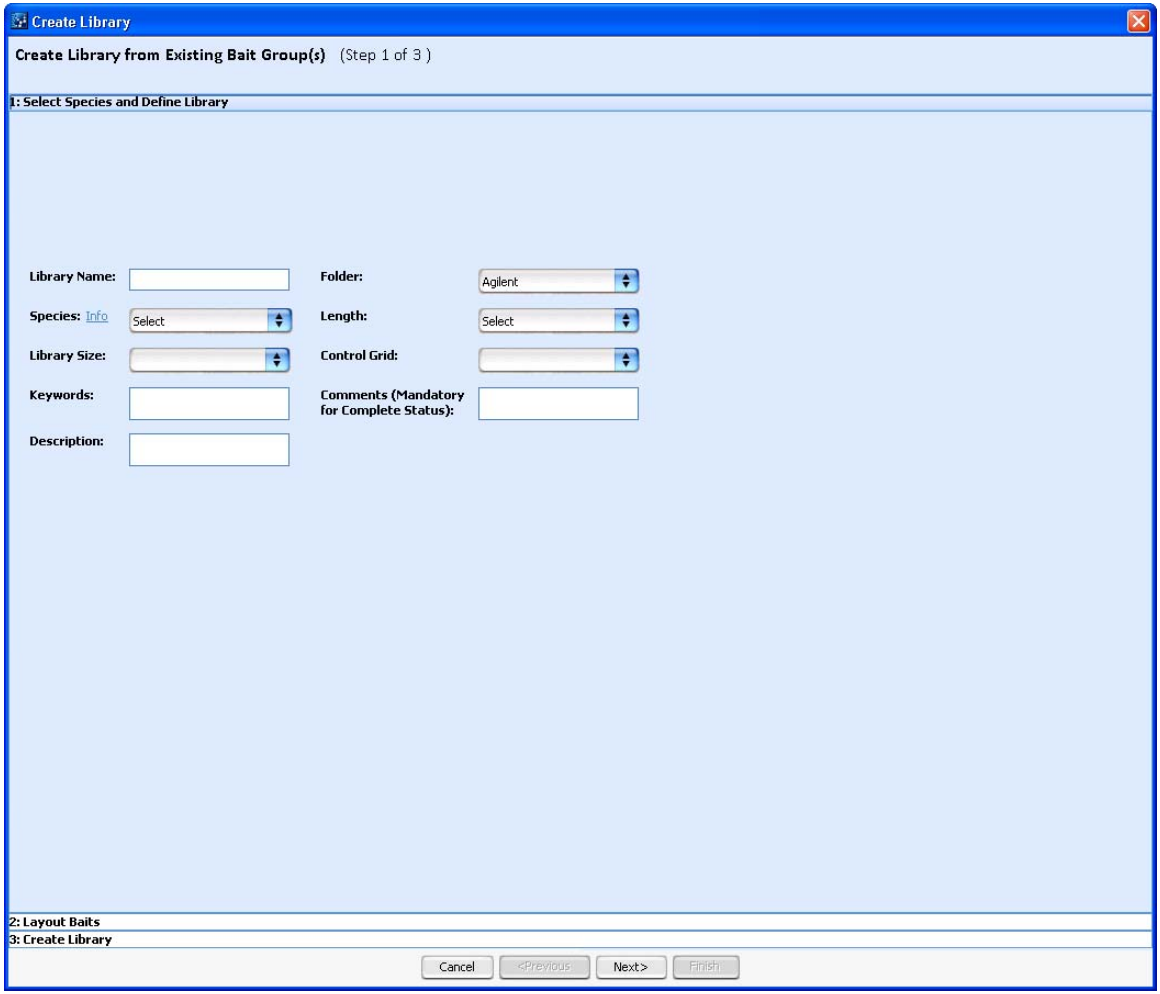


Figure 74 Create Library from Existing Bait Groups wizard – Step 1

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.
Species	Select the desired species.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in a library must have this length.
Library Size	(Read-only) Currently, eArray supports a library size of 55k baits.
Control Grid	This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process. Select an alternate control grid, if one is available.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to create the library with a status of Complete, which prevents further edits to the library, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

Step 2 – Layout Baits

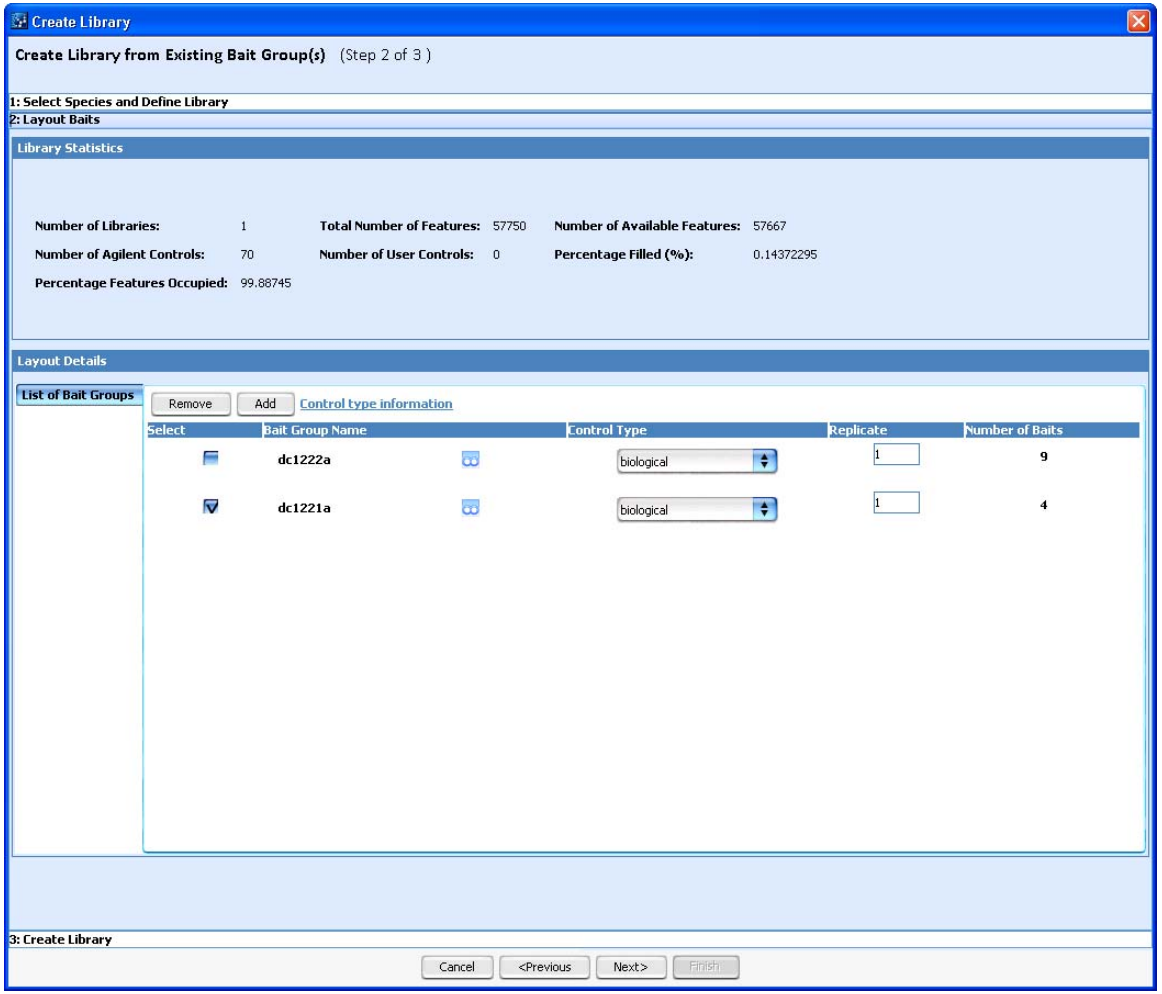


Figure 75 Create Library from Existing Probe Groups wizard – Step 2

The items in this step of the wizard are the same as items in the Edit Library dialog box. See "Edit Library" on page 740. These topics may be especially helpful:

- "Library Statistics Pane" on page 744

- "Layout Details – List of Bait Groups pane" on page 745
- "Layout Details – Add Bait Groups pane" on page 747

Step 3 – Create Library

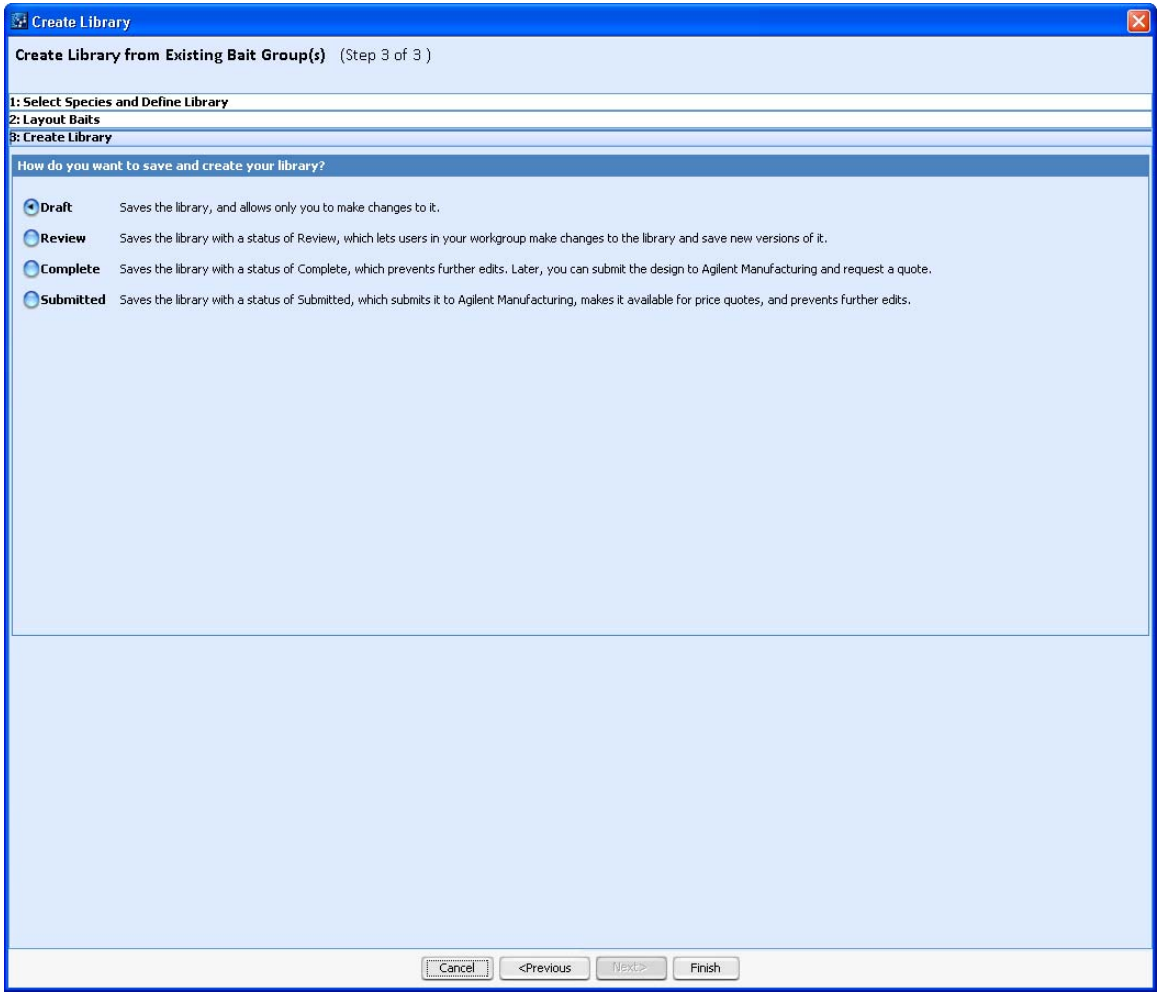


Figure 76 Create Library from Existing Bait Groups (wizard) – Step 3

How do you want to save and create your library?

Select one of these statuses for the library:

Status	Description
Draft	Lets only you edit the library. See "To edit a library" on page 447.
Review	Lets anyone with access to the library make changes to it, and save a new version. See "To review a library" on page 453.
Complete	Prevents further editing of the library, and lets the owner submit the library to Agilent Manufacturing. See "To submit a library to Agilent" on page 458.
Submitted	Prevents further editing of the library, and submits it to Agilent Manufacturing. You can then request a quote for the library. See "To request a quote for a library" on page 460. If you select this option, the **Show Checklist** button appears. You must click this button, and read and mark all items on the design checklist that appears. You can then finish the wizard. See "Design Checklists" on page 894.

Select Checklist

(Read-only, appears if you select Submitted as the status) The program marks this option after you view and mark all items on the design checklist.

Show Checklist

(Appears if you select Submitted as the status) Shows the library checklist. See "Design Checklists" on page 894.

NOTE

To save a library with a status other than Draft, you may need to transfer one or more bait groups from the eArray Web site to your server. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. You may also need to transfer bait data from the eArray Web site for the SureSelect Target Enrichment application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Create Library (Bait Tiling wizard)

Purpose: This wizard takes you through the steps that are required to design and submit a library using baits created by the Bait Tiling process. Bait tiling creates baits that evenly cover selected regions of a given genome. This wizard is available for the SureSelect Target Enrichment application type. See "To create a library using Bait Tiling (wizard)" on page 433.

To open: In the eArray$_{XD}$ tab, under Create Library Using, click **Bait Tiling.**

General Commands

These commands appear at the bottom of the wizard in all steps.

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step.

Finish (Available only for the last step of the wizard) Creates a new library based on all of the settings that you entered in the wizard.

This wizard has four steps:

- **Step 1 – Library Options and Target Details** – See "Step 1 – Library Options and Target Details" on page 631.
- **Step 2 – Define Library** – See "Step 2 – Define Library" on page 635.
- **Step 3 – Layout Baits** – See "Step 3 – Layout Baits" on page 637.
- **Step 4 –Create Library** – See "Step 4 – Create Library" on page 637.

Step 1 – Library Options and Target Details

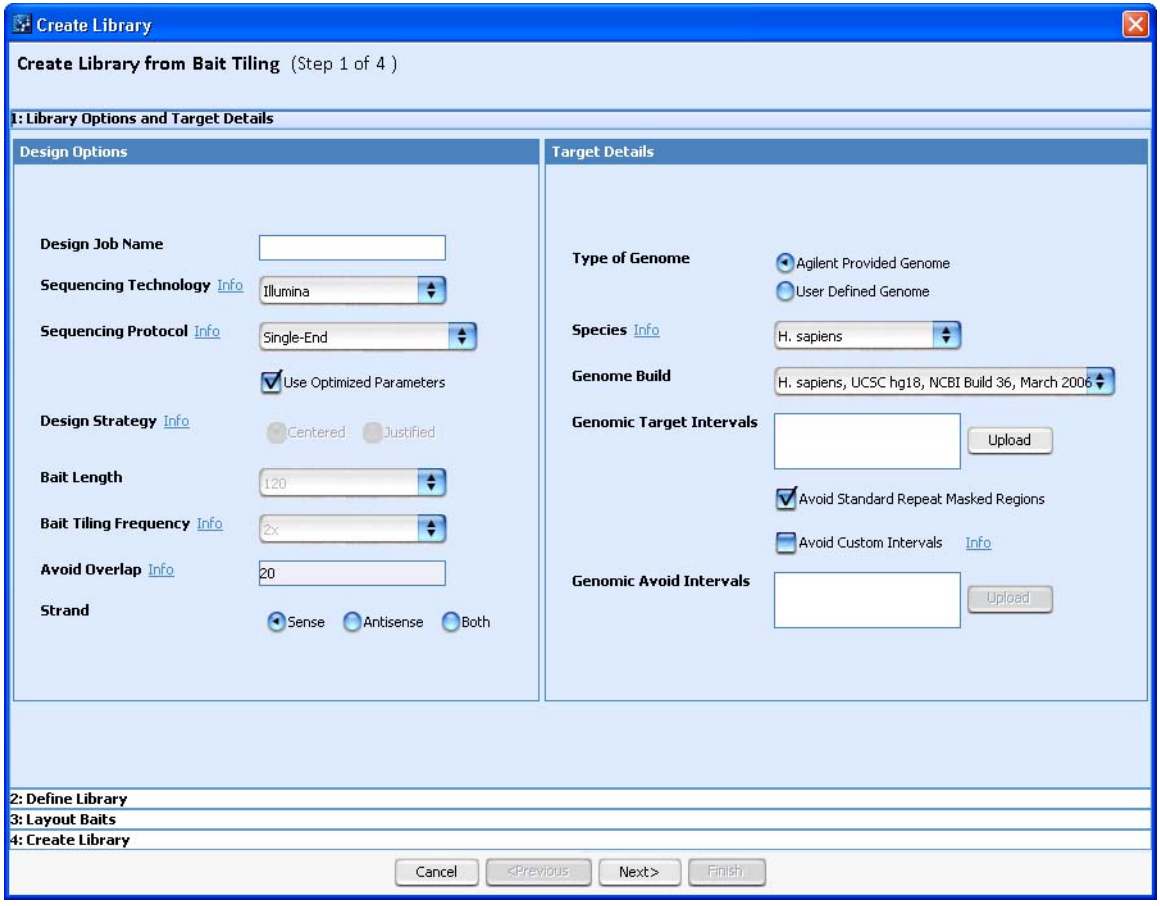


Figure 77 Create Library from Bait Tiling (wizard) – Step 1

Design Options

Parameter	Instructions/Details
Design Job Name	Type a name that will later enable you to identify this Bait Tiling job.
Sequencing Technology	From the list, select the type of DNA sequencer you will use to analyze your target DNA fragments.

Parameter	Instructions/Details
Sequencing Protocol	Select the desired protocol. In the list, eArray displays the available protocols for your chosen DNA sequencing technology.
Design Strategy	In general, mark **Use Optimized Parameters.** With this option, based on your selected sequencing technology and protocol, the program automatically sets the best values for Design Strategy, Bait Length, Bait Tiling Frequency, and Allowed overlap into avoid regions. To set options manually, clear **Use Optimized Parameters.** The options all become available. In **Design Strategy,** select one of these options: • **Centered** – eArray centers sets of tiled baits over their respective target intervals. That is, each set of baits hangs over both ends of its target interval by equal amounts. This option exactly respects the value you select for Bait Tiling frequency. • **Justified** – eArray designs sets of tiled baits to exactly cover their respective target intervals. This option adjusts the overlap of baits to achieve the precise and even tiling of only the target intervals, without any overhang into non-target regions. With this option, the actual tiling frequency can deviate from the value you select in Bait Tiling Frequency.
Bait Length	(Available only if you clear **Use Optimized Parameters.**) Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Bait Tiling Frequency	(Available only if you clear **Use Optimized Parameters.**) Select the desired tiling frequency. This setting controls the density of tiling. The density can also be affected by your choice of Design Strategy. • **2x** – eArray overlaps baits by 50% as it tiles each interval. Two baits cover each base in each interval. • **3x** – eArray overlaps baits as it tiles each interval so that three baits cover each base in each interval. • **4x** – eArray overlaps baits as it tiles each interval so that four baits cover each base in each interval. • **5x** – eArray overlaps baits as it tiles each interval so that five baits cover each base in each interval. **Note:** Depending on your other settings, the exact density of tiling may be somewhat less than that indicated above at the extreme 5' and 3' ends of each interval.

Parameter	Instructions/Details
Avoid Overlap	(Available only if you clear **Use Optimized Parameters.**) To change the value, select it, then type the desired distance in base pairs. eArray generates baits that may extend by this distance into the regions specified in Genomic Avoid Intervals (see below). For best results, set this distance to a maximum of 20 bp.
Strand	Select one of these options: • **Sense** – Produces baits that are similar in sequence to the sense strand of the target genomic DNA. • **Antisense** – Produces baits that are complementary to the sense strand of the target genomic DNA. • **Both** – Produces both a sense bait and an antisense bait for each target location. **Note:** In general, if you are going to use the library to enrich genomic targets, either sense or antisense baits will work. For the enrichment of cDNA targets, the selection of sense vs. antisense baits is important, since genes can appear on either strand.

Target Details

Parameter	Instructions/Details
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Lets you select one of the standard genomes available in eArray for the Bait Tiling job. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. • **User Defined Genome** – Lets you select a genome that you have uploaded to your server for the Bait Tiling job. The available species appear in Species. Once you select a species, the genome builds available for the species appear in Genome Build. To upload a genome, see "To import a new genome" on page 66.
Species	Select the desired species.
Genome Build	Select a different genome build of your selected species, if available. The program uses this build to generate baits. Only the most recent genome builds are available for Agilent-provided genomes.

Parameter	Instructions/Details
Genomic Target Intervals	Type target intervals using the format chrX:<start>-<end>. **Example:** `chr21:1000000-1500000`). Separate multiple intervals with pipe "|" characters. **Upload** – Opens a dialog box that lets you upload a list of intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—in a word processor, press **Enter** at the end of each line.
Avoid Standard Repeat Masked Region	If you mark this option, eArray excludes a standard set of repetitive genomic regions from the Bait Tiling process. These are regions of the genome that generally produce poor quality baits. This option is marked by default. If you are tiling a user-imported genome, these repeat regions are the sequences represented by lower case letters in your sequence files, if you marked Genome is Soft Masked when you imported it
Avoid Custom Intervals	If you mark this option, eArray excludes the genomic intervals that you enter in Genomic Avoid Intervals.
Genomic Avoid Intervals	• Available if you mark **Avoid Custom Intervals.** For intervals, use the format chrX:<start>-<end>. **Example:** `chr21:1000000-1500000` Separate multiple intervals with pipe "|" characters. **Upload** – Opens a dialog box that lets you upload a list of custom avoid intervals. Create the list as a *.txt file with one interval per line. End each line with a new line character—that is, in a word processor, press **Enter** at the end of each line.

Step 2 – Define Library

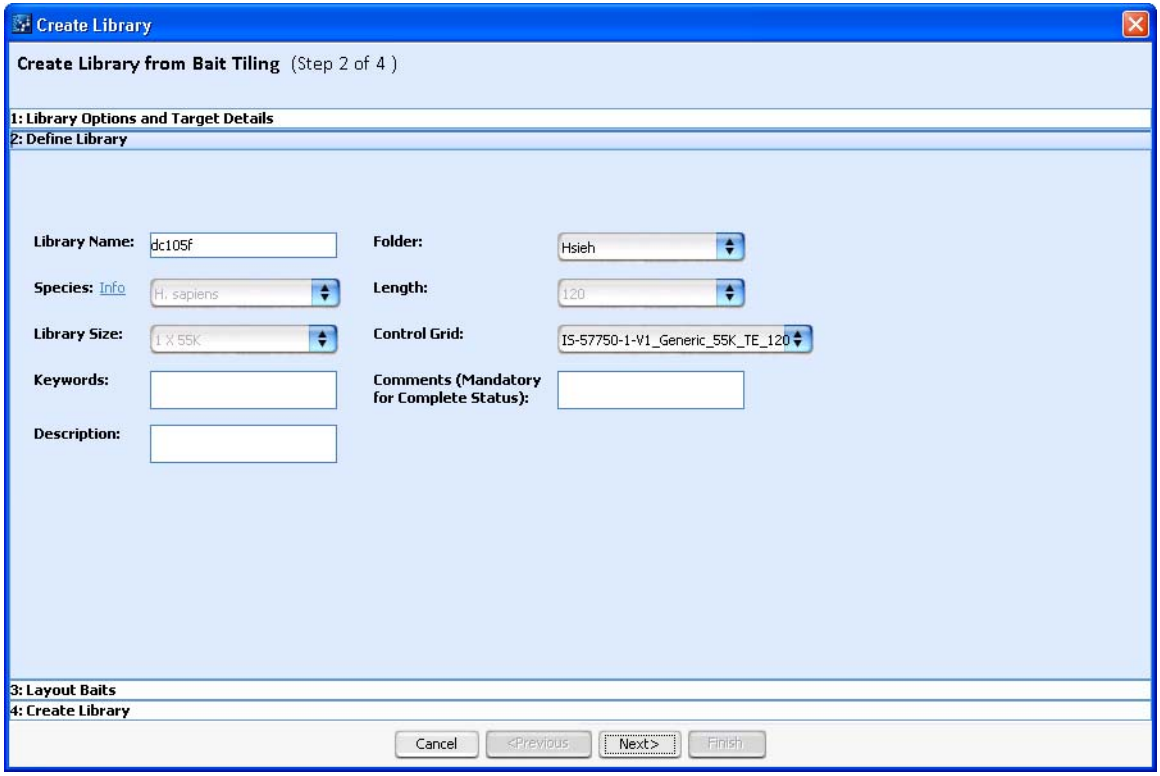


Figure 78 Create Library from Bait Tiling (wizard) – Step 2

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.

Parameter	Instructions/Details
Species	(Read-only) Displays the species that you selected in Step 1 of the wizard.
Length	(Read-only) Displays the bait length that you selected in Step 1 of the wizard.
Library Size	(Read-only) Displays the library size. **Example:** A library size of 1 X 55K can accommodate up to 57,750 baits.
Control Grid	This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process. If desired, select a different control grid, if one is available.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to create the library with a status of Complete, which prevents further changes to the library, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

Step 3 – Layout Baits

The Layout Baits step is the same for all library creation wizards. For details about this step, see the topic "Create Library from Existing Bait Groups (wizard)" on page 624, especially the section "Step 2 – Layout Baits" on page 627.

Step 4 – Create Library

The Create Library step is the same for all library creation wizards. For details about this step, see the topic "Create Library from Existing Bait Groups (wizard)" on page 624, especially the section "Step 3 – Create Library" on page 628.

Create Library (Bait Upload wizard)

Purpose: This wizard takes you through the steps that are required to design and submit a library using a file of bait sequences and annotation that you upload. This wizard is available for the SureSelect Target Enrichment application type. See "To create a library from a bait upload (wizard)" on page 422.

To open: In the eArray$_{XD}$ tab, under Create Library (Wizard), click **Bait Upload.**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step.

Finish (Available only for the last step of the wizard) Creates a new library based on all of the settings that you entered in the wizard.

This wizard has five steps:

- **Step 1 – Bait Parameter and File Details** – See "Step 1 – Bait Parameter and File Details" on page 639.
- **Step 2 – Preview of Uploaded Baits** – See "Step 2 – Preview of Uploaded Baits" on page 642.
- **Step 3 – Define Library** – See "Step 3 – Define Library" on page 643.
- **Step 4 – Layout Baits** – See "Step 4 – Layout Baits" on page 645.
- **Step 5 – Create Library** – See "Step 5 – Create Library" on page 645.

Step 1 – Bait Parameter and File Details

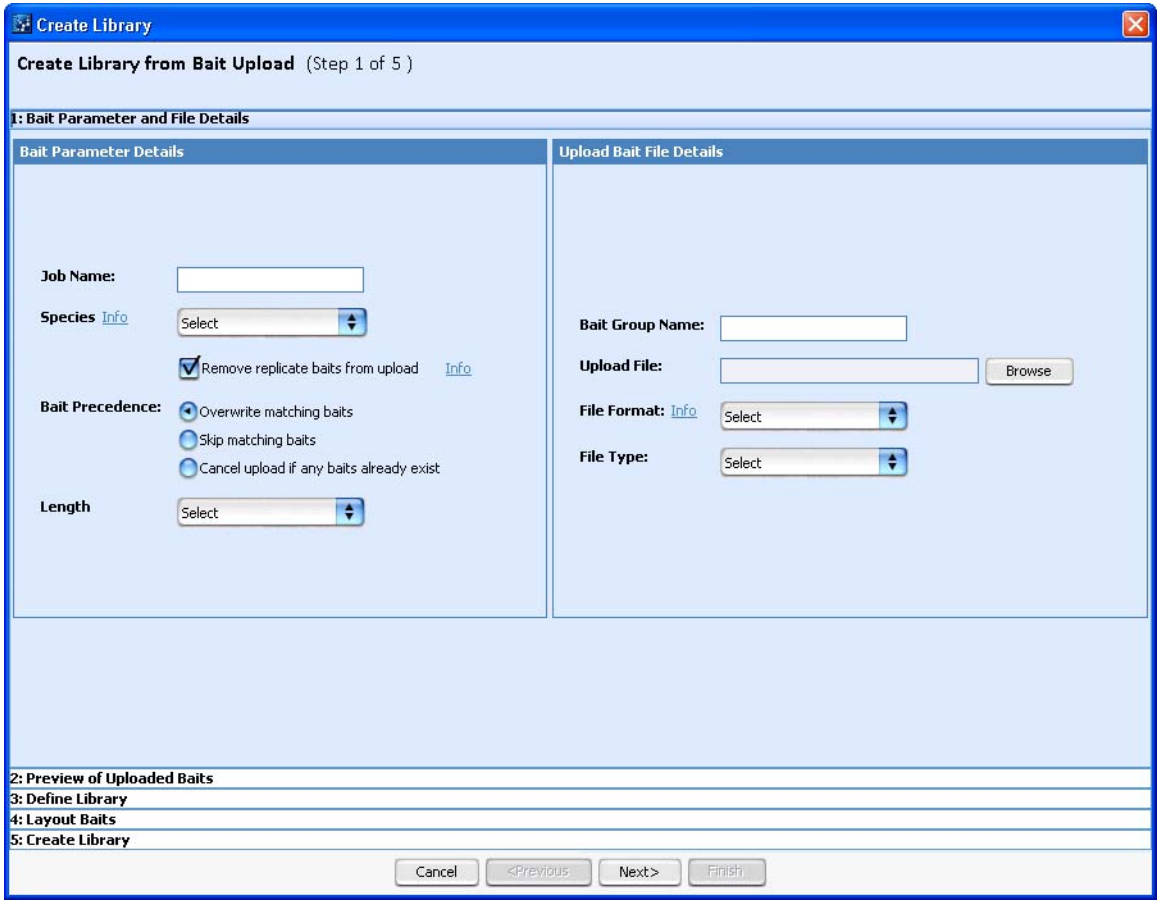


Figure 79 Create Library from Bait Upload (wizard) – Step 1

Bait Parameter Details

Parameter	Instructions/Details
Job Name	Type a name for the library. As the program creates the library, this name identifies the job in the Tasks pane of the Navigator. After the program creates the library, the name identifies the library in search results and the Design Data pane of the Navigator.
Species	Select the species associated with your baits. You can use this information later to search for the baits.
Remove replicate baits from upload	A replicate bait has the same Bait ID as another bait in the file. To ignore all but the first bait in each set of replicate baits in your file, mark this option. If your bait file contains replicate baits, and you do **not** mark **Remove replicate baits from upload,** the program displays an error message after you begin the upload, and does not upload your file.
Bait Precedence	These options tell the program what to do if it finds baits in your uploaded file that have the same Bait IDs as other baits that already exist in the system. Select one of these options: • **Overwrite matching baits** – The annotation of the matching uploaded bait replaces the annotation of the existing bait. This option is useful for reannotating baits. • **Skip matching baits** – The program ignores the matching uploaded baits, and only uploads new ones. • **Cancel upload if any baits already exist** – The program cancels the entire upload process if it finds a matching uploaded bait.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides. All baits in the file must have this length.

CAUTION If you select **Overwrite Matching Baits** in Bait Precedence, the program reannotates matching baits when you upload your bait file. The original annotation of these baits cannot be recovered.

Upload Bait File Details

Parameter	Instructions/Details
Bait Group Name	After the program uploads your bait data file, it creates a bait group that contains all of the baits from the file. Type a name for this bait group.
Upload File	The location of the file of baits and annotation to be uploaded. Your file must meet the requirements described in "To prepare a file of baits and annotation for upload" on page 371. **Browse** – Opens a dialog box that lets you select the desired file for upload.
File Format	Select either **MINIMAL** or **COMPLETE.** For details about these file formats, see "To prepare a file of baits and annotation for upload" on page 371.
File Type	Select the appropriate file type from the list. The program accepts Microsoft Excel (*.xls) files, and tab-delimited text (TDT) files with file extensions of .txt and .tdt **Note:** If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

Step 2 – Preview of Uploaded Baits

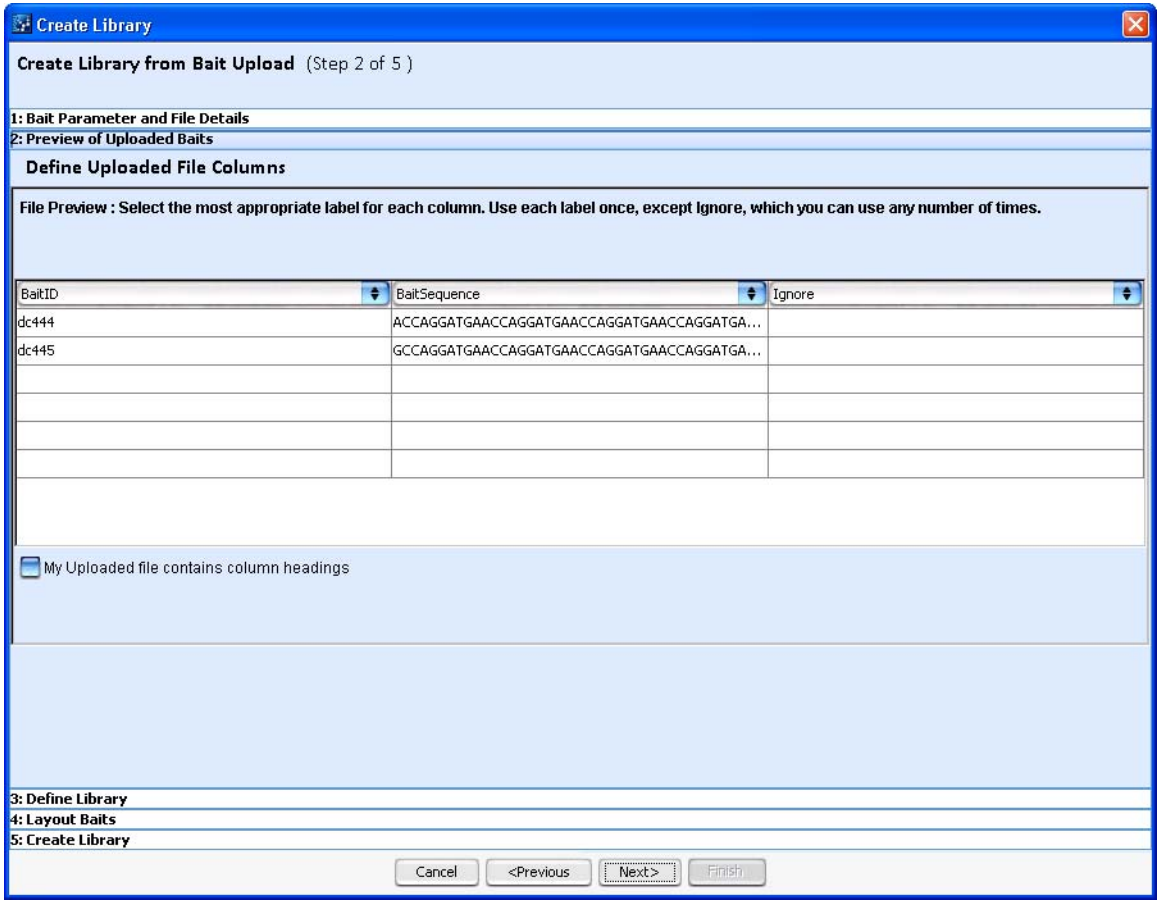


Figure 80 Create Library from Bait Upload (wizard) – Step 2

This step of the wizard lets you label the columns of data in your uploaded bait file. For each column, you select the column label that best identifies its contents.

Baits and annotation The first few lines of your uploaded file appear.

Column Labels Select the most appropriate label for each column. Every label must be used exactly once, except for Ignore, which can be used any number of times. Select **Ignore** for extra columns that do not apply to the selected upload format.

My uploaded file contains column headings If you select this option, the program ignores the first line of your file. This prevents the program from interpreting column headings in your file as actual bait data. The program does not interpret column headings, even if you mark this option.

Step 3 – Define Library

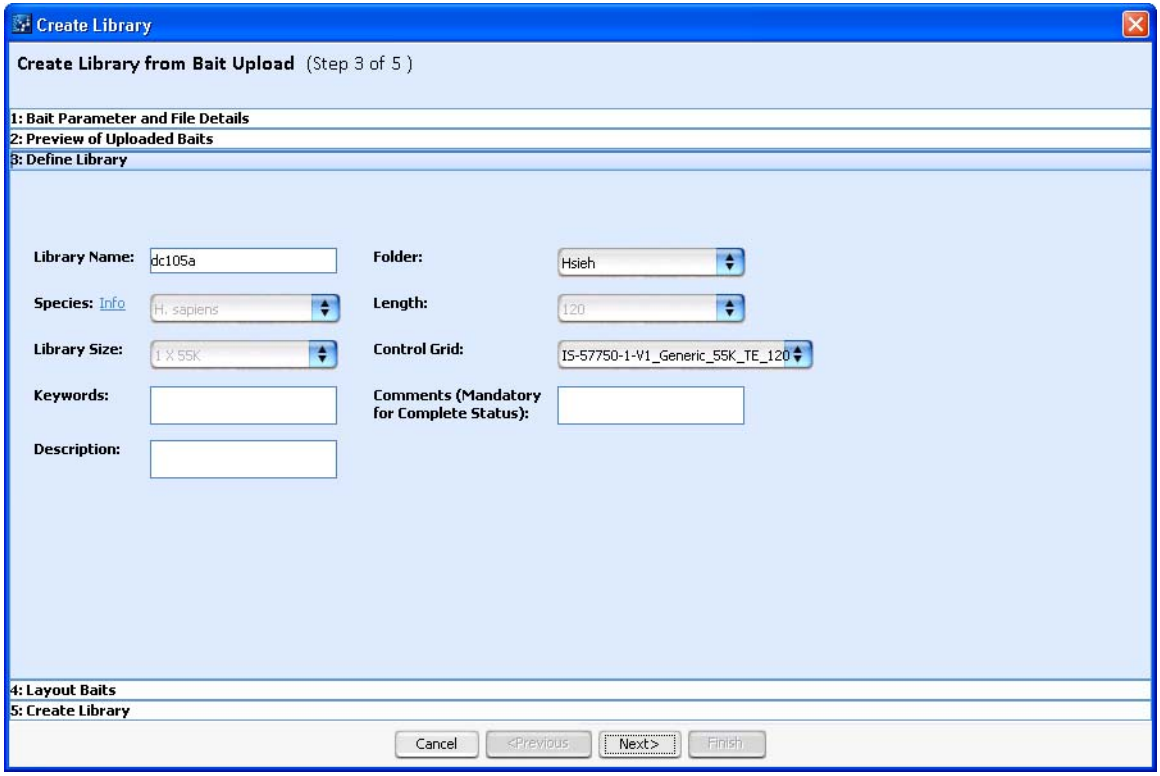


Figure 81 Create Library from Bait Upload (wizard) – Step 3

Parameter	Instructions/Details
Library Name	Type a name for the library. eArray$_{XD}$ uses this name as one of the search keys for libraries, and as a way to refer to the library in search results, lists, and the like. The name can contain up to 100 characters. Use only letters, numbers, hyphens, underscores, and periods.
Folder	Select a location for your new library. The folders to which you have access appear in the list.
Species	(Read-only) Displays the species that you selected in Step 1 of the wizard.
Length	(Read-only) The length of the baits in your uploaded file appears here.
Library Size	(Read-only) The capacity of the library appears. **Example:** A library size of 1 X 55K can accommodate up to 57,750 baits.
Control Grid	The program automatically selects an appropriate control grid for libraries. If desired, select an alternate control grid, if one is available. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process.
Keywords	(Optional) Type search keywords to associate with the library, separated by commas. Keywords can help you search for the library later.
Comments	Type comments to include with the library. If you intend to save the library with a status of Complete or Submitted, comments are required. Otherwise, comments are optional.
Description	(Optional) Type a brief description for the library.

Step 4 – Layout Baits

The Layout Baits step is the same for all library creation wizards. For details about this step, see the topic "Create Library from Existing Bait Groups (wizard)" on page 624, especially the section "Step 2 – Layout Baits" on page 627.

Step 5 – Create Library

The Create Library step is the same for all library creation wizards. For details about this step, see the topic "Create Library from Existing Bait Groups (wizard)" on page 624, especially the section "Step 3 – Create Library" on page 628.

Create Microarray Design

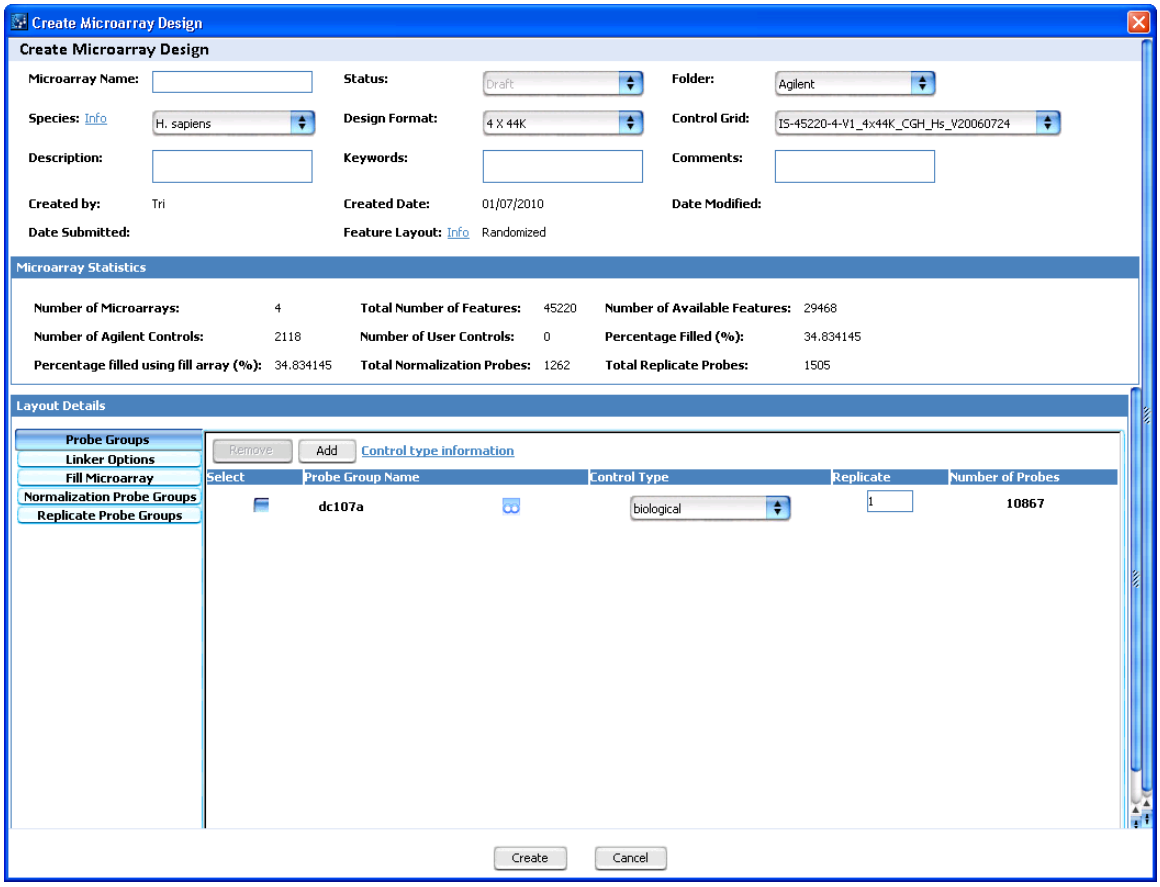


Figure 82 Create Microarray Design dialog box

Purpose: Lets you define the properties and probe group content of a new microarray design.

To open: In the results of a probe group search, select the desired probe group(s), then click **Create Microarray.** See "To search for probe groups" on page 224.

The options in this dialog box are identical to those in the Edit Microarray Design dialog box (see "Edit Microarray Design" on page 751), with the following exceptions:

- **Status** – The program creates all new microarray designs with a status of Draft.
- **Created by** – The program sets this property to your name.
- **Date Created** – The program sets this property to today's date.
- **Date Modified** – The program does not set this property for new microarray designs
- **Date Submitted** – The program does not set this property for new microarray designs.

NOTE

To create a microarray design that contains Agilent Catalog probes, or probes from the folders of your workgroup on the eArray Web site, you may first need to transfer probe data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. You may also need to transfer the probe group(s) from the eArray Web site to your server before you can save the design with a status of Review, Complete, or Submitted. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Create Microarray Design from Existing Probe Groups (Wizard)

Purpose: This wizard leads you through the microarray design creation process using existing probe groups as the source of probes. It is available for the CGH, ChIP-on-chip, methylation, microRNA, and expression application types. See "To create a microarray design from existing probe groups (Wizard)" on page 269.

To open: In the eArray$_{XD}$ tab, under Create Array Design (Wizard), click **Existing Probe Group(s).**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step.

Finish (Available only for the last step of the wizard) Creates a new microarray design based on all of the settings that you entered in the wizard.

This wizard has three steps:

- **Step 1 – Select Species and Define Design.** See "Step 1 – Select Species and Define Design" on page 649.
- **Step 2 – Layout Probes.** See "Step 2 – Layout Probes" on page 652.
- **Step 3 – Create Microarray Design.** See "Step 3 – Create Microarray Design" on page 654.

NOTE

To create a microarray design that contains Agilent Catalog probes, or probes from the folders of your workgroup on the eArray Web site, you may first need to transfer probe data from the eArray Web site for the given application type. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60. You may also need to transfer the probe group(s) from the eArray Web site to your server before you can save the design with a status of Review, Complete, or Submitted. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

Step 1 – Select Species and Define Design

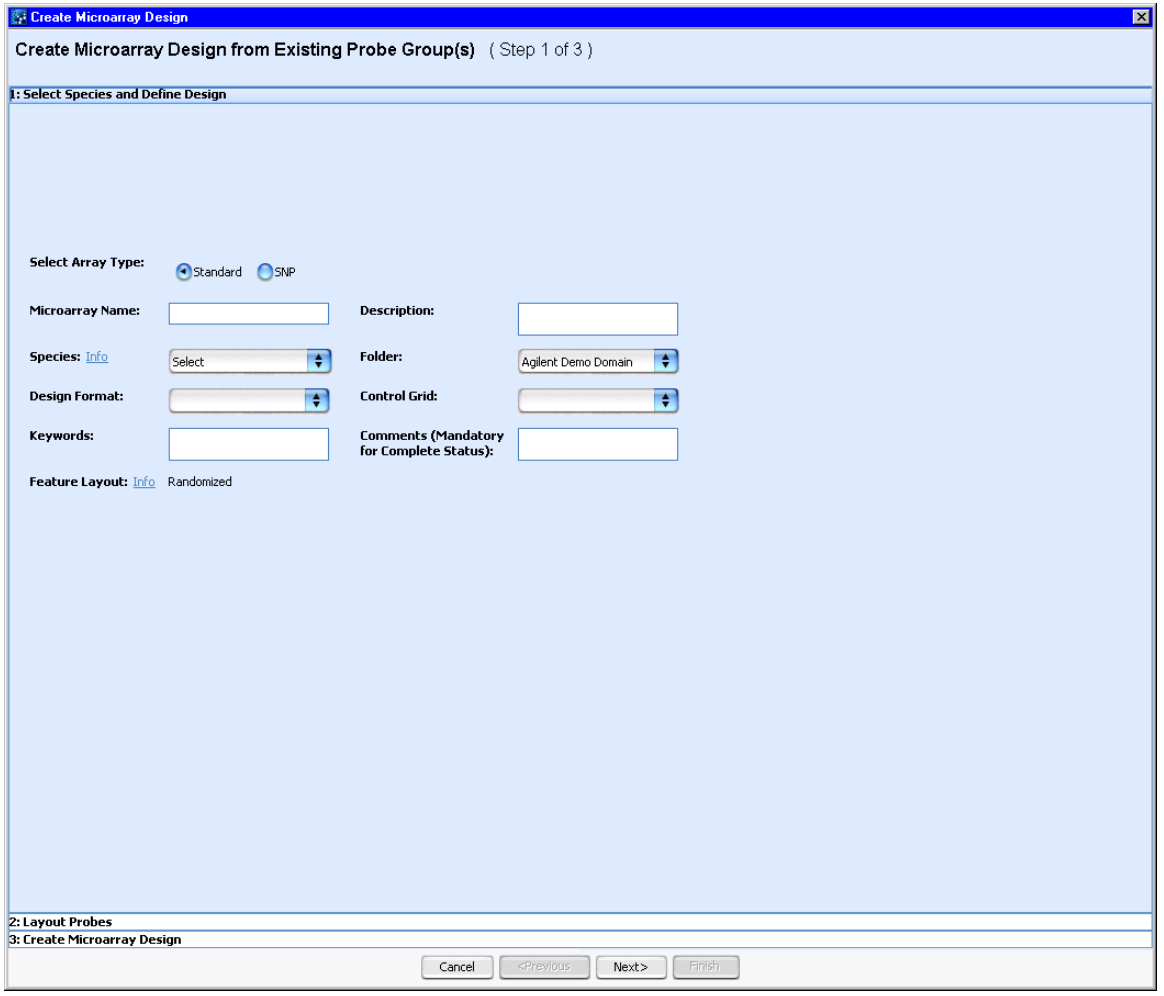


Figure 83 Create Microarray Design from Existing Probe Groups (Wizard) – Step 1

Parameter	Instructions/Details
Select Array Type	(CGH application type only) Select one of these options: • **Standard** – Creates a standard CGH microarray design. • **SNP** – Creates a CGH+SNP microarray design, which includes both CGH probes and Agilent SNP probes on the same array. See "To create a CGH+SNP microarray design" on page 301.
Microarray Name	Type a name for the microarray design. eArray uses this name as one of the search keys for microarray designs, and as a way to refer to the design in search results, lists, and the like. The name can be from 1 to 100 characters long, and can contain letters, numbers, hyphens, underscores, and periods.
Description	(Optional) Type a brief description for the microarray design.
Species	Select the desired species.
Folder	Select a location for your new microarray design. The folders to which you have access appear in the list.
Design Format	Select a design format from the list. Only the design formats that are available for your chosen application type and species appear in the list. When you select or change the design format, an appropriate control grid appears in Control Grid. The design format defines the number and location of features on a microarray slide. It also defines the number of replicate arrays that appear on the slide. **Example:** The 4x44K design format places four identical arrays on the slide. Each array contains approximately 44,000 features.
Control Grid	The program automatically selects a control grid that is appropriate for your application type, design format, and for CGH, ChIP-on-chip, and methylation applications, species. You can select an alternate control grid from the list, if one is available.
Keywords	(Optional) Type search keywords to associate with the design, separated by commas. Keywords can help you search for the microarray design later.

Parameter	Instructions/Details
Comments	Type comments to include with the microarray design. If you intend to save your microarray design with a status of Complete or Submitted, comments are required. Otherwise, comments are optional.
Feature Layout	(Read-only) The process always produces a design with **Randomized** feature layout, which assigns probes randomly to feature positions. **Note:** To create a microarray design in which probes are assigned to specific feature positions that you assign, you must create the design on the eArray Web site. For details, see the *Provide Feature Order* topic in the online help system on the eArray Web site.

Step 2 – Layout Probes

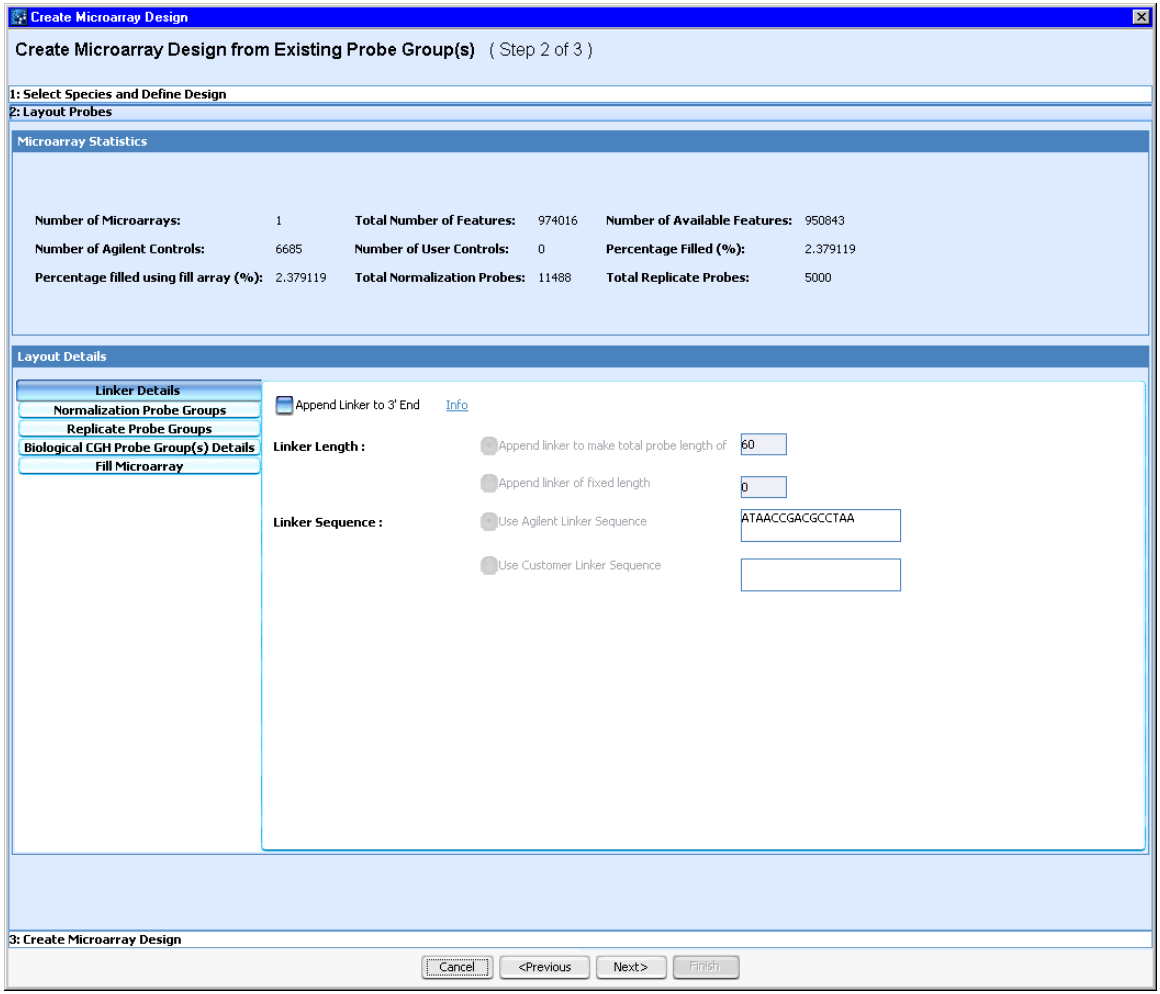


Figure 84 Create Microarray Design from Existing Probe Groups (Wizard) – Step 2

The items in this step of the wizard are identical to items in the Edit Microarray Design dialog box. See "Edit Microarray Design" on page 751. These topics may be especially useful:

- "Microarray Statistics" on page 754

- “Layout Details – Biological <type> Probe Groups pane” on page 762
- “Layout Details – Normalization Probe Groups pane” on page 759
- “Layout Details – Replicate Probe Groups pane” on page 760
- “Edit Probe Group” on page 771
- “Layout Details – Fill Microarray pane” on page 765

Step 3 – Create Microarray Design

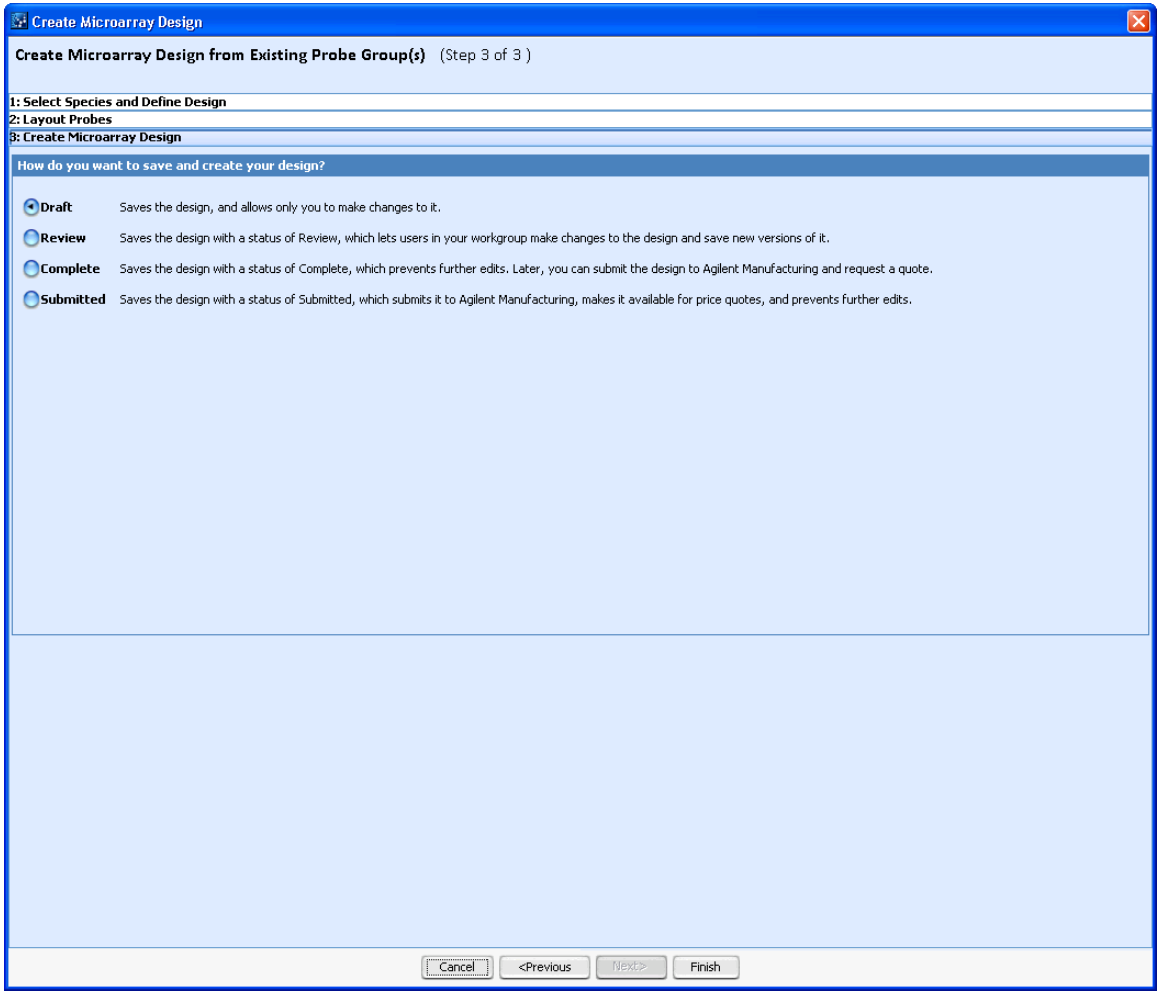


Figure 85 Create Microarray Design from Existing Probe Groups (Wizard) – Step 3

How do you want to save and create your design?

Select one of these status designations for the design:

Status	Description
Draft	Lets only you edit the design. See "To edit a microarray design" on page 310.
Review	Lets anyone with access to the design make changes to it, and save a new version of the design. See "To review a microarray design" on page 326.
Complete	Prevents further editing of the design, and lets the owner submit the design to Agilent Manufacturing. See "To submit a microarray design to Agilent" on page 346.
Submitted	Prevents further editing of the design, and submits it to Agilent Manufacturing. You can then request a quote for the design. See "To request a quote" on page 348. If you select this option, the **Show Checklist** button appears. You must click this button, and read and mark all items on the design checklist that appears. You can then finish the wizard. See "Design Checklists" on page 894.

Select Checklist

(Read-only, appears if you select Submitted as the design status) The program marks this option after you view and mark all items on the design checklist.

Show Checklist

(Appears if you select Submitted as the design status) Shows the design checklist relevant to your application type. See "Design Checklists" on page 894.

Create Microarray Design (HD Probes wizard)

Purpose: This wizard leads you through the microarray design creation process using a probe search of the Agilent High Density (HD) Probe Database as the source of probes. It is available for the CGH, ChIP-on-chip, and CH3 application types. See "To create a microarray design with HD probes" on page 297.

To open: In the eArray$_{XD}$ tab, under Create Array Design Using, click **HD Probes.**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step. After the first step of the wizard, this button submits an HD probe search job to the eArray Web site, and you must wait for the job to finish before you can continue.

Finish (Available only for the last step of the wizard) Creates a new microarray design based on all of the settings that you entered in the wizard.

This wizard has five steps:

- **Step 1 – Search Parameters.** See "Step 1 – Search Parameters" on page 657.
- **Step 2 – Create Probe Group.** See "Step 2 – Create Probe Group" on page 660.
- **Steps 3–5 – Define Design, Layout Probes, and Create Array Design.** See "Step 3–5 – Define Design, Layout Probes, and Create Array Design" on page 661.

Step 1 – Search Parameters

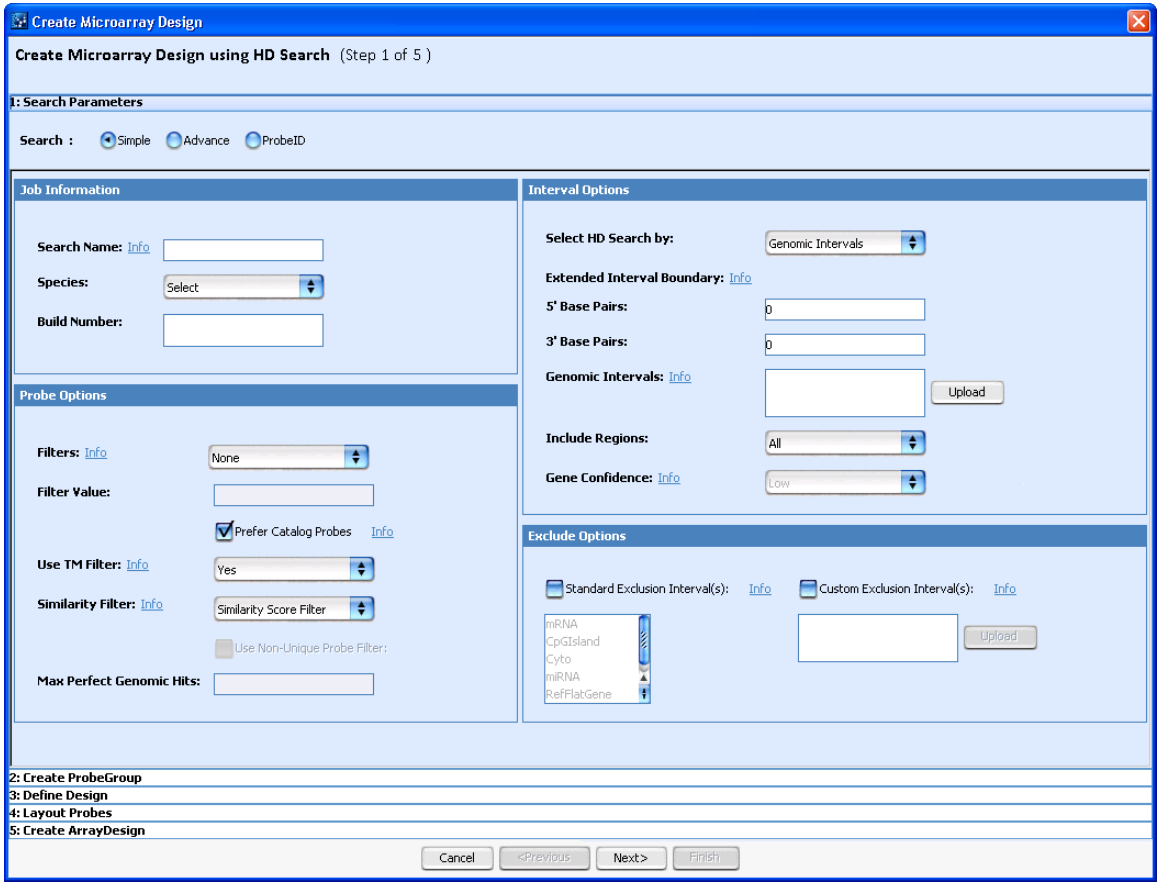


Figure 86 Create Microarray Design using HD Search (Wizard) – Step 1. This pane appears when you set up a Simple Genomic Intervals HD search.

The search pane that initially appears in this step lets you set up a Simple Genomic Intervals HD Search (see Figure 86). However, you can select options in **Search** and **Select HD Search by** to set up any available HD search. The table below describes these settings. For information about search parameters, see the reference given for each specific type of search.

Type of Search	Available for these application types	In *Search,* select this option	In *Select HD Search by,* select this option
Simple Genomic Intervals Retrieves probes from the Agilent HD probe database based on genomic intervals that you enter. For information about the search parameters, see "Simple HD Probe Search" on page 565.	• CGH • ChIP-on-chip • CH3	Simple	Genomic Intervals
Advanced Genomic Intervals Retrieves probes from the Agilent HD probe database based on genomic intervals that you upload. You supply the density of returned probes, and T_M and homology filtering characteristics on a per interval basis. For information about the search parameters, see "Advanced HD Probe Search" on page 527.	• CGH • ChIP-on-chip • CH3	Advanced	Genomic Intervals

Type of Search	Available for these application types	In *Search,* select this option	In *Select HD Search by,* select this option
Simple Gene Annotations Retrieves probes from the Agilent HD-CGH probe database based on their association with specific gene annotations that you enter. For information about the search parameters, see "Simple HD Probe Search" on page 565.	• CGH	Simple	Gene Annotations
Probe ID Retrieves probes from the Agilent HD probe database based on Probe IDs that you enter. For information about the search parameters, see "Probe ID Search (HD probes)" on page 557.	• CGH • ChIP-on-chip • CH3	Probe ID	Probe ID

Step 2 – Create Probe Group

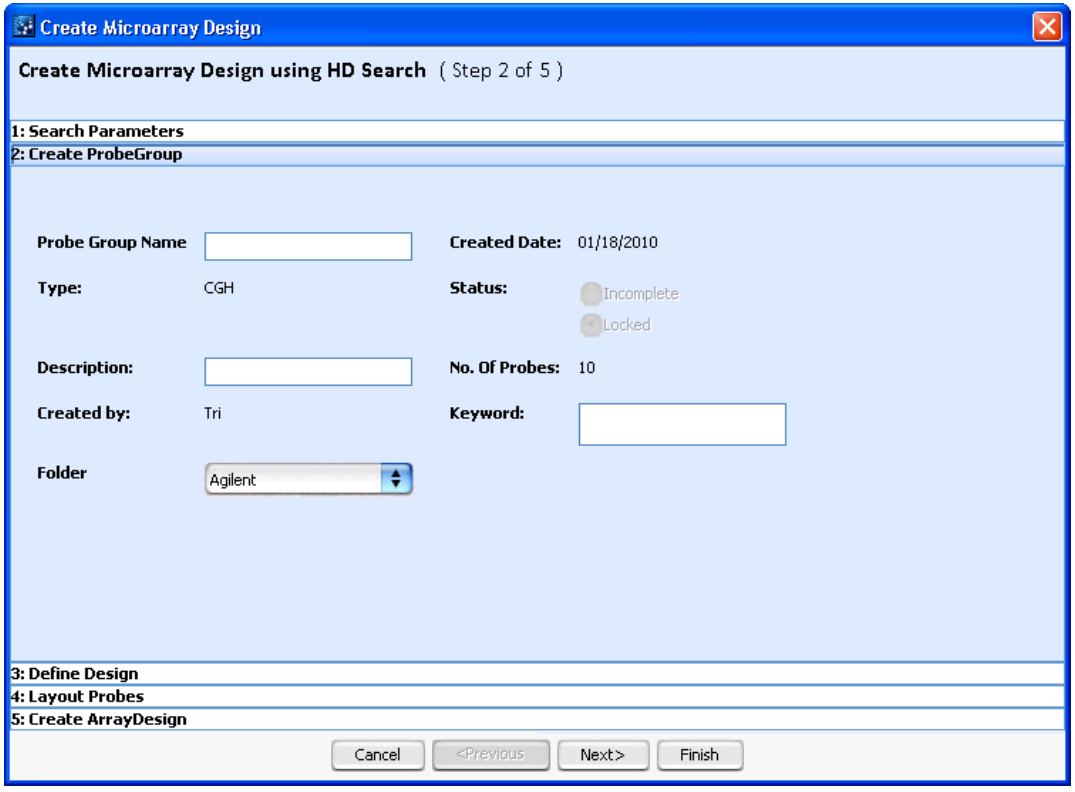


Figure 87 Create Microarray Design using HD Search (Wizard) – Step 2

Purpose: Creates a new probe group from the results of the HD probe search that you requested in the previous step. This probe group is available for your use both within and outside of the scope of the wizard.

To open: In the Tasks pane, in the **HD Search (Wizard)** folder, right-click the name of the applicable search job, then click **Create Probe Group.** The HD search job must have a status of Complete .

Probe Group Attributes

These probe group attributes appear:

Attribute	Description
Probe Group Name	Type a name for the probe group.
Type	(Read-only) The application type for which the probes were designed.
Description	(Optional) Type brief descriptive comments
Created by	(Read-only) Your name.
Folder	Select a location for the probe group. The folders to which you have access appear in the list.
Date Created	(Read-only) Today's date.
Status	(Read-only) The program always creates HD probe groups with a status of Locked. You cannot edit or unlock a locked probe group.
No. of Probes	(Read-only) The total number of probes in the probe group.
Keyword	Type one or more keywords, separated by commas.

Step 3–5 – Define Design, Layout Probes, and Create Array Design

These steps are the same for all microarray-related wizards. For information about the options in these steps, see the similarly named steps in "Create Microarray Design from Existing Probe Groups (Wizard)" on page 648.

Create Microarray from Target Sequences (wizard)

Purpose: This wizard lets you create a microarray design that uses Gene Expression Probe Design as a source of probes. It is available for the Expression application type. See "To create a microarray design from target transcripts" on page 289.

To open: In the eArray$_{XD}$ tab, under Create Array Design Using, click **Probe Design.**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Goes back to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. After step 3, you must wait for eArray to finish a gene expression probe design job before you can continue with the wizard.

Finish (Available only for the last step of the wizard) Creates a new microarray design based on all of the settings that you entered in the wizard.

This wizard has six steps:

- **Step 1 – Select Method.** See"Step 1 – Select Method" on page 663.
- **Step 2 – Select Parameters.** See "Step 2 – Select Parameters" on page 664.
- **Step 3 – Upload Target and Transcriptome.** See "Step 3 – Upload Target and Transcriptome" on page 668.
- **Steps 4–6 – Select Species and Define Design, Layout Probes, and Create Array Design.** See "Steps 4–6 – Select Species and Define Design, Layout Probes, and Create Array Design" on page 670.

Step 1 – Select Method

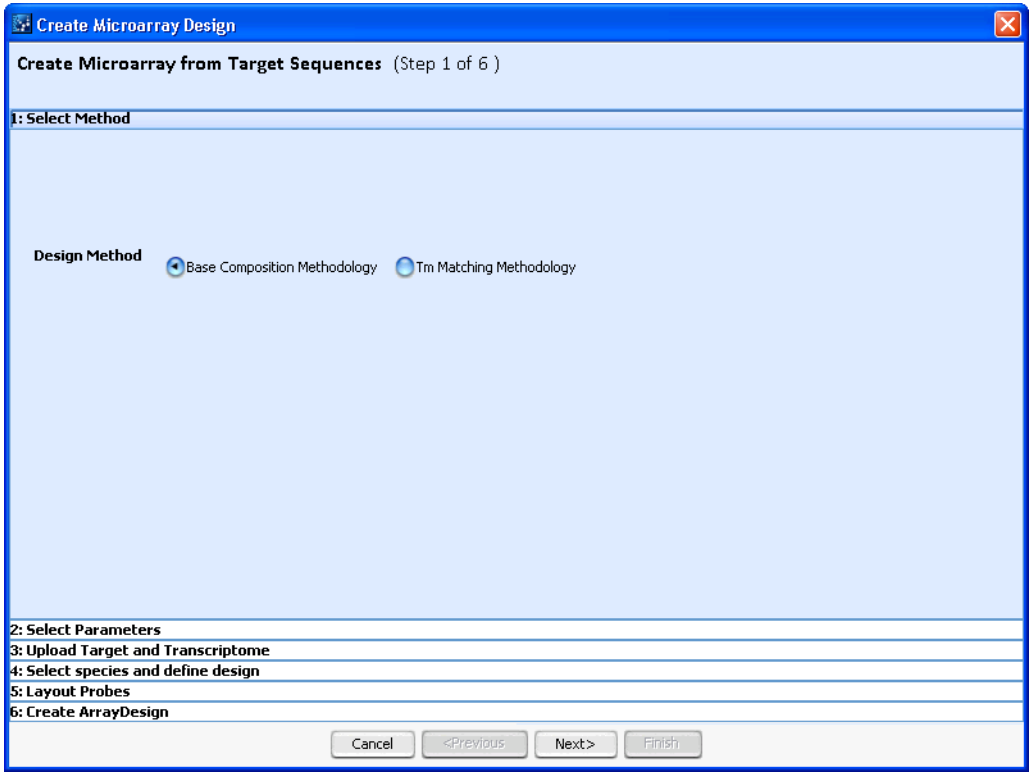


Figure 88 Create Microarray Design from Target Sequences (wizard) – Step 1

Design Method Select one of these options:

- **Base Composition Methodology** – The resulting probes adhere as closely as possible to the base composition profile that gives optimal performance on the Agilent platform, and they are all of equal length. This is the standard method, and it works best with Agilent protocols, and most eukaryotic organisms.
- **Tm Matching Methodology** – The resulting probes have melting temperatures (T_M) as similar as possible to a value that you enter. Probes can be all of equal length, or probes can be trimmed to increase compliance with the desired T_M. This methodology can work well when you design probes for prokaryotic organisms.

Step 2 – Select Parameters

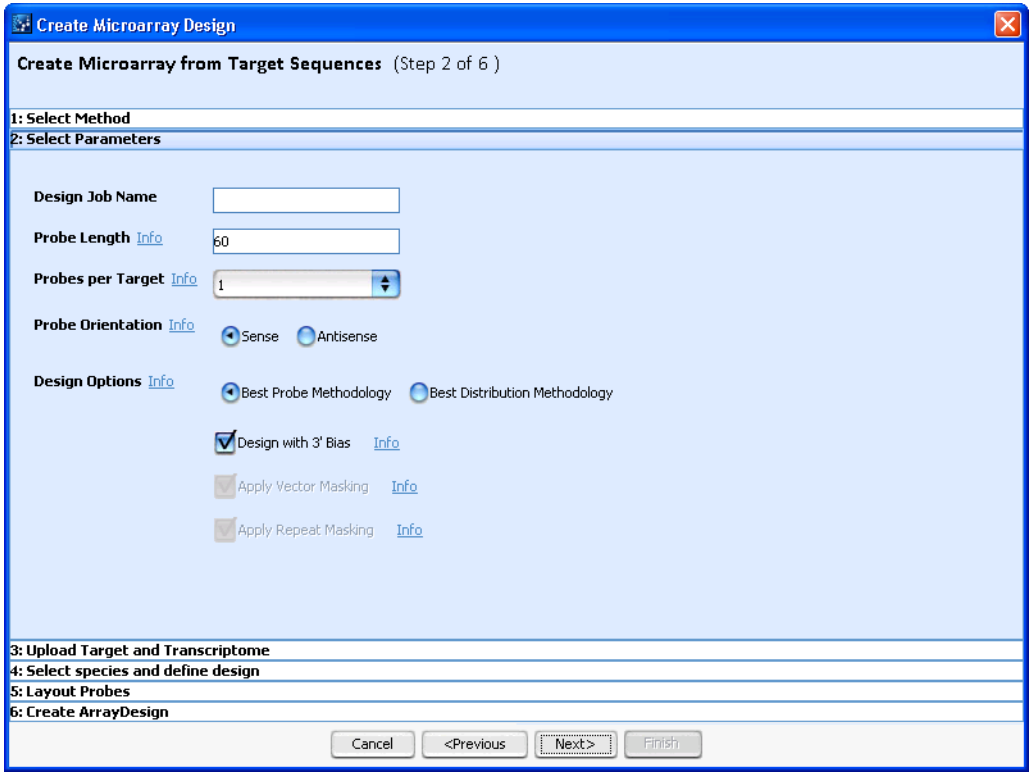


Figure 89 Create Microarray Design from Target Sequences (wizard) – Step 2

Parameters These job parameters appear:

Parameter	Instructions/Comments
Design Job Name	Type a name that will help you to later identify this specific GE probe design job. The job name can be from 1 to 50 characters in length, and can contain letters, numbers, underscores, periods, and dashes. Do not include spaces or special characters.
Probe Length	Type the maximum length for the generated probes. The allowable length is from 25 to 60 bases. Agilent has found that a probe length of 60 bases provides the optimal balance between sensitivity and specificity for most applications on the Agilent *in situ* microarray platform.
Probes per Target	Select from 1 to 10 probes per target. This is the maximum number of probes the probe design process returns for each uploaded target sequence. If the target sequences are of poor quality (for example, if they contain repetitive and/or vector sequences), the probe design process can return fewer probes than you enter. Because of the length and high quality of the generated probes, Agilent recommends that you create one probe per target sequence. However, if you design multiple probes per target sequence, you can select the best of those probes after a validation process.
Probe Orientation	Select one of these options: • **Sense** – Produces probes in the sense or "coding strand" orientation, similar in sequence to the mRNA targets. Use this option if the sample preparation methodology yields cDNA or cRNA molecules. • **Antisense** – Select this option if you want probes in antisense or "template" orientation, complementary in sequence to the mRNA targets. This is the best option if your samples are directly labeled RNA.
Design Options	Select one of these options: • **Best Probe Methodology** – The probe design process favors production of the highest quality probes, rather than even coverage of each target sequence. The selection process favors empirically validated probes, and probes that are closer to the 3' end of a given primary accession. • **Best Distribution Methodology** – The probe design process favors even coverage of each target sequence, rather than production of the highest quality probes.

Parameter	Instructions/Comments
Design with 3' bias	Mark this option to derive probes mainly from the first 1,000 bp from the 3' end of each of your target sequences. If you use an Agilent (or other) labeling protocol that uses linear amplification, it is important to select probes from the 3’ end of the sequence. Linear amplification generates sequences that are shorter than the initial template due to the attenuation of the polymerase reaction. Because of this, most of the labeled product represents only the first 1,000 bp from the 3' end of each target sequence. It is important to design probes that represent this region.
Masking	eArray always uses both of these options in the probe design process, and they cannot be disabled. • **Apply Vector Masking** – Identifies and ignores contaminant segments during probe design. Target sequences can contain contaminant segments not actually found in the sample under study. These segments are often artifacts from cloning vectors (e.g. plasmid, phage, BAC, YAC) used in cloning and amplification processes. • **Apply Repeat Masking** – Identifies and ignores repetitive sequences within your target sequences during probe design. The genome of any given organism contains interspersed repeats and low complexity DNA sequences. These sequences, which are unique at a species level, are replicated many times throughout the genome, and are found in the transcriptome as well. Replicate regions are poor candidates for unique probes.

Parameter	Instructions/Comments
Allow Probes to be Trimmed	(Available only for T_M-Matching GE Probe Design jobs) This option lets the program remove bases from candidate probes to increase compliance with the Preferred Probe T_M. eArray will not trim probes to shorter than 45 bases. In concept, a shorter probe has less complementary sequence available, which can reduce its specificity, or infringe on its ability to form a stable duplex with the desired target. However, the risk of this occurring to a significant extent is very low.
Preferred probe Tm	(Available only for T_M-Matching GE Probe Design jobs) Type the target T_M for the probe design process (in °C). The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms. Select a probe T_M based on these factors: • The mean and standard deviation of the T_M of all potential probes that could be generated for the target transcriptome. • The hybridization temperature identified in the hybridization protocol. In practice, the target T_M should be approximately 20°C higher than the hybridization temperature. For example, if the hybridization temperature is 60°C, then the target probe T_M should be 80°C.

Step 3 – Upload Target and Transcriptome

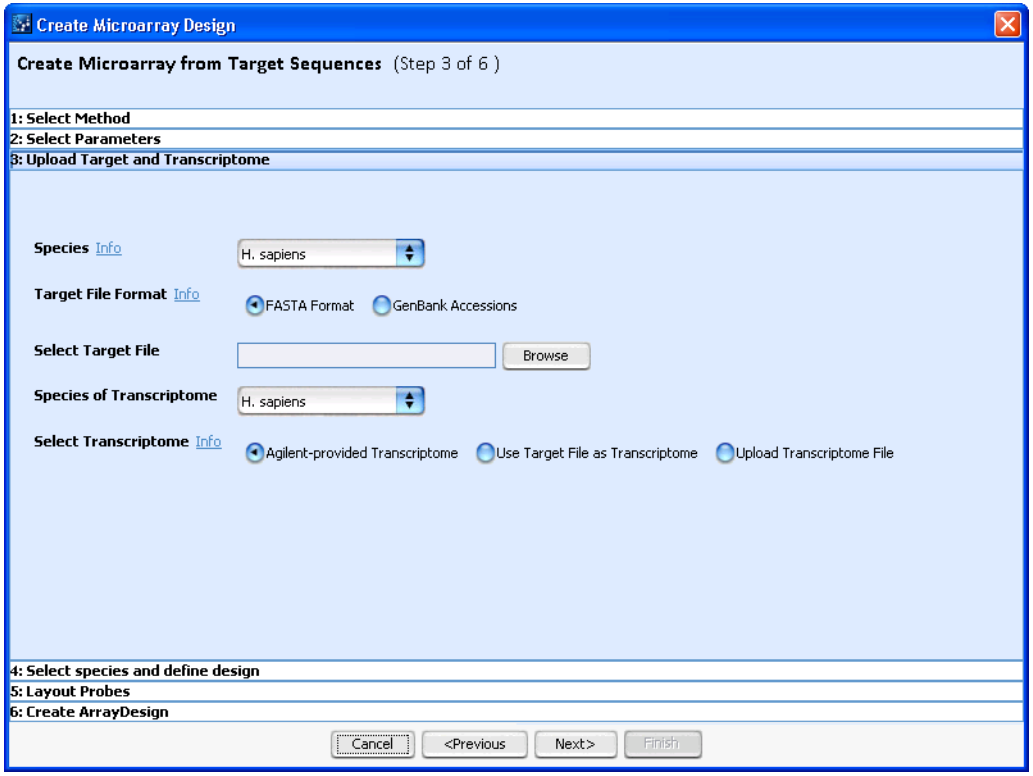


Figure 90 Create Microarray Design from Target Sequences (Wizard) – Step 3

Purpose: To assign the target and transcriptome sequences that will be used in the probe design process.

Parameter	Instructions/Comments
Species	Select the species that is associated with your target sequences.
Target File Format	Select one of these options • **FASTA format** – Select this option if you have a FASTA format file of target sequences that you want to use as the basis for the GE Probe Design process. • **GenBank Accessions** – Select this option if you have a *.txt file that contains GenBank accessions that you want to use as the basis for the GE Probe Design process. In either case, you must set the location of the file. See below, "Select Target File."
Select Target File	Displays the location of the target file. **Browse** – Opens an open dialog box where you can select the desired file. eArray resolves GenBank Accessions to actual sequence data before starting the GE Probe Design process.
Species of Transcriptome	Select the desired species. In general, select the same species as you did for the Target file. Alternatively, you can select a different species to eliminate certain cross-species hybridizations.

Parameter	Instructions/Comments
Select Transcriptome	Select the source of the transcriptome data that you want the probe design process to use. The process uses transcriptome data as a similarity database to eliminate potential probe sequences that would have significant cross-hybridization with targets other than the one of interest. • **Agilent-provided Transcriptome** – Uses one of Agilent's available species transcriptome databases. If a transcriptome is available for your species of interest, select this option. These databases have been specifically constructed for use in GE Probe Design. • **Use Target File as Transcriptome** – Uses the file you specified in Upload Target File as the transcriptome similarity database. Select this option if you are designing a "whole transcriptome" array for an organism that is not represented within the Agilent transcriptome set, and the target file represents most or all transcripts within the target transcriptome. This option works for uploaded target files containing either actual sequence data, or GenBank accessions. • **Upload Transcriptome File** – Uses a FASTA format transcriptome file that you upload as the similarity database. See below, "Upload Transcriptome File."
Upload Transcriptome File	(Available if you select **Upload Transcriptome File** in Select Transcriptome) Displays the location of the transcriptome file that will be uploaded. **Browse** – Opens an Open dialog box, where you can select a transcriptome file for upload.

Steps 4–6 – Select Species and Define Design, Layout Probes, and Create Array Design

These steps are essentially identical for all microarray-related wizards. For information about the options in these steps, see the similarly named steps in "Create Microarray Design from Existing Probe Groups (Wizard)" on page 648.

Create Microarray Design (Probe Upload wizard)

Purpose: This wizard leads you through the microarray design creation process using an uploaded file as the source of probes. You can also add additional probe groups. It is available for CGH, ChIP-on-chip, methylation, and expression applications. See "To create a microarray design from uploaded probes" on page 282.

To open: In the eArray$_{XD}$ tab, under Create Array Design Using, click **Probe Upload.**

General Commands

These commands appear at the bottom of the wizard in all steps:

Cancel Cancels the wizard and closes the dialog box.

Previous Returns to the previous step of the wizard. If this button is unavailable, you are either in the first step of the wizard, or you have progressed to a step from which you cannot go back.

Next Goes to the next step of the wizard. You can only go to the next step of the wizard if you enter all of the required settings in the current step.

Finish (Available only for the last step of the wizard) Creates a new microarray design based on all of the settings that you entered in the wizard.

This wizard has five steps:

- **Step 1 – Probe Parameter and File Details.** See "Step 1 – Probe Parameter and File Details" on page 672.
- **Step 2 – Preview of Uploaded Probes.** See "Step 2 – Preview of Uploaded Probes" on page 675.
- **Step 3 – Define Design Layout Probes, and Create Array Design.** See "Step 3–5 – Define Design, Layout Probes, and Create Array Design" on page 676

Step 1 – Probe Parameter and File Details

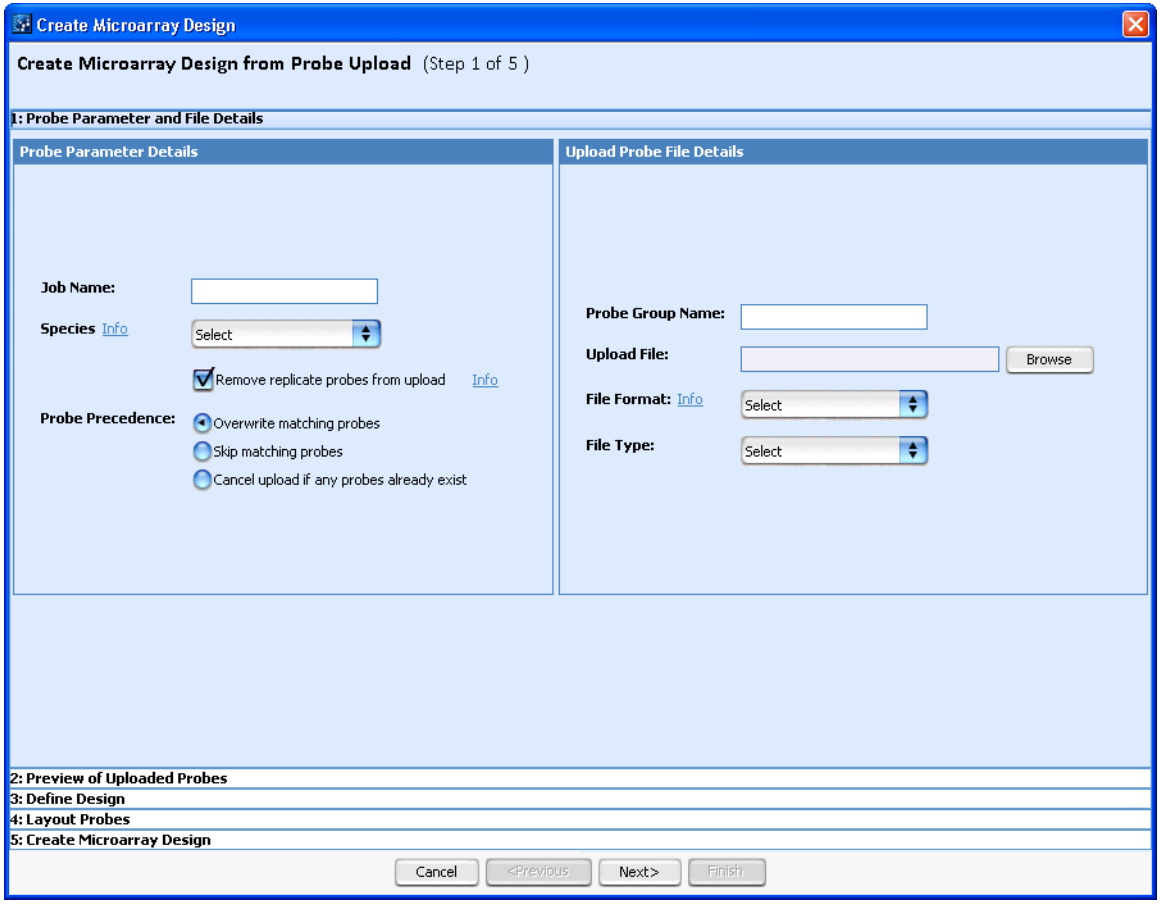


Figure 91 Create Microarray Design from Probe Upload – Step 1

Probe Parameter Details

These parameters appear:

Parameter	Description
Job Name	Type a name that will help you to identify this job.
Species	Select the desired species. The program associates all probes in the uploaded file with this species.

Parameter	Description
Remove replicate probes from upload	Mark this option to upload the first probe in each set of replicate probes in your file, and ignore the others. A replicate probe has the same Probe ID as another probe in the file. If your probe file contains replicate probes, and you do **not** mark **Remove replicate probes from upload,** the program does not upload your file.
Probe Precedence	These options tell the program what to do if it finds probes in your uploaded file that have the same Probe ID as probes that already exist in the system. Select one of these options: • **Overwrite matching probes** – The annotation of the matching uploaded probes replaces the annotation of the existing probes. You can use this option to reannotate existing probes. • **Skip matching probes** – The program ignores matching uploaded probes, but does upload other probes. • **Cancel upload if any probes already exist** – The program cancels the entire upload process if it finds a matching uploaded probe.

Upload Probe File Details

Parameter	Description
Probe Group Name	The program creates a probe group that contains the probes in your uploaded file. Type a name for this probe group.
Upload File	The location of the file that contains the probes and annotation to be uploaded. **Browse** – Opens an Open dialog box, where you can select a file of probes and annotation for upload.

Parameter	Description
File Format	The column content of your probe file. See "To prepare a file of probes and annotation for upload" on page 158. Select one of these options: • **COMPLETE** – The uploaded file contains the columns described in "Complete (for probes)" on page 881. • **MINIMAL** – The uploaded file contains the columns described in "Minimal (for probes)" on page 890.
File Type	The file type defines how the data items in the file are specified and separated. The program accepts tab-delimited text (*.tdt and *.txt) and Microsoft Excel (*.xls) files. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

CAUTION If you select **Overwrite Matching Probes** in Probe Precedence, the program reannotates matching probes when you upload you probe file. The original annotation of these probes cannot be recovered.

Step 2 – Preview of Uploaded Probes

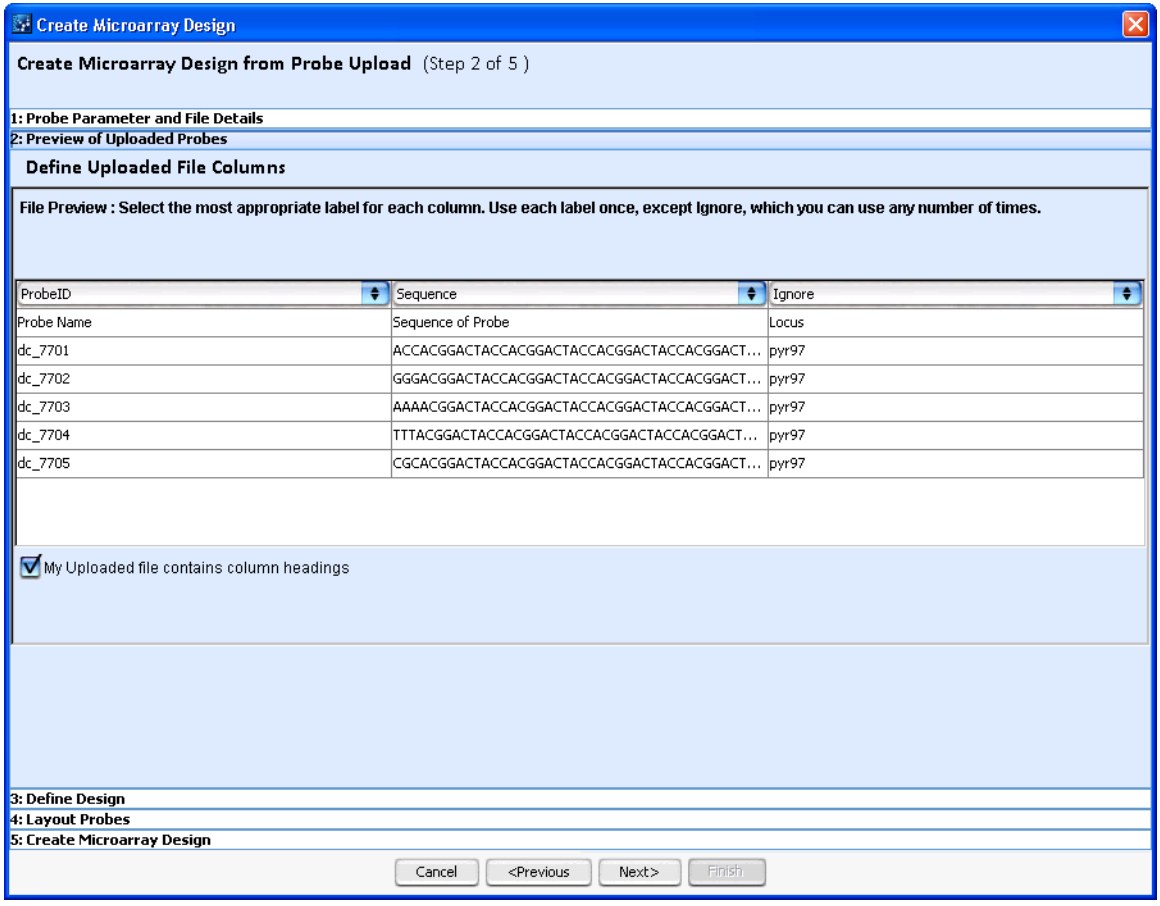


Figure 92 Create Microarray Design from Probe Upload – Step 2

This step of the wizard displays the first few rows of your probe file, and lets you identify the column content of the file.

Column headings Select the appropriate label for each column. Use every label exactly once, except Ignore, which you can use any number of times.

My uploaded file contains column headings

If you mark this option, the program ignores the first line of the file, and does not interpret it as actual probe data. The program does not interpret column heading information, even if you mark this option.

NOTE

After you click Next, the program submits a probe upload job to your server. You can continue with the rest of the wizard after the upload job has a status of Complete  .

Step 3–5 – Define Design, Layout Probes, and Create Array Design

These steps are essentially identical for all microarray-related wizards. For information about the options in these steps, see the similarly named steps in "Create Microarray Design from Existing Probe Groups (Wizard)" on page 648.

Create New Domain

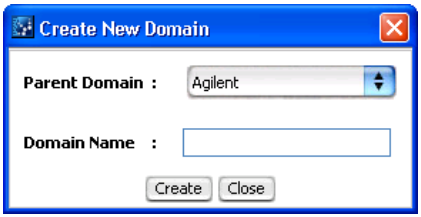


Figure 93 Create New Domain dialog box

Purpose: Lets you add a new domain (folder) to a selected location in the Design Data pane of the Navigator.

To open: In the **Design Data** pane of the Navigator, right-click your main "default" folder or any folder that you have created within it, then click **Create New Domain.**

Parent Domain The folder to which the new one will be added.

Domain Name Type a name for the new folder. Use only letters, numbers, spaces, and underscores.

Create Adds a new folder with the specified name to the selected folder in the Design Data pane of the Navigator. The program automatically adds empty Array Design and Probe Group nodes to the new folder.

Close Closes the dialog box without creating a new folder.

Create Probe Group

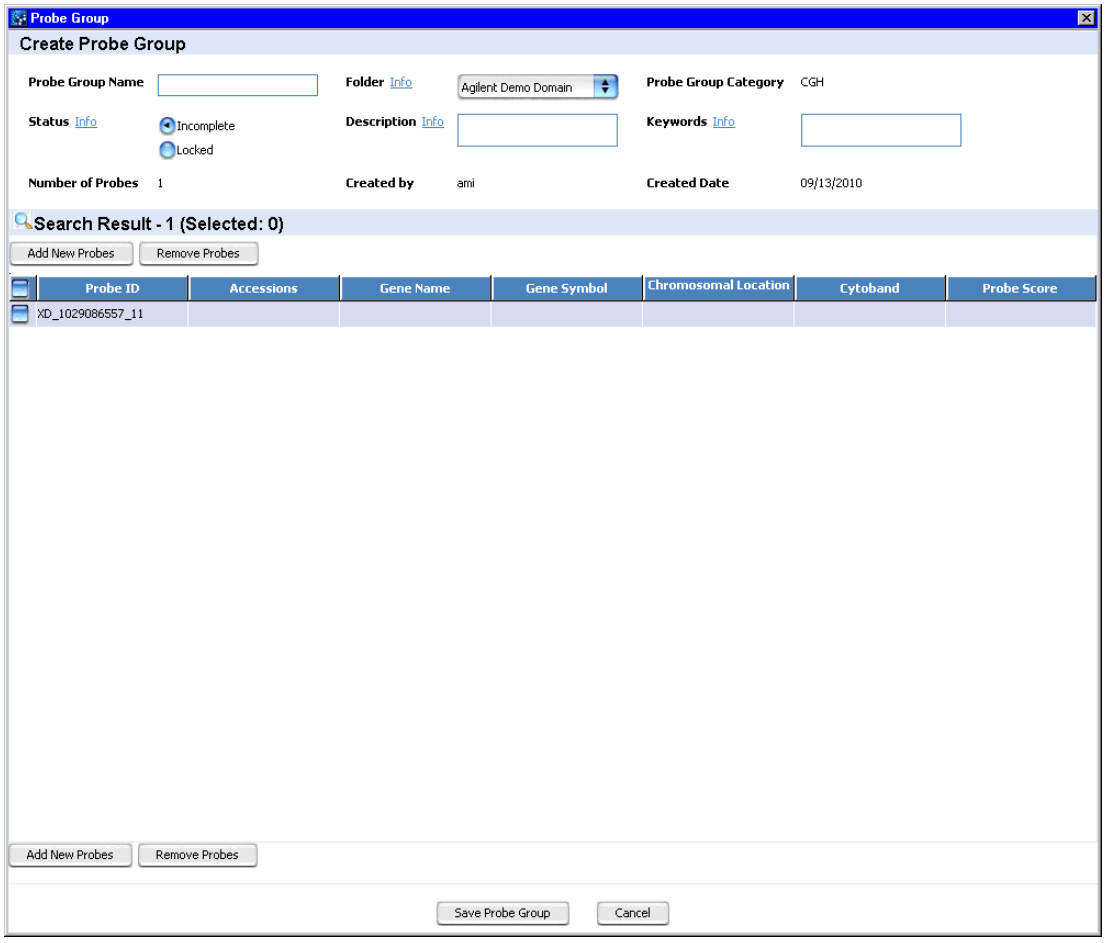


Figure 94 Create Probe Group dialog box

Purpose: Lets you define the properties of a new probe group that contains selected probes from a probe search. See "To create a new probe group" on page 204.

To open: Search for probes. In the search results, select the desired probes, then click **Create Probe Group.** See "To use the Probe Search tool to find probes" on page 92**.**

Properties

Parameter	Instructions/Details
Probe Group Name	Type a name for the probe group. eArray uses this name to reference the probe group in search results, probe group lists, view pages, and the like.
Folder	Select the desired location for the new probe group. Only the folders to which you have access appear in the list.
Probe Group Category	(Read-only, available for the CGH application type) One of these types appears: • **CGH** – The probe group is a standard CGH probe group that can included on standard CGH microarrays and on CGH+SNP microarrays. • **CGH+SNP** – The probe group is a SNP probe group that contains only Agilent SNP probes, and can be only used in CGH+SNP microarrays. See "To create a CGH+SNP microarray design" on page 301.
Status	Select one of these options: • **Incomplete** – The owner of the probe group can edit it. This option is selected by default. • **Locked** – Prevents further editing of the probe group**.** If you set the status to Locked, you cannot subsequently set the status to Incomplete.
Description	(Optional) Type a brief description of up to 4,000 characters.
Keywords	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. You can type up to 4,000 characters.
Number of Probes	(Read-only) The total number of probes in the probe group.
Created by	(Read-only) The name of the person who first saved the probe group. (Your name)
Date Created	(Read-only) The date that the probe group was first saved. (Today)

Search Result pane

The Search Result pane lists the probes that are currently in the probe group. The numbers in the title bar of the Search Result pane give the total number of probes in the probe group, and the number of probes that are currently selected.

Add New Probes Opens the Add Probes to Probe Group dialog box, where you can search for and select additional probes for the probe group. See "Add Probes to Probe Group" on page 578.

Remove Probes Removes selected probes from the probe group. To select a probe for removal, mark the check box next to the name of the probe.

Table of probes The table of probes has the columns listed below. Every probe has a Probe ID, but the availability of additional probe annotation varies.

- **Check boxes** – Mark the check box associated with an individual probe to select it for removal from the probe group. To select all of the probes on the current page for removal, mark the check box in the column heading.
- **Probe ID** – The unique probe name for each probe,
- **Additional Annotation Columns** – The availability of data for these columns varies by probe.

Page Navigation Buttons 

– (When available) Go to specific pages of probes.

Save Probe Group Saves the probe group to the selected folder, and closes the dialog box.

Cancel Closes the dialog box without creating a new probe group.

Create Probe Group (from HD or SNP search results)

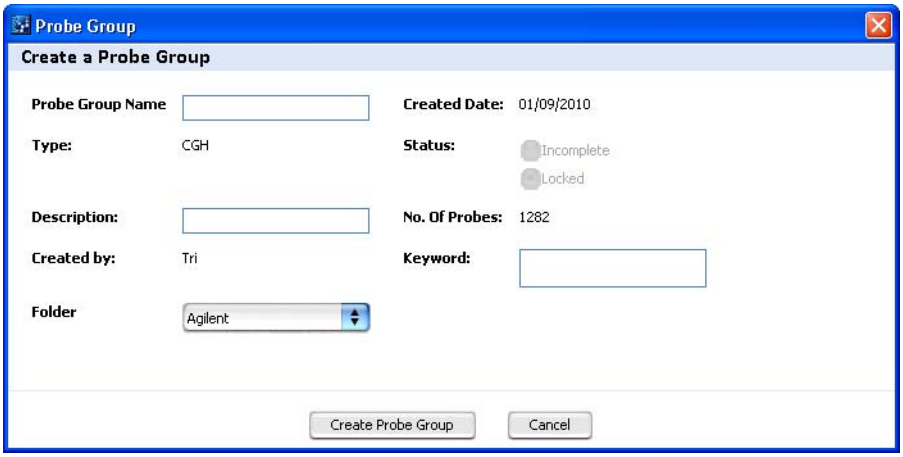


Figure 95 Create Probe Group dialog box

Purpose: Lets you create a probe group with the results of a completed HD or SNP Probe Search job. You can only create one probe group with the results of a particular probe search job. See "Searching for Agilent High Density (HD) Probes" on page 109 and "Searching for Agilent SNP Probes" on page 138.

To open: In the **Tasks** pane of the Navigator, in the **HD Search** folder, right-click the name of an HD search job, then click **Create Probe Group.** The job must have a status of Complete .

Probe Group Attributes

Attribute	Instructions/Details
Probe Group Name	Type a name for the probe group. The program uses this name to reference the probe group in search results, probe group lists, and the like.
Date Created	(Read-only) Today's date.
Type	(Read-only) • For the results of HD Probe Searches, gives the application type (CGH, ChIP-on-chip, or CH3) for which the probes were designed. • For the results of SNP Probe Searches, shows **CGH + SNP.**

Attribute	Instructions/Details
Status	• For the results of HD Probe Searches, this attribute is read-only. The program creates HD probe groups with a status of Locked. Locked probe groups cannot be edited or unlocked. • For the results of SNP Probe Searches, select one of these options: ◦ **Incomplete** – Gives the probe group a status of Incomplete, which lets you edit the probe group. ◦ **Locked** – Gives the probe group a status of Locked. Locked probe groups cannot be edited or unlocked.
Description	(Optional) Type a brief description, up to 4,000 characters in length.
No. of Probes	(Read-only) The total number of probes in the search result, and thus in the probe group that will be created. You cannot add or remove probes from an HD probe group.
Created by	(Read-only) Your name.
Keyword	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. The program can use keywords as search criteria.
Folder	Select a folder. eArray will save the new probe group to this location. Only the folders to which you have access appear in the list.

Create Probe Group Creates a new probe group with the attributes that you defined.

Cancel Closes the dialog box without creating a probe group.

Create Probes (TM Matching or Base Composition Methods)

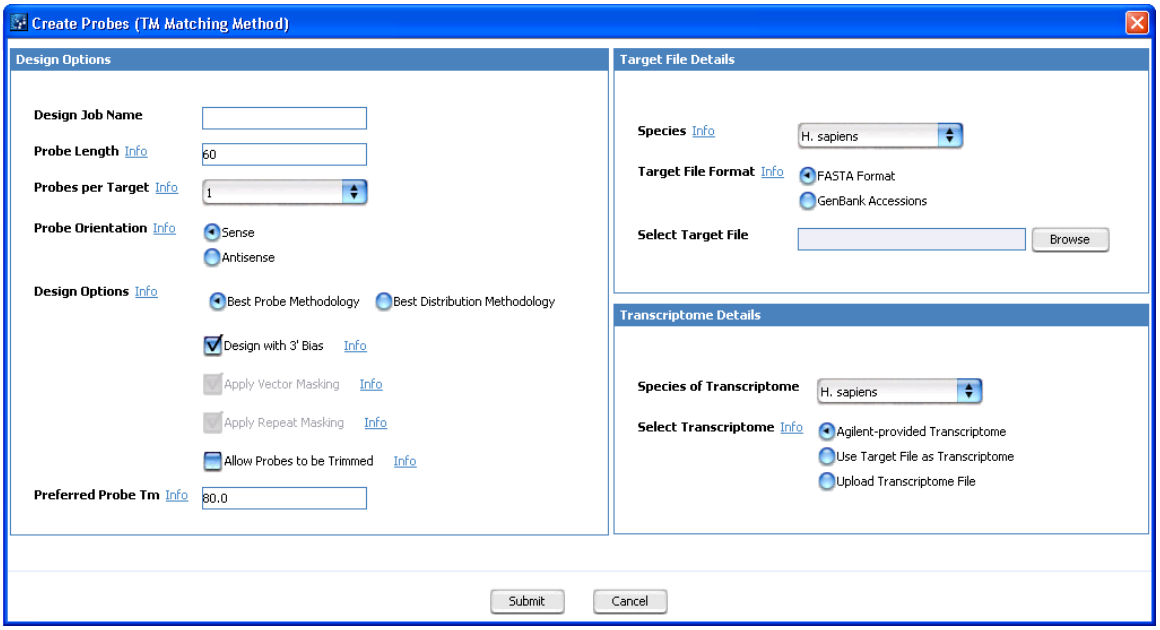


Figure 96 Create Probes dialog box as it appears for the TM Matching probe design method. The options for the Base Composition method are similar.

Purpose: Lets you set up a Gene Expression (GE) Probe Design job and submit it to the eArray Web site. GE Probe Design creates Expression type probes based on target transcript sequences that you upload, or transcripts that you identify in a file of GenBank accessions. See "To set up a GE Probe Design job" on page 167.

To open: In the eArray$_{XD}$ tab, under **Create Probes,** click one of these options:

- **Probe Design (TM)** – GE Probe Design (T_M-matching method)
- **Probe Design (BC)** – GE Probe Design (Base Composition method)

Design Options

Parameter	Instructions/Comments
Design Job Name	Type a name that will help you to later identify this specific GE probe design job.
Probe Length	Type the maximum length for the generated probes. The allowable length is from 25 to 60 bases. Agilent has found that a probe length of 60 bases provides the optimal balance between sensitivity and specificity for most applications on the Agilent *in situ* microarray platform.
Probes per Target	Select from 1 to 10 probes per target. This is the maximum number of probes the probe design process returns for each uploaded target sequence. If the target sequences are of poor quality (for example, if they contain repetitive and/or vector sequences), the probe design process can return fewer probes than you selected. Because of the length and high quality of the generated probes, Agilent recommends that you create one probe per target sequence. However, if you design multiple probes per target sequence, you can select the best of those probes after a validation process.
Probe Orientation	Select one of these options: • **Sense** – Produces probes in the sense or "coding strand" orientation, similar in sequence to the mRNA targets. Use this option if the sample preparation methodology yields cDNA or cRNA molecules. • **Antisense** – Select this option if you want probes in antisense or "template" orientation, complementary in sequence to the mRNA targets. This is the best option if your samples are directly labeled RNA.
Design Options	Select one of these options: • **Best Probe Methodology** – The probe design process favors production of the highest quality probes, rather than even coverage of each target sequence. The selection process favors empirically validated probes, and probes that are closer to the 3' end of a given primary accession. • **Best Distribution Methodology** – The probe design process favors even coverage of each target sequence, rather than production of the highest quality probes.

Parameter	Instructions/Comments
Design with 3' bias	Mark this option if you want probes derived mainly from the first 1,000 bp from the 3' end of each of your target sequences. If you use an Agilent (or other) labeling protocol that uses linear amplification, it is important to select probes from the 3′ end of the sequence. Linear amplification generates sequences that are shorter than the initial template due to the attenuation of the polymerase reaction. Because of this, most of the labeled product represents only the first 1,000 bp from the 3' end of each target sequence. It is important to design probes that represent this region.
Masking	eArray always uses both of these options in the probe design process, and they cannot be disabled. • **Apply Vector Masking** – Identifies and ignores contaminant segments during probe design. Target sequences can contain contaminant segments not actually found in the sample under study. These segments are often artifacts from cloning vectors (e.g. plasmid, phage, BAC, YAC) used in cloning and amplification processes. • **Apply Repeat Masking** – Identifies and ignores repetitive sequences within your target sequences during probe design. The genome of any given organism contains interspersed repeats and low complexity DNA sequences. These sequences, which are unique at a species level, are replicated many times throughout the genome, and are found in the transcriptome as well. Replicate regions are poor candidates for unique probes.

Parameter	Instructions/Comments
Allow Probes to be Trimmed	(Available only for T_M-Matching GE Probe Design jobs) This option lets the program remove bases from candidate probes to increase compliance with the Preferred Probe T_M. eArray will not trim probes to shorter than 45 bases. In concept, a shorter probe has less complementary sequence available, which can reduce its specificity, or infringe on its ability to form a stable duplex with the desired target. However, the risk of this occurring to a significant extent is very low.
Preferred probe Tm	(Available only for T_M-Matching GE Probe Design jobs) Type the target T_M for the probe design process (in °C). The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms. Select a probe T_M based on these factors: • The mean and standard deviation of the T_M of all potential probes that could be generated for the target transcriptome. • The hybridization temperature identified in the hybridization protocol. In practice, the target T_M should be ~20°C higher than the hybridization temperature. For example, if the hybridization temperature is 60°C, then the target probe T_M should be 80°C.

Target File Details

Parameter	Instructions/Comments
Species	Select the species associated with your target sequences.

Parameter	Instructions/Comments
Target File Format	Select one of these options • **FASTA format** – Select this option if you have a FASTA format file of target sequences that you want to use as the basis for the GE Probe Design process. • **GenBank Accessions** – Select this option if you have a *.txt file that contains GenBank accessions that you want to use as the basis for the GE Probe Design process. In either case, you must select the location of the file in Select Target File.
Select Target File	Displays the location of the target file for the GE Probe Design Process. **Browse** – Opens a dialog box, where you can select the desired target transcript file. eArray resolves GenBank Accessions to actual sequence data before it starts the GE Probe Design process.

Transcriptome Details

Parameter	Instructions/Comments
Species of Transcriptome	Select the desired species for the transcriptome similarity database. In general, the species that you select here is the same as the species represented in your uploaded file of target sequences. If you select Agilent-provided Transcriptome in Select Transcriptome (see the next parameter), the program uses the transcriptome of the selected species.
Select Transcriptome	Select the source of the transcriptome data that you want the probe design process to use. The process uses transcriptome data as a similarity database to eliminate potential probe sequences that would have significant cross-hybridization with targets other than the one of interest. • **Agilent-provided Transcriptome** – Uses one of Agilent's available species transcriptome databases. If a transcriptome is available for your species of interest, select this option. These databases have been specifically constructed for use in GE Probe Design. • **Use Target File as Transcriptome** – Uses the file you specified in Upload Target File as the transcriptome similarity database. Select this option if you are designing a "whole transcriptome" array for an organism that is not represented within the Agilent transcriptome set, and the target file represents most or all transcripts within the target transcriptome. This option works for uploaded target files containing either actual sequence data, or GenBank accessions. • **Upload Transcriptome File** – Uses a FASTA format transcriptome file that you upload as the similarity database. You select the file in Upload Transcriptome File.
Upload Transcriptome File	(Available if you select **Upload Transcriptome File** in Select Transcriptome) Displays the location of the transcriptome file that eArray will use as a similarity database in the probe design process. **Browse** – Opens a dialog box, where you can select the desired FASTA format transcriptome file.

Submit Submits the GE Probe Design job to the eArray Web site.

Cancel Cancels the GE probe design job, and closes the dialog box.

Design Probes

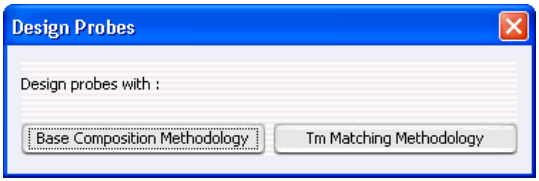


Figure 97 Design Probes dialog box

Purpose: Lets you select the type of Gene Expression Probe Design job to start, based on the selected results of a biological network search. This dialog box is available for the Expression application type. See "To use a biological network to find or create probes" on page 193.

To open: In the Network Inspector, after you have selected the desired nodes from the network, click **Design Probes.**

Base Composition Methodology Loads a file of selected nodes as GenBank accessions, and opens the Create Probes (Base Composition Method) dialog box. See "Create Probes (TM Matching or Base Composition Methods)" on page 683.

With base composition methodology, the resultant probes adhere as closely as possible to the base composition profile that gives optimal performance on the Agilent platform. The probes are all of equal length. This is the standard method, and it works best with Agilent protocols, and most eukaryotic organisms.

Tm Matching Methodology Loads a file of selected nodes as GenBank accessions, and opens the Create Probes (Tm Matching Method) dialog box. See "Create Probes (TM Matching or Base Composition Methods)" on page 683.

With Tm matching methodology, the resultant probes have melting temperatures (T_M) as similar as possible to a value that you enter. Probes can be all of equal length, or probes can be trimmed to increase compliance with the desired T_M. This methodology can work well when you design probes for prokaryotic organisms.

Design Results (Bait Tiling)

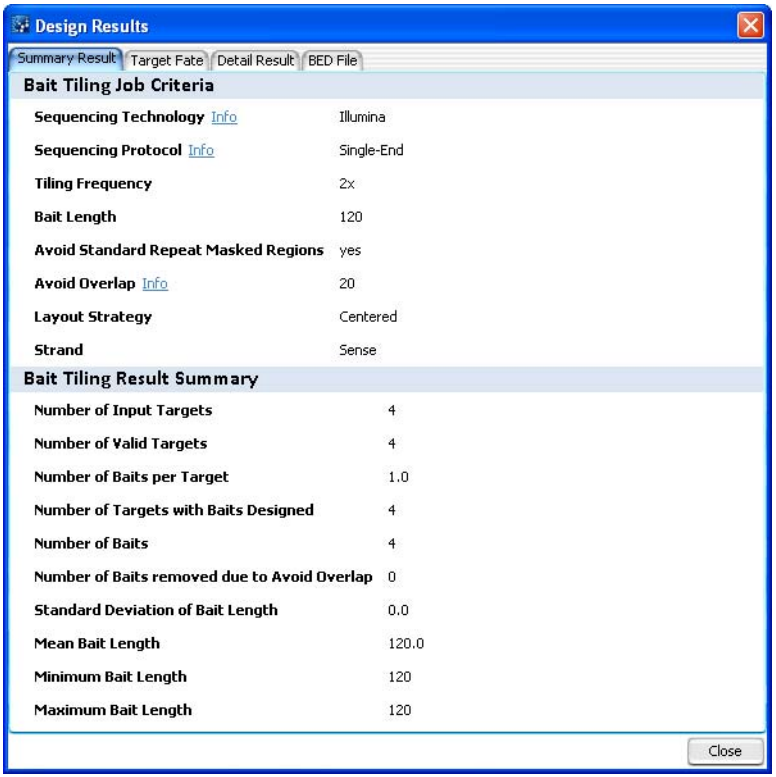


Figure 98 Design Results dialog box (Bait Tiling) – Summary Result tab

Purpose: (Available for the SureSelect Target Enrichment application type) Lets you view the results of a Bait Tiling job. See "To set up a Bait Tiling job" on page 378.

To open: In the Tasks pane of the Navigator, in the appropriate Bait Tiling folder, right-click the name of the desired Bait Tiling job, then click **View Design Details.**

This dialog box is organized into four tabs.

Summary Result tab

Bait Tiling Job Criteria

The criteria that were defined for the job by the user. For details, refer to "To set up a Bait Tiling job" on page 378.

Bait Tiling Result Summary

This information appears:

Parameter	Description
Number of Input Targets	The number of genomic intervals for which Bait Tiling was requested.
Number of Valid Targets	The number of genomic intervals that passed validation.
Number of Baits per Target	The average number of bats that were designed for each input genomic interval.
Number of Targets with Baits Designed	The number of input genomic intervals for which baits were designed.
Number of Baits	The total number of baits that were designed by the bait tiling process for this job.
Number of Baits Removed Due to Avoid Overlap	The number of designed baits that were removed from the final result because they were designed to avoided genomic regions.
Standard Deviation of Bait Length	The standard deviation in the length of the baits that were designed. Because Bait Tiling designs baits of uniform length, this value is always 0.0.
Mean Bait Length	The mean bait length of the probes that were designed by the Bait Tiling process. This value matches the bait length that was selected for the Bait Tiling process.
Minimum Bait Length	The length of the shortest bait that was designed by the Bait Tiling process. Because Bait Tiling designs baits of uniform length, this value matches the bait length that was selected for the Bait Tiling process.
Maximum Bait Length	The length of the longest bait that was designed by the Bait Tiling process. Because Bait Tiling designs baits of uniform length, this value matches the bait length that was selected for the Bait Tiling process.

Target Fate tab

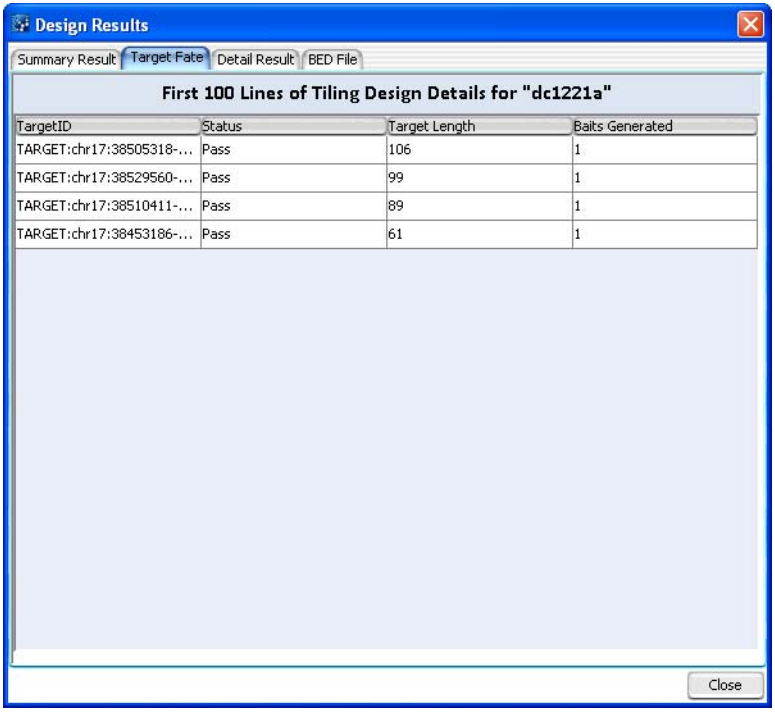


Figure 99 Design Results dialog box (Bait Tiling) – Target Fate tab

This tab lists the names of the target sequences that were submitted for Bait Tiling, and the number of baits that were produced from each. To change the width of a column, drag the border between the column and its neighbor left or right, as needed. These columns appear:

Target ID The genomic intervals that were submitted for tiling.

Status Indicates whether or not a given target genomic interval passed validation. To pass, intervals must refer to valid genomic locations for the given species, and they must be formatted correctly.

Target Length The length of the given target interval, in base pairs.

Baits Generated The number of baits that the Bait Tiling process produced from the given target sequence.

Detail Result tab

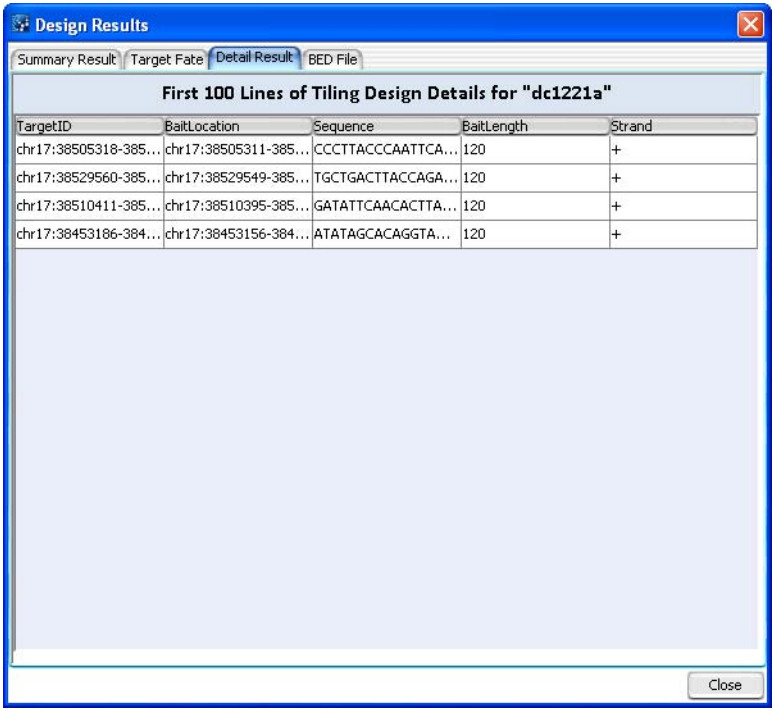


Figure 100 Design Results dialog box (Bait Tiling) – Detail Result tab

This tab lists up to the first 100 baits that were produced by the Bait Tiling process. To change the width of a column, drag the border between the column and its neighbor left or right, as needed. These columns appear:

Column	Description
Target ID	The input genomic interval to which the bait was designed.
Bait Location	The exact genomic coordinates to which the bait is designed.
Sequence	The nucleotide sequence of the bait, in 5' to 3' orientation.

Column	Description
Bait Length	The length of the bait in nucleotides.
Strand	The orientation of the bait, which can be + (sense) or – (antisense). Sense baits have a sequence that is similar to the sense strand of the DNA; antisense baits have a sequence that is complementary to it.

BED file tab

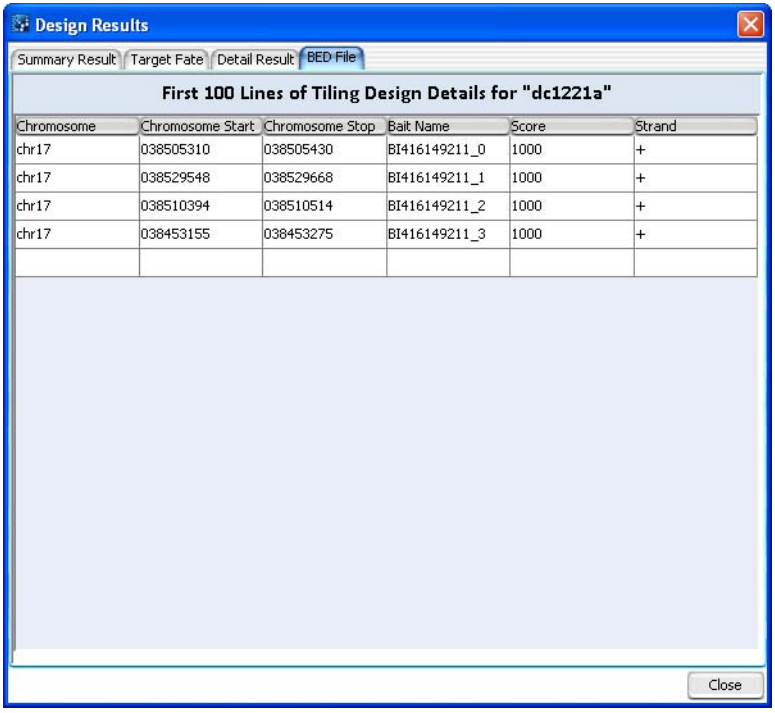


Figure 101 Design Results dialog box (Bait Tiling) – BED File tab

This tab displays up to the first 100 lines of the BED annotation track file that is generated by the Bait Tiling process. You can download the complete file, and view it in a compatible genome browser. See "To download Bait Tiling results" on page 387.

The following columns appear. Data for each bait appears on a separate line.

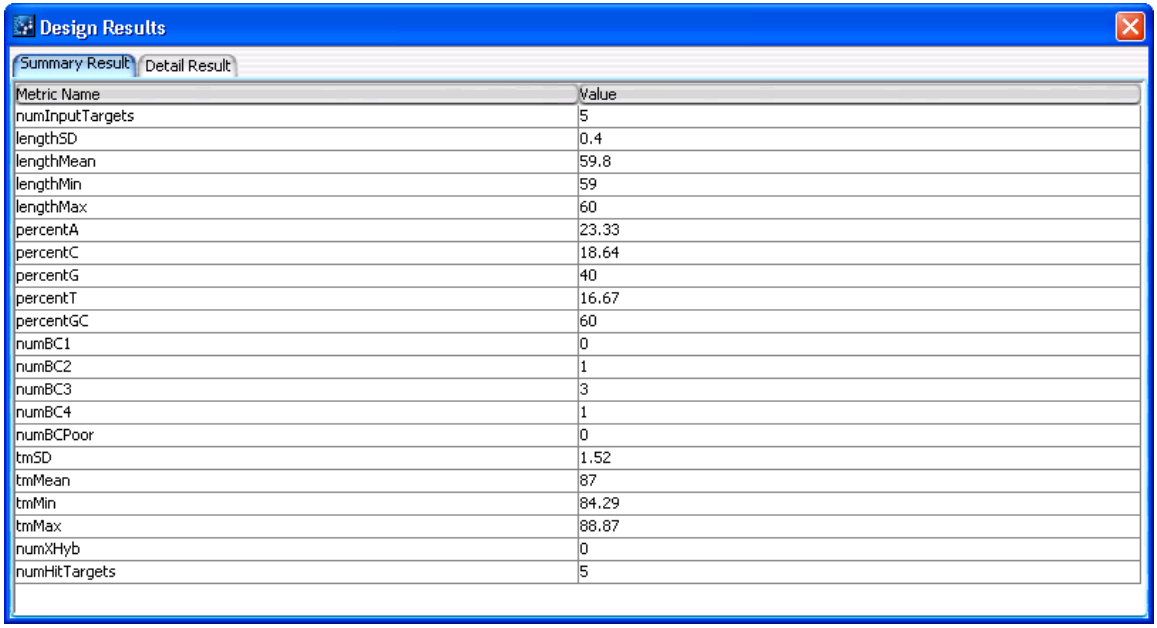
Column	Description
Chromosome	The chromosome to which the bait is designed.
Chromosome Start	On the given chromosome, the first base to which the bait is designed.
Chromosome Stop	On the given chromosome, the last base to which the bait is designed.
Bait Name	The ID of the bait, as it will appear in the genome browser.
Score	The level of gray with which the bait will appear. In general, the program sets a value of 1000, which displays the bait in black.
Strand	The strand of the DNA on which the bait will appear, which can be + (sense) or – (antisense).

Design Results (Gene Expression Probe Check)

Purpose: Lets you view the metrics and statistics that were calculated for the probes in a GE Probe Check job. "To check GE probe quality" on page 208.

To Open: In the Tasks pane of the Navigator, in the **Probe Check** folder, right-click the name of a GE Probe Check job, then click **View Result.** The results appear in two separate tabs.

Summary Result tab



Metric Name	Value
numInputTargets	5
lengthSD	0.4
lengthMean	59.8
lengthMin	59
lengthMax	60
percentA	23.33
percentC	18.64
percentG	40
percentT	16.67
percentGC	60
numBC1	0
numBC2	1
numBC3	3
numBC4	1
numBCPoor	0
tmSD	1.52
tmMean	87
tmMin	84.29
tmMax	88.87
numXHyb	0
numHitTargets	5

Figure 102 Design Results (GE Probe Check) – Summary File tab

This tab displays overall statistics about the submitted probes. These metrics appear:

Metric	Description
numInputTargets	The number of probes submitted for analysis.
lengthSD	The standard deviation of the lengths of the probes that were analyzed, in nucleotides.
lengthMean	The mean length (in nucleotides) of the probes that were analyzed.
lengthMin	The length (in nucleotides) of the shortest probe that was analyzed.
lengthMax	The length (in nucleotides) of the longest probe that was analyzed.
percentA	For all of the probes analyzed, the fraction of bases that are A bases.
percentC	For all of the probes analyzed, the fraction of bases that are C bases.
percentG	For all of the probes analyzed, the fraction of bases that are G bases.
percentT	For all of the probes analyzed, the fraction of bases that are T bases.
percentGC	For all of the probes analyzed, the fraction of bases that are G and C bases, collectively.
numBC1	The number of probes that have a base composition score of BC_1. This is the best base composition score.
numBC2	The number of probes that have a probe quality score of BC_2.
numBC3	The number of probes that have a probe quality score of BC_3.
numBC4	The number of probes that have a probe quality score of BC_4.
numBCPoor	The number of probes that have a probe quality score of BC_Poor. This is the worst base composition score.
tmSD	The standard deviation of the T_Ms (in °C) of the probes that were analyzed.
tmMean	The mean T_M (in °C) of the probes that were analyzed.
tmMin	The T_M (in °C) of the probe that has the lowest T_M
tmMax	The T_M (in °C) of the probe that has the highest T_M
numXHyb	The number of probes that are likely to hybridize to more than one location in the target genome.
numHitTargets	The number of probes that are likely to hybridize with at least one location in the target genome.

Detail Result tab

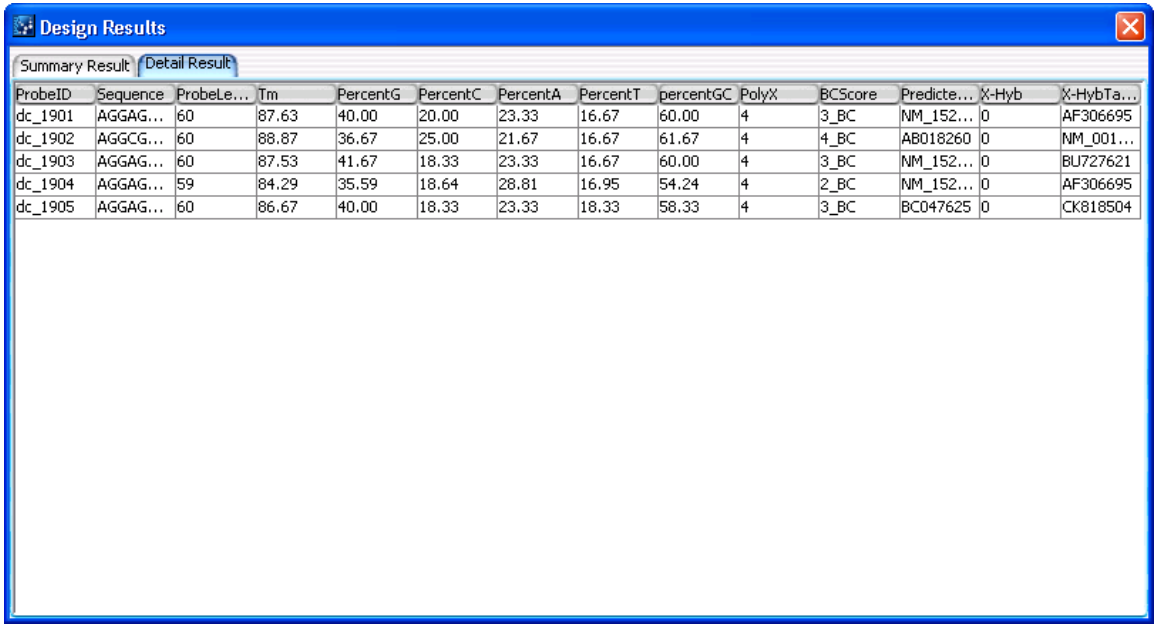


Figure 103 Design Results (GE Probe Check) – Detail Result tab

This tab displays identifying information and calculated statistics for each probe that was analyzed by the GE Probe Check job. These items appear:

Item	Description
ProbeID	The name of the probe.
Sequence	The nucleotide sequence of the probe, in 5' to 3' orientation.
ProbeLength	The length of the probe, in nucleotides.
Tm	The temperature (in °C) at which the probe and its target are expected to exist in a 50:50 mixture of duplex and single-stranded forms.
PercentG	The fraction of the bases in the probe that are G bases.
PercentC	The fraction of the bases in the probe that are C bases.
PercentA	The fraction of the bases in the probe that are A bases.

Item	Description
PercentT	The fraction of the bases in the probe that are T bases.
PercentGC	The fraction of the bases in the probe that are G and C bases, collectively.
PolyX	The longest homeomeric run (run of the same kind of base) in the probe. For example, the sequence ACCCGGGGTTTTTT has a polyX of 6, because of its 6 T bases.
BCScore	The base composition score of the probe. 1_BC is the best, and Poor_BC is the worst.
PredictedTarget	The transcript in the similarity database that forms the most energetically favorable duplex with the probe sequence.
X-Hyb	To effectively measure the expression level of a transcript, you must have probes that bind uniquely to this target transcript. If sequences other than the target transcript hybridize to a probe, this is a cross-hybridization (X-Hyb) event. The X-Hyb potential score is 0 if the only transcript predicted to form a duplex with a probe is the predicted target. If one or more other transcripts are predicted to form a duplex with a probe, the X-Hyb potential score is 1. A score of 0 is desirable.
X-Hyb Target	The transcript in the similarity database that forms the second most energetically favorable duplex with the probe sequence.

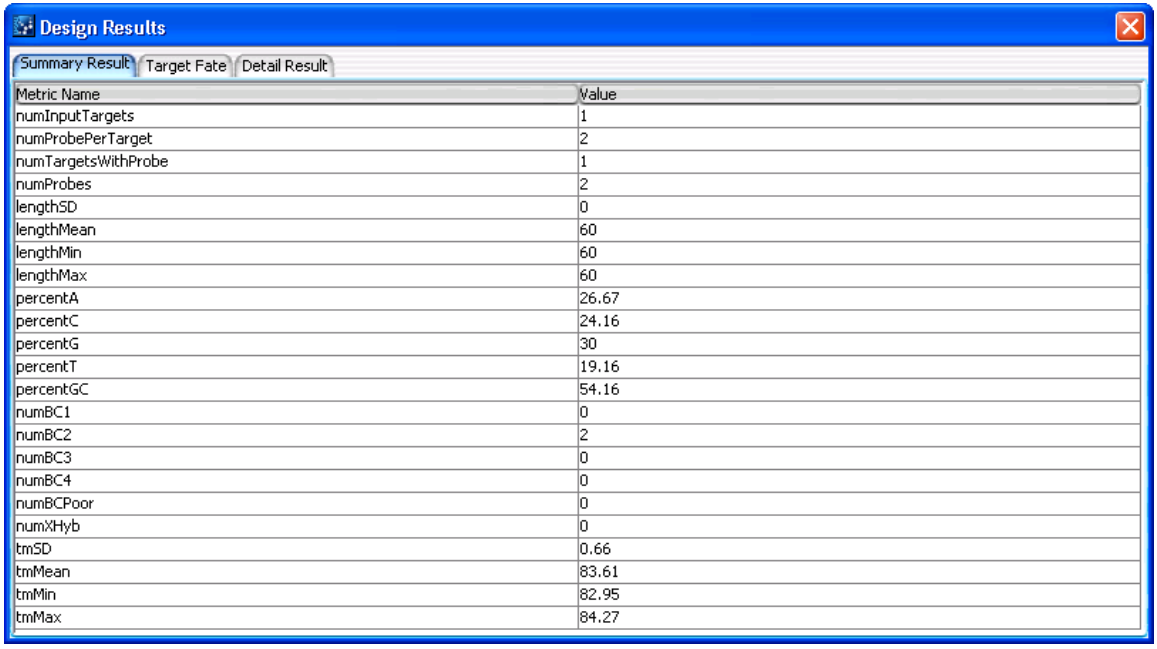
Design Results (Gene Expression Probe Design)

Purpose: Displays the results of a Gene Expression (GE) Probe Design job. See "To set up a GE Probe Design job" on page 167 and "To view the results of a probe design or tiling job" on page 181.

To open: In the tasks pane, in the Probe Design folder, right-click the name of the desired job, then click **View Result.** This option is only available after the probe design job has been completed.

Results are available in three tabs: Summary Result, Target Fate, and Detail Result. Each of these tabs corresponds to one of the result files available for GE Probe Design jobs. For information about downloading these results, see "To download probe design or tiling results" on page 182.

Summary Result tab



Metric Name	Value
numInputTargets	1
numProbePerTarget	2
numTargetsWithProbe	1
numProbes	2
lengthSD	0
lengthMean	60
lengthMin	60
lengthMax	60
percentA	26.67
percentC	24.16
percentG	30
percentT	19.16
percentGC	54.16
numBC1	0
numBC2	2
numBC3	0
numBC4	0
numBCPoor	0
numXHyb	0
tmSD	0.66
tmMean	83.61
tmMin	82.95
tmMax	84.27

Figure 104 Design Results (GE Probe Design) – Summary Result tab

This tab displays overall statistics about the designed probes. These statistics appear:

Statistic	Description
numInputTargets	The number of target sequences submitted for probe design.
numProbePer Target	The number of probes requested for each target sequence.
numTargetsWithProbe	The number of target sequences to which probe(s) were designed.
numProbes	The total number of probes that were designed.
lengthSD	The standard deviation of the lengths of the probes that were designed, in nucleotides.
lengthMean	The mean length (in nucleotides) of the probes that were designed.
lengthMin	The length (in nucleotides) of the shortest probe that was designed.

Statistic	Description
lengthMax	The length (in nucleotides) of the longest probe that was designed.
percentA	For all of the probes designed, the fraction of bases that are A bases.
percentC	For all of the probes designed, the fraction of bases that are C bases.
percentG	For all of the probes designed, the fraction of bases that are G bases.
percentT	For all of the probes designed, the fraction of bases that are T bases.
percentGC	For all of the probes designed, the fraction of bases that are G and C bases, collectively.
numBC1	The number of probes that have a base composition score of BC_1. This is the best score.
numBC2	The number of probes that have a base composition score of BC_2.
numBC3	The number of probes that have a base composition score of BC_3.
numBC4	The number of probes that have a base composition score of BC_4.
numBCPoor	The number of probes that have a base composition score of BC_Poor. This is the worst score.
numXHyb	The number of probes that are likely to hybridize to more than one location in the target genome.
tmSD	The standard deviation of the T_Ms (in °C) of the probes that were designed.
tmMean	The mean T_M (in °C) of the probes that were designed.
tmMin	The T_M (in °C) of the probe that has the lowest T_M
tmMax	The T_M (in °C) of the probe that has the highest T_M

Target Fate tab

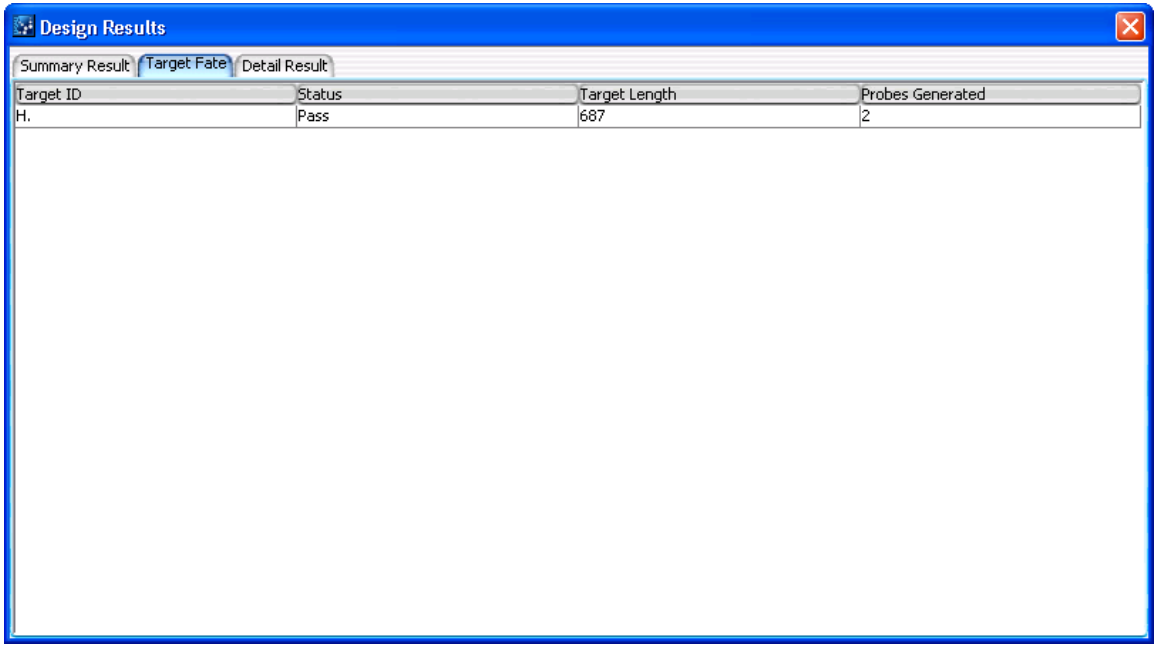


Figure 105 Design Results dialog box (GE Probe Design) – Target Fate tab

This tab gives general information about each target sequence that you submitted when you set up the GE Probe Design job.

These columns can appear:

Column	Description
Target ID	The name of each target, as defined in your uploaded FASTA-format target file.
Status	Whether or not each target sequence passed validation.
Target Length	The length of each target sequence, in base pairs.
Probes Generated	The number of probes designed to each specific target sequence.

Detail Result tab

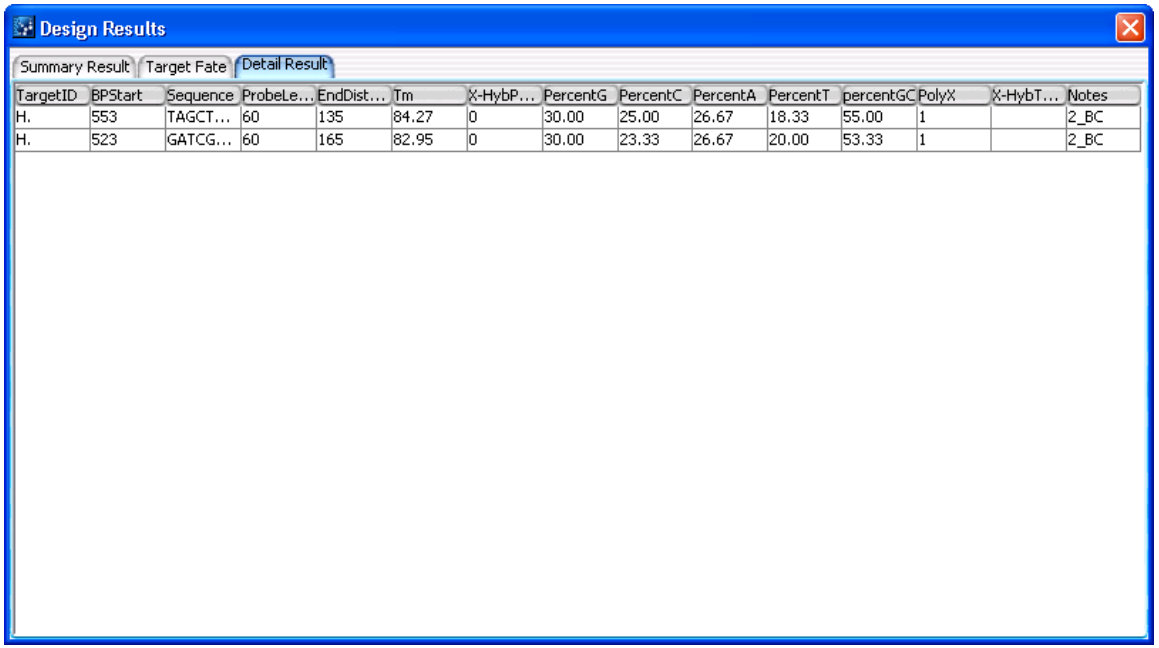


Figure 106 Design Results dialog box (GE Probe Design) – Detail Result tab

This tab displays identifying information and calculated statistics for each probe. The following columns can appear. You can change the width of a column—in the column heading row, drag its border with the neighboring column left or right, as needed.

Item	Description
TargetID	The name of the target to which the probe was designed.
BPStart	The location of the first base in the given target to which the probe is designed.
Sequence	The nucleotide sequence of the probe, in 5' to 3' orientation.
ProbeLength	The length of the probe, in nucleotides.
EndDistance	The number of base pairs from the 3' end of the given target to which the 5'-most nucleotide of the probe was designed.

Item	Description
Tm	The temperature (in °C) at which the probe and its target are expected to exist in a 50:50 mixture of duplex and single-stranded forms.
X-Hyb Potential	If you are trying to measure the expression level of a transcript, you must have probes that bind uniquely to this target transcript. If sequences other than the target transcript hybridize to a probe, this is a cross-hybridization (X-Hyb) event. The X-Hyb potential score is 0 if the only transcript predicted to form a duplex with a probe is the predicted target. If one or more other transcripts are predicted to form a duplex with a probe, the X-Hyb potential score is 1. A score of 0 is desirable.
PercentG	The fraction of the bases in the probe that are G bases.
PercentC	The fraction of the bases in the probe that are C bases.
PercentA	The fraction of the bases in the probe that are A bases.
PercentT	The fraction of the bases in the probe that are T bases.
PercentGC	The fraction of the bases in the probe that are G and C bases, collectively.
PolyX	The longest homeomeric run (run of the same kind of base) in the probe. For example, the sequence ACCCGGGGTTTTTT has a polyX of 6, because of its 6 T bases.
X-Hyb Target	The transcript in the similarity database that forms the second most energetically favorable duplex with the probe sequence.
Notes	The base composition score of the probe. 1_BC is the best, and Poor_BC is the worst.

Design Results (Genomic Tiling)

Purpose: Lets you view the results of a Genomic Tiling job. See "To set up a Genomic Tiling job" on page 176.

To open: In the Tasks pane of the Navigator, in the appropriate Genomic Tiling folder, right-click the name of the desired job, then click **View Result.** The dialog box contains several tabs

Tabs

- **Summary Result** – See "Summary Result Tab" on page 706
- **Target Fate** – See "Target Fate Tab" on page 708
- **Detail Result** – See "Detail Result Tab" on page 709
- **BED File** – See "BED File tab" on page 710

Close Closes the dialog box.

Summary Result Tab

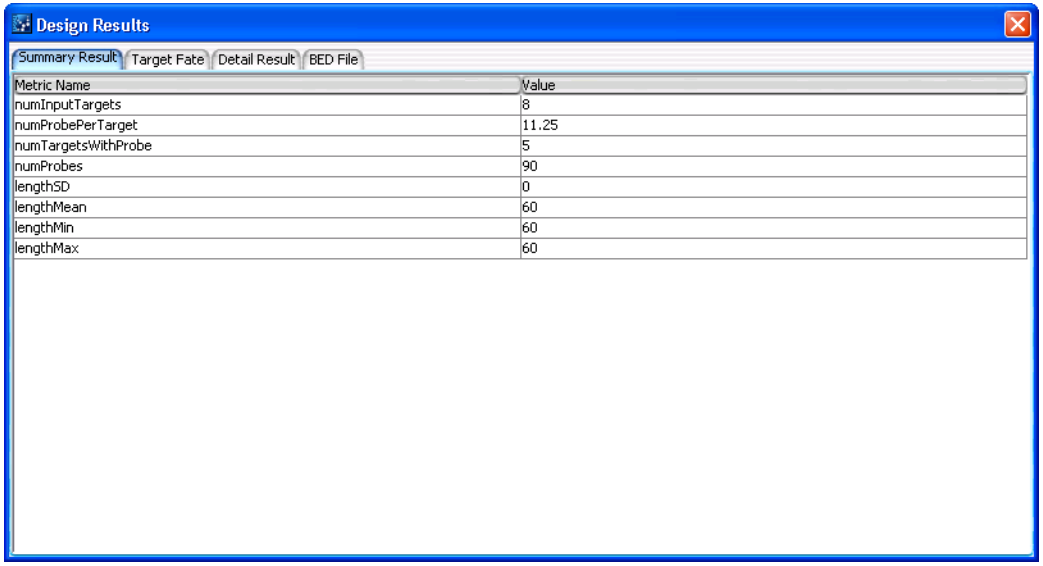


Figure 107 Design Results dialog box (Genomic Tiling) – Summary Result tab

Purpose: Lets you view overall statistics about the probes that were designed by the Genomic Tiling job.

These statistics appear:

Statistic	Details
numInputTargets	The number of separate target sequences that were submitted for tiling.
numProbePerTarget	The average number of probes designed to each genomic interval.
numTargetsWithProbe	The number of input target sequences to which probes were actually designed.
numProbes	The total number of probes designed by the tiling job.
lengthSD	For the population of probes generated by the tiling job, the standard deviation of the length of probes, in nucleotides.
lengthMean	The mean length, in nucleotides, of the population of probes generated by the tiling job.
lengthMin	The length in nucleotides of the shortest probe produced by the tiling job.
lengthMax	The length in nucleotides of the longest probe produced by the tiling job.

Target Fate Tab

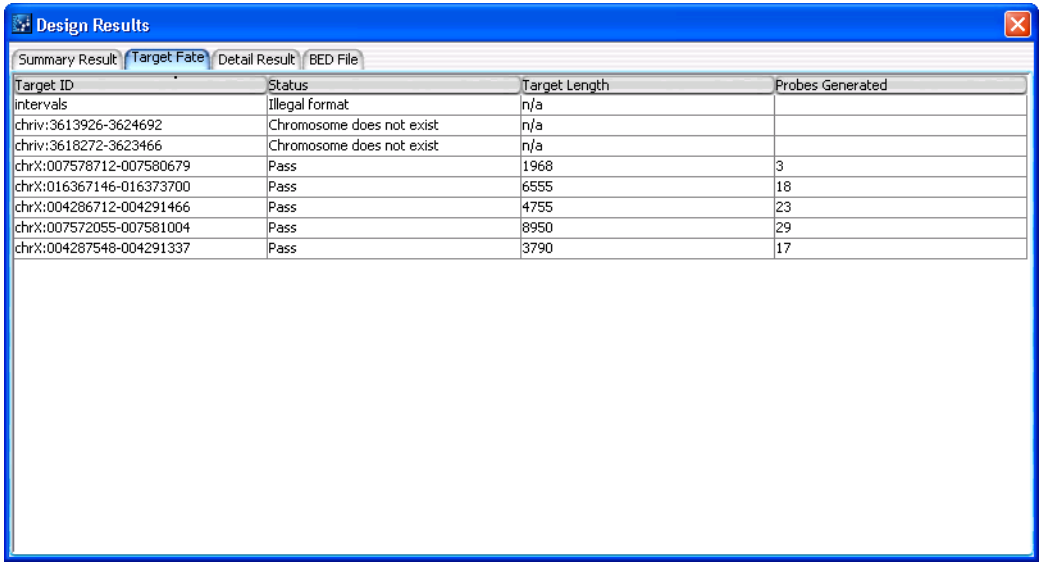


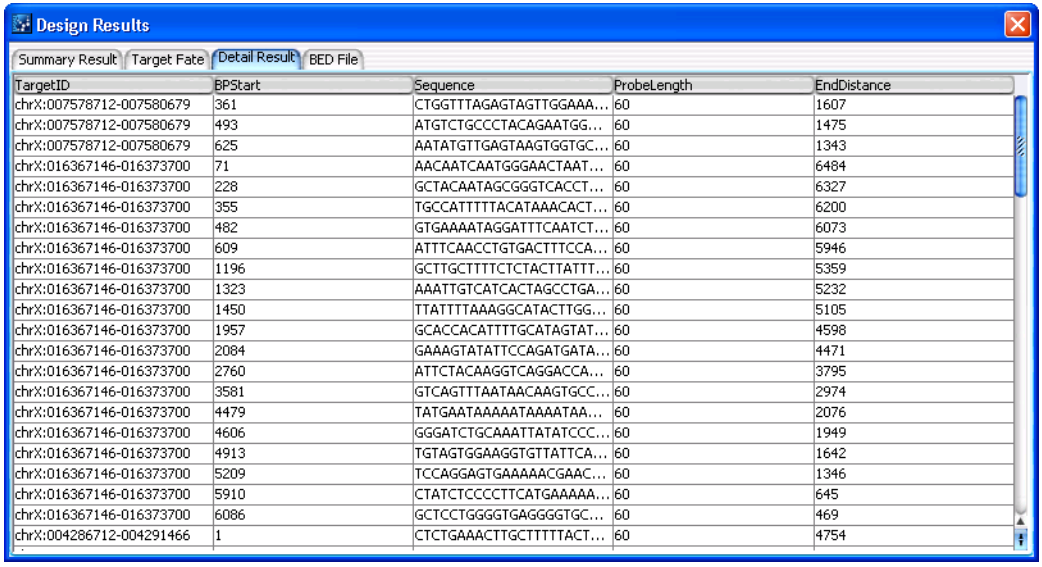
Figure 108 Design Results dialog box (Genomic Tiling) – Target Fate tab

This tab lists the names of the input genomic intervals for the Genomic Tiling job, and the number of probes that were designed from each.

The following columns appear:

Column	Description
Target ID	The name of each genomic interval that was supplied as input.
Status	Indicates whether or not a given interval passed validation.
Target Length	The length of the given target sequence or interval, in base pairs.
Probes Generated	The number of probes that the tiling job designed from each genomic interval.

Detail Result Tab



TargetID	BPStart	Sequence	ProbeLength	EndDistance
chrX:007578712-007580679	361	CTGGTTTAGAGTAGTTGGAAA...	60	1607
chrX:007578712-007580679	493	ATGTCTGCCCTACAGAATGG...	60	1475
chrX:007578712-007580679	625	AATATGTTGAGTAAGTGGTGC...	60	1343
chrX:016367146-016373700	71	AACAATCAATGGGAACTAAT...	60	6484
chrX:016367146-016373700	228	GCTACAATAGCGGGTCACCT...	60	6327
chrX:016367146-016373700	355	TGCCATTTTTACATAAACACT...	60	6200
chrX:016367146-016373700	482	GTGAAAATAGGATTTCAATCT...	60	6073
chrX:016367146-016373700	609	ATTTCAACCTGTGACTTTCCA...	60	5946
chrX:016367146-016373700	1196	GCTTGCTTTTCTCTACTTATTT...	60	5359
chrX:016367146-016373700	1323	AAATTGTCATCACTAGCCTGA...	60	5232
chrX:016367146-016373700	1450	TTATTTTAAAGGCATACTTGG...	60	5105
chrX:016367146-016373700	1957	GCACCACATTTTGCATAGTAT...	60	4598
chrX:016367146-016373700	2084	GAAAGTATATTCCAGATGATA...	60	4471
chrX:016367146-016373700	2760	ATTCTACAAGGTCAGGACCA...	60	3795
chrX:016367146-016373700	3581	GTCAGTTTAATAACAAGTGCC...	60	2974
chrX:016367146-016373700	4479	TATGAATAAAAAATAAAATAA...	60	2076
chrX:016367146-016373700	4606	GGGATCTGCAAATTATATCCC...	60	1949
chrX:016367146-016373700	4913	TGTAGTGGAAGGTGTTATTCA...	60	1642
chrX:016367146-016373700	5209	TCCAGGAGTGAAAAACGAAC...	60	1346
chrX:016367146-016373700	5910	CTATCTCCCCTTCATGAAAAA...	60	645
chrX:016367146-016373700	6086	GCTCCTGGGGTGAGGGGTGC...	60	469
chrX:004286712-004291466	1	CTCTGAAACTTGCTTTTTACT...	60	4754

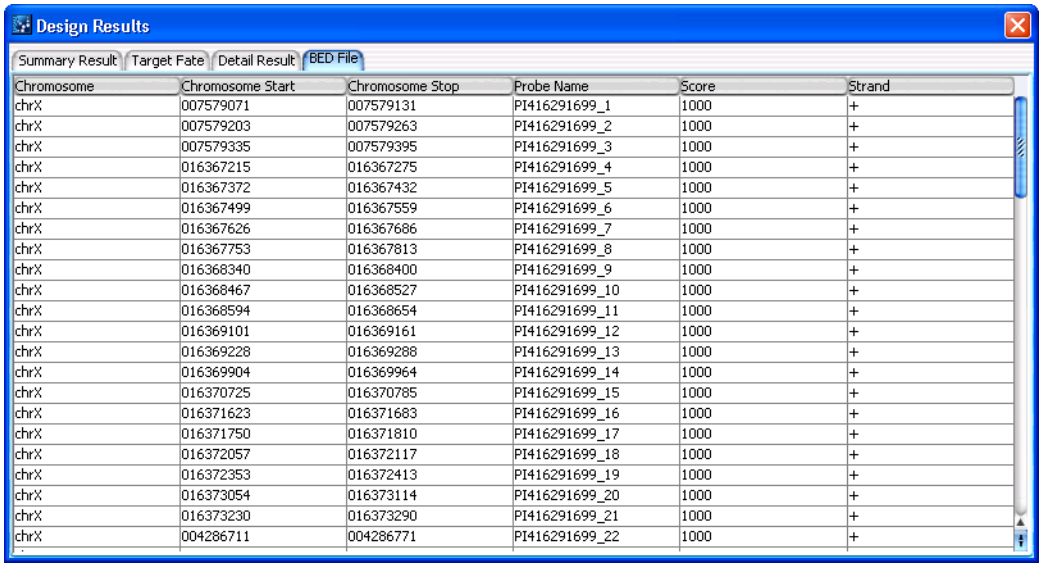
Figure 109 Design Results dialog box (Genomic Tiling) – Detail Result tab

This tab lets you view information about the first 100 probes generated by the Genomic Tiling job.

The following columns can appear. You can change the width of a column–In the column heading row, drag its border with the neighboring column left or right, as needed.

Column	Description
Target ID	The genomic interval from which the probe was derived.
BP Start	The location of the first base pair in the given interval to which the probe was designed.
Sequence	The nucleotide sequence of the probe in 5' to 3' orientation.
Probe Length	The number of nucleotides in the probe.
End Distance	The number of base pairs from the 3' end of the interval to which the last nucleotide in the probe binds.

BED File tab



Chromosome	Chromosome Start	Chromosome Stop	Probe Name	Score	Strand
chrX	007579071	007579131	PI416291699_1	1000	+
chrX	007579203	007579263	PI416291699_2	1000	+
chrX	007579335	007579395	PI416291699_3	1000	+
chrX	016367215	016367275	PI416291699_4	1000	+
chrX	016367372	016367432	PI416291699_5	1000	+
chrX	016367499	016367559	PI416291699_6	1000	+
chrX	016367626	016367686	PI416291699_7	1000	+
chrX	016367753	016367813	PI416291699_8	1000	+
chrX	016368340	016368400	PI416291699_9	1000	+
chrX	016368467	016368527	PI416291699_10	1000	+
chrX	016368594	016368654	PI416291699_11	1000	+
chrX	016369101	016369161	PI416291699_12	1000	+
chrX	016369228	016369288	PI416291699_13	1000	+
chrX	016369904	016369964	PI416291699_14	1000	+
chrX	016370725	016370785	PI416291699_15	1000	+
chrX	016371623	016371683	PI416291699_16	1000	+
chrX	016371750	016371810	PI416291699_17	1000	+
chrX	016372057	016372117	PI416291699_18	1000	+
chrX	016372353	016372413	PI416291699_19	1000	+
chrX	016373054	016373114	PI416291699_20	1000	+
chrX	016373230	016373290	PI416291699_21	1000	+
chrX	004286711	004286771	PI416291699_22	1000	+

Figure 110 Design Results dialog box (Genomic Tiling) – BED File tab

Purpose: This tab displays up to the first 100 lines of the BED annotation track file that is generated by the Genomic Tiling job. You can download the complete file, and view it with a compatible genome browser. See "To download probe design or tiling results" on page 182.

The following columns appear. Data for each probe appears on a separate line.

Column	Description
Chromosome	The chromosome to which the probe is designed.
Chromosome Start	On the given chromosome, the first base to which the probe is designed.
Chromosome Stop	On the given chromosome, the last base to which the probe is designed.
Probe Name	The ID of the probe, as it will appear in the genome browser.

Column	Description
Score	The level of gray with which the probe will appear. In general, the program sets a value of 1000, which displays the probe in black.
Strand	The strand of the DNA on which the probe will appear, which can be + (sense) or – (antisense).

Design Results (Simple Tiling)

Purpose: Lets you view the results of a Simple Tiling job. See "To set up a Simple Tiling job" on page 174.

To open: In the Tasks pane of the Navigator, in the appropriate Tiling folder, right-click the name of the desired job, then click **View Result.** The dialog box contains several tabs

Tabs

- **Summary Result** – See "Summary Result Tab" on page 712
- **Target Fate** – See "Target Fate Tab" on page 713
- **Detail Result** – See "Detail Result Tab" on page 715

Close Closes the dialog box.

Summary Result Tab

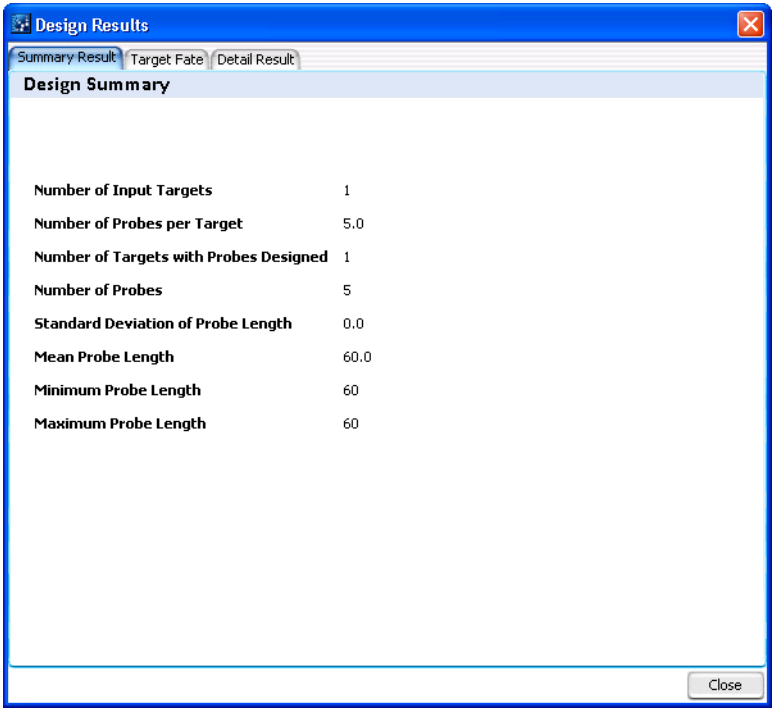


Figure 111 Design Results dialog box (Simple Tiling) – Summary Result tab

Purpose: Lets you view overall statistics about the probes that were designed by the Simple Tiling job.

These statistics appear:

Statistic	Details
Number of Input Targets	The number of separate target sequences that were submitted for tiling.
Number of Probes per Target	The average number of probes designed to each target sequence.
Number of Targets with Probes Designed	The number of input target sequences to which probes were actually designed.
Number of Probes	The total number of probes designed by the tiling job.

Statistic	Details
Standard Deviation of Probe Length	For the population of probes generated by the Simple Tiling job, the standard deviation of the length of probes, in nucleotides.
Mean Probe Length	The mean length, in nucleotides, of the population of probes generated by the tiling job.
Minimum Probe Length	The length in nucleotides of the shortest probe produced by the tiling job.
Maximum Probe Length	The length in nucleotides of the longest probe produced by the tiling job.

Target Fate Tab

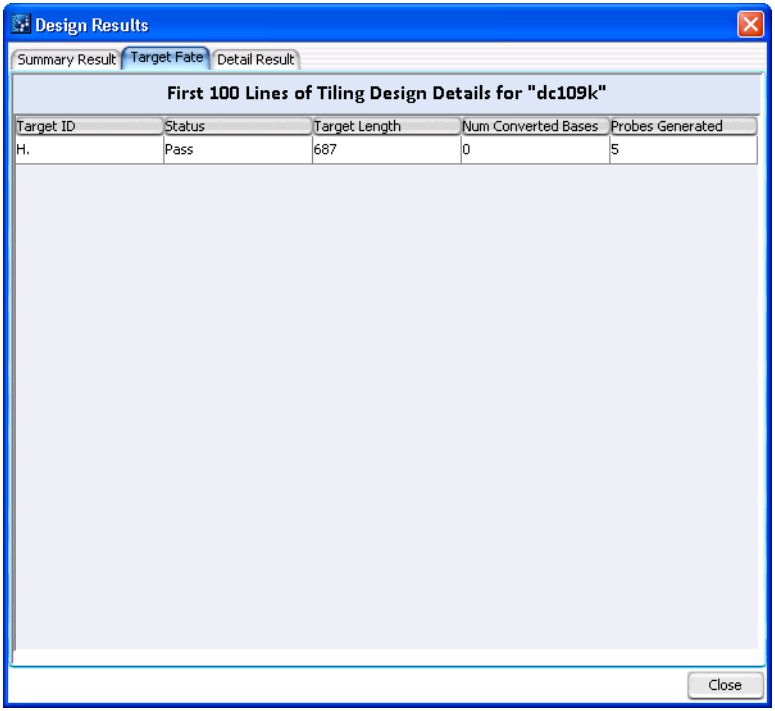


Figure 112 Design Results dialog box for Simple Tiling – Target Fate tab

This tab lists the names of the input target sequences for the Simple Tiling job, and the number of probes that were designed from each.

The following columns appear:

Column	Description
Target ID	The name of each input target sequence.
Status	Indicates whether or not a given target sequence passed validation.
Target Length	The length of the given target sequence or interval, in base pairs.
Num Converted Bases	For each sequence, the number of non-conforming (non-A, C, G, T) bases that were converted to “N” characters.
Probes Generated	The number of probes that the tiling job designed from each target sequence.

Detail Result Tab

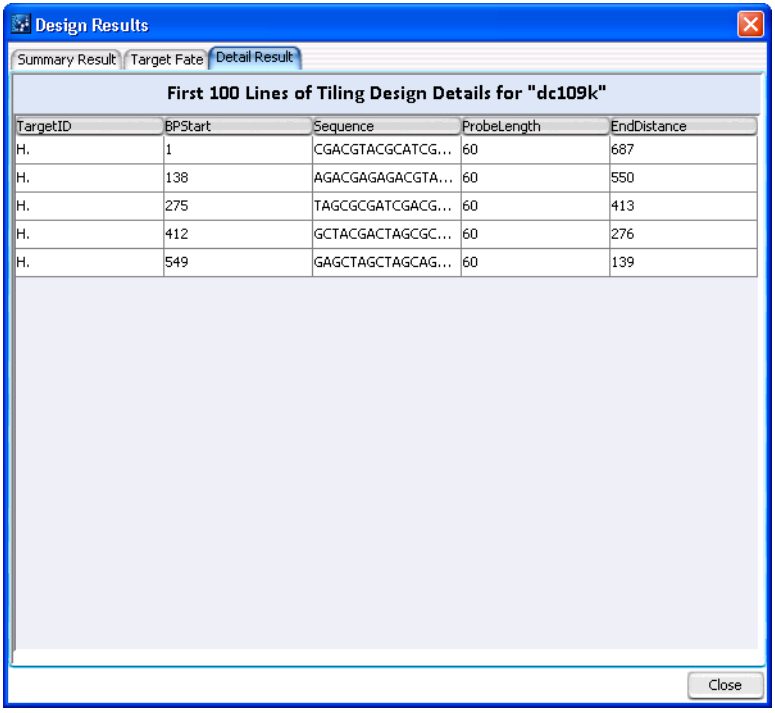


Figure 113 Design Results dialog box (Simple Tiling) – Detail Result tab

This tab lets you view information about the first 100 probes generated by a Simple Tiling job.

The following columns can appear. You can change the width of a column—In the column heading row, drag its border with the neighboring column left or right, as needed.

Column	Description
Target ID	The name of the target sequence from which the probe was derived. This is the name in description line of the target in the uploaded FASTA format file.
BP Start	The location of the first base pair in the given target sequence to which the probe was designed.

Column	Description
Sequence	The nucleotide sequence of the probe in 5' to 3' orientation.
Probe Length	The number of nucleotides in the probe.
End Distance	The number of base pairs from the 3' end of the target sequence to which the last nucleotide in the probe was designed.

Download Bait Group

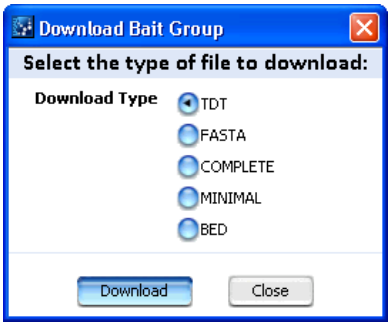


Figure 114 Download Bait Group dialog box

Purpose: Lets you select the file type for a bait group download. See "To download a bait group" on page 409.

To open: In the Design Data pane of the Navigator, right-click the name of the bait group that you want to download, then click **Download.**

Alternatively, search for bait groups. In the Search Result pane, in the **Actions** column, next to the desired bait group, click . See "To search for bait groups" on page 396.

Download type

For Bait Groups, you can download these types of files:

- **TDT** – Tab delimited text file that contains the attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the attributes indicated in the table below.
- **COMPLETE** – Tab delimited text file that contains the attributes indicated in the table below.
- **MINIMAL** – Tab delimited text file that contains the attributes indicated in the table below.
- **BED** – Tab delimited text file that contains the attributes indicated in the table below. This file is A BED format track file that you can view in a compatible genome browser

These file types contain the attributes indicated in the table below:

Attribute	TDT	FASTA	COMPLETE	MINIMAL	BED
BaitID	•	•	•	•	•
Sequence	•	•	•	•	
TargetID	•		•		
Species	•				
GeneName	•				
GeneSymbol	•		•		
Description	•		•		
ControlType	•				
Accessions	•		•		
BaitGroups	•				
Status	•				
ValidationMethod	•				
Chromosomal Location	•		•		•
Cytoband	•				
GOID	•				
Strand			•		

• – Attribute included in file format

Download Opens a Save dialog box, where you can select a location for the downloaded file.

For large files, the program submits a job to the download. You can view the job in the Tasks pane of the Navigator, in the Download Bait Group Folder.

Close Closes the dialog box without downloading the bait group.

Download Baits

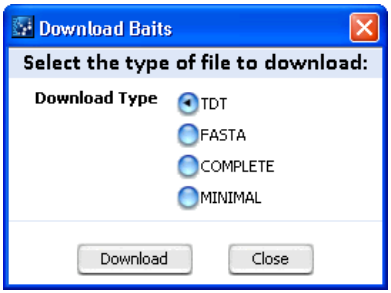


Figure 115 Download Baits dialog box

Purpose: Lets you select the file type for a bait download. See "To download baits" on page 389.

To open: Search for baits. In the Search Result pane, select the desired baits, then click **Download.** See "To search for baits" on page 358

Download Type For baits, you can download these types of files:

- **TDT** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892.
- **FASTA** – FASTA format text file that contains the bait attributes indicated in the table below. See "FASTA" on page 884.
- **COMPLETE** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892.
- **MINIMAL** – Tab delimited text file that contains the bait attributes indicated in the table below. See "TDT files" on page 892

These file types contain the attributes indicated in the table below.

Attribute	TDT	FASTA	COMPLETE	MINIMAL
BaitID	•	•	•	•
Sequence	•	•	•	•
TargetID	•		•	
Species	•			

Attribute	TDT	FASTA	COMPLETE	MINIMAL
GeneName	•			
GeneSymbol	•		•	
Description	•		•	
ControlType	•			
Accessions	•		•	
BaitGroups	•			
Status	•			
ValidationMethod	•			
ChromosomalLocation	•		•	
CytoBand	•			
GO IDs	•			
Strand			•	

• – Attribute included in file format

Download Opens a dialog box that lets you select a location for the downloaded file.

Close Closes the dialog box without downloading baits.

Download Library

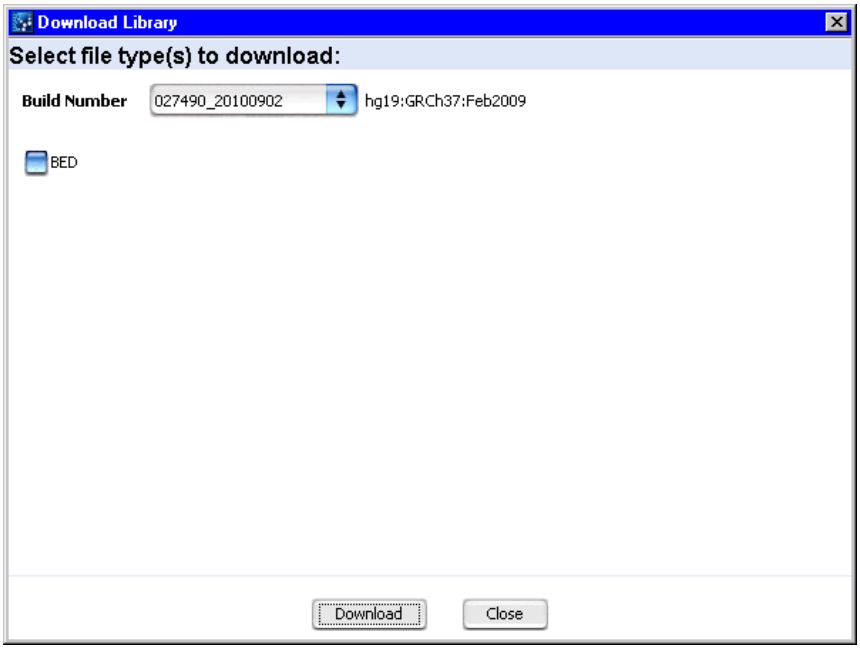


Figure 116 Download Library dialog box

Purpose: (Available for the SureSelect Target Enrichment Application type) For libraries with a status of Review, Complete, or Submitted, lets you select the type(s) of files to download. See "To download library design files" on page 461.

To open: In the Design Data Pane of the Navigator, right-click the desired library, then click **Download.**

Alternatively, search for the desired library. In the Search Result pane, in the **Actions** column, next to the desired library, click . See "To search for libraries" on page 416.

Build Number Shows a list of library IDs/timestamps. Each is associated with a specific set of available design files. Also shows the genome build that is associated with the particular

Example: In Figure 116, **027490_20100902** appears as an option in Build Number. This refers to the library with a library ID of 027490, specifically the version of the design files that has a timestamp of 20100902. Next to the library ID and timestamp, the genome build that is associated with them appears, in this case **hg19:GRCh37:Feb2009.**

When you select an option, all of the design files that are associated with the selected library ID and timestamp appear.

Select All (Appears when more than one file is available) Marks all available file types.

File Types These file types can be available:

- **BED** – Browser Extensible Data (BED) format track file that contains the columns indicated in the table below. You can import this file into a compatible genome browser. This file is available for libraries with a status of Complete or Submitted.
- **TDT** – Tab-delimited text file that contains the columns indicated in the table below. This file can be available for libraries with a status of Review, Complete, or Submitted.

Column	BED	TDT
BaitID	•	•
Sequence		•
ReplicateCount		•
Chromosome	•	
BPStart	•	
BPEnd	•	
Strand	•	•

NOTE The TDT file is available for all libraries with a status of Review. To make this file available for libraries with a status of Complete or Submitted, you must set the file writer preferences. See "To select the types of design files that the program creates" on page 343.

Download Opens a Save dialog box, where you can select a location for the downloaded file(s).

Close Closes the dialog box without downloading any files.

Availability of design files

eArray$_{XD}$ handles the design files for libraries in specific ways, described in the table below.

Type of library	Comments
Agilent Catalog libraries	To download design files for Agilent Catalog libraries to your computer, you must first transfer the content of the library from the eArray Web site to your server. The first time such a transfer is needed, appears next to the name of the library in the Design Data pane of the Navigator. If you search for such a library, (Download from eArray.com) is the only action available. After this transfer, the program lets you download a BED file. **Note:** • If Agilent updates an Agilent Catalog library on the eArray Web site after you transfer it, you can transfer it again. A **Download from eArray.com** option appears for this purpose when you right-click the name of the library in the Navigator. • You can also download a TDT file. To do this, you must set the Writer Preferences in the User Preferences dialog box *before* you first transfer the design from the eArray Web site to your server. See "To select the types of design files that the program creates" on page 343. • If you need the TDT file, but you did not retrieve it when you transferred the library from the eArray Web site to your server, you can download this file from the eArray Web site. See the online help on the eArray Web site for details.

Type of library	Comments
Workgroup custom libraries on the eArray Web site	When you install your Agilent Genomic Workbench server, it transfers the names of all custom libraries from the folders of your workgroup on the eArray Web site to your server. However, the information that maps specific baits to a given library must be separately transferred from the eArray Web site to your server. If such a transfer is needed,  appears next to the name of the library in the Design Data pane of the Navigator. If you search for such a library,  (Download from eArray Web site) is the only action available. After this transfer, the program lets you download a BED file. **Note:** • You can also download a TDT file. To do this, you must set the Writer Preferences in the User Preferences dialog box *before* you first transfer the design from the eArray Web site to your server. See "To select the types of design files that the program creates" on page 343. • If you use eArray$_{XD}$ to add baits to this kind of library, or change the annotation of baits, the program creates new versions of the design files. • If your custom library contains Agilent baits or bait groups, and Agilent updates this content, your library can use this new content. Download the appropriate updated Agilent Catalog bait group(s). See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64. • If you create a custom library on the eArray Web site *after* you install your Agilent Genomic Workbench server, it appears in the **Custom Designs** folder in the Design Data pane of the Navigator, and you can download the BED file for it.

Type of library	Comments
Custom libraries created within eArray$_{XD}$	If the library has a status of Review, you can download a TDT file. if the library has a status of Complete or Submitted, you can download both a TDT and a BED file. When you first save libraries with these statuses, the program creates the design files locally, which can take time. If you try to download such a library during this time, a dialog box tells you that the design files are not available. **Note:** • If you use eArray$_{XD}$ to add baits to this kind of library, or change the annotation of baits, the program creates new versions of the design files. • To download a TDT file for libraries with a status of Complete or Submitted, you must set the Writer Preferences in the User Preferences dialog box *before* you save the library with one of those statuses. See "To select the types of design files that the program creates" on page 343. • If your custom library contains Agilent baits or bait groups, and Agilent updates this content, your library can use this new content. Download the appropriate updated Agilent Catalog bait group(s). See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

NOTE

- Your server keeps every version of the design files for a given library that is transferred from the eArray Web site, or that is created in eArray$_{XD}$. When you download design files from your server, you can select any available version. Each available set of design files is associated with a specific library ID and timestamp, which you select in **Build Number.** Each set of files also maps to a specific genome build. More than one version (set) of files can map to a given genome build or library ID.
- For design files that have been transferred from the eArray Web site, the timestamp that is associated with the transferred files is the same as the timestamp of this set of files on the eArray Web site, without regard to when the files were transferred to your server.
- You may need to transfer bait data to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Download Microarray Design

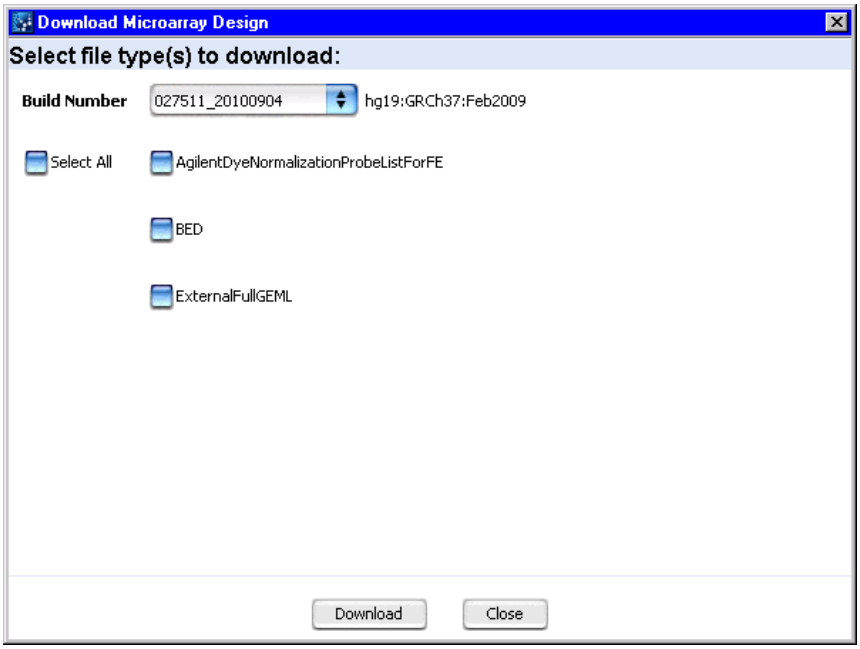


Figure 117 Download Microarray Design dialog box

Purpose: For microarray designs with a status of Review, Complete, or Submitted, lets you select the type(s) of files to download. See "To download microarray design files" on page 341.

To open: In the Design Data Pane of the Navigator, right-click the desired microarray design, then click **Download.**

Alternatively, search for microarray designs. In the Search Result pane, in the **Actions** column, next to the desired microarray design, click  See "To search for microarray designs" on page 251.

Build Number Shows a list of design IDs/timestamps. Each is associated with a specific set of available design files.

Example: In Figure 117, **027511_20100904** appears as an option in Build Number. This refers to the microarray with a design ID of 027511, specifically the version of the design files that has a timestamp of 20100904. Next to the design ID and timestamp, the genome build that is associated with them appears, in this case **hg19:GRCh37:Feb2009.**

When you select an option, all of the design files that are associated with the selected design ID and timestamp appear.

Select All Mark this option select all of the available files for the microarray design for download.

File Types The table below lists the file types that can be available for you to download. File types are available for all microarray application types unless otherwise indicated.

File Type	Description
All Annotations	(Expression application type only) Lists all annotation fields for probes on the microarray.
BED	Browser Extensible Data format. Gives you a flexible way to define the data lines that appear in an annotation track. BED files that you download from eArray contain genomic coordinates and probe names.
ExternalFullGEML (GEML 1.0)	Gene Expression Markup Language. Used by Agilent Feature Extraction, Rosetta Resolver, and Rosetta Luminator. For details, go to http://rosettabio.com/tech/geml/default.htm. This file is supplied in Agilent scanner orientation.
ExternalFullGEML2 (GEML 2.0)	Gene Expression Markup Language Version 2. Used by Rosetta Resolver and Rosetta Luminator. For details, go to http://rosettabio.com/tech/geml/default.htm. This file is supplied in Agilent scanner orientation.
FASTA	A list of probes in FASTA format. The FASTA format begins with a single-line description (which is defined by a starting ">" character), followed by lines of biological sequence in standard IUB/IUPAC amino acid or nucleic acid code. FASTA probe files that you download from eArray contain probe names on the description lines, and probe DNA sequence data.

File Type	Description
GAL	GenePix Array List, conforming to the Axon Text File (ATF) format. The GAL file format is used in Axon's GenePix image analysis software. For more details, go to: http://www.axon.xom/gn_GenePixSoftware.html This file is supplied in Axon scanner orientation.
GeneList	GeneID file for BioDiscovery Imagene software. This file is supplied in Agilent and Axon scanner orientation.
GEO	Gene Expression Omnibus file. Use this file to submit the microarray design to the GEO repository. For details, go to http://ncbi.nlm.nih.gov/geo/
Imagene	File format used by BioDiscovery's Imagene image analysis software.
SequenceList	A tab-delimited list of probe ID/probe sequence pairs.
TDT	Tab Delimited Text file. This file supplies a representation of the microarray features and their annotation, suitable for use in a spreadsheet or database. This file is supplied in Agilent and Axon scanner orientation.
NormalizedProbeTDT	(CGH application type only) Normalization probe list file. Used by Agilent Feature Extraction software for dye normalization for 2-color microarrays.
CrossSpeciesHits	(microRNA application type only) Cross-species annotation file. This file is only available for microarrays that have probes that have annotations to more than one species.

Download Opens a Save dialog box that lets you select a location for the downloaded files. The program downloads all of the requested files as a *.zip file.

Close Closes the dialog box without downloading any files.

Availability of design files

The design files for a particular microarray contain the information that is needed to manufacture the microarray. They also contain information that is required for downstream analysis of microarray sample data by the Feature Extraction program, and by the application-specific data analysis programs in Agilent Genomic Workbench. You can download these design files from eArray$_{XD}$. See "To download microarray design files" on page 341.

eArray$_{XD}$ handles designs in specific ways, described in the table below.

Type of microarray design	Comments
Agilent Catalog designs	To download Agilent Catalog design files to your computer, you must first transfer the design from the eArray Web site to your server. The first time such a transfer is needed, appears next to the name of the design in the Design Data pane of the Navigator. If you search for such a microarray design,  (Download from eArray.com) is the only action available. By default, the program lets you download these files: • GEML design file • NormalizedProbeTDT (CGH application type) • AllAnnotations (Expression application type) • BED For descriptions of these files, see "Download Microarray Design" on page 726. **Note:** • If Agilent updates an Agilent Catalog design on the eArray Web site after you transfer it, you can transfer it again. A **Download from eArray.com** option appears for this purpose when you right-click the name of the design in the Navigator. • You can download additional types of files. To do this, you must set the Writer Preferences in the User Preferences dialog box *before* you first transfer the design from the eArray Web site to your server. See "To select the types of design files that the program creates" on page 343. • Once the design files for a particular Agilent Catalog design are available for you to download, the kinds of design files that you can download appear in the Download Microarray Design dialog box. You may be able to download additional types of files for the design from the eArray Web site. See the online help on the eArray Web site for details.

Type of microarray design	Comments
Workgroup custom designs on the eArray Web site	When you install your Agilent Genomic Workbench server, it transfers the names of all custom microarray designs from the folders of your workgroup on the eArray Web site. To download design files for these microarrays, you must first transfer their content from the eArray Web site. If such a transfer is needed, appears next to the name of the design in the Design Data pane of the Navigator. If you search for such a microarray design,  (Download from eArray Web site) is the only action available. By default, the program lets you download these files: • GEML design file • NormalizedProbeTDT (CGH application type) • AllAnnotations (Expression application type) • BED For descriptions of these files, see "Download Microarray Design" on page 726. **Note:** • You can download additional types of files. To do this, you must set the Writer Preferences in the User Preferences dialog box *before* you transfer the design from the eArray Web site to your server. See "To select the types of design files that the program creates" on page 343. • If you use eArray$_{XD}$ to add probes to this kind of design, or change the annotation of probes, the program creates new versions of the design files. • If your custom design contains Agilent probes or probe groups, and Agilent updates this content, your design can use this new content. Download the appropriate updated Agilent Catalog probe group(s). See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64. • When you transfer a custom microarray design from the eArray Web site to your server, you cannot download design files until the program completes the transfer and also creates an additional file for internal use. If you try to download design files during this time, an error message appears. • If you create a custom design on the eArray Web site *after* you install your Agilent Genomic Workbench server, it appears in the **Custom Designs** folder in the Design Data pane of the Navigator, and you can download the ExternalFullGEML file for it.

Type of microarray design	Comments
Custom designs created within eArray$_{XD}$	You can download the design files for this kind of microarray design if the design has a status of Complete or Submitted. When you first save designs with these statuses, the program creates the design files locally, which can take time. If you try to download such a design during this time, a dialog box tells you that the design files are not available. By default, the program lets you download these files: • GEML design file • NormalizedProbeTDT (CGH application type) • AllAnnotations (Expression application type) • BED For descriptions of these files, see "Download Microarray Design" on page 726. **Note:** • The program can also create additional types of files. To select the additional types of files that the program creates, see"To select the types of design files that the program creates" on page 343. • When you save a microarray design with a status of Review, the program creates a TDT file. After the program creates this file, you can download it. • If you use eArray$_{XD}$ to add probes to this kind of design, or change the annotation of probes, the program creates new versions of the design files. • If your custom design contains Agilent probes or probe groups, and Agilent updates this content, your design can use this new content. Download the appropriate updated Agilent Catalog probe group(s). See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

NOTE

- Your server keeps every version of the design files for a given microarray design that is transferred from the eArray Web site, or that is created in eArray$_{XD}$. When you download design files from your server, you can select any available version. Each available set of design files is associated with a specific design ID and timestamp, which you select in **Build Number.** Each set of files also maps to a specific genome build. More than one version (set) of files can map to a given genome build or design ID.
- For design files that have been transferred from the eArray Web site, the timestamp that is associated with the transferred files is the same as the timestamp of this set of files on the eArray Web site, without regard to when the files were transferred to your server.
- You may also need to transfer probe data for the given application type to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Download Probe Group

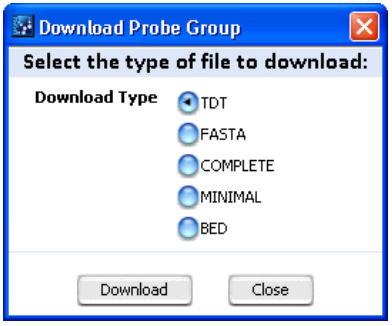


Figure 118 Download Probe Group dialog box

Purpose: Lets you save probe group data to your computer in one of several available file formats. See "To download a probe group" on page 240.

To open: In the **Actions** column of the search results of a probe group search, next to the desired probe group, click . See "To search for probe groups" on page 224. Alternatively, in the **Design Data** pane of the Navigator, right-click the name of the desired probe group, then click **Download.**

List of file types Lists the file types available for download. Select one.

- **TDT** – Tab delimited text file that contains the attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the attributes indicated in the table below.
- **COMPLETE** – Tab delimited text file that contains the attributes indicated in the table below.
- **MINIMAL** – Tab delimited text file that contains the attributes indicated in the table below.
- **BED** – Tab delimited text file that contains the attributes indicated in the table below. This file is A BED format track file that you can view in a compatible genome browser.

Attribute	TDT	FASTA	COMPLETE	MINIMAL	BED
ProbeID	•	•	•	•	•
Sequence	•	•	•	•	
TargetID	•		•		
Species	•				
GeneName	•				
GeneSymbol	•		•		
Description	•		•		
ControlType	•				
Accessions	•		•		
ProbeGroups	•				
Status	•				
ValidationMethod	•				
Chromosomal Locations	•		•		•
Cytoband	•				
GoIDs	•				

• – Attribute included in file format

Download Opens a dialog box, where you can select a location for the downloaded file.

Close Closes the dialog box without downloading the probe group.

NOTE

- For microRNA microarrays, probes are grouped by the microRNA to which they are designed. One to four probes act in concert to measure a given microRNA. In downloaded files, each probe appears on a separate line, but the file lists the probes for a given microRNA on consecutive lines. The name of the microRNA to which each probe binds appears explicitly in the downloaded TDT and COMPLETE format files, in the TargetID column.
- You may also need to transfer probe data for the given application type to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Download Probes

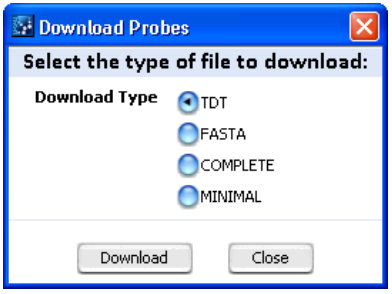


Figure 119 Download Probes dialog box

Purpose: Lets you save probe data to your computer in one of several available file formats. See "To download probes" on page 206.

To open: In the Search Result pane of a Probe Search, select the desired probes, then click **Download.** See "To use the Probe Search tool to find probes" on page 92.

Download Type Lists the file types available for download. Select one.

- **TDT** – Tab delimited text file that contains the attributes indicated in the table below.
- **FASTA** – FASTA format text file that contains the attributes indicated in the table below.

- **COMPLETE** – Tab delimited text file that contains the attributes indicated in the table below.
- **MINIMAL** – Tab delimited text file that contains the attributes indicated in the table below.

Attribute	TDT	FASTA	COMPLETE	MINIMAL
ProbeID	•	•	•	•
Sequence	•	•	•	•
TargetID	•		•	
Species	•			
GeneName	•			
GeneSymbol	•		•	
Description	•		•	
ControlType	•			
Accessions	•		•	
ProbeGroups	•			
Status	•			
ValidationMethod	•			
Chromosomal Locations	•		•	
Cytoband	•			
GoIDs	•			

• – Attribute included in file format

Download Opens a Save dialog box, where you can select a location for the downloaded file.

Close Closes the dialog box without downloading the probes.

NOTE

For microRNA microarrays, probes are grouped by the microRNA to which they are designed. One to four probes act in concert to measure a given microRNA. In downloaded microarray files, each probe appears on a separate line, but the file lists the probes for a given microRNA on consecutive lines. The name of the microRNA to which each probe binds appears explicitly in the downloaded TDT and COMPLETE format files, in the TargetID column.

Edit Bait Group

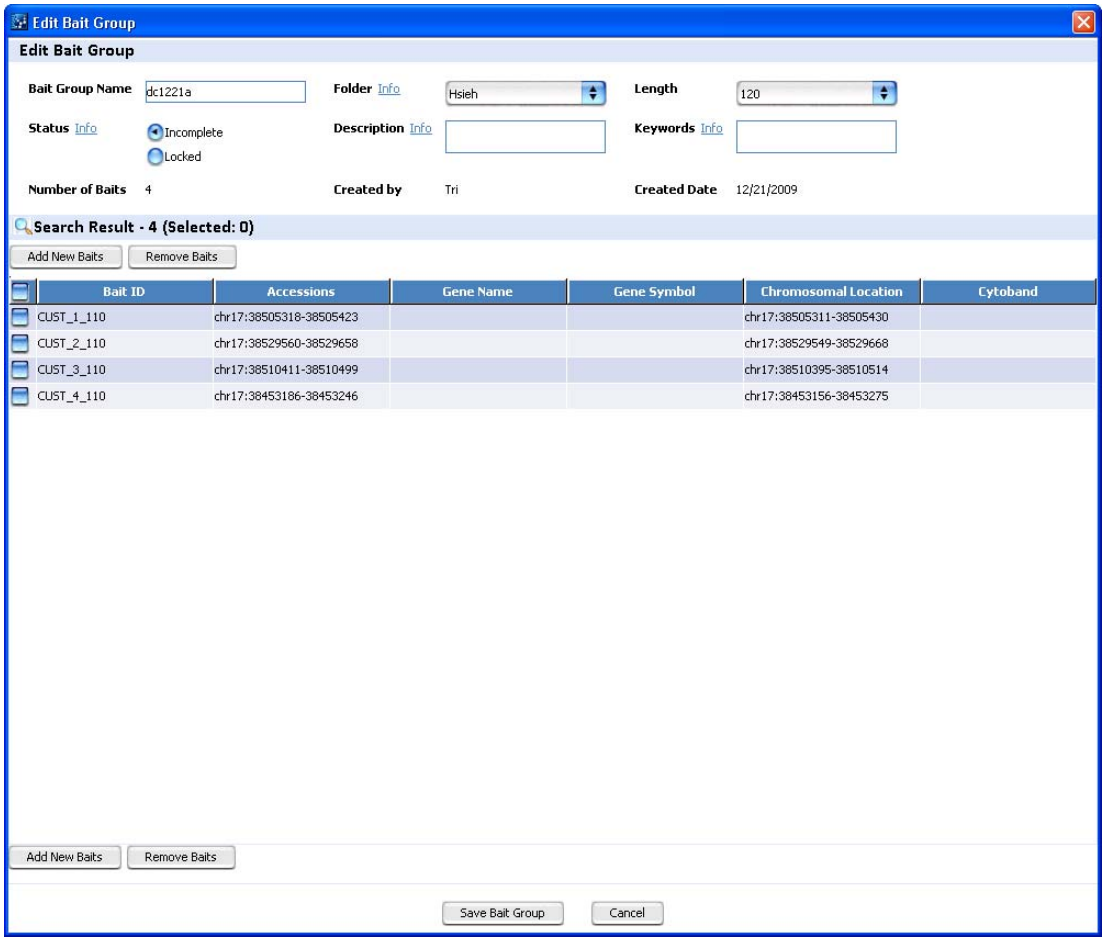


Figure 120 Edit Bait Group dialog box

Purpose: Lets you make changes to the attributes and bait content of a bait group. You can edit bait groups with a status of Incomplete. See "To edit a bait group" on page 406.

To open: In the Design Data pane of the Navigator, right-click the name of the bait group that you want to edit, then click **Edit.**

Alternatively, search for bait groups. In the Search Result pane, in the Actions column, next to the desired bait group, click  . See "To search for bait groups" on page 396.

Edit Bait Group pane

Attribute	Description
Bait Group Name	Type a name in the box. This name is the way the program references the bait group in search results, bait group lists, view pages, and the like.
Folder	Select the folder where you want the program to save the new bait group. The folders to which you have access appear in the list.
Length	Select a value of 120. Agilent currently supports a bait length of 120 nucleotides.
Status	Select one of these options: • **Incomplete** – After you save the bait group, you can still edit it. • **Locked** – After you save the bait group, the bait group cannot be edited further. **Note:** • Once you lock a probe group, you cannot subsequently unlock it. • You can use both locked and incomplete bait groups in a library.
Description	(Optional) Type a brief description.
Keyword	(Optional) Type a keyword, or multiple keywords separated by pipe "|" characters, commas, or semicolons. Keywords can make it easier to find the bait group when you search for it.
Number of Baits	(Read-only) The total number of baits in the bait group. The program updates this value as you make changes to the bait content of the bait group.
Created by	(Read-only) The name of the person who created the bait group.
Date Created	(Read-only) The date the bait group was first saved.

Search Result pane

Add New Baits Opens the Add Baits to Bait Group dialog box, where you can search for and select additional baits for the bait group. See "Add Baits to Bait Group" on page 576.

Remove Baits Removes selected baits from the bait group. To select a bait for removal, mark the check box next to the name of the bait.

Table of baits The table of baits has the columns listed below. Every bait has a Bait ID, but the availability of additional bait annotation varies.

- **Check boxes** – Mark the check box associated with an individual bait to select it for removal from the bait group. To select all of the baits on the current page for removal, mark the check box in the column heading.
- **Bait ID** – The unique bait name for each bait.
- **Additional annotation columns** – The availability of data for these columns varies by bait.

Page navigation buttons 

– (Page Links) Navigates to a specific page

Save Bait Group Saves the bait group with any changes that you made. This overwrites the original bait group, even if you change the location.

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

NOTE

To edit a bait group, you may need download the bait group from the eArray Web site. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61. Yummy also need to transfer bait data to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Edit Library

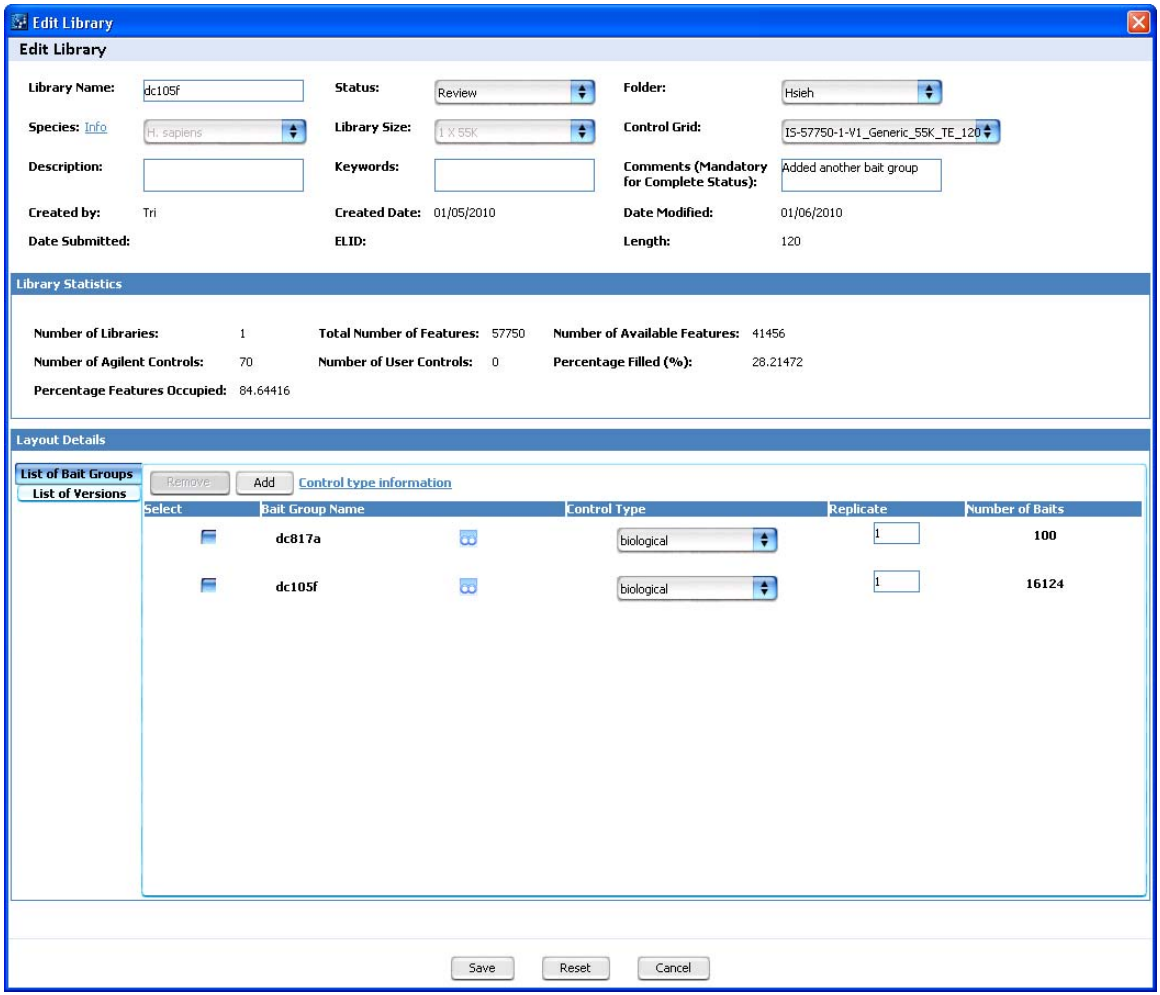


Figure 121 Edit Library dialog box.

Purpose: Lets you make changes to the attributes and bait group content of a library with Draft status. See "To edit a library" on page 447.

You also use this dialog box to review libraries. The library must have a status of Review. Anyone with access to a library with a status of Review can make changes to it and save new versions of it. See "To place a library in review" on page 451 and "To review a library" on page 453.

When you save a library that you have reviewed, the program saves a new version of the library with a new version number, and retains all previous versions of the library. By default, all reviews use the original version of the library as a starting point. However, the owner of the library can select any version as the starting point for subsequent reviews. See "To place a different version of a library in review" on page 452.

To open: Do one of the following:

- In the **Actions** column of the search results of a library search, next to the desired library, click  (for libraries with a status of Draft) or  (for libraries with a status of Review). See "To search for libraries" on page 416.
- In the **Design Data** pane of the Navigator, right-click the name of the desired library, then click **Edit** (for libraries with a status of Draft) or **Review** (for libraries with a status of Review).

Edit Library pane

The table below describes the attributes that appear in this pane.

Property	Instructions/Details
Library Name	Type a new name for the library. The name can be from 1 to 100 characters long. Use only letters, numbers, spaces, hyphens, underscores, and periods.
Status	Select one of these options: • **Draft** – (Not available for libraries with a status of Review) The library will continue to have a status of Draft, which lets only the owner edit it. • **Review** – Places (or keeps) the library in review, which lets anyone with access to the library make changes and save new versions of it. See "To review a library" on page 453. • **Complete** – Assigns a status of Complete to the library. The library can subsequently be submitted to Agilent. It cannot be edited. Only the owner of a library can change its status to COmplete. **Caution:** Library status follows a one-way order from Draft to Review to Complete. Once you save a library with a given status, you cannot change the status to a previous one in the order.
Folder	Select a new location for the library. Only the folders to which you have access appear in the list.
Species	(Read-only) The species that was defined for the library when it was created.
Library Size	Select the desired library size. **Example:** A library size of 1 X 55K can accommodate up to 57,750 total baits.
Control Grid	Select a different control grid, if one is available. This required Agilent control grid contains baits that are used for quality control purposes in the library manufacturing process.
Description	Edit the description, as desired.
Keywords	Edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Edit comments, as desired. If you intend to save the library with a status of Complete, comments are required. Otherwise, comments are optional.
Created by	(Read-only) The person who first saved the library.

Property	Instructions/Details
Date Created	(Read-only) The date the library was first saved.
Date Modified	(Read-only) • For libraries with a status of Draft, this is the date the library was last saved. • For libraries with a status of Review, this is the date that the currently selected version of the library was created.
Date Submitted	(Read-only) The date the library was submitted to Agilent Manufacturing. To be submitted to Agilent, libraries must have a status of Complete. Thus, for libraries that you can edit, which have a status of Draft, this attribute is blank.
ELID	(Read-only) An ELID (Enrichment Library ID) is a unique Agilent ID number for a library. The system assigns an ELID when you complete or submit a library. Thus, for libraries that you can edit, which have a status of Draft, this attribute is blank.
Length	(Read-only) The length of each of the baits in the library, in nucleotides. All baits in a library must have the same length. Agilent currently supports a bait length of 120 nucleotides.
Unique Baits	(Read-only, available for libraries with a status of Complete or Submitted) The total number of distinct baits, not including any replicate baits.
Base Coverage	(Read-only, available for libraries with a status of Complete or Submitted.) If all baits in the library have chromosomal locations defined for them, this statistic is the total number of bases (in Mb) in the genome of interest that are covered by at least one bait in the library. If one or more baits in the library do not have chromosomal locations defined for them, this statistic is an estimate of the number of bases (in Mb) in the genome of interest that are covered by at least one bait in the library. The estimate is based on the number of unique baits in the library, the bait length, and the bait tiling density. Unless otherwise warranted, eArray assumes a bait tiling density of 2x.

Library Statistics Pane

These statistics appear in the pane. The program updates these statistics as you change the bait group content of your library. All statistics are read-only.

Statistic	Description
Number of Libraries	Number of libraries required to accommodate all baits, including Agilent control baits as well as the baits that you selected for the library. Currently, Agilent manufactures single libraries only, thus all baits must fit within one library.
Total Number of Features	Total number of baits that can be accommodated in the given number of libraries. Currently, Agilent manufactures single libraries only.
Number of Available Features	Number of additional baits that can be accommodated in the library.
Number of Agilent Controls	Number of baits in the required Agilent control bait group. This bait group contains baits that Agilent uses as quality controls in the library manufacturing process. In addition, the program replicates this bait group the same number of times as your least-replicated bait group. These control baits count against the available features in the library.
Number of User Controls	Number of baits that you have identified as positive **(pos)** or negative **(neg)** user control baits in the Control Type column of the List of Bait Groups tab (see the next section). The control type of a bait group does not affect the composition of a library, but the program saves the control type designations with the library for future user reference.
Percentage Filled (%)	The percentage of the available space in the library that is currently occupied by the selected user bait groups and the Agilent control bait group. **Example:** Your library contains 12,000 baits, including the required Agilent control baits. The capacity of the 1 X 55K library format is 57,750 baits. Thus, Percentage Filled = 12,000/57,750 = 20.8%

Layout Details – List of Bait Groups pane

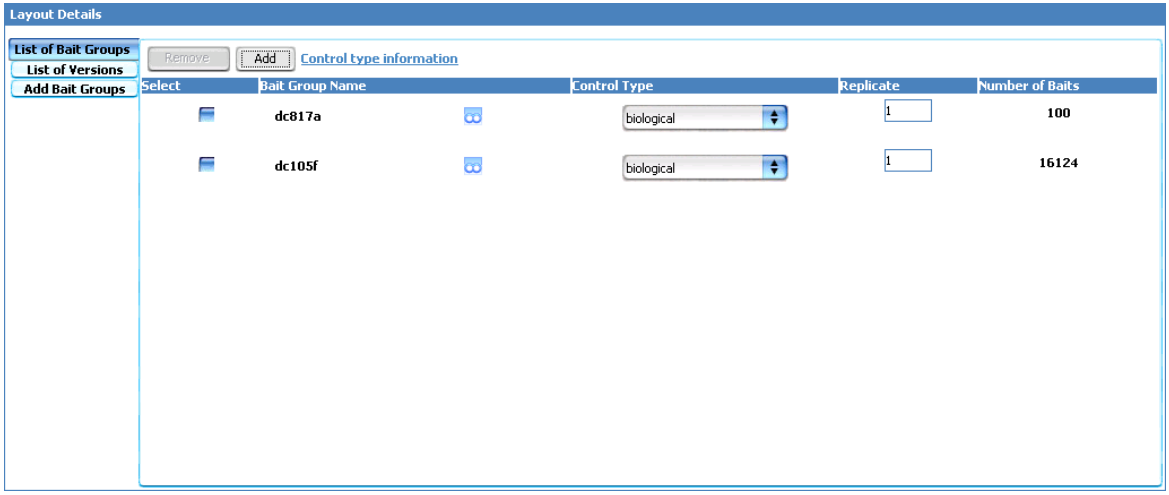


Figure 122 Edit Library – List of Bait Groups pane

This tab lists the bait groups that are currently included in the library. It contains these columns and commands:

Column/Button	Description
Select	Mark the check box next to a bait group to select it for removal. The program removes selected bait groups from your library when you click **Remove.**
Bait Group Name	The names of the user bait groups that are currently in the library. – Opens the View Bait Group dialog box, where you can view the properties and bait content of the bait group. See "View Bait Group" on page 867.

Column/Button	Description
Control Type	The control types of bait groups do not have any effect on the composition of a library, and they are not used in the SureSelect Target Enrichment protocol or in downstream sequence analyses. They are included in the library design files for user reference. For each bait group, you can select one of these options: • **neg, pos,** or **ignore** – Indicates that the bait group contains control baits that are designed to monitor the quality of capture, or other control or QC applications. • **biological** – Indicates that the bait group contains biological baits that are designed to capture desired genomic regions.
Replicate	The number of copies of the bait group that will be included in the library. **Note:** The program also replicates the required Agilent control bait group the same number of times as your least-replicated bait group.
Number of Baits	The number of individual baits in the bait group.
Remove	Removes the selected bait group(s) from the library.
Add	Opens the Add Bait Groups tab within the dialog box. See the next section.

Layout Details – Add Bait Groups pane

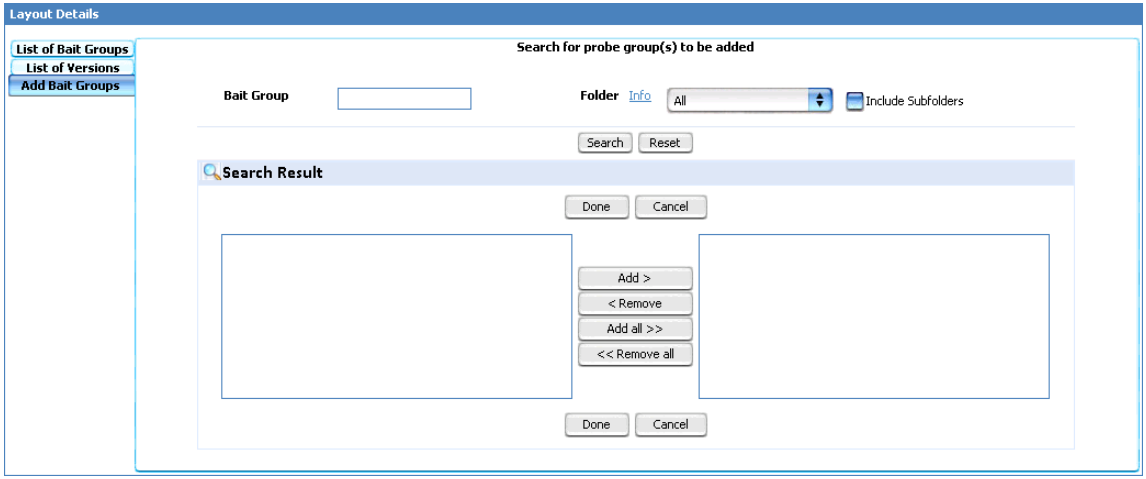


Figure 123 Edit Library – Add Bait Groups pane

Purpose: Lets you search for, select, and add bait groups to your library.

To open: Under Layout Details, in the List of Bait Groups pane, click **Add.**

The Add Bait Groups pane contains these items:

Item	Description
Bait Group	Type all or part of the name of a desired bait group. To return all bait groups available to you, leave this search criterion blank.
Folder	This item lets you set the folder(s) for the bait group search. • To limit returned bait groups to those in a specific folder, select the desired folder. • To return bait groups without regard to their folder locations, select **All.** • To also return bait groups that are found in the subfolders of the selected folder, mark **Include Subfolders.**
Search	Starts a search for bait groups that whose names contain the term that you typed in Bait Group. Matching bait groups appear on the left side of the Search Result pane.
Reset	Clears your search term and any returned results.

Item	Description
Search Result pane	
Left box	Contains the bait group search results, if any. These bait groups are available for you to add to your library. To select bait groups from the search results: • To select a single bait group, click its name. • To select multiple bait groups, control-click their names. • To select a contiguous block of bait groups, click the first bait group in the block, then shift-click the last bait group.
Right box	Contains the names of the bait groups that you select for inclusion in your library. The list accumulates bait groups as you transfer them, including transfers from multiple searches. You can also remove bait groups from this box. To select bait groups for removal: • To select a single bait group, click its name. • To select multiple bait groups, control-click their names. • To select a contiguous block of bait groups, click the first bait group in the block, then shift-click the last bait group.
Add	Transfers the selected bait groups from the left box to the right box. These bait groups will be included in your library.
Remove	Transfers the selected bait groups from the right box to the left box. These bait groups will no longer be included in your library.
Add all	Transfers all of the bait groups from the left box to the right box. All of these bait groups will be include in your library.
Remove all	Clears the right box. The bait groups that appeared in there will no longer be included in your library.
Done	Adds the bait groups in the right box to your library.
Cancel	Closes the tab without adding any bait groups to your library.

NOTE

When you select bait groups for a library, the program tells you if a bait group is *Local* or if it is *Not Downloaded.* If you select one or more bait groups that are *Not Downloaded,* you can only save the new library with a status of Draft. After you download the given bait group(s) from the eArray Web site, you can save the library with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64. You may also need to transfer bait data to your server from the eArray Web site. See "To transfer probe, bait, and exon data from the eArray Web site" on page 60.

Layout Details – List of Versions pane

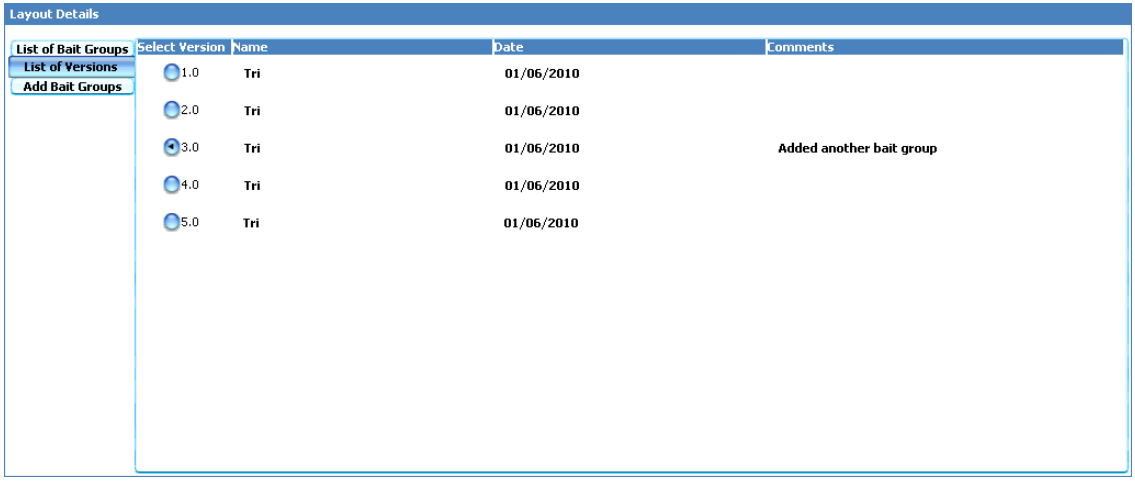


Figure 124 Edit Library – List of Versions pane

Purpose: This tab lets you view a list of all of the versions of the library. It is available for libraries with a status of Review. See "To review a library" on page 453. Only the owner of the library can select a different version for review.

To open: In the Layout Details pane of the Edit Library dialog box, click **List of Versions.**

Select Version Lists the version numbers of all of the versions of a library. The program uses the selected version as the starting point for all reviews of the library. If you are the owner of a library, you can select a different version to use as the starting point for subsequent reviews. See "To place a different version of a library in review" on page 452.

Also, when the owner of the library changes the status of the library to Complete, the program saves the current version of the library, only. See "To complete a library" on page 457.

Name Lists the name of the person who saved each version of the library.

Date Gives the date on which each version of the library was saved.

Comments Lists any comments that were saved with each version of the library.

Other buttons

Save Saves the library with any changes that you made. This replaces the previous version of the library, even if you changed the location.

Reset Restores all settings to the what they were before you made any changes.

Cancel Closes the dialog box without saving any of your changes.

Edit Microarray Design

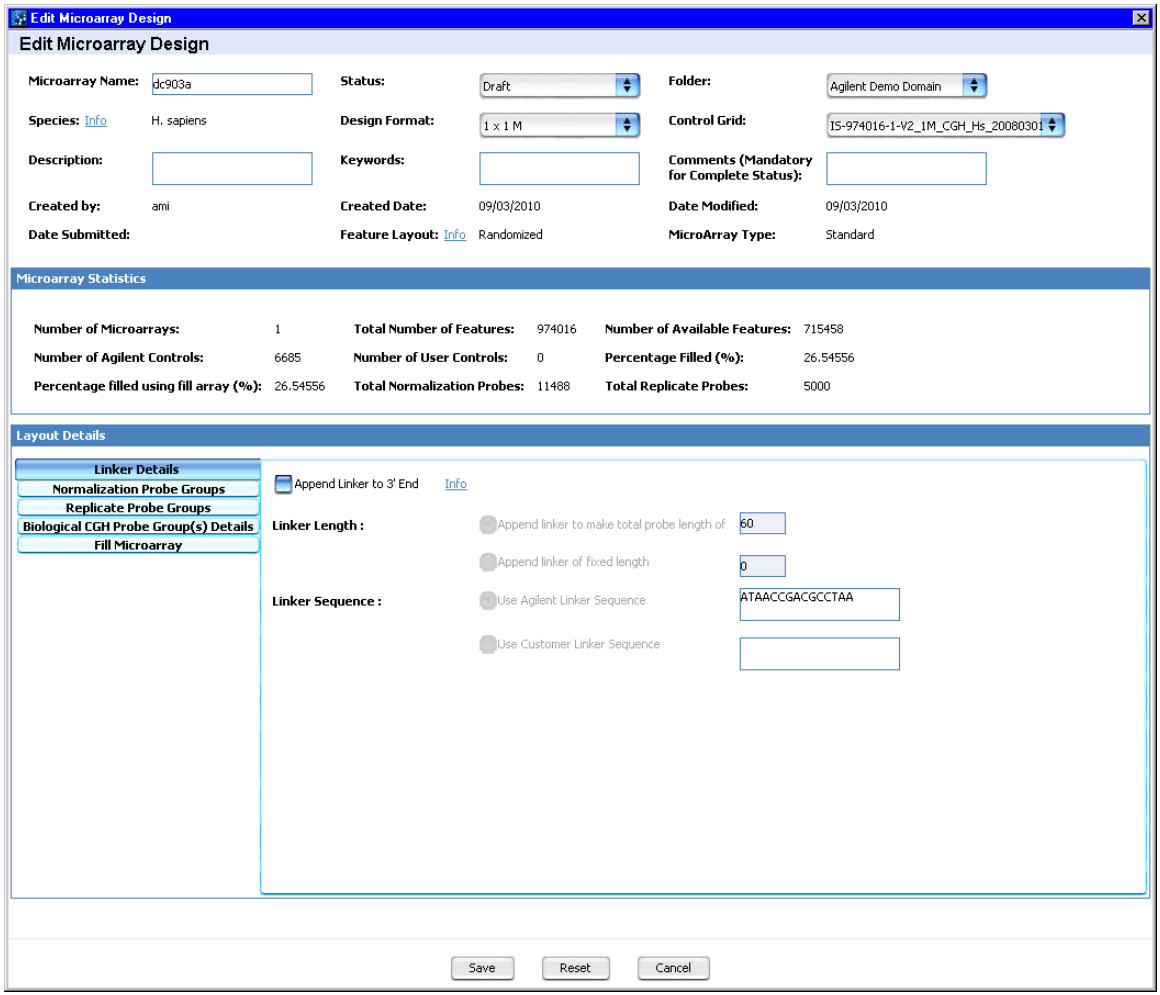


Figure 125 Edit Microarray Design dialog box

Purpose: Lets you make changes to the properties and probe group content of a microarray design that you own. The design must have a status of Draft. See "To edit a microarray design" on page 310.

You also use this dialog box to review microarray designs. The design must have a status of Review. Anyone with access to a design with a status of Review can make changes to it and save new versions of it. See "To place a microarray design in review" on page 324 and "To review a microarray design" on page 326.

When you save a reviewed design, the program saves a new version of the design with a new version number, and retains all previous versions of the design. By default, all reviews use the original version of the design as a starting point. However, the owner of the design can select any version as the starting point for subsequent reviews. See "To place a different version of a design in review" on page 325.

To open: Do one of the following:

- In the **Actions** column of the search results of a microarray design search, next to the desired design, click  (for designs with a status of Draft) or  (for designs with a status of Review). See "To search for microarray designs" on page 251.
- In the **Design Data** pane of the Navigator, right-click the name of the desired microarray design, then click **Edit** (for designs with a status of Draft) or **Review** (for designs with a status of Review).

Properties

Property	Instructions/Details
Microarray Name	Type a new name for the microarray design. The name can be from 1 to 100 characters long, and can contain letters, numbers, hyphens, underscores, and periods.
Status	Select one of these options: • **Draft** – (Not available for designs with a status of Review) The design will continue to have a status of Draft, which lets only the owner edit it. • **Review** – Places (or keeps) the design in review, which lets anyone with access to the design make changes and save new versions of it. See "To review a microarray design" on page 326. • **Complete** – Assigns a status of Complete to the design. The design can subsequently be submitted to Agilent. It cannot be edited. Only the owner of a design can assign it a status of Complete. **Caution:** Design status follows a one-way order from Draft to Review to Complete. Once you save a design with a given status, you cannot change the status to a previous one in the order.

Property	Instructions/Details
Folder	Select a new location for the design. Only the folders to which you have access appear in the list.
Species	(Read-only) The species associated with the probes in the design.
Design Format	Select a different design format, if one is available. The design format reflects the number of replicate arrays and the approximate total number of features in each array on a slide. **Example:** The 4x44K format contains four replicate arrays on a single glass slide. Each of these arrays contains approximately 44,000 features.
Control Grid	Select an alternate control grid, if one is available. The name of the currently selected Agilent control grid appears in the list. This is a required group of probes that is included in each design for quality control, background subtraction, and the like. The control grid can vary based on the application type, species, design format, and user choice. It occupies a portion of the features in each design.
Description	Edit the description, as desired.
Keywords	Edit search keywords, as desired. Separate multiple keywords with commas.
Comments	Edit comments, as desired. If you intend to save the microarray design with a status of Complete, which prevents further editing, comments are required. Otherwise, comments are optional.
Created by	(Read-only) The person who first saved the design.
Date Created	(Read-only) The date the design was first saved.
Date Modified	(Read-only) • For designs with a status of Draft, this is the date the design was last saved. • For designs with a status of Review, this is the date that the currently selected version of the design was created. • (Only applies to the View Microarray Design dialog box) For designs with a status of Complete or Submitted, this property is the date that the design was last saved, not the date that it was downloaded to your server.

Property	Instructions/Details
Features per microRNA	(microRNA application type only) In Feature per microRNA, select the desired number of features. This property reflects the total number of features on the array assigned to each microRNA. Each microRNA has from one to four different probes associated with it. eArray adjusts the number of replicates of each of these probes to achieve the specified number of features per target (microRNA). A higher number generates slightly more robust data, while a lower setting lets you measure more microRNAs per array. The default value is 16 features per microRNA target. Agilent Catalog arrays use 16 features per microRNA target for human arrays, and 20 features per microRNA target for mouse and rat arrays.
Date Submitted	(Available only for submitted designs) The date the design was submitted to Agilent. See "To submit a microarray design to Agilent as part of a wizard" on page 347. Because you cannot edit a microarray with a status of Submitted, this property is blank in the Edit Microarray Design dialog box.
Feature Layout	(Read-only) eArray$_{XD}$ supports only **Randomized** feature layout, in which probes are assigned randomly to feature positions. To create a microarray design with a Customer Specified probe layout, you must use the eArray Web site.
Microarray Type	(Read-only, available for the CGH application type) One of these terms appears: • **Standard** – The microarray is a standard CGH microarray. • **CGH+SNP** – The microarray is a CGH+SNP microarray, which combines both CGH and SNP probes on the same array. See "To create a CGH+SNP microarray design" on page 301.

Microarray Statistics

All of these statistics are calculated by the program. You cannot directly edit them.

Statistic	Description
Number of Microarrays	The number of copies of the microarray design that will appear on the slide.
Total Number of Features	The number of features, both occupied and unoccupied, in your design.
Number of Available Features	The number of unoccupied features in your design. These features are available to accommodate additional probes.

Statistic	Description
Number of Agilent Controls	Number of required Agilent control probes in the design. These probes count toward the total number of probes that you can include in the design.
Number of User Controls	Number of probes in the design that you have identified as positive or negative control probes.
Percentage Filled (%)	The percentage of features that are occupied, collectively, by Agilent control probes and the probes that you have selected for the design. This does not include probes from any filler probe group. If this value exceeds 100%, you must either remove probe group(s) from your design, or select a different design format with a higher capacity.
Percentage Filled Using Fill Array (%)	You can fill the unused features of your design with probes from the probe group of your choice. This statistic reflects the percentage of the features in the design that are occupied by any type of probe, including those from a filler probe group. See "Layout Details – Fill Microarray pane" on page 765.
Total Normalization Probes	(Available for CGH arrays) The number of normalization probes in the microarray design. You assign normalization probe groups in the Normalization Probe Groups pane. See "Layout Details – Normalization Probe Groups pane" on page 759.
Total Replicate Probes	(Available for CGH and Expression arrays) The number of replicate probes in the microarray design. You assign replicate probe groups in the Replicate Probe Groups pane of the dialog box. See "Layout Details – Replicate Probe Groups pane" on page 760. These probe groups are distinct from any user biological probe groups that you have specified in the Probe Groups pane.
Number of SNP Probes	(Available for CGH+SNP microarrays) The total number of Agilent SNP probes selected for the microarray design.
Number of microRNA targets covered	(microRNA application type) Total number of microRNA targets associated with probes on the array.

Statistic	Description
Number of distinct microRNA targets covered	(microRNA application type) Total number of microRNA targets associated with probes on the array, excluding microRNAs with duplicate sequences. For example, for a multi-species array, if two microRNAs have the same sequence, this value considers them together as a single microRNA. eArray treats microRNAs that have the same sequence as a single species of microRNA, and lays out only one set of probes for it. This avoids the problem of two sets of probes competing for the same target material. The competition would otherwise compromise the specificity of the assay.
Number of distinct microRNA targets that can be covered by remaining space	(microRNA application type) Number of microRNAs that you can still select for the array, without exceeding its capacity. **Note:** The program treats microRNAs that have the same sequence as a single species of microRNA, and lays out only one set of probes for it.

Layout Details pane

The Layout Details Pane lets you edit the probe group content and configuration for the microarray. These panes can be available:

Pane	See this section
Linker Details	"Layout Details – Linker Details pane" on page 757
Normalization Probe Groups	"Layout Details – Normalization Probe Groups pane" on page 759
Replicate Probe Groups	"Layout Details – Replicate Probe Groups pane" on page 760
Biological <type> Probe Groups	"Layout Details – Biological <type> Probe Groups pane" on page 762
SNP Probe Groups	"Layout Details – SNP Probe Groups pane" on page 764
Fill Microarray	"Layout Details – Fill Microarray pane" on page 765
Add Probe Groups	"Layout Details – Add Probe Groups pane" on page 767
List of Versions	"Layout Details – List of Versions pane" on page 769

Layout Details – Linker Details pane

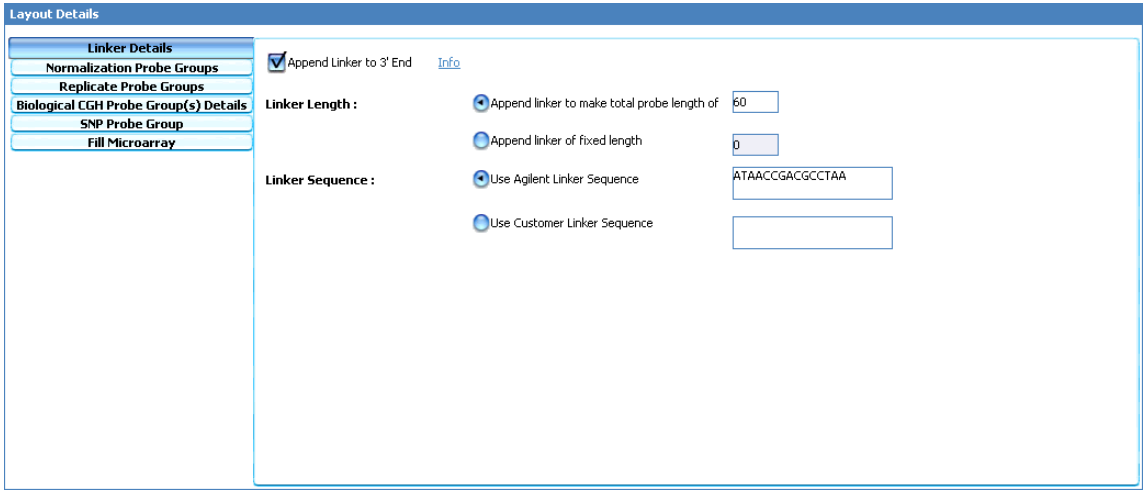


Figure 126 Edit Microarray Design – Linker Options pane

Purpose: This pane lets you view and configure linkers for your microarray design. Linkers are nucleotide sequences that eArray can add to the 3' ends of probes to raise the active, hybridizing probe sequences farther above the glass microarray substrate. This can reduce steric hindrance, and improve hybridization.

To open: Under Layout Details, click **Linker Details.**

These options are available:

Option	Description
Append linker to 3' end	Adds linkers to the 3' ends of probes according to the options that you select in the pane. When you mark this option, the rest of the options in the pane become available. To remove linkers, clear this option.
Linker length	Select one of these options: • **Append linker to make total probe length of** – Adds nucleotides to the 3' ends of probes so that the resulting probes have the length specified. In the box, type a number of nucleotides from 20 to 60. If there are probes in your microarray design longer than the length that you enter, the program leaves them alone. They are not trimmed, and no linkers are added to them. • **Append linker of fixed length** – Adds the specified number of nucleotides to the 3' ends of probes. In the box, type a number of nucleotides from 1 to 49. The program truncates the linker on a probe, as necessary, to keep the total length of the probe from exceeding 60 nucleotides. If the linker sequence is shorter than the length that you enter, eArray replicates the linker sequence to fill in the length.
Linker sequence	Select one of these options: • **Use Agilent Linker Sequence** – You cannot edit the Agilent-provided linker sequence. • **Use Customer Linker Sequence** – Type a DNA base sequence for the linker. Use a random sequence, or derive it from a sequence not found in nature. **Note:** eArray adds the Agilent linker sequence to Agilent probes, even if you select Use Customer Linker Sequence.

Layout Details – Normalization Probe Groups pane

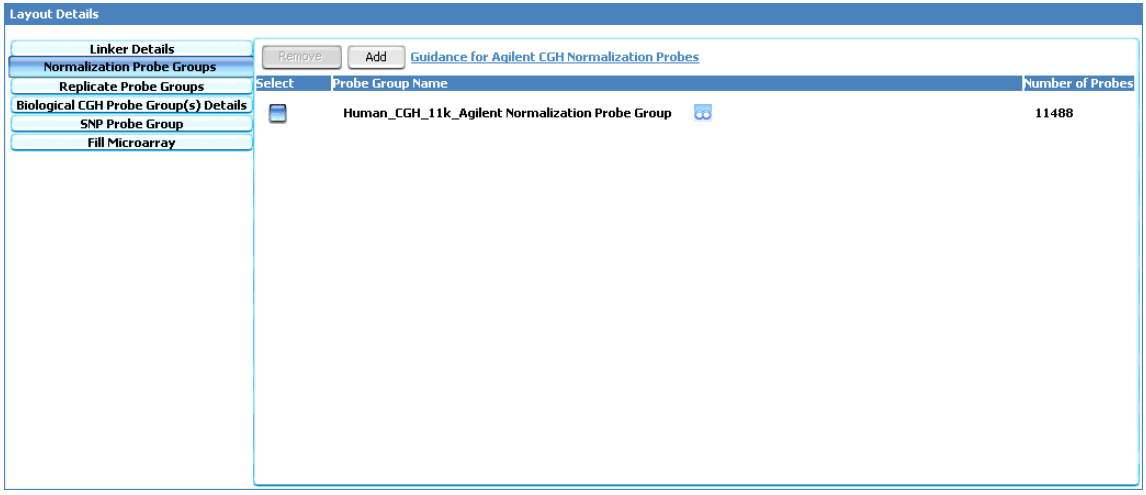


Figure 127 Edit Microarray Design – Normalization Probe Groups pane

Purpose: (Available for CGH arrays) This pane shows the normalization probe group(s) that are currently included in your microarray design. A normalization probe group is a special control probe group that supplies data that can be used to normalize the two dye channel data generated from the array. See "CGH array design guidance" on page 900.

To open: Under Layout Details, click **Normalization Probe Groups.**

These items are available:

Item	Description
Table columns	
Select	Mark the check box next to a normalization probe group to select it for removal. To remove the selected probe group(s) from the design, click **Remove.**
Probe Group Name	The name(s) of the normalization probe group(s) currently included in the design.
Number of Probes	The number of probes in each normalization probe group.

Item	Description
Buttons	
Remove	Removes the selected probe group(s) from the design.
Add	Opens the Add Probe Groups tab within the dialog box, where you can add additional normalization probe group(s) to the design. See "Layout Details – Add Probe Groups pane" on page 767.

NOTE

When you create an array for certain species and design formats, eArray automatically adds a default Agilent normalization probe group. If normalization probe group(s) appear in your design, you can download a list of unique probes to use in the Agilent Feature Extraction program. The name of this file is *NormalizedProbeTDT*. See "To download microarray design files" on page 341.

You can also create your own normalization probe group. See "CGH array design guidance" on page 900.

Layout Details – Replicate Probe Groups pane

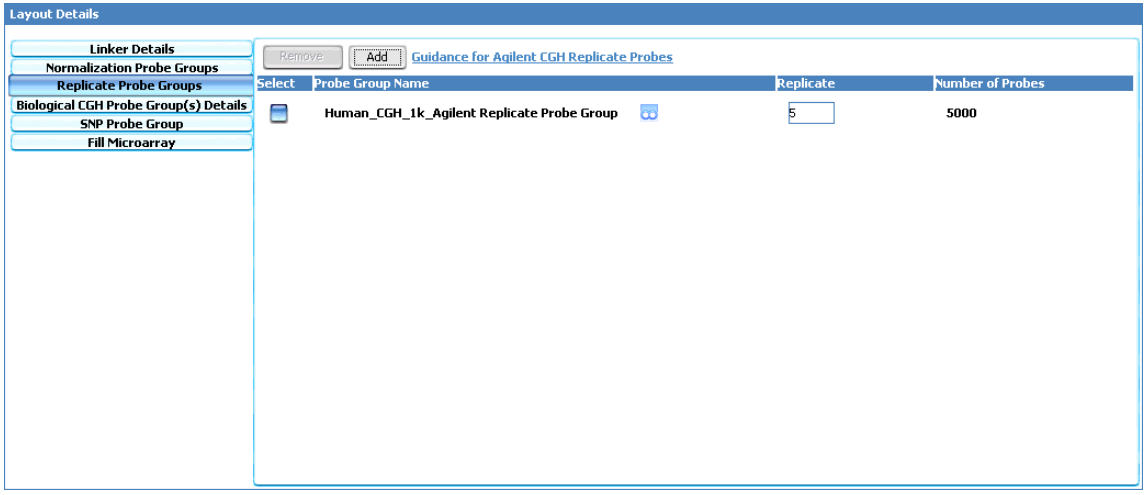


Figure 128 Edit Microarray Design – Replicate Probe Groups pane

Purpose: (Available for CGH and Expression arrays) This pane displays the replicate probe groups that are currently included in your microarray design. The replicate probe groups that you edit in this pane are distinct from the user probe groups that you can include in designs in multiple copies. These are special control probe groups that the Feature Extraction and DNA Analytics programs can use to calculate the Reproducibility QC Metric. For each channel, this metric is the median %CV of background-subtracted signal for the replicate probes after outlier rejection.

To open: Under layout Details, click **Replicate Probe Groups.**

These items are available in the pane:

Item	Description
Table columns	
Select	Mark the check box next to a replicate probe group to select it for removal. To remove the selected probe group(s) from the design, click **Remove.**
Probe Group Name	The names of the replicate probe groups currently included in the design.
Replicate	The number of copies of the replicate probe group in the design. The default is 5.
Number of Probes	The number of probes in each replicate probe group.
Buttons	
Remove	Removes the selected replicate probe group(s) from the design.
Add	Opens the Add Probe Groups tab within the dialog box, where you can add additional replicate probe group(s) to the design. See "Layout Details – Add Probe Groups pane" on page 767.

NOTE

When you create an array for certain species and design formats, eArray automatically adds a default Agilent replicate probe group.

You can also create your own replicate probe group. See "Expression array design guidance" on page 898 and "CGH array design guidance" on page 900.

Layout Details – Biological <type> Probe Groups pane

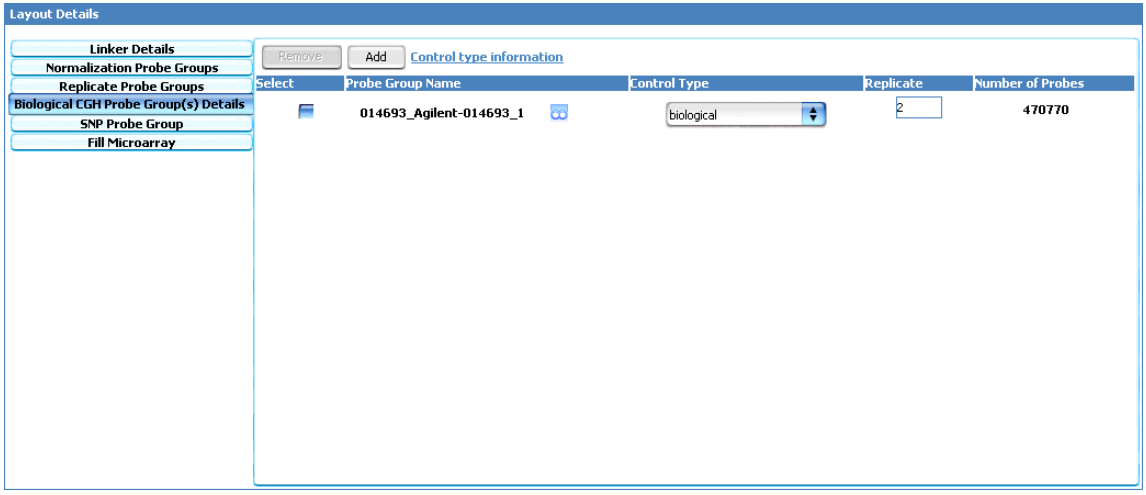


Figure 129 Edit Microarray Design dialog box – Biological <type> Probe Groups pane

Purpose: This pane shows the biological and user control probe groups that are currently included in your microarray design. It also lets you add and remove probe groups.

To open: Under Layout Details, click **Biological <type> Probe Groups.** ("<type>" is the given application type, such as CGH or Expression.)

The items and options in the table below are available in this pane.

Item	Description
Table columns	
Select	Mark the check box next to a probe group to select it for removal. To remove the selected probe group(s) from the design, click **Remove.**
Probe Group Name	(Read-only) The names of the probe groups currently included in the design. To view a given probe group, click .

Item	Description
Control Type	You can select a new control type for any probe group in the list. The control type of a probe group influences how the data from the probe group are handled in downstream analysis. Positive and negative control probe groups cannot collectively occupy more than 50% of the available features in your design. These options are available: • **biological** – Identifies the probe group as a non-control probe group (condition= **FALSE**). It is the default option for biological probes, which should comprise at least 50% of your design. • **ignore** – Omits the probe group from the Feature Extraction analyses and output. Once a microarray design is submitted, the control types of its probe groups cannot be changed, so the only way to "re-activate" these probe groups, if desired, would be to modify the ControlType field of the design file. • **neg** – Identifies the probe group as a negative user control. Negative control groups are intended to have no hybridization. The control grid that is automatically assigned to each microarray design contains an adequate number of negative controls. If you assign your own additional group of negative controls, these controls will be used by Feature Extraction, whether or not they report only background signal. • **pos** – Identifies the probe group as a positive user control. Positive controls are excluded from many of the statistical QC metrics in Feature Extraction, but are available for downstream analysis by the user. In general, positive controls have predictable signals, but this is not a requirement. An example of positive controls is the Agilent spike-in probes that are present on Agilent control grids. These controls are used in the gene expression application to calculate QC metrics following addition of spike-in controls to the sample.
Replicate	(Available only for biological (non-control) probe groups) The number of copies of the probe group to be included in the design.
Number of Probes	(Read-only) The number of probes in each probe group.
Buttons	
Remove	Removes the selected probe group(s) from the design.
Add	Opens the Add Probe Groups tab within the dialog box, where you can add additional probe group(s) to the design. See "Layout Details – Add Probe Groups pane" on page 767.

Layout Details – SNP Probe Groups pane

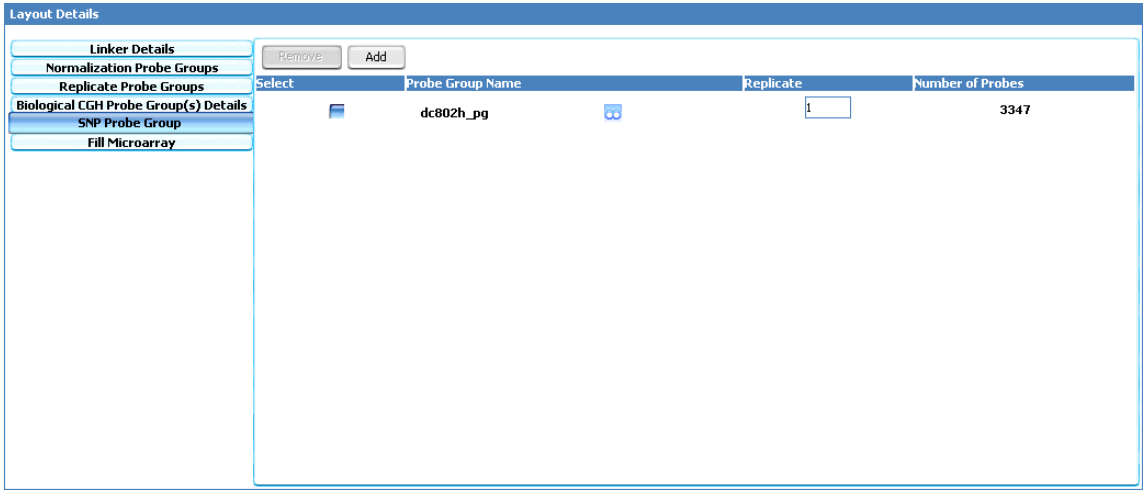


Figure 130 Edit Microarray Design – SNP Probe Groups pane

Purpose: (Available for CGH+SNP microarrays in the CGH application type) This pane shows the SNP probe groups that are currently included in your microarray design. It also lets you add and remove SNP probe groups.

To open: Under Layout Details, click **SNP Probe Groups.**

The items and options in the table below are available in this pane.

Item	Description
Table columns	
Select	Mark the check box next to a SNP probe group to select it for removal. To remove the selected probe group(s) from the design, click **Remove.**
Probe Group Name	(Read-only) The names of the SNP probe groups that are currently included in the design. To view a given probe group, click .
Replicate	The number of copies of the given SNP probe group to be included in the design.
Number of Probes	(Read-only) The number of probes in each SNP probe group.

Item	Description
Buttons	
Remove	Removes the selected probe group(s) from the design.
Add	Opens the Add Probe Groups pane within the dialog box, where you can add additional probe group(s) to the design. See "Layout Details – Add Probe Groups pane" on page 767. When you use the Add Probe Groups pane, search results show only SNP probe groups.

Layout Details – Fill Microarray pane

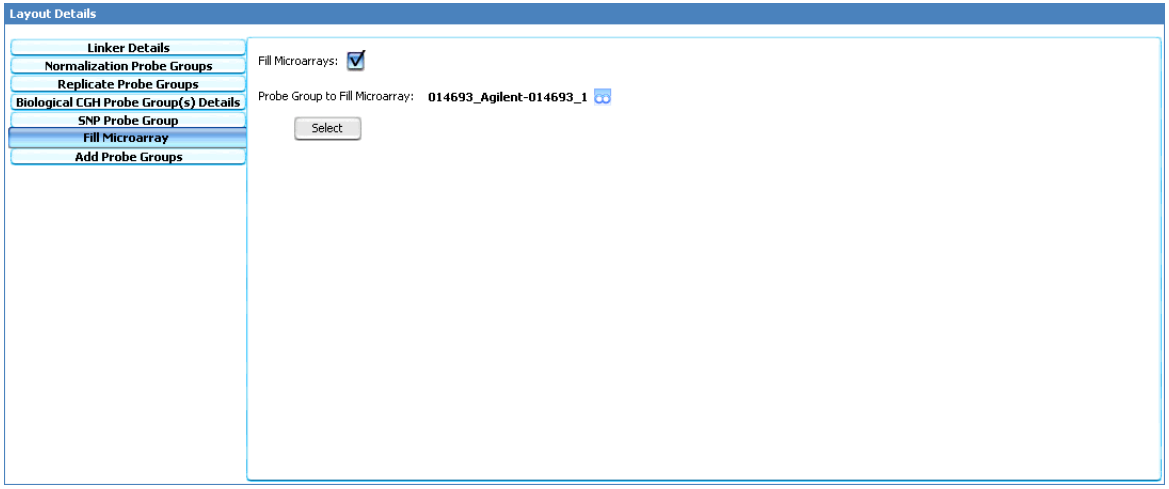


Figure 131 Edit Microarray Design – Fill Microarray pane

Purpose: The options in the Fill Microarray pane let you to select a probe group with which to fill the unused features of your microarray design.

To open: Under Layout Details, click **Fill Microarray.**

These items appear in the pane:

Item	Description
Fill Microarrays	Mark this option to fill the unused features in your design with probes from the probe group of your choice. The program applies probes from the selected probe group, multiple times if needed, until all features are filled.
Probe Group to Fill Microarray	Displays the name of the currently selected filler probe group, if any. **Note:** For microRNA microarrays, the program always fills unused features with a structural filler probe group.
	Opens the View Probe Group dialog box, where you can view the properties and probe content of the currently selected filler probe group. See "View Probe Group" on page 873.
Select button	Opens the Select Probe Group to Fill Microarray tab within the dialog box, where you can select a filler probe group. This tab is identical to the Add Probe Groups tab, but you can only select one probe group. See "Layout Details – Add Probe Groups pane" on page 767. The probe group that you select replaces any previously selected filler probe group.

Layout Details – Add Probe Groups pane

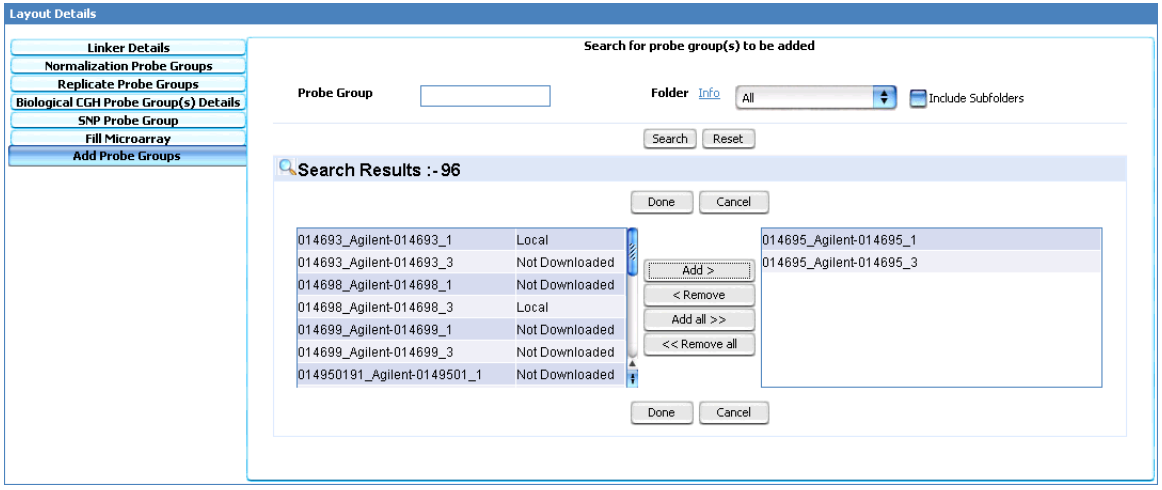


Figure 132 Edit Microarray Design – Add Probe Groups pane

Purpose: Lets you search for, select, and add probe groups to your microarray design. Depending upon how you open this tab, the program adds the probe group(s) as normalization, replicate, SNP, filler, or user biological or control probe groups.

To open: Under Layout Details, do one of the following:

- Click **Biological <type> Probe Groups,** then click **Add.**
- (CGH Designs only) Click **Normalization Probe Groups,** then click **Add.**
- (CGH and Expression designs, only) Click **Replicate Probe Groups,** then click **Add.**
- (CGH+SNP designs only) Click **SNP Probe Groups,** then click **Add.**
- Click **Fill Microarray,** mark **Fill Microarray,** then under **Probe Group to Fill Microarray,** click **Select.**

The Add Probe Groups tab contains the following items:

Item	Description
Probe Group	Type all or part of the name of a desired probe group. To return all probe groups available to you, leave this search criterion blank.
Folder	Select a folder. The program limits the probe group search to only the folder that you select. To return probe groups without regard to their folder locations, select **All.** To include the subfolders of the selected folder in your search, mark **Include Subfolders.**
Search	Starts a search for all probe groups that are available to you that contain the term you typed in Probe Group. Search results appear on the left side of the Search Result pane.
Reset	Clears your search term and any returned results.
Search Result pane	
1 2 3	(Appears if there are multiple pages of search results) Click a number to navigate to a specific page of search results.
Left box	Contains a page of probe group search results, if any. These probe groups are available for you to add to your microarray design. To select probe groups from a page of search results: • To select a single probe group, click its name. • To select multiple probe groups, control-click their names. • To select a contiguous block of probe groups, click the first probe group in the block, then shift-click the last probe group.
Add	Transfers the selected probe groups from the left box to the right box. These probe groups will be included in your microarray design.
Remove	Transfers the selected probe groups from the right box to the left box. These probe groups will no longer be included in your microarray design.
Add all	Transfers all of the probe groups from the left box to the right box. All of these probe groups will be included in your microarray design.
Remove all	Clears the right box. The probe groups that appeared in there will no longer be included in your microarray design.
Done	Adds the probe groups in the right box to your microarray design.

Item	Description
Cancel	Closes the tab without adding any probe groups to your microarray design.
Add	Transfers the selected probe groups from the left box to the right box. These probe groups will be included in your microarray design.

NOTE

When you select probe groups for a microarray design, the program tells you if a probe group is *Local* or if it is *Not Downloaded.* If you select one or more probe groups that are *Not Downloaded,* you can only save the new microarray design with a status of Draft. After you download the given probe group(s) from the eArray Web site, you can save the microarray design with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

Layout Details – List of Versions pane

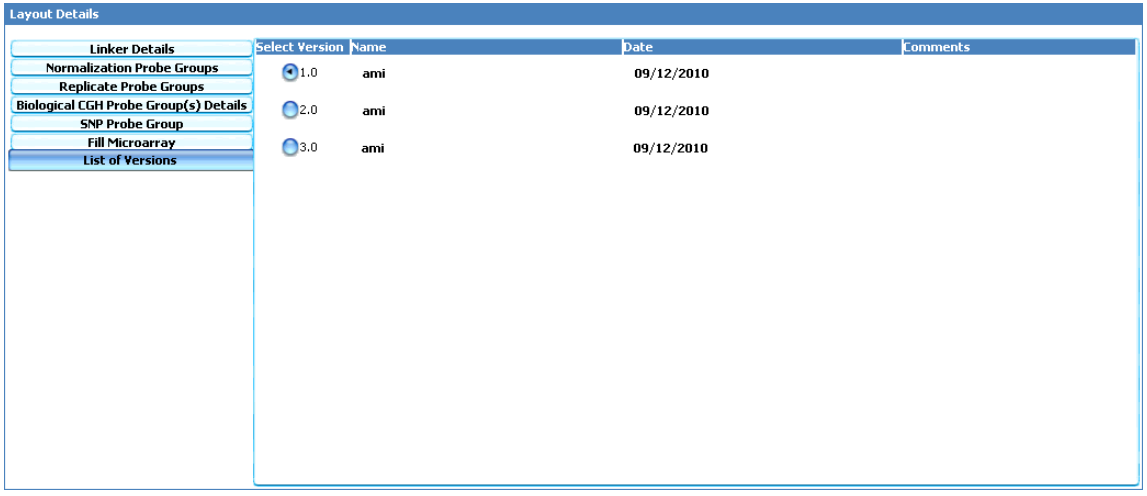


Figure 133 Edit Microarray Design – List of Versions pane

Purpose: This pane lets you view a list of the current and previous review versions of the microarray design. It is available for designs with a status of Review. See "To review a microarray design" on page 326.

To open: When you review a microarray design, Under **Layout Details,** click **List of Versions.**

Select Version Lists the version numbers of all of the versions of a microarray design. The selected version is the one that the program uses as the starting point for all reviews of the design. If you are the owner of the design, you can select a different version to use as the starting point for subsequent reviews of the design. See "To place a different version of a design in review" on page 325.

Also, when the owner of the design changes the status of the design to Complete, the program saves the current version of the design, only. See "To prevent further edits or reviews of a design" on page 335.

Name Lists the name of the person who saved each version of the design.

Date Gives the date on which each version of the design was saved.

Comments Lists any comments that were saved with each version of the design.

Buttons

These buttons appear at the bottom of the dialog box:

Save Saves the microarray design with any changes that you have made, and closes the dialog box. The changed design overwrites the original one, even if you have selected a different folder location.

Reset Restores the properties and probe group content of the microarray design to what they were before you made any changes.

Cancel Closes the dialog box without making any changes.

Edit Probe Group

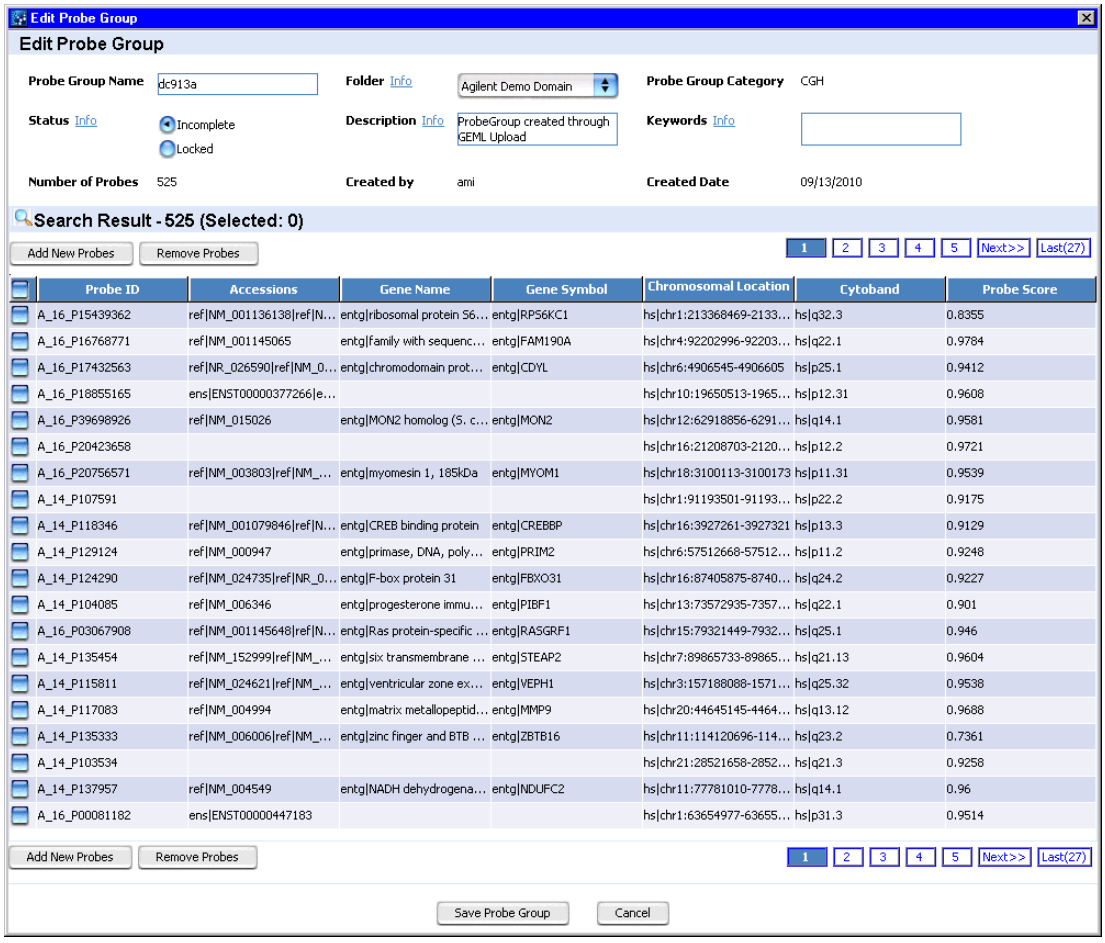


Figure 134 Edit Probe Group dialog box

Purpose: Lets you make changes to the content and properties of a probe group with Incomplete status. See "To edit a probe group" on page 234.

To open: In the **Actions** column of the search results of a probe group search, next to the desired probe group, click . See "To search for probe groups" on page 224.

Alternatively, in the **Design Data** pane of the Navigator, right-click the name of the desired probe group, then click **Edit.**

Properties

Property	Instructions/Details
Probe Group Name	Type a new name, if desired. Use only letters and numbers.
Folder	Select a new location for the probe group. Only the folders to which you have access appear in the list.
Probe Group Category	(Read-only, available for the CGH application type) One of these types appears: • **CGH** – The probe group is a standard CGH probe group that can included on standard CGH microarrays and on CGH+SNP microarrays. • **CGH+SNP** – The probe group is a SNP probe group that contains only Agilent SNP probes, and can be only used in CGH+SNP microarrays. See "To create a CGH+SNP microarray design" on page 301.
Status	Select one of these options: **Incomplete** – This option lets you make additional edits to the probe group after you save it. This is the default option. **Locked** – This option prevents edits to the probe group after you save it. Locked probe groups cannot be unlocked.
Description	Type brief descriptive information, if desired, up to 4,000 characters in length.
Keywords	Type search keyword(s), if desired, up to a total length of 4,000 characters. Separate multiple keywords with pipe " | " characters, commas, or semicolons.
Number of Probes	(Read-only) The total number of probes in the probe group.
Created by	(Read-only) The name of person who first saved the probe group.
Date Created	(Read-only) The date the probe group was first saved.

Search Result pane

Add New Probes (Not available for SNP probe groups) Opens the Add Probes to Probe Group dialog box, where you can search for and select additional probes for the probe group. See "Add Probes to Probe Group" on page 578.

Remove Probes (Not available for SNP probe groups) Removes selected probes from the probe group. To select a probe for removal, mark the check box next to the name of the probe.

Table of probes The table lists the probes in the probe group. Every probe has a Probe ID, but the availability of additional probe annotation varies.

- **Check boxes** – Mark the check box associated with an individual probe to select it for removal from the probe group. To select all of the probes on the current page for removal, mark the check box in the column heading.
- **Probe ID** – The unique probe name for each probe,
- **Additional Annotation Columns** – The availability of data for these columns varies by probe.

1 2 3 (Page navigation buttons) If available, these buttons let you display different pages of probes.

Save Probe Group Saves the probe group with any changes that you have made. This overwrites the original probe group, even if you change the location.

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

File Upload

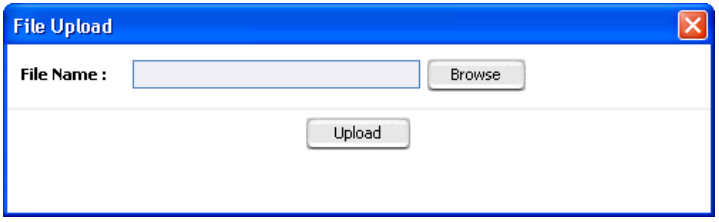


Figure 135 File Upload dialog box

Purpose: Lets you upload a file that contains parameter value(s) for specific types of searches.

To open: In certain search panes (such as the Simple HD Probe Search pane), click **Upload.**

File Name (Read-only) Displays the location of the file selected for upload.

Browse Opens an Open dialog box, where you can select a file for upload.

Upload Uploads the values in the file to the associated search parameter in the search pane.

File Writer Preferences

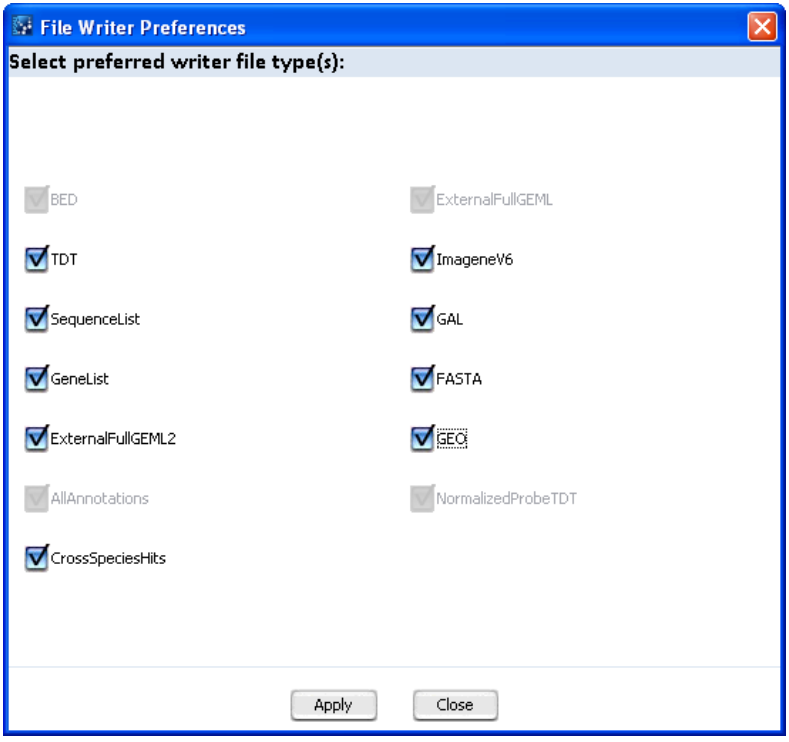


Figure 136 File Writer Preferences dialog box

Purpose: The eArray$_{XD}$ File Writer is the part of the program that creates design files for libraries and microarray designs. By default, the program only creates the annotation files that are required for data analysis in Agilent Genomic Workbench, or in GeneSpring. This dialog box lets you select the

additional design files that the program creates. After the program creates design files, you can download them. See "To select the types of design files that the program creates" on page 343.

NOTE The options that you select affect the files that are available for libraries and microarray designs that you *subsequently* transfer from the eArray Web site, or save with a status of Complete or Submitted.

To open: In the Miscellaneous tab of the User Preferences dialog box, click **Change Writer Preferences.** See "User Preferences – Miscellaneous tab" on page 864.

Select preferred writer file type(s)

Mark the file types that you want the program to create. Some file types are only available for particular application types. Also, you cannot clear several of the options—the program creates these files whenever they are appropriate. Descriptions of file types appear in the table below.

File Type	Description
All Annotations	(Expression application type only) Lists all annotation fields for probes on the microarray.
BED	Browser Extensible Data format. Gives you a flexible way to define the data lines that appear in an annotation track. BED files that you download from eArray contain genomic coordinates and probe names.
ExternalFullGEML (GEML 1.0)	Gene Expression Markup Language. Used by Agilent Feature Extraction, Rosetta Resolver, and Rosetta Luminator. For details, go to http://rosettabio.com/tech/geml/default.htm. This file is supplied in Agilent scanner orientation.
ExternalFullGEML2 (GEML 2.0)	Gene Expression Markup Language Version 2. Used by Rosetta Resolver and Rosetta Luminator. For details, go to http://rosettabio.com/tech/geml/default.htm. This file is supplied in Agilent scanner orientation.

File Type	Description
FASTA	A list of probes in FASTA format. The FASTA format begins with a single-line description (which is defined by a starting ">" character), followed by lines of biological sequence in standard IUB/IUPAC amino acid or nucleic acid code. FASTA probe files that you download from eArray contain probe names on the description lines, and probe DNA sequence data.
GAL	GenePix Array List, conforming to the Axon Text File (ATF) format. The GAL file format is used in Axon's GenePix image analysis software. For more details, go to: http://www.axon.xom/gn_GenePixSoftware.html This file is supplied in Axon scanner orientation.
GeneList	GeneID file for BioDiscovery Imagene software. This file is supplied in Agilent and Axon scanner orientation.
GEO	Gene Expression Omnibus file. Use this file to submit the microarray design to the GEO repository. For details, go to http://ncbi.nlm.nih.gov/geo/
Imagene	File format used by BioDiscovery's Imagene image analysis software.
SequenceList	A tab-delimited list of probe ID/probe sequence pairs.
TDT	Tab Delimited Text file. This file supplies a representation of the microarray features and their annotation, suitable for use in a spreadsheet or database. This file is supplied in Agilent and Axon scanner orientation.
NormalizedProbeTDT	(CGH application type only) Normalization probe list file. Used by Agilent Feature Extraction software for dye normalization for 2-color microarrays.
CrossSpeciesHits	(microRNA application type only) Cross-species annotation file. This file is only available for microarrays that have probes that have annotations to more than one species.

Genome Information

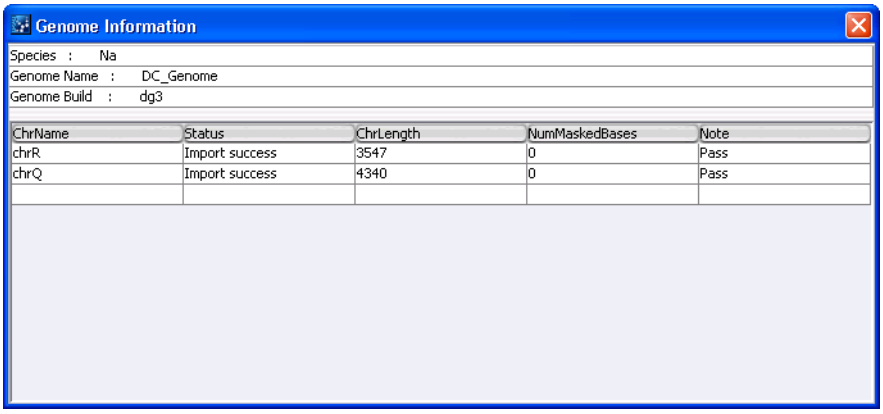


Figure 137 Genome Information dialog box

Purpose: Lets you view the names and statistics of custom genome sequences that you have imported, and see whether or not the sequences passed validation. See "To import a new genome" on page 66. The imported sequences can also represent chromosomes to be added to an existing custom genome. See "To add more chromosomes to a custom genome" on page 68.

To open: In the Tasks pane of the Navigator, in the Import Genome folder, right-click the desired job, then click **View Genome Information.**

Species The species that was selected by the user when the genome was imported.

Genome Name The name of the job, as entered by the user when the sequences were imported.

Genome Build The specific genome build represented by the imported sequences, as entered by the user when the genome was imported.

List of Chromosomes This list shows all of the chromosomes that were submitted. These columns appear:

Column	Description
ChrName	Name of each chromosome that was uploaded, as specified on the description line of each imported FASTA format file.
Status	Whether or not the given chromosome was successfully imported.

Column	Description
ChrLength	The number of base pairs in each chromosome.
NumMaskedBases	The number of bases in the sequence that were interpreted as "soft-masked" bases. These bases are represented by lower-case characters in the sequence file. The program only identifies soft-masked bases if you mark **Genome is soft-masked** when you import the genome. Soft masked bases are ignored by the Bait Tiling and Genomic Tiling tools when you mark **Avoid Standard Repeat Masked Regions.**
Note	Whether or not the given chromosome passed validation.

Genomic Tiling

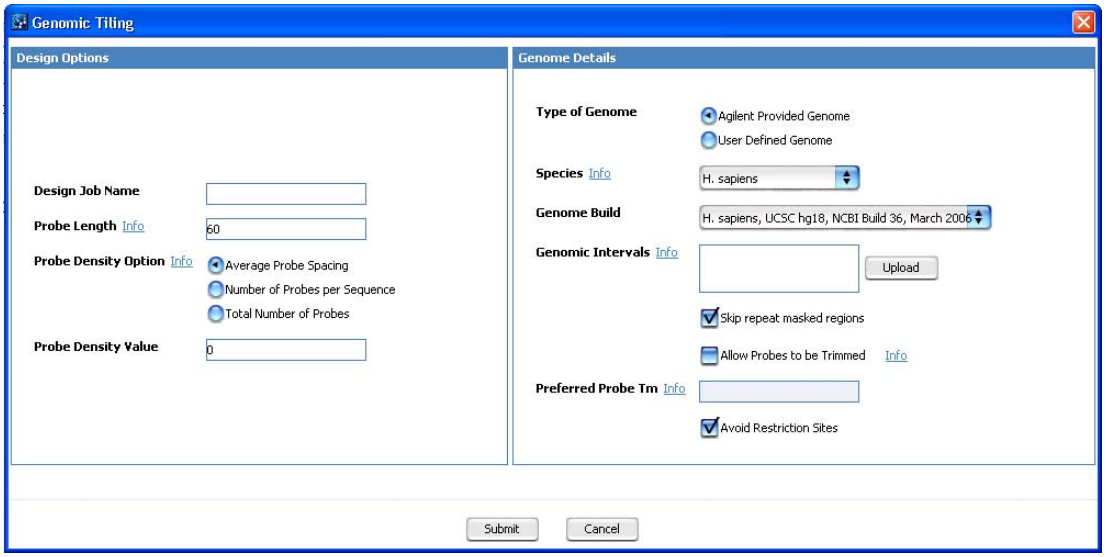


Figure 138 Genomic Tiling dialog box

Purpose: Lets you set up and submit a Genomic Tiling job. Genomic Tiling creates probes for the CGH, ChIP-on-chip, and CH3 application types that span specified regions of a genome at even intervals. See "To set up a Genomic Tiling job" on page 176.

To open: In the eArray$_{XD}$ tab, under **Create Probes,** click **Genomic Tiling.**

Design Options

Parameter	Instructions/Details
Design Job Name	Type a name to identify this Genomic Tiling job.
Probe Length	Type the desired length (from 45 to 60 bp) for the generated probes. If you intend to T_M trim probes, keep the length set to its default value of 60 bp.

Parameter	Instructions/Details
Probe Density Option	Select one of the following options, then type an appropriate number in **Probe Density Value.** • **Average Probe Spacing** – Defines the average distance (in bp) between the center points of the probes. Because of repeat regions, the actual spacing between probes may deviate from the ideal average probe spacing. • **Number of Probes per Sequence** – Defines the average number of probes designed for each target sequence. eArray uses this value to calculate average probe spacing on a per-sequence basis. The actual number of probes designed for each sequence may deviate from the specified value, because of repeat regions and rounding, but this deviation should not be large unless sequence length limits the design process. • **Total Number of Probes** – Defines the total probes generated, to be spaced evenly over all of the target sequences. eArray first calculates the number of probes to be generated for each sequence, and then uses these numbers to calculate average probe spacing.
Probe Density Value	Type the desired number of probes, or the desired probe spacing that applies to your selection in **Probe Density Option.**

Genome Details

Parameter	Instructions/Details
Type of Genome	Select one of these options: • **Agilent Provided Genome** – Select this option to use a genome that is available on the eArray Web site. • **User Defined Genome** – Select this option to use a genome that has been previously uploaded to your server. To upload a genome, see "To import a new genome" on page 66. In either case, the available genomes of the selected type appear in Species.
Species	Select the desired species. Only the genomes of the type that you selected in Type of Genome appear in the list.
Genome Build	The specific genome build of the selected species to which probes will be designed. Select an alternate build, if one is available.

Parameter	Instructions/Details
Genomic Intervals	Type the genomic intervals to be tiled. Separate multiple intervals with pipe " | " characters. You can enter genomic intervals in several ways, illustrated in the following examples: • `chr1` (all of chromosome 1) • `chr1:1000` (chromosome 1, from base 1000 to the end) • `chr1:1000-5000` (chromosome 1, bases 1000 to 5000) **Upload** – Opens a File Upload dialog box, where you can select a file of genomic intervals to upload as an alternative to typing them. See "File Upload" on page 773. The file must be a plain text file that contains one genomic interval per line. See "Genomic Intervals (Genomic Tiling)" on page 888.
Skip repeat masked regions	Select this option to ignore repeat regions within the selected genomic intervals during the tiling process.
Allow Probes to be Trimmed	This option lets the program trim probes to shorter than the size in Probe Length. This can yield tighter compliance with the desired T_M. eArray will not trim probes to shorter than 45 bases. To T_M trim probes, you must set **Probe Length** to 60 bases.
Preferred Probe Tm	Type the preferred probe T_M (in °C). The probe tiling algorithm trims probes so that they have a T_M close to the requested one. Set the Preferred Probe T_M approximately 20°C higher than your intended hybridization temperature. The T_M is the temperature at which equal populations of a probe and its target sequence exist as a 50:50 mixture of duplex and single-stranded forms.
Avoid Restriction Sites	(Available for the CGH application type) Mark this option if you use the Agilent CGH enzymatic labeling protocol. This option avoids RsaI and AluI restriction enzyme recognition sites within the selected genomic intervals during the Genomic Tiling process. The CGH enzymatic labeling protocol uses these two enzymes. Because the target DNA is always cut at these sequences, probes that contain these sequences may not be able to hybridize effectively with the labeled DNA.

Submit For Agilent-provided genomes, submits the Genomic Tiling job to the eArray Web site. For user-defined genomes, creates the probes locally on your server.

Cancel Cancels the Genomic Tiling job, and closes the dialog box.

HD Search Criteria

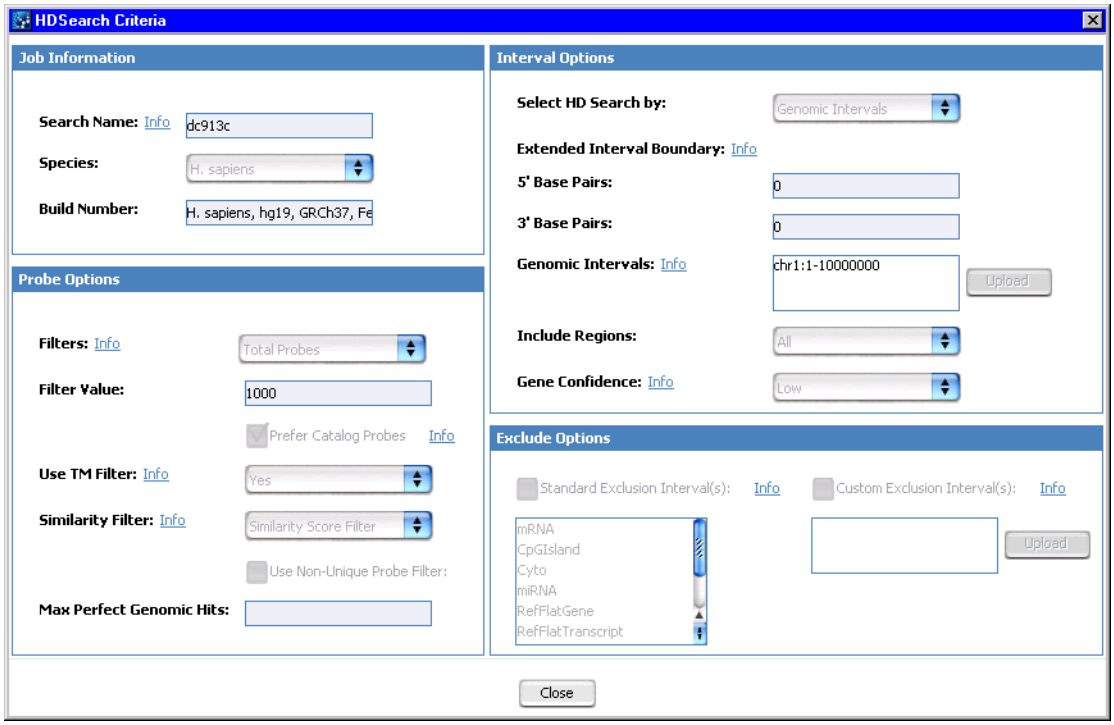


Figure 139 HD Search Criteria dialog box, with the search criteria for a Simple HD-CGH Genomic Intervals probe search

Purpose: Lets you view the search criteria that were used in a specific High Density (HD) Probe Search. See "Searching for Agilent High Density (HD) Probes" on page 109.

To open: In the **Tasks** pane of the Navigator, in the **HD Search** or **HD Search (Wizard)** folder, right-click the name of the desired job, then click **View Search Criteria.**

Search Criteria

The search criteria that appear in the dialog box vary by the type of HD probe search that was requested. All search criteria are read-only. See these topics:

- "Simple HD Probe Search" on page 565
- "Advanced HD Probe Search" on page 527

- "Probe ID Search (HD probes)" on page 557

Close Closes the dialog box.

HD Search Results

Purpose: Lets you view the search criteria that were used in a specific HD probe search, and statistics about the probes that were returned. See "To view HD probe search results" on page 134.

To open: In the Tasks pane of the Navigator, in the HD Search folder, right-click the name of the desired HD Search job, then click **View Result.**

This dialog box displays the results in several tabs:

- **Search Criteria** – Shows the search criteria that were submitted for the HD Probe Search. See "Search Criteria tab" on page 784.
- **Summary Result** – Shows overall statistics about the probes that were returned by the HD Probe Search. See "Summary Result tab" on page 785.
- **Detail Result** – Shows information about each genomic interval that was submitted for the HD Search, and a summary of the probes that were returned for each interval. See "Detail Result tab" on page 787

Search Criteria tab

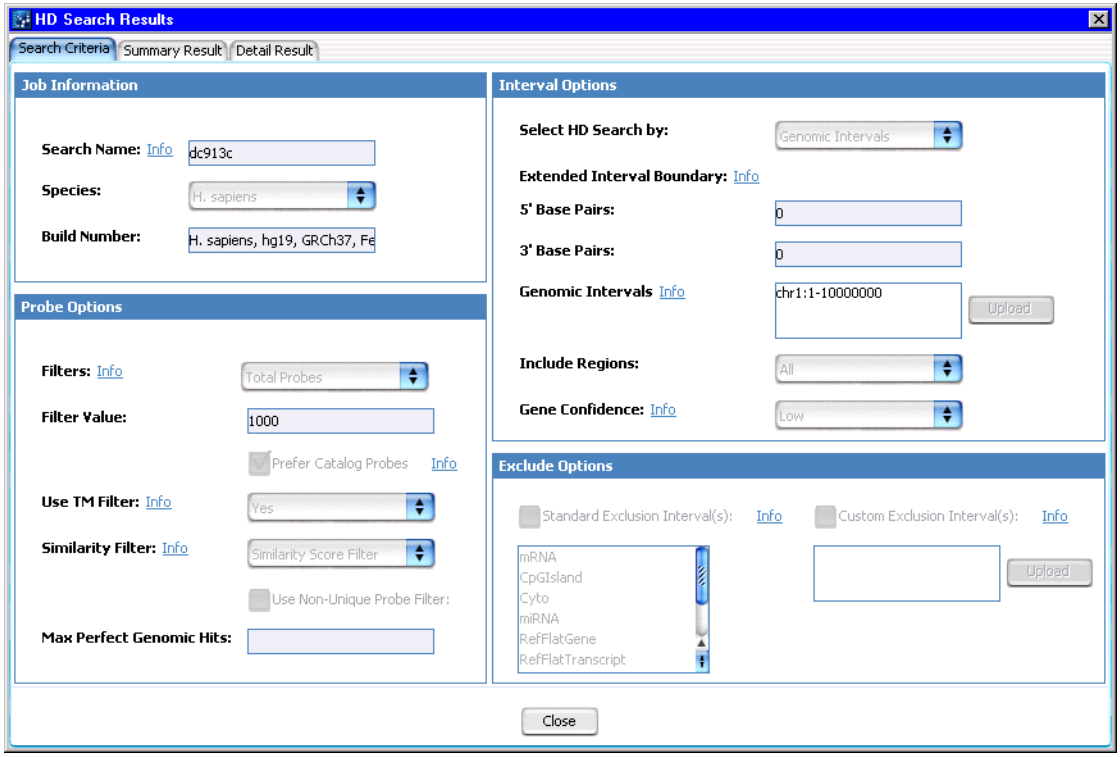


Figure 140 HD Search Results dialog box – Search Criteria tab. Criteria for an Simple Genomic Intervals HD Probe Search shown

This tab lets you view the search criteria that were used in a specific High Density (HD) Probe Search. See "Searching for Agilent High Density (HD) Probes" on page 109.

The search criteria that appear in the dialog box vary by the type of HD Probe Search that was requested. All search criteria are read-only. See these topics for details about specific criteria:

- "Simple HD Probe Search" on page 565
- "Advanced HD Probe Search" on page 527
- "Probe ID Search (HD probes)" on page 557

Summary Result tab

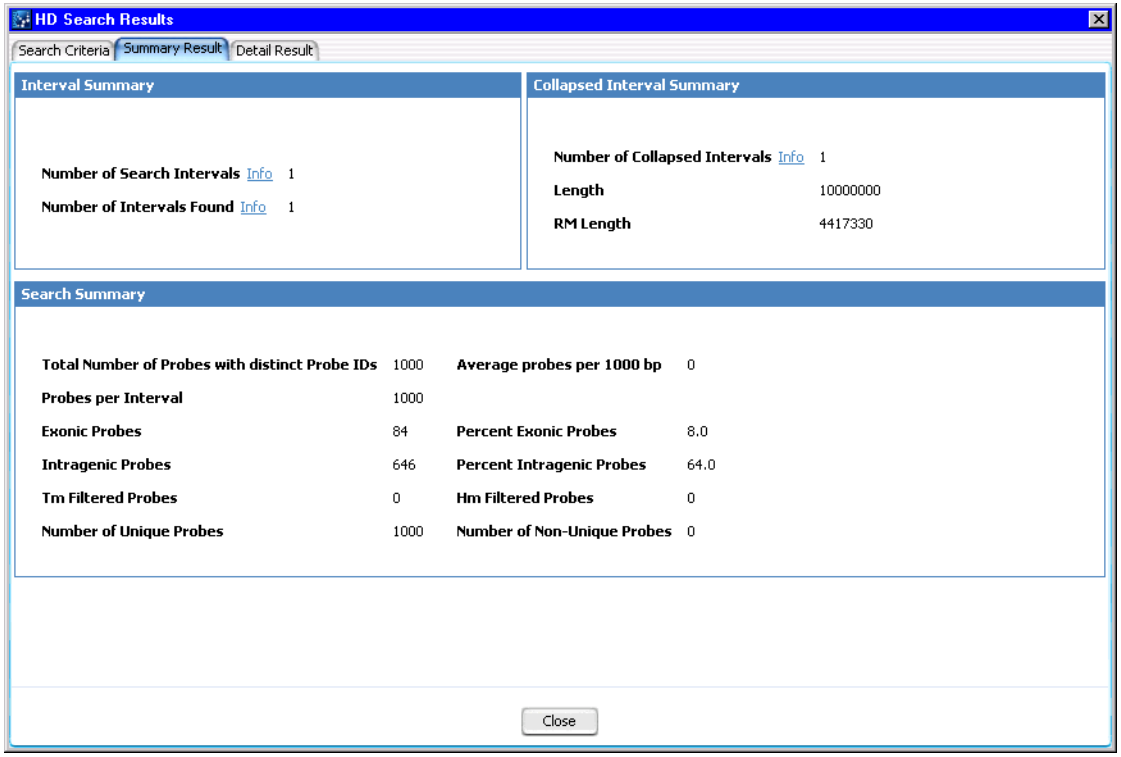


Figure 141 HD Search Results dialog box – Summary Result tab

This tab shows overall statistics about the probes that were returned by the HD Probe Search. All information in this pane is read-only. The table below lists the statistics that can appear. For Probe ID HD Searches, the only statistic available is Total Number of Probes.

Item	Description
Interval Summary	
Number of Search Intervals	Number of search intervals that were entered as search criteria.
Number of Intervals Found	Number of search intervals that were correctly formatted, and for which probes were actually present.

Item	Description
Collapsed Interval Summary	
Number of Collapsed Intervals	Number of intervals after overlapping intervals were combined.
Length	Total number of base pairs considered in the search.
RM Length	(Repeat-masked length) Number of base pairs considered in the search, not including repeat regions.
Search Summary	
Total Number of Probes with Distinct Probe IDs	Total number of resultant probes before filtering, not including replicate probes.
Average Probes per 1000 bp	Average number of probes retrieved per 1,000 input base pairs.
Probes per Interval	Average number of probes retrieved for each interval in the search criteria.
Exonic Probes	Number of probes in final result that map within exons.
Percent Exonic Probes	Fraction of the retrieved probes that map within exons.
Intragenic Probes	Number of probes in final result that map within genes.
Percent Intragenic Probes	Fraction of the retrieved probes that map within genes.
TM Filtered Probes	Number of probes removed by the T_M filter.
HM Filtered Probes	Number of probes removed by the homology (Hm) filter.
Number of Unique Probes	Number of retrieved probes that map to a single genomic region.
Number of Non-Unique Probes	Number of retrieved probes that map to more than one genomic region.

Detail Result tab

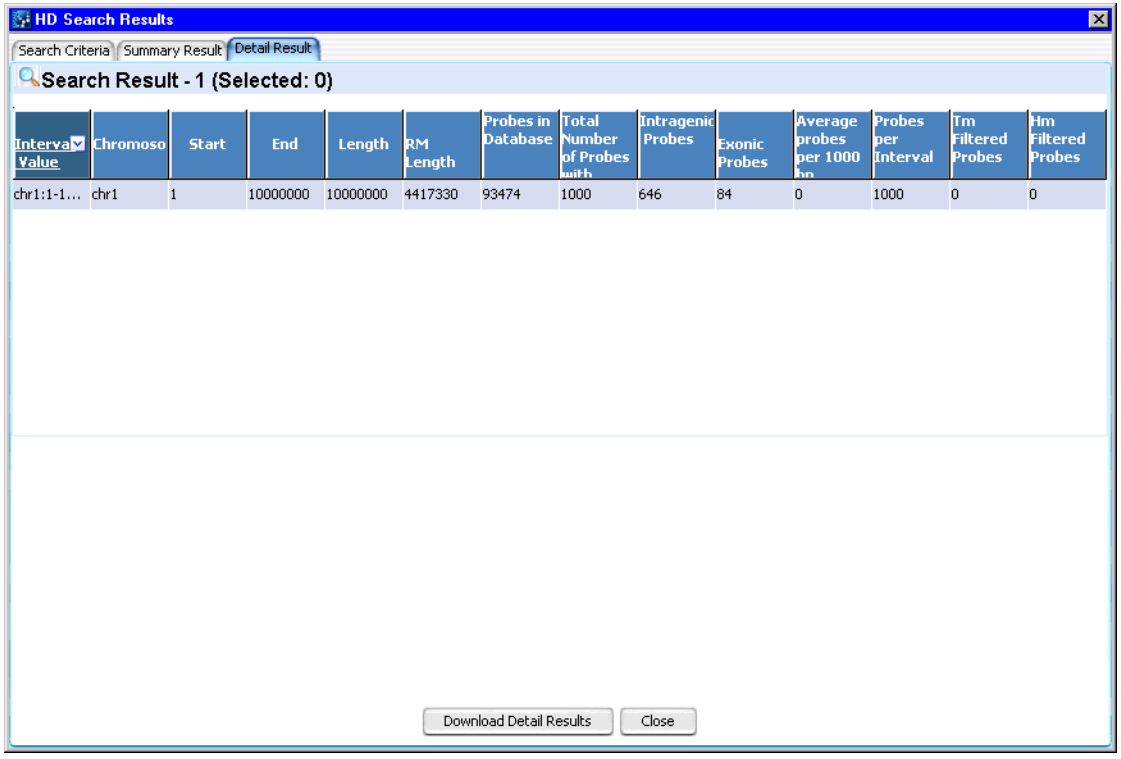


Figure 142 HD Search Results dialog box – Detail Result tab

This tab displays the statistics of a completed High Density (HD) Probe Search job, broken down by genomic interval or gene annotation. The statistics are reported for each interval that was requested in the HD search. All information in the dialog box is read-only. See "Searching for Agilent High Density (HD) Probes" on page 109.

NOTE This tab is not available for Probe ID HD Search results.

Columns

Column	Description
Interval Value	Chromosomal location ranges, cytobands, or gene annotations entered as search criteria.
Chromosome	Chromosome that contains the given interval.
Start	First base pair in the interval on the given chromosome.
End	Last base pair in the interval on the given chromosome.
Length	Total number of base pairs in the interval.
RMLength	(Repeat masked length) Number of base pairs in the interval, not including repeat regions.
Total Number of Probes	Total number of resultant probes before filtering.
Intragenic Probes	Number of probes in final result that map within genes.
Exonic Probes	Number of probes in final result that map within exons.
Average Probes per 1000 bp	Average number of probes retrieved per 1,000 base pairs.
Probes per Interval	Number of probes returned for each interval in the search criteria.
TM Filtered Probes	Number of probes removed by the T_M filter.
HM Filtered probes	Number of probes removed by the homology (Hm) filter.

(Page navigation buttons) If available, these buttons let you display different pages of statistics.

Download Detail Results Opens a Save dialog box, where you can select a location for a downloaded TDT format file. This file contains the same information that you see in the Detail Result tab of the HD Search Results dialog box. You can open the file in a word processing or spreadsheet program.

Close Closes the dialog box.

Import Genome

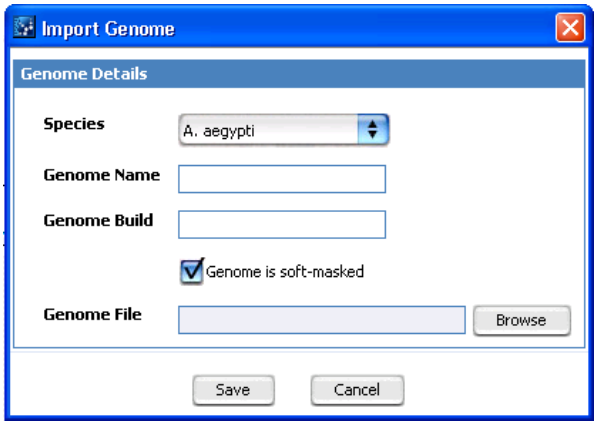


Figure 143 Import Genome dialog box

Purpose: Lets you upload a user defined genome for use with the Genomic Tiling and Bait Tiling tools. See these topics:

- "To import a new genome" on page 66
- "To set up a Genomic Tiling job" on page 176
- "To set up a Bait Tiling job" on page 378

To open: In the **Home** tab, click **Import > Custom Genome for Tiling.**

Genome Details

Parameter	Instructions/Details
Species	Select the species of the user-defined genome that you will import. The species list contains all of the species currently available in the system. To upload a genome for a species that does not appear in this list, select **NA.**
Genome Name	Type a name for the genome upload job. The program lists the job in the Tasks pane of the Navigator under this name.
Genome Build	Type the name of the specific build of the genome that is represented in your genome files. Use only letters, numbers, underscores, periods, and dashes.

Parameter	Instructions/Details
Genome is soft-masked	Mark this check box if repeat sequences in your genome file are represented by lower-case letters. Otherwise, the program converts lower case characters to upper case upon upload.
Genome File	Displays the location of the genome file for import. The genome file must be a ZIP archive that contains the FASTA format chromosomal sequence files. See "Genome" on page 886. **Browse** – Opens an Open dialog box, where you can select the desired genome file for import.

Save Imports the genome and saves it to your server. Imported genomes are available to all users who are connected to your server.

Cancel Closes the dialog box without importing a genome.

Job Queue Management Console

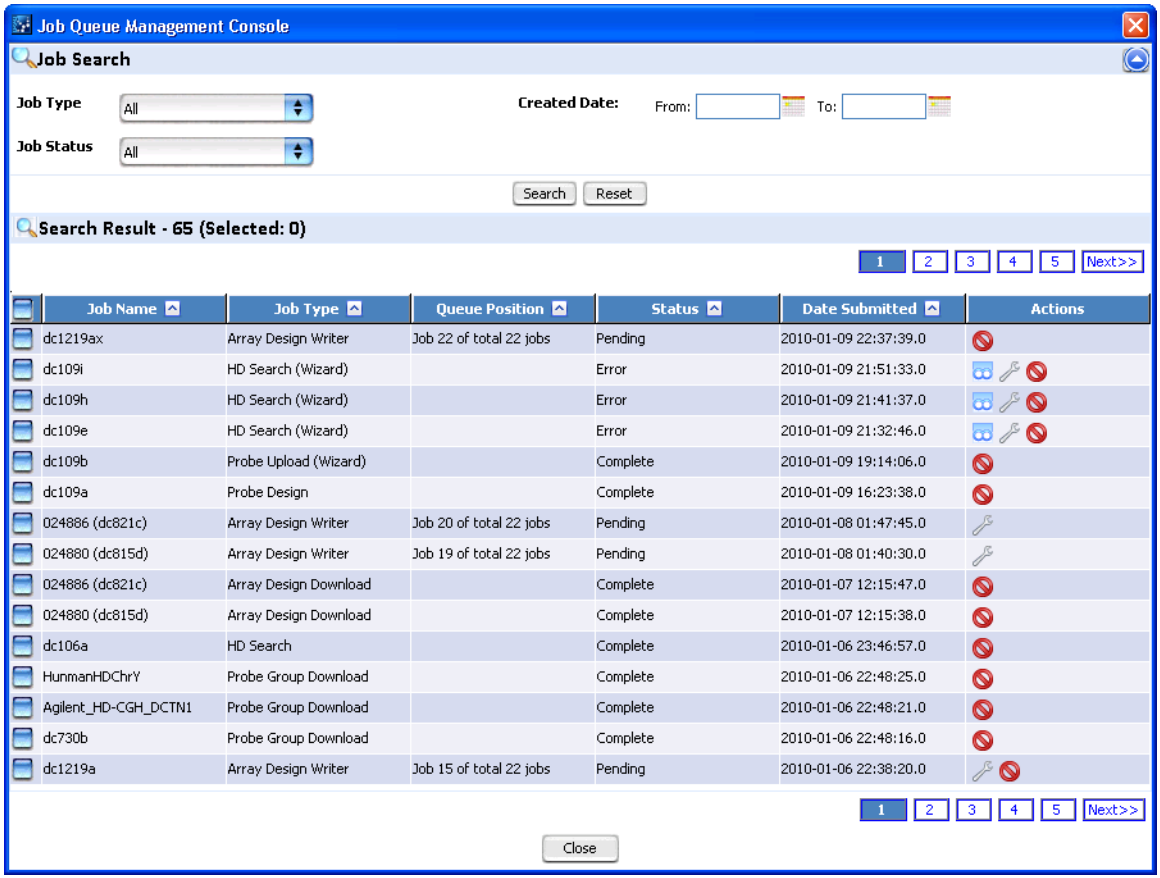


Figure 144 Job Queue Management Console

Purpose: Lets you retrieve a list of jobs (tasks). You can delete, view, or troubleshoot the retrieved jobs.

To open: In the eArray$_{XD}$ tab, under Job Queue Management, click **Tasks.**

Job Search pane

The job search pane contains these options and commands:

Item	Description
Job Type	Limits the list of jobs that are retuned to those of a specific type. Select the desired job type.
Date Created	Enter a range of dates. Use yyyy-mm-dd as the date format, for example `2009-03-20`. Alternatively, to select the desired dates from calendars, click  next to **From** and **To.** To return only designs that were created before a given date, select the desired date in **To**, and do not select a date in **From.**
Job Status	Limits the list of jobs that are returned to those that have a specific status. Select one of these options: • **All** – Does not limit the list based on job status • **COMPLETE** – Displays only jobs that are finished. • **ERROR** – Displays only jobs that have generated an error during processing. • **PENDING** – Displays only jobs that have been submitted to the system, but that have not yet been started. • **PROCESSING** – Displays only jobs that are currently being processed.
Search	Submits the search.
Reset	Clears all search criteria and results.

Search Result pane

The jobs that match the search criteria appear in this pane.

1 2 3 (Page buttons) Click one of these buttons to go to a different page of search results.

Column headings To sort the results based on the contents of a column, click any column heading except Actions. To reverse the order of the jobs, click the same column heading again.

Columns

Column	Description
	These check boxes are for future expansion. They are not currently used by eArray$_{XD}$.
Job Name	The name of the job, as assigned by the user who created the job.
Job Type	The specific type of job, which usually matches the name of the folder in the Tasks pane of the Navigator that contains it.
Queue Position	The place the job holds in the queue. The lower the number, the sooner the job will be processed by the system.
Status	The status of the job: • **PENDING** – The job has been submitted to the system, but no action has been taken on it yet. • **PROCESSING** – The job is currently being processed. • **COMPLETE** – The job is finished. • **ERROR** – The system processed the job, but it generated an error. The job must be resubmitted.
Date Submitted	The date and time that the job was submitted to the system.
Actions	The actions that you can take on a specific job. One or more of these buttons can appear in the Actions column:  – Opens the Troubleshoot Job dialog box, where you can submit an error log to Agilent Technical Support. See "Troubleshoot Job" on page 863.  – Opens a dialog box that can display an error message for the job.  – Deletes the job from the Job Queue Management Console, cancels the job, and removes the job from the Tasks pane of the Navigator. See "To delete a task" on page 75.

Close Closes the dialog box.

Literature Network Inspector

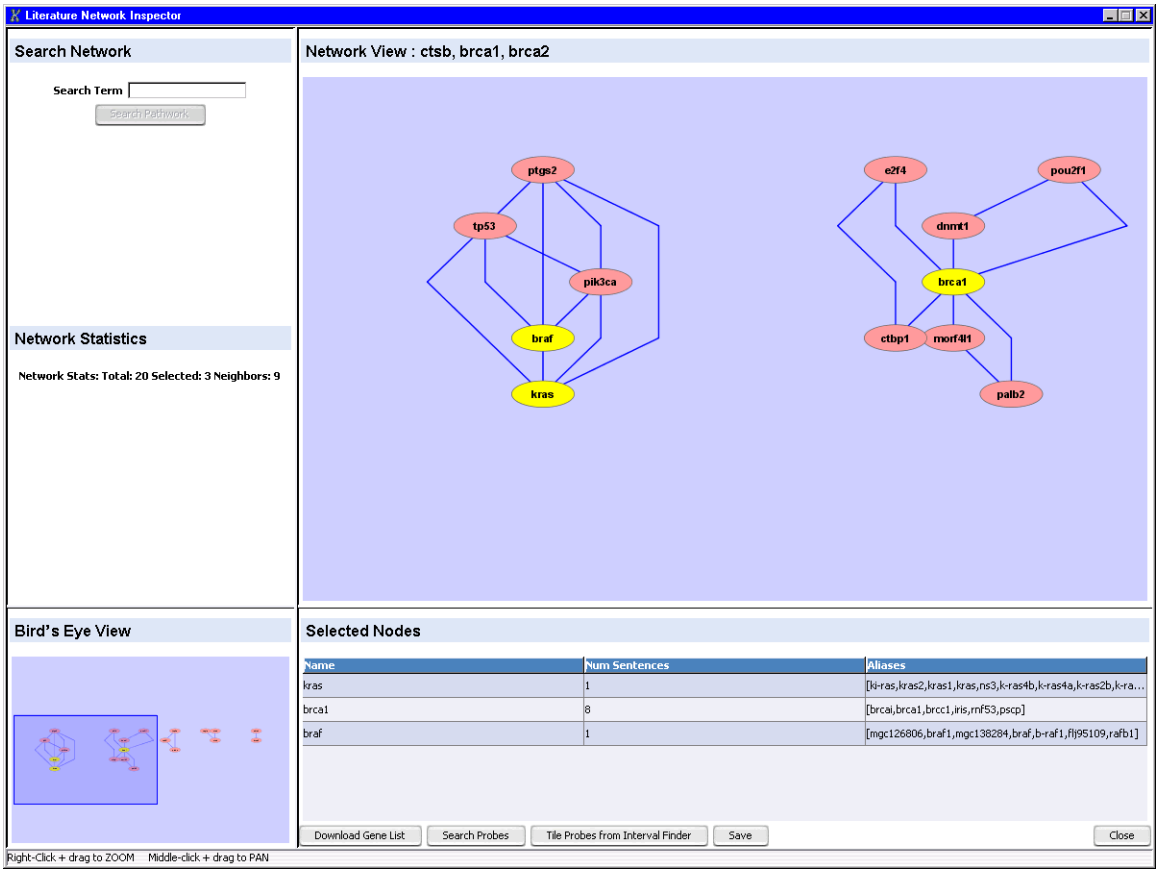


Figure 145 Literature Network Inspector, results from a literature search shown

Purpose: Displays the custom biological network that is created by a literature search. Lets you select specific nodes to use as a basis to find or create probes or baits. Also lets you get additional information about specific elements of the network.

To open: Do a Literature Search. The Literature Network Inspector appears automatically when the search finishes. See "To use a literature search to create a custom network" on page 186.

A description of each pane of the Literature Network Inspector appears below.

Search Network pane

Figure 146 Literature Network Inspector – Search Network pane

This pane lets you search the created custom network for nodes that match a search term that you enter.

Search Term Type a single term. The search returns nodes whose names match exactly. You can use an asterisk (*) to represent an unspecified group of characters.

Search Network Searches the network that currently appears in the Literature Network Inspector. Nodes that match the search term become yellow in color in Bird's Eye View and in Network View, and their names appear in the Selected Nodes pane.

Network Statistics pane

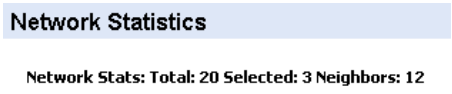


Figure 147 Literature Network Inspector – Network Statistics pane

These statistics about the network that appears in the Literature Network Inspector are available:

Statistic	Description
Total	Total number of nodes in the network
Selected	Number of nodes that you have selected in Network View
Neighbors	The number of unselected nodes that are neighbors of the selected one(s). A "neighbor" of a node is a node that is directly connected to it in the network.

Bird's Eye View

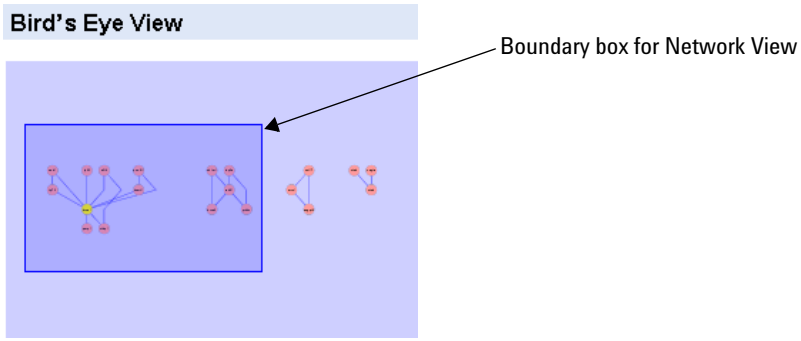


Figure 148 Literature Network Inspector – Bird's Eye View

This pane shows all of the nodes that are available in the Literature Network Inspector, and lets you select the part of the network that appears in Network View.

Unselected node – These pink nodes do not appear in the Selected Nodes pane.

Selected node – These yellow nodes appear in the Selected Nodes pane.

Boundary box for Network View

This purple box shows the portion of the network that appears in Network View. To display a different part of the network, drag the boundary box to the desired location.

The size of the boundary box can change as you increase or decrease the zoom level of Network View. See "Network View" on page 797.

Network View

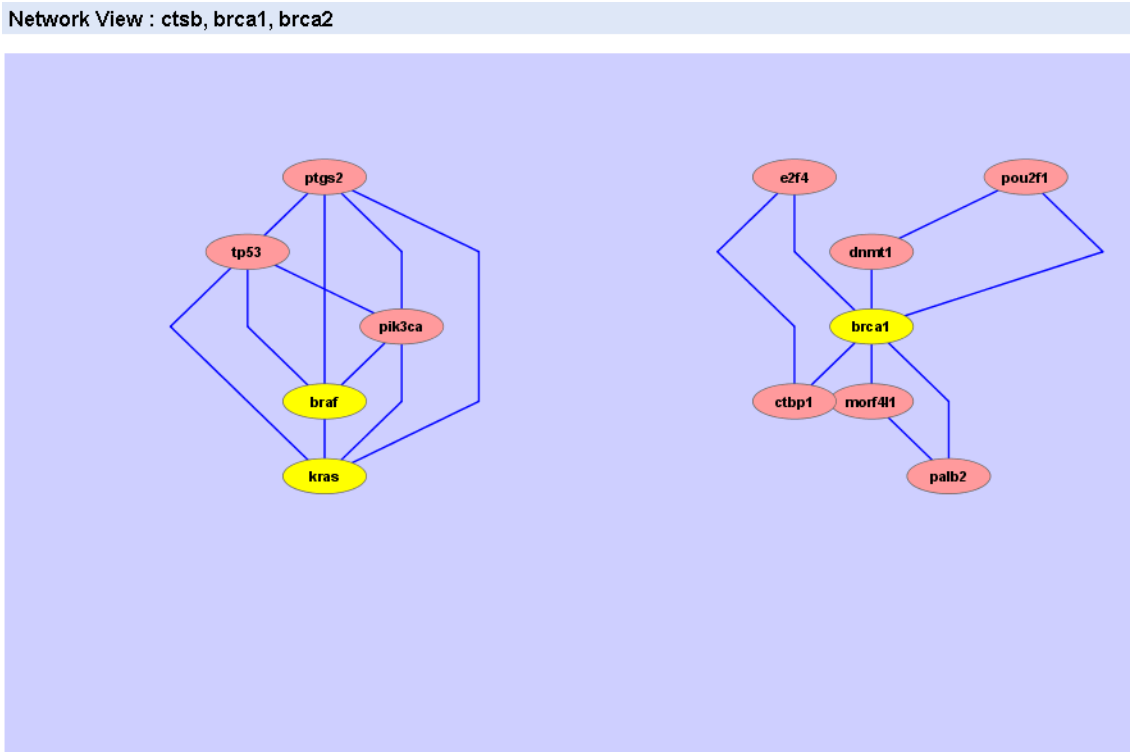


Figure 149 Literature Network Inspector – Network View

This pane lets you view and select the nodes in the current network. It also lets you view reference information about each node, find neighbors of nodes, and find the hubs in the network (see below).

General navigation

You can do the following to change the way the network appears in Network View:

Task	Instructions/Details
Change the zoom level	Right-click-drag a blank area of Network View to change the zoom level. • To zoom in, drag upward. • To zoom out, drag downward. As you change the zoom level, the size of the purple boundary box in Bird's Eye view, which shows the portion of the network that appears in Network View, can change in size.
Pan the view	In Bird's Eye View, drag the purple boundary box to the desired location. If your mouse has three buttons, you can also pan the network in Network View. Hold down the middle mouse button, and drag the pointer in the desired direction

Nodes

You can do the following with the nodes in Network View:

Action	Result
Click a node	Selects the node. Selected nodes appear in yellow. If a selected node represents a metabolite or a gene product. its name appears in the Selected Nodes pane.
Shift-click a node	Lets you select additional node(s). **Note:** The shift key also limits your pointer to vertical movement only. Release the shift key before you shift-click each additional node.
Drag-enclose nodes	Selects the enclosed nodes.
Click a blank area of Network View	Clears your node selections.
Drag a node	Changes the position of the node in Network View. This can be useful if two or more nodes overlap, and you want to see or select hidden node(s).

Action	Result
Right-click a node	Opens a shortcut menu with these options: • **LinkOut** – Opens another menu with a list of database types. Each of these options opens another menu that lists one or more specific databases. When you select a specific database, the program passes the name of the node to the database as a search string, and opens the relevant site in your Web browser. Your browser displays the relevant page of results. • **Show Sentences** – Opens the Agilent Literature Search Sentences dialog box, where you can view the sentences that were found in the returned abstracts that contained the name of the node. See "Agilent Literature Search Sentences" on page 581. • **Select All** – Selects all of the nodes in the network. • **Zoom Selected** – (Available if at least one node is selected) Zooms and re-centers Network View so the selected nodes occupy the entire view. • **Zoom In** – Zooms in Network View by approximately 10%. • **Zoom Out** – Zooms out Network View by approximately 10%. • **Show Query** – Selects and highlights the nodes whose names match one of the search terms in the literature search. • **Show Hubs** – Selects the nodes in the network that have at least a minimum number of neighbors. The minimum number of neighbors is set so that less than 25% of nodes are hubs. This number varies for different networks. • **Show Neighbors** – (Available if you select at least one node) Adds the neighbors of the selected node(s) to the list of selected nodes. A neighbor node is directly connected to your node of interest in the network.

Unselected node – These pink nodes do not appear in the Selected Nodes pane.

Selected node – These yellow nodes appear in the Selected Nodes pane.

Network "edge" – These blue lines show a relationship that was found between two nodes during the analysis of the abstracts that were returned by the literature search.

Selected Nodes pane

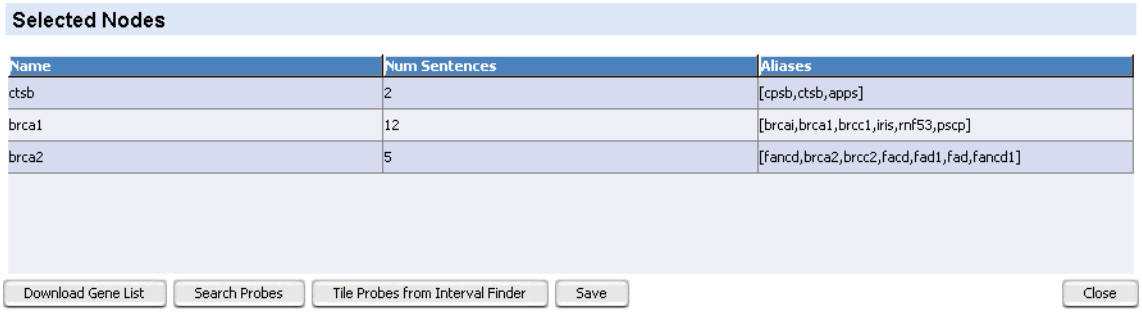


Figure 150 Literature Network Inspector – Selected Nodes pane

This pane displays information about the selected nodes in the network. To select nodes, see above, "Network View" on page 797 and "Search Network pane" on page 795.

Columns These columns appear:

Column	Description
Name	The name of the node.
Num Sentences	The number of sentences from the retrieved abstracts that contained the particular term, that were used to construct the custom network.
Aliases	Other names for the given node.

- To change column widths, drag one of the borders between columns right or left, as desired.

Buttons

Download Gene List Opens a Save dialog box, where you can select a location for a *.txt file that contains the names of the selected nodes, one node per line.

Search Probes (Available for all application types except SureSelect Target Enrichment) Opens the Probe Search pane, and transfers the names of the selected nodes as search terms for a Gene Symbol search. The species is also transferred. See "To use the Probe Search tool to find probes" on page 92 and "Probe Search" on page 560.

Search Baits (Available for the SureSelect Target Enrichment application type) Opens the Bait Search pane, and transfers the names of the selected nodes as search terms for a bait search. The species is also transferred. See "To search for baits" on page 358 and "Bait Search" on page 538.

Design Probes (Available for the Expression application type) Opens the Design Probes dialog box, where you can start a Gene Expression Probe Design job based on the selected nodes. See "Design Probes" on page 689.

Tile Probes from Interval Finder (Available for the CGH, ChIP-on-chip, CH3 application types) Opens the Advanced Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Genomic Tiling job. See these topics:

- "To do an Advanced Interval Finder Search" on page 129
- "To set up a Genomic Tiling job" on page 176
- "Advanced Interval Finder" on page 531

Tile Baits from Exon Finder (Available for the SureSelect Target Enrichment application type) Opens the Advanced Exon Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Bait Tiling job. See these topics:

- "To do an Advanced Exon Interval Finder Search" on page 367
- "To set up a Bait Tiling job" on page 378
- "Advanced Exon Interval Finder" on page 525

Tile Baits from Interval Finder (Available for the SureSelect Target Enrichment application type) Opens the Advanced Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Bait Tiling job. See these topics:

- "To do an Advanced Interval Finder Search" on page 364
- "To set up a Bait Tiling job" on page 378

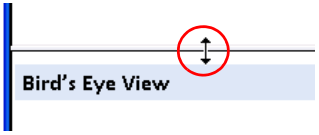
- "Advanced Interval Finder" on page 531

Save Opens the Save a Search Result dialog box, where you enter a name for the literature search (and the associated custom network). When you click OK in this dialog box, the program saves the search in the My Networks pane of the Navigator. See "To save a literature search" on page 199.

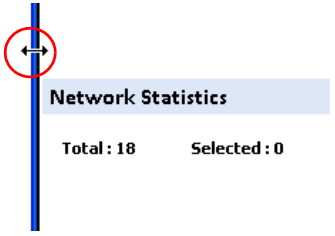
Close Closes the Literature Network Inspector.

Other actions

- To change the relative size of the panes in the Literature Network Inspector, drag a thick internal border in the desired direction.



- To change the overall size of the Literature Network Inspector, drag the bottom border or one of the side borders in the desired direction.



Literature Search

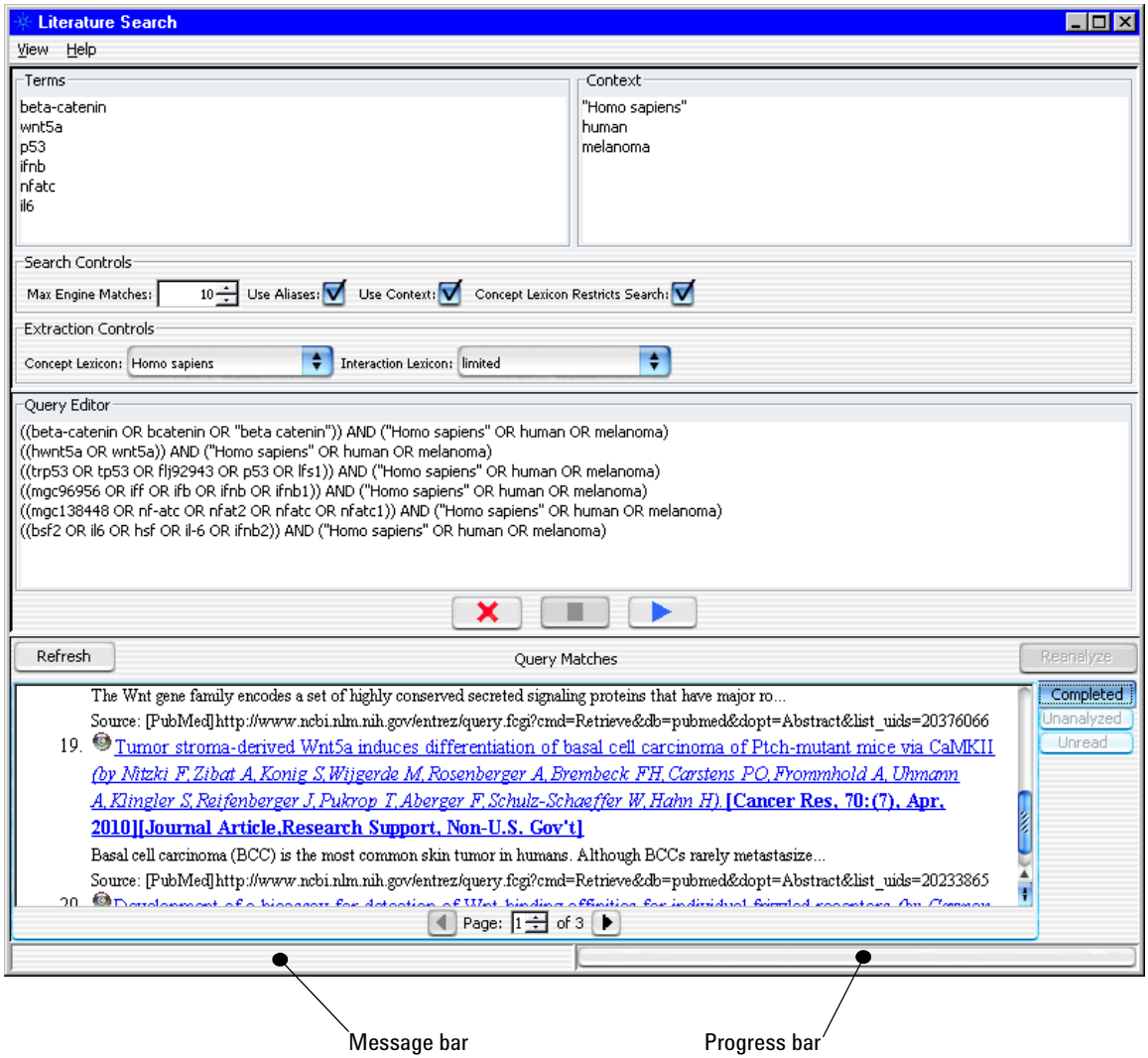


Figure 151 Literature Search dialog box, with example search criteria and results shown

Purpose: Lets you set up and submit a search of the biomedical literature to one or more Web-based search engines. The program uses the results to construct a custom biological network based on meaningful terms that it finds in the returned abstracts. See "To use a literature search to create a custom network" on page 186. Literature searches are available for all application types in eArray$_{XD}$. When a literature search is complete, the resulting custom network appears in the Network Inspector. See "Network Inspector" on page 815.

To open: In the eArray$_{XD}$ tab, under Search, click **Literature Search.**

View menu Opens a menu with an Engine Selections option. This option opens a dialog box that lets you select the search engine(s) that will be used in the literature search. These search engines are available:

Search engine	Description
PubMed	(This option is selected by default) Index of life sciences citations maintained by the U.S. National Library of Medicine at the National Institutes of Health. For more information, go to ncbi.nlm.nih.gov/pubmed/.
OMIM	**Online Mendelian Inheritance in Man** – Database of human genes and genetic phenotypes maintained by the McKusick-Nathans Institute of Genetic Medicine at the Johns Hopkins University School of Medicine. For more information, go to ncbi.nlm.nih.gov/omim.
USPTO	**United States Patent and Trademark Office** – Database of patents and published patent applications. For more information, go to uspto.gov.

Help menu Opens a menu with these options:

Option	Description
Contents	Opens a separate help system for the Agilent Literature Search tool. **Note:** Some of the features that are described in this separate help system are not available for literature searches in eArray$_{XD}$.
About	Opens an About dialog box that gives version and copyright details for the Agilent Literature Search tool.

Terms The Terms box lets you enter the main search terms for the literature search, such as the names of genes and gene products. Also, you can automatically include any alternate names for each term that you enter. See *Use Aliases*, in Search Controls, below.

You can include multiple search terms. The program interprets all of the text on a given line as a single search term.

Context

The Context box lets you enter any terms that must appear in an abstract, in addition to the entries under Terms, for the program to return the given abstract. Context terms include, for example, names of diseases or therapeutic drugs. You can also add the current species of interest to the list of context terms. See *Concept Lexicon Restricts Search,* in Search Controls, below.

You can include multiple context terms. The program interprets all of the text on a given line as a single context term. To use context term(s) in the literature search, you must mark **Use Context,** under Search Controls.

Search Controls

The Search Controls group contains these options:

Parameter	Instructions/Details
Max Engine Matches	This value defines the maximum number of abstracts that can be returned by each selected search engine for each query line. To change the number, click the up and down arrow buttons next to the number, or edit the number. The default value for this parameter is 10 abstracts, which is a good starting point for literature searches that balances comprehensive coverage of interactions with the creation of a custom network of manageable size. **Note:** The program also limits the total number of abstracts that can be returned for all queries from a given search engine during a literature search. For PubMed searches, this limit is 1,000 abstracts. For OMIM and USPTO searches, this limit is 100 abstracts.
Use Aliases	If you mark this option, the program automatically includes all known aliases for the terms that you enter under Terms. Aliases are alternate names for terms. The program uses the concept lexicon for the selected species to find aliases.

Parameter	Instructions/Details
Use Context	If this option is marked, the program uses any terms under Context in the literature search. **Note:** If you clear this option, the program also clears **Concept Lexicon Restricts Search.**
Concept Lexicon Restricts Search	If this option is marked, the program includes the species name of the concept lexicon as a context term in the literature search. By default, literature searches include as a context term the name of the species that is selected for the concept lexicon. **Note:** If you mark this option, the program also marks **Use Context** if it is not already marked.

Extraction Controls

The extraction controls define how returned abstracts are analyzed to supply the nodes and interactions in the custom network. These options are available:

Parameter	Instructions/Details
Concept Lexicon	Lets you select the desired concept lexicon for the literature search, by species. A concept lexicon is a list of meaningful terms for a given species that represent biological entities such as genes and gene products. The species associated with the available concept lexicons appear in the list. When the program analyzes the text of a given abstract, it looks for the presence of terms from the concept lexicon. By default, literature searches use the human concept lexicon. Also, the selected concept lexicon is the source of aliases for the literature search.
Interaction Lexicon	Lets you set the stringency with which interactions are created from the sentences of retrieved abstracts. Interaction lexicons are lists of terms (verbs) that describe molecular interactions. These options are available: • **empty** – The interaction lexicon contains no terms. The program returns interactions without regard to the presence of terms that describe interactions. This is the least stringent setting, and returns interaction(s) for every sentence that contains at least two terms from the concept lexicon. • **limited** – (This is the default, most stringent setting) This interaction lexicon contains a subset of the terms found in the relaxed interaction lexicon. The program returns interaction(s) for a sentence if it contains at least one term from this lexicon, and two terms from the concept lexicon. • **relaxed** – This interaction lexicon contains a larger number of terms than does the limited interaction lexicon. The program returns interaction(s) for a sentence if it contains at least one term from this lexicon, and two terms from the concept lexicon.

Query Editor

The Query Editor shows the exact query strings that the program constructs based on your search criteria. When you start the search, every query string is passed to each selected search engine. The program uses several general rules to construct query strings:

- One query string appears per line.
- Each term that you enter in **Terms** creates a separate query string.
- If you mark **Use Aliases,** the program includes in each query string any aliases for the given term. The term and any aliases are joined by Boolean OR operators.

- If any terms appear in **Context,** and you mark **Use Context,** the program joins these terms with Boolean OR operators, and includes the terms in every query string. It joins the context terms to the other terms in each query string with a Boolean AND operator.
- If you mark **Concept Lexicon Restricts Search,** the program treats the species, and any alternative name that is available for the species, as a Context term. See the previous item.

Also, you can manually edit the query strings that appear in the query editor. However, if you change any of the items that the program uses to automatically create query strings, such as search terms or options, the program discards your manual edits.

Clear – (Available if no literature search is in progress, and there is at least one term in Terms, Context, or in the Query Editor pane.) Clears all entries in Terms, Context, and in the Query Editor pane.

Stop – (Available if a literature search is in progress.) Stops the literature search. Search results that were retrieved before you stopped the search remain available, however, you cannot continue the search.

Start (or **Continue**) – (Available if no literature search is in progress and there is at least one term in Terms or in the Query Editor pane. Also available if a literature search is paused.) If no literature search is in progress, this button starts the literature search. If a literature search is paused, this button resumes the search.

Pause – (Available if a literature search is in progress) Temporarily pauses the literature search. To resume the search, click the  (Continue) button.

Query Matches Pane

List of matches

The Query Matches pane shows the abstracts that were returned by the literature search. Several types of information can appear for each abstract:

-  icon – If present, this icon indicates that the given abstract supplied interaction(s) that the program used to create the custom network. To highlight the nodes and interactions in the Literature Network Search dialog box that were derived from the abstract, click the icon.
- Citation – Can include title, author, date, and journal information. The citation appears as a hyperlink. If you click the hyperlink, the abstract opens in your Web browser.

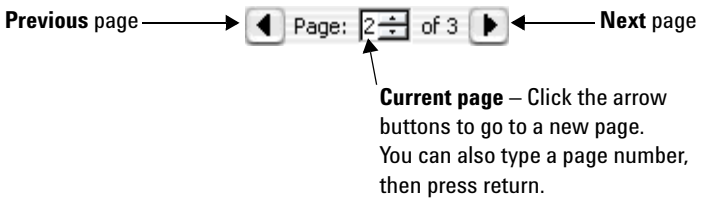
- Key sentence(s) – Up to one line of text can appear that contains sentence(s) from the abstract that contain meaningful terms.
- Source information – This information includes the search engine that returned the abstract, and a URL for the abstract.

Reanalyze Once a literature search is complete, you can change analysis settings, such as the interaction lexicon setting, or search terms. The program can then reanalyze the previously retrieved abstracts and build a network based on the new settings. This process takes much less time than a new literature search.

Tabs Query matches can appear in up to three tabs in the Query Matches pane:

- **Completed** – Abstracts in this tab have been retrieved, and their text has been analyzed for interactions. When a literature search is complete, listings for all abstracts appear in this tab.
- **Unanalyzed** – (Available at certain times when a literature search is in progress) Abstracts in this tab have been retrieved, but their text has not yet been analyzed for interactions.
- **Unread** – (Available at certain times when a literature search is in progress) Abstracts in this tab have been identified, but their text has not yet been retrieved from the Web.

Page controls These controls let you go to different pages of query matches:



Message bar Displays messages about the progress of the literature search. Several statistics can also appear:

- **Completed Queries** – The number of query lines that have been passed to the selected search engine(s).
- **Articles Read** – The number of abstracts whose text has been retrieved from the Web.
- **Articles Analyzed** – The number of retrieved abstracts whose text has been analyzed for interactions.

Progress bar Shows the progress of the literature search graphically.

Move Array Design

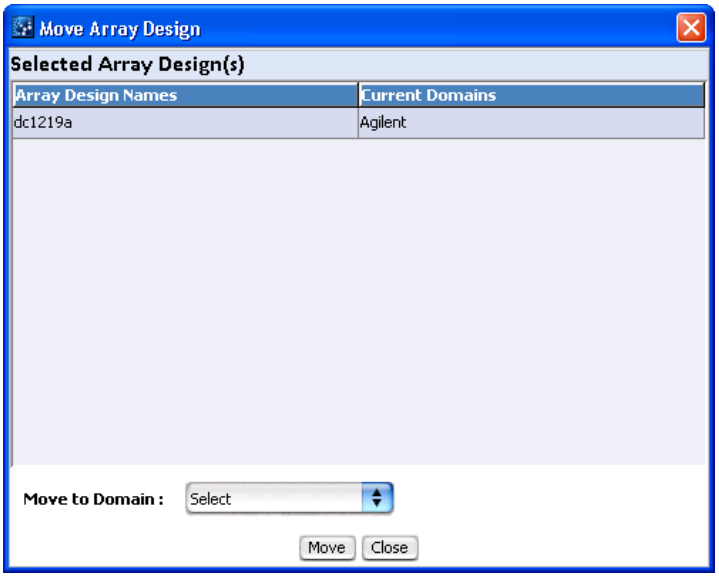


Figure 152 Move Array Design dialog box

Purpose: Lets you move one or more microarray designs to another folder. You must own the design(s), and you must have access to the destination folder. See "To move a microarray design" on page 338.

To open: Search for the microarray designs that you want to move. See "To search for microarray designs" on page 251. In the search results, select the designs that you want to move, then click **Move.**

Alternatively, in the **Design Data** pane of the Navigator, select the design(s) that you want to move. Right-click the name of one of the designs, then click **Move.**

Array Design Names The names of the designs to be moved.

Current Domains The current location of each of the designs to be moved.

Move to Domain Select the destination folder for the designs.

Move Moves the designs to the selected folder.

Close Closes the dialog box without moving the designs.

Move Bait Group

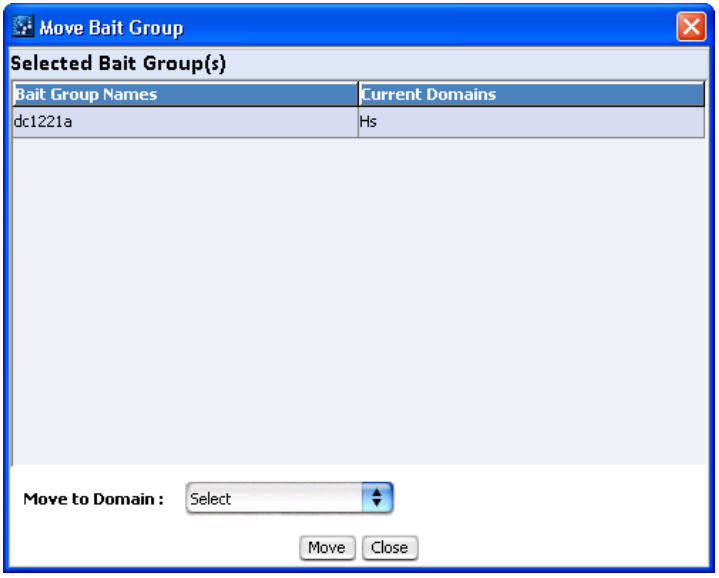


Figure 153 Move Bait Group dialog box

Purpose: Lets you move one or more bait groups to another folder. You must own the bait group(s), and you must have access to the destination folder. See "To move bait group(s)" on page 408.

To open: Do one of the following:

- Search for the bait groups that you want to move. See "To search for bait groups" on page 396. In the search results, select the bait groups that you want to move, then click **Move.**
- In the **Design Data** pane of the Navigator, select the bait group(s) that you want to move. Right-click the name of one of the bait groups, then click **Move.**

Bait Group Names (Read-only) The name(s) of the bait group(s) to be moved.

Current Domains (Read-only) The current location of each of the bait groups to be moved.

Move to Domain Select the destination folder for the bait groups.

Move Moves the bait groups to the selected folder.

Close Closes the dialog box without moving the bait groups.

Move Library

Figure 154 Move Library dialog box

Purpose: Lets you move one or more libraries to another folder. You must own the librar(ies), and you must have access to the destination folder. See "To move libraries" on page 456.

To open: Do one of the following:

- Search for the libraries that you want to move. See "To search for libraries" on page 416. In the search results, select the libraries that you want to move, then click **Move.**

- In the **Design Data** pane of the Navigator, select the librar(ies) that you want to move. Right-click the name of one of the libraries, then click **Move.**

Library Names The names of the librar(ies) to be moved.

Current Domains The current location of each of the libraries to be moved.

Move to Domain Select the destination folder for the libraries.

Move Moves the libraries to the selected folder.

Close Closes the dialog box without moving the libraries.

Move Probe Group

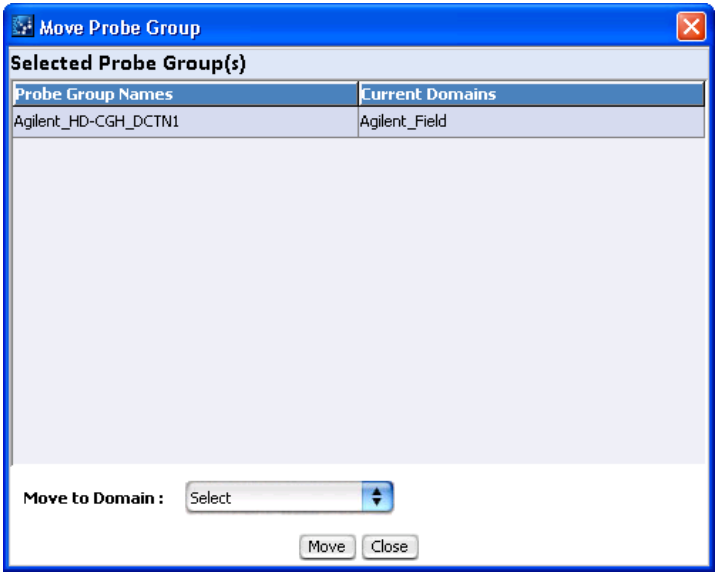


Figure 155 Move Probe Group dialog box

Purpose: Lets you move one or more probe groups to another folder. You must own the probe group(s), and you must have access to the destination folder. See "To move probe groups" on page 239.

To open: Do one of the following:

- Search for the probe groups that you want to move. See "To search for probe groups" on page 224. In the search results, select the probe groups that you want to move, then click **Move.**
- In the **Design Data** pane of the Navigator, select the probe group(s) that you want to move. Right-click the name of one of the probe groups, then click **Move.**

Probe Group Names The name(s) of the probe group(s) to be moved.

Current Domains The current location of each of the probe groups to be moved.

Move to Domain Select the destination folder for the probe groups.

Move Moves the probe groups to the selected folder.

Close Closes the dialog box without moving the probe groups.

Network Inspector

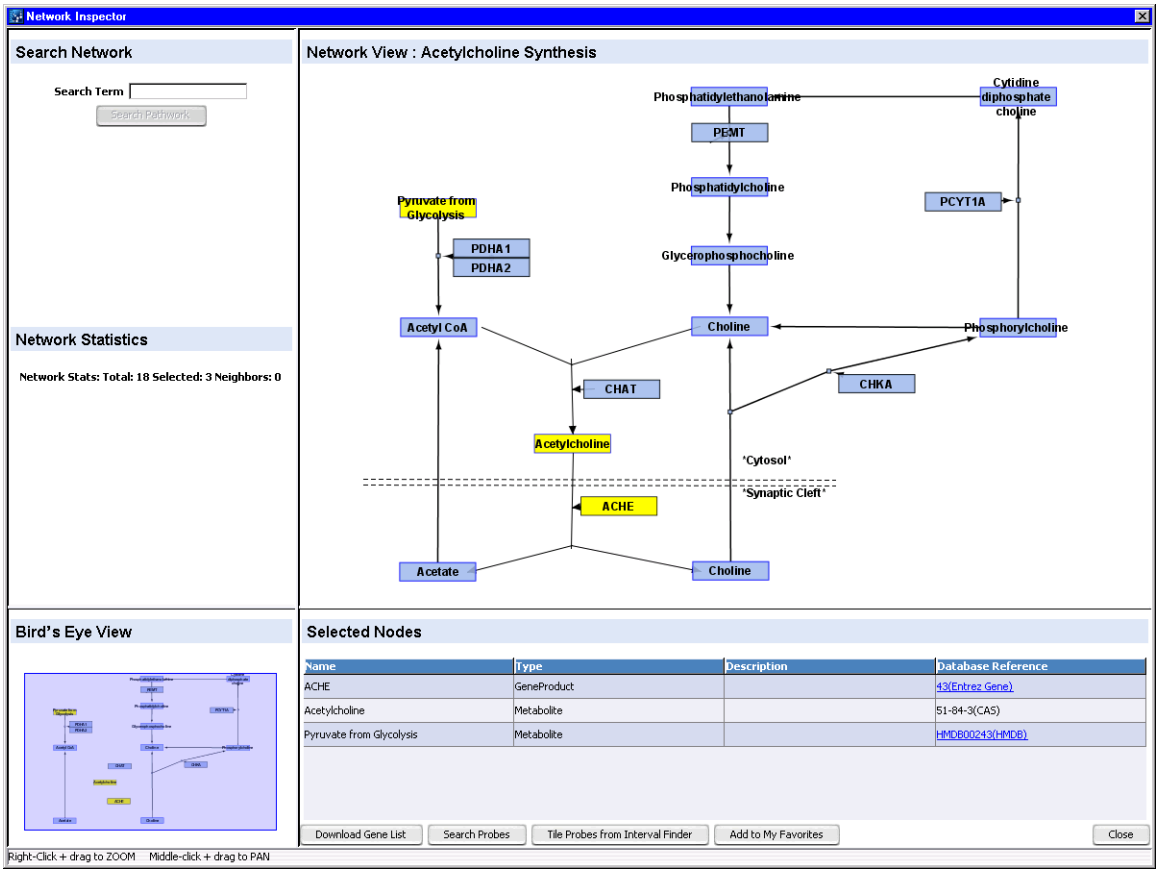


Figure 156 Network Inspector, human acetylcholine biosynthesis shown

Purpose: Displays a selected biological network that you retrieve in a Network Search. Lets you select specific nodes to use as a basis to find or create probes or baits. Also lets you get additional information about specific elements of the network. See "Using Biological Networks to Find or Create Probes or Baits" on page 184.

To open: Do a Network Search. In the Actions column of the Search Result pane, click in the row of the desired network.

A description of each pane of the Network Inspector appears below.

Search Network pane

Figure 157 Network Inspector – Search Network pane

This pane lets you search for nodes that match a search term that you enter.

Search Term Type a single term. The search returns nodes whose names match exactly. You can use an asterisk (*) to represent an unspecified group of characters.

Search Network Searches the network that currently appears in the Network Inspector. Nodes that match the search term become yellow in color in Bird's Eye View and in Network View, and their names appear in the Selected Nodes pane.

Network Statistics pane

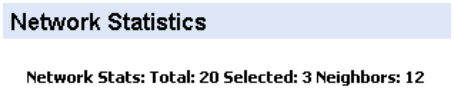


Figure 158 Network Inspector – Network Statistics pane

These statistics about the network that appears in the Network Inspector are available:

Statistic	Description
Total	Total number of nodes in the network.
Selected	Number of nodes that you have selected in Network View.
Neighbors	The number of unselected nodes that are neighbors of the selected one(s). A “neighbor” of a node is a node that is directly connected to it in the network.

NOTE

Biological networks can contain “non-referenced” graphical nodes that are not directly linked to database references. Although you can select these nodes, they do not appear in the Selected Nodes pane, nor are they included in neighbor and hub analyses. Also, these nodes are not included in the values in the Network Statistics pane.

Bird's Eye View

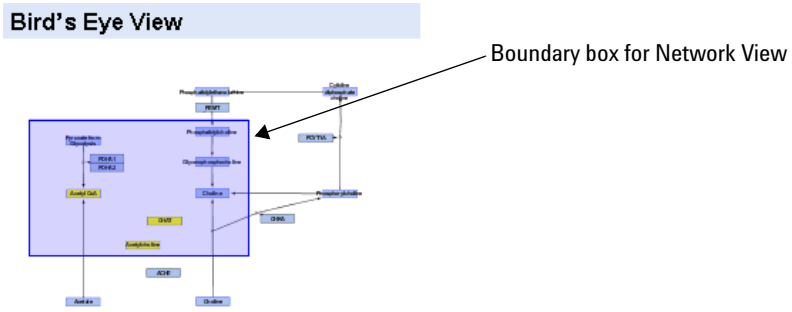


Figure 159 Network Inspector – Bird's Eye View

This pane shows all of the nodes in the pane, and lets you select the part of the network that appears in Network View.

Acetyl CoA

Unselected node – These blue nodes do not appear in the Selected Nodes pane.

Acetyl CoA

Selected node – These yellow nodes appear in the Selected Nodes pane, unless they are "non-referenced" nodes that are not directly linked to database references.

Boundary box for Network View

This purple box shows the portion of the network that appears in Network View. To display a different part of the network, drag the boundary box to the desired location.

The size of the boundary box can change as you increase or decrease the zoom level of Network View. See "Network View" on page 819.

Network View

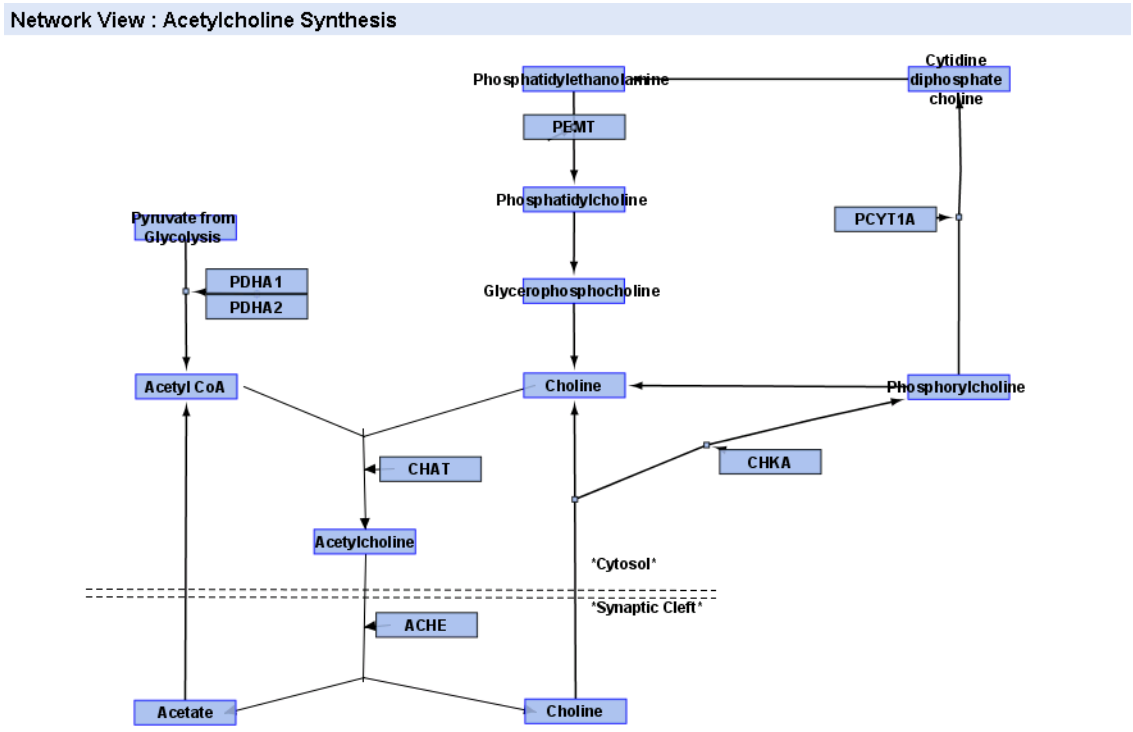


Figure 160 Network Inspector – Network View, human acetylcholine biosynthesis shown

This pane lets you view and select the nodes in the current network. It also lets you view reference information about each node, and search and display networks that interact with specific nodes.

General navigation

You can do the following to change the way the network appears in Network View:

Task	Instructions/Details
Change the zoom level	Right-click-drag a blank area of Network View to change the zoom level. • To zoom in, drag upward. • To zoom out, drag downward. As you change the zoom level, the size of the purple boundary box in Bird's Eye view, which shows the portion of the network that appears in Network View, can change in size.
Pan the view	In Bird's Eye View, drag the purple boundary box to the desired location. If your mouse has three buttons, you can also pan the network in Network View. Hold down the middle mouse button, and drag the pointer in the desired direction

Nodes

You can do the following with the nodes in Network View:

Action	Result
Click a node	Selects the node. Selected nodes appear in yellow. If a selected node represents a metabolite or a gene product. its name appears in the Selected Nodes pane.
Shift-click a node	Lets you select additional node(s). **Note:** The shift key also limits the pointer to vertical movement only. Release the shift key before you shift-click each additional node.
Drag-enclose nodes	Selects the enclosed nodes.
Click a blank area of Network View	Clears your node selections.
Drag a node	Changes the position of the node in Network View. This can be useful if two or more nodes overlap, and you want to see or select hidden node(s).

Action	Result
Right-click a node	Opens a shortcut menu with these options: • **LinkOut** – Opens another menu with a list of database types. Each of these options opens another menu that lists one or more specific databases. When you select a specific database, the program passes the name of the node to the database as a search string, and opens the relevant site in your Web browser. Your browser displays the relevant page of results. • **Select All** – Selects all of the nodes in the network. The program ignores non-referenced nodes. See the note at the bottom of this table. • **Zoom Selected** – (Available if at least one node is selected) Zooms and re-centers Network View so the selected nodes occupy the entire view. • **Zoom In** – Zooms in Network View by approximately 10%. • **Zoom Out** – Zooms out Network View by approximately 10%. • **Show Query** – Selects and highlights the nodes whose names match one of your original search terms. The program ignores non-referenced nodes. See the note at the bottom of this table. • **Show Hubs** – Selects the nodes in the network that have at least a minimum number of neighbors. The minimum number of neighbors is set so that less than 25% of nodes are hubs. This number varies for different networks. • **Show Neighbors** – (Available if you select at least one node) Adds the neighbors of the selected node(s) to the list of selected nodes. A neighbor node is directly connected to your node of interest in the network.

NOTE Biological networks can contain "non-referenced" graphical nodes that are not directly linked to database references. Although you can select these kinds of nodes, they do not appear in the Selected Nodes pane, nor are they included in neighbor and hub analyses. Also, these nodes are not included in the values in the Network Statistics pane.

- 

– An unselected node that represents a metabolite. Note the blue border of the node.
- 

– An unselected node that represents a gene product. Note the gray border of the node.

- Acetyl CoA – A selected node. The program highlights selected nodes in yellow, and also includes them in the Selected Nodes pane.
- Network elements that appear in forms other than those listed above are not nodes. You cannot select them.

Selected Nodes pane

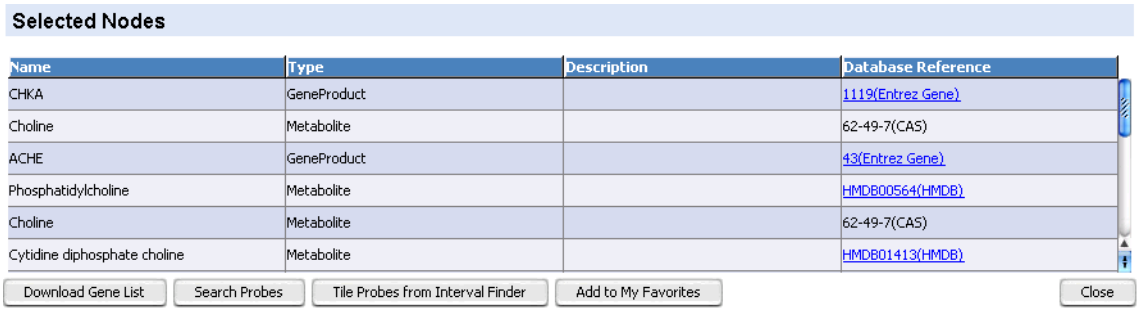


Figure 161 Network Inspector – Selected Nodes pane

This pane displays information about the nodes that you have selected. To select nodes, see above, "Network View" and "Search Network pane."

Columns These columns appear:

Column	Description
Name	The name of the node
Type	The type of network element that the node represents, such as a gene product or metabolite.
Description	A brief description of the node.
Database Reference	The link that can appear in this column opens your Web browser, and displays the relevant page from the applicable database for the given node.

- To change column widths, drag one of the borders between columns right or left, as desired.

NOTE Biological networks can contain "non-referenced" graphical nodes that are not directly linked to database references. These nodes do not appear in the Selected Nodes pane

Buttons

Download Gene List Opens a Save dialog box, where you can select a location for a *.txt file that contains the names of the selected nodes, one node per line.

Search Probes (Available for all application types except SureSelect Target Enrichment) Opens the Probe Search pane, and transfers the names of the selected nodes as search terms for a Gene Symbol search. The species is also transferred. See "To use the Probe Search tool to find probes" on page 92 and "Probe Search" on page 560.

Search Baits (Available for the SureSelect Target Enrichment application type) Opens the Bait Search pane, and transfers the names of the selected nodes as search terms for a bait search. The species is also transferred. See "To search for baits" on page 358 and "Bait Search" on page 538.

Design Probes (Available for the Expression application type) Opens the Design Probes dialog box, where you can start a Gene Expression Probe Design job based on the selected nodes. See "Design Probes" on page 689.

Tile Probes from Interval Finder (Available for the CGH, ChIP-on-chip, CH3 application types) Opens the Advanced Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Genomic Tiling job. See these topics:

- "To do an Advanced Interval Finder Search" on page 129
- "To set up a Genomic Tiling job" on page 176
- "Advanced Interval Finder" on page 531

Tile Baits from Exon Finder (Available for the SureSelect Target Enrichment application type) Opens the Advanced Exon Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Bait Tiling job. See these topics:

- "To do an Advanced Exon Interval Finder Search" on page 367
- "To set up a Bait Tiling job" on page 378
- "Advanced Exon Interval Finder" on page 525

Tile Baits from Interval Finder

(Available for the SureSelect Target Enrichment application type) Opens the Advanced Interval Finder pane, and transfers the names of the selected nodes as search terms to the Gene Symbol search criterion. The species is also transferred. You can use the intervals that the search returns to set up a Bait Tiling job. See these topics:

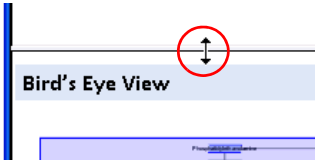
- "To do an Advanced Interval Finder Search" on page 364
- "To set up a Bait Tiling job" on page 378
- "Advanced Interval Finder" on page 531

Add to My Favorites

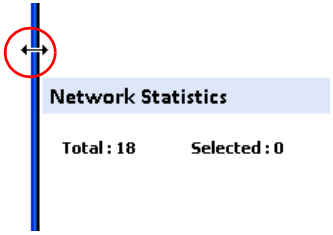
Adds the network that is currently displayed in the Network Inspector to your My Favorites list. This can make it easier for you to retrieve the network in future searches. See "To add a network to My Favorites" on page 197.

Other actions

- To change the relative size of the panes in the Network Inspector, drag a thick internal border in the desired direction.



- To change the overall size of the Network Inspector, drag the bottom border or one of the side borders in the desired direction.



Note

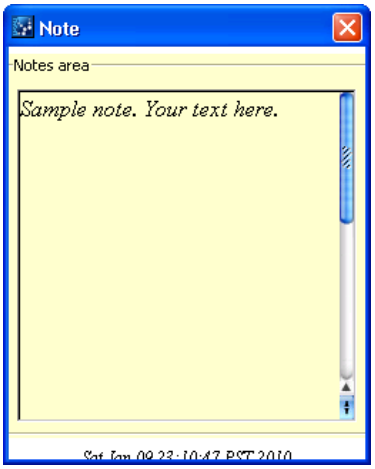


Figure 162 Note dialog box

Purpose: Lets you create or view a text note that is attached to a microarray design, library, probe group, or bait group. See these topics:

- "To add an attachment to a probe group" on page 243
- "To add an attachment to a microarray design" on page 320
- "To attach a file, note, or URL to a bait group or library" on page 444

To open: In the Add/Remove Attachments dialog box, in the Total Attachments pane, in the row of an attached note, click .

Notes area Type your text note in the box. You can also paste text into the box from the clipboard.

Closes the dialog box, and saves the note as an attachment to the given probe group or microarray design.

Probe Group

See these topics:

- "Create Probe Group" on page 678

- "Create Probe Group (from HD or SNP search results)" on page 681

Probe Quality

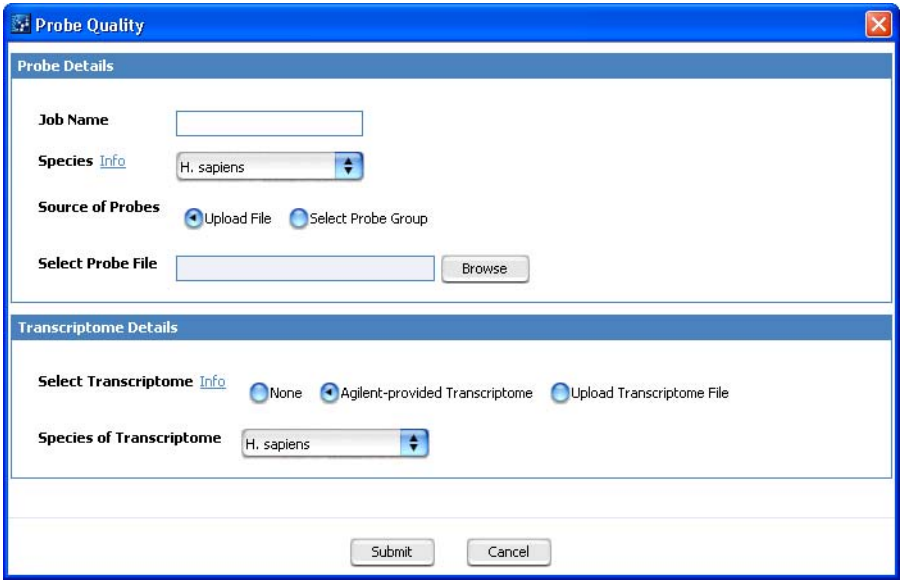


Figure 163 Probe Quality dialog box, set to check the quality of probes in an uploaded file using the Agilent-provided human transcriptome as a similarity database.

Purpose: Lets you set up a job to evaluate gene expression probes to see how they will work on the Agilent platform using Agilent protocols. You use this dialog box to submit a job to the eArray Web site. The eArray Web site calculates the base composition and other statistics of the probes, as well as a base composition score. It can also report potential cross-hybridization problems. See "To check GE probe quality" on page 208.

To open: In the eArray$_{XD}$ tab, under **Quality,** click **Probe.** This tool is only available for the Expression application type.

Probe Details

Parameter	Description
Job Name	A name that will help you to identify this job.
Species	The species that is associated with the probes to be checked.
Source of Probes	The source of the probes to be checked: • **Upload File** – Checks the quality of the probes in a file that you upload. If you select this option, the Select Probe File option appears. The file must be a tab-delimited text file in the MINIMAL format, with no column headings. See "Minimal (for probes)" on page 890. • **Select Probe Group** – Checks the quality of the probes in an existing probe group. This option is useful if you want to check the quality of probes that you have already uploaded. The program can check one probe group at a time. If you select this option, the Select a Probe Group option appears.
Select Probe File	(Appears if you select **Upload File** in Source of Probes) Displays the location of the probe file. **Browse** – Opens an Open dialog box, where you can select the file of probes to be checked.
Select a Probe Group	(Appears if you select **Select Probe Group** in Source of Probes) Displays the name of the probe group that contains the probes to be checked. **Select and Add** – Opens the Select and Add dialog box, where you can search for, select, and add the desired probe group. See "Select and Add : Probe Group" on page 843.

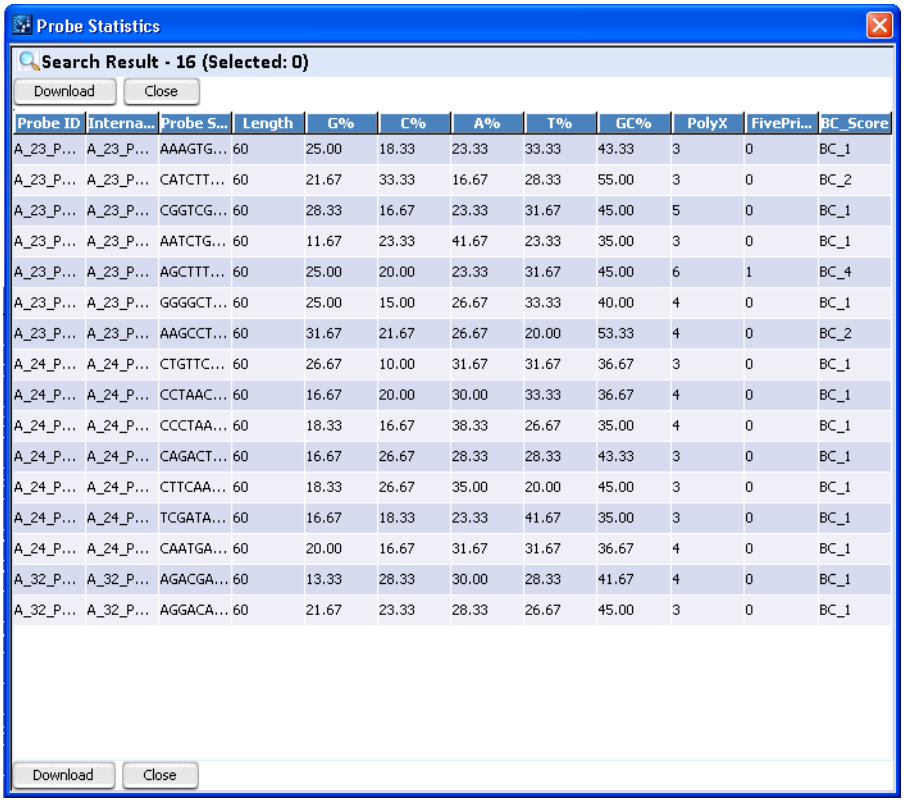
Transcriptome Details

Parameter	Description
Select Transcriptome	The source of the transcriptome that the program will use as a similarity database to derive the identity of potential targets and cross-hybridization problems: • **None** – No transcriptome will be used. The job returns an analysis based upon the base composition of probes, only. • **Agilent-provided transcriptome** – Uses a transcriptome that is available on the eArray Web site. Select this option if an Agilent transcriptome is available for your species of interest. To see a list of the available transcriptomes, select this option, then view the list in **Species of Transcriptome.** • **Upload Transcriptome File** – Uses a FASTA-format transcriptome file that you upload. Select this option if an Agilent transcriptome is not available for your species of interest.
Species of Transcriptome	(Appears if you select **Agilent-provided Transcriptome** in Select Transcriptome) Select the desired species.
Upload Transcriptome File	(Appears if you select **Upload Transcriptome File** in Select Transcriptome) Displays the location of your FASTA-format transcriptome file. **Browse** – Opens an Open dialog box, where you can select the desired FASTA-format transcriptome file.

Submit Submits the job to the eArray Web site.

Cancel Closes the dialog box without submitting a job.

Probe Statistics



Probe ID	Interna...	Probe S...	Length	G%	C%	A%	T%	GC%	PolyX	FivePri...	BC_Score
A_23_P...	A_23_P...	AAAGTG...	60	25.00	18.33	23.33	33.33	43.33	3	0	BC_1
A_23_P...	A_23_P...	CATCTT...	60	21.67	33.33	16.67	28.33	55.00	3	0	BC_2
A_23_P...	A_23_P...	CGGTCG...	60	28.33	16.67	23.33	31.67	45.00	5	0	BC_1
A_23_P...	A_23_P...	AATCTG...	60	11.67	23.33	41.67	23.33	35.00	3	0	BC_1
A_23_P...	A_23_P...	AGCTTT...	60	25.00	20.00	23.33	31.67	45.00	6	1	BC_4
A_23_P...	A_23_P...	GGGGCT...	60	25.00	15.00	26.67	33.33	40.00	4	0	BC_1
A_23_P...	A_23_P...	AAGCCT...	60	31.67	21.67	26.67	20.00	53.33	4	0	BC_2
A_24_P...	A_24_P...	CTGTTC...	60	26.67	10.00	31.67	31.67	36.67	3	0	BC_1
A_24_P...	A_24_P...	CCTAAC...	60	16.67	20.00	30.00	33.33	36.67	4	0	BC_1
A_24_P...	A_24_P...	CCCTAA...	60	18.33	16.67	38.33	26.67	35.00	4	0	BC_1
A_24_P...	A_24_P...	CAGACT...	60	16.67	26.67	28.33	28.33	43.33	3	0	BC_1
A_24_P...	A_24_P...	CTTCAA...	60	18.33	26.67	35.00	20.00	45.00	3	0	BC_1
A_24_P...	A_24_P...	TCGATA...	60	16.67	18.33	23.33	41.67	35.00	3	0	BC_1
A_24_P...	A_24_P...	CAATGA...	60	20.00	16.67	31.67	31.67	36.67	4	0	BC_1
A_32_P...	A_32_P...	AGACGA...	60	13.33	28.33	30.00	28.33	41.67	4	0	BC_1
A_32_P...	A_32_P...	AGGACA...	60	21.67	23.33	28.33	26.67	45.00	3	0	BC_1

Figure 164 Probe Statistics dialog box, as it appears for Expression type probes.

Purpose: Displays the IDs and sequences of selected probes. For Expression type probes, also displays statistics based on base composition. See "To view probe sequences and statistics" on page 202.

To open: Search for probes. In the Search Result pane, select the desired probes, then click **Show Statistics.** See "To use the Probe Search tool to find probes" on page 92.

Alternatively, view a probe group, then click **Show Statistics.** See "To view a probe group" on page 228.

Probe ID The name of each probe. For user probes, this is the user-supplied name of the probe.

Internal ID The system-generated identification code of the probe within the database on your server.

Probe Sequence The nucleotide sequence of each probe in 5' to 3' orientation.

Additional Statistics (Available for Expression type probes) These statistics are derived from the base composition of each probe.

Statistic	Description	Example
Length	The number of nucleotides in the probe	Agilent expression probe A_12_P119943 contains 60 nucleotides. Length = 60.
G%	Percentage of bases in the probe sequence that are G bases	Same probe as above: 11 Gs; %G = 18.33%
C%	Percentage of bases in the probe sequence that are C bases	Same probe as above: 16 Cs; %C = 26.67%
A%	Percentage of bases in the probe sequence that are A bases	Same probe as above: 13 As; %A = 21.67%
T%	Percentage of bases in the probe sequence that are T bases	Same probe as above: 20 Ts; %T = 33.33%
GC%	Percentage of bases in the probe sequence that are, collectively, G and C bases	Same probe as above: 11 Gs and 16 C's. %GC = 45%
PolyX	The longest homeomeric run (run of one type of base) in the probe sequence, represented as the number bases in the run.	ATTAGTTTATG has a PolyX of 3 because it contains a run of three Ts. Same probe as above: contains a run of 5 Ts; therefore, the PolyX = 5.
FivePrimeAs	The length of any poly A sequence on the 5' end of the probe	Same probe as above: FivePrimeAs = 0
BC_Score	Base Composition Score – A numeric value that defines the quality of the probe, based upon its base composition and distribution	BC_1 is the best, and BC_Poor is the worst.

Download Opens a Save dialog box, where you can download the information in the dialog box as a TDT format file. You can open this file in a word processing or spreadsheet program.

Close Closes the dialog box.

1 2 3 (Page buttons) If available, these buttons let you go to a specific page of probe statistics.

Probe Upload

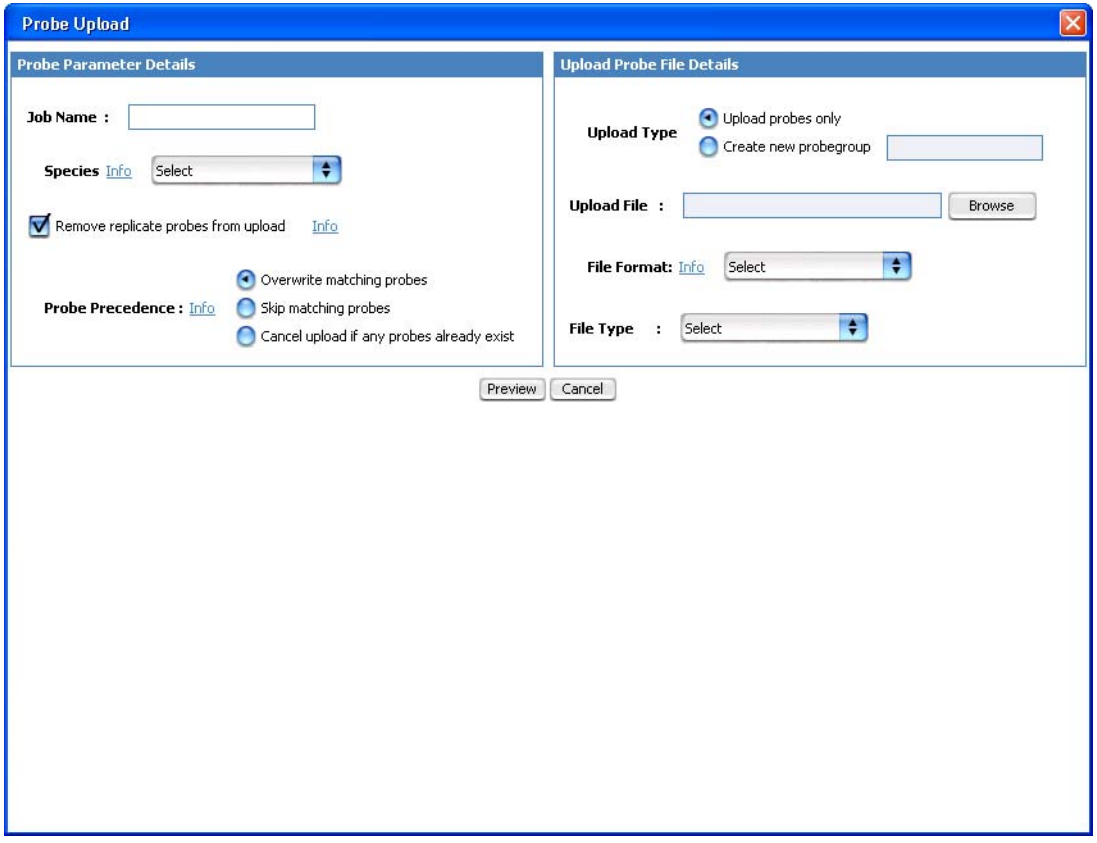


Figure 165 Probe Upload dialog box

Purpose: Lets you set up and start a probe upload. Probe uploads are available for the CGH, ChIP-on-chip, CH3, and Expression application types. A probe upload transfers probe sequences and annotation to your server. See "To upload probes and annotation" on page 161.

NOTE In the CGH application type, you cannot upload probes as SNP probes.

To open: In the eArray$_{XD}$ tab, under Create Probes, click **Probe Upload.**

Probe Parameter Details

Detail	Instructions/Comments
Job Name	Type a name to identify this probe upload job in the Tasks pane of the Navigator as eArray$_{XD}$ completes it.
Species	Select the desired species. The program associates all probes in the uploaded file with this species.
Remove replicate probes from upload	Mark this check box to upload the first probe in each set of replicate probes in your file, and ignore the others. A replicate probe has the same Probe ID as another probe in the file. If your probe file contains replicate probes, and you do **not** mark **Remove replicate probes from upload,** the program does not upload your file.
Probe Precedence	These options tell the program what to do if it finds probes in your uploaded file that have the same Probe IDs as probes that already exist in the system. Select one of these options: • **Overwrite matching probes** – The annotation of the matching uploaded probes replaces the annotation of the existing probes. You can use this option to reannotate existing probes. • **Skip matching probes** – The program ignores matching uploaded probes, but does upload other probes. • **Cancel upload if any probes already exist** – The program cancels the entire upload process if it finds a matching uploaded probe.

Upload Probe File Details

Detail	Instructions/Comments
Upload Type	Select one of these options: • **Upload probes only** – Creates probes from the data in the uploaded file, and makes them available to you in the program as individual probes. • **Create new probe group** – Creates probes from the data in the uploaded file, and puts all of the probes into a probe group. In the box, type a name for the probe group. The probe group name can contain up to 100 characters.
Upload File	Displays the location of the file of probes and annotation to be uploaded. **Browse** – Opens an Open dialog box, where you can select the desired file of probes and annotation.
File Format	The file format defines the specific types of data available in the uploaded file. See "To prepare a file of probes and annotation for upload" on page 158. Select one of these options: • **COMPLETE** – Your file contains the columns of data described in "Complete (for probes)" on page 881. • **MINIMAL** – Your file contains the columns of data described in "Minimal (for probes)" on page 890.
File Type	Select the appropriate file type from the list. The file type defines how the data items in the file are specified and separated. • **MS-EXCEL** – Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format. • **TDT** – Tab-delimited text file (*.tdt or *.txt)

Preview Opens the Define Uploaded File Columns pane in the dialog box, which lets you view the first few lines of your uploaded file, and label the content of each column of data within it. See below, "Define Uploaded File Columns pane."

Cancel Cancels the upload and closes the dialog box.

Define Uploaded File Columns pane

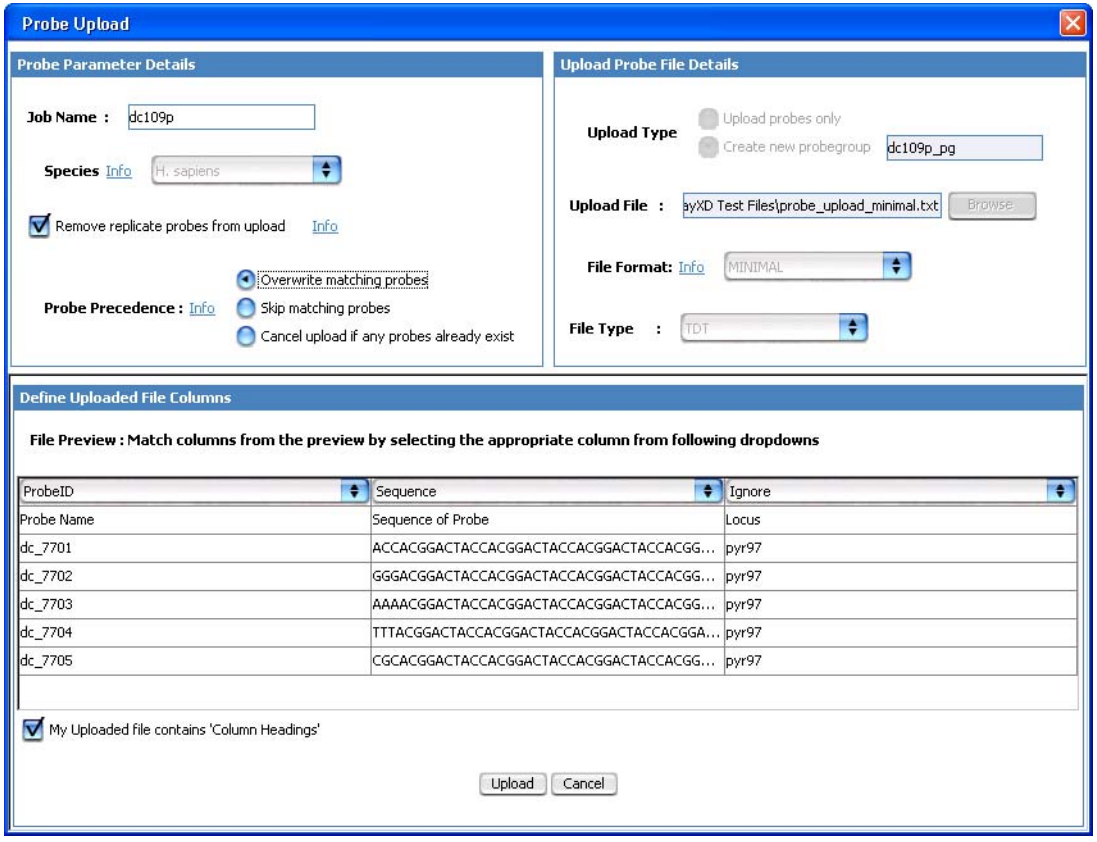


Figure 166 Probe Upload dialog box, with Define Uploaded File Columns pane visible

This pane displays the first few rows of your probe upload file, and lets you label the columns of data in it.

Column Labels From the list at the top of each column, select the most appropriate label. Use each label exactly once, except Ignore, which you can use any number of times. Select **Ignore** for columns that do not apply to the other labels.

My uploaded file contains column headings Mark this option if the first row of your file is actually a row of column headings. This prevents the program from interpreting the column headings as actual probe data. Even if you mark this option, eArray does not interpret any column heading information in your file.

Upload Submits your probe upload job to the upload queue, and closes the dialog box.

Cancel Cancels your probe upload, and closes the dialog box.

Score Custom Probes

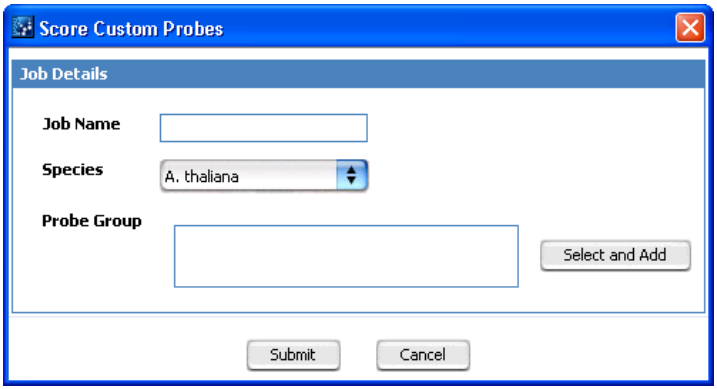


Figure 167 Score Custom Probes dialog box

Purpose: (Available for the CGH, ChIP-on-chip, and CH3 application types) Lets you set up a Probe Score job. This type of job calculates performance scores for non-Agilent probes in a probe group, and associates these scores with the appropriate probes in the probe database on your server. Probe performance scores indicate how likely it is that a probe will produce a good log ratio response on the Agilent microarray platform. See "To calculate probe performance scores" on page 214.

To open: In the eArray$_{XD}$ tab, under Quality, click **Probe Score.**

Job Details Pane

Job Name Type a name for the Probe Score job. The program uses this name to refer to the job in the Tasks pane of the Navigator.

Species Select the species that is associated with the probes. eArray supports probe scoring only for the species that appear in this list.

Probe Group Shows the name of the probe group that contains the probes to be scored. The probe group must contain at least one non-Agilent probe. Probe Score jobs can score one probe group at a time.

Select and Add – Opens the Select and Add dialog box for probe groups, where you can search for and select the probe group to be scored. See "Select and Add : Probe Group" on page 843.

Submit Submits the Probe Score job. The job appears in the Tasks pane in the Probe Score folder.

Cancel Closes the dialog box, and does not submit a Probe Score job.

Select and Add : Bait Group

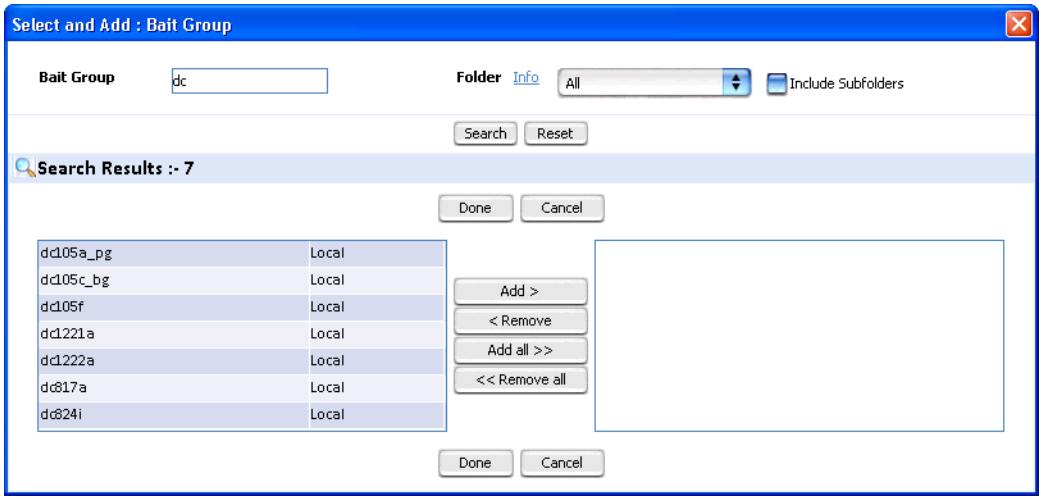


Figure 168 Select and Add Bait Group dialog box

Purpose: Lets you search for, select, and add bait group(s) in several locations in the program.

To open: The dialog box opens when you need to select one or more bait groups. For example, it opens when you click **Select and Add** in the **Used in Bait Groups** criterion of a Bait Search. (See "To search for baits" on page 358.)

Bait Group Type some or all of the name of the desired bait group. This search term is not case sensitive.

Folder This item lets you set the folder(s) for the bait group search.

- To limit returned bait groups to those in a specific folder, select the desired folder.
- To return bait groups without regard to their folder locations, select **All.**
- To also return bait groups that are found in the subfolders of the selected folder, mark **Include Subfolders.**

Search Searches all folders to which you have access for bait groups that match your search term. The results, if any, appear in the left box of the Search Result pane.

Reset Clears your search term and any results.

Search Result pane

(Page buttons) If available, these buttons let you display to a specific page of bait group search results.

Left box Lists bait group(s) that match your search term. To select a bait group, click its name. To select additional bait groups, control-click their names.

Right box Lists bait groups that you have transferred from the left box. These bait groups will be the one(s) selected for your search or other process.

Add Transfers the selected bait groups from the left box to the right box.

Remove Removes the selected bait group from the right box, and restores it to its original position in the left box. To select a bait group for removal, click its name.

Add all Transfers all of the bait groups from the left box to the right box.

Remove all Removes all of the bait groups in the right box, and restores them to their original positions in the left box.

Done Closes the dialog box, and adds the bait groups in the right pane to your search or other process. These entries replace any existing ones.

Cancel Closes the dialog box without adding any bait groups to your search or other process.

NOTE

When you select bait groups for a library, the program tells you if a bait group is *Local* or if it is *Not Downloaded.* If you select one or more bait groups that are *Not Downloaded,* you can only save the new library with a status of Draft. After you download the given bait group(s) from the eArray Web site, you can save the library with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

Select and Add : Library Name

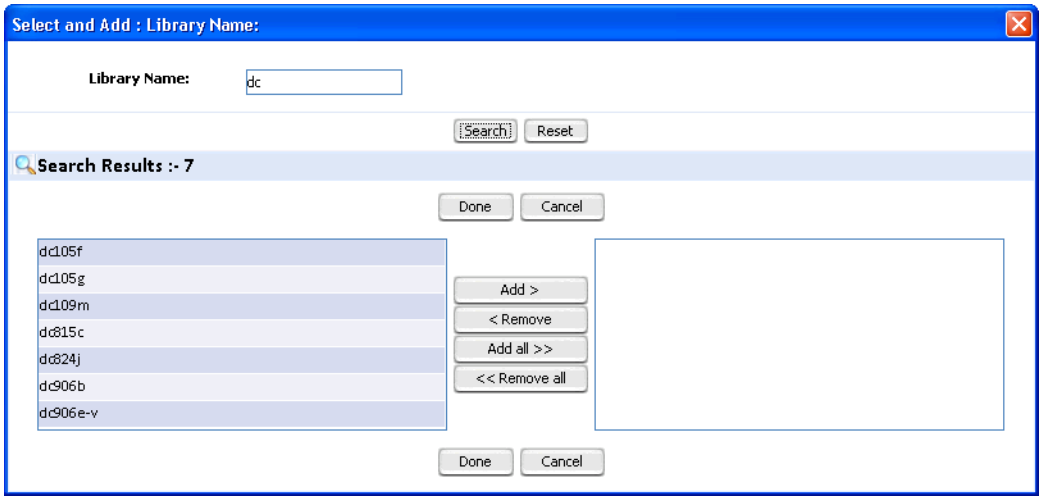


Figure 169 Select and Add : Library Name dialog box

Purpose: Lets you search for, select, and add library names as search criteria in a Bait Search. See "To search for baits" on page 358.

To open: In the Bait Search pane, in Used in Libraries, click **Select and Add.** See "Bait Search" on page 538.

Library Name Type some or all of the name of the desired library. This search term is not case sensitive.

Search Searches all folders to which you have access for library names that match your search term. The results, if any, appear in the left box of the Search Result pane.

Reset Clears your search term and any results.

Search Result pane

Left box Lists librar(ies) that match your search term. To select a library, click its name. To select additional libraries, control-click their names.

Right box Lists libraries that you have transferred from the left box. These libraries will be the one(s) selected for your search or other process.

Add Transfers the selected libraries from the left box to the right box.

Remove Removes the selected bait group from the right box, and restores it to its original position in the left box. To select a bait group for removal, click its name.

Add all Transfers all of the libraries from the left box to the right box.

Remove all Removes all of the libraries in the right box, and restores them to their original positions in the left box.

Done Closes the dialog box, and adds the libraries in the right pane to your search. These entries replace any existing ones.

Cancel Closes the dialog box without adding any libraries to your search.

Select and Add : Microarray Name

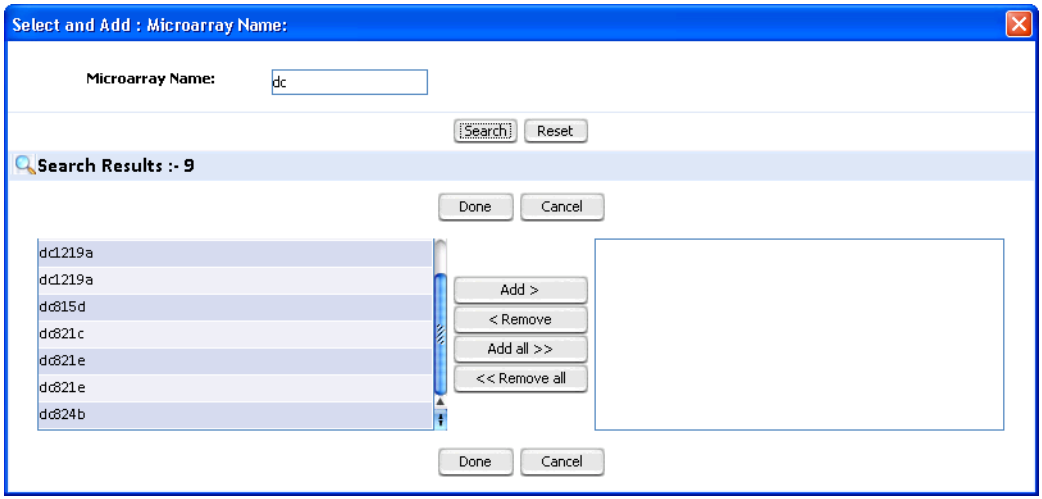


Figure 170 Select and Add Microarray Name dialog box

Purpose: Lets you search for, select, and add microarray names as search criteria in a Probe Search. See "To use the Probe Search tool to find probes" on page 92.

To open: In the Probe Search pane, in Used in Array Designs, click **Select and Add.** See "Probe Search" on page 560.

Microarray Name Type some or all of the name of the desired microarray design. This search term is not case sensitive.

Search Searches all folders to which you have access for microarray design names that match your search term. The results, if any, appear in the left box of the Search Result pane.

Reset Clears your search term and any results.

Search Result pane

Left box Lists microarray designs that match your search term. To select a microarray design, click its name. To select additional microarray designs, control-click their names.

Right box Lists microarray designs that you have transferred from the left box. These microarray designs will be the one(s) selected for your search or other process.

Add Transfers the selected microarray designs from the left box to the right box.

Remove Removes the selected bait group from the right box, and restores it to its original position in the left box. To select a bait group for removal, click its name.

Add all Transfers all of the microarray designs from the left box to the right box.

Remove all Removes all of the microarray designs in the right box, and restores them to their original positions in the left box.

Done Closes the dialog box, and adds the microarray designs in the right pane to your search. These entries replace any existing ones.

Cancel Closes the dialog box without adding any microarray designs to your search.

Select and Add : Probe Group

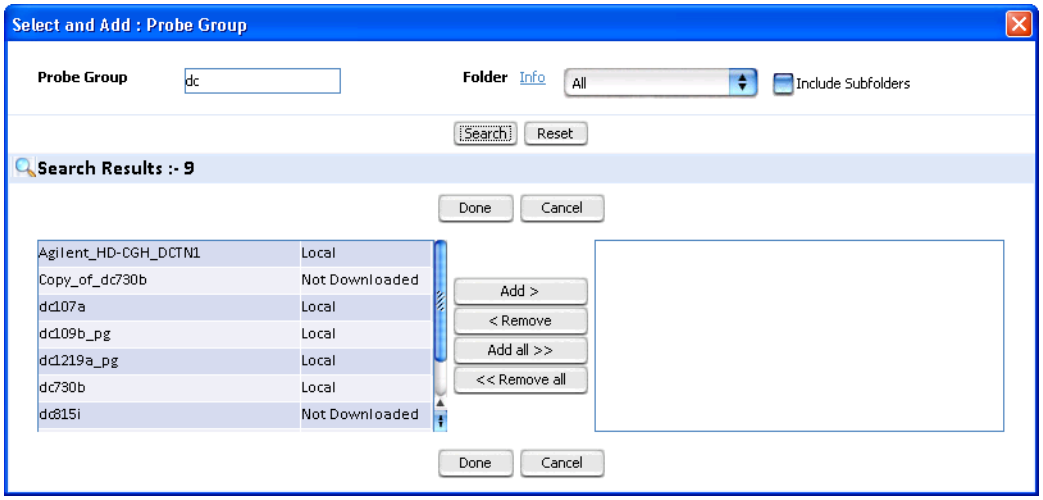


Figure 171 Select and Add Probe Group dialog box

Purpose: Lets you search for, select, and add probe group(s) in several locations within the program. For instructions on how to use this dialog box, see "To select probe groups for searches or microarrays" on page 106.

To open: The dialog box opens when you need to select one or more probe groups. For example, it opens when you click **Select and Add** in the **Used in Probe Groups** criterion of a Probe Search. (See "To use the Probe Search tool to find probes" on page 92.)

Probe Group Type some or all of the name of the desired probe group. This search term is not case sensitive.

Folder Limits the search to the selected folder. To search all folders, select **All.** The folders to which you have access appear in the list.

Include Subfolders – Includes the subfolders of the selected folder in your search.

Search Searches all folders to which you have access for probe groups that match your search term. The results, if any, appear in the left box of the Search Result pane.

Reset Clears your search term and any results.

Search Result pane

Left box Lists probe group(s) that match your search term. To select a probe group, click its name. To select additional probe groups, control-click their names.

Right box Lists probe groups that you have transferred from the left box. These probe groups will be the one(s) selected for your search or other process.

Add Transfers the selected probe groups from the left box to the right box.

Remove Removes the selected probe group from the right box, and restores it to its original position in the left box. To select a probe group for removal, click its name.

Add all Transfers all of the probe groups from the left box to the right box.

Remove all Removes all of the probe groups in the right box, and restores them to their original positions in the left box.

Done Closes the dialog box, and add the probe groups in the right pane to your search or other process. These entries replace any existing ones.

Cancel Closes the dialog box without adding any probe groups to your search or other process.

NOTE

When you select probe groups for a microarray design, the program tells you if a probe group is *Local* or if it is *Not Downloaded.* If you select one or more probe groups that are *Not Downloaded,* you can only save the new microarray design with a status of Draft. After you download the given probe group(s) from the eArray Web site, you can save the microarray design with a status of Complete or Submitted. See "To obtain updates of Agilent Catalog probes, baits and annotation from the eArray Web site" on page 64.

Select and Add : Species

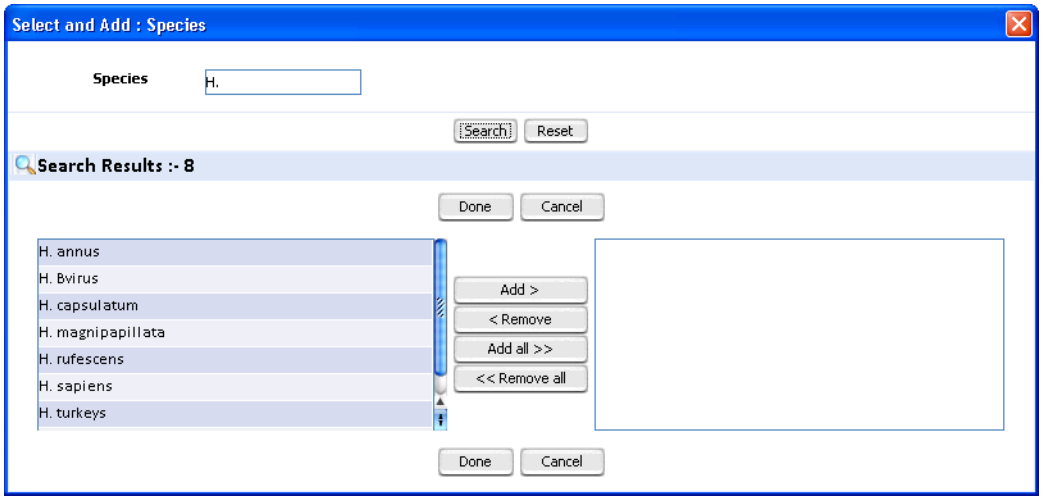


Figure 172 Select and Add Species dialog box

Purpose: Lets you select one or more species for microarray design or bait library searches. See "To search for microarray designs" on page 251 and "To search for libraries" on page 416.

To open: In the Array Design Search pane, or the Library Search pane, in **Species,** click **Select and Add.** See "Array Design Search" on page 533 and "Library Search" on page 551.

Species Type some or all of the name of the desired species. This search term is not case sensitive.

Search Searches the program for species that match your search term. The results, if any, appear on the left side of the Search Result pane.

Reset Clears your search term and any results.

Search Result pane

Left box Lists species that match your search term. To select a species, click its name. To select additional species, control-click their names.

Right box Lists species that you have transferred from the left box. These species will become search criteria for your microarray design search. To select a species for removal from this list, click its name.

Add Transfers the selected species from the left box to the right box.

Remove Removes the selected species from the right box, and restores it to its original position in the left box.

Add all Transfers all of the species from the left box to the right box.

Remove all Removes all of the species in the right box, and restores them to their original positions in the left box.

Done Closes the dialog box, and adds the species from the right box to your search. Multiple entries appear there in pipe "|" separated format. These entries replace any existing ones.

Cancel Closes the dialog box without adding any species to the search.

Select Array Type

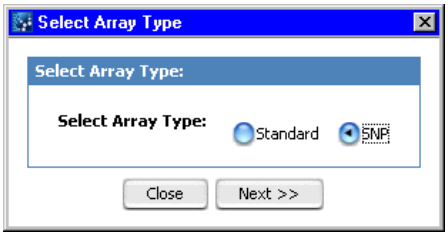


Figure 173 Select Array Type dialog box

Purpose: (Available for the CGH application type) Lets you set the specific type of microarray to create, either a standard CGH microarray, or a CGH+SNP microarray. CGH+SNP microarrays include both CGH and SNP probes on the same array. See "To create a CGH+SNP microarray design" on page 301.

To open: In the CGH application type, do a probe group search. In the search result pane, select one or more probe groups, then click **Create Microarray.**

Select Array Type Select one of these options:

- **Standard** – Creates a standard CGH microarray design.
- **SNP** – Creates a CGH+SNP microarray design, which includes both CGH and SNP probes on the same array. See "To create a CGH+SNP microarray design" on page 301.

Close Closes the dialog box, and does not create a microarray design.

Next Opens the Create Microarray Design dialog box, where you can enter the properties and select probe groups for a new microarray design. See "Create Microarray Design" on page 646.

Select Background Color

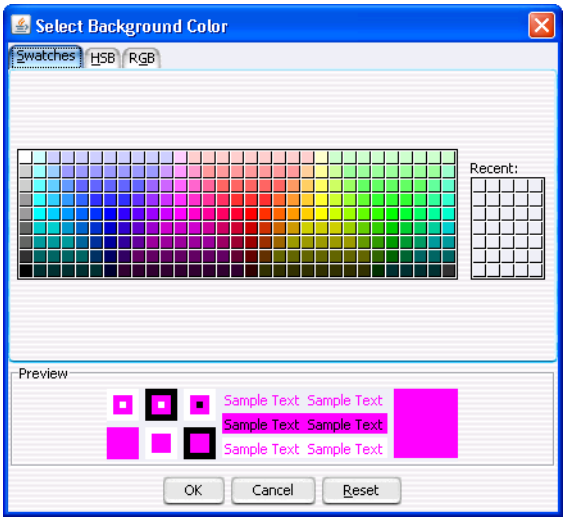


Figure 174 Select Background Color dialog box – Swatches tab

Purpose: Lets you select a color to represent particular probes when you use the Array Visualizer tool. See "To view the layout of probes on a microarray graphically" on page 306.

To open: In the Array Layout dialog box, under Color Legend, click a color swatch. See "Array Layout" on page 583.

Swatches tab

Swatches To select a color, click a swatch. The new color appears in the Preview pane and also under Recent. The color that you select also becomes the selected color in the HSB and RGB tabs, where you can further refine the color.

Recent Displays the colors that you have recently selected in the Swatches tab. To select one of these recent colors, click it.

HSB tab

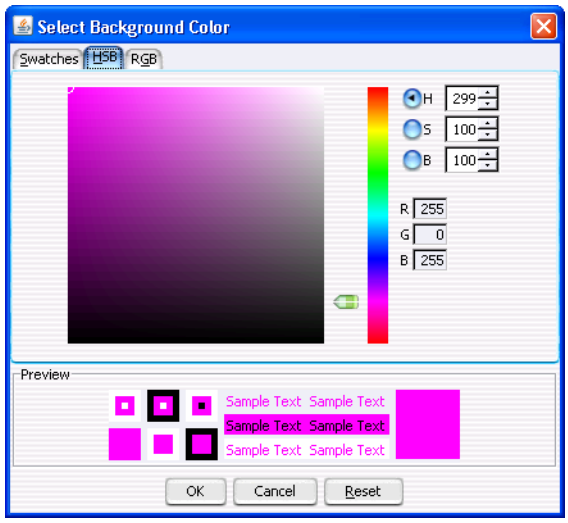


Figure 175 Select Background Color dialog box – HSB tab

This tab lets you define the hue (H), saturation (S), and brightness (B) levels of for a color. These three values uniquely define a color. The initial color settings in this tab reflect any changes that you have made to the currently selected color in the other tabs. You can set these values in several ways:

- Directly edit the numbers in **H, S,** and **B.** You can also click the up or down button to the right of each value to increase or decrease it. In addition, to use the up and down arrow keys on your keyboard to change values, click the number that you want to change, then press the up or down arrow key, as desired.
- Use the green slider to change values. Select **H, S,** or **B,** as desired, then drag the slider up or down to change the selected value.
- Use the green slider and the large, square color selection box. Select **H, S,** or **B,** then drag the slider up or down to set the desired value. The color selection box shows all of the available colors given the particular setting of the slider. To select a color, click anywhere within the color selection box. This sets the remaining two HSB values.

H **Hue** – A number from 0 to 359 that represents the basic color. The color spectrum is a 360 degree color circle.

S **Saturation** – A number from 0 to 100 that represents the intensity of the color. A setting of 100 gives maximum color intensity. A setting of 0 gives no color, and reduces the available color spectrum to grayscale, only.

B **Brightness** – A number from 0 to 100 that represents the amount of black that is mixed in with the color. A setting of 100 gives maximum brightness, with no black added, and a setting of 0 results in the color black, regardless of the other settings.

R, G, B Show the color settings of the selected color using the RGB (Red, Green, Blue) color model. You cannot directly edit the values from HSB tab, but they change when you select a different color. You can set specific RGB values in the RGB tab.

RGB tab

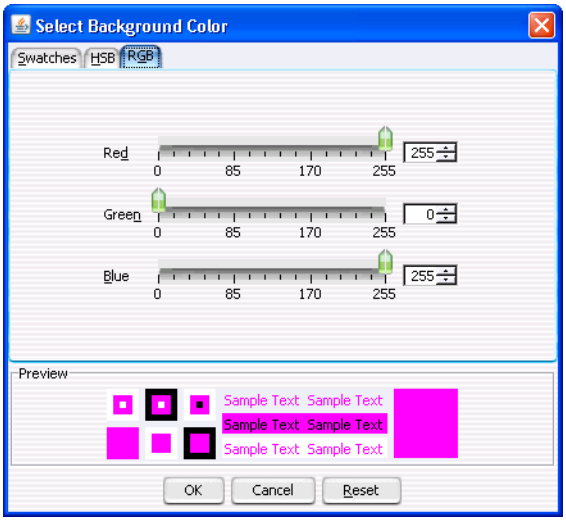


Figure 176 Select Background Color dialog box – RGB tab

This tab lets you use the RGB (red-green-blue) color model to define a color. In this model, you select the amounts of red, green, and blue to combine to form the desired color. All colors can be defined.

You can change the R, G, or B value of the selected color in two ways:

- In **Red, Green,** or **Blue,** drag the green slider to the desired value.

- Directly edit the number in **R, G,** or **B.** You can also click the up and down buttons to the right of the value to increase or decrease it. In addition, to use the up and down arrow keys on your keyboard to change a value, click the number that you want to change, then press the up or down arrow key, as desired.

R **Red** – A number from 0 to 255 that represents the amount of red. 0 is the minimum and 255 is the maximum.

G **Green** – A number from 0 to 255 that represents the amount of green. 0 is the minimum and 255 is the maximum.

B **Blue** – A number from 0 to 255 that represents the amount of blue. 0 is the minimum and 255 is the maximum.

Items that appear in all tabs

Preview Shows the selected color in a number of contexts. The right-most diagram in this pane shows two colors:

- **Top color** – The color that is currently in use in the Color Legend in the Array Layout dialog box.
- **Bottom color** – The color that is currently selected to replace it.

OK Accepts any changes that you made to the color, and closes the dialog box.

Cancel Closes the dialog box, and discards any changes that you made to the color.

Reset Restores the color settings in the dialog box to what they were before you made any changes. The dialog box remains open.

Simple Tiling

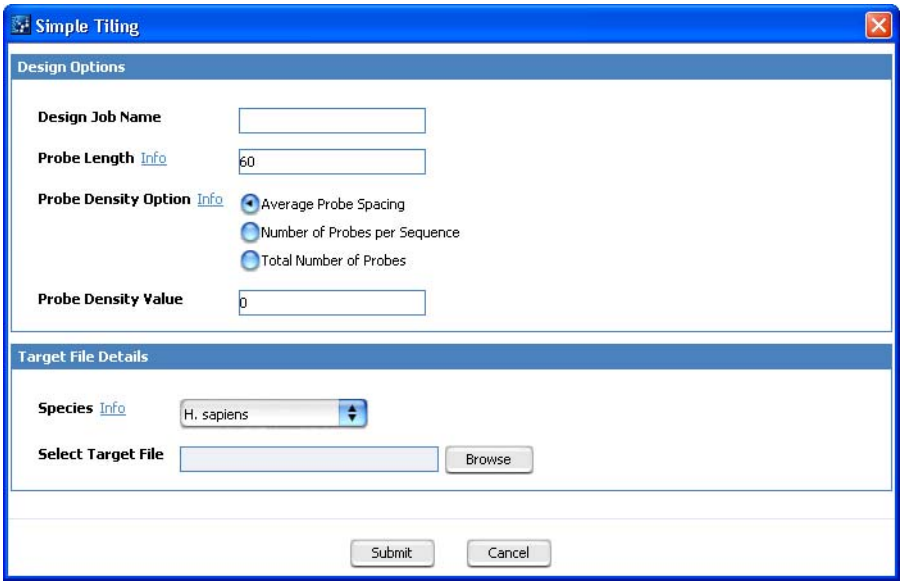


Figure 177 Simple Tiling dialog box

Purpose: Lets you set up and submit a Simple Tiling job. Simple Tiling creates Expression type probes that span uploaded sequences at even intervals. See "To set up a Simple Tiling job" on page 174.

To open: In the eArray$_{XD}$ tab, under **Create Probes,** click **Simple Tiling.**

Design Options

Parameter	Instructions/Details
Design Job Name	Type a name to identify this Simple Tiling job.
Probe Length	Type the desired length (from 45 to 60 bp) for the generated probes. Type the number of base pairs, without units. Agilent has found that a probe length of 60 bp provides the optimal balance between sensitivity and specificity for most applications on the Agilent *in situ* microarray platform.

Parameter	Instructions/Details
Probe Density Option	Select one of these options, then type the appropriate value in **Probe Density Value.** • **Average Probe Spacing** – Defines the average distance (in bp) between the centers of the generated probes. • **Number of Probes per Sequence** – Defines the average number of probes designed for each target sequence. eArray uses this value to calculate average probe spacing on a per-sequence basis. The actual number of probes designed for each sequence may deviate from the specified value, because of repeat regions and rounding, but this deviation should not be large unless sequence length limits the design process. • **Total Number of Probes** – Defines the total number of probes generated, to be spaced evenly over all of the target sequences. eArray first calculates the number of probes to be generated for each sequence, and then uses these numbers to calculate average probe spacing.
Probe Density Value	Type the desired number of probes, or probe spacing (in bp), as applies to your selection in **Probe Density Option.** In all cases, type an integer that is greater than 0.

Target File Details

Parameter	Instructions/Details
Species	Select the species that applies to the data in your uploaded target sequence file. The program uses the selected species name to properly classify the new probes in the probe database on your server.
Select Target File	Displays the location of the file that contains the sequences to be tiled. **Browse** – Opens an Open dialog box, where you can select the file that contains the desired FASTA format sequence file.

Submit Starts the Simple Tiling Job.

Cancel Cancels the job and closes the dialog box.

SNP Search Criteria

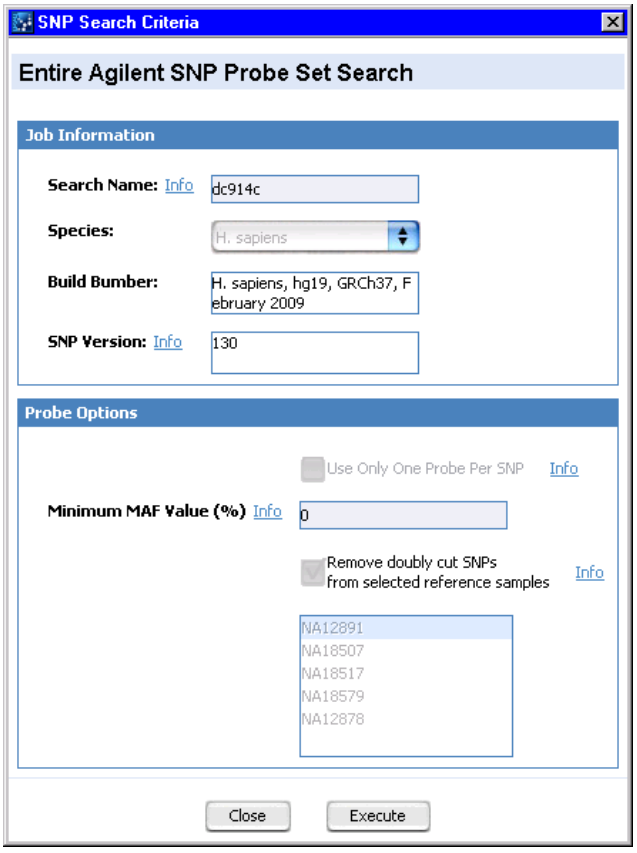


Figure 178 SNP Search Criteria dialog box, as it appears for an Entire Agilent SNP Probe Set search

Purpose: Displays all of the search criteria that were used in an existing SNP probe search job, and lets you use the criteria for that job to set up a new search. See "To view the search criteria for a SNP probe search job" on page 154 and "To use existing SNP probe search criteria to set up a new search" on page 154.

To open: In the Tasks pane of the Navigator, right-click the name of the desired job, then click **View Search Criteria.**

Search Criteria The search criteria that appear in this dialog box are a read-only version of the criteria that appear in the corresponding SNP probe search pane. See these topics for details:

- "Entire Agilent SNP Probe Set Search" on page 542
- "Genomic Interval Search (SNP Probe Search)" on page 546
- "Probe ID Search (SNP probes)" on page 558
- "SNP ID Search (SNP probe search)" on page 572

Close Closes the dialog box.

Execute Opens the corresponding SNP probe search pane, and transfers the search criteria from the selected SNP probe search job. All parameters except Job Name are transferred.

SNP Search Results (Except Gene Interval searches)

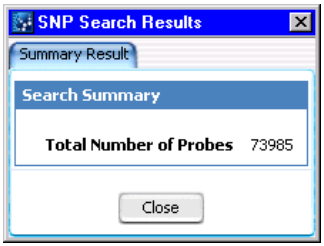


Figure 179 SNP Search Results dialog box for an Agilent SNP Probe search.

Purpose: A SNP Probe Search returns Agilent SNP probes specifically for use in Agilent CGH+SNP microarray designs. See "Searching for Agilent SNP Probes" on page 138. This dialog box tells you the total number of probes that were returned by one of these types of Agilent SNP probe searches:

- Entire Agilent SNP Probe Set Search – See "To do an Entire Agilent SNP Probe Set Search" on page 141.
- SNP ID Search – See "To do a SNP probe search by SNP ID" on page 150.
- Probe ID Search – See "To do a SNP probe search by probe ID" on page 148.

A different dialog box shows the results of a SNP probe search by genomic intervals. See "SNP Search Results (Genomic Interval Search)" on page 857.

To open: In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired SNP probe search job, then click **View Result.** (Note: The SNP probe search job must have a status of Complete .)

Summary Result tab – Search Summary

Total number of probes The number of probes that were returned by the search.

Close Closes the dialog box.

SNP Search Results (Genomic Interval Search)

Purpose: This dialog box lets you view statistics about the results of a SNP probe search by genomic intervals, both overall and on a per-interval basis. Two tabs are available, as described below.

Summary Result tab

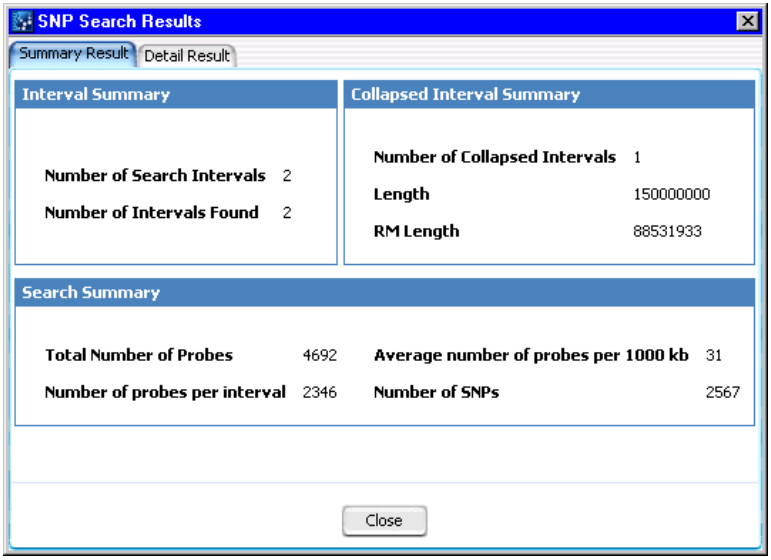


Figure 180 SNP Search Results dialog box for a SNP probe search by genomic intervals – Summary Result tab

Purpose: This tab shows overall statistics about the selected SNP probe search by gene interval. The statistics report an aggregate summary for all search intervals that were entered for the search. See "To do a SNP probe search by genomic intervals" on page 143.

To open: In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired SNP probe search job, then click **View Result.** The Summary Result tab appears by default. (Note: The SNP probe search job must have a status of Complete .)

Interval Summary These statistics appear:

Statistic	Description
Number of Search Intervals	The total number of genomic intervals that were entered as search criteria.
Number of Intervals Found	The number of entered genomic intervals that passed validation. (The number of entered genomic intervals that actually exist for the given species.)

Collapsed Interval Summary These statistics appear:

Statistic	Description
Number of Collapsed Intervals	The total number of intervals after overlapping entered intervals were combined.
Length	The total number of base pairs of DNA that were considered in the search.
RM Length	(Repeat-masked length) The total number of base pairs of DNA that were considered in the search, after repetitive regions were removed.

Search Summary These statistics appear:

Statistic	Description
Total Number of Probes	The total number of probes that were returned by the SNP probe search
Probes per Interval	The average number of probes that were returned for each interval that was entered as a search criterion.
Average probes per 1000 kb	The average number of probes that were returned for each 1,000 kb of DNA.
Number of SNPs	The number of SNP sites that are represented by the returned probes.

Close Closes the dialog box.

Detail Result tab

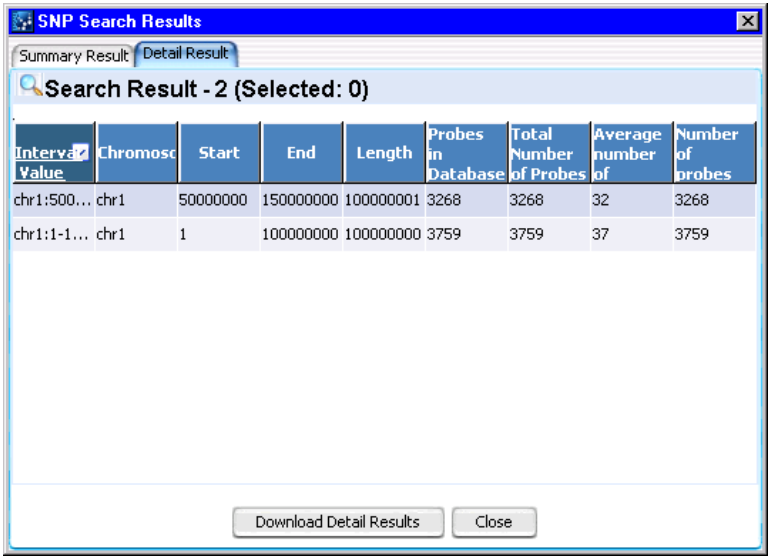
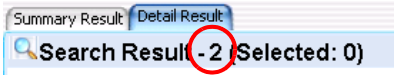


Figure 181 SNP Search Results dialog box for a SNP probe search by genomic intervals – Detail Result tab

Purpose: This tab shows statistics about the selected SNP probe search by genomic interval. Statistics appear for each interval that was entered for the search. See "To do a SNP probe search by genomic intervals" on page 143.

To open: In the Tasks pane of the Navigator, in the SNP Search folder, right-click the name of the desired SNP probe search job, then click **View Result.** When the SNP Search Results dialog box appears, click the **Detail Result** tab. (Note: The SNP probe search job must have a status of Complete .)

Search Result The first number that appears is the total number of intervals that appear in the search results in the Detail Result tab.



Columns The table below describes the columns that appear.

Column	Description
Interval Value	Each genomic interval that was entered as a search criterion.
Chromosome	The chromosome on which each interval is located.
Start	The first base pair in the interval on the given chromosome.
End	The last base pair in the interval on the given chromosome.
Length	The total length of the interval in bp
Probes in Database	The total number of SNP probes in the Agilent SNP probe database for each interval.
Total Number of Probes	The total number of SNP probes that the search returned for each interval. This value can be less than the total number of probes in the database for the interval because of filters and other options that were selected for the search.
Average Number of Probes per 1000 kb	For each interval, the average number of probes that the search returned per 1,000 kb.
Number of Probes per Interval	Same as Total Number of Probes.

Other actions You can customize the appearance of this dialog box in several ways:

- Drag a column heading to change the order of columns.
- Drag the border between column headings to change the relative width of adjacent columns.
- Drag the bottom or side borders of the dialog box to adjust its size.
- Click the column heading of the Interval Value column to reverse the order of the intervals.

Download Detail Results Opens a Save dialog box, where you can select a location to download a file that contains the data that appears in the Detail Result tab of the dialog box. The program saves the results as a *.tdt file with column headers that you can open in a spreadsheet program.

Close Closes the dialog box.

Submit Library

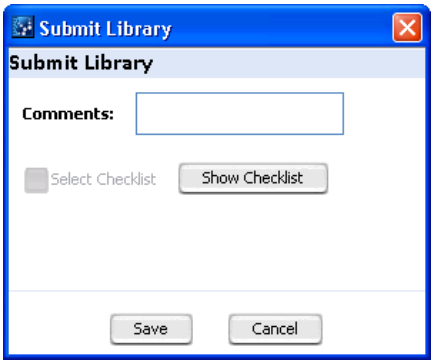


Figure 182 Submit Library dialog box

Purpose: Lets you submit a library to Agilent Manufacturing. After you submit a library, you can request a quote for it, and search for it on the eArray Web site. See "To submit a library to Agilent" on page 458.

To open: In the results of a library search, click . See "To search for libraries" on page 416. Alternatively, in the Design Data pane of the Navigator, right-click the name of the desired library, then click **Submit.**

Comments Type comments for future reference to be saved with the library. Comments are required. Agilent does not monitor these comments—if you have a question or request, contact Agilent Technical Support or your Agilent sales representative.

Select Checklist (Read-only) The program marks this option after you view and mark all items on the library checklist. To view this checklist, click **Show Checklist.**

Show Checklist Opens the library checklist. See "Design Checklists" on page 894.

Save Submits your library to Agilent Manufacturing.

Cancel Closes the dialog box without submitting your library.

Submit Microarray Design

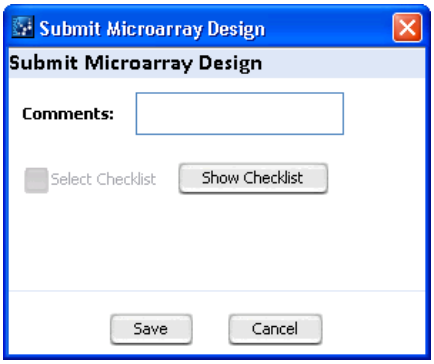


Figure 183 Submit Microarray Design dialog box

Purpose: Lets you submit a microarray design to Agilent Manufacturing. After you submit a microarray design, you can request a quote for it, and search for it on the eArray Web site. See "Submitting Microarray Designs to Agilent" on page 346.

To open: In the results of a microarray design search, click . See "To search for microarray designs" on page 251.

Alternatively, in the Design Data pane of the Navigator, right-click the name of the desired microarray design, then click **Submit.**

Comments Type comments for future reference to be saved with the microarray design. Comments are required. Agilent does not monitor these comments—if you have a question or request, contact Agilent Technical Support or your Agilent sales representative.

Select Checklist (Read-only) The program marks this option after you view and mark all items on the design checklist. To view the design checklist, click **Show Checklist.**

Show Checklist Opens the design checklist appropriate to your application type. See "Design Checklists" on page 894.

Save Submits your microarray design to Agilent Manufacturing.

Cancel Closes the dialog box without submitting your microarray design.

Troubleshoot Job

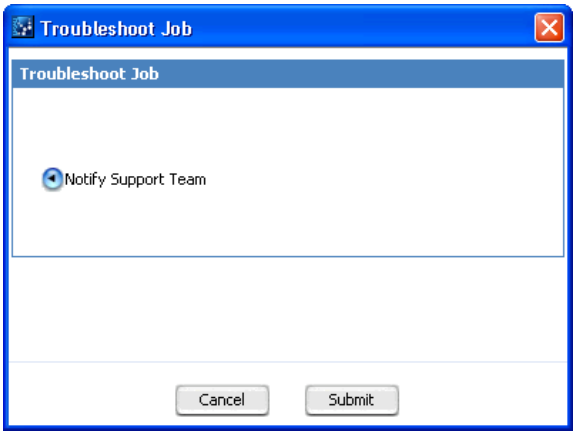


Figure 184 Troubleshoot Job dialog box

Purpose: Lets you submit an error log for the job to Agilent Technical Support. See "To troubleshoot a task" on page 74.

To open: In the Job Queue Management Console, in the row of the desired job, in the **Actions** column, click .

Options The Notify Support Team option sends an error log to Agilent Technical Support. If you contact Agilent Technical Support, this log can help them resolve your issue. This is the only option, and it is selected by default.

Cancel Closes the dialog box.

Submit Sends the error log to Agilent Technical Support.

User Preferences – Miscellaneous tab

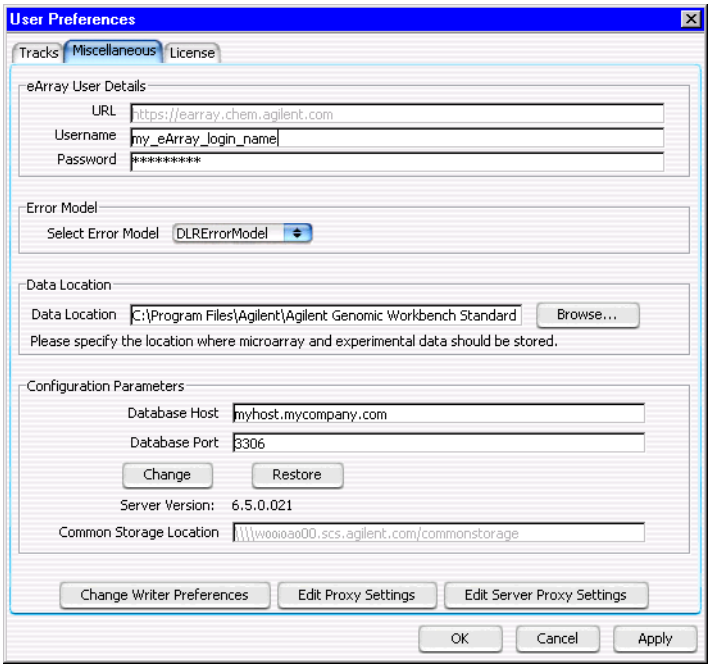


Figure 185 Preferences dialog box – Miscellaneous tab

Purpose: The Preferences dialog box lets you customize many aspects of Agilent Genomic Workbench for your specific purposes. The Miscellaneous tab contains settings for eArray$_{XD}$ that let you enter the login name and password of your existing account on the eArray Web site. You must have an account on the eArray Web site to use eArray$_{XD}$. The dialog box also lets you view or change the location and the configuration parameters of your Agilent Genomic Workbench server. See these topics:

- "To become a registered user on the eArray Web site" on page 39
- "To link the Agilent Genomic Workbench client program to a different account on the eArray Web site" on page 38.
- "To display or change the location of your Agilent Genomic Workbench server" on page 37

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

eArray User Details

URL (Read-only) The address of the eArray Web site, currently https://earray.chem.agilent.com

Username Your eArray login name. Usually, this is your e-mail address.

Password Your password for the eArray Web site. Passwords are case-sensitive.

NOTE The settings above let you record your existing username and password for the eArray Web site. To change either of these pieces of information, you must log in to the eArray Web site, and change it in the My Account tab.

Configuration Parameters

Database host The name of the machine upon which the Agilent Genomic Workbench server software is running.

Database port The TCP/UDP port number assigned to the MySQL service on the machine that is running the Agilent Genomic Workbench server software. Typically, this is port 3306.

Change Opens a dialog box that asks if you really want to change the database configuration parameters. If you click Yes, the Database host and Database port setting become available. Otherwise, these settings are read-only, and cannot be edited.

Restore Resets the database configuration parameters to their settings before you made any changes.

Server Version The version number of the Agilent Genomic Workbench server software for the server to which your client program is connected.

Common Storage Location The location of the Agilent Genomic Workbench server database files. This location is generated by the program, and cannot be edited.

CAUTION The configuration parameters must refer to a valid Agilent Genomic Workbench server installation to which you have access. Otherwise, the program will not function properly.

Change Writer Preferences Opens the File Writer Preferences dialog box, where you can select the types of microarray and library design files that the program creates. See "File Writer Preferences" on page 774

Edit Proxy Settings Opens a dialog box where you can enter these settings. Your network administrator can tell you if you need to change them. For more information, see the *Product Overview Guide*.

Edit Server Proxy Settings Opens a dialog box where you can enter these settings. Your network administrator can tell you if you need to change them. For more information, see the *Product Overview Guide*.

Other Commands

OK Accepts your changes and closes the dialog box.

Cancel Discards your changes and closes the dialog box.

Apply Accepts your changes, but leaves the dialog box open.

The other options in this tab of the Preferences dialog box are only relevant to DNA Analytics data analysis applications, and do not affect eArray$_{XD}$.

View Bait Group

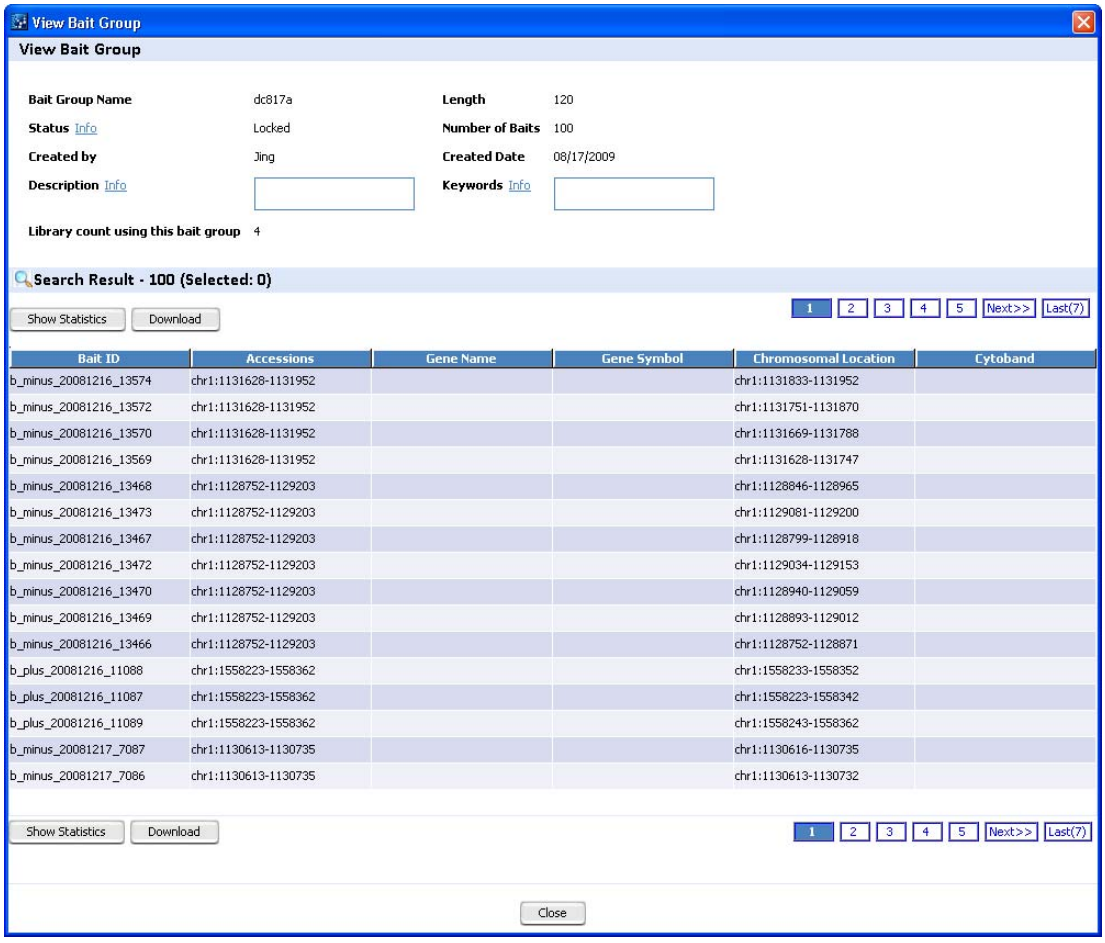


Figure 186 View Bait Group dialog box

Purpose: Lets you view the properties and bait content of a bait group. See "To view a bait group" on page 399.

To open: In the **Actions** column of the search results of a bait group search, next to the desired bait group, click . See "To search for bait groups" on page 396.

Alternatively, in the **Design Data** pane of the Navigator, right-click the name of the desired bait group, then click **View.**

Properties All properties in the top pane of the dialog box are read-only.

Property	Details
Bait Group Name	Name of the bait group, assigned by its creator.
Length	The length of each of the baits in the bait group, in nucleotides. All baits in a bait group (and in a library) must have the same length. Agilent currently supports a bait length of 120 nucleotides.
Status	**Incomplete** – Bait group can be edited. **Locked** – Bait group cannot be edited, nor can it be unlocked.
Number of Baits	Total number of baits in the bait group.
Created by	User who first saved the bait group.
Date Created	Date the bait group was first saved.
Description	Brief description of bait group, assigned by its creator.
Keyword	One or more search keywords.
Library count using this Bait Group	The number of libraries on your server that use this bait group.

Search Result Pane

Table of baits The table lists the baits in the bait group by Bait ID. Additional columns of annotation may be available, depending on the bait.

Show Statistics Opens the Bait Statistics dialog box, where you can view the Bait IDs and sequences of the baits in the bait group. See "Bait Statistics" on page 596.

Download Opens the Download Bait Group dialog box, where you can download the bait group in one of several formats. See "Download Bait Group" on page 717 and "To download a bait group" on page 409.

(Page buttons) If available, these button let you to go to different pages of the bait list.

Close Closes the dialog box.

View Library

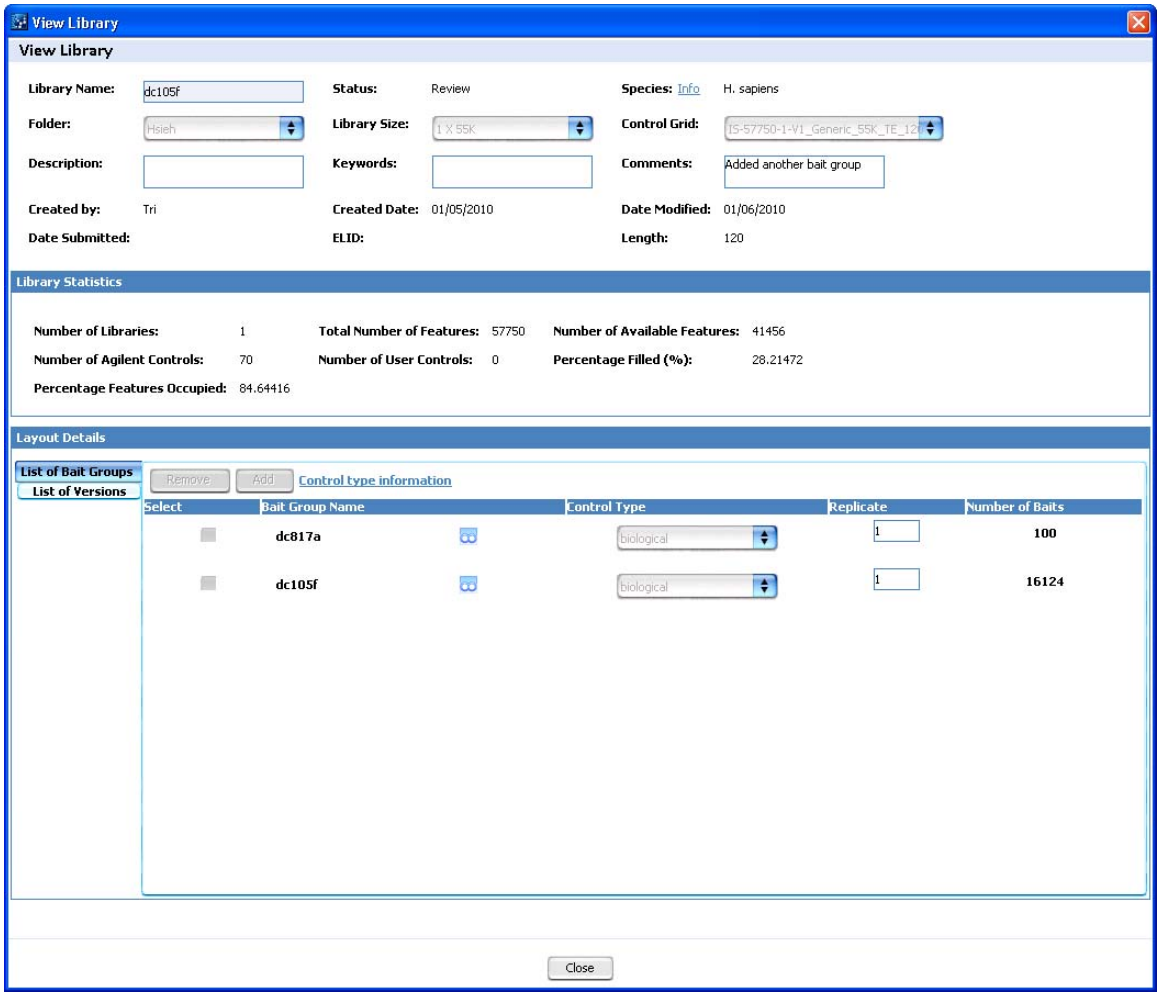


Figure 187 View Library dialog box

Purpose: Lets you view the properties, statistics, and bait group content of libraries. Anyone with access to a folder can view the libraries within it. See "To view a library" on page 443.

To open: In the Search Result pane of a library search, next to the desired library, in the **Actions** column, click  . See "To search for libraries" on page 416.

Alternatively, in the Design Data pane of the Navigator, right-click the name of the desired library, then click **View.**

This dialog box is a read-only version of the Edit Library dialog box. See "Edit Library" on page 740.

View Microarray Design

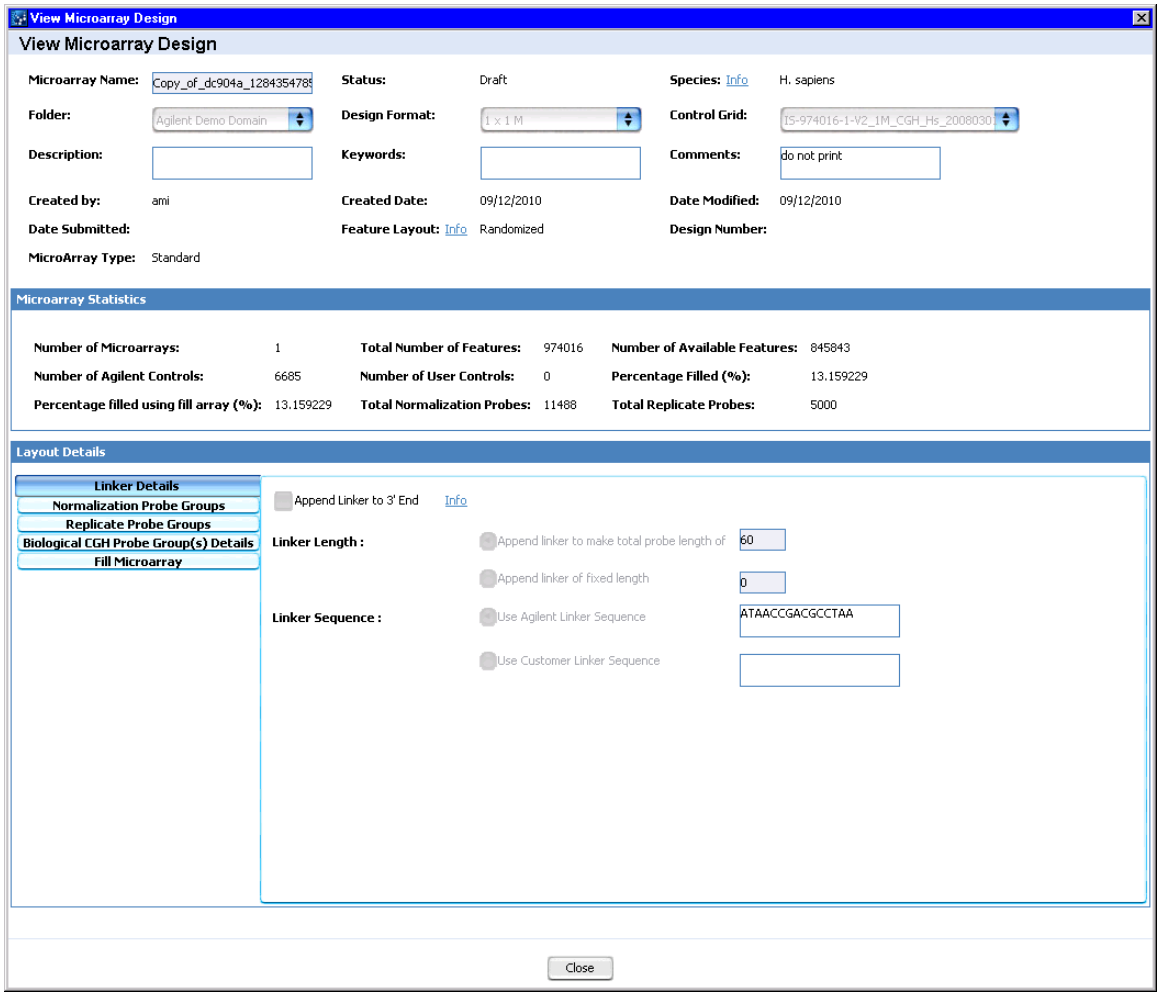


Figure 188 View Microarray Design dialog box

Purpose: This dialog box is a read-only version of the Edit Microarray Design dialog box. It lets you view the properties, statistics, and probe group content of microarray designs. See "Edit Microarray Design" on page 751. Anyone with access to a folder can view the microarray designs within it.

To open: In the Actions column of the search results of a microarray design search, next to the desired design, click  . See "To search for microarray designs" **on page 251**.

Alternatively, in the Design Data pane of the Navigator, right-click the name of the desired microarray design, then click **View.**

View Probe Group

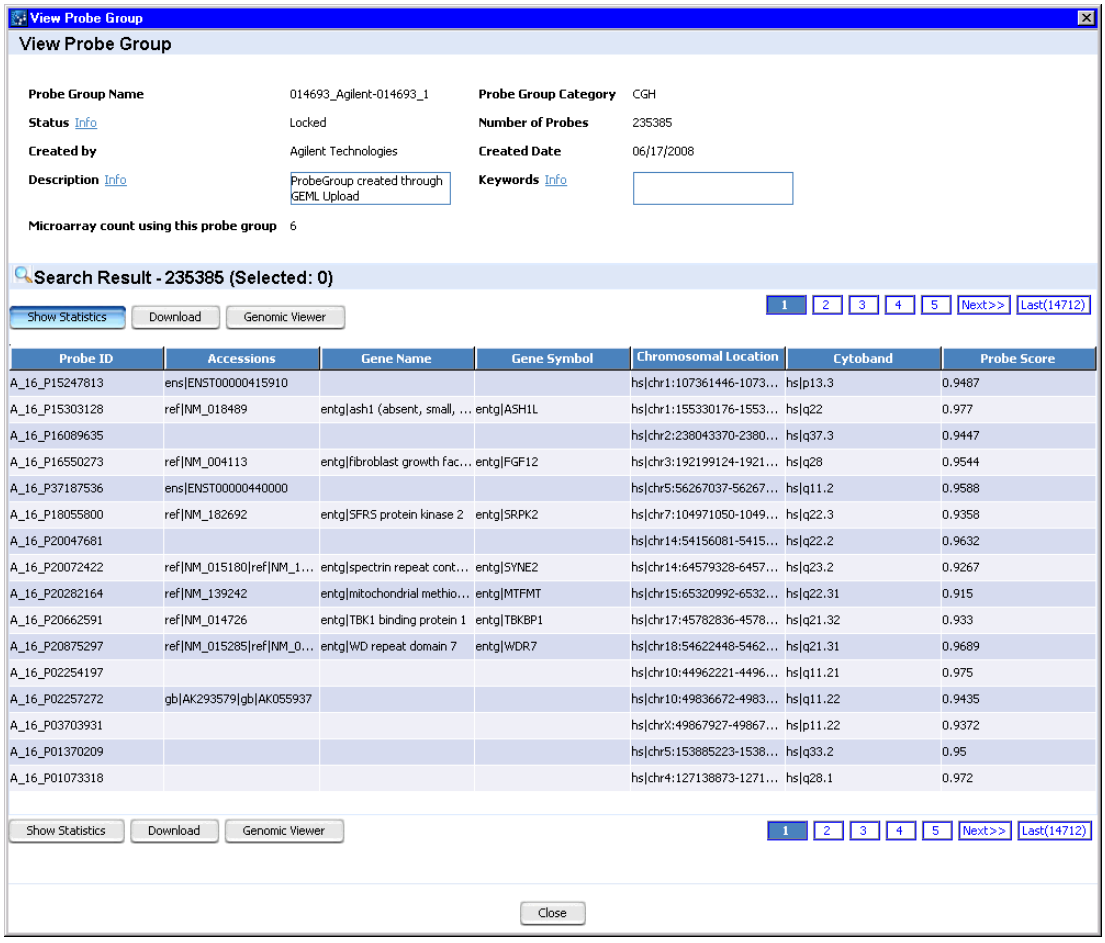


Figure 189 View Probe Group dialog box

Purpose: Lets you view the properties and probe content of a probe group. See "To view a probe group" on page 228.

To open: In the **Actions** column of the search results of a probe group search, next to the desired probe group, click . See "To search for probe groups" on page 224.

Alternatively, in the **Design Data** pane of the Navigator, right-click the name of the desired probe group, then click **View.**

Properties All properties in the top pane of the dialog box are read-only.

Property	Details
Probe Group Name	Name of the probe group, assigned by its creator.
Probe Group Category	(CGH Application type only) One of these terms appears: • **CGH** – The probe group is a standard CGH probe group, and can be used in both standard and CGH+SNP microarray designs. • **CGH+SNP** – The probe group contains only Agilent SNP probes, and can only be used in CGH+SNP microarray designs.
Status	**Incomplete** – Probe group can be edited. **Locked** – Probe group cannot be edited, nor can it be unlocked.
Number of Probes	Total number of probes in the probe group.
Created by	User who defined the probe group and saved it.
Date Created	Date the probe group was first saved.
Description	Brief description of probe group, assigned by its creator.
Keywords	One or more search keywords. Multiple keywords are separated by commas.
Microarray count using this Probe Group	The number of microarrays on your server that use this probe group.

Search Result Pane

Table of probes The table lists the probes in the probe group by Probe ID. Additional annotation can also appear.

Show Statistics Opens the Probe Statistics dialog box, where you can view the Probe IDs and sequences of the probes in the probe group. See "Probe Statistics" on page 829.

Download Opens the Download Probe Group dialog box, where you can download the probe group in one of several formats. See "Download Probe Group" on page 732.

Genomic Viewer (Available for the CGH, ChIP-on-chip, and CH3 application types) Opens the Genomic Viewer, where you can view the locations of the probes in the probe group graphically next to the chromosomes and genes of the genome. See "To plot the genomic locations of probes" on page 203.

(Page buttons) If available, these buttons let you to go to different pages of the probe list.

Close Closes the dialog box.

File Formats

This section contains descriptions of the files that you can upload and download through eArray$_{XD}$. Formats appear in alphabetical order.

Accessions

Purpose: For upload of accession values for the searches referenced in the following topics:

- "To use the Probe Search tool to find probes" on page 92
- "To search for baits" on page 358
- "To set up a GE Probe Design job" on page 167
- "To do an Advanced Interval Finder Search" on page 364
- "To do an Advanced Exon Interval Finder Search" on page 367

Details: Create a plain text file (*.txt) that contains one accession per line. Enter accession values without sources, as the sources are already supplied by eArray. So sgd|Q0055 will be only `Q0055`.

Advanced Search Interval

Purpose: For upload of genomic intervals, spacing, and filter settings for an Advanced HD Genomic Intervals Search for probes. See "To do an Advanced Genomic Intervals HD Search for probes" on page 117.

Details: Create a plain text (*.txt) file that contains one interval per line. You can include column headings in the first line of the file, but eArray does not interpret them. Each line must contain the following entries, separated by tabs, in this order:

1 **Genomic Interval** – A cytoband (for example, 1p36.33) or a chromosomal location, for example:

`chr1:1-500001`

`chr1` (all of chromosome 1)

`chrX:2000500` (X chromosome from 2000500 to the end)

For a given search, all the intervals must be of the same type (for example, all chromosomal locations or all cytobands).

2 **Average Spacing** – Average number of base pairs between each of the retrieved probes within the interval.

3 **TM Filtered** – Yes or No. For this interval, removes probes with TMs that lead to poor performance on the Agilent platform.

4 **HM Filtered** – Yes or No. Removes probes that bind to more than one location on the genome. (Homology filtering)

Example:

```
chr1:1-1000000        500   Yes  Yes
chr2:500-5000000      1000  Yes  No
chr2:5000000-8000000 1000  Yes  Yes
```

BaitID

Purpose: For upload of bait IDs for a bait search. See "To search for baits" on page 358.

Details: Create a plain text (*.txt) file that contains one bait ID per line.

Example:

```
AGN_PPRID379037179
AGN_PPRID379045351
AGN_PPRID379045442
AGN_PPRID379045617
AGN_PPRID379035501
AGN_PPRID379036391
```

Bait Sequence

Purpose: For upload of bait sequence data for a bait search. See "To search for baits" on page 358.

Details: Create a plain text (*.txt) file that contains one sequence per line.

Example:

```
ACGTAGCTAGAGCTAGCTGAGCTGAGCTGAGATCGATGCTAGTGATCGAT
ATTATGGATGATTGATGAGTAGTAGAGAGGCGCGCTAGCATCGCTAGCTA
ACGTACGATAGCGCGCAGCTAATGATGACGCAGATCAGAGACGATCGCGA
CCTACCGATGTCTGCTACAGACGGCGGGGATGACGATACGATACGGCGTGA
```

NOTE In the example above, the search sequences would actually need to be of a length that is supported by the program. The program currently supports a bait length of 120 nucleotides for all users.

BED

Purpose: Downloadable file that contains annotation track data that can be read by a compatible genome browser. In general, for downloads from eArray, BED files contain probe names and their associated genomic locations.

Details: A bed file is a tab-delimited text file with an extension of .bed. For downloads from eArray, the BED file has the columns listed below, with no header row. Each line contains information for one probe.

1. Chromosome
2. Starting base pair
3. Ending base pair
4. Probe ID

Example:

```
chr1    1003797    1003857    A_18_P21423305
chr1    1007923    1007972    A_16_P00298861
chr1    1012399    1012447    A_18_P21424558
```

NOTE

- For BED format bait downloads, the file also contains strand information. Baits can have a sequence similar to the sense strand of the DNA (+), or the antisense strand (–).
- Chromosomal locations are given in UCSC format (zero-based, half open format). For SNP probes, chromosomal locations refer to the position in the genome of the given SNP.

Chromosomal Location

Purpose: For upload of chromosomal locations for a Simple Search for probes or baits. See "To use the Probe Search tool to find probes" on page 92 and "To search for baits" on page 358.

Details: Create a plain text (*.txt) file that contains one chromosomal location per line. Use the format illustrated in the following examples:

- `chr1:1-500001` (Chromosome 1, base pairs 1 to 500001)
- `chr1` (all of chromosome 1)
- `chrX:2000500` (X chromosome from 2000500 to the end)

Complete (for baits)

Purpose: For upload or download of bait data. See "To upload baits and annotation" on page 374 and "To download baits" on page 389.

NOTE The Complete file format is different for the Expression, CGH, CH3. and ChIP-on-chip application types. See "Complete (for probes)" on page 881.

Details:

- For downloads, the files are tab-delimited text (*.tdt) files that contain the columns indicated in the table below. You can open the file in a spreadsheet program.

- For uploads, create a tab-delimited text (*.txt or *.tdt) file that contains the columns in the table below. You can also create a Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format

Type of data	Requirements
BaitID	A unique identifier for the bait sequence, containing up to 15 characters. Bait ID cannot be blank.
Bait Sequence	The base sequence of the bait, in 5' to 3' orientation. It must contain only the capital characters A, C, G, and T. All baits in the file must have the same length. Sequence cannot be blank. The program supports a bait length of 120 nucleotides for all users.
Genomic Interval	The segment of the genome associated with the bait, for example `chr1:1-10000`. This column can be blank.
Bait genomic location	The exact position of the bait in the genome, for example `chr1:1-169`. This column can be blank.
Accessions	Unique identifier(s) that refer to a nucleotide sequence that is a target for the associated probe and/or a protein sequence that is a product of the target. Accessions are represented in a <source>|<ID> pair format. <source> is the symbol of the database from which the accession was derived and <ID> is the unique identifier accession. For example, `ref|NM_015752` is a <source>|<ID> pair where `ref` (NCBI Refseq) is the source and `NM_015752` is the unique identifier for that source. The Accessions field can contain multiple <source>|<ID> pairs, delimited by pipe "|" characters. For example, `gi|7657630|ref|NM_015752` is an allowable accession that gives both an NCBI gene identifier (`gi`), and a Refseq identifier (`ref`) for the same probe sequence. Accessions can be blank.
GeneSymbols	A unique abbreviation for a gene name. GeneSymbols can be blank.
Description	A description of a phenotype, gene product, or its function. Description can be blank.
Strand	The orientation of the bait, which can be + (sense) or – (antisense). The program interprets blank entries as **sense.**

Complete (for probes)

Purpose: For upload or download of probe data. See "Uploading Probes" on page 158 and "To download probes" on page 206.

NOTE The Complete file format is different for the SureSelect Target Enrichment application type. see "Complete (for baits)" on page 879.

Details:

- For downloads, the files are tab-delimited text (*.tdt) files that contain the columns indicated in the table below. You can open the file in a spreadsheet program.
- For uploads, create a tab-delimited text (*.txt or *.tdt) file that contains the columns in the table below. You can also create a Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

Type of data	Requirements
ProbeID	A unique identifier for the probe sequence, containing up to 15 characters. Probe ID cannot be blank.
Sequence	The base sequence of the probe, in 5' to 3' orientation. The sequence must be from 20 to 60 nucleotides in length, and must only contain the capital characters A, C, G, and T. Sequence cannot be blank.
TargetID	Also referred to as the primary accession, TargetID uniquely identifies the sequence that most exemplifies the target transcript. Only one annotation value is allowed, and it can include or omit the source designation. For example, both `ref|AK075564` and `AK075564` are acceptable. TargetID can be blank.

Type of data	Requirements
Accessions	Unique identifier(s) that refer to a nucleotide sequence that is a target for the associated probe and/or a protein sequence that is a product of the target. Accessions are represented in a <source>|<ID> pair format. <source> is the symbol of the database from which the accession was derived and <ID> is the unique identifier accession. For example, `ref|NM_015752` is a <source>|<ID> pair where `ref` (NCBI Refseq) is the source and `NM_015752` is the unique identifier for that source. The Accessions field can contain multiple <source>|<ID> pairs, delimited by pipe "|" characters. For example, `gi|7657630|ref|NM_015752` is an allowable accession that gives both an NCBI gene identifier (`gi`), and a Refseq identifier (`ref`) for the same probe sequence. Accessions can be blank.
GeneSymbols	A unique abbreviation for a gene name. GeneSymbols can be blank.
Description	A description of a phenotype, gene product, or its function. Description can be blank.
ChromosomalLocation	The chromosome number and the location of the sequence on the chromosome, expressed in the following example notation: `chr19:11392326-11391822` Enter only one chromosomal location. It can include or omit the source, and it can be blank.

Custom Exclusion Interval

Purpose: For upload of genomic intervals to exclude in HD probe searches. See "Searching for Agilent High Density (HD) Probes" on page 109.

Details: Create a plain text (*.txt) file that contains one genomic interval per line.

Cytoband

Purpose: For upload of cytobands for the types of searches referenced in the following topics:

- "To use the Probe Search tool to find probes" on page 92
- "To search for baits" on page 358
- "To do an Advanced Interval Finder Search" on page 364
- "To do an Advanced Exon Interval Finder Search" on page 367

Details: Create a plain text (*.txt) file that contains one cytoband per line. For cytobands, use the format illustrated by the examples below:

- `1p12.123` (Chromosome 1, p arm, band 1, sub band 2, sub sub band 1, micro band 2, sub micro band 3)
- `1p1` (Chromosome 1, p arm, band 1)
- `1p1-1p2` (Gene interval range from the beginning of 1p1 to the end of 1p2)

FASTA

Purpose: The FASTA file format is widely used to represent biosequence information. eArray specifically uses FASTA format files to upload nucleic acid sequence information, such as user-defined genomes, and target sequences for generating probes with Simple Tiling and Gene Expression (GE) probe design. It is also available as a file format when you download probes and baits.

Refer to these topics:

- "To set up a GE Probe Design job" on page 167
- "To set up a Simple Tiling job" on page 174
- "To download probes" on page 206
- "To download baits" on page 389

Details: FASTA files are plain text (*.txt) files that conform to specific guidelines:

- A sequence in FASTA format begins with a single description line, followed by one or more lines of sequence data. More than one sequence can be specified in a single FASTA format file.
- The description line is distinguished from the sequence data by a greater-than (">") symbol as the first character in the line. In general, include only the sequence identifier in the description line. If you include other annotation in the description line, it must not exceed 255 characters (including spaces).
- The program interprets the sequence ID for a given FASTA record as the character string that occurs after the ">" symbol, before the first space, on the annotation line. The sequence ID must not exceed 64 characters (including spaces).
- The associated sequences must be represented in an abbreviated version of the IUB/IUPAC nucleic acid code. All sequence data must contain only the capital characters A, T, C, G. eArray masks all other characters out of the sequence.

Example of two FASTA-formatted sequences in a file:

```
>NM_012514 Rattus norvegicus breast cancer 1 (Brca1), mRNA
CGCTGGTGCAACTCGAAGACCTATCTCCTTCCCGGGGGGGCTTCTCCGGCATTTAGGC
CTCGGCGTTTGGAAGTACGGAGGTTTTTCTCGGAAGAAAGTTCACTGGAAGTGGAAGA
AATGGATTTATCTGCTGTTCGAATTCAAGAAGTACAAAATGTCCTTCATGCTATGCAG
```

```
AAAATCTTGGAGTGTCCAATCTGTTTGGAACTGATCAAAGAACCGGTTTCCACACAGT
GCGACCACATATTTTGCAAATTTTGTATGCTGAAACTCCTTAACCAGAAGAAAGGACC
TTCCCAGTGTCCTTTGTGTAAGAATGAGATAACCAAAAGGAGCCTACAAGGAAGTGCA
AGG
>NM_012515
TGTGGATCTTTCCAGAACAGCAGTTGCAATCACTATGTCTCAATCCTGGGTACCCGCC
GTGGGCCTCACTCTGGTGCCCAGCCTGGGGGGCTTCATGGGAGCCTACTTTGTGCGTG
GTGAGGGCCTCCGCTGGTATGCTAGCTTGCAGAAACCCTCCTGGCATCCGCCTCGCTG
GACACTCGCTCCCATCTGGGGCACACTGTATTCGGCCATGGGGTATGGCTCCTACATA
ATCTGGAAAGAGCTGGGAGGTTTCACAGAGGAGGCTATGGTTCCCTTGGGTCTCTACA
CTGGTCAGCT
```

GEML

The Gene Expression Markup Language (GEML) is a file format for storing DNA microarray and gene expression data. GEML is an open-standard XML format that enables exchange of data between gene expression databases and analysis systems. GEML stores the data collection methodology used, but does not make assumptions about the meanings of measurements. This lets the program normalize, integrate, and compare data across methodologies. GEML handles expression profile data and allows scan images and chip layouts (or patterns) to be easily referenced and tracked. GEML is independent of any particular database schema.

Gene Annotations

Purpose: For upload of gene annotation data for HD-CGH Gene Annotations Searches for probes. See "To do a Simple Gene Annotations HD Search for probes" on page 120.

Details: Create a plain text (*.txt) file that contains one annotation per line. Annotations can be either accession numbers (for example, `NM_016660` or `AY884282`) or gene symbols (for example, `H3N2` or `CTSB`), but for a given search the annotations must all be of the same type.

Gene Symbols

Purpose: For upload of gene symbols as search criteria for the types of searches referenced in the following topics:

- "To search for baits" on page 358
- "To use the Probe Search tool to find probes" on page 92
- "To do an Advanced Interval Finder Search" on page 364
- "To do an Advanced Exon Interval Finder Search" on page 367

Details: Create a plain text (*.txt) file that contains on gene symbol per line.

Example:

```
ACOX2
BRCA1
HRH4
TXNDC1
```

Genome

Purpose: For import of a user-defined genome. See "To import a new genome" on page 66.

Details: Create a *.zip file that contains one or more FASTA format sequence files. Typically, each FASTA formatted sequence file contains the name and sequence of one of the chromosomes of the organism. The *.zip file must contain sequences for a single genome. In addition, the *.zip file must contain the sequence data for all of the desired chromosomes of the genome—to "add" sequences to the genome, you must re-import the entire genome with the added sequences.

Each FASTA file must adhere to the standard FASTA format (see "FASTA" on page 884) and also the following specific guidelines:

- Each FASTA file within the *.zip file must have a unique name.

- The header line in each sequence file must be the name of the specific chromosome associated with the sequence in the file. The name must not match any other chromosome name in your genome import. This name becomes the identifier that you must use throughout eArray$_{XD}$ to identify genomic intervals on this chromosome, chromosomal locations, and the like.
- The header must start with a greater than ">" character, and contain fewer than 20 characters. Further, the header must contain only letters and numbers (no spaces, underscores, or other special characters).
- Each file must contain exactly one nucleotide sequence.
- The sequence in each file must be at least 60 nucleotides in length.
- You can "soft mask" repeat sequences. Within the sequence, enter repeat regions as lower case letters. If you mark **Genome is Soft-Masked** when you import the genome, this information is retained. Otherwise the program converts these characters to capital characters before it stores the sequences in the database.
- When the program imports your sequence files, it removes all tabs, spaces, and blank lines from each sequence, and converts other non-ACGT characters to N characters.

Example of one FASTA format chromosome file:

```
>chr1
ACGACGATACGAGACTAGACTACGACTACGATACGATCGGCGCATCTACGTgtgcata
gcaggcgctagcgctagcgatcgatcagcatcagtTAACTGACGCGCGATCGATACGA
TAGAGCTACGATCGAGATAGCATAGCATCGCGCGCGCGATATATCGATCAGCATGCGC
GATCGATGCTACGCGCGATAGATATGACTGCATGCAGCGATCGATGCTAGCGATCGTA
GCTGATCGATCGTAGTGCGCGAGCTATCGTAGTCGATT
```

Genomic Intervals (Genomic Tiling)

Purpose: For upload of genomic intervals to be tiled by the Genomic Tiling process. See "To set up a Genomic Tiling job" on page 176.

Details: Create a plain text (*.txt) file that contains one genomic interval per line. The intervals must be associated with the genome of the species you select when you set up the Genomic Tiling job. Use the genomic interval format illustrated in these examples:

- `chr1:1-500001` (Chromosome 1, base pairs 1 to 500001)
- `chr1` (all of chromosome 1)
- `chrX:2000500` (X chromosome from 2000500 to the end)

Genomic Intervals (Simple HD and SNP Probe Searches)

Purpose: For upload of genomic intervals for a Simple Genomic Intervals HD Search for probes or a SNP Probe Search. See "To do a Simple Genomic Intervals HD Search for probes" on page 111 and "To do a SNP probe search by genomic intervals" on page 143.

Details: Create a plain text (*.txt) file that contains one genomic interval per line. You can enter cytobands or chromosomal locations, but all intervals must be of the same type.

Examples:

Chromosomal locations:

- `chr1:1-500001` (Chromosome 1, base pairs 1 to 500001)
- `chr1` (all of chromosome 1)
- `chrX:2000500` (X chromosome from 2000500 to the end)

Cytobands:

- `1p12.123` (Chromosome 1, p arm, band 1, sub band 2, sub sub band 1, micro band 2, sub micro band 3)
- `1p1` (Chromosome 1, p arm, band 1)
- `1p1-1p2` (Gene interval range from the beginning of 1p1 to the end of 1p2)

Minimal (for baits)

Purpose: For upload or download of bait data. See "To upload baits and annotation" on page 374 and "To download baits" on page 389.

NOTE The Minimal file format is different for microarray-related application types (Expression, CGH, ChIP-on-chip, CH3, and microRNA). See "Minimal (for probes)" on page 890.

Details:

- For downloads, the files are tab-delimited text (*.tdt) files that contain the columns indicated in the table below.
- For uploads, create a tab-delimited text (*.txt or *.tdt) file that contains the columns in the table below. You can also create a Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format. Your file can contain column headings, although the program does not interpret them.

Type of data	Requirements
BaitID	A unique identifier for the bait sequence, containing up to 15 characters. BaitID cannot be blank.
Sequence	The base sequence of the bait, in 5' to 3' orientation. The sequence must only contain the capital characters A, C, G, and T. All baits in the file must have the same length. The program supports a bait length of 120 nucleotides for all users.

Minimal (for probes)

Purpose: For upload or download of probe data. See "Uploading Probes" on page 158 and "To download probes" on page 206.

NOTE The Minimal file format is different for the SureSelect Target Enrichment application type. See "Minimal (for baits)" on page 889.

Details:

- For downloads, the files are tab-delimited text (*.tdt) files that contain the columns indicated in the table below.
- For uploads, create a tab-delimited text (*.txt or *.tdt) file that contains the columns in the table below. You can also create a Microsoft Excel (*.xls) file. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format. For most probe uploads, your file can contain column headings, although the program does not interpret column headings. For GE Probe Quality checks, do *not* include column headings in your probe file.

Type of data	Requirements
ProbeID	A unique identifier for the probe or bait sequence, containing up to 15 characters. Probe ID cannot be blank.
Sequence	The base sequence of the probe, in 5' to 3' orientation. The sequence must be from 20 to 60 nucleotides in length, and must only contain the capital characters A, C, G, and T. Sequence cannot be blank.

ProbeID

Purpose: For upload of Probe IDs for a Probe Search or an HD Probe ID Search for probes. See "To use the Probe Search tool to find probes" on page 92 and "To do a Probe ID HD Search for probes" on page 125.

Details: Create a plain text (*.txt) file that contains one probe ID per line.

Example:

```
A_14_P100053
A_14_P100055
A_14_P100056
A_14_P100057
A_14_P100059
A_14_P100227
```

Probe Sequence

Purpose: For upload of probe sequence data for a Search for probes. See "To use the Probe Search tool to find probes" on page 92.

Details: Create a plain text (*.txt) file that contains one sequence per line.

Example:

```
ACGTAGCTAGAGCTAGCTGAGCTGAGCTGAGATCGATGCTAGTGATCGAT
ATTATGGATGATTGATGAGTAGTAGAGAGGCGCGCTAGCATCGCTAGCTA
ACGTACGATAGCGCGCAGCTAATGATGACGCAGATCAGAGACGATCGCGA
CCTACCGATGTCTGCTACAGACGGCGGGGATGACGATACGATACGGCGTG
```

TDT files

The Tab-Delimited Text (TDT) file format is a general purpose file format used extensively in eArray to both upload and download tables of data. TDT files are plain text files that can be created and read by word processing and spreadsheet programs.

In a TDT file, items within a row of the data table are separated by <TAB> characters, and each row ends with a <RETURN> character. Blank or missing data items still require a <TAB> character. In this way, TDT files can represent the structure and content of a data table with any number of rows and columns.

For example, if you have a data table that looks like this:

blue	2334	Lincoln
red		Jefferson
green	12	
	38	Washington

Then the TDT file would look like this:

```
blue <TAB> 2334 <TAB> Lincoln <RETURN>
red <TAB> <TAB> Jefferson <RETURN>
green <TAB> 12 <TAB> <RETURN>
<TAB> 38 <TAB> Washington <RETURN>
```

Note: If you create this TDT file with a word processor, <TAB> indicates you press the **Tab** key, and <RETURN> indicates that you press the **Return** or **Enter** key on your keyboard.

TDT is not the native file format for most word processing and spreadsheet programs. When you save the file, use the **Save As** command, and save the file as a text file. In spreadsheet programs, you may need to identify the type of text file as **tab-delimited.** Similarly, when you open a downloaded TDT file in a spreadsheet program, you may need to select **tab-delimited** as the file type.

In a TDT file from eArray, the first line of the file is usually a row of column headers. However, when you upload a TDT file, the program does not interpret column header data, and treats column headers in your file as actual data,

unless you mark **My uploaded file contains column headings** during the upload process. For GE Probe Quality checks, *do not* include column headings in your file.

In the special case of a TDT file that represents a table with a single column of data, the “tab-delimited” text file actually contains no <TAB> characters. The data items are actually separated by <RETURN> characters.

Design Checklists

Before you submit a library or microarray design to Agilent Manufacturing, you must read and mark all of the items on the appropriate design checklist. The questions in the checklist are intended to be reminders to help increase the quality of your microarray design or library before you submit it to Agilent.

CGH design checklist

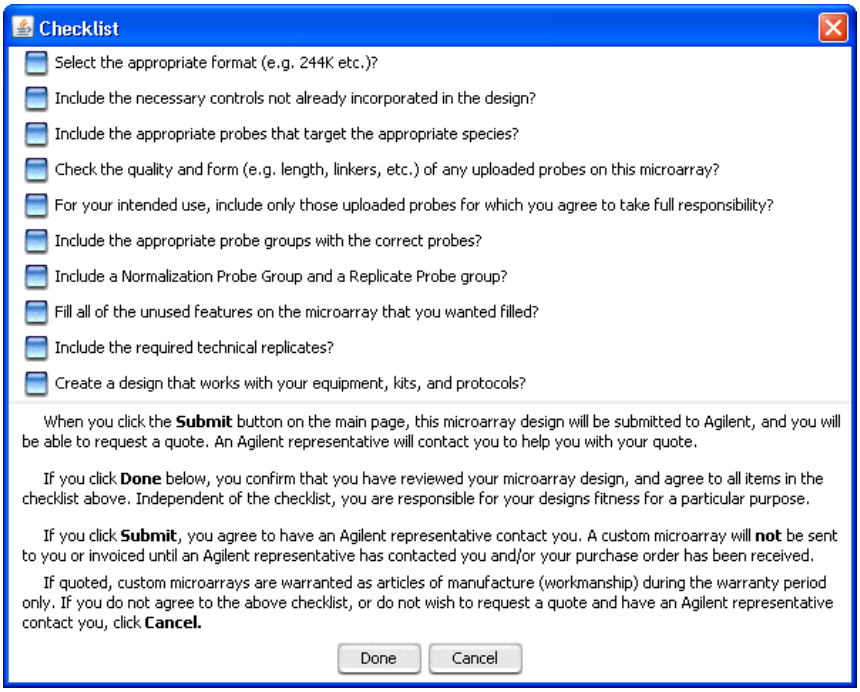


Figure 190 Checklist for CGH designs

ChIP, CH3, and Expression design checklist

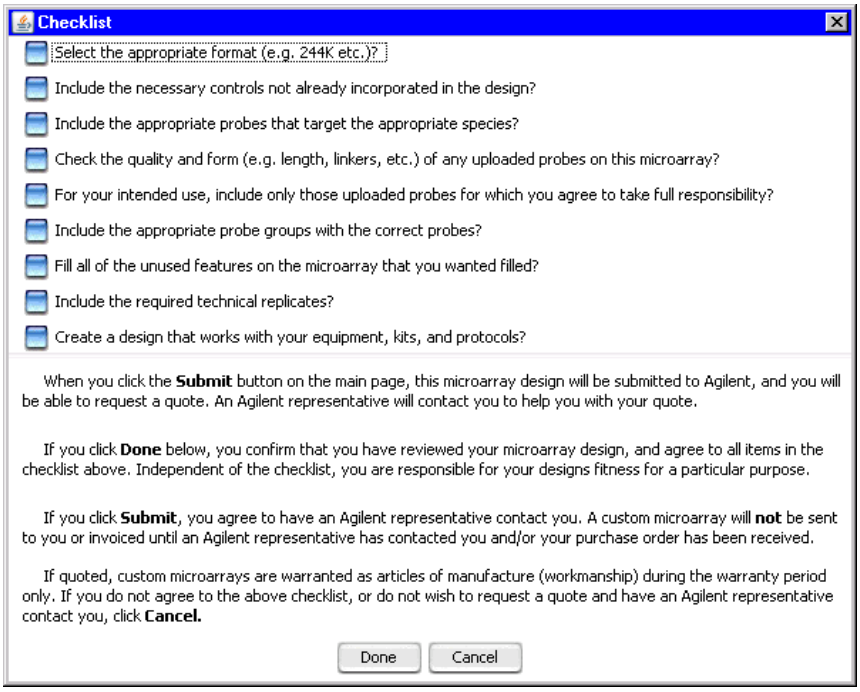


Figure 191 Checklist for ChIP, CH3, and Expression designs

microRNA design checklist

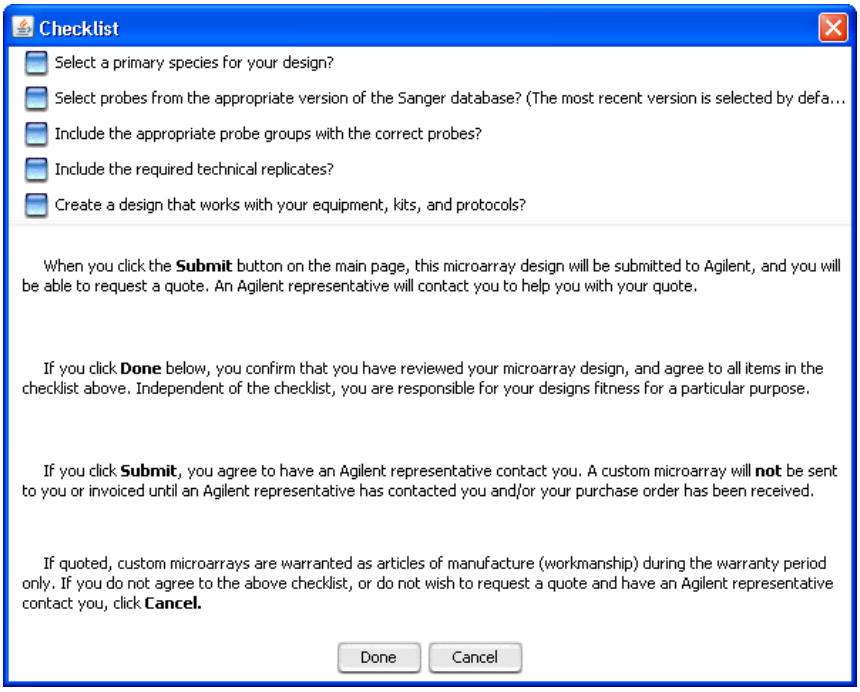


Figure 192 Checklist for microRNA designs

SureSelect Target Enrichment library checklist

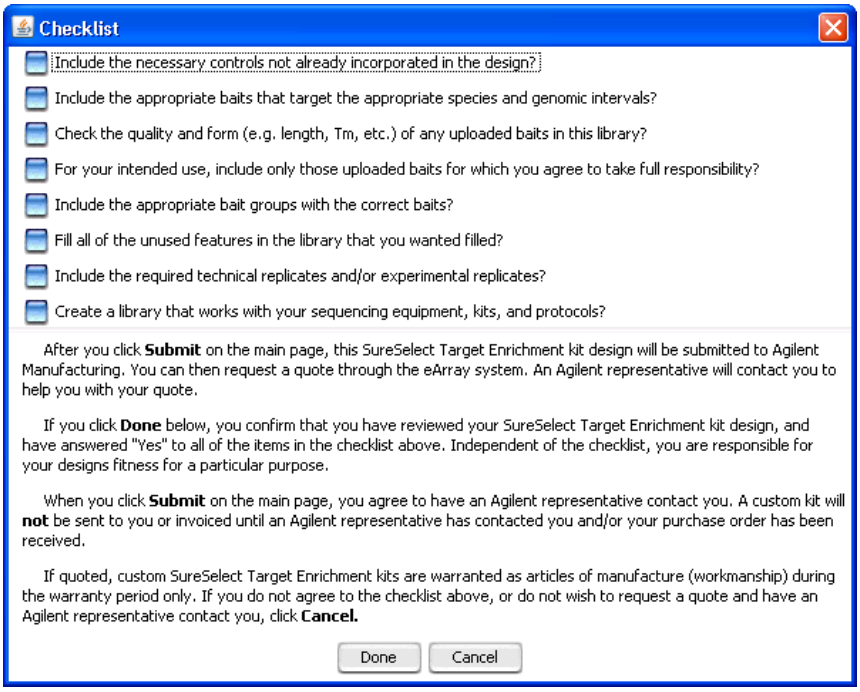


Figure 193 Checklist for SureSelect Target Enrichment libraries

Custom Design Guidance

Agilent offers the following application-specific guidance to help you create optimal microarray designs.

Expression array design guidance

When you create custom Gene Expression microarray designs, design and include the following types of probe sets:

- Agilent's negative control probes for optimal background-subtraction with the Agilent Feature Extraction software. Agilent negative control probes are included in Agilent's QC grid. If you use custom negative control probes, identify them as non-control probes when you use them with Agilent Feature Extraction software.
- Replicated non-control probes for use in the Multiplicative Detrending step of the Agilent Feature Extraction software. The Multiplicative Detrending step detects and corrects for trends in array uniformity and uses replicated non-control probes as a default. A minimum of 15 probes should be replicated 5-10 times on each microarray design. If replicated probes are not used, the default settings should be adjusted in the Feature Extraction protocol.
- Probe set representing non-differentially expressed genes for use in accurate normalization of microarray experiments, where typical normalization assumptions about differential expression are not met due to a relatively low probe count or strong bias in differential expression. These probes should span the full range of signal intensity for optimal normalization. Agilent recommends that a minimum of 1% of the non control probes be part of this list for each custom design. If prior knowledge of non-differentially expressed genes is unavailable, we recommend that these probes be selected to randomly cover the dynamic range of the experiment. For these custom Gene Expression designs, microarray data should be normalized using data from these control probes. For custom "whole genome" type arrays, inclusion of a normalization gene list is generally not necessary.

The process for generation and use of a DyeNorm Gene List for two-color microarray data analysis is described in the *Feature Extraction Software User Guide*. The non-differentially expressed gene list can also be used for one-color microarray data normalization in downstream applications such as GeneSpring GX, as described in the *GeneSpring GX Software User Manual*.

How eArray handles highly homologous sequences

Before it designs probes, eArray first clusters target sequences and transcriptome sequences. Highly homologous sequences are considered as a single entity when the program evaluates cross-hybridization problems. Two sequences are clustered together if they are over 95% identical over 95% of both sequence lengths.

Highly homologous sequences can simply be a result of errors during the preparation of input sequence files. Also, it is usually not possible to find distinctive sequences that are long enough to place probes for highly homologous sequences. Because the program clusters these kinds of sequences, file processing errors are ignored and high-quality probes that do not cross-hybridize to other sequences can be selected for all targets.

If eArray designs a probe that binds to more than one of the target or transcriptome sequences within a cluster, it does not report or consider any potential cross-hybridization problems (X-hyb). Thus, if you notice that a probe binds to more than one target, but eArray does not report this, those targets might be members of the same cluster. After you submit a GE Probe Design job, and eArray completes it, you can download a MOST_cluster file that lists the clusters that eArray generated during the design process. See "To download probe design or tiling results" on page 182.

CGH array design guidance

CGH Normalization Probes

When you create a custom CGH design, the design should contain content that enables accurate dye normalization during downstream data processing. The dye normalization step corrects systematic differences in overall signal intensities between the red and green channels. The assumption is that these overall intensities should be the same. If your custom design fails this assumption, Agilent recommends that you add a normalization probe group to serve this purpose.

If an Agilent Normalization Probe Group exists for a given array format and species, the program adds it to your array automatically. If you remove this probe group, you should include a set of probes that represent non-aberrant/non-variant regions for proper normalization, ideally selected to cover all autosomes. When you design a whole genome array, you do not need to include a specific normalization probe group, since there should be enough non-aberrant regions for proper normalization.

The Agilent or user-defined normalization probe group should be used in Feature Extraction to properly normalize the array. A dye normalization probe group has a minimum size requirement. Its probes must occupy at least 1% of the total number of features on the array after filtering. If you do not use an Agilent or user-defined normalization probe group, and the assumptions of dye normalization are not met within reason, Feature Extraction will not be able to correct all of the systematic dye bias. This will affect copy number estimates. For information on how to use the normalization probe group for normalization in Feature Extraction, see the section *View or change grid template properties* in the *Feature Extraction Software User Guide*. Under *Browse File*, the topic *Change the default DyeNorm gene list* may be especially useful.

CGH Replicate Probes

When you create a custom CGH design, you should include a set of replicate probes. If an Agilent replicate probe group exists for a given array format and species, the program adds it to your array automatically. Replicate this probe group five times. These probes are used to calculate the Reproducibility QC metric in Feature Extraction and DNA Analytics. This metric is set to the median %CV of background-subtracted signal for these replicate probes after outlier rejection. If you remove this probe group, include a set of replicate probes so that these metric can be calculated. For user-defined replicate probe groups, include a minimum of 300 probes replicated five times. For more information on the Reproducibility QC metric, see the microarray QC metrics in the *DNA Analytics User Guide*.

Additional guidance

An extensive, additional set of FAQs about the design of CGH microarrays is available in the online help on the eArray Web site. To view these FAQs, follow these steps:

1 Go to https://earray.chem.agilent.com

The eArray login page appears. You do not need to log in to view the online help.

2 Click **Help.**

The online help opens.

3 Click **FAQ.**

microRNA Design Guidance

The Agilent microRNA microarray solution is a robust and sensitive method for the detection of microRNAs from total RNA. Agilent makes Human, Mouse and Rat catalog arrays that have been designed and empirically tested to supply sensitive and specific measurements of all microRNAs from the Sanger miRBase database for these species.

eArray lets you design custom microRNA microarrays. You can design microarrays that measure the microRNAs of your choice from the Sanger miRBase database. The principles used in the design of Agilent catalog arrays, outlined below, are also applied for these custom arrays. This approach reduces uncertainty in the design of custom microarrays, while continuing to supply the most sensitive and robust assay to meet your research needs. eArray gives you the flexibility to study the microRNAs of your choice on the 8x15K format.

Agilent microRNA array design principles

Before designing a custom microRNA array, it is useful to understand some of the underlying principles of the Agilent microRNA platform:

- **Probe design and labeling methods that are linked.** The mature microRNAs are labeled via the ligation of a Cy3 conjugated pCp molecule to the 3' end of the microRNA This labeling reaction adds an additional "C" base to the 3' end of all of the labeled RNA molecules. During probe design, we take advantage of this "C" base, by adding an additional "G" to the 5' end of the active probe sequence. The addition of this G:C base pair to the probe:microRNA interaction helps stabilize the interaction, and gives some additional selectivity to labeled mature microRNAs.
- **Multiple probes and probe replicates for each microRNA.** Each microRNA represented on an Agilent microRNA array is measured by multiple probes. In addition, each probe sequence is replicated multiple times. This replication allows for both improved robustness, as outlier features are removed during data summarization in Feature Extraction, and improved sensitivity, as the presence of the probe replicates helps drive the hybridization reaction towards equilibrium.

- **Robust data summarization.** The data summarization procedures used in the Agilent Feature Extraction software allow for the summarization of the multiple probes and probe replicates into a robust measurement for each microRNA. This measurement, the "TotalGeneSignal," is found in both of the Feature Extraction output files: the full text and "GeneView" files. Details about data summarization can be found in the Feature Extraction Reference Guide.

Guidance for design of microRNA custom microarrays

Agilent has predesigned probes to all the mature microRNAs for all species* in the most recent Sanger miRBase release. Both the identification of the appropriate probe sequences and the methods implemented for custom microRNA microarray design are designed to supply robust, sensitive, and specific measurements of your microRNAs of interest. All designs are based on the 8x15K format.

NOTE

Although Agilent has designed probes for all species in the Sanger miRBase database, users should be aware that the Agilent labeling protocol requires an accessible hydroxyl group on the 3′ end of the microRNA for ligation of a dye-conjugated pCp molecule. microRNAs from some species (mostly plants) have a 3′ modification which can interfere with the Agilent labeling method. To study 3′-modified microRNAs, you will likely need to use alternative labeling methods, and should conduct experiments to optimize the assay conditions.

General Design Guidance

- **Probe search:** Searching for probes in eArray is based on the premise that each microRNA is represented by multiple probes. Probes are therefore returned in groups, based on the microRNA to which they are designed. You can search for probes against multiple miRBase builds, but probes for a microRNA present in the latest build are returned only when that build is included in the search. See below for more information on multiple miRBase build designs.

- **Microarray Formats:** Currently, only the 8x15K format is enabled for microRNA microarrays, because microRNA probe and assay design, including probe replicates, RNA input requirements, and labeling reaction conditions are based on that format. To measure more microRNAs than can be included on this format, a *microarray set* can be created. To create microarray sets, you must use the eArray Web site. For more information on microarray sets, see the online help on the eArray Web site.
- **Microarray Layout:** Selected probes will be laid out using the design principles outlined above. You can select whether to represent each microRNA with 16 or 20 features. Twenty features returns slightly more robust data, while 16 features lets you include more microRNAs on each array. All probes are randomly distributed on the array. This yields the most robust downstream data because probe replicates are spread across the entire array. Any space that is not used for the selected probes is filled by a structural control and considered "blank." These "blank" features are ignored in the downstream analysis.

Guidance for specific cases

- **Creating an array from multiple miRBase build designs**

  The eArray probe database contains probes that are designed to the current Sanger miRBase release. It also contains probes to microRNAs that were present in selected former database builds that may have been removed or changed in the intervening periods. For the earliest Sanger miRBase builds, eArray only contains probes for selected species (9.1, human only; 10.1 and 11.0, human, mouse and rat).

  It is possible to design an array containing probes to microRNAs from multiple database builds. The systematic ID given to the "old-build specific" microRNAs will be appended with the database version (e.g., hsa-miR-139_v9.1). Note that not all microRNA sequence changes will result in new probes being designed (e.g., addition of one base to the 5' end). If the probe sequences did not change, the microRNA is considered unchanged.

  - Due to the data processing steps in Feature Extraction, each microRNA sequence being measured must have a unique systematic name, to enable proper TotalGeneSignal calculation.
  - Combined with the fact that some microRNAs may be present in multiple database builds with the same name, but different sequences, requires us to alter the previous names.

microRNA sequences from previous builds that are unchanged in the current build can be searched in the most recent build only. microRNAs with name changes between builds can be searched in both builds, but the primary annotation comes from the newest build.

- **Creating multi-species arrays** – It is possible to design a multi-species array using eArray. Due to the similarity of certain cross-species microRNAs and the design of the microRNA assay, the layout of such designs needs to be done very carefully. This system is designed to give you as much flexibility as possible to design multi-species arrays while maintaining the Agilent microRNA microarray design principles.

  Primary species must be identified. When microRNAs are selected for a given design from multiple species and those microRNAs are identical, probes to only one of those microRNAs will be included in the design. A species priority order is used to select which probes to include in the design, with the primary species getting top priority. Users must select the primary species when creating a microarray. Agilent's pre-defined species priority order is used to assign priority to the remaining species.

  - Probes for all microRNAs of the first priority species will be incorporated in the design.
  - Probes for all microRNAs for the 2nd priority species that are not already measured by the existing probes are added to the design.
  - Probes for the microRNAs for the remaining species are added to the design according to the species priority order.

  Annotation considerations. Probes are annotated on the array using the priority order described above.

Species Priority Order

Agilent has defined the following species priority list for multi-species microRNA microarray designs. For details, see Creating multi-species arrays, above.

Priority Order	Species Name	Common Name
1	Homo sapiens	human
2	Mus musculus	mouse
3	Rattus norvegicus	rat
4	Pan troglodytes	chimp
5	Macaca mulatta	rhesus monkey
6	Gallus gallus	chicken
7	Oryza sativa	rice
8	Ornithorhynchus anatinus	platypus
9	Physcomitrella patens	moss
10	Populus trichocarpa	poplar
11	Arabidopsis thaliana	arabadopsis
12	Danio rerio	zebrafish
13	Canis familiaris	dog
14	Caenorhabditis elegans	worm
15	Xenopus tropicalis	frog
16	Drosophila melanogaster	fruit fly
17	Vitis vinifera	grape
18	Bos taurus	cow
19	Monodelphis domestica	opossum
20	Fugu rubripes	fugu (Japanese pufferfish)
21	Tetraodon nigroviridis	pufferfish
22	Zea mays	corn
23	Caenorhabditis briggsae	worm

Priority Order	Species Name	Common Name
24	Pan paniscus	bonobo
25	Gorilla gorilla	gorilla
26	Pongo pygmaeus	orangutan
27	Drosophila erecta	fruit fly
28	Chlamydomonas reinhardtii	alga
29	Drosophila ananassae	fruit fly
30	Drosophila sechellia	fruit fly
31	Sorghum bicolor	sorghum
32	Drosophila yakuba	fruit fly
33	Drosophila virilis	fruit fly
34	Glycine max	soybean
35	Macaca nemestrina	pig-tailed macaque
36	Drosophila pseudoobscura	fruit fly
37	Drosophila grimshawi	fruit fly
38	Drosophila mojavensis	fruit fly
39	Drosophila willistoni	fruit fly
40	Drosophila persimilis	fruit fly
41	Drosophila simulans	fruit fly
42	Selaginella moellendorffii	spikemoss
43	Oikopleura dioica	tunicate
44	Sus scrofa	boar
45	Schmidtea mediterranea	flatworm
46	Ateles geoffroyi	spider monkey
47	Bombyx mori	silkworm
48	Anopheles gambiae	mosquito
49	Apis mellifera	honey bee

Priority Order	Species Name	Common Name
50	Brassica napus	rapeseed
51	Lagothrix lagotricha	brown woolly monkey
52	Tribolium castaneum	beetle
53	Saguinus labiatus	tamarin
54	Pinus taeda	pine
55	Ciona intestinalis	tunicate
56	Triticum aestivum	wheat
57	Epstein Barr	human virus
58	Medicago truncatula	clover
59	Solanum lycopersicum	tomato
60	Ciona savignyi	tunicate
61	Mouse cytomegalovirus	mouse virus
62	Rhesus lymphocryptovirus	rhesus viru
63	Mareks disease	chicken virus
64	Mareks disease	
65	Saccharum officinarum	sugarcane
66	Kaposi sarcoma-associated	human virus
67	Lemur catta	ring-tailed lemur
68	Human cytomegalovirus	human virus
69	Gossypium hirsutum	cotton
70	Mouse gammaherpesvirus	mouse virus
71	Symphalangus syndactylus	gibbon
72	Pygathrix bieti	black snub-nosed monke
73	Herpes Simplex	human virus
74	Rhesus monkey	rhesus monkey
75	Xenopus laevis	frog

Priority Order	Species Name	Common Name
76	Human immunodeficiency	human virus
77	Ovis aries	sheep
78	BK polyomavirus	human virus
79	Dictyostelium discoideum	amoeba
80	Gossypium rammindii	cotton
81	JC polyomavirus	human virus
82	Simian virus	monkey virus
83	Brassica oleracea	wild mustard
84	Brassica rapa	cabbages
85	Cricetulus griseus	Chinese hamster
88	Carica papay	papaya
87	Gossypium herbecium	cotton

Frequently Asked Questions (FAQs)

When I design probes, why do I get back the same probe for different target sequences?

Ideally, the eArray probe design algorithms select unique probes for each input target sequence. However, they return a “shared” probe if no other unique probes are available. This often occurs if two or more sequences within the target sequence set are overall very similar to each other, or are similar/identical in the region of the transcript from which candidate probes are selected (3' bias).

How many probes can I upload to eArray$_{XD}$ at a time?

Agilent has tested the 64-bit version of eArray$_{XD}$, and has successfully uploaded 150,000 probes from a Complete format file. The file size was approximately 32 MB. See “To upload probes and annotation” on page 161, and “Complete (for probes)” on page 881.

How do I search for the probes that I have designed with the GE Probe Design tool?

When you use the GE Probe Design tool to create probes, the program saves the probes in files that you can download, sort, and analyze. However, you must save the probes as a probe group before eArray commits them to the database, and makes them searchable.

What is the purpose of the controls on an array?

Agilent control grids contain these categories of controls:

- Positive controls that, depending upon application type, show predictable signal intensities. Positive controls include spike in (e1A) controls and endogenous target (housekeeping) controls;
- Negative controls that are designed to show no signal after hybridization, and are used as part of the background subtraction algorithms; and
- Manufacturing controls that Agilent uses for quality control, and to troubleshoot arrays that do not perform as expected.

How many features do I have available to me on an array?

The number of probes that you can include on an array depends upon the application type, array format, and target species. To determine the number of probes available on an array, you can use the microarray statistics that appear as you select and configure the probe groups for a microarray design.

Can I omit the control grid for my array?

No, all arrays require a control grid. The specific grid depends on the application type and the array format. For CGH, ChIP-on-chip, and methylation applications, the control grid is species-specific.

I have registered on the eArray Web site, but I cannot log in to my account. Why?

When you submit a registration request, you complete the first step in the registration process. Your account must also be approved and enabled.

How does transcriptome selection affect design?

The ability of the program to design probes that are specific for each of the transcripts depends on how well your chosen transcriptome is characterized. Similar results are also observed if ESTs or predicted genes comprise the majority of transcripts in your target transcriptome. In other words, you should select the reference sequence that best represents what is in your DNA sample.

If I want to design a non-randomized array, how do I do this?

Agilent does not recommend the creation of non-randomized arrays, and eArray$_{XD}$ does not let you do this. However, you can create microarray designs with customer-provided feature order if you use the eArray Web site. In the online help on the Web site, see *Provide feature order*.

Can I design a CGH array with tiling coverage for specific genomic intervals of interest?

Yes. You can search the CGH HD database for probes in specific intervals of interest. This function lets you return all probes in the specified intervals, or a specific number or density of probes. See "Searching for Agilent High Density (HD) Probes" on page 109.

If I download a sequence list for a catalog probe group and then modify the list and upload it, will eArray recognize the probes as catalog probes?

No. If you download catalog probes, and re-upload them, the system recognizes them as new probes. If you create a subset of catalog probes with off-line tools, use the Probe Search tool to retrieve probes by probe ID, and then save the returned probes as a probe group.

What are the attributes of probes that can be uploaded?

In addition to probe ID and sequence, you can also upload target IDs, multiple accession numbers, gene symbols, a description line, and a chromosomal location for each probe. To enter these attributes, use the **Complete** file format for the probe upload. See "Uploading Probes" on page 158 and "Complete (for probes)" on page 881.

Why do you select species in eArray? What does it affect?

- (For all application types) To supply another variable on which probes can be searched.
- (For the CGH, ChIP-on-chip, and CH3 application types) To let the system select the proper, required species-specific control grid for each array.

What if my organism of interest is not defined in eArray? How can I design controls for these organisms?

If your organism of interest is not available, select NA as your organism type in the appropriate species lists. To add your organism to the species database, contact Agilent Technical Support. If you choose this route, do not upload your probes as NA.

Why would I want to use a linker?

Linkers move the "active" hybridizing parts of probes farther away from the glass microarray substrate, reducing steric hindrance. Within eArray$_{XD}$, you can apply linkers to probes that are less than 60 nucleotides long to increase the biological availability of the active probe.

For example, if you have 25mer probes, you can add a linker that stilts them to be 40mers, making the 25mer sequence more available for duplex formation. eArray applies the linker to the 3' end of the probe. Derive the linker sequence from a sequence that is not found in nature, or is random. The program has a default linker sequence that you can use for this purpose.

Does the eArray probe design algorithm take into account phred scores (poor middle reads)?

No. eArray does not accept phred scores as part of the probe design process.

Can you suggest literature or references that speak to the performance of computationally generated probes compared to empirically validated probes?

Not at this time. However, customers have anecdotally reported great success using Agilent's computationally generated probes to define and solve biological problems.

How often does Agilent update annotation on the eArray Web site?

Agilent updates annotation on the eArray Web site every 3-4 months. After an update occurs, any probe groups or microarray designs that use the updated content become unavailable on your server. To make them available, you must manually request an update. See "To transfer a probe/bait group, microarray design, or library from the eArray Web site to your server" on page 61.

How does Agilent annotate its gene expression probes?

To provide annotation for its gene expression probes, Agilent uses BLAST and/or BLAT to align probes to various database transcripts. For more information on these sequence alignment tools, go to ncbi.nih.gov/BLAST and genomeblat.com. The exact procedure depends on the species.

Each probe is annotated to a primary transcript and secondary transcripts to assist you in probe searches.

After the transcript alignments are established, Agilent uses public domain linkages from the transcript identifiers to derive additional annotations such as title lines, gene names, gene symbols, or Gene Ontology terms. The additional annotations are derived from the primary transcript whenever possible, and from the secondary transcripts if unavailable from the primary.

To compute genomic annotation for each probe, Agilent uses BLAT to align the primary transcripts to the genome. Probes are aligned to the transcripts, and subsequently the probe alignment to the genome is computed. This multi-step process provides a more robust result when a probe spans a splice site.

Why does probe annotation change?

The most common reason for annotation changes is the addition or removal of a sequence from a public database. For example, if a probe aligns to a RefSeq transcript, eArray uses that annotation. If a particular RefSeq transcript is withdrawn later, the probe annotation could switch to a GenBank or Ensembl identifier.

Changes to the primary transcript annotation often cause several additional annotations to change, as they are derived by linkage to the primary transcript annotation. In addition, probe annotations can change when public databases change assignments of gene names, gene symbols, GO terms, and the like.

Agilent updates its probe annotation approximately every 3–4 months. For most application types, the eArray Web site contains only the most recent annotations.

Under what circumstances does Agilent update microRNA probe annotation?

Agilent updates microRNA probe annotation when new versions of the Sanger database become available. Several types of changes can occur:

- **Change in microRNA name** – If this type of change occurs, the primary accession for the probe will reflect the name in the latest version of the Sanger database. In the Accessions field, previous names will appear, each appended with the last version of the database in which they appeared. **Example: miR-hsa-###_v9.1**
- **Change in microRNA sequence that results in new probe sequences** – If this type of change occurs, the new probes will be annotated with the microRNA name. eArray annotates old probes with the microRNA name, and appends the last version of the database in which that sequence appeared.
- **Deletion of a microRNA from the database** – eArray annotates the probes that are associated with the deleted microRNA with the old name, and appends the last version of the database in which that microRNA appeared.

Can I access other application types?

You can use the Switch Application menu to access all of the application types that are available within eArray$_{XD}$. See "To set the application type" on page 48. Additional application types are available on the eArray Web site, including the SureSelect Capture Array application type, which

lets you create microarrays for array-based DNA capture, a methodology that helps harvest specific genomic DNA fragments of interest for sequencing.

Additional FAQs

Additional FAQs are available in the online help on the eArray Web site, including an extensive set of FAQs about the design of CGH microarrays. To view these FAQs, follow these steps:

1 Go to https://earray.chem.agilent.com

The eArray login page appears. You do not need to log in to view the online help.

2 Click **Help.**

The online help opens.

3 Click **FAQ.**

www.agilent.com

In this book

This User Guide describes how to use the eArray$_{XD}$ program to create and submit custom microarray designs and SureSelect Target Enrichment libraries.

eArray$_{XD}$ is part of the Agilent Genomic Workbench 6.5 suite of microarray creation, data processing, and analysis programs.

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