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# REMBRANDT 1.5.8 User's Guide

## REMBRANDT 1.5.8 User's Guide

The *REMBRANDT 1.5.8 User's Guide* has the following sections.

- [About This REMBRANDT User's Guide v1.5.8](#)
- [Credits and Resources v1.5.8](#)
- [1 Getting Started with REMBRANDT v1.5.8](#)
- [2 Conducting Simple Searches v1.5.8](#)
- [3 Conducting Advanced Searches v1.5.8](#)
- [4 High Order Analysis v1.5.8](#)
- [5 Viewing REMBRANDT Results v1.5.8](#)
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## About This REMBRANDT User's Guide v1.5.8

### About This REMBRANDT User's Guide v1.5.8

This section introduces you to the following topics:

- [About This Guide](#)
  - [Purpose](#)
  - [Audience](#)
  - [Topics Covered](#)
  - [Text Conventions Used](#)

### About This Guide

#### Purpose

This guide provides an overview of REMBRANDT. This book is organized into chapters that parallel REMBRANDT's workflow.

#### Audience

This guide is designed for researchers who want to perform ad hoc querying and reporting across multiple domains, such as gene expression, chromosomal aberrations, and clinical data.

#### Topics Covered

If you are new to REMBRANDT, read this brief overview, which explains what you will find in each chapter.

- [Chapter 1](#) provides instructions to start using REMBRANDT.
- [Chapter 2](#) describes how to search by gene keyword and reporter identifier and to create gene expression plots, Kaplan-Meier survival plots, and copy number-based graphs from those search results.
- [Chapter 3](#) describes how to add gene expression, copy number, and clinical queries to REMBRANDT, and group them to create and generate results for compound queries.
- [Chapter 4](#) extends the basic knowledge of the previous chapters and shows you how to work with class comparisons, hierarchical clustering, and principal component analysis.

- [Chapter 5](#) describes how to view all the results generated from advanced searches and high order analyses.
- [Chapter 6](#) describes how to download data from caArray application developed by the NCI Center for Biomedical Informatics and Information Technology.
- [Chapter 7](#) describes how to manage user-defined or study-defined patient ID, gene, and reporters lists.

## Text Conventions Used

This section explains conventions used in this guide. The various typefaces represent interface components, keyboard shortcuts, toolbar buttons, dialog box options, and text that you type.

Convention	Description	Example
Bold	Highlights names of option buttons, check boxes, drop-down menus, menu commands, command buttons, or icons.	Click <b>Submit</b> .
<a href="#">link</a>	Indicates a Web address or a link to another section or wiki page.	<a href="http://domain.com">http://domain.com</a>
capital letters	Indicates a keyboard shortcut.	Press ENTER.
capital letters-capital letters	Indicates keys that are pressed simultaneously.	Press SHIFT-CTRL.
Italics	Highlights new terms.	A <i>coin plot</i> is...
<b>Note:</b> Important information.	Highlights information of particular importance	This concept is used throughout the document.

## Credits and Resources v1.5.8

### Credits and Resources v1.5.8

The following table lists the REMBRANDT Development and Management Teams.

Development	Product and Program Management	Documentation	Application Support

<ul style="list-style-type: none"> <li>• Subha Madhavan</li> <li>• Alex Jiang</li> <li>• Kevin Rosso</li> <li>• Ryan Landy</li> <li>• Himanso Sahni</li> <li>• David Bauer</li> <li>• Huaitian Liu</li> <li>• Michael Harris</li> <li>• Ram Bhattaru</li> <li>• David Hall</li> <li>• Ye Wu</li> <li>• Ying Long</li> <li>• Don Swan</li> <li>• Dana Zhang</li> <li>• Vesselina Bakalov</li> <li>• Vesselina Bakalov</li> <li>• Jean-Claude Zenklusen</li> <li>• Yuri Kotliarov</li> <li>• Gregg Silk</li> <li>• Hangjiong Chen</li> <li>• Shine Jacob</li> <li>• Nonna Rabinovich</li> <li>• Leonie Misquitta</li> <li>• Mervi Heiskanen</li> <li>• Hangjiong Chen</li> <li>• Thiagaran Prakash</li> </ul>	<ul style="list-style-type: none"> <li>• Subha Madhavan</li> <li>• Anand Basu</li> <li>• Mervi Heiskanen</li> <li>• JJ Pan</li> <li>• Debra Hope</li> </ul>	<ul style="list-style-type: none"> <li>• Laura Jackel</li> <li>• Huaitian Liu</li> <li>• Jill Hadfield</li> </ul>	<p><b>Application Support</b></p> <ul style="list-style-type: none"> <li>• Telephone: 301-451-4384</li> <li>• Toll free: 888-478-4423</li> </ul>
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## 1 Getting Started with REMBRANDT v1.5.8

### 1 Getting Started with REMBRANDT v1.5.8

This section introduces you to the following topics:

- [About REMBRANDT](#)
  - [How to Cite REMBRANDT Data](#)
- [Launching REMBRANDT](#)
- [REMBRANDT's Opening Page](#)
- [New User Registration](#)
- [Logging In](#)
  - [Accepting REMBRANDT Provisions](#)
- [REMBRANDT Menu](#)
- [REMBRANDT Tabs](#)
- [REMBRANDT Side Bar](#)
- [Application Support](#)
- [Logging Out](#)

### About REMBRANDT

REMBRANDT (REpository for Molecular BRAin Neoplasia DaTa) is a joint initiative of NIH's National Cancer Institute (NCI) and the National Institute of Neurological Disorder

s and Stroke (NINDS). REMBRANDT provides a bioinformatics knowledge base framework that leverages data warehousing technology to host and integrate clinical and functional genomics data from clinical trials involving patients suffering from gliomas (tumors).

Researchers can use REMBRANDT to answer questions related to a patient or patient population and view integrated datasets in a variety of contexts. REMBRANDT also includes tools that link data to other annotations, such as cellular pathways, gene ontology terms, and genomic information. Researchers can also perform various higher-order analyses on clinical and genomic datasets.

## How to Cite REMBRANDT Data

When referencing the REMBRANDT data set, please cite National Cancer Institute as the source, including year of first production release (2005), the REMBRANDT website (<http://rembrandt.nci.nih.gov>) and the accessed date.

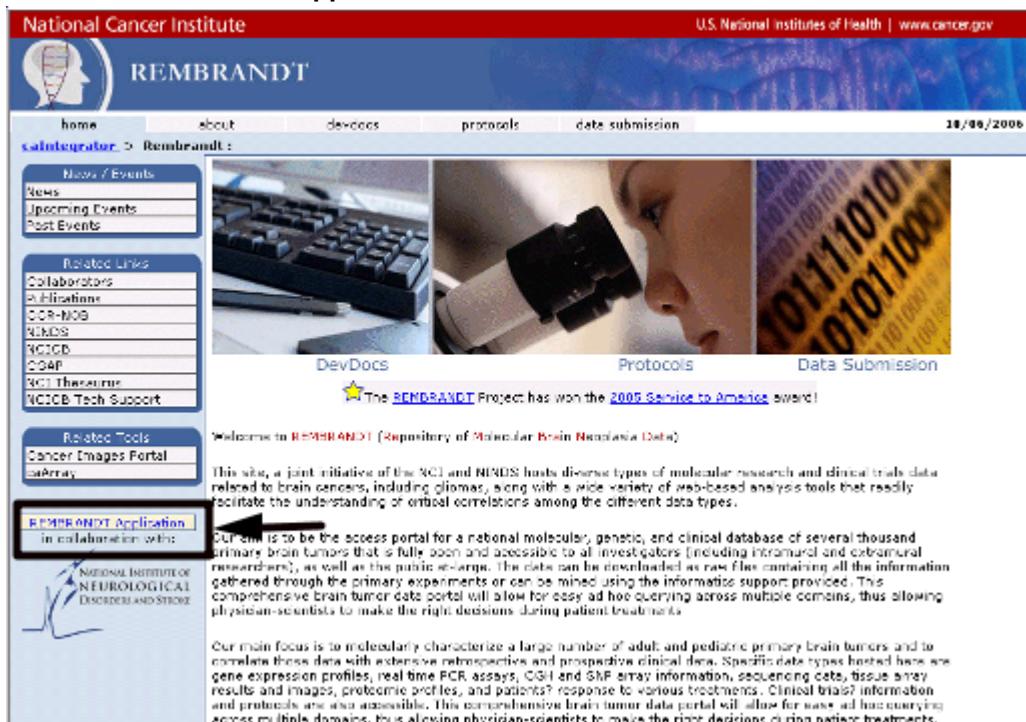
*For Example:*

National Cancer Institute. 2005. REMBRANDT home page. <<http://rembrandt.nci.nih.gov>>. Accessed 2007 September 24

## Launching REMBRANDT

To launch REMBRANDT, follow these steps:

1. Go to the REMBRANDT portal on the NCICB website: <http://rembrandt.nci.nih.gov/>.
2. Click the **REMBRANDT Application** button located in the lower left-hand blue column.



3. The REMBRANDT login page appears.

National Cancer Institute  
U.S. National Institutes of Health | www.cancer.gov

REMBRANDT

home help support tutorials user guide LogIn

About this application

Release 1.5

REpository for Molecular BRAin Neoplasia DaTa (REMBRANDT) is a robust Bioinformatics knowledgebase framework that leverages data warehousing technology to host and integrate clinical and functional genomics data from clinical trials involving patients suffering from Gliomas. The knowledge framework will provide researchers with the ability to perform ad hoc querying and reporting across multiple data domains, such as Gene Expression, Chromosomal aberrations and Clinical data.

Scientists will be able to answer basic questions related to a patient or patient population and view the integrated data sets in a variety of contexts. Tools that link data to other annotations, such as cellular pathways, gene ontology terms and genomic information will be embedded.

Please visit <http://rembrandt.nci.nih.gov> for more information.

Repository for Molecular Brain Neoplasia Data.  
Empowering translational research for brain tumor studies.

Browse Rembrandt Data

For Access, new and existing users click the button below:

[Browse Rembrandt Data](#)

Additional Information:

- Download User Guide (PDF)
- View Tutorial
- Provide us your feedback

Throughout the application please click the Help icon for context sensitive application help.

HOME | SUPPORT | NOTIFICATION

## REMBRANDT's Opening Page

REMBRANDT's opening page enables you to perform the following tasks:

- Register new users and log in current users with the button.
- Access REMBRANDT 1.5.8 Help with the link.
- Run REMBRANDT tutorials that will assist you in using new REMBRANDT options with the link.
- Provide the REMBRANDT team with any feedback about the product with the **Provide us with your feedback** link.

## New User Registration

First-time REMBRANDT users need to register first to obtain a username and password. To register in REMBRANDT, follow these steps:

1. Fill in the the and information. Department is optional.

- For security purposes, in the Verification text box, type the alpha-numeric characters that you see in the image. The entry is case-sensitive.
  - To clear all of the fields and start again, click the **Reset** button.
  - To submit your registration, click the **Register** button.

**i Note**

If you do not enter the information properly, a message appears at the top. Correct the information and continue.

- If you successfully register, the Logging In panel fills in with a temporary username and password that you can use immediately.
- You should receive an e-mail registration confirmation and then an additional e-mail containing your new account information. Once you receive your username and password, do not use the temporary account.
- If you have any problems with the form, click the link at the top of the REMBRANDT window.

## Logging In

To log into REMBRANDT, you need a username and password. You should have received an e-mail with this information once you registered.

**i Note**

If you are a first-time REMBRANDT user, you must register to obtain a username and password.

- On the login panel, enter your username and password.
- Click the **Login** button. If your login is successful, the Legal Rules of the Road page appears.
- From the Registration/Login page, you can join (or remove yourself from) the Rembrandt List Serve. Enter the appropriate information in the lower left corner of the page.

- On the login panel, enter your Username and Password.
- Click the **Login** button. If your login is successful, the Legal Rules of the Road page appears.

## Accepting REMBRANDT Provisions

Once you log in, the Legal Rules of the Road page appears. After reading the provisions, click the link in the lower right-hand corner.



The REMBRANDT workspace appears.



## REMBRANDT Menu

Information about how to use REMBRANDT is easily accessed from REMBRANDT's menu in the top left of the REMBRANDT workspace.



The following table describes each item on the REMBRANDT menu.

Menu Option	Function
Help	<p>Click to access a complete version of online REMBRANDT help.</p> <p>For complete page-level help, click  on any REMBRANDT page.</p> <p>To open a help page to the field's information, click .</p>
Support	Click to obtain support for REMBRANDT.
Tutorials	Click <b>REMBRANDT</b> to access online tutorials to walk you through REMBRANDT.
User's Guide	Click to access the <i>REMBRANDT 1.5.8 User's Guide</i> .

## REMBRANDT Tabs

The following table describes each REMBRANDT tab on the workspace.

Tab Name	Function
Simple Search	<p>Search the database and view the following search results:</p> <ul style="list-style-type: none"> <li>• Gene Expression plots</li> <li>• Kaplan-Meier Survival plots</li> </ul> <p>For more information, see <a href="#">Chapter 2</a>.</p>
Advanced Search	<p>Create the following types of queries and group them to generate results for compound queries:</p> <ul style="list-style-type: none"> <li>• Gene Expression analysis</li> <li>• Copy Number Data analysis</li> <li>• Clinical Study analysis</li> </ul> <p>For more information, see <a href="#">Chapter 3</a>.</p>
High Order Analysis	<p>Run higher order analyses, including class comparisons, hierarchical clustering, and principal component analyses. For more information, see <a href="#">Chapter 4</a>.</p>
View Results	<p>View Advanced Search and High Order Analysis results. Also download static, archive files for use in BRB-ArrayTools. For more information, see <a href="#">Chapter 5</a>.</p>
??Download	<p>Download data from caArray. For more information, see <a href="#">Chapter 6</a>.</p>

My Workspace	Manage user- or study-defined patient identifier, gene, or reporter lists. For more information, see <a href="#">Chapter 7</a> .
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## REMBRANDT Side Bar

The side bar appears on the right side of the REMBRANDT workspace. The following table provides an overview of the information that may appear as you use additional REMBRANDT functions.

Information Displayed	Function
Filter Settings	Displays the filter settings for the following: <ul style="list-style-type: none"> <li>• A Principal Component Analysis (see <a href="#">Performing a Principal Component Analysis</a>)</li> <li>• A Hierarchical Clustering Analysis (see <a href="#">Performing Hierarchical Clustering Analysis</a>)</li> </ul>
Queries	Lists queries created with the Advanced Queries function and enables you to add, copy, edit, and delete existing queries. See <a href="#">Managing Individual and Compound Queries</a> .
PatientDID List	Displays the default provided with REMBRANDT, and displays in red any PatientDID lists added to REMBRANDT. See <a href="#">Adding New Lists</a> . To display the items in any type of list, hover over the name and a popup displays the data items. To export a list to a spreadsheet file, double-click the list name.
Gene List	Displays in red any added to REMBRANDT. See <a href="#">Adding New Lists</a> .
Reporter List	Displays in red any added to REMBRANDT. See <a href="#">Adding New Lists</a> .

## Application Support

For any general information about the application, application support or to report a bug, contact NCICB Application Support.

Email: <a href="mailto:ncicb@pop.nci.nih.gov">ncicb@pop.nci.nih.gov</a>	When submitting support requests via email, please include: <ul style="list-style-type: none"> <li>• Your contact information, including your telephone number.</li> <li>• The name of the application/tool you are using</li> <li>• The URL if it is a Web-based application</li> <li>• A description of the problem and steps to recreate it.</li> <li>• The text of any error messages you have received</li> </ul>
Application Support URL	<a href="http://ncicb.nci.nih.gov/NCICB/support">http://ncicb.nci.nih.gov/NCICB/support</a>

**Telephone: 301-451-4384 Toll free: 888-478-4423**

Telephone support is available:  
Monday to Friday, 8 am – 8 pm Eastern Time,  
excluding government holidays.

## Logging Out

To log out of REMBRANDT, follow these steps.

1. On the REMBRANDT workspace, click the link in the upper right-hand corner.



2. The Logout page appears.

A screenshot of the "Logout" page. It starts with a "Logout" header. Below it is a message: "Thank you for visiting the REMBRANDT application. You cannot save the current session if you are logged in a guest user (RBUser)." There are three radio button options:

- Save my current session and logout. [?]
- Do not save my current session and logout. [?]
- Continue working in the application and do not logout.

At the bottom is a "Submit" button with a mouse cursor icon hovering over it.

3. Select one of the following options:

- To return to REMBRANDT, select **Continue working in the application** and do not logout.
- To log out of REMBRANDT *without* saving the session, select **Do not save my current session** and logout.
- To log out and save your session, select **Save my current session** and logout.
- To fill out a three-question survey, click **Click Here** to take a quick feedback survey. Answer the questions.

4. Click the **Submit** button.

## 2 Conducting Simple Searches v1.5.8

### 2 Conducting Simple Searches v1.5.8

This section describes how to use REMBRANDT to conduct simple searches of the REMBRANDT repository and create graphs from the results obtained. Topics in this section include:

- [Simple Search Overview](#)
- [Gene Expression Simple Search](#)
  - [Eliminating Aliases](#)
  - [Understanding a Gene Expression Plot](#)
  - [Median Plot Details](#)
  - [Geometric Mean Plot Details](#)
  - [Log2 Intensity Gene Expression Plot Details](#)
  - [Box and Whisker Log2 Intensity Gene Expression Plot Details](#)
    - [Displaying a Coin Plot](#)
  - [Saving, Printing, and E-mailing a Gene Expression Plot](#)
- [K-M Gene Expression Simple Search](#)
  - [Redrawing the K-M Survival Plot for Gene Expression Data](#)
  - [Understanding K-M Survival Plot for Gene Expression Data](#)
    - [Notes about Probe Set to Gene Summarization](#)
- [K-M Copy Number Simple Search](#)
  - [Redrawing the K-M Survival Plot for Copy Number Data](#)
  - [Understanding K-M Survival Plot for Copy Number Data](#)
- [K-M Sample Search](#)
  - [Understanding K-M Survival Plot for Sample Data](#)

## Simple Search Overview

The Simple Search page enables you to perform the following types of searches:

- Gene Expression search (see [Gene Expression Simple Search](#))
- [Kaplan-Maier](#) survival plot for the following:
  - Gene Expression Data search (see [K-M Gene Expression Simple Search](#))
  - Copy Number Data search (see [K-M Copy Number Simple Search](#))
  - Sample Data search (see [K-M Sample Search](#))
- Results are generated for each search. The Kaplan-Meier survival plots also create Clinical reports and plots (see [Clinical Reports](#)).

**i Note**

It is not possible to save queries launched as simple searches in Rembrandt. For information about saving advanced queries, see [Chapter 3](#)

## Gene Expression Simple Search

To create a gene expression plot, follow these steps:

1. From the Simple Search page, select **Gene Keyword**.

**i Note**

If you do not enter a valid gene symbol, the following message appears: *The gene you entered is either invalid, or not in the database. Please select another.* Close the message window, and enter another gene symbol.

2. Enter a gene keyword, for example, enter a [HUGO](#) gene symbol such as EGFR or WT1, to plot a gene expression profile based on the expression of your gene of interest.

- Click the Go button.

## Eliminating Aliases

If a message indicates that one or more genes or their aliases have been found, follow these steps:

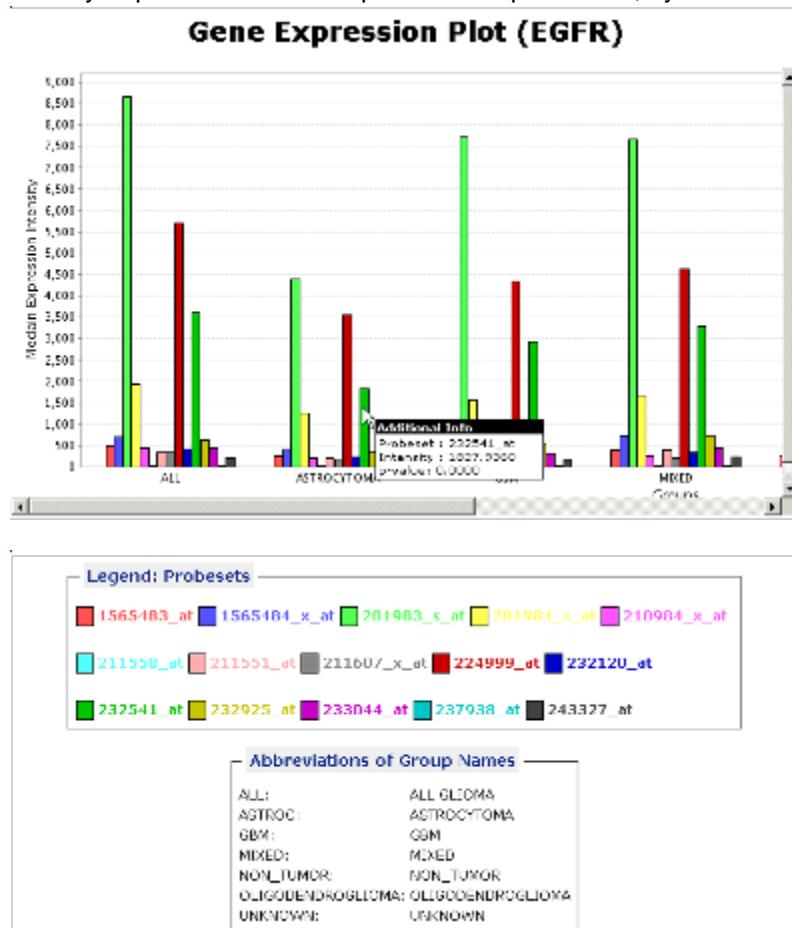
- Select the appropriate option from the drop-down list.



- To end the search, click **Cancel** button.
- To continue, click the **Go** button.

## Understanding a Gene Expression Plot

When you perform a Gene Expression simple search, by default the Median Gene Expression Plot appears.



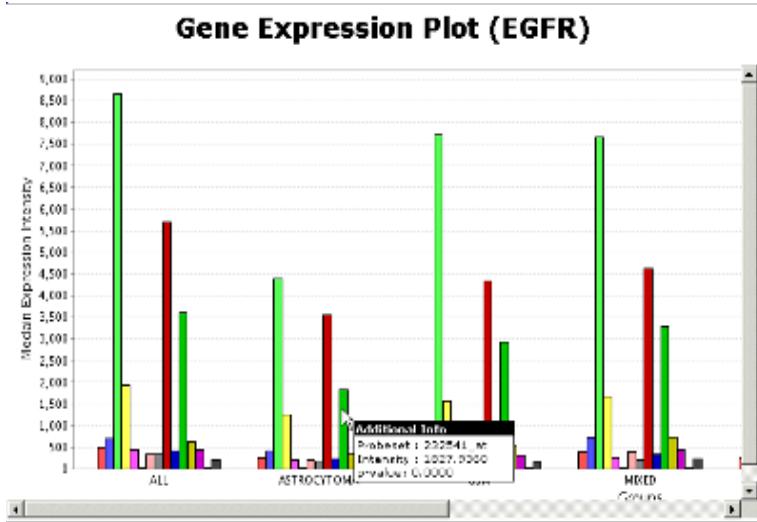
The following table describes each area of the Gene Expression Plot page.

Item	Special Instructions
------	----------------------

Data Selection	Select the link to repaint the graph.  Select the link to view a unified gene expression with lesser reporters. This displays a gene-based view of the expression data. To obtain the unified gene expression values, the probe-level data is processed with custom CDF (Chip Definition Files) that rearranges Affymetrix probes into splice-form based probesets. Probes mapped to alternatively spliced exons are grouped into a distinct probeset. The most 3` probes are selected for processing. Non-specific probes are masked before processing.
Graph Type	Displays different versions of the Gene Expression Plot. <ul style="list-style-type: none"> <li>• <b>Median</b> is the default graph shown when you perform a simple search. For additional graph details, see <a href="#">Median Plot Details</a>.</li> <li>• <b>Geometric Mean</b> displays mean expression intensity (Geometric mean) versus Groups. For additional graph details, see <a href="#">Geometric Mean Plot Details</a>.</li> <li>• <b>Log2 Intensity</b> displays average expression intensities for the gene of interest. For additional graph details, see <a href="#">Log2 Intensity Gene Expression Plot Details</a>.</li> <li>• <b>Box and Whisker Log2 Intensity</b> displays a Box and Whisker plot or box plot. For additional graph details, see <a href="#">Box and Whisker Log2 Intensity Gene Expression Plot Details</a>.</li> </ul>
Click here to open plot in a new window	Click the link to open the current graph in a new window and adjust the display. You can then save, print, and e-mail the graph.  See <a href="#">Saving, Printing, and E-mailing a Gene Expression Plot</a> .
Legend Probesets	Indicates the color for each probeset appearing in the graph.
Abbreviations of Group Names	Lists the complete name of each group abbreviation in the plot.
Print this Graph	Click to print the graph.

## Median Plot Details

The **Median** Gene Expression Plot displays the median expression versus Groups.

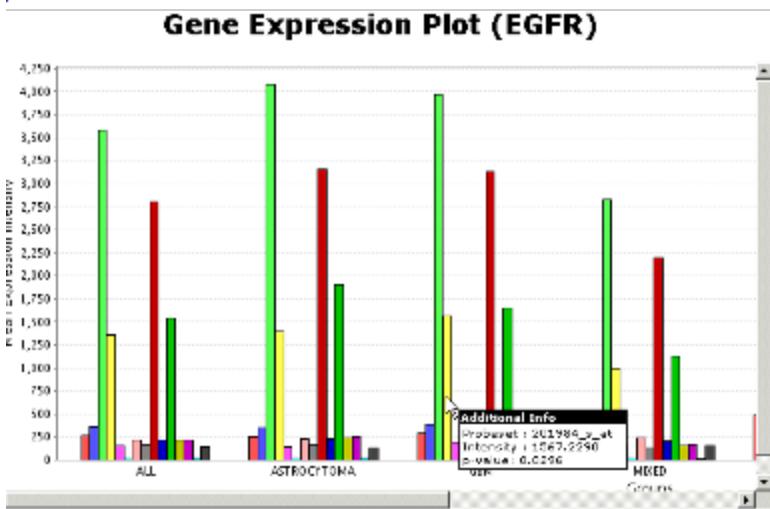


Mouse-over a bar on the graph to display **Additional Information**. The following table describes Additional Information details.

Item	Special Instructions
Probeset	Each probeset contains multiple probe pairs. Each probe pair consists of two groups of probes—one called a perfect match (PM) and the other called a mismatch (MM). The perfect match is a set of oligonucleotide whose sequence exactly matches the gene of interest; the mismatch differs from the perfect match at one base position in the middle of the sequence.
Intensity	The median value calculated for each comparison group.
p-value	The probability for obtaining the differences in expression values between tumor (or a subtype of tumor) and non-tumor samples.

### Geometric Mean Plot Details

The Geometric Mean Gene Expression Plot displays mean expression intensity (Geometric mean) versus Groups.



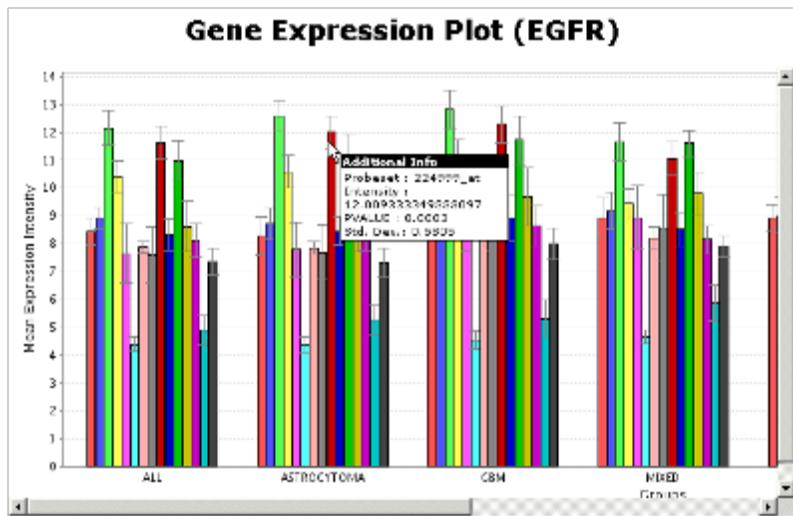
Mouse-over a bar on the graph to display **Additional Information**. The following table describes Additional Information details.

Item	Special Instructions
Probeset	Each probeset contains multiple probe pairs. Each probe pair consists of two groups of probes—one called a perfect match (PM) and the other called a mismatch (MM). The perfect match is a set of oligonucleotide whose sequence exactly matches the gene of interest; the mismatch differs from the perfect match at one base position in the middle of the sequence.
Intensity	The geometric mean value calculated for each comparison group.
p-value	The probability for obtaining the differences in expression values between tumor (or a subtype of tumor) and non-tumor samples.

## Log2 Intensity Gene Expression Plot Details

The Log2 Intensity Gene Expression Plot (*Figure 2.5*) displays average expression intensities for the gene of interest based on Affymetrix GeneChip arrays (U133 Plus 2.0 arrays). Multiple probesets (for some genes) are designed to measure the expression of the gene of interest. For more information on the probeset design strategy for human genes, go to <http://www.affymetrix.com> **INSERT OUTSIDE JUMP**.

Group average (sample averages based on tumor subtypes in six categories, Glioblastoma Multiforme, Oligodendrogloma, Astrocytoma, Mixed, Unclassified, and Unknown tumors) is calculated for each probeset and is plotted on the Y-axis for each tumor type.



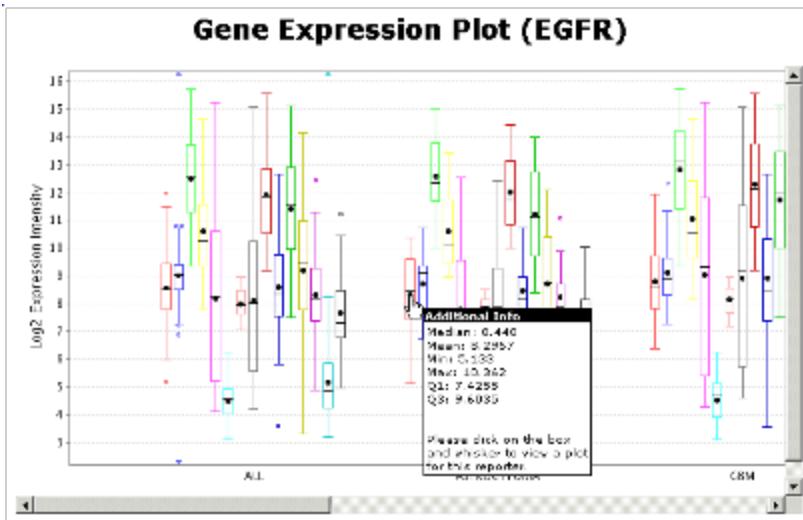
Mouse-over a bar on the graph to display **Additional Information**. The following table describes Additional Information details.

Item	Special Instructions
Probeset	Each probeset contains multiple probe pairs. Each probe pair consists of two probes—one called a perfect match (PM) and the other called a mismatch (MM). The perfect match is an oligonucleotide whose sequence exactly matches the gene of interest; the mismatch differs from the perfect match at one base position in the middle of the sequence.
Intensity	The mean value calculated for each comparison group.
p-value	The probability for obtaining the differences in expression values between tumor (or a subtype of tumor) and non-tumor samples.
Std. Dev.	The standard deviation value of a comparison group, such as GBM or Astrocytoma, for a particular probeset or gene. Standard deviation is a statistical measure of spread or variability.

### Box and Whisker Log2 Intensity Gene Expression Plot Details

The Gene Expression Plot displays a box plot without all the individual data points. Example uses of box and whisker plots include the following:

1. Indicate whether a distribution is skewed and whether there are potential unusual observations (outliers) in the dataset.
2. Perform a large number of observations.
3. Compare two or more datasets.
4. Compare distributions because the centre, spread, and overall range are immediately apparent.



A box and whisker plot or box plot is a graph that presents information from a five-number summary. To display the summary about a probeset for one group, mouse over the probe-set on the plot to display the . The following table describes **Additional Information** details.

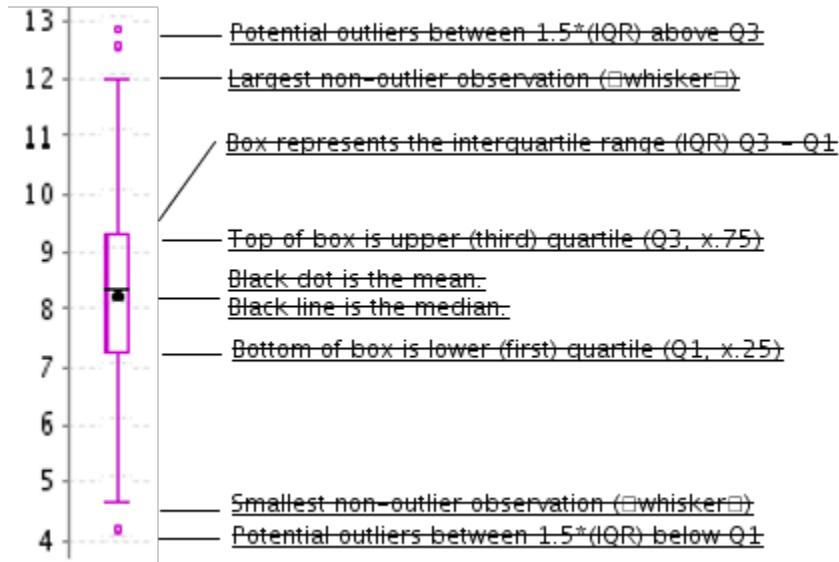
Item	Special Instructions
Median	Median value of log 2 (or ratio) gene expression values for a particular probeset or unified gene.
Mean	Mean value of log 2 (or ratio) gene expression values for a particular probeset or unified gene
Min.	The minimum value.
Max.	The maximum value.
Q1	The bottom of the box. The first quartile is the median of the lower part of the data.
Q3	The top of the box. The third quartile is the median of the upper part of the data.
...plot	Represents the probeset name.

#### **Note**

To display a coin plot for the reporter, in the box. A is a box-and-whisker plot with all the individual data points (see [Displaying a Coin Plot](#)).

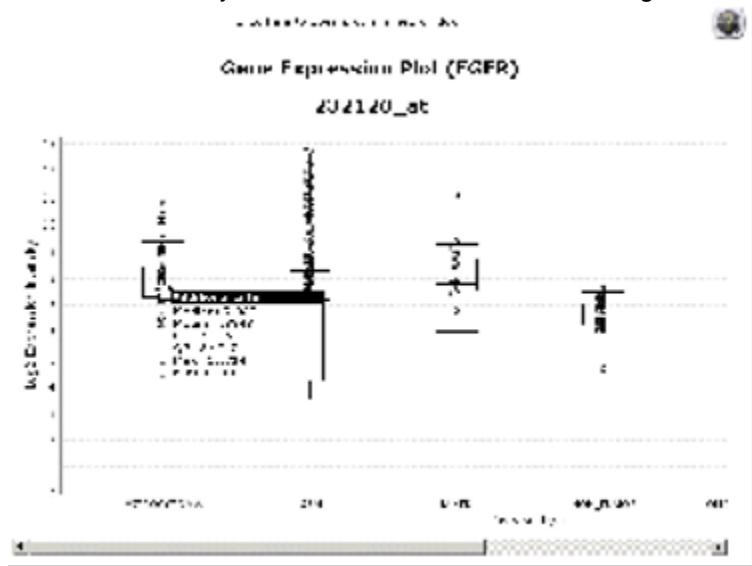
In the box-and-whisker plot, the individual probeset summary is represented as follows (). Horizontal lines (the "whiskers") extend to, at the most, 1.5 times the box length (the interquartile range) from either or both ends of the

box. They end at an observed value, thus connecting all the values outside the box that are not more than 1.5 times the box width away from the box.



### Displaying a Coin Plot

A is box-and-whisker plot () with all individual data points. This enables you to obtain a diagram representing a statistical summary of the data without the disadvantage of concealing the real data.

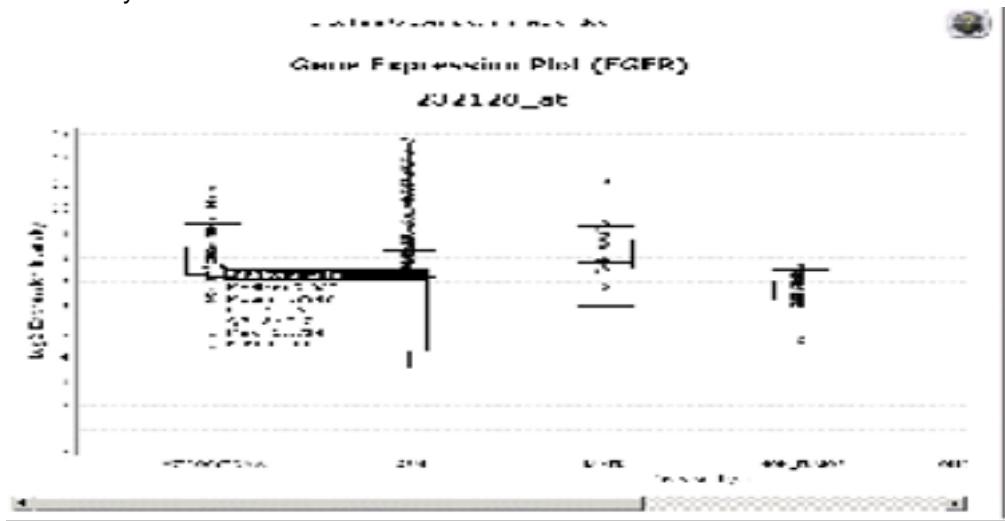


The coin plot is a graph that presents information from a five-number summary. To display the summary about a probeset for one group, mouse over the probe-set on the plot to display the **Additional Information**. The following table describes Additional Information details.

Item	Special Instructions
Median	Median value of log 2 (or ratio) gene expression values for particular a probeset or unified gene.

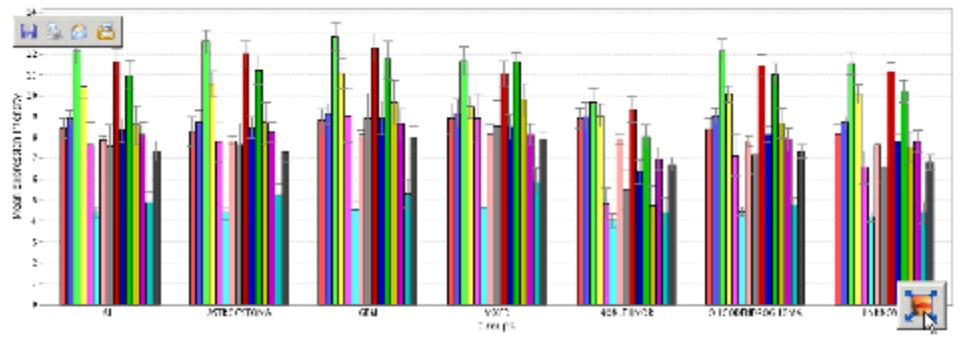
Mean	Mean value of log 2 (or ratio) gene expression values for particular a probeset or unified gene
Min.	The minimum value.
Max.	The maximum value.
Q1	The bottom of the box. The first quartile is the median of the lower part of the data.
Q3	The top of the box. The third quartile is the median of the upper part of the data.
...plot	Represents the probeset name.

In the coin plot, the individual probeset summary is represented as follows (). Horizontal lines (the "whiskers") extend to, at the most, 1.5 times the box length (the interquartile range) from either or both ends of the box. They end at an observed value, thus connecting all the values outside the box that are not more than 1.5 times the box width away from the box.



### Saving, Printing, and E-mailing a Gene Expression Plot

By opening a Gene Expression plot in a new window, you can perform a number of tasks with the Gene Expression plot.



The following table describes the tasks you can perform when you open a Gene Expression plot in a new window.

Item	Special Instructions
<b>INSERT SQUARE ICONS</b>	Mouse-over the graph, and the icon appears in the lower right-hand corner. Click the icon to enlarge or reduce the size of the graph.
<b>INSERT STANDARD ICONS</b>	Mouse-over the graph, and standard icons appear in the upper left-hand corner. Click the appropriate icon to save, print, or e-mail the graph.

## K-M Gene Expression Simple Search

To create a survival plot for gene expression data (K-M Gene Expression), follow these steps:

1. From the Simple Search page, select **Create Kaplan-Meier survival plot for Gene Expression Data**.
2. Enter a gene keyword, for example, enter a [HUGO](#) gene symbol, such as EGFR or WT1, to plot a gene expression profile based on the expression of your gene of interest.

**Note**

If you do not enter a valid gene symbol, the following message appears: *The gene you entered is either invalid, or not in the database. Please select another.* Close the message window, and enter another gene symbol. If you do not enter a valid gene symbol, the following message appears: *The gene you entered is either invalid, or not in the database. Please select another.* Close the message window, and enter another gene symbol.

3. From the **Restrict to Sample Group** drop-down list, select a saved sample group.
4. Click the **Go** button.

For information about the Gene Expression Plot, see [Understanding a Gene Expression Plot](#).

## Redrawing the K-M Survival Plot for Gene Expression Data

To redraw a K-M Gene Expression data, follow these steps:

**Note**

If you restricted the search to a group, Constrained to group appears at the top.

1. To dynamically modify the fold change thresholds and redraw the plot, adjust the **Up-Regulated** and **Down-R**

egulated values.

2. Specify a **Unified** or a **Affymetrix Reporter Type**.
3. To visualize the K-M plot for the unified probeset, click the **Reporters** drop-down list.



4. Select an individual reporter or one of the following options:
  - **Median** is the median value of all Reporters (default).
  - **Mean** is the mean value of all Reporters.

5. Click the **Redraw Graph** button.

For information about the Gene Expression Plot, see [Understanding a Gene Expression Plot](#).

## Understanding K-M Survival Plot for Gene Expression Data

A K-M Survival Plot for Gene Expression Data () displays the survival rate at each time point for samples with certain expression characteristics (e.g., EGFR expression levels in tumor samples greater than those in the non-tumor samples by 3 fold or higher). Kaplan-Meier estimates are calculated based on the last follow-up time and the censor status (0=alive, 1=dead) from the samples of interest. The Kaplan-Meier estimates are then plotted against the survival time. The points that correspond to the events with censor status of 0 are indicated on the graph. You can dynamically modify the fold change (up and down regulation) thresholds and redraw the plot.

### Note

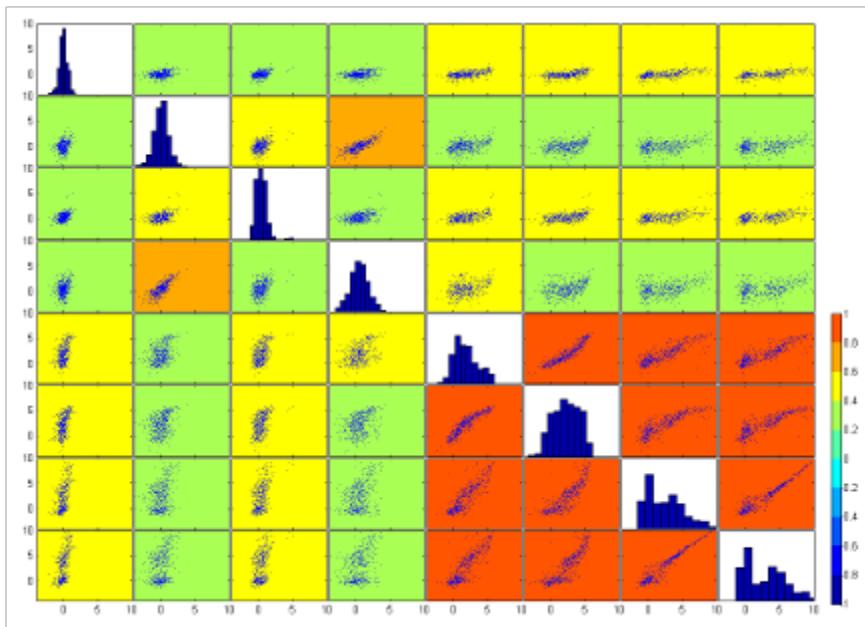
Samples for which there is no survival information and censor status are excluded from the Kaplan Meier Plot Analysis.

The following discussion summarizes the relationships between Affymetrix probe sets to genes, as annotated by NetAffx.

## Notes about Probe Set to Gene Summarization

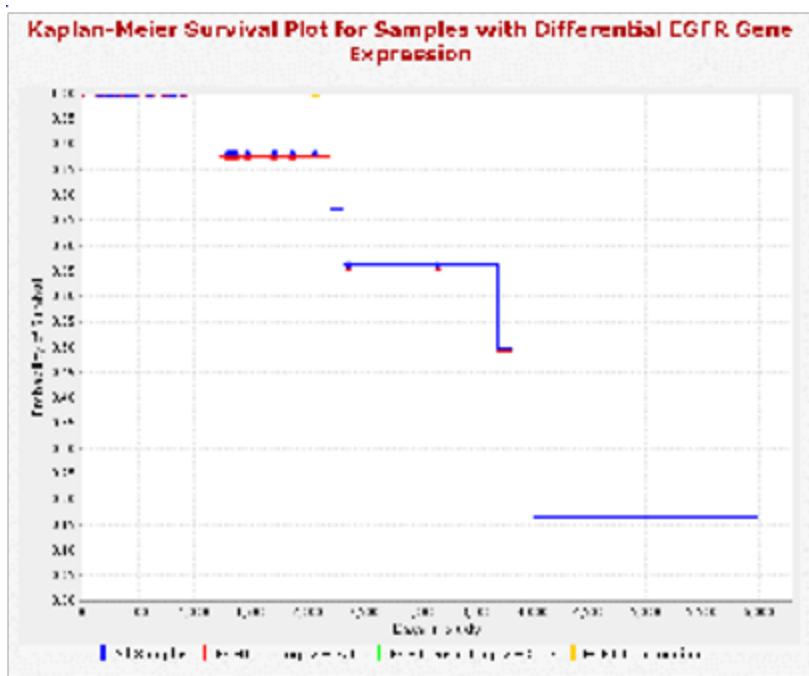
NetAffx annotation of Affymetrix expression probe sets contains a relationship between probe sets and genes, and many genes are represented by multiple probe sets. Often researchers need to calculate expression of a particular gene in a sample as a single value. Several methods are widely used: (1) selecting the "best" single probe set for each gene by either highest mean, or median, or maximum expression across all the samples in the dataset; (2) combining probes into a re-annotated sets and creating a custom CDF file; (3) simply averaging expression values of all probe sets associated with the same gene. The second method, while perhaps biologically more relevant, requires re-processing the whole data set starting from raw data in CEL files. The third method, although quite simple, should be avoided.

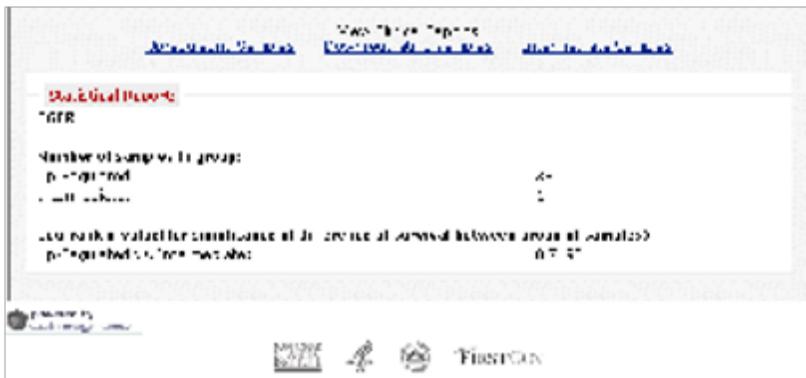
The following figure shows pair-wise correlations between all probe sets associated with the EGFR gene. The histograms on the diagonal are distributions of expression values (log2-transformed) for each probe set. On the correlation plots, each dot represents a sample, and color corresponds to Pearson's correlation coefficient. The probe sets (eight in the case of the EGFR gene) are sorted by their mean expression across all the samples. Thus low expressing probe sets are located in the upper left corner of the figure, and high expressing in the lower right corner.



It is clear that different probe sets have very different expression ranges, and averaging them by either mean or median is (a) simply incorrect, because values do not belong to the same population (one-way ANOVA analysis gives zero p-value), and (b) results in lower values and larger noise, making any further analysis very difficult. Another observation from the figure is that probe sets with highest expression are usually correlated with each other very well, in contrast to low expression probe sets, suggesting that a single probe set with relatively high expression can be used to represent the gene (method 1 above). The EGFR gene has been chosen only because of its known wide range of expression in brain tumors. However, this pattern is very similar for the majority of genes represented by multiple probe sets on Affymetrix platform.

To redraw the survival plot, see [Redrawing the K-M Survival Plot for Gene Expression Data](#).





### Kaplan-Meier Survival Plot for Gene Expression Data

The following table describes areas on the Kaplan-Meier Survival Plot for Gene Expression data page.

Item	Special Instructions
<b>INSERT STANDARD ICONS</b>	Mouse-over the graph, and standard icons appear in the upper left-hand corner. Click the appropriate icon to save, print, or e-mail the graph. See .
<b>View Clinical Reports</b>	When you apply a gene expression filter, REMBRANDT provides links to display the gene expression for , , and . For more information, see .
<b>Statistical Report</b>	<ol style="list-style-type: none"> <li>1. Displays the gene keyword entered as search criteria for the plot.</li> <li>2. Displays the reporter selected for the plot.</li> <li>3. specifies the number of Up-Regulated, Intermediate, Down-Regulated samples, if any.</li> <li>4. indicates the significance of the difference in survival between any two groups of samples segregated based on gene expression of the gene of interest. The log rank -value is calculated using Mantel-Haenszel procedure. The -values are recalculated every time a new threshold is selected.</li> </ol>

### K-M Copy Number Simple Search

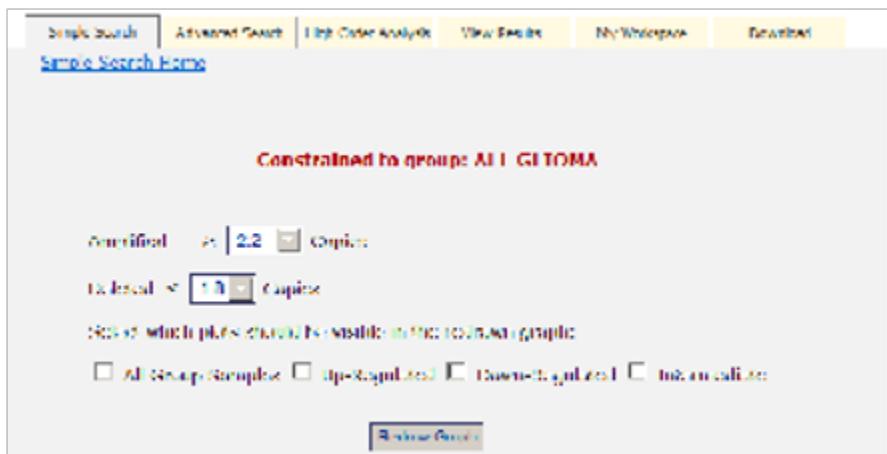
To create a survival plot for copy number-based data (K-M Copy Number), follow these steps:

1. From the Simple Search page, select **Create Kaplan-Meier survival plot for Copy Number Data**.
2. Select **Gene Keyword** and enter a [HUGO](#) gene symbol, such as EGFR or WT1, to plot a Kaplan-Meier survival plot based on the calculated copy number of your gene of interest.
3. To search on a sample group saved in a previous search, select a group from the **Restrict to Sample Group** list box.
4. Click the **Go** button.

For information about the K-M Copy Number plot, see [Understanding K-M Survival Plot for Copy Number Data](#).

### Redrawing the K-M Survival Plot for Copy Number Data

When the K-M survival plot displays, the following figure shows above the graph.



To redraw a KM Copy Number graph, follow these steps:

**Note**

If you restricted the search to a group, **Constrained to group** appears at the top.

1. Select the amplification and deletion criteria.
2. Select the plot(s) to be visible in the redrawn graph.
3. Click the **Redraw Graph** button.

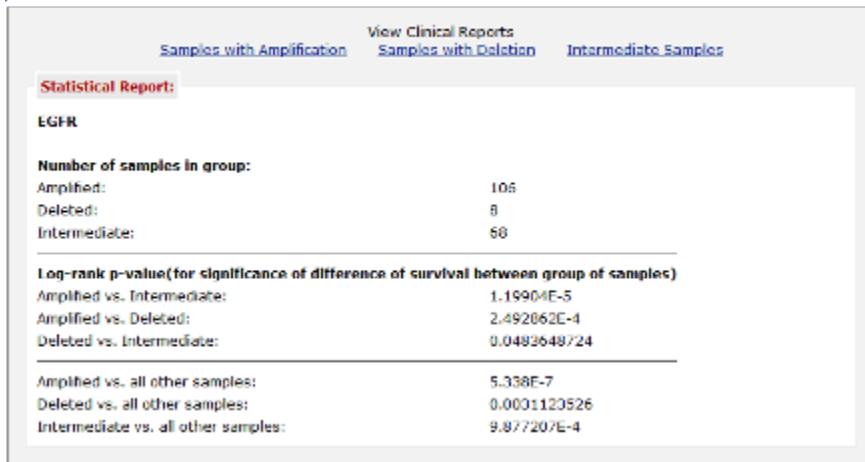
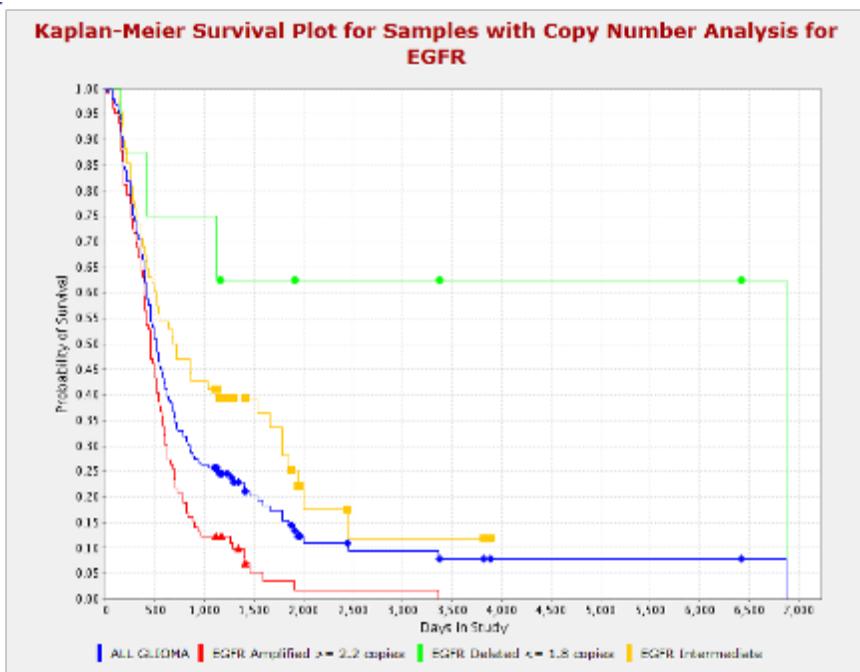
### Understanding K-M Survival Plot for Copy Number Data

A gene keyword search displays a plot for samples with certain amplification/deletion characteristics (for example, amplification of the cytoband that EGFR maps to 7p11.2). Kaplan-Meier estimates are calculated based on the last follow-up time and the censor status (0=alive, 1=dead) from the samples of interest. The Kaplan-Meier estimates are then plotted against the survival time. The points that correspond to the events with censor status of 0 are indicated on the graph. You can dynamically modify the calculated copy number (amplified and deleted) thresholds and redraw the plot.

**Note**

Samples for which there is no survival information and censor status are excluded from the Kaplan Meier Plot Analysis.

To redraw the survival plot, see [Redrawing the K-M Survival Plot for Gene Expression Data](#).



The following table describes areas on the Copy Number-based Plot page.

Item	Special Instructions
<b>INSERT STANDARD ICONS</b>	Mouse-over the graph and standard icons appear in the upper left-hand corner. Click the appropriate icon to save, print, or e-mail the graph..
<b>View Clinical Reports</b>	When you apply a copy number filter, REMBRANDT provides links to display the copy number data for samples. For more information, see .

Statistical Report	<ol style="list-style-type: none"> <li>1. Displays the search criteria for the plot.</li> <li>2. Displays the reporter selected for the plot.</li> <li>3. specifies the number of different types of samples, if any.</li> <li>4. indicates the significance of the difference in survival between any two groups of samples segregated based on gene expression of the gene of interest. The log rank -value is calculated using Mantel-Haenszel procedure. The -values are recalculated every time a new threshold is selected.</li> </ol>
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## K-M Sample Search

To create a survival plot for sample data (K-M Sample), follow these steps:

1. From the **Simple Search** tab, select **Create Kaplan-Meier survival plot for Sample Data**.
2. Select a sample from each drop-down list for comparison purposes.
3. Click the **Go** button. The Kaplan-Meier survival plot appears.

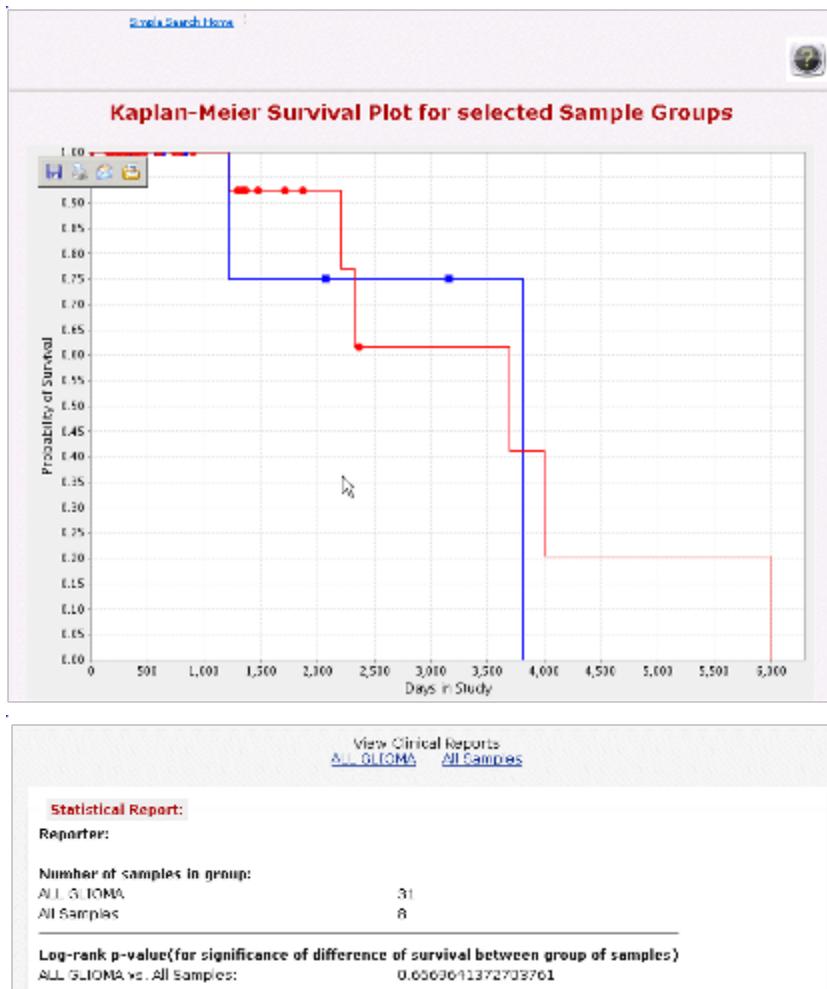
For information about the Gene Expression Plot, see [Understanding a Gene Expression Plot](#).

## Understanding K-M Survival Plot for Sample Data

A Kaplan-Meier Survival Plot for Sample Data () shows the survival rate at each time point for samples. Kaplan-Meier estimates are calculated based on the last follow-up time and the censor status (0=alive, 1=dead) from the samples of interest. The Kaplan-Meier estimates are then plotted against the survival time. The points that correspond to the events with censor status of 0 are indicated on the graph.

 **Note**

Samples for which there is no survival information and censor status are excluded from the Kaplan Meier Plot Analysis.



The following table describes areas on the Kaplan-Meier Survival Plot for Sample Data page.

Item	Special Instructions
<b>INSERT STANDARD ICONS</b>	Mouse-over the graph, and standard icons appear in the upper left-hand corner. Click the appropriate icon to save, print, or e-mail the graph. See .
<b>View Clinical Reports</b>	To display clinical data for the selected sample groups, click the group link. For more information, see .
<b>Statistical Report</b>	<ol style="list-style-type: none"> <li>1. Displays the search criteria for the plot.</li> <li>2. Displays the reporter selected for the plot.</li> <li>3. specifies the number of groups of samples.</li> <li>4. indicates the significance of the difference in survival between any two groups of samples segregated based on groups of samples. The log rank -value is calculated using Mantel-Haenszel procedure.</li> </ol>

## 3 Conducting Advanced Searches v1.5.8

## 3 Conducting Advanced Searches v1.5.8

This section describes how to create compound queries to generate graphs.

Topics in this section include:

- [Advanced Searches Overview](#)
- [Gene Expression Advanced Search](#)
  - [Selecting a Gene Ontology \(GO\) Classification](#)
  - [Selecting a Pathway](#)
- [Copy Number Advanced Search](#)
- [Clinical Study Advanced Search](#)
- [Managing Individual and Compound Queries](#)
- [Refining a Query](#)

### Advanced Searches Overview

The Advanced Search function enables you to add individual queries to REMBRANDT and then group the queries to create and generate results for a . The following is an overview.

1. The Advanced Search - Build Query page enables you to define advanced searches in three categories:
  - a. Gene Expression Analysis (see [Gene Expression Advanced Search](#))
  - b. Copy Number Analysis (see [Copy Number Advanced Search](#))
  - c. Clinical Analysis (see [Clinical Study Advanced Search](#))
- Once you create a query, you can add, copy, edit, and delete queries from the side bar.  
To create a compound query, click the button or the option.
2. Validate the compound query and generate results on the View Results page.

#### Note

To save queries, when you select to log out, Rembrandt prompts you to save the session. If you do so, when you log back in, advanced queries are saved and display in the right sidebar of the browser window. You cannot save the current session if you are logged in as a guest user.

### Gene Expression Advanced Search

To define an advanced gene expression search, follow these steps:

1. On the Gene Expression page, in the box, you are required to enter a name for the gene expression query. The name must be unique among all the queries in the current session. The following is the Advanced Gene Expression page (top portion)

## Gene Expression

The screenshot shows the REMBRANDT Gene Expression search interface. At the top, there are tabs for Simple Search, Advanced Search, High Order Analysis, View Results, and Manage Lists. Below these are links for Advanced Search Help and Refine Query.

**Query Name:** Gene Expression 1 (should be unique)

**Gene:**

- Type Genes: Name/Symbol: ESR1
- Choose a saved Gene List:
- All Genes Query

**Region:**

Chromosome Number:

Cytoband:  -to-  Mip Browser...  
 Base Pair Position (kb):  -to-

2. You are required to enter at least one search criteria for the query. The following table lists the available search criteria:

Criteria	Item Name	Special Instructions
Gene	Type Genes	Select a gene identifier option (Name/Symbol, <b>Locus Link ID</b> , or GenBank AccNo.), and then enter or paste comma-delimited values for the genes to be searched.
Gene	Choose a Saved Gene List	Drop down the list box and select a saved gene list. If you have not added a <u><a href="#">Gene List</a></u> with the REMBRANDT My Workspace function, none appears (see <u><a href="#">Managing Lists Overview</a></u> ).
Gene	All Genes	Click if you do not wish to specify a list of genes but want to display data for all the genes analyzed.  You must apply this option to a pre-existing result set, as described in Step 1 of <u><a href="#">Refining a Query</a></u> .
Region	Chromosome Number	Select the chromosomal region of interest (1-22, X or Y). Cytoband fills in based on the selected chromosome number.

Region	Cytoband	A context-sensitive list displays only the relevant cytobands for the selected chromosome. Select a cytband range.
Region	Map Browser	Click to conduct a search of cytoband ranges.
Region	Base Pair Position	Enter the start and end base pair positions.
Clone Id/Probe Set ID	Type Reporters	Select an option (Probeset ID or <b>MAGE ID</b> ), and then enter or paste comma-delimited values for the identifiers to be searched. IMAGE identifiers must start with IMAGE:.
Clone Id/Probe Set ID	Choose a Saved Reporters List	Drop down the list box and select a saved Reporters list. If you have not added a Reporters list with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Gene Ontology (GO) Classifications	(list box)	Enter a <a href="#">Gene Ontology (GO)</a> ID in the format GO:##### to search for one or more branches of the GO hierarchy.  For example, enter GO:0005006 (epidermal growth factor receptor activity (12)).
Gene Ontology (GO) Classifications	Go Browser	Click the button to search for and select a GO classification.  See <a href="#">Selecting a Gene Ontology (GO) Classification</a> .
Pathways		Click the button to search for and select a pathway.  See <a href="#">Selecting a Pathway</a> .
Pathways		Click the button to search for and select a pathway.  See <a href="#">Selecting a Pathway</a> .

Pathways	clear text area	Click the button to search for and select a pathway.  See <a href="#">Selecting a Pathway</a> .
Clone Location	3' UTR	<i>Future implementation</i>
Clone Location	5' UTR	<i>Future implementation</i>

3. At the bottom of the Gene Expression page, you can optionally add disease type criteria to the search

The screenshot shows a search interface for 'Disease Type'. It includes a list of diseases like 'Huntington's Chd', 'Huntington's Chd', 'GEP', 'MCF7', 'Hep G2', 'Oncoprotein', 'Tumor', and 'Tumor'. Below this is a 'Sample Identifier' input field with 'ANTENORAD' entered. There are two checkboxes for 'Exclude Re-Program Tumor Samples': one checked and one unchecked. Under 'Add Change', there are three radio buttons: 'Up-regulation' (selected), 'Down-regulation' (unchecked), and 'None'. A dropdown menu is open, showing 'Up-regulation' and 'Down-regulation' again. At the bottom is an 'Array Platform' section with a dropdown menu.

4. Optionally, you can combine a disease type with the query. The following table lists the Disease Type items:

Criteria	Item Name	Special Instructions
Disease Type	(list box)	To select a disease, click on the name. To select more than one disease, click the first name and +click the remaining disease types. To display the tumor sub-types for a disease type, mouse over the disease type name.
Disease Type	Grade	<i>Future Implementation</i>

Sample Identifier	(list boxes)	To further filter the search, enter or paste comma-delimited sample identifiers to be searched.  OR  Drop down the list box and select a saved sample identifier list. If you have not added a PatientDID List with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Re-resection Tumor Samples	checkbox	Select to exclude subsequent re-resection tumor samples from the query. Typically re-resection specimens labels are appended with letter "B" for second resection or "C" for third resection and so on.
Fold Change	Up-Regulation Down-Regulation Unchanged	Specify the threshold for the differential regulation. This returns differential expression ratios between tumor and non-tumor samples for a particular reporter. To create an <b>All Genes</b> query, you must select a fold change threshold of 4 or above.
Array Platform	(list box)	Select an array platform.

5. For the last step, you submit the search. Submitting the search saves the search criteria, and the Advanced Search - Build Query page appears. No results are generated until you create a query from your saved searches.

To save the search and return to the Advanced Search tab, click the **Submit** button.

6. You can also use the other buttons as follows:

- To clear the values entered on the page and enter new values, click the **Clear** button.
- To clear the values and return to the Advanced Search page, click the **Cancel** button.
- To display a preview of the report generated by the search results, click the **Preview** button.

### Tip

A search initiated with this button cannot be saved.

## Selecting a Gene Ontology (GO) Classification

Once you select the button on the Gene Expression page, a list of GO IDs appears.



The screenshot shows a dropdown menu with a list of GO terms. The menu has a blue header bar with the text "Select a GO ID". Below the header, there is a list of items, each consisting of a blue link and a corresponding GO ID in purple. The items are organized into categories:

- [biological process](#) : GO:0008150
  - [biological process unknown](#) : GO:0000004
  - [cellular process](#) : GO:0009987
    - [cell adhesion](#) : GO:007155
    - [cell communication](#) : GO:0077124
    - [cell differentiation](#) : GO:0030154
    - [cell recognition](#) : GO:0009037
    - [cellular physiological process](#) : GO:0050875
    - [regulation of cellular process](#) : GO:0050794
  - [development](#) : GO:0007275
    - [aberration](#) : GO:0009838
    - [agen](#) : GO:0007568
    - [appendage development](#) : GO:0048736
    - [cell differentiation](#) : GO:0030154
    - [cellularization](#) : GO:0077349
    - [circle tracing](#) : GO:0017593
    - [developmental growth](#) : GO:0045589
    - [embryon](#) : GO:0107582
    - [embryo implantation](#) : GO:0007556
    - [embryonic development](#) : GO:0009790
    - [fraying body formation](#) : GO:0030582
    - [genetic transfer](#) : GO:0019292
    - [hatching](#) : GO:0035138
    - [maturation](#) : GO:0021700
    - [meristem development](#) : GO:0048507
    - [ovule development](#) : GO:0009824

To add the GO ID to your advanced search, click on the appropriate GO term. The GO ID is added to the Gene Expression page.

## Selecting a Pathway

To select a pathway of interest, follow these steps.

1. Browse the pathway list, and check the pathways of interest.



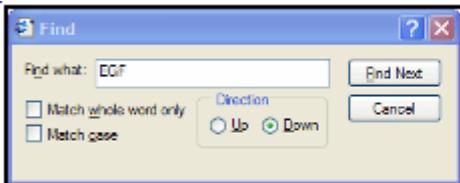
The screenshot shows a pathway browser interface with a blue header bar. The main area displays a list of pathways, each with a small icon, a name, and a brief description. The pathways listed are:

- [!\[\]\(c71a20455d83e51067809b2e3cc6a33a\_img.jpg\) \*\*Cardiovascular Disease\*\*](#) Cardiovascular disease is a broad category of diseases that affect the heart and blood vessels.
- [!\[\]\(197d309be7e34263cad894cbccc9888f\_img.jpg\) \*\*Chemical carcinogenesis\*\*](#) Chemical carcinogenesis is the process by which chemicals cause cancer.
- [!\[\]\(075352c6d2c04b517d934e6a3ddc9b91\_img.jpg\) \*\*Alzheimer's Disease\*\*](#) Alzheimer's disease is a progressive neurodegenerative disorder.
- [!\[\]\(787ae2401c34f8f70c7428194f9c4fa7\_img.jpg\) \*\*Chronic Disease\*\*](#) Chronic disease is a long-term condition that requires ongoing medical attention and management.
- [!\[\]\(a10cd3ddb81af3df48735c7d1fce6d11\_img.jpg\) \*\*Fracture\*\*](#) Fracture is a break in a bone, often caused by trauma or osteoporosis.
- [!\[\]\(ce0ea221c24d38490c15ffe362ce9a32\_img.jpg\) \*\*Obesity\*\*](#) Obesity is a state of having excess body fat.
- [!\[\]\(e5e24af5fb425a3f653ff1cb25aa8696\_img.jpg\) \*\*Diabetes\*\*](#) Diabetes is a metabolic disorder characterized by high blood sugar levels.
- [!\[\]\(9efb3b97c664304fa6cfdedd63258c8b\_img.jpg\) \*\*Stroke\*\*](#) Stroke is a sudden loss of brain function due to a disturbance in the blood supply.

**Note**

For more information about a pathway, click the pathway name.

2. To quickly find the pathway of interest, type CTRL-F. The Search dialog box appears.



3. Enter the pathway into the search text box, and click the **Find Next** button.  
The pathway(s) fulfilling the search criteria appear.
4. Select the check box next to the pathway of interest and click the **Done** button. The selected pathways are added to the query.

## Copy Number Advanced Search

To add a copy number data analysis to a query, follow these steps:

1. On the Copy Number Data page, in the **Query Name** box, you are required to enter a name for the query.  
The name must be unique among all the queries in the current session.

A screenshot of the Copy Number Advanced Search interface. At the top, there's a navigation bar with tabs like 'Simple Search', 'Advanced Search', 'High Order Analysis', 'New Results', 'My Workspaces', and 'Download'. Below the tabs, a 'Query Name' input field is shown with the placeholder '(should be unique)'. To the right of the input field is a 'Gene/Region' button. Below the input field, there are two radio buttons: 'Gene View' (selected) and 'Region View'. Under 'Gene View', there's a 'Gene' section with a dropdown menu set to 'Type Genome' and a 'Name/Symbol' input field containing 'checkplease'. There's also a 'checkplease' link. At the bottom, there's a radio button for 'Choose a saved Gene List' followed by a browse button.

2. You are required to enter at least one search criterion for the copy number query. The following table lists the available search criteria:

Criteria	Item Name	Special Instructions

Gene	Type Genes	Select a gene identifier option ( <b>Name/Symbol</b> ) and then enter or paste comma-delimited values for the genes to be searched.
Gene	Choose a Saved Gene List	Drop down the list box and select a gene list. If you have not added a <a href="#">Gene List</a> with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Region	Chromosome Number	Select the chromosomal region of interest (1-22, X or Y). Cytoband fills in based on the selected chromosome number.
Region	Cytoband	A context-sensitive list displays only the relevant cytobands for the selected chromosome. Select a cytoband range.
Region	Base Pair Position (kb)	Enter the start and end base pair positions.

3. At the bottom of the Advanced Copy Number page, you can add disease type criteria to the search. The following table lists the Disease Type options:

Criteria	Item Name	Special Instructions
Disease Type	(list box)	To select a disease, click on the name. To select more than one disease, click the first name and +click the remaining disease types. To display the tumor sub-types for a disease type, mouse over the disease type name.
Disease Type	Grade	<i>Future implementation</i>

Sample Identifier	(list boxes)	To further filter the search, enter or paste comma-delimited sample identifiers.  OR  Drop down the list box and select a saved sample identifier list. If you have not added a PatientDID List with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Analysis Type	Paired Tissue Samples	Tissue vs Blood paired samples
Analysis Type	Unpaired Tissue Samples	Tissue vs. Reference samples
Analysis Type	Normal samples	Blood vs. Reference samples
Calculated Copy Number	None	Specify the threshold for the copy number. <ul style="list-style-type: none"><li>• Amplified</li><li>• Deleted</li><li>• Amplified or Deleted</li></ul> Calculated copy number = $2 * 2^{\text{Segment Mean}}$ .
Segment Mean	None	Circular binary segmentation (CBS) output. Select <b>Mean ≥</b> or <b>Mean ≤</b> or <b>Unchanged</b> .
Array Platform	(list box)	Select the array platform.

- For the last step, submit the search. Submitting the search saves the search criteria, and the Advanced Search - Build Query page appears. No results are generated until you create a query from your saved searches.
- To save the search and return to the Advanced Search tab, click the **Submit** button.

You can also use the other buttons as follows:

- To clear the values entered on the page and enter new values, click the **Clear** button.
- To clear the values and return to the Advanced Search page, click the **Cancel** button.
- To display a preview of the report generated by the search results, click the **Preview** button.

## Clinical Study Advanced Search

To add a clinical data analysis to a query, follow these steps:

- On the Clinical Data page, in the **Query Name** box, you are required to enter a name for the query. The name must be unique among all the queries in the current session.

**Clinical Data**

Graph Search Advanced search High Order Analysis View Results Manage Lists

Advanced Search Home : [Save Query](#)

Query Name [\[?\]](#)  
 (should be unique)

Disease Type [\[?\]](#)

ALL  
 ASTROCYTOMA  
 GBM  
 MNGD

Grade:  AI [\[?\]](#)

Mouseover disease types and any relevant sub-type will be displayed.

**ASTROCYTOMA MIXED, OLIGODENDROGLIOMA**

**ASTROCYTOMA Tumor Sub-types**

Sample ID  
 Occurred  
 First Pres  
 Prior therapy [\[?\]](#)

1. Anaplastic Astrocytoma  
 2. Brain Astrocytoma  
 3. Diffuse Astrocytoma  
 4. Intramedullary Astrocytoma  
 Astrocytoma  
 5. Pilocytic Astrocytoma  
 6. Filamentous Astrocytoma  
 7. Pleomorphic Xanthoastrocytoma  
 8. Spinal Cord Astrocytoma  
 9. Subependymal Astrocytoma

2. You must specify a disease type, and optionally complete the remaining information. The following table lists the Disease Type items:

Criteria	Item Name	Special Instructions
Disease Type	(list box)	To select a disease, click on the name. To select more than one disease, click the first name and CTRL-click the remaining disease types.  To display the tumor sub-types for a disease type, mouse over the disease type name.
Disease Type	Grade	<i>Future implementation</i>
Sample Identifier	(list box)click	To further filter the search, enter or paste comma-delimited sample identifiers.  OR  Drop down the list box and select a saved sample identifier list. If you have not added a PatientDID List with the REMBRANDT My Workspace function, <b>none</b> appears (see <a href="#">Managing Lists Overview</a> )
Occurrence	First Presentation Recurrence	<i>Future implementation</i>

Prior Therapy	Radiation Radiation Type	Select <b>Radiation</b> and then select the type of radiation that the patient received prior to enrollment in the current study.
Prior Therapy	Chemo Agent	Select <b>Chemo</b> and then select the agent that the patient received prior to enrollment in the current study.
Prior Therapy	Surgery Title Outcome	Select <b>Surgery</b> and then enter the name of the surgery that the patient had prior to enrollment in the current study and the outcome of the surgery.
Onstudy Therapy	Radiation Radiation Type	Select <b>Radiation</b> and then select the type of radiation that the patient received after enrollment in the current study.
Onstudy Therapy	Chemo Agent	Select <b>Chemo</b> and then select the agent that the patient received after enrollment in the current study.
Onstudy Therapy	Surgery Title Outcome	Select <b>Surgery</b> and then enter the name of the surgery that the patient had after enrollment in the current study and the outcome of the surgery
Survival Range	Lower Upper	Specify the upper and lower limits (in months) for filtering the clinical data based on the age (in years) at which a patient was diagnosed.
Age at Dx	Lower Upper	Specify the upper and lower limits for filtering the clinical data based on the age at which a patient was diagnosed with the disease.
Gender	None	Select the appropriate gender of the patient.
Race	None	Select the appropriate race of the patient.

Clinical Evaluation	<a href="#">Karnofsky</a>	Score from the Karnofsky Performance status scale, representing the functional capabilities of a person.
Clinical Evaluation	<a href="#">Lansky</a>	Score from an enumerated set of values representing performance status according to the Lansky scale. The Lansky scale is intended for use only with subjects under 12 years old.
Clinical Evaluation	Neuro Exam	The participant's neurologic exam score. Score identifiers are the following: +2 DEFINITELY BETTER +1 POSSIBLY BETTER 0 STABLE -1 POSSIBLY WORSE -2 DEFINITELY WORSE
Clinical Evaluation	MRI	Relates to the disease evaluation as measured by scan (MRI/CT). Score definitions are the following: +3 DISAPPEARANCE OF TUMOR (CR) +2 DEFINITELY BETTER (PR) +1 POSSIBLY BETTER 0 UNCHANGED -1 POSSIBLY WORSE -2 DEFINITELY WORSE (PD) -3 DEVELOPMENT OF A NEW LESION (PD)

- For the last step, you submit the search. Submitting the search saves the search criteria, and the Advanced Search - Build Query appears. No results are generated until you create a query from your saved searches.
- To save the search and return to the Advanced Search - Build Query, click the **Submit** button.

You can also use the other buttons as follows:

- To clear the values entered on the page and enter new values, click the **Clear** button.
- To clear the values and return to the Advanced Search page, click the **Cancel** button.
- To display a preview of the report generated by the search results, click the **Preview** button.

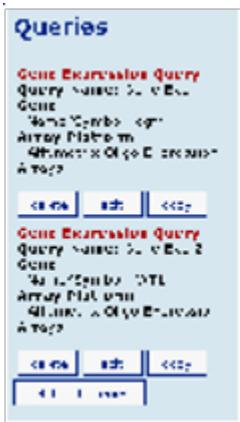
## Managing Individual and Compound Queries

Once you submit an individual query, you are returned to the Advanced Search - Build a Query page. Your search is added to the counter next to the Analysis button. The following list describes how to manage your individual and compound queries (if defined):

- Add more individual queries: Click the **Gene Expression Analysis**, **Copy Number Analysis**, or **Clinical**

**Analysis** button on the Advanced Search - Build a Query page.

2. Copy, edit, or delete existing individual queries. Find the query listed in the right side bar and use the **Copy**, **Edit**, and **Delete** buttons.



3. Create a compound query. Click the **Finalize Query** button or the Refine Query option on the Advanced Search page, and see [Refining a Query](#).
4. Delete a compound query. Find the compound query listed in the right side bar and click the Delete button.

**Note**

The **Delete All Queries** button deletes all compound *and* individual queries listed in the sidebar.



## Refining a Query

The Refine Query page enables you to group multiple queries into a single, compound query. You must validate the query to generate a result.

1. Fill in the Refine Query criteria.



2. The following table lists the Refine Query options:

Item Name	Special Instructions
Step 1	<p>You can group the queries to obtain a particular result set, or select all queries.</p> <p>To group queries click <b>Please refine your results by grouping queries</b>.</p> <ul style="list-style-type: none"> <li>• Select the open parentheses, (.</li> <li>• Select a <b>Query Name</b>.</li> <li>• Select a closing parentheses ).</li> <li>• Select an <b>and/or operator</b> at the end of a query row to enable the next row where you can select another query of interest.</li> <li>• Repeat for each query name to be grouped. Go to Step 3.</li> </ul> <p><b>- OR -</b></p> <p>To select all queries, click <b>Please select an All Genes query</b>. The drop-down list appears from which you can choose an All Genes query. Go to Step 2.</p>
Step 2. Select result set (mandatory for "All Genes" queries)	Select a previously saved result set to which to apply these queries. You will not see any result sets if you have not saved a sample set from a previous query, for example from a Clinical report page. The available sets are also listed in the side bar under PatientDID Lists in red type.

Step 3. Validate your query	REQUIRED. Click to validate the syntax of the query is correct.
Step 4. Select a view	Select a report from the drop-down list. The available reports vary based type of queries selected.
Step 5. Select data source(s) to filter the query by (Optional)	<p>Optionally select a datasource to filter the query by the institute providing data. You can select more than one institute.</p> <div style="border: 1px solid #ccc; padding: 10px; margin-top: 10px;"> <p><b>Note</b></p> <p>The Simple Search function and Preview assigns all the institutes to which you have access.</p> </div>

3. To return to the Advanced Search - Build Query page and not save the information, click the **<< Back** button.
4. To generate a report from the defined criteria, click the **Run Report >>** button.

**Note**

If the **Run Report** button does not appear, click the **Validate Query** button first to check the query syntax.

## 4 High Order Analysis v1.5.8

### 4 High Order Analysis v1.5.8

This section describes how to use REMBRANDT to run higher order analyses, including class comparisons, hierarchical clustering, and principal component analyses.

Topics in this section include:

- [High Order Analysis Overview](#)
- [Performing a Class Comparison](#)
- [Performing a Principal Component Analysis](#)
- [Performing Hierarchical Clustering Analysis](#)
- [Performing an Integrative Genomic Viewer Analysis](#)
- [Performing a GenePattern Analysis](#)
- [Launching GenePattern](#)

#### High Order Analysis Overview

REMBRANDT stores preprocessed gene expression data (filtering and normalization). The [High Order Analysis](#) tab includes buttons, described below, to further analyze gene expression data.

- Class Comparison Analysis (See [Performing a Class Comparison](#).)
- Principal Component Analysis (PCA) (See [Performing a Principal Component Analysis](#).)
- Hierarchical Clustering Analysis (See [Performing Hierarchical Clustering Analysis](#).)

Additionally, REMBRANDT can integrate with the GenePattern application in two ways, using its tools to analyze gene expression data.

- You can send gene expression data to GenePattern for up to four methods of analysis. GenePattern returns the analysis results to REMBRANDT where they can be reviewed on the View Results tab. (See [Performing a GenePattern Analysis](#).)
- You can launch GenePattern itself, giving you the option to perform your tasks right in the GenePattern application. (See [Launching GenePattern](#).)

A high order analysis generates results that you can review on the View Results page. (See [High Order Analysis Results](#).)

## Performing a Class Comparison

To create a High Order Analysis with [Class Comparisons](#), follow these steps:

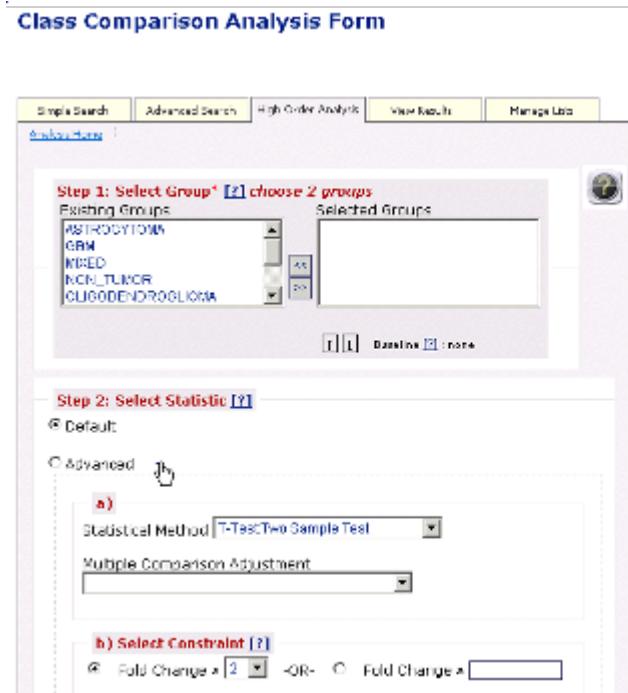
1. On the High Order Analysis tab, click the **Class Comparison Analysis** button.

The Class Comparison Analysis Form page enables you to define the criteria to perform a class comparison.

### Note

Clicking the plus (+) sign in Step 1 expands and displays the Advanced Statistic options.

**Class Comparison Analysis Form**



Step 1: Select Group\* [?] choose 2 groups

Existing Groups

- ASTROCYTOMA
- GEM
- IMR32
- NCI\_TUMOR
- GLIOBLASTOMA

Selected Groups

Basins [?]

Step 2: Select Statistic [?]

Default

Advanced [?]

a)

Statistical Method: T-Test Two Sample Test

Multiple Comparison Adjustment:

b)

Select Constraint [?]

Fold Change > 2 OR  Fold Change < -2

Step 3: Select Array Platform [?]  
Oligo (Affymetrix U133 Plus 2.0)

Step 4: Name Analysis Result [?]  
(should be unique)

clear cancel submit

2. You are required to complete at least one step for the class comparison. The following table lists the available criteria:

Criteria	Item Name	Special Instructions
Step 1: Select Group	Existing Groups Selected Groups	<p>A <i>group</i> is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics (See <a href="#">Managing Lists Overview</a>).</p> <div style="border: 1px solid #ccc; padding: 10px; margin-top: 10px;"> <p><b>Note</b></p> <p>User-defined PatientDID lists appear in red type in the side bar.</p> </div> <p>Select two groups in the <b>Existing Groups</b> box and move them to the <b>Selected Groups</b> box.</p>
Step 1: Select Group	Baseline	<p>To select a baseline, follow these steps:</p> <ul style="list-style-type: none"> <li>• Select a group in the <b>Selected Groups</b> box.</li> <li>• Use the <b>Baseline</b> up or down arrows to move the group to the bottom of the list.</li> <li>• Once you correctly select the baseline, (<b>baseline</b>) appears next to your selection.</li> </ul>
Step 2: Select Statistic	Default	Select to perform a default statistical analysis.
Step 2: Select Statistic	Advanced	Select to define additional statistical analysis options.
Step 2: Select Statistic	+	Click to access (and close) the advanced options.

Step 2: Select Statistic	Statistical Method	<p>a. Select the appropriate statistical method:</p> <ul style="list-style-type: none"> <li>• <b>T-test:</b> Two Sample Test to identify genes showing statistically significant differences between two samples.</li> <li>• <b>Wilcoxon Test:</b> Man-Whitney Test is the non-parametric test analog to the independent two-sample t-test. This test is used in place of a two-sample t-test when the populations being compared are not normal.</li> <li>• <b>F-test:</b> One Way ANOVA to identify genes showing statistically significant differences across two or more groups.</li> </ul> <p>b. If there are three or more predefined groups, F-test: One Way ANOVA is the default statistical method.</p> <p>c. When you select the F-test option to test a hypothesis of the means of two or more populations, the technique is called the <i>Analysis of Variance (ANOVA)</i>. The ANOVA simplifies the F-test, where F-test is the mean square for each main effect and the interaction effect divided by the <i>within</i> variance. A one-way ANOVA or single factor ANOVA tests differences between the groups classified only on one independent variable.</p> <p>d. Using ANOVA instead of multiple t-tests reduces the probability of a type-I error.</p>
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Step 2: Select Statistic	Multiple Comparison Adjustment	<u>Family-wise Error Rate (FWER):</u> Bonferroni  <u>False Discovery Rate (FDR):</u> Benjamini-Hochberg
Step 2: Select Statistic	Select constraint	Select the fold change ( through ) or enter an additional fold change to specify a range.
Step 2: Select Statistic	p-value	Enter a p-value.
Step 3: Select Array Platform	Select Array Platform	Select the array platform.

3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create a Class Comparison report, click the **Submit** button.

## Performing a Principal Component Analysis

To create a High Order Analysis with [Principal Component Analysis](#), follow these steps:

1. On the High Order Analysis tab, click the **Principal Component Analysis (PCA)** button.
2. The Principal Component Analysis (PCA) Form page enables you to define criteria to perform a PCA. When you access the page, Current Filter Settings display in the side bar. To modify the filter settings, see the following table.

3. You are required to complete at least one step for the Principal Component analysis. The following table lists the available criteria:

Criteria	Item Name	Special Instructions
Step 1: Select Group	Show all samples	Select to show all samples.

Step 1: Select Group	Select samples	<p>Select to specify the groups to include in the sample.</p> <p>A <i>group</i> is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics (See <a href="#">Managing Lists Overview</a>).</p> <div style="border: 1px solid #ccc; padding: 5px; margin-top: 10px;"> <span style="color: blue;">i</span> <b>Note</b>            User-defined PatientDID lists appear in red type in the side bar.         </div>
Step 1: Select Group	<ul style="list-style-type: none"> <li>• Existing Groups</li> <li>• Selected Groups</li> </ul>	Select at least two groups in the <b>Existing Groups</b> box and move them to the <b>Selected Groups</b> box.
Step 2. Filter Genes/Reporters	View Filter Settings	To use the default filter settings, continue to Step 3. Current settings display in the side bar.
Step 2. Filter Genes/Reporters	+ 	Click to access (and close) the advanced options.
Step 2. Filter Genes/Reporters	<ul style="list-style-type: none"> <li>• Constrain reporters by variance (Gene Vector) percentile: %</li> </ul>	Enter a percentage which selects the reporters whose variances of the log ratio (or Log2 signals) across all experiments were among the top percentile of variance of all reports identified. For example, 70% chooses reporters with the top 30 (100 - 70) percentile of variance.
Step 2. Filter Genes/Reporters	<ul style="list-style-type: none"> <li>• Use differentially expressed genes</li> </ul>	Drop down the list box and select a saved list of differentially expressed genes identified by class comparison. If you have not added a <a href="#">Gene List</a> with the REMBRANDT My Workspace function, none appears (see <a href="#">Adding New Lists</a> ).

Step 2. Filter Genes/Reporters	<ul style="list-style-type: none"> <li>• Use differentially expressed reporters</li> </ul>	Drop down the list box and select a saved list of differentially expressed reporters identified by class comparison. If you have not added a reporter list with the Class Comparison report, none appears (see <a href="#">Adding New Lists</a> ).
Step 2. Filter Genes/Reporters	<ul style="list-style-type: none"> <li>• Set These Filters as Default</li> </ul>	Click to save the options as default filter settings.
Step 3: Select Array Platform	Select Array Platform	Select the array platform.

4. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
5. To submit your criteria and create a Principal Comparison Analysis report, click the **Submit** button.
6. To clear the form, click **Clear**.
7. To cancel the analysis, click **Cancel**.

## Performing Hierarchical Clustering Analysis

To create a [High Order Analysis](#) with Hierarchical Clustering, follow these steps:

1. On the High Order Analysis tab, click the **Hierarchical Clustering Analysis** button.
2. The Hierarchical Clustering Analysis Form enables you to perform a clustering. When you access the page, Current Filter Settings display in the side bar. To modify the filter settings, see the following table

3. You are required to enter at least one step for the hierarchical clustering. The following table lists the available criteria:

Criteria	Item Name	Special Instructions
Step 1. Filter Genes/Reports	View Filter Settings	To use the default filter settings, continue to Step 3. Current settings display in the side bar.
Step 1. Filter Genes/Reports	+	Click to access (and close) the advanced options.

Step 1. Filter Genes/Reports	<ul style="list-style-type: none"> <li>Constrain reporters by variance (Gene Vector) percentile: %</li> </ul>	Enter a percentage which selects the reporters whose variances of the log ratio (or Log2 signals) across all experiments were among the top percentile of variance of all reports identified. For example, 70% chooses reporters with the top 30 (100 - 70) percentile of variance.
Step 1. Filter Genes/Reports	<ul style="list-style-type: none"> <li>Use differentially expressed genes</li> </ul>	Drop down the list box and select a saved list of differentially expressed genes identified by class comparison. If you have not added a <a href="#">Gene List</a> with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Step 1. Filter Genes/Reports	<ul style="list-style-type: none"> <li>Use differentially expressed reporters</li> </ul>	Drop down the list box and select a saved list of differentially expressed reporters identified by class comparison. If you have not added a reporter list with the REMBRANDT My Workspace function, none appears (see <a href="#">Managing Lists Overview</a> ).
Step 1. Filter Genes/Reports	<ul style="list-style-type: none"> <li>Set These Filters as Default</li> </ul>	Click to save the options as default filter settings.
Step 2. Select Statistic	Distance Matrix	Select a distance matrix option: <ul style="list-style-type: none"> <li><b>Pearson</b> correlation measures the relative shape of the gene regulations rather than the absolute levels. This is a natural choice, because it is widely used to measure gene correlations.</li> <li><b>Euclidean</b> distance is the most common distance measure. It measures the absolute level of gene regulation.</li> </ul>

Step 2. Select Statistic	Linkage Method	Select a linkage option to affect the shape of the resulting clusters: <ul style="list-style-type: none"> <li>• <b>Average</b> linkage is the average of all pair-wise distances between members of the two clusters.</li> <li>• <b>Single</b> linkage is the minimum distance between two clusters.</li> <li>• <b>Complete</b> linkage is the maximum distance between two clusters.</li> </ul>
Step 3. Cluster By	Cluster By	Leave the default to cluster on <b>Samples</b> or cluster by <b>Genes</b> .
Step 4. Select Array	Select Array Platform	Select the array platform.

4. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
5. To submit your criteria and create a Hierarchical Clustering Analysis report, click the **Submit** button.
6. To clear the form, click **Clear**.
7. To cancel the analysis, click **Cancel**.

## Performing an Integrative Genomic Viewer Analysis

This section describes sending data from REMBRANDT to Integrated Genomics Viewer (IGV) for analyses whose results can then be viewed in IGV. REMBRANDT uses Integrated Genomics Viewer (IGV) to visualize gene expression and segmented copy number data.

The IGV is a high-performance visualization tool for interactive exploration of large, integrated datasets. It supports a wide variety of data types including sequence alignments, microarrays, and genomic annotations.

For more information about the Integrative Genomics Viewer or to connect independently to the IGV home page, see [Integrative Genomics Viewer](#)



. You may also want to refer to the [IGV User Guide](#)



To perform an IGV analysis of gene expression data, or segmented copy number data, or both gene expression and segmented copy number data follow these steps:

1. On the High Order Analysis tab, click the **Integrated Genomics Viewer** button. The Integrated Genomics Viewer Integration Form page that opens enables you to define the criteria to perform Integrated Genomics Viewer data visualization.

**Integrative Genomics Viewer Integration Form**

Simple Search Advanced Search High Order Analysis View Results My Workspace Downloaded

[Analysis Home](#)

**Step 1: Select Group\* [?]**

Select 1 or More Groups

Existing Groups  
 ASTROCYTOMA  
 MIXED  
 NON\_TUMOR  
 OLIGODENDROGLIOMA  
 UNKNOWN

Selected Groups  
 GBM

**Step 2: Select Array Platform (Select at least one) [?]**

100K SNP Array  Affymetrix HG\_U133 Plus 2.0

**Step 3: Select SNP Analysis Method**

[Select Box]

**Step 4: Name Analysis Result\* [?]**

GBM analysis [ ] (should be unique)

Clear Cancel Submit

2. Complete the form is described in the following table:

Criteria	Item Name	Special Instructions
Step 1: Select Group	Existing Groups Selected Groups	A <i>group</i> is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics. Note that user-defined PatientDID lists appear in red type in the side bar.  Select one or more groups in the <b>Existing Groups</b> box and move them to the <b>Selected Groups</b> box.
Step 2: Select Array Platform	Select Array Platform	Select the array platform. For the current version of REMBRANDT, Affymetrix HG_U133 Plus 2.0 is for gene expression, 100K SNP array is for copy number.

Step 3: Select SNP Analysis Method	Select SNP Analysis Method	If 100K SNP array is selected, the user can Select the Analysis Method. Paired Tissue Samples (Tumor vs Blood), Unpaired Tissue Samples (Tumor vs Reference Samples), Blood Samples (Blood vs Reference Samples)
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3. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.
4. To submit your criteria and create an Integrated Genomics Viewer Analysis report, click the **Submit** button.
5. Once the data has been sent to Integrated Genomics Viewer, REMBRANDT directs you to the View Result page.

The screenshot shows a window titled "GenePattern Job Results [?]" with the following content:

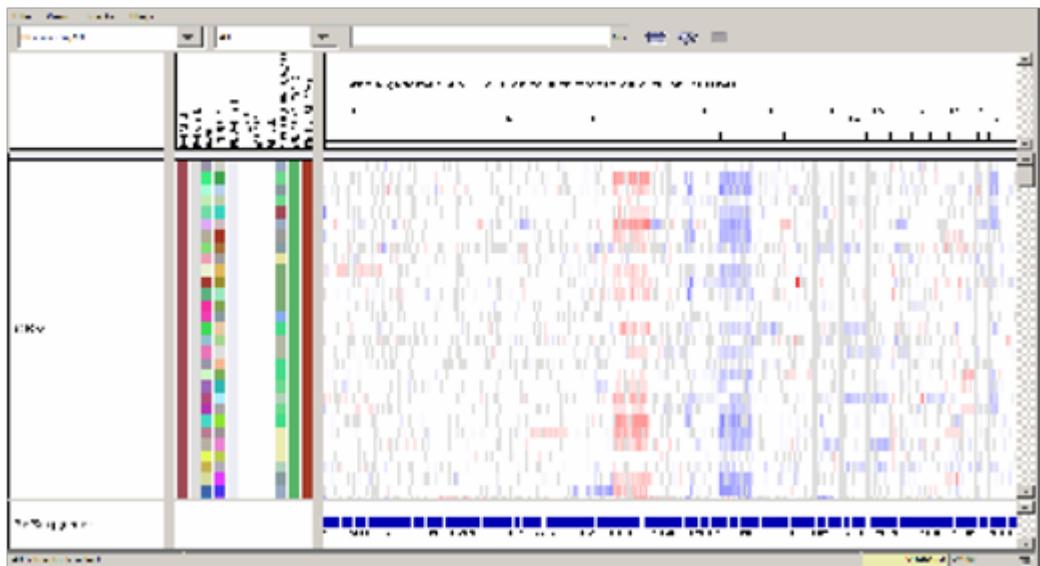
Your request has been sent to GenePattern for processing, and your job id is : **1353**. When your task is complete, your data will be ready for visualizer. Just click next to the link below to launch the visualizer you have selected. The approximate processing time is 2-8 minutes depending on the size of the dataset.

• [IGV Job# 1353 \(ibhtest\)](#)  running

All available GenePattern jobs

Please click the above link to launch GenePattern or to launch Visualizer. If your task does not appear in the sidebar, please wait a minute and refresh the GenePattern page to try again. If some of your jobs are not listed in the sidebar, they have been moved to the Job results menu.

6. Click the forward button next to the completed analysis to open the results. An example is below. IGV results display from the analysis criteria you set in REMBRANDT.



- To clear the form, click **Clear**. To cancel the analysis, click **Cancel**.

## Performing a GenePattern Analysis

REMBRANDT provides two means to use GenePattern to analyze gene expression data.

- This section describes sending data from REMBRANDT to GenePattern for analyses whose results can then be viewed in REMBRANDT.
- The following section describes how to launch GenePattern itself so you can work within that application.

To perform a GenePattern analysis of gene expression data, follow these steps:

- On the High Order Analysis tab, click the **Send Data to GenePattern** button.
- The GenePattern Integration Form page that opens enables you to define the criteria to perform GenePattern

data analyses.

- Complete the form as described in the following table:

Criteria	Item Name	Special Instructions
Step 1. Select Group	Existing Groups Selected Groups	A is a pre-defined or user-defined PatientDID list comprising patient identifiers with certain characteristics (See on page 89). Note that user-defined PatientDID lists appear in red type in the side bar.  Select two groups in the box and move them to the box.

Step 2. Select Array Platform	Select Array Platform	Select the array platform. For the current version of REMBRANDT, Affymetrix is the sole option.
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4. You must enter a title/name for this analysis in the **Name Analysis Result** text box. This name must be unique among all your queries in this session.

5. To submit your criteria and create a GenePattern Analysis report, click the **Submit** button.

Once the data has been sent to GenePattern, REMBRANDT directs you to the View Result page. For more information, see [GenePattern Analysis Reports](#).

- To clear the form, click **Clear**.
- To cancel the analysis, click **Cancel**.

## Launching GenePattern

To launch a session in the GenePattern application, on the High Order Analysis page, click **Launch Gene Pattern Application**. You can perform many gene expression analyses working within GenePattern itself. For more information about using GenePattern, click the online help links within the application.

## 5 Viewing REMBRANDT Results v1.5.8

### 5 Viewing REMBRANDT Results v1.5.8

This section describes reports and search results that REMBRANDT returns after advanced searches and high order analyses. You can also download the product BRB Array Tools and the static BRB-ArrayTools archive files.

Topics in this section include the following:

- [Results Overview](#)
- [Notification of Prolonged Queries](#)
- [Clinical Reports](#)
  - [Viewing Clinical Plots](#)
- [Advanced Search or Query Results](#)
  - [Gene Expression Sample Report](#)
    - [Filtering Results by Gene or Reporter \(Filter Toolbar\)](#)
    - [Highlighting Results By Value \(Highlight Toolbar\)](#)
    - [Selecting and Saving Sample Results \(Select Samples Toolbar\)](#)
    - [Differentiating Data \(Show All Values Toolbar\)](#)
    - [Removing Columns \(Hide Diseases toolbar\)](#)
    - [Showing Additional Information](#)
  - [Copy Number Sample Report](#)
- [High Order Analysis Results](#)
  - [Class Comparison Report](#)
    - [Filtering a -value \(Filter p-value Toolbar\)](#)
    - [Selecting and Saving Reporters \(Select Reporters toolbar\)](#)
    - [Resorting Column Results](#)

- [Principal Component Analysis Plot](#)
  - [Viewing a Three-dimensional Principal Component Analysis \(PCA\)](#)
  - [PCA Icons](#)
- [Hierarchical Clustering Report](#)
- [GenePattern Analysis Reports](#)

## Results Overview

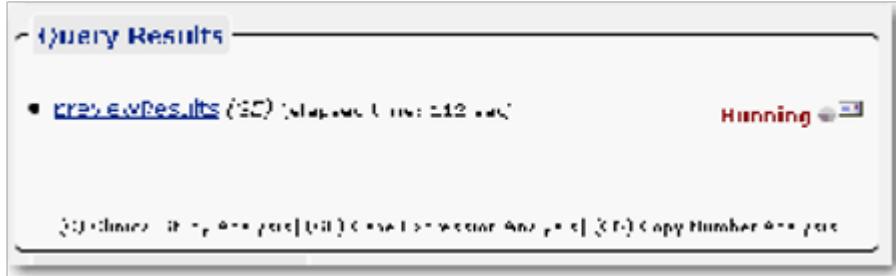
When you open the View Results tab after launching an advanced query, the page displays queries in progress or newly completed. If you have opened this tab using the Preview, the Finalize Query or Refine Query buttons, you may see the icon that monitors the timing of the query.

The View Results page shows a collection of reports previously viewed in a particular user session. This allows you to compare reports by opening them in separate windows or even in spreadsheet format. For example, you can compare clinical and gene expression reports with a set of patient samples. You can view Clinical reports, results generated with the Advanced Search function and the High Order Analysis function.

## Notification of Prolonged Queries

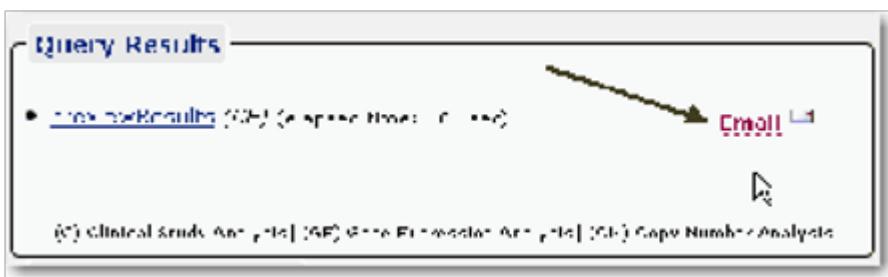
Once you execute an advanced query, either through the **Preview**, **Finalize Query** or **Refine Query** button, if the query takes longer than 45 seconds, REMBRANDT provides you the option of being notified by email when the query ends.

1. After you execute the search by clicking any of those buttons, the system opens the View Results tab which displays a monitor of the elapsed time for the query.



The Checking Status monitor refreshes every 10 seconds.

2. After 45 seconds, REMBRANDT displays a letter icon (✉) on the tab. If you click the icon, a dialog box opens where you can enter your email address. The system first validates your email address, then displays an email link.



3. If you mouse over the link, a popup indicates that you will be notified by email when the results are ready. The results are saved in REMBRANDT for 5 days.

4. In the email you receive, you can click the link to the query. After you log into REMBRANDT, click the View Results tab to retrieve the query results.
- The query report is available only to the user who generates the report. Other logged in users will not be able to see the report.

**Note**

The query continues even if you log out of REMBRANDT.

## Clinical Reports

A Clinical report displays patient demographics, therapy, and outcome data. This information is displayed in a single domain, such as gene expression, or in multiple domains that combine queries, such as gene expression, chromosomal aberrations, and clinical areas. On the Clinical page, you can save samples to a [PatientDID list](#) stored in the My Workspace function. To save samples, follow these steps:

**Note**

When either a gene expression filter and/or a copy number filter is applied with the Advanced Search function, hyperlinks are provided in this report to display the gene expression and/or copy number data for a particular sample.

1. There are two ways to select samples on the Clinical window:

The screenshot shows the REMBRANDT Clinical interface. At the top, there's a header with the REMBRANDT logo and some navigation icons. Below the header, a search bar says "Clinical (Query Name: Rembrandt\_results\_1)" and has a link "Show Clinical Plots for these samples". There are also "Show Help Form Tools" and "Show Help Form Tools" buttons. A note "Displaying: 1 - 20 of 30 records" is shown with a "2 pages(s) [1] [2]" link and a "per page" dropdown set to 25. The main area is a table with the following columns: Sample, Age at Dx (years), Gender, Survival (months), Disease, Grade, Race, Karnofsky, and N. The table contains 15 rows of sample data, each with a checkbox in the first column. The data includes various tumor types like Astrocytoma, Glioblastoma, and Meningeal tumor, along with their respective demographic and clinical details.

Sample	Age at Dx (years)	Gender	Survival (months)	Disease	Grade	Race	Karnofsky	N
HF0017	45-49	M	>30M	ASTROCYTOMA	II	--	--	--
HF0023	50-64	F	10-60M	ASTROCYTOMA	II	--	--	--
HF0050	50-54	F	24-30M	GBM	IV	--	--	--
HF0087	50-64	F	>60M	OLIGODENDROGLIOMA	--	--	--	--
HF0083	55-69	F	08-09M	GBM	IV	--	--	--
HF0189	30-34	M	>30M	ASTROCYTOMA	II	--	--	--
HF0223	45-49	M	42-60M	ASTROCYTOMA	II	--	--	--
HF0252	35-39	M	>60M	MENINGEAL	II	--	--	--
HF0305	30-34	M	48-60M	MENINGEAL	II	--	--	--
HF0350	55-59	F	18-24M	GBM	IV	--	--	--
HF0434	50-64	M	05-06M	OLIGODENDROGLIOMA	II	--	--	--
HF0442	45-49	M	10-24M	GBM	IV	--	--	--

2. To select an individual sample, select the box in the **Sample** column.

**Note**

Selecting individual items in the list may not be available for all Clinical reports.

Sample	Age at Dx (years)	Gender	Survival (months)	Disease	Grade	Race	Ka
HF0017	45-49	M	>60M	ASTROCYTOMA	II	-	-
HF0026	60-64	F	48-50M	ASTROCYTOMA	II	-	-
HF0050	50-54	F	24-30M	GEM	N	-	-
HF0007	60-64	F	>60M	OLIGODENDROGLIOMA	--	-	-
HF0083	65-69	F	06-08M	GEM	N	-	-

3. To select all of the samples, select the **All** box. To display a list of the **selected samples**, click the samples selected link.

Clinical (Query Name: Rembrandt_results_0) Show Clinical Info for these samples Show Help Page in Tools				
<input checked="" type="checkbox"/> Rembrandt_results_0   <input type="checkbox"/> Other selected samples   <input checked="" type="checkbox"/> All 33 samples selected (View samples)				
<b>Displaying:</b> 1 - 25 of 33 samples selected   <b>2 pages</b>   <b>Help</b>   <b>Selected Samples:</b>				
Sample	Age at Dx (years)	Gender	Survival (n)	
<input checked="" type="checkbox"/> HF0017	45-49	M	>60M	
<input checked="" type="checkbox"/> HF0018	60-64	F	<60M	

To clear all of the samples, click the clear samples link.

- To save the selected samples, enter a unique name for the PatientDID list next to **Select Samples**, or maintain the current name.

ClinicalQuery Name:Rembrandt_Results(0) Show Clinical Data for these samples [Download CSV Tools]								
My Samples		Selected samples		<input checked="" type="checkbox"/> All 30 samples selected (clear samples)				
Displaying 1 - 20 of 30 records <a href="#">Next</a>		2 pages( <a href="#">1</a> <a href="#">2</a> )		25 per page <a href="#">Change</a>				
Sample	Age of Dx (years)	Gender	Survival (months)	Disease	Grade	Race	Kar	Notes
<input checked="" type="checkbox"/> HF0017	45-49	M	>60M	ASTROCYTOMA	III	--	--	
<input checked="" type="checkbox"/> HF0026	60-64	F	48-60M	ASTROCYTOMA	III	--	--	
<input checked="" type="checkbox"/> HF0050	50-54	F	24-30M	ASTROCYTOMA	IV	--	--	
<input checked="" type="checkbox"/> HF0087	60-64	F	>60M	ASTROCYTOMA	IV	--	--	
<input checked="" type="checkbox"/> HF0099	65-69	F	06-09M	ASTROCYTOMA	IV	--	--	
<input checked="" type="checkbox"/> HF0189	30-34	M	>60M	ASTROCYTOMA	III	--	--	
<input checked="" type="checkbox"/> HF0223	45-49	M	42-48M	ASTROCYTOMA	III	--	--	

5. Click the **Save Selected Samples** button. *Sample List Saved* appears.
  6. Click the **OK** button.
  7. Once saved, the sample set is listed in red type under PatientDID List in the side bar.
  8. Note: The sample set name will also appear on the Refine Query page, in the **Select the Result set to apply the above query** drop-down list. This enables you to add the saved sample set to another query.
  9. To show clinical plots for the selected samples, click **Show Clinical Plots for these Samples** at the top of the window (see [Viewing Clinical Plots](#)).
  10. To export only the samples you select to an Excel spreadsheet, select the samples and click the **Download for Excel** icon. The spreadsheet opens displaying data for the selected samples.

	A	B	C	D	E	F	G	H	I	J	K
1	Sample	Age at Di.	Gender	Residence	Diabetes	Smokes	Phone	Health Risk	Comorbidity	Drugs being M.	
2	388021	30-54	M	10-14	NMEDU	-	WHITE	JUST	-	-	-
3	309109	50-54	M	--	EDU	-	WHITE	4 MEDU	-	-	-
4	309161	50-54	M	--	UNKNOWN	-	WHITE	4-H MEDU	100 100	100 100	-
5	388167	65-69	M	12-15N	EDU	-	WHITE	JAN4-A	5	-	4

## Viewing Clinical Plots

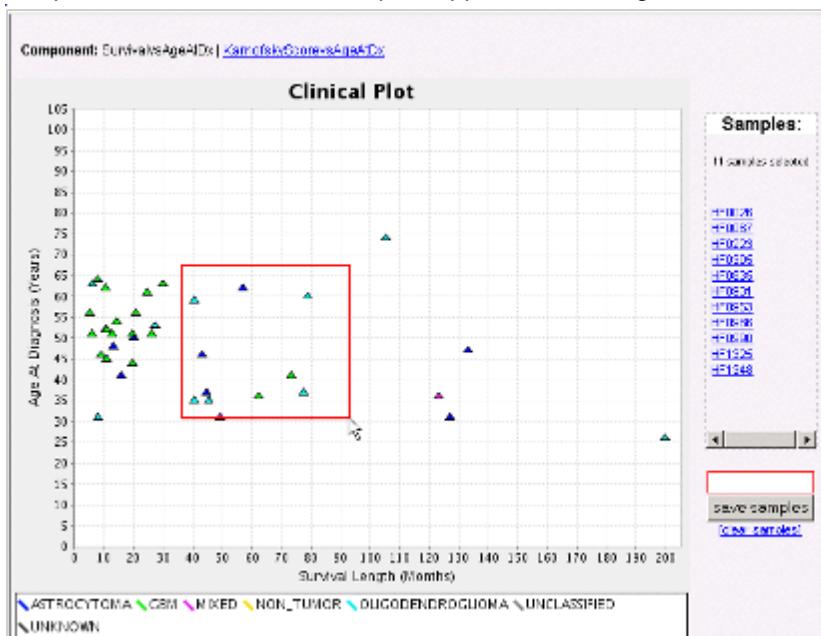
On certain clinical plots, you can display two kinds of clinical plots:

- **Survival vs Age at Dx** (diagnosis in years) indicates the survival or number of months versus the age at diagnoses in years. The data points are colored by disease type.
- **Karnofsky score** (Neurological assessment) Vs Age at Dx (diagnosis in years) indicates the [Karnofsky score](#) or neurological assessment versus the age at diagnosis in years. The data points are colored by disease type.

To toggle between the different types of plots, click the [SurvivalvsAgeatDx](#) link or the [KarnofskyscoreVsAgeatDx](#) link.

To select the samples of interest, follow these steps:

1. Click and drag a rectangle around the samples to save for future use. A red rectangle appears around the samples, and the list of the samples appears on the right-hand side.



To clear the samples, and select another group, click the **clear samples** link under the **Save Samples** button

2. To help lasso the points on the plot and identify the location of these points, mouse over a sample name in the list. A yellow circle appears on the plot where the sample is located.
3. To save the selected samples to a file, enter a name for the samples in the text box, and click the **Save Samples** button.

## Advanced Search or Query Results

The following Advanced Search reports are generated:

- [Gene Expression Sample Report](#)
- [Copy Number Sample Report](#)

View Results display the query name and the output generated for the query. To view the report, click the report name and the file opens in a new window.

The screenshot shows the REMBRANDT Query Results interface. At the top, there are tabs for 'Compound Query', 'Institutions', and 'View'. Below these, a 'Clinical View' section is selected. Underneath, there are two main links: 'Gene Expression Data for Sample View' and 'Gene Expression Data for IMAGE clone View'.

All Advanced Search options (Gene Expression, Copy Number Data, and Clinical) generate a Clinical report. For more information about Clinical Reports, see [Clinical Reports](#).

## Gene Expression Sample Report

The Gene Expression Sample report displays gene expression ratios (between the tumor sample and the geometric mean of non-tumor samples) for each probeset (or IMAGE clone) for the genes selected in the queries. Each column represents a sample, and the samples are grouped by tumor sub-type. For Affymetrix probesets, the ratio of the absolute expression values of the tumor sample and the geometric mean of the expression value of the non-tumor samples displays. For each IMAGE clone, missing values are handled and the ratio of expression values between the tumor and geometric mean of the non-tumor group is calculated for each sample.

### Note

To display a clinical report for all samples, click the **View Clinical Report for All Samples** link. For more information, see [Clinical Reports](#).

When two queries are included in the results, the results are separated by a double line and the query information is listed at the bottom.

The screenshot shows the REMBRANDT Gene Expression Sample report for 'ASTROCYTOMA Samples'. The interface includes a toolbar with various icons, a filter toolbar, and a main data grid.

**Filter Toolbar:**

- Show Only: Radio button selected.
- Hide: Radio button.
- Gene: Drop-down menu.
- Filter: Button.
- Reset: Button.

**Highlight:** Buttons for 'Highlight values', 'Highlight', and 'Clear Highlighting'.

**Select Samples:** Buttons for 'Gene expression query', 'Save Sample', 'Checklist', and 'Unchecklist'.

**Show All Values:** Buttons for 'Show all values in this report' and 'Show Previous Report'.

**Hide Diseases:** Checkboxes for 'ASTROCYTOMA', 'CNS', 'CNS tumor', 'CNS/extra CNS tumor', and 'EXCLUDED'.

**Displaying:** Text indicating '1 - 5 of 15 records' and '25 per page'.

**Gene Reporter:** Column header for the data grid.

**Data Grid:** Shows expression values for genes EGFR\_1565483\_at, EGFR\_1565484\_x\_at, EGFR\_201983\_s\_at, EGFR\_237930\_at, and EGFR\_243327\_at across samples F00137 through F00223.

Gene Reporter	ASTROCYTOMA Samples									
	F00137	F00214	F00262	F00117	F00206	F00189	F00223	F00208	F00220	F00221
EGFR_1565483_at	0.3100	0.4000	0.1800	2.3200	5.3300	2.7700	2.5500	8.8900	0.2	0.2
EGFR_1565484_x_at	0.5400	1.2200	0.2800	1.5400	2.0600	0.9200	1.8100	4.0300	0.3	0.3
EGFR_201983_s_at	1.2500	5.8300	4.3500	12.0800	8.3400	6.6400	6.4500	31.9100	4.2	4.2
EGFR_237930_at	2.2600	0.6900	0.0000	0.6700	2.9900	2.7800	2.6500	1.0000	1.0	1.0
EGFR_243327_at	0.6200	0.0000	1.0400	2.2100	2.1100	2.0900	1.9800	14.2100	0.4	0.4

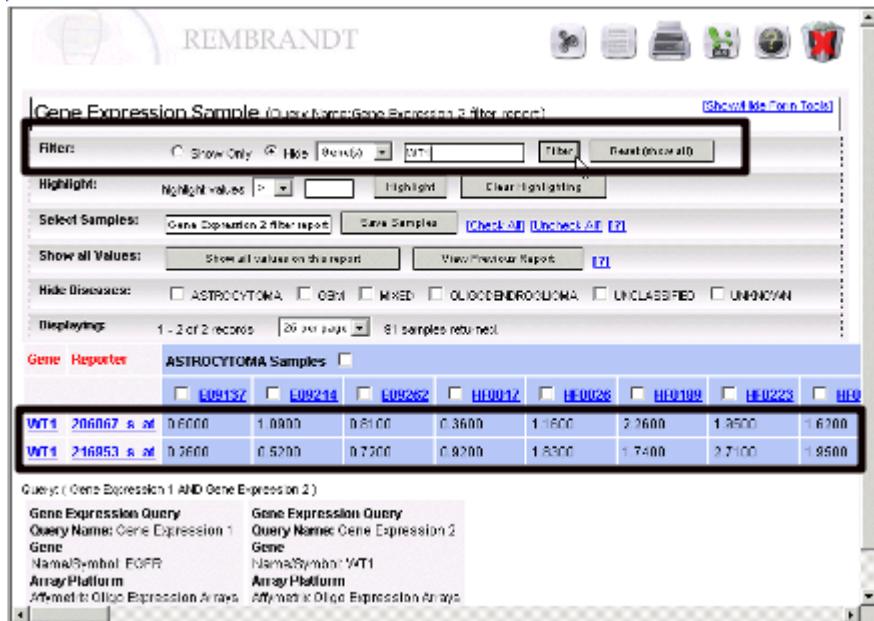
## Filtering Results by Gene or Reporter (Filter Toolbar)

To filter a report, follow these steps:

- From the **Filter** toolbar, select the filter mode **Show only** or **Hide**.
  - Select **Gene** or **Reporter** from the drop-down list, and enter gene or reporter to be filtered.
- For example, if you click **Show Only**, select **Gene**, and enter WT1. Only WT1 samples appear in the list.

3. Click the **Filter** button.

The results are filtered based on your selections.



4. To show all of the samples again, click the **Reset (show all)** button.

**Note**

You can use more than one toolbar to limit the samples shown in the results. For example, you can filter the results and then highlight certain filtered results.

## Highlighting Results By Value (Highlight Toolbar)

To highlight certain data, follow these steps:

1. From the **Highlight** toolbar, select an operator and a threshold value.  
For example, select < 5 to highlight all values less than 5.
2. Click the **Highlight** button.  
The values that meet this criteria are highlighted in yellow.

- To restore the report to its original state and clear the highlighting, click the **Clear Highlighting** button.

**Note**

You can use more than one toolbar to limit the samples shown in the results. For example, you can filter the results and then highlight certain filtered results.

### Selecting and Saving Sample Results (Select Samples Toolbar)

You can save samples to a PatientDID list stored in the My Workspace function. PatientDID lists enable you to further filter advanced queries. To save samples, follow these steps:

- On the sample report, there are several ways to select samples.
- To select all the listed samples on the **Select Samples** toolbar, click the **Check All** link. To deselect all the listed samples, click the **Uncheck All** link.

- To select (or deselect) all the samples in a sample group, click the box next to the sample group name, for example, the box next to **ASTROCYTOMA Samples**. All the samples in the group are selected.
- To select (or deselect) an individual sample within a group, click the box in the column next to the sample

name.

Gene	Reporter	ASTROCYTOMA Samples			
WT1	206067 s. ar	E09137	E09214	E09262	HR0017
		0.6000	1.0000	0.5700	0.3600
WT1	216953 s. ar	0.3600	0.5200	0.7300	0.9200

5.  
6. To save the selected samples, enter a unique name for the PatientDID list next to **Select Samples**, or maintain the current name.



7. Click the **Save Samples** button.  
8. Once saved, the sample set is listed in red type under PatientDID List in the side bar.

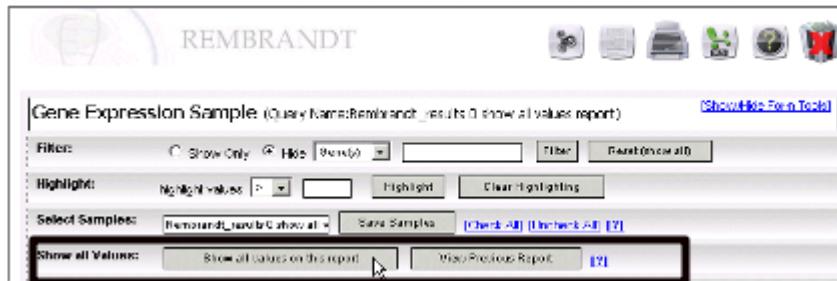
#### Note

The sample set name will also appear on the Refine Query page, in the Select the Result set to apply the above query drop-down list. This enables you to add the saved sample set to another query.

### Differentiating Data (Show All Values Toolbar)

To differentiate between missing values in the array and data that did not meet your search criteria, follow these steps:

1. Click **Show All Values** on this Report on the Show all Values toolbar.



2. The samples that did not meet your criteria, appear in gray. A value of Null indicates a missing value for that reporter.  
3. To display the previous report before you clicked the **Show All Values on this Report** button, click the **View Previous Report** button.

### Removing Columns (Hide Diseases toolbar)

To remove a disease from the report, select the check box for the disease in the **Hide Diseases** toolbar. The checked disease is NOT included in the results.

Gene	Reporter	MIXED Samples	UNKNOWN Samples						
FGFR	<a href="#">1565483_at</a>	<input type="checkbox"/> <a href="#">HGU252</a>	<input type="checkbox"/> <a href="#">HGU358</a>	<input type="checkbox"/> <a href="#">HGU297</a>	<input type="checkbox"/> <a href="#">HGU412</a>	<input type="checkbox"/> <a href="#">HGU298</a>	<input type="checkbox"/> <a href="#">HGU299</a>	<input type="checkbox"/> <a href="#">HGU295</a>	<input type="checkbox"/> <a href="#">HGU296</a>
FGFR	<a href="#">1565484_x_at</a>	1.9800	2.3800	3.0300	0.4800	0.5700	0.6800	1.9400	0.7200
FGFR	<a href="#">201963_s_at</a>	1.3800	1.5400	1.7300	1.2300	0.9500	0.7600	1.6600	0.7900

## Showing Additional Information

When results are listed in a report, row or column items may appear as links. These links may be for genes, reporters, cytobands, or sample names. Click the link to display additional information about the item.

For example, to display more information about a gene, click the gene symbol link.



The Cancer Genome Anatomy Project (CGAP) browser opens.

## Copy Number Sample Report

The Copy Number Data Per Sample report displays the copy number data from Affymetrix 100K SNP arrays. The CHP files from the Affymetrix Gene Chip Operating System were processed using the Affymetrix GDAS (GeneChip® DNA Analysis Software). Copy number data was collected for each mapping SNP reporter on the Chip, for all the tumor samples. Each column represents a sample, and the samples are grouped based on the tumor sub-type.

### Note

To display a clinical report for all samples, click the [View Clinical Report for All Samples](#) link.  
For more information, see [Clinical Reports](#).

Cytoband	Genes	Reporter	ASTROCYTOMA Samples		
			<a href="#">900_00_1961 (00715851_B)</a>	<a href="#">900_00_1961 (00715851_T)</a>	<a href="#">900_00_5</a>
7p11.2	EGFR	<a href="#">SNP_A-1701575</a>	0.9116	2.2551	0.8110
7p11.2	EGFR	<a href="#">SNP_A-1671426</a>	3.3968	2.1946	3.1835
7p11.2	EGFR	<a href="#">SNP_A-1676976</a>	3.8239	2.1141	3.2781
7p11.2	EGFR	<a href="#">SNP_A-1648981</a>	2.2841	3.1123	2.0798
7p11.2	EGFR	<a href="#">SNP_A-1650715</a>	1.8950	2.4480	4.2884

## High Order Analysis Results

The following High Order Analysis reports are generated:

- [Class Comparison Report](#)
- [Principal Component Analysis Plot](#)
- [Hierarchical Clustering Report](#)
- [GenePattern Analysis Report](#)

[View Results \(\)](#) displays the query name and lists the output generated for the query.

Compound	Query	Institution	Status
Gene_Exp_1			<a href="#">Clinical View</a> <a href="#">Gene Expression Data Per Sample View</a> <a href="#">Gene Expression Data Per Sample Sheet View</a>
Gene_Exp_2			<a href="#">Clinical View</a> <a href="#">Gene Expression Data Per Sample View</a> <a href="#">Gene Expression Data Per Sample Sheet View</a>

## Class Comparison Report

The Class Comparison report displays group average, fold change, and *p*-value based on the Advanced Search parameters that you selected. The output varies based on the statistical method chosen.

For **T-test or Wilcoxon Statistical Method** analysis, the Class Comparison report is as follows.

- The report displays the group average, where the numerator is the mean of log(base 2) expression signals from the samples in the first group. The denominator is the mean of log(base 2) expression signals from the samples in the second group.
- The fold change for the reporter between the selected groups appears along with *p*-value.
- Gene symbol annotations appear for each reporter. To obtain extensive annotations, click the Excel icon on the upper right-hand corner of the report.

The screenshot shows the REMBRANDT Class Comparison interface. The main window displays a table of gene expression data. The columns include Reporter ID, Group Avg, P-Value, Fold Change, and Gene Symbol. The table lists 29 genes, each with a corresponding URL in blue. The 'Displaying' section at the top indicates 1 - 29 of 716 records.

Reporter	Group Avg	P-Value	Fold Change	Gene Symbol
<a href="#">202456_s_at</a>	7.480475.3897	2.66e-3	3.1238	ZNF11BL
<a href="#">232328_st</a>	4.151215.3740	4.34e-2	2.1777	ZNF552
<a href="#">232228_st</a>	6.703877.7833	1.81e-2	-2.1134	ZNF520
<a href="#">213819_st</a>	0.727175.7180	1.51e-2	-0.9708	ZNF302
<a href="#">210780_s_at</a>	6.675877.3420	2.51e-2	2.5209	ZNF300
<a href="#">234701_st</a>	6.863375.2410	1.39e-3	3.0785	ZNF326
<a href="#">213820_st</a>	7.162275.0310	1.88e-2	2.1934	ZNF208
<a href="#">232408_st</a>	0.329074.8170	2.22e-2	9.2781	ZNF192
<a href="#">202317_s_at</a>	4.804575.9800	2.07e-2	-2.8235	ZF

For an **F-test** Statistical Method analysis, the difference is that in the results there is a group average displayed for each group.

The screenshot shows the REMBRANDT Class Comparison F-Test interface. The main window displays a table of gene expression data. The columns include Reporter ID, GRM Group Avg, NON\_TUMOR Group Avg, MZFO Group Avg, P-Value, and Fold Change. The table lists 6 genes, each with a corresponding URL in blue. The 'Displaying' section at the top indicates 1 - 6 of 11 records.

Reporter	GRM Group Avg	NON_TUMOR Group Avg	MZFO Group Avg	P-Value	Fold Change
<a href="#">232172_st</a>	1.3040	1.5103	2.514	8.80e-13	11.2387
<a href="#">200855_s_at</a>	14.0808	13.2773	14.1057	1.58e-12	3.6514
<a href="#">201645_st</a>	12.3876	8.3444	11.4177	3.34e-12	16.4869
<a href="#">220735_s_at</a>	8.4072	10.0793	8.3992	9.37e-12	2.1861
<a href="#">211862_st</a>	12.7108	9.5293	12.9117	6.09e-12	10.1498
<a href="#">209820_s_at</a>	9.1604	7.7208	8.7900	7.45e-12	2.6841

### Filtering a -value (Filter p-value Toolbar)

To filter a *p*-value, follow these steps:

- From the **Filter p-value** toolbar, select an operator from **Show Values** and enter a threshold value.
- Click the **Filter** button.

The results are filtered based on your selections.

Reporter	Group Avg	P-Value	Fold Change	Gene Symbol
<a href="#">20144_st</a>	11.5530	9.7364	4.50e-6	3.5225
<a href="#">213074_st</a>	8.3009	7.5033	5.11e-6	2.0002
<a href="#">155566_st</a>	4.6903	3.1205	5.85e-6	2.9583
<a href="#">206896_st</a>	9.0019	5.1386	8.30e-6	14.5532
<a href="#">228810_st</a>	19.4552	12.1808	1.29e-6	2.4531
<a href="#">200159_st</a>	10.5928	7.1103	1.26e-6	2.4006
<a href="#">201661_st</a>	6.4218	7.0064	2.20e-6	2.6662

- To show all of the samples again, click the **Reset (show all)** button.

**Note**

You can use more than one toolbar to limit the samples shown in the results. For example, you can filter the results and then highlight certain filtered results.

### Selecting and Saving Reporters (Select Reporters toolbar)

- There are several ways to select reporters in the result list:
  - From the **Select Reporters** toolbar, select a reporter type from the **Type** drop-down list. The reporters with the selected criteria are displayed.
  - To select all of the results, click the **All on all pages** box.
  - To select one row of results at a time, click the box on the left side of the result row.

Reporter	Group Avg	p-value	Fold Change	Gene Symbol
<a href="#">202108_st</a>	11.7264	0.4651	1.64e-13	4.8073
<a href="#">201546_st</a>	13.3876	8.3444	3.09e-13	16.4866
<a href="#">203620_st</a>	9.1584	7.7288	4.40e-13	2.6941
<a href="#">201524_st</a>	7.5968	5.2674	5.40e-13	4.9568
<a href="#">203620_st</a>	12.7108	9.5203	8.59e-13	9.1201
<a href="#">202472_st</a>	6.3208	4.7308	7.55e-13	11.2357
<a href="#">215306_st</a>	11.8665	9.7890	7.71e-13	4.1915

- To clear the selected reporters, click the **clear reporters** link.
- To save the selected reporters, enter a unique name for the Reporters list next to **Select Reporters**, or

maintain the current name. The name varies based on the type of Statistical Method selected for the analysis.

4. Click the **Save Reporters** button.
5. Once saved, the Reporters list appears in red type under Reporter Lists in the side bar.
6. Click the **OK** button.

**Note**

You can use more than one toolbar to limit the samples shown in the results. For example, you can filter the results and then highlight certain filtered results.

## Resorting Column Results

To sort a column in a report, follow these steps:

1. If a report column has red triangles pointing up and down next to the name, you can sort a column of numeric or alphabetical values.

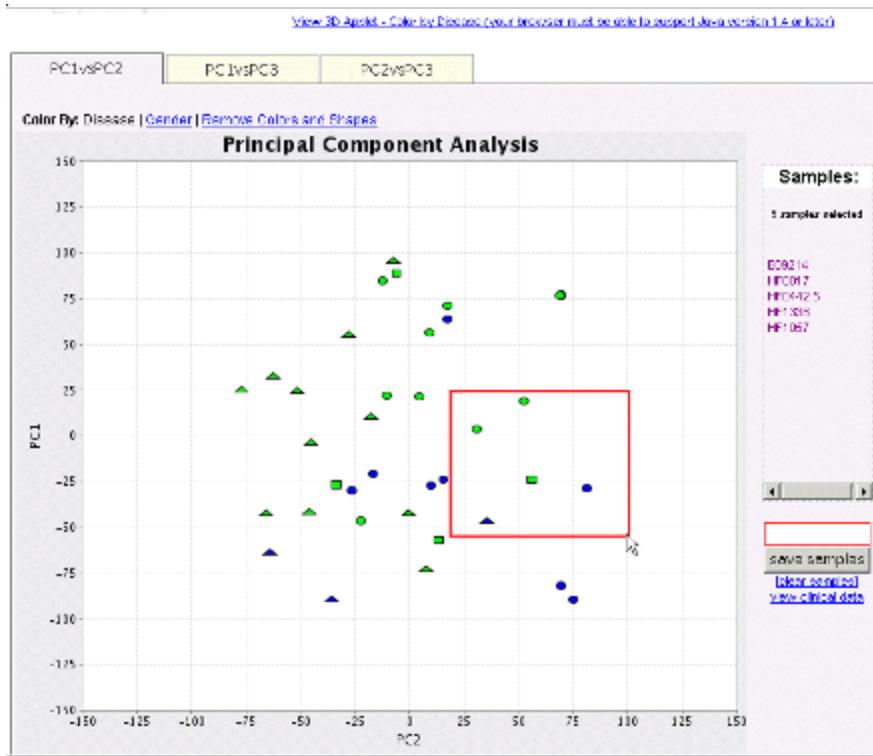
Field Change	▲▼
-0.1824	
-6.7056	
6.5246	
-5.3992	
-5.3720	
5.1233	
-4.9571	

2. To sort a column in ascending order, select the red triangle pointing up. To sort a column in descending order, select the red triangle pointing down.

## Principal Component Analysis Plot

The Principal Component Analysis plot is a two-dimensional graph which plots the various principal components from the analyses. The following list describes the different areas of the plot:

- To review a three-dimensional version of the color by disease PCA, click the **View 3D Applet - Color by Disease** link at the top of the page (see [Viewing a Three-dimensional Principal Component Analysis \(PCA\)](#)).
- The three tabs at the top of the page enable you to display **PC1 versus PC2**, **PC1 versus PC3**, or **PC2 versus PC3**.
- Each point on the graph represents a sample. By default, the samples are colored by Disease. To color by gender, click the **Gender** link or **Remove Colors and Shapes**.
- At the bottom of the graph, there is a legend defining how the different shapes on the graph indicate different survival ranges for patients.
- The Samples area enables you to select, review, and save samples in the plot (see [Viewing Clinical Plots](#)). You can also display clinical data for the PCA analysis, by clicking the **view clinical data** link.



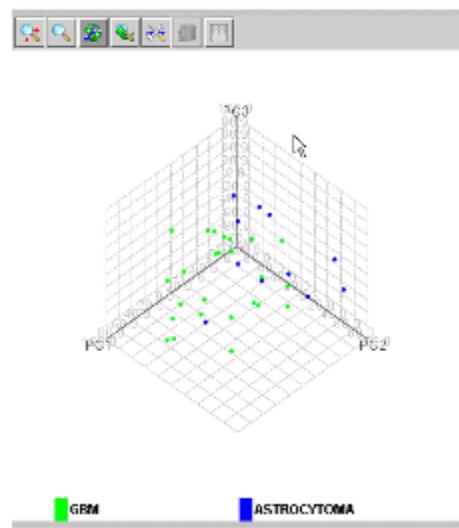
## Viewing a Three-dimensional Principal Component Analysis (PCA)

The three-dimensional Principal Component Analysis enables you to view PCA plot data in three dimensions. For more information about the PCA plot, see [Principal Component Analysis Plot](#). The applet supports Java Plugin versions 1.4.x and 1.5.x. For assistance with the plugin, refer to the links at the top of the page.

The following table provides general tasks you can perform with the three-dimensional PCA view:

Task	Instructions
Highlight all points in a data set (in black)	Click on a legend label or click on a single point in the plot.
Rename a dataset	Double-click on a legend label and enter a new name.
Show the values for a single point	Right-click on a point in the plot. Right-click again to remove the values.
Open the points of a dataset into a spreadsheet view	Double-click on a point on the plot.

Don't know what browser you have installed? If you'd like help installing the plug-in? Visit this site: <http://www.jnsoftware.com/help/index.html> for details.



## PCA Icons

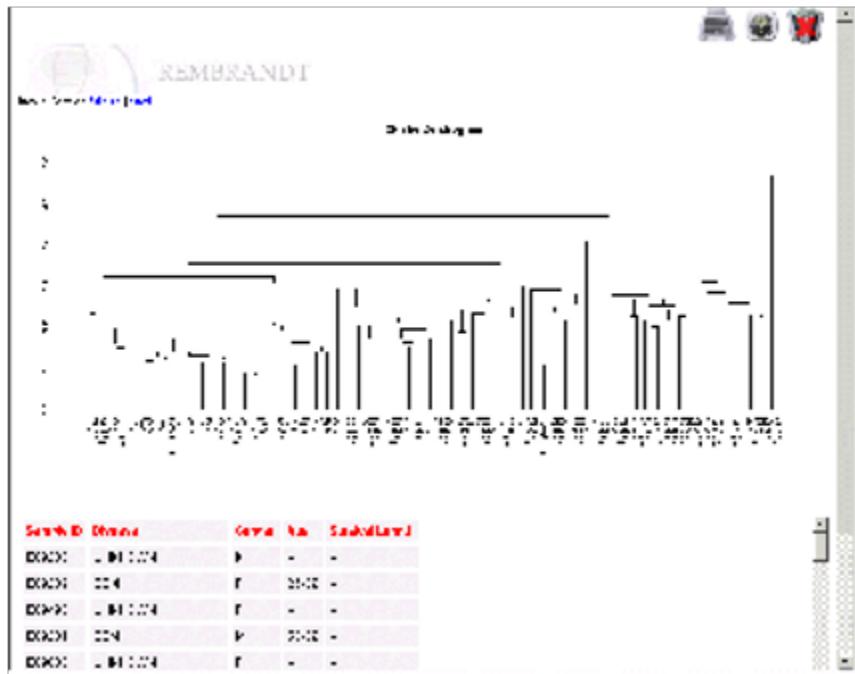
The following table describes the icons:

Icon	Special Instructions
	Moves the plot around the page. Click the button, and click and drag the plot.  To return to the original 3-D view, click .
	Magnifies a selected area on the plot. Click the button, and click and drag the box around an area on the plot. The selected area is magnified.  To move within the area, click  . To return to the original 3-D view, click .
	Moves and spins the plot, so you can display clusters. Default tool selected when the page displays. Click the button, and click and drag the plot to rotate the plot in the 3-D space.
	Returns to the original 3-D view. Click the button to cancel a zoom or return to the original axes or placement on the page.
	Not applicable to a Principal Component Analysis plot.

	Not available.
	<p>Displays a spreadsheet view of the data with each dataset in a separate tab. Click the button, and the spreadsheet view appears. From the spreadsheet view, you can perform the following tasks:</p> <ul style="list-style-type: none"> <li>• To remove a dataset, uncheck  . All data from the set is removed from the main plot.</li> <li>• To copy the data to the clipboard, click  .</li> <li>• To change the color of a data group, click the color box next to  .</li> </ul>

## Hierarchical Clustering Report

The Hierarchical Clustering report displays the dendrogram from the hierarchical clustering analysis. To display the image at full resolution, click on **full size** at the top left-hand corner of the graph. Based on the cluster parameter that you select, the report displays either sample or reporter annotations beneath the dendrogram.



To perform a Hierarchical Clustering analysis, see [Performing Hierarchical Clustering Analysis](#).

## GenePattern Analysis Reports

If you have launched a GenePattern Analysis from the High Order Analysis tab, REMBRANDT directs you to the View Results tab where you can monitor the status of the task you have initiated. From this tab, you can also launch GenePattern itself to perform tasks within that application.

The GenePattern Job Results (lower panel) in the View Results tab indicates that your query has been sent to GenePattern. It displays the number assigned to the job and its current status. When the status shows **Completed**, the job number appears in the Gene Pattern Modules section in the upper portion of the page.

In the GenePattern Modules section, you can select your data and an analysis method by which GenePattern will analyze it.

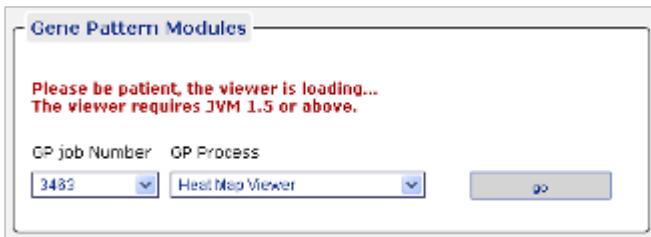
1. Select a completed job by number. If you have more than one job in the queue, select from the drop down list the data to be analyzed.
  2. Select the analysis (described in the following table) that you want GenePattern to perform on your data.

Analysis Method	Description
HeatMap Viewer	Displays values in a heat map format where the largest values are displayed as the reddest (hot), the smallest values are displayed as the bluest (cool), and intermediate values are a lighter color of either blue or red.
Hierarchical Clustering	Genes or other expression data are clustered according to predetermined algorithms.
K-Nearest Neighbors	Classifies a sample by assigning it the label most frequently represented among the k nearest samples.

Comparative Marker Selection	Finds the genes in a dataset that are most closely correlated with the two phenotypes (ALL and AML).
------------------------------	--

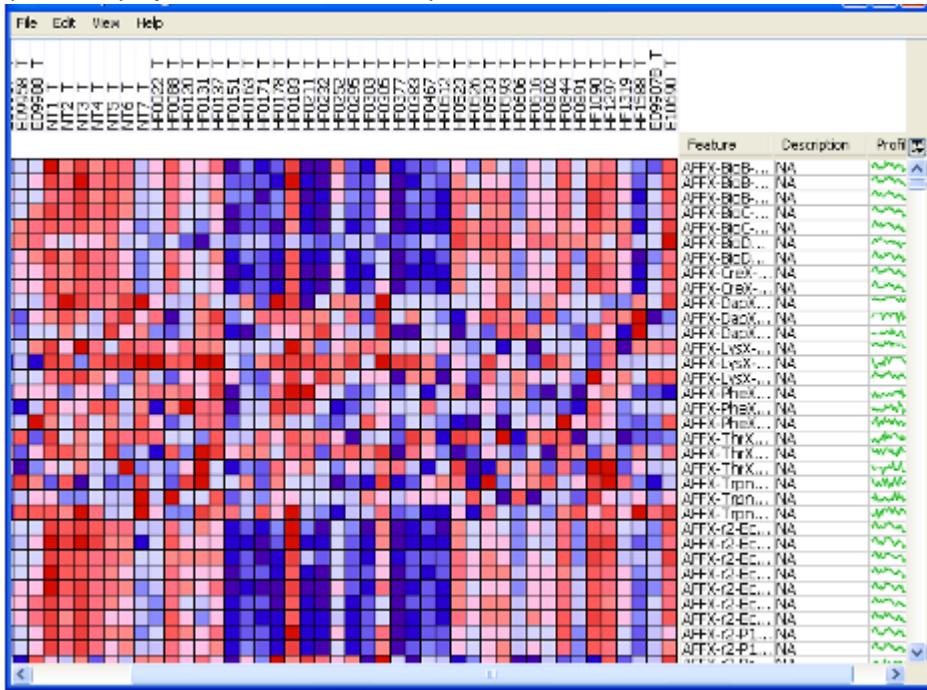
3. Click **Go** to launch the analysis.

The Gene Pattern Modules section of the page displays a message telling you to be patient. Your results should be finished shortly.

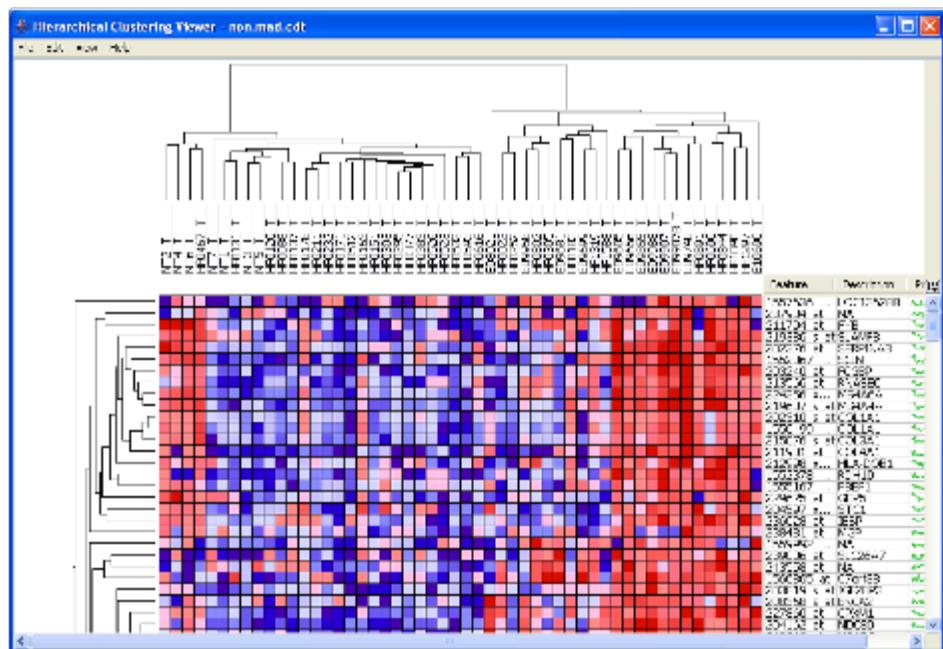


REMBRANDT displays the following results, based on your analysis selection:

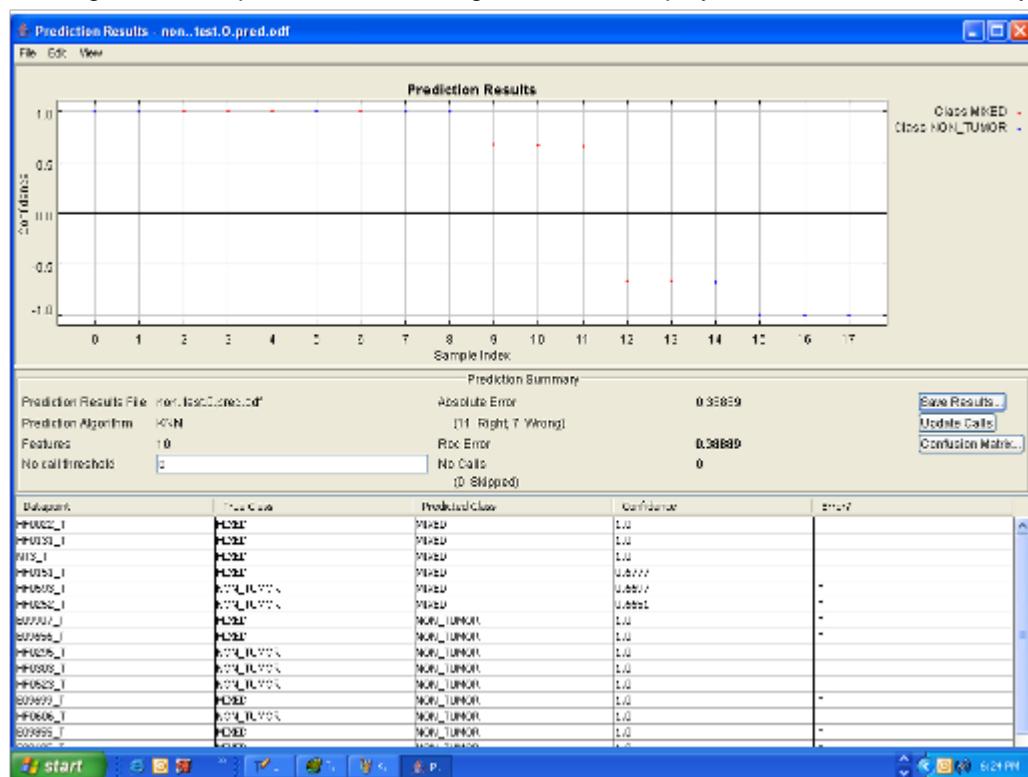
4. If HeatMap viewer was selected as the Analysis Method, then the GenePattern HeatMap Viewer Applet opens up and display the values in heat map format.



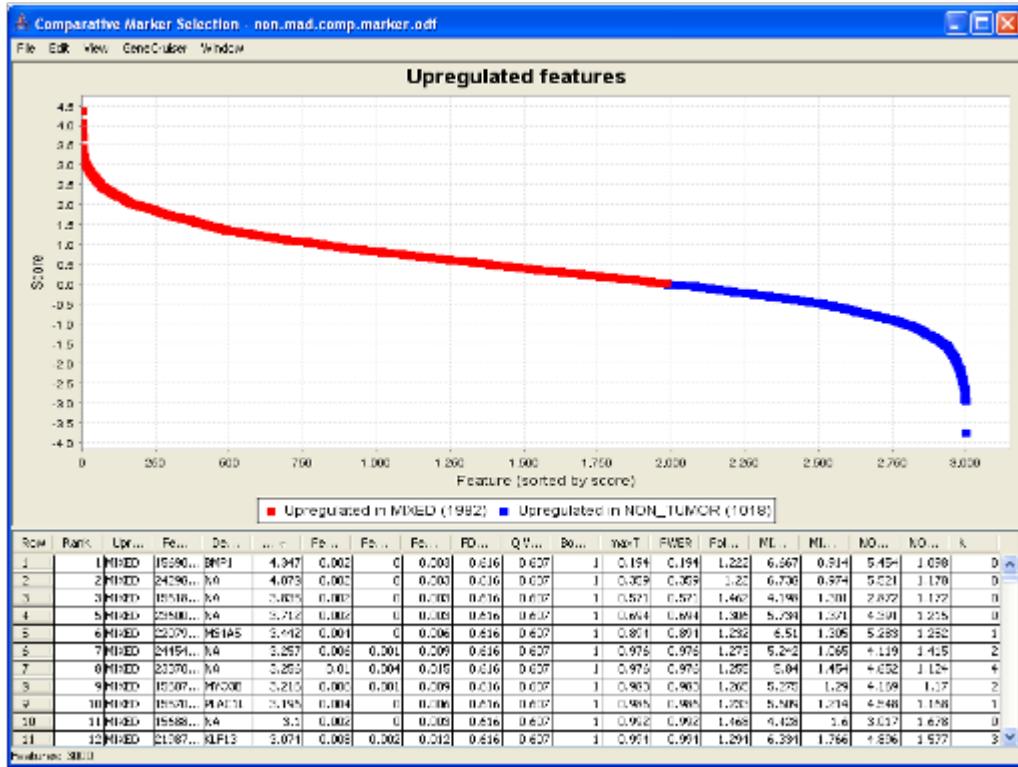
5. If Hierarchical Clustering, K-Nearest Neighbors or Comparative Marker Selection was selected, a GenePattern job is launched from REMBRANDT. The status of the job is displayed as GenePattern Analysis Results (, , )



The following is an example of K-nearest neighbors result displayed as a GenePattern analysis result.



The following example of Comparative Marker Selection (CMS) result displayed as a GenePattern analysis result.



- When your task is complete, the task will be ready for the visualizer. Launch the associated visualizer by clicking the (  ) icon next to the job link.
- If you click on the job hyperlink, GenePattern is launched.

## 6 Downloading Data from caArray v1.5.8

This section describes two options available in REMBRANDT for downloading data.

Topics in this section include the following:

- [Data Download Overview](#)
  - [Downloading caArray Tools and Files](#)
  - [Downloading BRB Array Tools and Files](#)

### Data Download Overview

REMBRANDT enables you to download data from the caArray application developed by the NCI Center for Biomedical Informatics and Information Technology. It also enables you to analyze data using BRB-ArrayTools created by the Biometric Research Branch of the National Cancer Institute.

#### Downloading caArray Tools and Files

caArray guides the annotation and exchange of array data using a federated model of local installations whose results are sharable across the cancer Biomedical Informatics Grid (caBIG®). To download caArray data files, follow these steps.

1. Select the **Download** tab. The page that opens displays a section for downloading caArray data ()�.

The screenshot shows a web-based interface for downloading data from caArray. It consists of three main sections: Step 1: Choose the saved List, Step 2: Choose Array Platform, and Step 3: Select file type to download. In Step 1, 'ASTROCYTOMA' is selected in a dropdown. In Step 2, 'Oligo (Affymetrix U133 Plus 2.0)' is selected in a dropdown. In Step 3, 'CEL' is selected in a dropdown. At the bottom of the interface is a blue 'download' button.

2. Select the download criteria described in the following table:

<b>Step 1. Select Data</b>	Select from the drop-down list the data set corresponding to the dataset you want to download from caArray
<b>Step 2. Select Array Platform</b>	Select the array platform. For the current version of REMBRANDT, Oligo U133 Plus 2.0 and 100 K SNP gene Chip are the two options.
<b>Step 3. Select File Type</b>	Select the file type to download. The options are .chp and .cel.

3. Click the **Download** button.

The Download Results section of the page monitors the download status. You can stop the download process at any time by clicking the **Stop Updating** link.

4. Upon completion, REMBRANDT generates a hyperlink to a zip file which contains the downloaded file from caArray.

## Downloading BRB Array Tools and Files

REMBRANDT enables you to analyze data using BRB-ArrayTools created by the Biometric Research Branch of the National Cancer Institute. BRB-ArrayTools is a comprehensive state-of-the-art statistical analysis system for microarray gene expression data. It is free for non-commercial purposes and can be licensed for commercial purposes from the NIH. BRB-ArrayTools installs as an Excel plug-in using a self-installer.

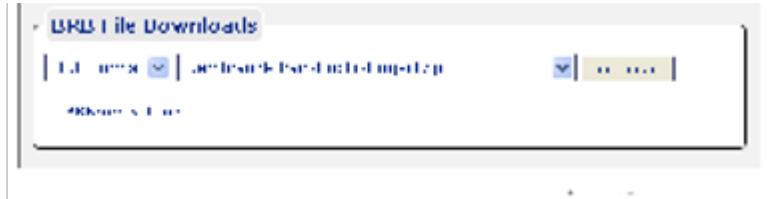
The Bulk Downloads drop-down list box enables you to download the static BRB archive files which enable you to obtain the appropriate files based on your as follows:

- Public users receive the Public dataset file ()
- Institution users receive the institution data and public dataset files.
- Super users receive all dataset files.

To download BRB-Array Tools and the appropriate files, follow these steps.

1. To download BRB-ArrayTools, select the **Download** tab.

The lower portion of the page displays the **BRB File Downloads** section.



The format and name of the available file(s) are predetermined.

2. Click the **BRB-Array Tools** link for more information about using the BRB website and tools. On the web site that appears, select and download the appropriate version of the product, and follow the prompts.
3. Once you have downloaded and installed BRB-Array Tools, select the files to download to analyze a dataset with BRB-Array Tools.
4. Click the **Download** button.
5. Unzip the REMBRANDT static BRB archive file(s).
6. Open the project worksheet in Excel on a Microsoft Windows PC.

## 7 Managing Workspace v1.5.8

### 7 Managing Workspace v1.5.8

This section describes how to manage your workspace by editing and or reorganizing existing lists and queries, adding new items or creating new custom lists from existing lists and queries. Additionally, this chapter describes import and export functions, allowing you to share lists and queries with others.

Topics in this section include:

- [Managing Lists Overview](#)
  - [Adding New Lists](#)
    - [Combining Existing Lists to Create a New List](#)
    - [Uploading a List](#)
    - [Manually Entering a List](#)
  - [Viewing the Data Items in a List](#)
  - [Removing Data Items](#)
  - [Deleting an Entire List](#)
- [Organizing Existing Lists and Queries](#)
- [Importing Lists and Queries](#)
- [Exporting Lists and Queries](#)

#### Managing Lists Overview

The REMBRANDT My Workspace tab centralizes all activities pertaining to the creation and management of user-defined, as well as study-defined, [PatientDID lists](#), [Gene lists](#), and [Reporter lists](#), as well as queries that you have saved in Rembrandt. Lists and queries are managed in the same way. You can further refine queries or facilitate analysis. You can also organize, import and export lists and queries. When working with lists and queries on the My Workspace/Manage Lists page, you can minimize the number of lists displayed by clicking the PatientDID Lists, Gene Lists, and Reporters Lists heading.

### Tip

You can add a saved gene or IMAGE clone list to an advanced gene expression search. You can also add a saved Gene List or probeset list to an advanced copy number search.

## Adding New Lists

The following table lists how to add each list type to REMBRANDT.

List Type	How to Add a List
PatientDID List	<p>REMBRANDT provides a collection of default PatientDID Lists list from glossary.</p> <p>To create a new PatientDID list, see the following:</p> <ul style="list-style-type: none"><li>• <a href="#">Combining Existing Lists to Create a New List</a></li><li>• <a href="#">Uploading a List</a></li><li>• <a href="#">Manually Entering a List</a></li><li>• Save patients from a Clinical report. See <a href="#">Clinical Reports</a>.</li></ul> <p>Save patients from a Gene Expression Sample report. See <a href="#">Selecting and Saving Sample Results (Select Samples Toolbar)</a>.</p>
Gene List	<p>To add a Gene List, see the following:</p> <ul style="list-style-type: none"><li>• <a href="#">Combining Existing Lists to Create a New List</a></li><li>• <a href="#">Uploading a List</a></li><li>• <a href="#">Manually Entering a List</a></li></ul>
Reporter List	<p>To add a Reporter List, see the following:</p> <ul style="list-style-type: none"><li>• <a href="#">Combining Existing Lists to Create a New List</a></li><li>• <a href="#">Uploading a List</a></li><li>• <a href="#">Manually Entering a List</a></li></ul> <p>Save Reporters from a Class Comparison report. See <a href="#">Selecting and Saving Sample Results (Select Samples Toolbar)</a>.</p>

### Combining Existing Lists to Create a New List

You can create new lists from existing lists. To create a custom list from existing lists, follow these steps:

1. Select the **My Workspace** tab.

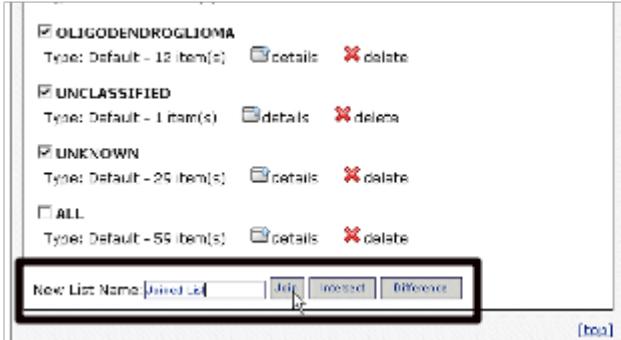
On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. Click the type of list you would like to view (**PatientDID List**, **Gene List**, **Reporter List**). The names for the lists appear.

3. Click the box next to the list name(s) to be combined to create a new list.

### Note

You cannot select more than two lists to use the **Difference** option.

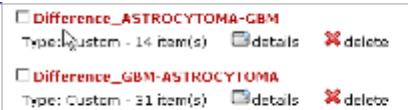


The screenshot shows a list management interface. At the top, there are four checked items: "OLIGODENDROGLIOMA" (Type: Default - 12 item(s)), "UNCLASSIFIED" (Type: Default - 1 item(s)), "UNKNOWN" (Type: Default - 25 item(s)), and "ALL" (Type: Default - 55 item(s)). Below this is a toolbar with buttons: "New" (highlighted), "Join", "Intersect", and "Difference". The "Difference" button is also highlighted with a red box. At the bottom right of the toolbar is a "[back]" link.

4. Enter a unique name for the new list you are creating, and then click the appropriate button:

- **Join** combines two or more lists into one new list.
- **Intersect** creates a new list from only the items that appear on more than one selected list.
- **Difference** creates up to two lists each comprising items that appeared in one of the selected lists. For example, if you select Astrocytoma and GBM, the new lists are “Astrocytoma-GBM” comprising the items that appeared in the Astrocytoma list only and “GBM-Astrocytoma” comprising the items appearing in the GBM list only.

5. The new list appears on the My Workspace page and in the side bar in red.



The screenshot shows the My Workspace page with two new lists created: "Difference\_ASTROCYTOMA-GBM" (Type: Custom - 14 item(s)) and "Difference\_GBM-ASTROCYTOMA" (Type: Custom - 31 item(s)). Both lists are displayed in red text.

### New Difference lists

## Uploading a List

You may add a new list type by a list from your computer.

This feature is for creating a new list from scratch, one item per line in a simple text file. This is in contrast to the Import file feature which imports files save in XML format. See .

To upload a list, follow these steps:

1. Select the **My Workspace** tab.

On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. At the top of the Manage List page, click **Add List**.

The **Upload List or Manually type List** block appears.

3. Click **Upload List** at the top of the box.



The screenshot shows a form titled "Upload List or Manually type List". It has three main sections: "Choose the list type:" with a dropdown menu set to "Reporter-DGNC", "Upload file:" with a "Browse..." button, and "Name list:" with a text input field containing "Astrocytoma".

4. From the **Choose the list type** drop-down list box, select the list to be uploaded.
5. Click the **Browse** button beside the **Upload file** box. Navigate to and select the file on your computer that you would like to upload.
6. Enter a unique name for the list, and then click the **Add List** button.  
The name of the list appears on the My Workspace page or in the side bar under the appropriate list type.

## Manually Entering a List

You can create a new list type by a list. To enter a list manually, follow these steps:

1. Select the **My Workspace** tab.

On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. At the top of the Manage List page, click **Add List**.

The **Upload List or Manually type List** block appears.

3. Click **Manually Type List** at the top of the box.

4. From the **Choose the list type** drop-down list box, select the type of list to be entered.
5. The following table lists examples of correctly formatted codes for each list type.

List Type	Correctly Formatted Examples
PatientDID	CB160831 K03193
Gene-GENBANK_ACCESSION_NUMBER	AF125253 S75264
Gene-GENESYMBOL	BPIL2 IVL
Gene-LOCUS_LINK	10 100 10017
Reporter-AFFY_GHU133PLUS2_PROBE_SET	1007_s_at 1053_at
Reporter-IMAGE_CLONE	IMAGE:1407831 IMAGE:143995

Reporter-DBSNP	rs1000015 rs1000025
Reporter-AFFY_100K SNP PROBE_SET	SNP_A-1708471 SNP_A-1655302

*List type code formats*

6. In the **Type Ids** box, enter items into the text block by typing them one to a line.
7. Enter a unique name for the list, and then click the **Add List** button.

The new list name appears under the appropriate category on the My Workspace page and in the side bar in red.

8. To display the values in the list, click **Details**.

 **Note**

If the format of the values entered in the Type Ids box was not correct, you must Delete the list and start again.



## Viewing the Data Items in a List

To view the individual data items on a list, follow these steps:

Select the **My Workspace** tab.

On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

1. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID Lists**, **Gene Lists**, **Reporter Lists**).
2. Find a list to be viewed, and click the **details** icon to display all of the items in the list.

PatientDID Lists

ALL GLIOMA  
Type: Default - 52 item(s)

- 1) E09197 [\[details\]](#) [\[delete\]](#)
- 2) E09198 [\[details\]](#) [\[delete\]](#)
- 3) E09199 [\[details\]](#) [\[delete\]](#)
- 4) E09151 [\[details\]](#) [\[delete\]](#)
- 5) E09192 [\[details\]](#) [\[delete\]](#)

The side bar displays each list type and the associated lists. You can mouse-over a list and display the data items.

3. To export the list, see [Exporting Lists and Queries](#).

## Removing Data Items

You may delete items from an existing list, then view the new list or save the list on your computer. Follow these steps:

1. Select the My Workspace tab. On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.
2. At the top of the Manage List page, click on the type of lists you would like to view (PatientDID List, Gene List, Reporter List).
3. Find the list you want to change, and click on the box next to the list name.
4. Click the **details** icon to display all the items in the selected list.
5. Click the **delete** link beside the item you want to delete. The item is removed from the list.

PatientDID Lists

ALL GLIOMA  
Type: Default - 52 item(s)

- 1) E09197 [\[details\]](#) [\[delete\]](#)
- 2) E09199 [\[details\]](#) [\[delete\]](#)

6. Once you remove the items, you can view the new list or export the list to your computer. See [Exporting Lists and Queries](#).

## Deleting an Entire List

To delete one or more lists from a list type, follow these steps:

1. Select the My Workspace tab. On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.
2. At the top of the Manage List page, click on the type of lists you would like to view (**PatientDID List, Gene List, Reporter List**).
3. Find the list you want to delete, and click the box next to the list name. Click more than one box to select multiple lists for deletion.
4. To delete the selected lists, click an **x delete** icon. The selected categories are removed .



The list(s) are deleted.

5. This delete function is completely different than deleting lists and queries in the Organize function. For clarification, see [Organizing Existing Lists and Queries](#).

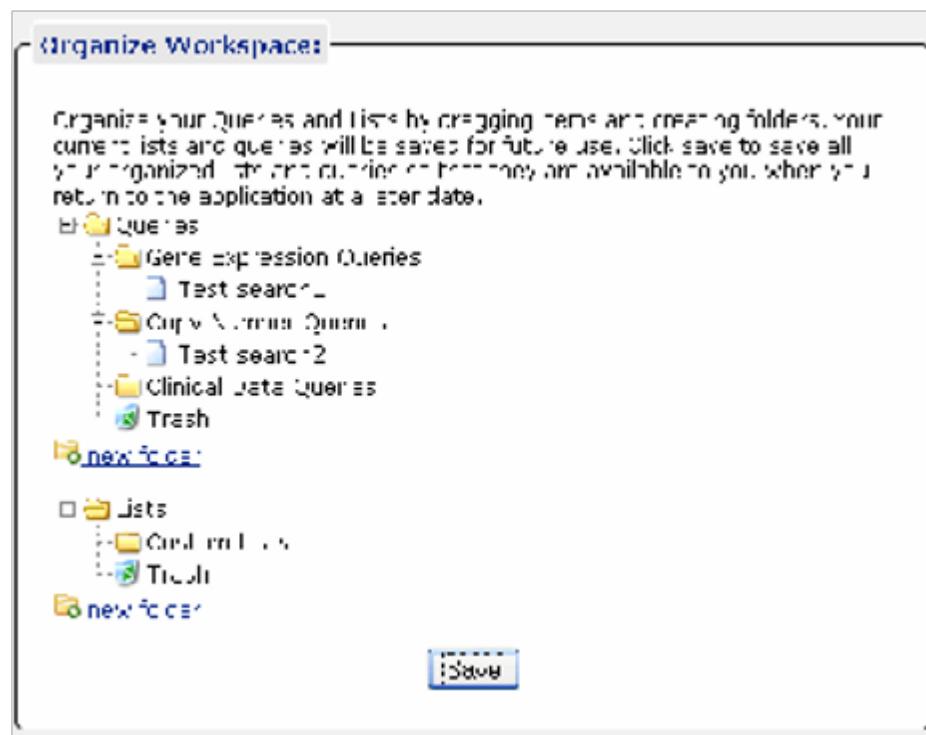
## Organizing Existing Lists and Queries

To organize lists and queries, follow these steps:

1. Select the **My Workspace** tab.

On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. At the top of the Manage List page, click the Organize hypertext link. This opens the Organize Workspace page.



3. The Organize Workspace text describes how you can organize lists and queries displayed on the page.
  - Create a new folder by clicking the **New Folder** link.
  - To name the folder, double click the folder. Enter the name in the text box.
  - Click and drag items to new locations, reorganizing the directory structure.
  - To delete items from the hierarchy, drag and drop them in the Trash bin.
4. Click **Save** to save the new hierarchy.
  - If you navigate to another location in Rembrandt without saving your "organized" lists and queries, Rembrandt prompts you to click **Save**. If you do not confirm that you want to save them, your organization will be lost.
  - When you click **Save**, the Trash bin empties, and any empty folders in the structure are deleted.

## Importing Lists and Queries

To import a list or a query that you have saved in XML format at an external location, follow these steps:

1. Select the **My Workspace** tab.

On the page that opens, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. At the top of the Manage List page, click the **Import** hypertext link.

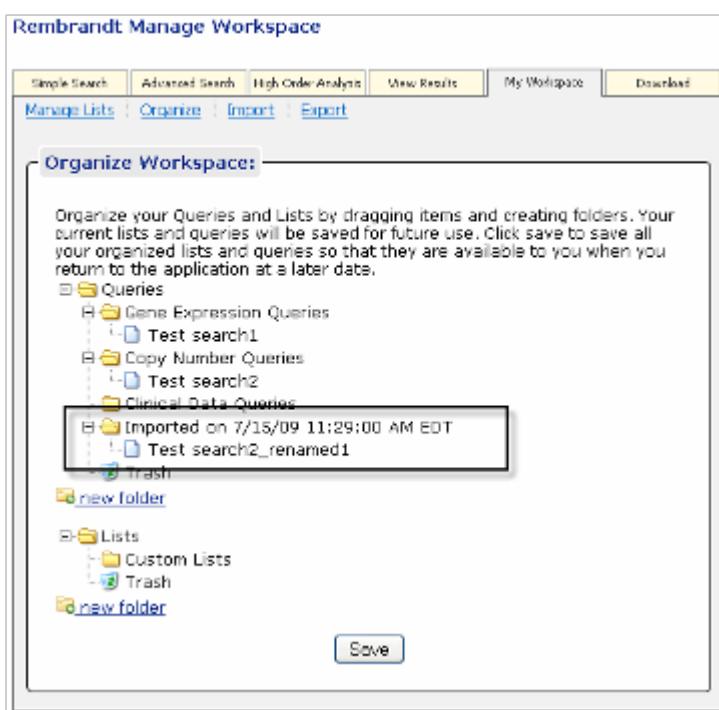
The Import Workspace text describes how you can import lists and queries.

3. At the bottom of the page, select the file type you are importing, **Query** or **List**.

4. Click the **Browse** button to navigate for the file(s).

5. Click the **Import** button.

Rembrandt informs you if the file you are trying to import does not comply with acceptable format standards. If it does meet requirements, the system opens the Organize Workspace page where you will see the imported file displaying in a new "Imported" folder named with the date and time stamp. If a file with an identical name already exists in Rembrandt, the program renames the imported file. The Organize Workspace page displays imported file folders. Rembrandt renames files where duplicates exist in the database.



6. You can import only one file at a time; import of a "batch" of files is not possible.

## Exporting Lists and Queries

To export a list, follow these steps:

1. Select the **My Workspace** tab.

On the page, Rembrandt displays the following sub-categories as hypertext links: Manage Lists, Organize, Import, and Export. By default, the page opens to the Manage Lists subcategory.

2. At the top of the Manage List page, click the **Export** hypertext link.

3. In the directory, locate and click on the query or list you want to export. You can select one file in an existing folder or you can select an entire folder. In each case, your selection is exported as an one XML file. If you are exporting a folder of multiple files, they will all be part of one large XML file.

4. This opens an Opening... dialog box which indicates the file and file type. Select the option to open or to save the file on your local drive.

 **Note**

When you select to log out, Rembrandt will prompt you to save lists or queries you may have been working with.

## Glossary v1.5.8

### Glossary v1.5.8

Acronyms, objects, tools and other terms referred to in the chapters or appendixes of this REMBRANDT 1.5 User's Guide are described in this glossary.

Term	Definition
allele	Mutually exclusive alternative forms of the same gene occupying the same locus on homologous chromosomes, differing in DNA sequence and governing the same biochemical and developmental process.
Astrocytic tumors: Astrocytoma	Neoplasms of the brain and spinal cord derived from glial cells. Also called an astrocytoma.
Benjamini-Hochberg Multiple Testing Correction	The concept of False Discovery Rate (FDR) was introduced in multiple testing by Benjamini and Hochberg (1995).
CCR	Center of Cancer Research
CCR-NOB	CCR Neuro-Oncology Branch
CGAP	Cancer Genome Anatomy Project
Class Comparison	Differential gene expression across the tumor types will be evaluated by calculating the typical <i>t</i> -statistic for each reporter. Both parametric and non-parametric <i>p</i> -value will be computed.
False Discovery Rate (FDR)	The expected proportion of Type I errors among rejected hypotheses in simultaneous testing of multiple null hypotheses.
Family-wise Error Rate (FWER)	Denotes the probability of having at least one false significant test result within the set of tested hypotheses.

Gene List	A pre-defined or user-defined list in REMBRANDT comprising genes with a set of characteristics. Used to filter a query.
Gene Ontology (GO) Classification	A collaborative effort to address the need for consistent descriptions of gene products in different databases. The goal of the Gene Ontology project is to produce a controlled vocabulary that can be applied to all organisms even as knowledge of gene and protein roles in cells is accumulating and changing.
Glioblastoma	Malignant form of astrocytoma histologically characterized by pleomorphism of cells, nuclear atypia, microhemorrhage, and necrosis.
Gliomas	Any of the largest group of primary tumors of the brain, composed of malignant glial cells. Kinds of gliomas are astrocytoma, ependymoma, glioblastoma multiforme, medulloblastoma, and oligodendrogioma.
Hierarchical Clustering	A statistical method for finding relatively homogeneous clusters of cases based on measured characteristics. It starts with each case in a separate cluster and then combines the clusters sequentially, reducing the number of clusters at each step until only one cluster is left.
High Order Analysis	After data preprocessing (filtering and normalization), further statistical analysis of gene expression data are performed.
HUGO [gene symbol] [Human Genome Organization]	HUGO is an international organization of scientists involved in human genetics. Established in 1989 by a collection of the world's leading human geneticists, the primary ethos of the Human Genome Organization is to promote and sustain international collaboration in the field of human genetics.
Kaplan-Maier	The Kaplan Maier method is used for survival analysis. Kaplan-Maier curves are used to estimate survival probability as a function of time, and survival differences are analyzed by the log-rank test.
Karnofsky Performance Status	A standard way of measuring the ability of cancer patients to perform ordinary tasks. The scores range from 0 to 100, with a higher score indicating a better ability to carry out daily activities. KPS may be used to determine a patient's prognosis, to measure changes in functioning, or to decide if a patient could be included in a clinical trial.

Lansky Play-Performance Status	The play-performance scale for children is a parent-rated instrument which records usual play activity as the index of performance. It is similar to the Karnofsky Performance Scale for adults.
Mann-Whitney Test	A nonparametric test (distribution-free) used to compare two independent groups of sampled data. Unlike the parametric <i>t</i> -test, this non-parametric makes no assumptions about the distribution of the data (e.g., normality).
Multiple Comparison Adjustment	Since tens of thousands of genes are compared, many genes can be false positives. However, genes are not all independent and genes in the same pathway could have similar <i>t</i> -statistics or <i>p</i> -values. Multiple-comparison adjusted <i>p</i> -values have been proposed to handle the multiple comparison issues in the context of microarray data.
NCIA	National Cancer Imaging Archive
NCI	National Cancer Institute
NCICB	National Cancer Institute Center for Bioinformatics
NINDS	National Institute of Neurological Disorders and Stroke
Oligodendroglial tumor: Oligodendroglioma	Rare, slow-growing tumor that grows in the oligodendrocytes (brain cells that provide support and nourishment for nerve cells). Also called an oligodendroglioma.
PatientDID List	A pre-defined or user-defined list in REMBRANDT comprising patients with a set of characteristics. Used to filter a query.
Pleomorphic Xanthoastrocytoma	Astrocytic tumor with a relatively favorable prognosis (WHO grade II) and is typically encountered in children and young adults. It has a superficial location in the cerebral hemispheres and involvement of the meninges.
Principal Component Analysis	Commonly used in microarray research as a tool. It is designed to capture the variance in a dataset in terms of principle components. In effect, one is trying to reduce the dimensionality of the data to summarize the most important, for example defining parts, while simultaneously filtering out noise.

Protoplasmic [astrocytoma]	Rare variant of Diffuse Astrocytoma. It is predominantly composed of neoplastic astrocytes showing a small cell body with few, flaccid processes with a low content of glial filaments and scant GFAP expression.
Reporter List	A pre-defined or user-defined list in REMBRANDT comprising reporters with a set of characteristics. Used to filter a query.
SNP	Single nucleotide polymorphisms or SNPs (pronounced "snips") are DNA sequence variations that occur when a single nucleotide (A,T,C or G) in the genome sequence is altered.
Wilcoxin Test	Nonparametric statistics for testing hypotheses about whether two samples differ.