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Revision History

Part #	Revision	Date	Description of Change
11319130	B	November 2010	
11319130	A	November 2008	Initial GenomeStudio release.

Table of Contents

Notice	iii
Revision History	v
Table of Contents	vii
List of Tables	ix
Chapter 1 Overview	1
Introduction	2
Audience and Purpose	3
Installing the Methylation Module.	4
Methylation Module Workflow	6
Chapter 2 Creating a New Project.	7
Introduction	8
Starting the Methylation Module	9
Selecting an Assay Type	10
Choosing a Project Location	11
Selecting Your Project Data	12
Defining Groupsets and Groups.	14
Defining the Analysis Type and Parameters.	17
Creating a Mask File.	19
Chapter 3 Viewing Your Data.	21
Introduction	22
Scatter Plots.	23
Scatter Plot Functions	24
Scatter Plot Context Menu Selections.	27
Finding Items in the Scatter Plot	28
Histogram Plots	33
Histogram Plot Context Menu	34
Heat Maps	36
Heat Map Tools Menu	37
Heat Map Context Menu	38
Cluster Analysis Dendrograms	39
Similarities and Distances	39
Analyzing Clusters	40
Dendrogram Context Menu Selections	42
Viewing the Sub-Tree List Directly in the Dendrogram	43
Copy/Paste Gene Clusters.	45
From Scatter Plot to Dendrogram	45
From Dendrogram to Scatter Plot	45

Chapter 4	Applying Methylation Algorithms	47
	Methylation Analysis Algorithms	48
	Normalization Methods and Algorithms	49
	Average Normalization	49
	Normalization to Internal Controls.	49
	Background Subtraction	50
	Differential Methylation Analysis Algorithms	51
	Illumina Custom Model	51
	Mann-Whitney Model	51
	T-Test Model	52
Chapter 5	Comparing Methylation and Gene Expression Data	53
	Introduction	54
	Importing Gene Expression Data.	55
	Visualize the Correlation of Methylation and Expression Levels Data.	58
Chapter 6	User Interface Reference	59
	Introduction	60
	Detachable Docking Windows.	61
	Control Probe Profile Table.	61
	Infinium Methylation Controls Dashboard.	63
	GoldenGate Methylation Control Summary Graph.	70
	Group Methylation Profile Table	72
	Sample Methylation Profile Table	80
	Samples Table.	88
	Project Window	90
	Log Window	90
	Main Window Menus	91
	Context Menus	94
Appendix A	Sample Sheet Format.	97
	Introduction	98
	Data Section	99
	Sample Sheet Template	100
	Sample Sheet Examples	101
	Technical Assistance	103

List of Tables

Table 1	Scatter Plot Control Panel Functions and Descriptions	24
Table 2	Scatter Plot Tools Menu Item Descriptions	26
Table 3	Scatter Plot Context Menu Item Descriptions	27
Table 4	Histogram Plot Context Menu Item Descriptions	35
Table 5	Heat Map Tools Menu Item Descriptions	37
Table 6	Heat Map Context Menu Item Descriptions	38
Table 7	Dendrogram Context Menu Selections	43
Table 8	Control Probe Profile Table	62
Table 9	GoldenGate Assay Control Summary Graph	71
Table 10	Group Methylation Profile Table, Infinium HD Assay	73
Table 11	Group Methylation Profile Table, Infinium Assay	76
Table 12	Group Methylation Profile Table, GoldenGate Assay	79
Table 13	Sample Methylation Profile Table, Infinium HD Assay	81
Table 14	Sample Methylation Profile Table, Infinium Assay	84
Table 15	Sample Methylation Profile Table, GoldenGate Assay	86
Table 16	Samples Table, Infinium Assay	88
Table 17	Samples Table, GoldenGate Assay	89
Table 18	Main Menu Elements and Functions	91
Table 19	Context Menu Elements and Functions	94
Table 20	Data Section, Required and Optional Columns	99
Table 21	Illumina General Contact Information	103
Table 22	Illumina Customer Support Telephone Numbers	103

List of Tables

Overview

Introduction	2
Audience and Purpose.	3
Installing the Methylation Module	4
Methylation Module Workflow	6



Introduction

DNA methylation is an important regulatory mechanism of gene expression in many eukaryotic cell types. In humans and most mammals, DNA methylation mostly affects the cytosine base (C) when it is followed by a guanosine (G). Thus, in these organisms, DNA methylation generally occurs at CpG sites.

The pattern of methylation is cell-type-specific and established during the development of an organism. Changes in methylation patterns play critical roles in the regulation of gene expression in development, differentiation, and diseases such as multiple sclerosis, diabetes, schizophrenia, aging, and cancers.

The GenomeStudio Methylation Module is a software application you can use to analyze methylation data from scanned microarray images collected from the Illumina iScan System, HiScan or HiScanSQ System, BeadXpress Reader, or BeadArray Reader. You can also use the resulting GenomeStudio output files with most standard data analysis programs.

The GenomeStudio Methylation Module allows you to perform two types of data analysis:

- ▶ Methylation Analysis—calculating methylation levels
- ▶ Differential Methylation Analysis—determining whether methylation levels have changed between a reference group and another experimental group.

You can perform these analyses on individual samples, or on groups of samples treated as replicates.

The GenomeStudio Methylation Module includes tools that provide a quick, visual means for exploratory analysis, including:

- ▶ Line plots
- ▶ Bar graphs
- ▶ Scatter plots
- ▶ Histograms
- ▶ Dendrograms
- ▶ Box plots
- ▶ Heat maps
- ▶ Control summary reports

Also included with the GenomeStudio Methylation Module are the following powerful data visualization and analysis tools:

- ▶ Illumina Genome Viewer (IGV)
- ▶ Illumina Chromosome Browser (ICB)
- ▶ Methylation/Gene Expression Comparison Tool

This manual describes Illumina's GenomeStudio Methylation Module software application and its component tools, and presents guidelines for evaluating the quality of your methylation experiments.

For information about the IGV and the ICB, see the *GenomeStudio Framework User Guide*.

Audience and Purpose

This guide is written for researchers who want to use the GenomeStudio Methylation Module software application to analyze data obtained by performing one or more of the following assays:

- ▶ Illumina's Infinium Assay for Methylation
- ▶ Illumina's Infinium HD Assay for Methylation
- ▶ Illumina's GoldenGate Assay for Methylation
- ▶ Illumina's VeraCode Assay for Methylation

This guide includes procedures and user interface information for the GenomeStudio Methylation Module. For information about performing Methylation assays, see the related Methylation Assay Guide.

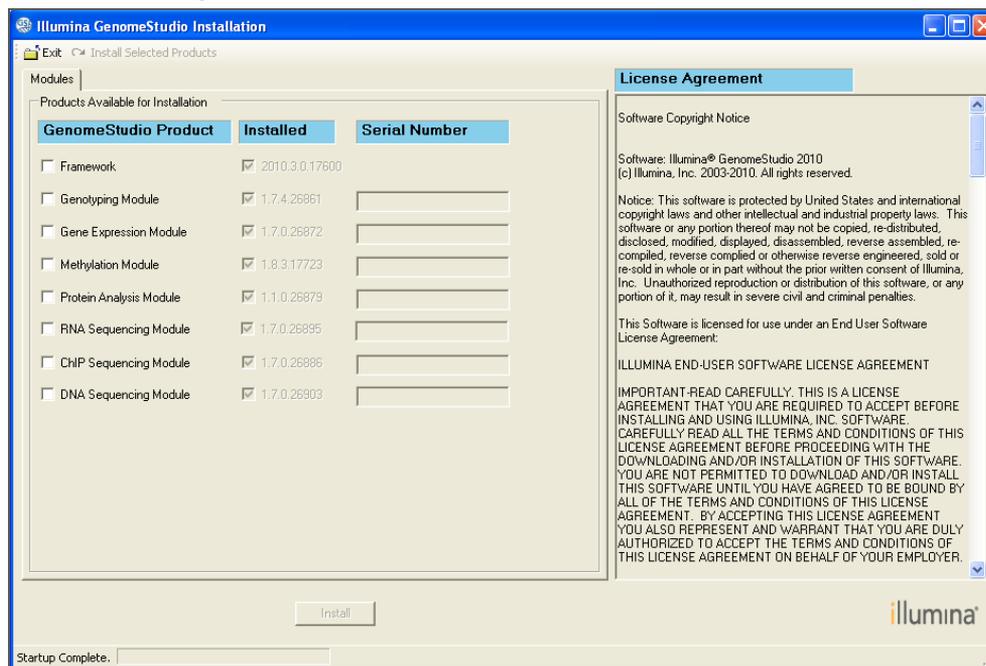
Installing the Methylation Module

To install the GenomeStudio Methylation Module:

- 1 Put the GenomeStudio CD into your CD drive or navigate to the GenomeStudio installer.

The GenomeStudio application suite unzips, then the Illumina GenomeStudio Installation dialog box opens.

Figure 1 Selecting GenomeStudio Software Modules



- 2 Read the software license agreement in the right-hand side of the Illumina GenomeStudio Installation dialog box.
- 3 In the GenomeStudio Product area, select **Methylation Module**.



NOTE

The GenomeStudio Framework works in conjunction with GenomeStudio software modules. Select the Framework and one or more GenomeStudio modules to install, and have your serial number(s) available.

- 4 In the Serial Number area, enter your serial number for the Methylation Module.



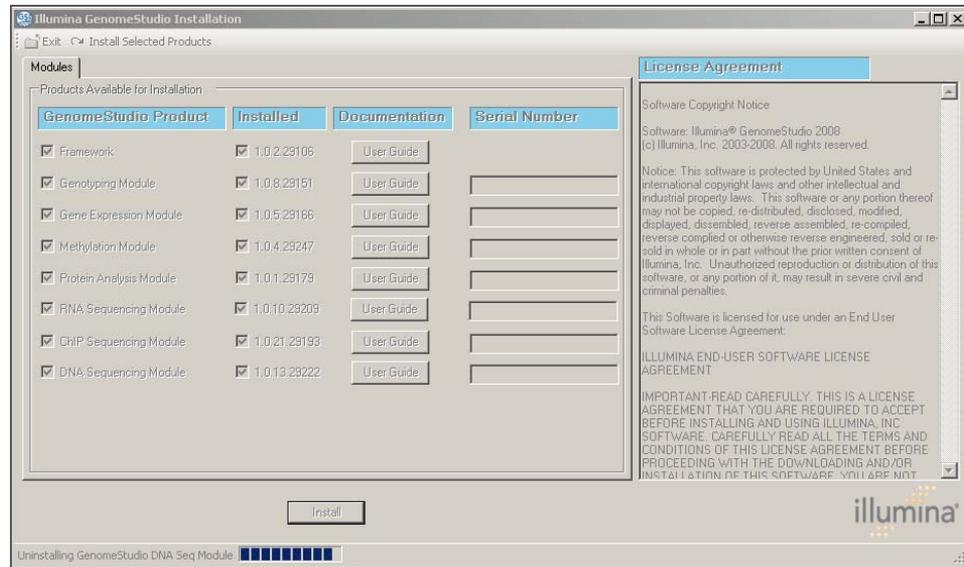
NOTE

Serial numbers are in the format ####-####-####-#### and can be found on an insert included with your GenomeStudio CD.

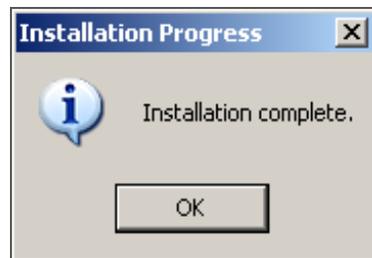
- 5 **[Optional]** Enter the serial numbers for additional GenomeStudio modules if you have licenses for additional GenomeStudio modules and want to install them now.
- 6 Click **Install**.
The Software License Agreement dialog box opens.

Figure 2 License Agreement

- 7 Click **Yes** to accept the software license agreement. The GenomeStudio Framework and Methylation Module are installed on your computer, along with any additional GenomeStudio modules you selected.

Figure 3 Installing GenomeStudio

The Installation Progress dialog box notifies you that installation is complete.

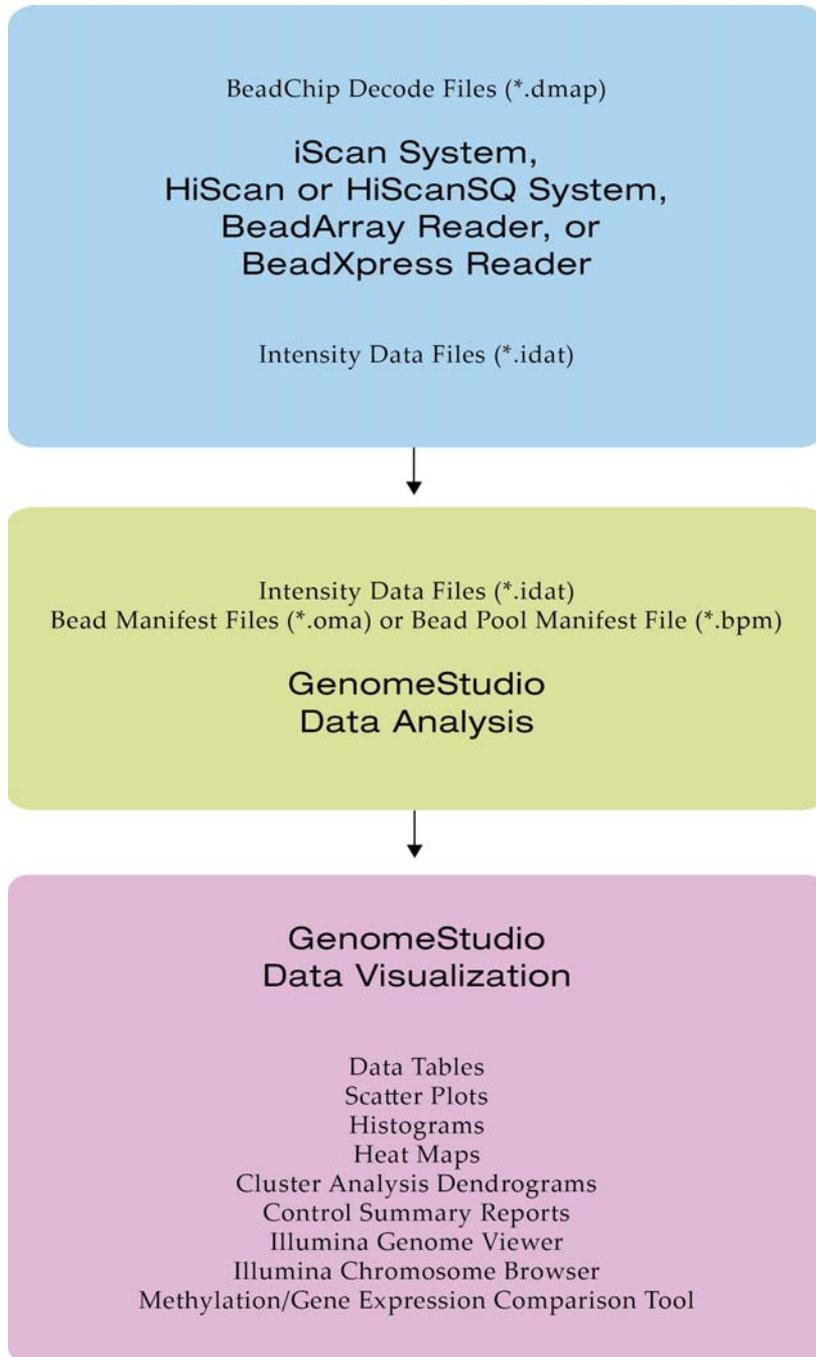
Figure 4 Installation Complete

- 8 Click **OK**.
- 9 In the Illumina GenomeStudio Installation dialog box, click **Exit**. You can now start a new GenomeStudio project using any GenomeStudio module you have installed. See Chapter 2, *Creating a New Project*, for information about starting a new Methylation project.

Methylation Module Workflow

The basic workflow for methylation is shown in Figure 5.

Figure 5 GenomeStudio Methylation Module Workflow



Creating a New Project

Introduction	8
Starting the Methylation Module	9
Selecting an Assay Type	10
Choosing a Project Location	11
Selecting Your Project Data	12
Defining Groupsets and Groups	14
Defining the Analysis Type and Parameters.	17
Creating a Mask File	19



Introduction

Using the intensity files produced by the Illumina iScan System, HiScan or HiScanSQ System, or BeadArray Reader, GenomeStudio's Methylation Module allows you to produce data tables containing:

- ▶ CpG locus lists
- ▶ Methylation levels for individual CpG loci (normalized or raw)
- ▶ Associated hybridization intensities in the red and green channels
- ▶ Information about system controls

In addition, GenomeStudio's Differential Methylation Analysis capability allows you to produce data tables determining the probability that the methylation level between two samples or groups of samples has changed.

Using these data tables, GenomeStudio's data visualization tools can create sophisticated plotting analyses, including:

- ▶ Bar plots
- ▶ Line plots and scatter plots
- ▶ Heat maps
- ▶ Histograms
- ▶ Cluster analysis dendrograms
- ▶ Control summary reports

For another level of analysis, you can also use the Illumina Genome Viewer (IGV), the Illumina Chromosome Browser (ICB), or a tool included in the Methylation Module that compares methylation with gene expression levels.



NOTE

For more information about the IGV and the ICB, see the *GenomeStudio Framework User Guide*.

For more information about the Methylation/Gene Expression Comparison Tool, see Chapter 5, *Comparing Methylation and Gene Expression Data* of this manual.

To run a methylation analysis, you must first define a GenomeStudio **project**. Within a project, you define one or more **groupsets**, one or more **groups** (sample sets that can be compared against each other for the purpose of identifying differences in methylation), and one or more **analyses**. For more information about groups and groupsets, see *Defining Groupsets and Groups* on page 14.

In the simplest experiment, each group may have only one sample. However, if your experiment includes replicate samples, or samples that belong to similar biological conditions, you can assign these to the same group.

In a project and within a group, GenomeStudio averages the values for each gene across the samples. Its algorithms automatically take advantage of the replicates' statistical power to provide a sensitive determination of methylation detection and differential methylation.

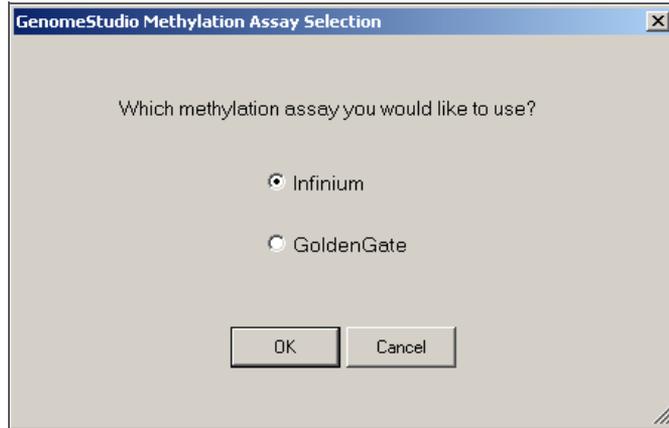
The GenomeStudio Project Wizard walks you through each step of creating a project:

- ▶ Starting the Methylation module
- ▶ Defining a project
- ▶ Creating groupsets and groups
- ▶ Applying normalization, methylation analysis, and differential methylation analysis algorithms

Starting the Methylation Module

- ▶ Start the GenomeStudio Methylation Module by doing one of the following:
 - Go to **File | New Project | Methylation**.
 - On the Start page, in the New Project pane, click **Methylation**.The GenomeStudio Methylation Assay Selection dialog box opens.

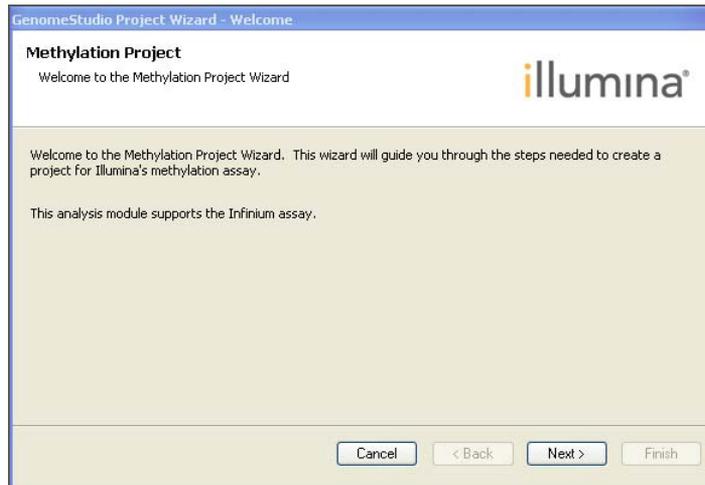
Figure 6 GenomeStudio Methylation Assay Selection



Selecting an Assay Type

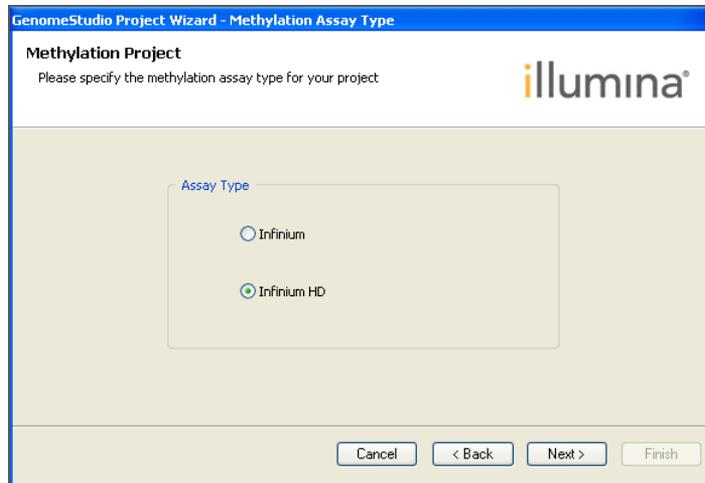
- 1 Select the **Infinium** or **GoldenGate** assay, as appropriate for the run you are analyzing, then click **OK**.
The examples in the following sections of this chapter reflect the choices available if you select **Infinium** and might not match the choices shown on your screen.

Figure 7 GenomeStudio Project Wizard - Welcome



- 2 Click **Next** to continue.
The GenomeStudio Project Wizard - Methylation Assay Type dialog box opens.

Figure 8 GenomeStudio Project Wizard - Methylation Assay Type



- 3 Verify that the assay type is correct, and click **Next**.
The GenomeStudio Project Wizard - Project Location dialog box opens.

Choosing a Project Location

- 1 In the **Projects Repository** area of the Project Location dialog box, browse to the location where you want to save your project.
- 2 In the **Project Name** area, enter a name for your project.
The full path for your project appears beneath the name you enter.

Figure 9 GenomeStudio Project Wizard - Project Location

GenomeStudio Project Wizard - Project Location

Methylation Project
Please specify the name and location for your project

Projects Repository
C:\Documents and Settings\carrier\My Documents\Data\GenomeStudio\MyProjects Browse...

Project Name
450KMethylation

Project will be created in:
C:\Documents and Settings\carrier\My Documents\Data\GenomeStudio\MyProjects\450KMethylation

Cancel < Back Next > Finish

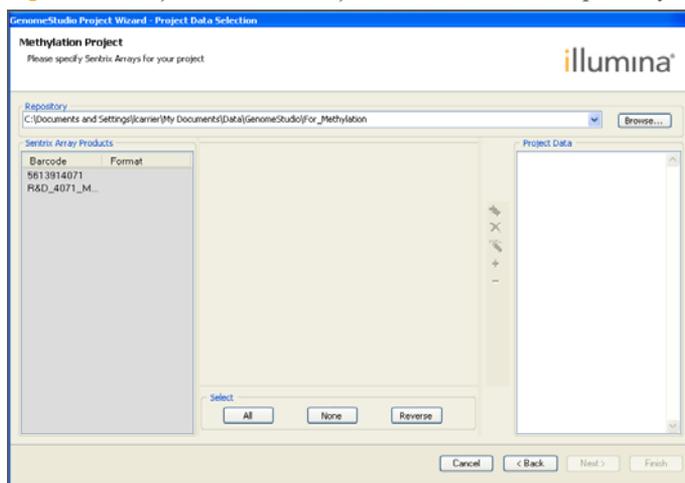
- 3 Click **Next** to continue.
The GenomeStudio Project Wizard - Project Data Selection dialog box opens.

Selecting Your Project Data

- 1 In the **Repository** area of the Project Data Selection dialog box, do one of the following:
 - Use the dropdown menu to select the repository folder where your intensity data (*.idat file) is stored.
 - Type the path to the repository folder.
 - Browse to the repository folder by using the **Browse** button to the right of the Repository area.

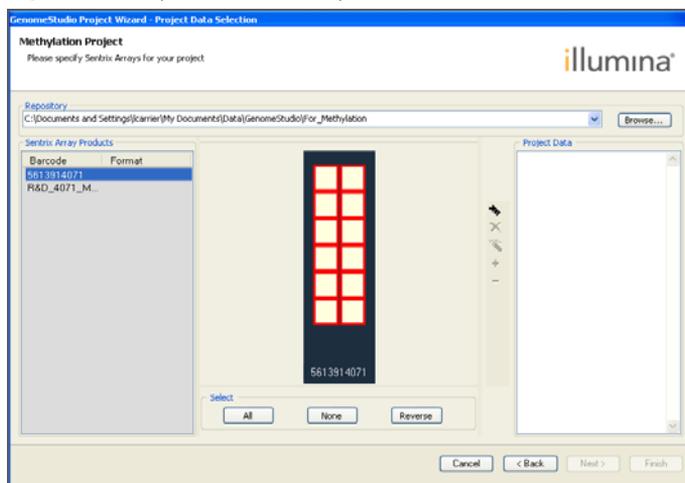
When you browse to a repository folder, GenomeStudio displays all subfolders containing *.idat files.

Figure 10 Project Wizard - Project Data Selection - Repository



- 2 In the Sentrix Array Products pane, select the product that you want to include in your project.
All samples are selected by default.

Figure 11 Project Wizard - Project Data Selection



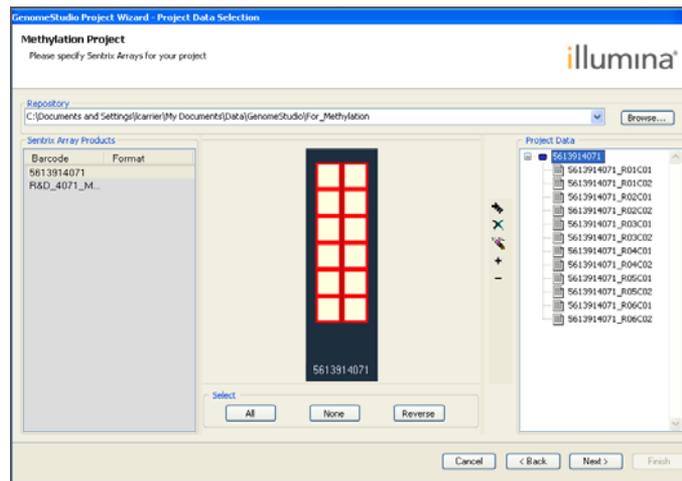
NOTE

The image of the Sentrix Array Product is different for each product.

- 3 To change the selected samples, in the Select area, do one or more of the following:
 - To select a single sample, click the sample on the image.
 - To select multiple samples, hold **Ctrl** and click each sample you want to select.
 - To select all samples, click **All**.
 - To select no samples, click **None**.
 - To select the reverse of the samples currently selected (for example, samples 1, 2, and 3 are currently selected, but you want to select samples 4, 5, and 6), click **Reverse**.

- 4 Click  to add the selected samples to your project.
 The selected samples appear under the name of the Sentrix Array Product in the Project Data pane.

Figure 12 Project Wizard - Project Data Selection - Selecting Samples



- 5 **[Optional]** Click  (to the left of the group symbol) to display the list of samples chosen for the current project for the given array. A project can contain several arrays, but the + corresponds to only one array.

- 6 Click **Next** to advance to the GenomeStudio Project Wizard - Groupset Definition screen.

Defining Groupsets and Groups

GenomeStudio projects are structured in a hierarchical manner.

A project includes one or more groupsets.

A groupset is a collection of groups that you choose to be analyzed simultaneously.

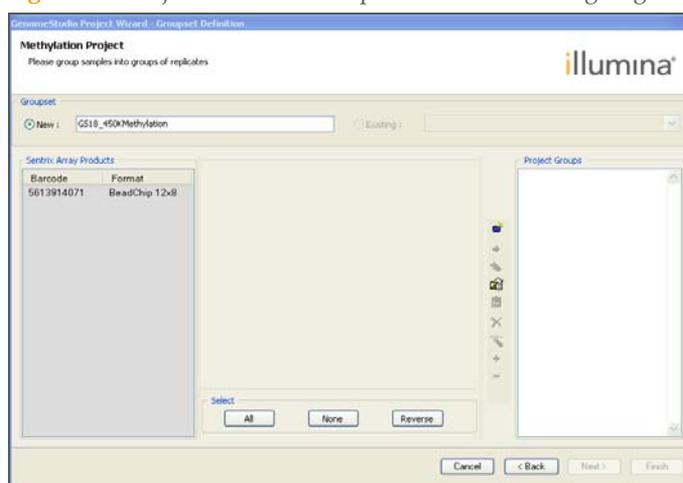
A groupset includes one or more groups.

A group is a set of arrays that share a functional relationship (e.g., replicates, zero time points, reference group). Within a groupset, an array can be included in more than one group (e.g., analyzed individually in addition to being analyzed as a member of a reference group).

Perform the following steps to define a groupset for your project.

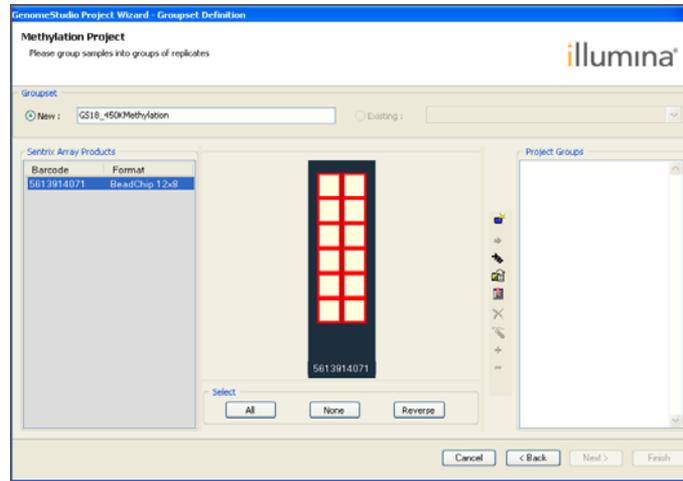
- 1 Assign a name to your groupset by doing one of the following:
 - Select **New** and type a name for your new groupset.
 - Select **Existing** and choose a groupset from the dropdown menu.

Figure 13 Project Wizard - Groupset Definition - Assigning Groupset Name



- 2 In the Sentry Array Products pane, select the product that contains the samples you want to assign to a groupset.
All samples are selected by default.

Figure 14 Project Wizard - Groupset Definition - Selecting Sentrix Array Product



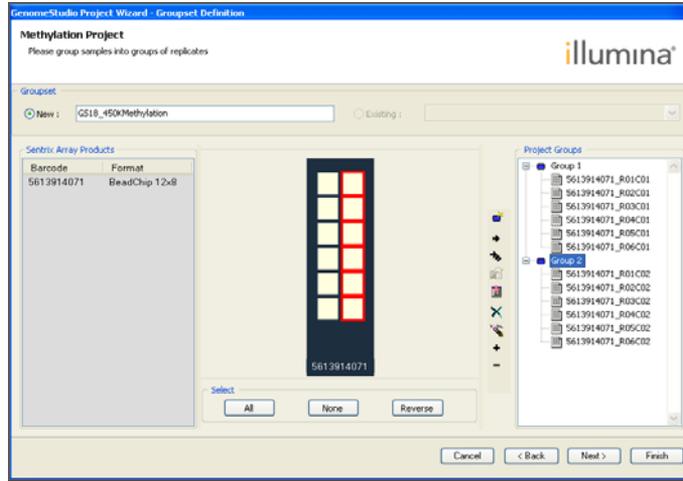
NOTE

The image of the Sentrix Array Product is different for each product.

- 3 To change the selected samples, in the Select area, do one or more of the following:
 - To select a single sample, click the sample on the image.
 - To select multiple samples, hold **Ctrl** and click each sample you want to select.
 - To select all samples, click **All**.
 - To select no samples, click **None**.
 - To select the reverse of the samples currently selected (for example, samples 1, 2, and 3 are currently selected, but you want to select samples 4, 5, and 6), click **Reverse**.
- 4 Do any of the following to define project groups in a groupset:

To...	Click...
Create a new group	
Add selected samples to a selected group	
Create a separate group for each selected sample	
Load data from a sample sheet	
Apply a group layout file	
Remove selected groups and samples from the project	
Remove all groups and samples from the project	

Figure 15 Project Wizard - Groupset Definition - Selecting Samples



- 5 Click **Next** to continue.
The GenomeStudio Project Wizard - Project Analysis Type and Parameters dialog box opens.

Defining the Analysis Type and Parameters

- 1 In the Analysis Type area of the Project Analysis Type and Parameters dialog box, select **Methylation** or **Diff Methylation**.

Figure 16 Project Wizard - Project Analysis Type and Parameters

The screenshot shows the 'Methylation Project' dialog box in GenomeStudio. The 'Analysis Type' section has 'Methylation' selected. The 'Analysis' section has 'GS18_450K' selected for 'Groupset' and a 'Name' field. The 'Parameters' section has 'none' selected for 'Normalization' and a 'Subtract Background' checkbox. The 'Differential Methylation' section has 'A431' selected for 'Ref Group' and 'Illumina custom' selected for 'Error Model'. The 'OMA Manifest' section has a 'Use Mask File' checkbox. Navigation buttons at the bottom include 'Cancel', '< Back', 'Next >', and 'Finish'.

- 2 In the Name area, enter a name for this analysis.
- 3 In the Parameters area, select the normalization method you want to use:
 - **Average**
 - **Controls**
 - **Background**
 - **None**



NOTE

These normalization methods are not supported for all products. For information about normalization methods, see Chapter 4, *Applying Methylation Algorithms*.

- 4 Select an appropriate Content Descriptor for your project: *.bpm for Infinium assays or *.oma for GoldenGate or VeraCode assays.
- 5 If you are performing a differential methylation analysis, select a **Reference Group** and **Error Model** in the Differential Methylation area.

- If you want to compute the false discovery rate, select the **Compute false discovery rate** check box.



NOTE

If you select Compute false discovery rate, the p-values (in the p-value column in the table) are adjusted accordingly. The p-values are not adjusted if you do not select Compute false discovery rate.

- [Optional, GoldenGate assay only]** Select the **Use Mask File** check box and browse to the location of the mask file you want to use.

The mask file must contain the following columns:

- TargetID
- ProbeID
- 0/1

To create a mask file, copy the TargetID and ProbeID columns from the table, and add the 0/1 column in Excel.

For more information about mask files, see the section *Creating a Mask File* on page 19.



NOTE

A mask file allows you to choose which probes to include in your analysis.

- Click **Finish**.
GenomeStudio begins to run your analysis. A progress bar indicates the completion level of your analysis.

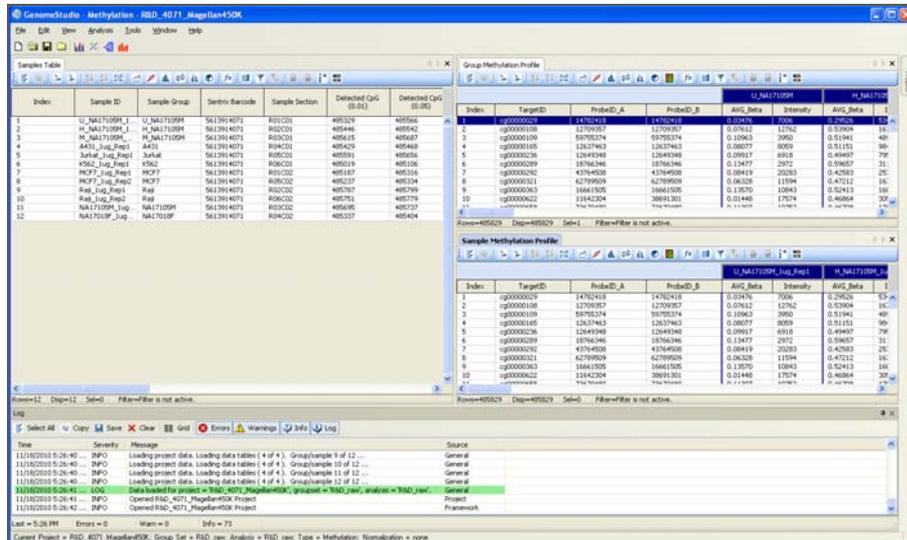


NOTE

The time it takes for your analysis to be processed depends on the number of samples and groups, and the type of analysis.

Your GenomeStudio Methylation project opens.

Figure 17 GenomeStudio - Methylation Analysis Default View



For information about the graphical user interface of the GenomeStudio Methylation Module, see Chapter 6, *User Interface Reference*.

Creating a Mask File

Some custom GoldenGate assay probes may not provide reproducibly robust results and should be removed from analysis. The detection p-value reported in GenomeStudio can be used as an objective measure of overall probe performance.



NOTE

Illumina recommends excluding probes that have a detection p-value of greater than 0.05 in the assay; however, you may define your own criteria.

To exclude a probe:

- 1 Export the TargetID and ProbeID columns from the Group Methylation Profile table or the Sample Methylation Profile table.
- 2 Create an additional column, in which 1 represents the probe to display, and 0 represents the probe to hide.
- 3 Save the mask file as a *.csv file in the same repository where the content descriptor file is stored. The mask file need not conform to a naming convention.



NOTE

Any *.csv file present in the same repository as Content Descriptor files will appear in the Experiment Parameters pulldown menu. To avoid confusion, Illumina advises the use of separate repositories for Content Descriptor and for SAM/BeadChip data.

Figure 18 Mask File Example

	A	B	C	D	E	F	G
1	Illumina Inc.						
2	Normalization = none						
3	Array Content = GS0007005-OMA						
4	Error Model = none						
5	DateTime = 12/11/06						
6	Local Settings = en-US						
7							
8	TargetID	ProbetID	0/1				
9	AATK_E63_R	2976	1				
10	AATK_P519_R	3	1				
11	AATK_P709_R	10	0				
12	ABCA1_E120_R	5366	1				
13	ABCA1_P45_F	4214	1				
14	ABCB4_E429_F	2983	1				
15	ABCB4_P51_F	23	1				
16	ABCB4_P892_F	21	0				
17	ABCC2_E16_R	67	1				
18	ABCC2_P88_F	3072	1				
19	ABCC5_P444_F	27	1				
20	ABCG2_P178_R	3089	1				
21	ABCG2_P310_R	2985	1				
22	ABL1_P53_F	2249	1				
23	ABL2_P459_R	4216	1				
24	ABO_E110_F	2986	1				
25	ABO_P312_F	30	1				
26	ACTG2_E98_R	2988	1				
27	ACTG2_P346_F	33	1				
28	ACTG2_P455_R	36	0				
29	ACVR1_E328_R	5829	1				
30	ACVR1_P983_F	5799	1				
31	ACVR1B_E497_R	5834	1				

Viewing Your Data

Introduction	22
Scatter Plots	23
Histogram Plots	33
Heat Maps	36
Cluster Analysis Dendrograms	39
Copy/Paste Gene Clusters	45



Introduction

This chapter describes the data visualization functions of the GenomeStudio Methylation Module, which are used to create:

- ▶ Scatter plots
- ▶ Histogram plots
- ▶ Heat maps
- ▶ Dendrograms
- ▶ Control summary reports

Use these tools to explore the data you generate using Bead Studio's Methylation Analysis or Differential Methylation Analysis (described in Chapter 4).

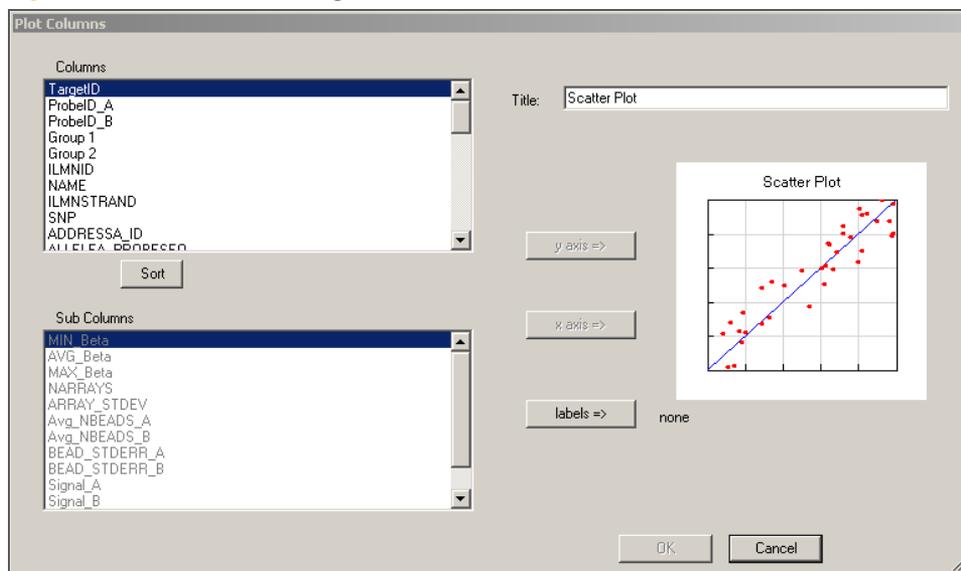
Scatter Plots

Once you have performed a methylation analysis or differential methylation analysis, you can create scatter plots of your data.

To create a scatter plot:

- 1 Click  **Scatter Plot**.
The Plot Columns dialog box opens.

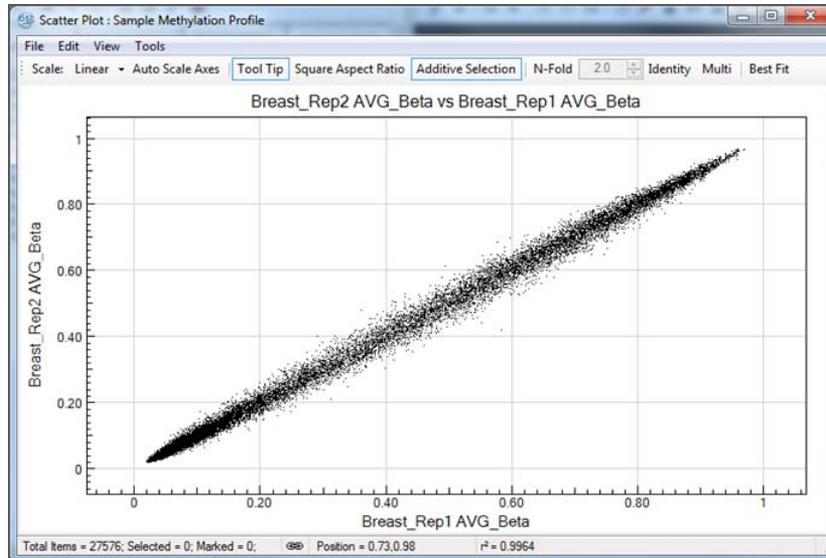
Figure 19 Plot Columns dialog box



- 2 In the Plot Columns dialog box, select options from the Columns and Sub Columns areas for:
 - Y-axis
 - X-axis
 - Labels

You can choose any subcolumn that contains numerical data for the axes. The tooltip displays the column information you choose as a label.
- 3 Click **OK** to create and display the scatter plot.

Figure 20 Scatter Plot



Scatter Plot Functions

- ▶ Click and drag to move the scatter plot.
- ▶ Shift-click to zoom into a particular region of the scatter plot.
- ▶ Use the mouse wheel to zoom in and out.
- ▶ Control-click, hold, and move the mouse to select a specific gene or group of genes.

Table 1 lists and describes Control Panel functions.

Table 1 Scatter Plot Control Panel Functions and Descriptions

Function	Item	Description
Scale	Linear	When enabled, X and Y axes are on a linear scale.
	Logarithmic	When enabled, X and Y axes are on a logarithmic scale.
	Power	When enabled, X and Y axes are on nth root scale (where n is an odd number from 3 to 9).
N-Fold	Show	When checked, shows n-fold lines and allows you to select the fold value.
	N-fold setting selector	When Show is checked, allows you to select the fold change.
	Identity	When checked, GenomeStudio displays the identity line in bold red color. If a gene is on this line, its X and Y intensities are equal.
	Multi	When checked, GenomeStudio displays additional incremental fold change regions.

Table 1 Scatter Plot Control Panel Functions and Descriptions (Continued)

Function	Item	Description
Options	Best Fit	When checked, presents the Scatter Plot in the optimal fit for the genes of interest (linear equation is displayed in Control Panel next to r2 values).
	Mouse Drag/ Zoom	When checked, allows you to drag and zoom in/out using the mouse. Use the mouse wheel to zoom in or out. If your mouse does not have a wheel: <ol style="list-style-type: none"> 1. Press the Shift key while pressing the left mouse button. 2. Drag to create a rectangle around an area to zoom in on. 3. Release the Shift key and the mouse button to zoom. To return to normal view, select Scatter Plot Tools Auto Scale Axes .
	Tooltip	When checked, the scatter plot displays the label you chose.
	Square Aspect Ratio	When checked, X axis scale is equal to Y axis scale.
	Additive Selection	When checked, any new gene selection will be added to the scatter plot, along with previous selections. When not checked, any new selection replaces the previous selection(s).
	Close Control Panel	Click to close the Control Panel.
Status Bar	# total items () =	Displays the number of CpG loci visible in the scatter plot.
	# selected =	Displays the number of selected CpG loci in the scatter plot.
	Linking	Clicking  toggles synchronization of marking and selection of the data shown in the scatter plot with data in the table.
	Position	Displays current X/Y position of gene (mouse pointer) on the Scatter Plot.
	r2	Square of the correlation coefficient. Note: If the scatter plot is in linear scale, the r2 value is calculated in linear space; if the scatter plot is in logarithmic scale, r2 is calculated in log space.

- 4 To use additional plot tools, select **Tools** from the scatter plot main menu.

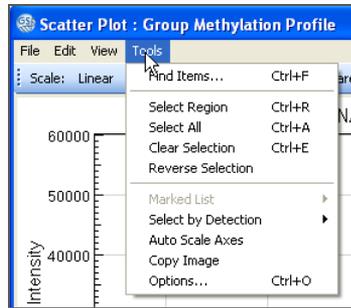
Figure 21 Scatter Plot Tools Menu

Table 2 lists and describes the various scatter plot tools.

Table 2 Scatter Plot Tools Menu Item Descriptions

Tool Name	Description
Find Items	Opens the Find Items dialog box, where you can enter a list of items separated by commas or load a search item list from a text file.
Select Region	Converts the cursor to a crosshair tool, which you can use to draw a boundary around any region in the scatter plot. All loci within the boundary are selected.
Select All	Selects all CpG loci in the scatter plot. Loci are displayed in the currently-selected color.
Clear Selection	Clears any previous selections.
Reverse Selection	Reverses the current selection (selects items that are unselected).
Marked List	Includes operations you can perform on items you mark in the scatter plot: <ul style="list-style-type: none"> • View in Web Browser—Displays a list of the marked items in a web browser. • Save in Text File—Brings up the Save Marked Items List As dialog box and allows you to save genes in a file in a location you specify. • Show Item Symbols—Shows item symbols.
Auto Scale Axes	Automatically scales the X and Y axes of the scatter plot.
Copy Image	Copies the current image to the clipboard.

Table 2 Scatter Plot Tools Menu Item Descriptions (Continued)

Tool Name	Description
Options	<p>Opens the Scatter Plot dialog box, in which you can set the following parameters:</p> <ul style="list-style-type: none"> • Axes—Displays the minimum and maximum X and Y axis values. When Square Aspect Ratio is not checked, you can set new X and Y axis vales. • Labels— Allows you to choose font properties for the scatter plot title and axes. • Data Points— Allows you to select a point size and style for the Scatter Plot data points. • Scale— Allows you to select a power (3, 5, 7, or 9) for the Power Setting. • Colors— Click in each box to bring up the color palette and set colors for: <ul style="list-style-type: none"> • Axes • Background • Grid • Data Points • Selection

Scatter Plot Context Menu Selections

Right-click anywhere in the scatter plot to view the context menu. The context menu contains options that can be applied to the selected project.

Figure 22 Scatter Plot Context Menu

Table 3 lists context menu items and their functions.

Table 3 Scatter Plot Context Menu Item Descriptions

Item	Description
Fold Change	If fold change lines are present, displays the fold change limits for the current cursor location. Allows you to select or deselect all genes inside the fold change.

Table 3 Scatter Plot Context Menu Item Descriptions (Continued)

Item	Description
Select Region	Allows you to select a region that contains samples of interest.
Select All	Allows you to select all samples.
Clear Selection	Clears your selection.
Copy Selection	Copies your selection to the clipboard.
Paste Selection	Pastes the contents of the clipboard to the current location.
Reverse Selection	Allows you to select the samples that were previously unselected.
Mark Selected Items	Allows you to mark items of interest.
Clear Marks	Clears your marks.
Disconnect Selections/ Marking	Disconnects synchronization between the graph and the table.
Marked List	Includes operations you can perform on genes you mark in the scatter plot: <ul style="list-style-type: none"> • View in Web Browser—Displays a list of the marked genes in a web browser. • Save in Text File—Brings up the Save Marked Genes List As dialog box and allows you to save genes in a file in a location you specify. • Show Item Symbols—Shows item symbols.
Auto Scale Axes	When selected, automatically scales the scatter plot X and Y axes.
Copy Image	When selected, places the scatter plot image on the clipboard.
Options	<ul style="list-style-type: none"> • Axes—Displays the minimum and maximum X and Y axis values. When Square Aspect Ratio is <i>not</i> checked, you can set new X and Y axis values. • Labels—Allows you to choose font properties for the Scatter Plot title, X axis, and Y axis. • Data Points—Allows you to select a point size and style for the Scatter Plot data points. • Scale—Allows you to select a power (3, 5, 7, or 9) for the Power setting. • Colors—Click in each box to bring up the color palette and set colors for: <ul style="list-style-type: none"> • Axes • Background • Grid • Data Points • Selection

Finding Items in the Scatter Plot

The GenomeStudio Methylation Module provides a path to gene property information, including gene ID, intensities, and gene ontology information.

To find items in the scatter plot:

- 1 From the Scatter Plot menu bar, select **Tools | Find Items**.

Figure 23 Find Items Tool Selected

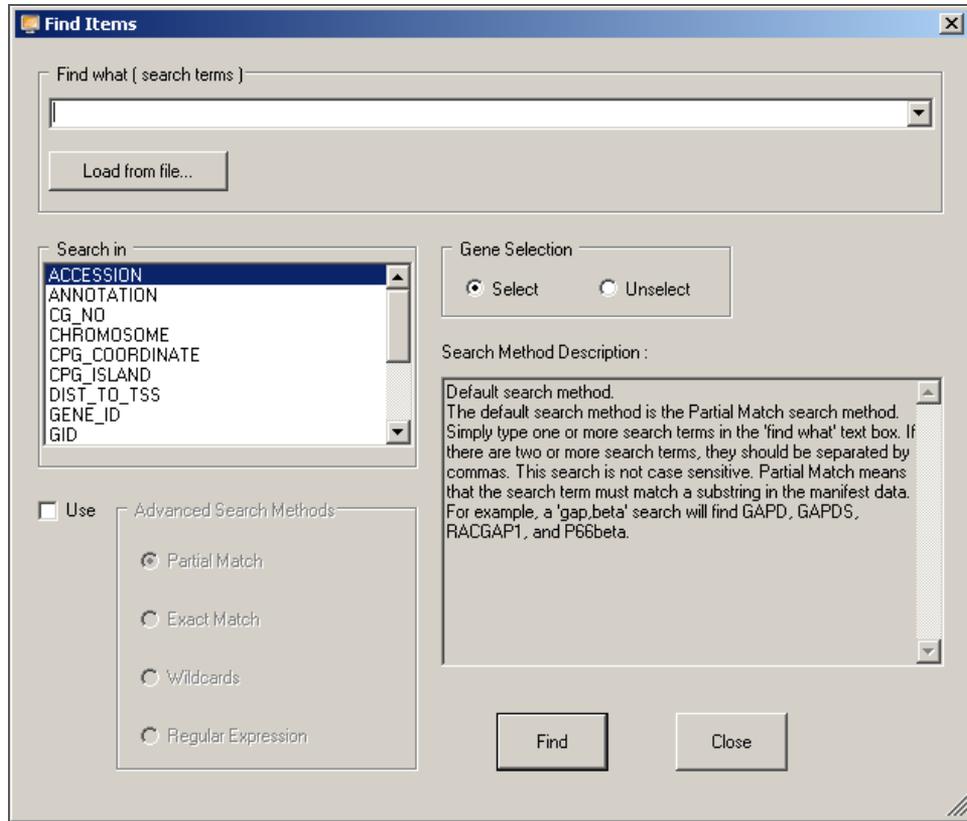


- 2 In the Find Items dialog box, select specific items based on the following fields in the manifest (which includes GenBank database information):

- Accession
- Annotation
- Chromosome
- CpG coordinate
- CpG island
- Dist. to TSS
- Gene ID
- GID
- Input sequence
- Probe ID
- Product
- Ref seq
- Search key
- Symbol
- Synonym

This list of fields reflects the columns in a *.bpm or *.oma file. It can vary for different *.bpm and *.oma files. Not all of the fields may be populated in a particular manifest. In the Search in pane, select the manifest column you want to search.

Figure 24 Find Items dialog box



- 3 In the Find what (search terms) text field, enter the search text.

**NOTE**

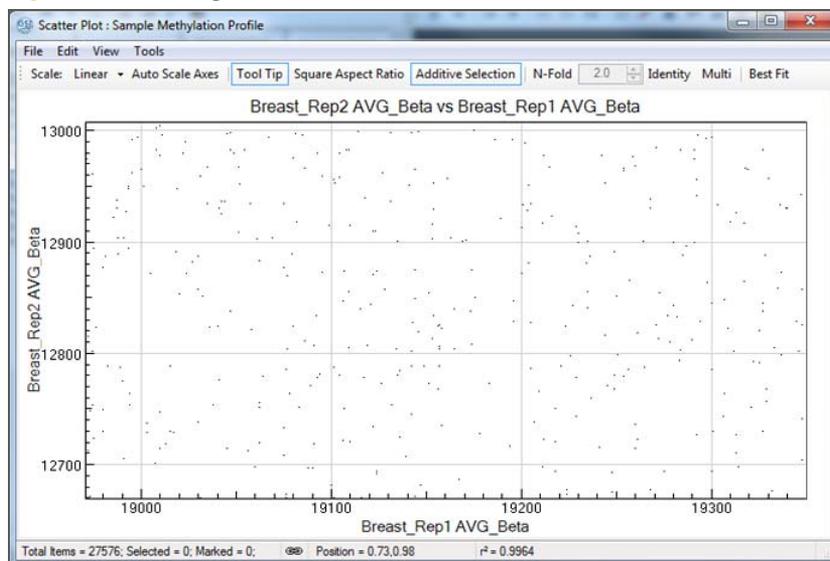
By default, searches are partial. For example, if you search the word 'VEGF' in the Symbol field, the search will return not only VEGF, but also, VEGFB and VEGFC.

Multiple search terms can be used, separated by commas.

Search terms can also be loaded from a text file. The file should have each term on a separate line.

- 4 Do one of the following:
 - Click **Select** to select found items.
 - Click **Unselect** to unselect found items that were previously selected.
- 5 Click **Find** to return to the scatter plot with the identified items highlighted. For more advanced search options, select **Use** (to the left of the Advanced Search Methods pane). Advanced search methods are described in the Search Method Description box. The scatter plot displays the selected item.
- 6 **[Optional]** Use the mouse wheel to zoom in for a magnified view.

Figure 25 Zooming in to See Selected Items



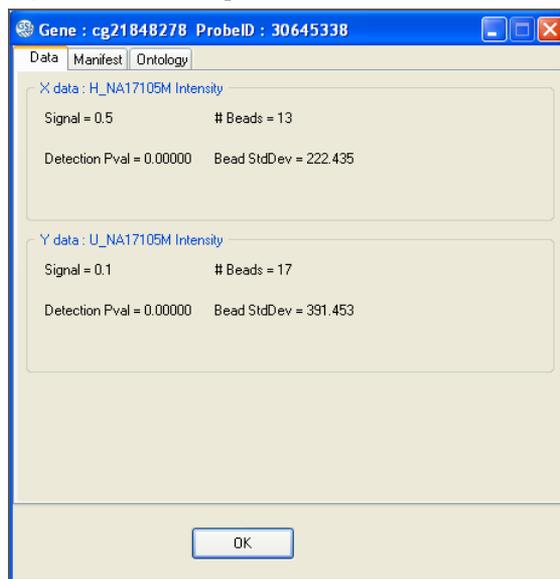
- 7 To display the Gene Properties dialog box:
 - a Right-click the selected item.
 - b Click **Gene Symbol** in the context menu.
 The Gene Properties dialog box opens.

The following paragraphs illustrate the functions of the Gene Properties dialog box.

Data Tab

Figure 26 illustrates the Data tab of the Gene Properties dialog box.

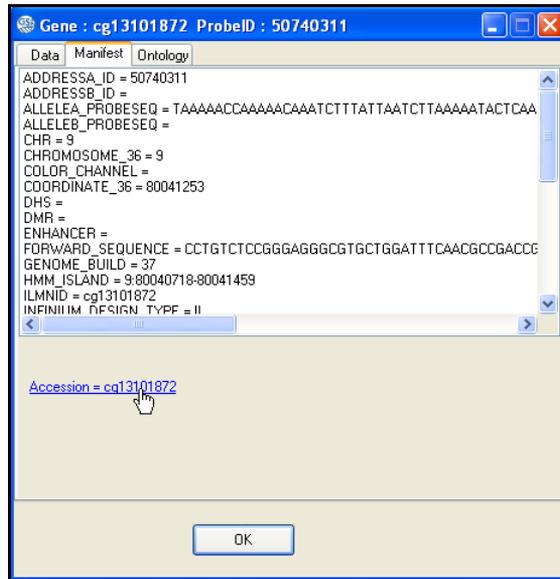
Figure 26 Gene Properties Window Data Tab



Manifest Tab

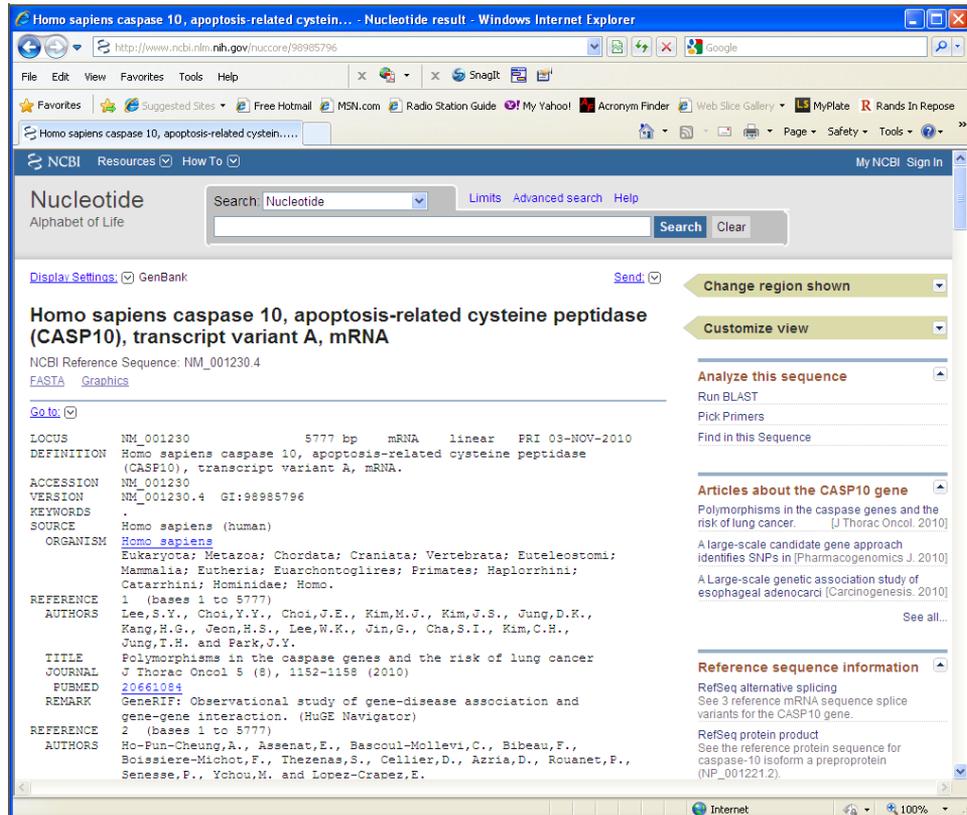
- 1 On the Manifest tab, click the **Accession** link to view the National Center for Biotechnology Information (NCBI) record for the selected gene.

Figure 27 Gene Properties Window Manifest Tab



GenomeStudio jumps to the NCBI website.

Figure 28 NCBI Website



Histogram Plots

Once methylation analysis or differential methylation analysis has been completed, you can create histogram plots using GenomeStudio data tables.



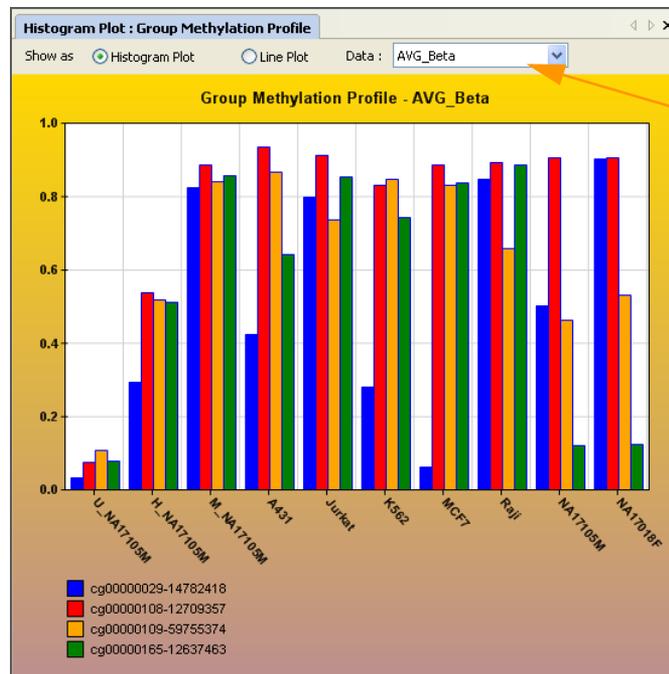
NOTE

A histogram plot shows data from the currently-selected data table. If no data is selected, a warning message will appear, prompting you to select some data..

To create a histogram plot:

- 1 Click  **Histogram Plot**.
The histogram plot appears.

Figure 29 Histogram Plot of Sample Probe Profile



If you want to view the same data in a line plot, select **Line Plot**.

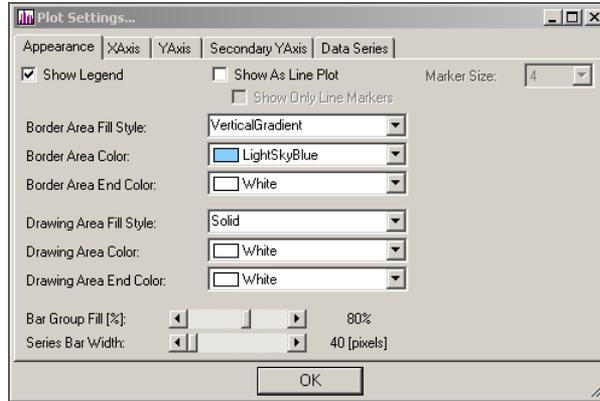
- 2 In the Data dropdown menu, select the type of data to plot.



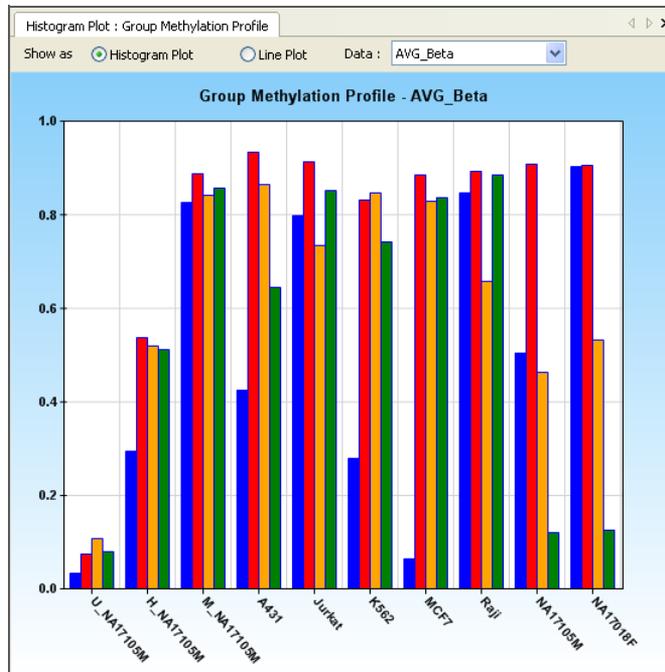
NOTE

The graph only displays the data that are shown in the table. To change which columns are displayed in the table, use the Column Chooser tool, described in the GenomeStudio Framework User Guide, Part # 11204578.

- 3 Right-click and select **Properties** from the context menu.
The Plot Settings dialog box opens.

Figure 30 Plot Settings dialog box

- 4 Select attributes for the following aspects of the histogram plot:
 - Appearance
 - X Axis
 - Y Axis
 - Data Series
- 5 Click **OK**.
The histogram plot is displayed with the attributes you have chosen.

Figure 31 Histogram Plot With User-Selected Attributes

Histogram Plot Context Menu

Right-click anywhere in the histogram plot to view the context menu. The context menu contains features that can be applied to the selected project.

Figure 32 Histogram Plot Context Menu

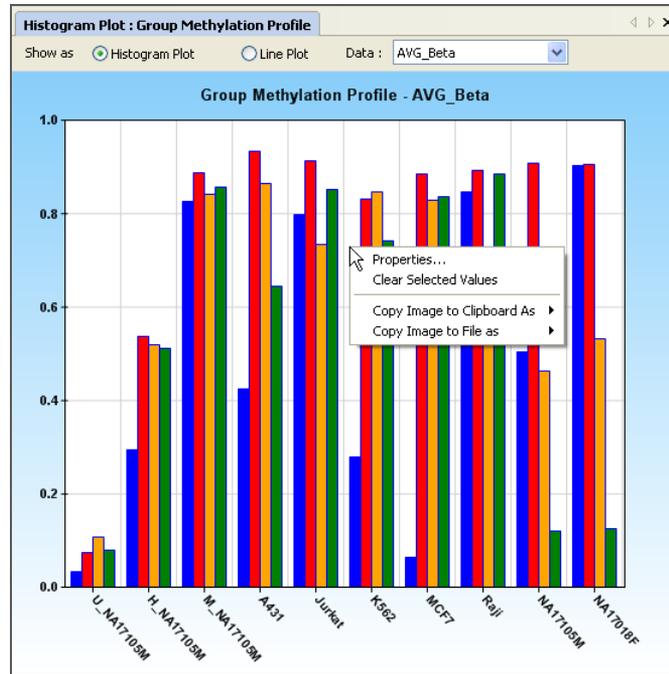


Table 4 lists context menu items and their functions.

Table 4 Histogram Plot Context Menu Item Descriptions

Item	Description
Properties	Displays the Plot Settings dialog box, which allows you to change the characteristics of the histogram plot.
Clear Selected Values	Clears the selected values.
Copy As	Copies the histogram plot image to the clipboard in any of the following file formats: BMP, JPEG, PNG, GIF, or TIFF.

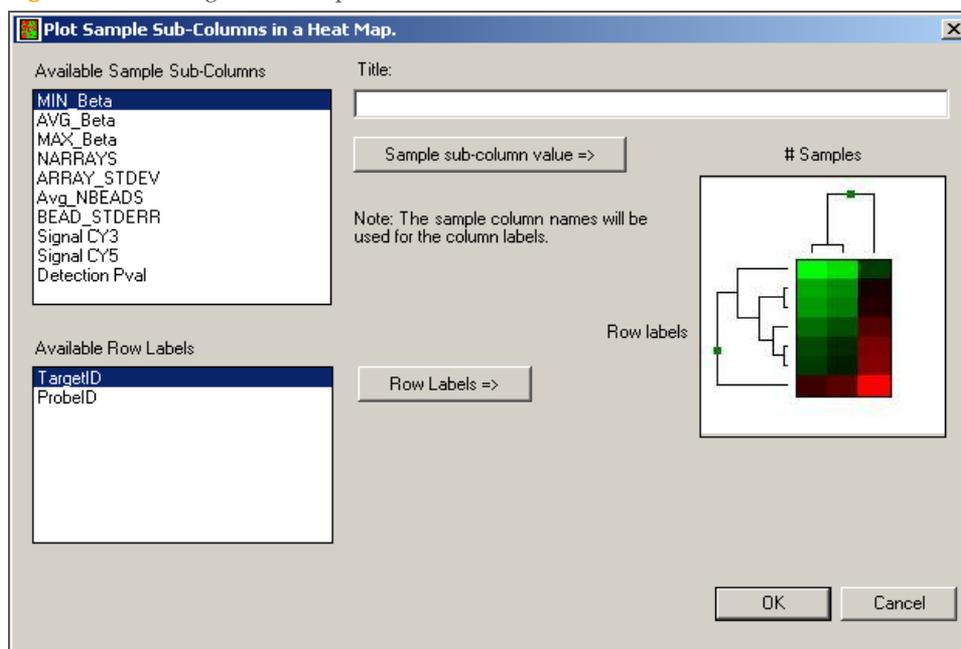
Heat Maps

Once gene analysis or differential analysis has been completed, you can create heat maps using GenomeStudio output files.

To create a heat map:

- 1 Click  **Column Chooser**.
The Column Chooser dialog box opens.
- 2 Select rows and columns from the data table that you want to display in a heat map.
- 3 Click **OK**.
The Column Chooser dialog box closes.
- 4 In the table toolbar, click  **Heat Map**.
The Plot Sample Subcolumns in a Heat Map dialog box opens.

Figure 33 Creating a Heat Map



- 5 **[Optional]** Type a title in the Title text field.
- 6 Select an attribute in the Available Sample Subcolumns area.

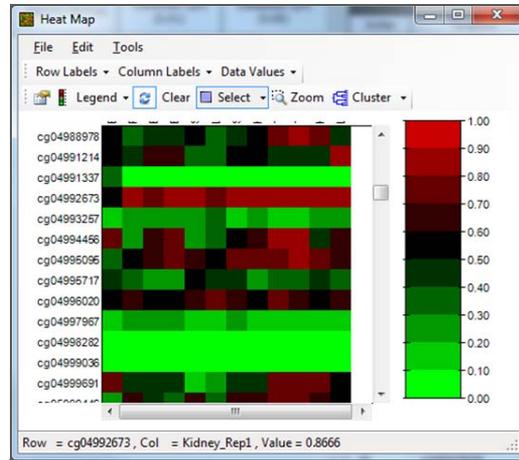


NOTE

Available sample subcolumns must contain plottable (numerical) data.

- 7 Select an attribute in the Available Row Labels area.
- 8 Click **OK** to create and display the heat map.

Figure 34 Heat Map



Heat Map Tools Menu

To use additional heat map tools:

- 1 On the menu bar, click **Tools**.
- 2 Select **Cluster** or **Generate Presentation Image**.

Figure 35 Heat Map Tools Menu

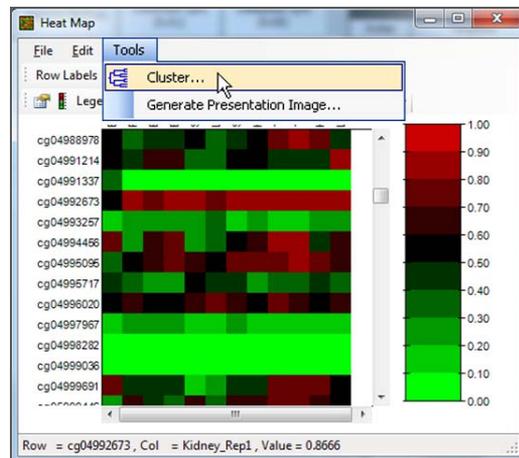


Table 5 describes the available heat map tools.

Table 5 Heat Map Tools Menu Item Descriptions

Tool	Description
Cluster	Displays the Cluster Options window, from which you can select whether to cluster rows or columns, as well as which hierarchical clustering method to use (COR, ACOR, Manhattan, or Euclidian). See “Cluster Analysis Dendrograms” on page 39 for more information about clustering methods.
Generate Presentation Image	Displays the Presentation Image Setup window, from which you can configure and generate a presentation image.

Heat Map Context Menu

Right-click anywhere in the Heat Map to view the context menu. The context menu contains options that can be applied to the selected Heat Map.

Figure 36 Heat Map Context Menu

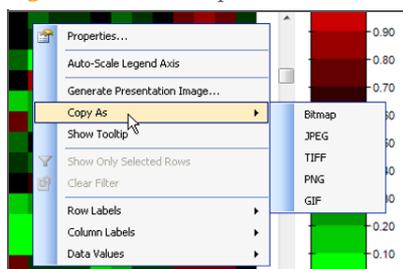


Table 6 lists heat map context menu items and their functions.

Table 6 Heat Map Context Menu Item Descriptions

Item	Description
Properties	Displays the Heat Map Properties dialog box, from which you can alter the visual properties of the title, legend, rows, columns, and scroll bars of the heat map.
Auto-Scale Legend Axis	Automatically scales the legend axis.
Generate Presentation Image	Displays the Presentation Image Setup window, from which you can configure and generate a presentation image.
Copy As	Copies the heat map to the clipboard as any of the following image types: BMP, JPEG, TIFF, PNG, or GIF.
Show Tooltip	Displays a tooltip when the cursor is positioned over the heat map.
Show Only Selected Rows	Limits the data shown in the heat map to only include data from rows selected in the data table.
Clear Filter	Shows all data in the heat map.
Row Labels	Enables you to change the row labels while the heat map is open.
Column Labels	Enables you to change the column labels while the heat map is open.
Data Values	Enables you to change what data is displayed in the heat map.

For more information about working with heat maps, see the Heat Maps section in the *GenomeStudio Framework User Guide*, Part # 11204578.

Cluster Analysis Dendrograms

Clustering is an analysis method used to group sets of objects into subsets or clusters. Objects assigned to the same cluster are more closely related to one another than to objects assigned to different clusters. In the context of methylation, the method can be used to answer two basic questions:

- ▶ Which genes show similar patterns of methylation across a series of samples?
Knowing this is useful for identifying genes in common pathways, or genes that coordinately respond to the same stimuli.
- ▶ Which samples are most similar based on the methylation levels of genes within them?
Knowing this is useful for identifying conditions that generate a common metabolic response. For example, in a toxicology study, if an unknown compound induces a pattern of expression similar to that induced by a panel of genotoxins, it is likely that the unknown is a genotoxin.

Mathematicians have devised dozens of clustering methods using different metrics to establish relationships between sets of values. In GenomeStudio, clustering occurs using the nesting with average linkage method. GenomeStudio offers four clustering metrics for calculating dissimilarities:

- ▶ **Correlation (COR)**
Computes the Pearson correlation using a $1 - r$ distance measure.
- ▶ **Absolute Correlation (ACOR)**
Computes the Pearson correlation using a $1 - |r|$ distance measure.
- ▶ **Manhattan**
Computes the distance between two points if a grid-like path is followed.
- ▶ **Euclidian**
Computes the shortest distance between two points.



NOTE

Illumina recommends using multiple clustering methods to validate results. Groupings with a true biological basis will usually show up regardless of the algorithm used.

Similarities and Distances

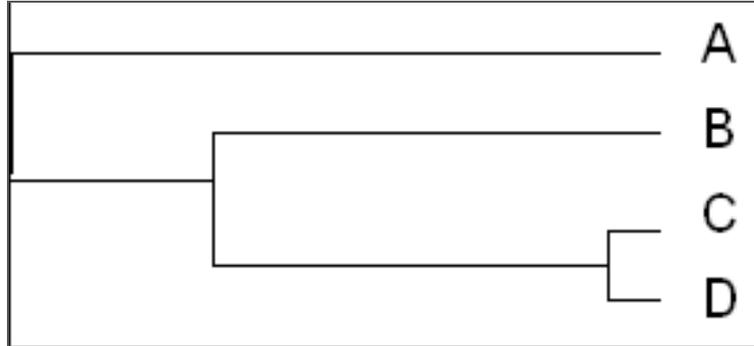
There are several ways to compute the similarity of two series of numbers. The most commonly used similarity metric is the Pearson correlation. The Pearson correlation coefficient between any two series of numbers $X = \{X_1, X_2, \dots, X_N\}$ and $Y = \{Y_1, Y_2, \dots, Y_N\}$ is defined as:

$$r = \frac{1}{N} \sum_{i=1}^N \left(\frac{X_i - \bar{X}}{\sigma_X} \right) \left(\frac{Y_i - \bar{Y}}{\sigma_Y} \right)$$

Distance is then defined as $1 - r$ for Correlation and $1 - |r|$ for Absolute Correlation. GenomeStudio also uses Manhattan ($\sum |X_i - Y_i|$) and squared Euclidean ($\sum (X_i - Y_i)^2$) distances.

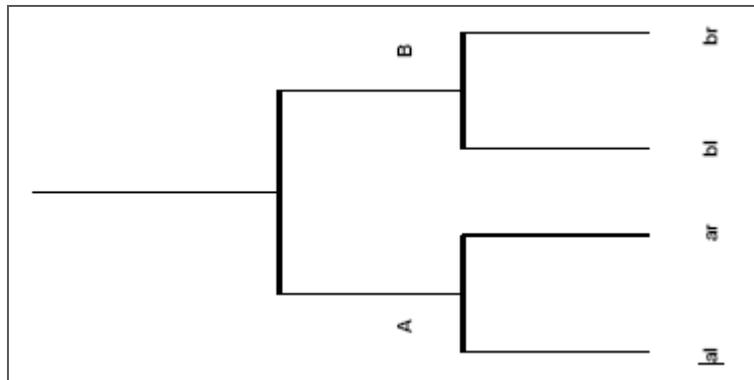
GenomeStudio presents the clustering information in the form of a dendrogram, a tree-like structure with branches that correspond to genes or samples, depending on how the analysis is run. The distance on the X axis establishes the similarity relationships among the genes or samples. For example, if the dendrogram plots the similarity of samples based on methylation, samples C and D are very similar to each other, less similar to B, and even less similar to A.

Figure 37 Dendrogram Similarity Example



After clustering, nodes are reordered starting near the top to ensure that node “ar” is closer to “B” than node “al”, and node “bl” is closer to “A” than node “br”.

Figure 38 Dendrogram, Showing Nodes



Analyzing Clusters

To analyze clusters:

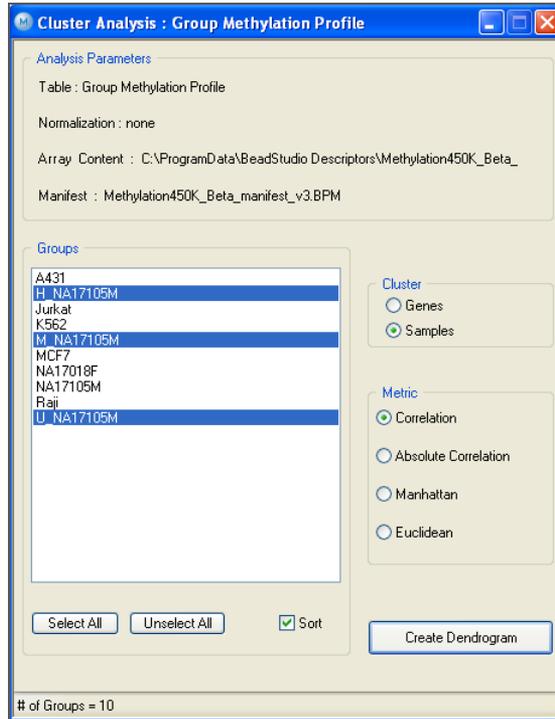
- 1 Click  **Run Cluster Analysis** to open the cluster analysis tool.
- 2 In the Cluster Analysis dialog box:
 - a Groups pane—highlight the group(s) whose clusters you wish to analyze (or click **Select All**).
 - b Select the **Sort** check box to sort the items in the Groups listbox alphabetically in ascending order.
 - c Cluster pane—Click **Genes** or **Samples**.
If you select **Genes**, the dendrogram displays a cluster of genes.
If you select **Samples**, the dendrogram displays a cluster of samples.

**NOTE**

Clustering samples is much faster than clustering genes. Clustering thousands of genes can take hours.

- d Metric pane—Select the metric you would like GenomeStudio to use to calculate clusters.

Figure 39 Cluster Analysis dialog box

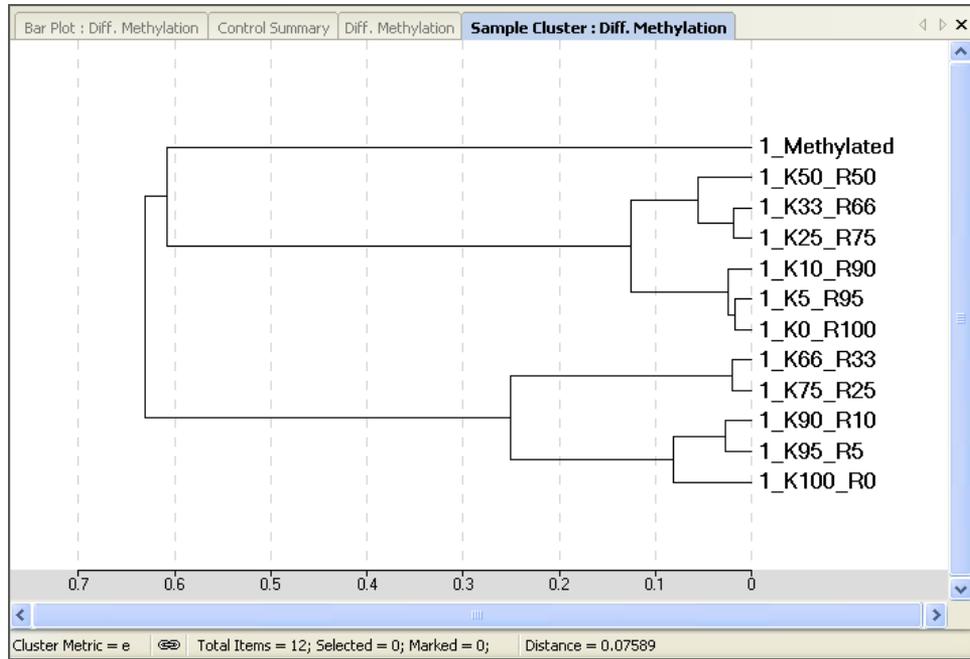


- e Click **Create Dendrogram** to view the graph.

**NOTE**

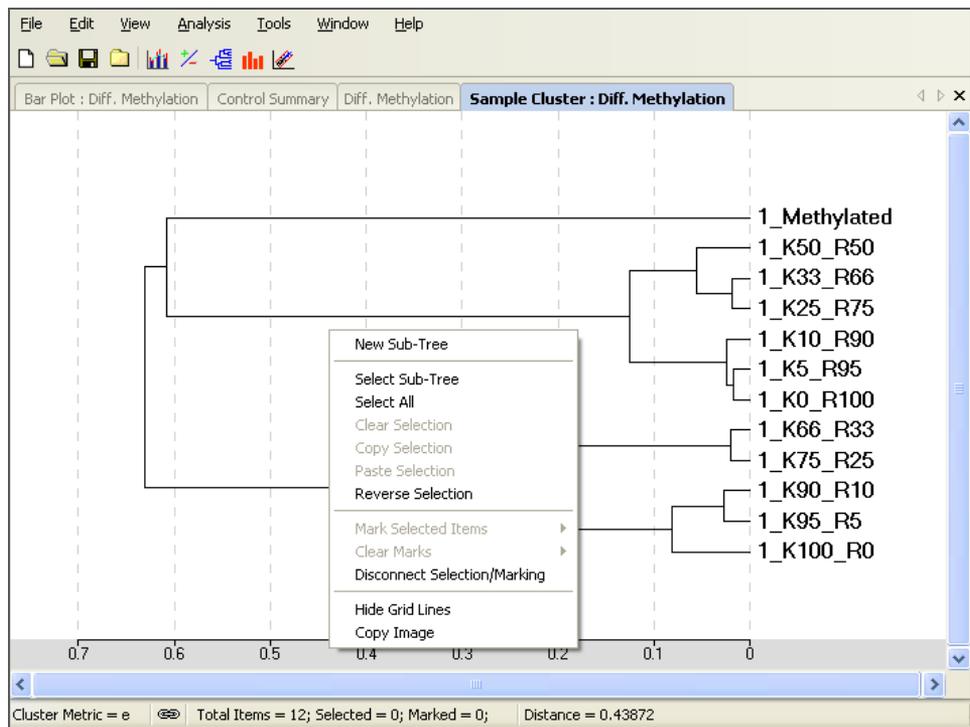
The scale at the bottom of the dendrogram shows dissimilarity between nodes. See “Similarities and Distances” on page 39.

Figure 40 Dendrogram



- 3 Right-click in the dendrogram to view the context menu.

Figure 41 Dendrogram with Context Menu



Dendrogram Context Menu Selections

Table 7 lists and describes the dendrogram context menu selections.

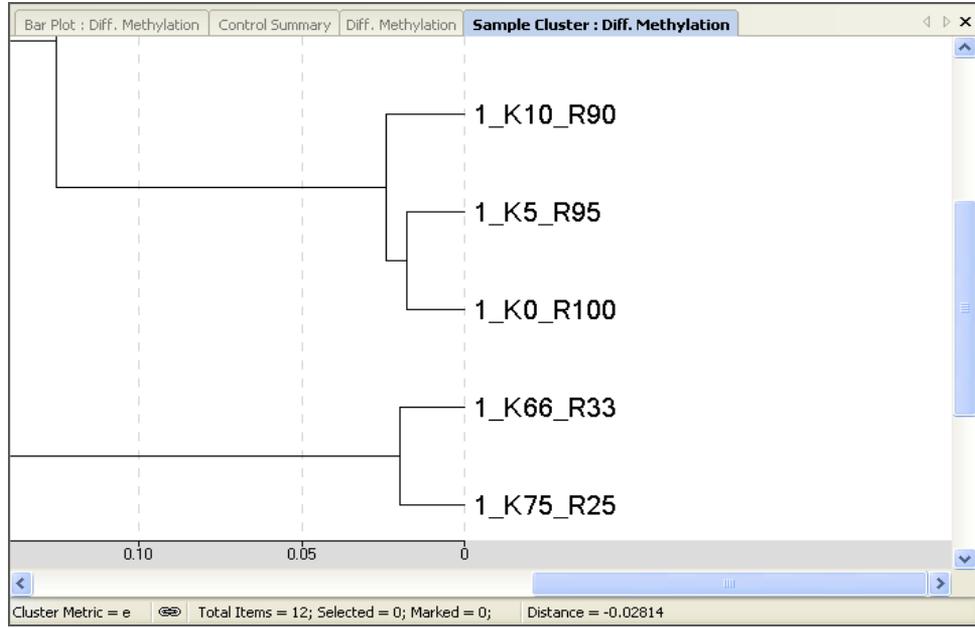
Table 7 Dendrogram Context Menu Selections

Item	Description
New Sub-Tree	Displays the selected sub-tree in a new window. This feature is disabled when the cursor is outside of any tree.
Select Sub-Tree	Highlights the sub-tree in blue. This feature is disabled when the cursor is outside of any tree.
Select All	Selects all sub-trees.
Clear Selection	Clears any selection.
Copy Selection	Copies the current selection(s) to the clipboard.
Paste Selection	Pastes the current clipboard contents to a location you choose.
Reverse Selection	Reverses the last selection made.
Mark Selected Items	Marks the currently-selected items.
Clear Marks	Clears all marks.
Marked List	Includes operations you can perform on genes you mark in the scatter plot: <ul style="list-style-type: none"> • View in Web Browser—Displays a list of the marked genes in a web browser. • Save in Text File—Brings up the Save Marked Genes List As dialog box and allows you to save genes in a file in a location you specify. • Show Item Symbols—Shows item symbols.
Disconnect Selection/ Marking	Disconnects synchronization between the graph and the table.
Hide Grid Lines	Hides background grid lines.
Copy Image	Copies the current image to the clipboard.

Viewing the Sub-Tree List Directly in the Dendrogram

- ▶ To view the sub-tree list directly in the dendrogram, zoom in by using the mouse wheel.
The sub-tree list appears to the right of the dendrogram.
- ▶ To resize the dendrogram, press **Ctrl** and the right or left arrow keys on your keyboard.
The scale adjusts appropriately.
- ▶ To return the dendrogram to its default size, click the mouse wheel.

Figure 42 Zooming In to View a Sub-Tree List



Copy/Paste Gene Clusters

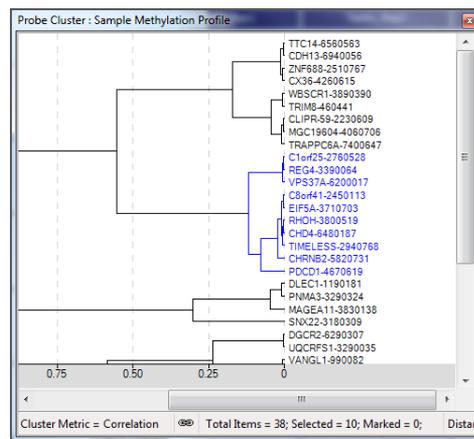
You can copy and paste gene clusters from a scatter plot to a dendrogram and vice versa.

From Scatter Plot to Dendrogram

- In the scatter plot, do one of the following:
 - Select **Tools | Select Region** from the pulldown menu.
 - Open the context menu and click **Select Region**.
- Using the crosshair tool, draw a shape around the genes you want to copy. The selected genes change color (blue by default, or the color you have set in **Scatter Plot Options**).
- Open the context menu and click **Copy Selection**.
- To paste the selection into the dendrogram, do one of the following:
 - Select **Tools | Paste Selection** from the pulldown menu.
 - Open the context menu and click **Paste Selection**.

From Dendrogram to Scatter Plot

- In the dendrogram, position the cursor over the sub-tree you want to copy.
- Open the context menu and click **Select Sub-Tree**. The selected sub-tree appears in blue.



- Open the context menu and click **Copy Selection**.
- To paste your selection into a scatter plot, do one of the following:
 - Select **Tools | Paste Selection** from the pulldown menu.
 - Open the context menu and click **Paste Selection**.

Applying Methylation Algorithms

Methylation Analysis Algorithms	48
Normalization Methods and Algorithms.	49
Differential Methylation Analysis Algorithms	51



Methylation Analysis Algorithms

Methylation analysis is used to extract methylation information for individual loci in individual samples and sample groups, and provides intensity, beta, and detection data. Samples are not compared to each other in any way, as they are in differential methylation.

The beta value (β) is used to estimate the methylation level of the CpG locus using the ratio of intensities between methylated and unmethylated alleles.

For the GoldenGate and VeraCode Methylation Assays, β is calculated as:

$$\beta = \frac{\text{Max}(\text{Cy5},0)}{\text{Max}(\text{Cy3},0) + \text{Max}(\text{Cy5},0) + 100}$$

For the Infinium Methylation Assay, β is calculated as:

$$\beta = \frac{\text{Max}(\text{SignalB},0)}{\text{Max}(\text{SignalA},0) + \text{Max}(\text{SignalB},0) + 100}$$

For Infinium I assays, signal A and signal B are produced by two different bead types and reported in the same color. For Infinium II assays, signal A corresponds to the signal in the Red channel and signal B corresponds to the signal in the Green channel.

Normalization Methods and Algorithms

Normalization algorithms transform sample signals in order to minimize the effects of variation arising from non-biological factors. However, when using the GenomeStudio Methylation Module to analyze your data, it is also possible to use raw data without applying a normalization algorithm.

In gene expression analysis, most normalization algorithms operate under the assumption that the majority of genes are not differentially expressed. However, we cannot make this same assumption for the purposes of methylation analysis. For this reason, the GenomeStudio Methylation Module offers simple normalization algorithms that do not rely on the assumption that the majority of genes are differentially expressed.

The following sections of this chapter contain detailed descriptions of the GenomeStudio Methylation Module normalization algorithms used for methylation analysis:

- ▶ Average
- ▶ Controls
- ▶ Background

Average Normalization

Average normalization is applied across Sentrix Array Products, with the goal of minimizing scanner-to-scanner variation. The assumption is that biological conditions are balanced across Sentrix Array Products.

Suppose that you are using three SAMs. Let I_1 , I_2 , and I_3 be the average intensity values for the first color channel of each SAM, and let m equal the average across SAMs. The average is computed across all loci and all bundles, so $m = (I_1 + I_2 + I_3) / 3$. Multiply the intensity values of color channel 1 in SAM 1 by m / I_1 . Normalize the other two SAMs and the other color channel in the same way.

At the end of this procedure, every SAM has the same average intensity in each color channel. When the first SAM is divided by I_1 , the mean is scaled to 1. When it is multiplied by m , the mean is scaled to m . In other words, the three SAMs initially have mean intensity values of I_1 , I_2 , and I_3 , but after scaling, they all have mean m .

Normalization to Internal Controls

This method is available for the Infinium HumanMethylation450 assay.

Normalization control probe pairs are designed to target the same region within housekeeping genes and have no underlying CpG sites in the probe.

One probe will extend to incorporate a base in Green channel, and the corresponding probe will incorporate a base in the Red channel. Over 90 probe pairs are used for normalization.

- ▶ Normalization values are calculated and used separately in two channels separately. For the Green channel, CG controls values are used; for the Red channel, AT controls values are used.
- ▶ For normalization, probe intensity in the given sample is multiplied by a constant normalization factor (for all samples) and divided by the average of normalization controls in the probe's channel in the given sample.
- ▶ The normalization factor is calculated as the average of AT and CG normalization controls in sample 0, the reference sample. It is the first sample in the list of samples. It does not matter which sample is use, as long as there is one reference sample.
- ▶ Outliers are not removed for normalization controls.

Background Subtraction

The background value is derived by averaging the signals of built-in negative control bead types. Outliers are removed using the median absolute deviation method.

Background normalization is capable of minimizing the amount of variation in background signals between arrays. This is accomplished using the signals of built-in negative controls, which are designed to be thermodynamically equivalent to the regular probes but lack a specific target in the transcriptome.

Negative controls allow for estimating the expected signal level in the absence of hybridization to a specific target. The average signal of the negative controls is subtracted from the probe signals. As a result, the expected signal for unexpressed targets is equal to zero.

Half of the unexpressed targets are expected to have negative signals because the average signal of negative controls is subtracted. Assuming symmetry, half the negative controls are lower than average, and half are higher. Therefore, half of the negative controls will be negative after the average is subtracted. The negative controls represent unexpressed targets, half of which are expected to be negative after subtraction.

For HumanMethylation450 array, background subtraction is calculated differently.

- ▶ Background is calculated in two channels separately.
- ▶ Channel background is 5% percentile of the negative controls in the given channel. Negative probes outliers are not removed.
- ▶ Background is subtracted from probe intensities in the same channel. If intensity becomes negative, it is set to 0.
- ▶ Background is also used in probe detection calculations. In this case, backgrounds are subtracted from negative controls only. This guarantees that probe detection does not change with background subtraction. If the intensity of a negative control becomes negative, it is set to 0. There might be slight changes in detection p-values between data sets with and without background subtraction. This might happen because of the nonlinear nature of replacing negative values of probes and negative values of controls with 0.

Differential Methylation Analysis Algorithms

All differential methylation analysis algorithms compare a group of samples (referred to as the **condition group**) to a **reference group**. This comparison is made using the following error models:

- ▶ Illumina Custom Model
- ▶ Mann-Whitney Model
- ▶ T-Test Model

Illumina Custom Model

This model operates under the assumption that the methylation value β is normally distributed among replicates corresponding to a set of biological conditions.

The variation in the estimate of β is a function of β . The function was estimated for all values of β by repeatedly measuring loci with known methylation fractions ranging from 0 to 1, and then fitting a parabola to the standard deviation as a function of β . The standard deviation estimate is then given by $s = A\beta^2 + B\beta + C$, where:

For GoldenGate and Infinium Methylation:

$A = -0.1511$, $B = 0.1444$, and $C = 0.01646$

For VeraCode Methylation:

$A = -0.1582$, $B = 0.1554$, and $C = 0.00756$

We produce p-values using the following approach:

$$p = z \left(\frac{|\beta_{cond} - \beta_{ref}|}{\sqrt{\frac{s_{ref}^2}{N_{ref}} + \frac{s_{cond}^2}{N_{cond}}}} \right)$$

where z is the two-sided tail probability of the standard normal distribution.

A diff score for a probe is computed as:

$$DiffScore = 10 \operatorname{sgn}(\beta_{cond} - \beta_{ref}) \log_{10} p$$

For a locus with multiple probes, the DiffScores across probes are averaged. In addition, a concordance value between probes is reported.

Mann-Whitney Model

This implementation produces exact p-value if:

$$\min(N_{ref}, N_{cond}) < 3$$

or

$$\max(N_{ref}, N_{cond}) < 22$$

Otherwise, normal approximation with continuity correction is used. Differential scores are computed as described for the Illumina Custom model (page 51).

T-Test Model

When either the reference group or a condition group contains at least two samples, variance is estimated across replicate samples. Otherwise, variance is estimated from bead-to-bead variation. We use t-test with the assumption of equal variance. Differential scores are computed the same way as described for the Illumina Custom model (page 51).

Comparing Methylation and Gene Expression Data

Introduction	54
Importing Gene Expression Data	55
Visualize the Correlation of Methylation and Expression Levels Data	58



Introduction

This chapter describes how to analyze the correlation between:

- ▶ levels of DNA methylation for particular CpG loci
- ▶ levels of the expression of this gene in the same sample

Use the Methylation/Gene Expression Comparison tool if you have expression data collected for the genes present on the BeadChip or in the OMA pool (oligo pool for the Methylation Assay).

Importing Gene Expression Data

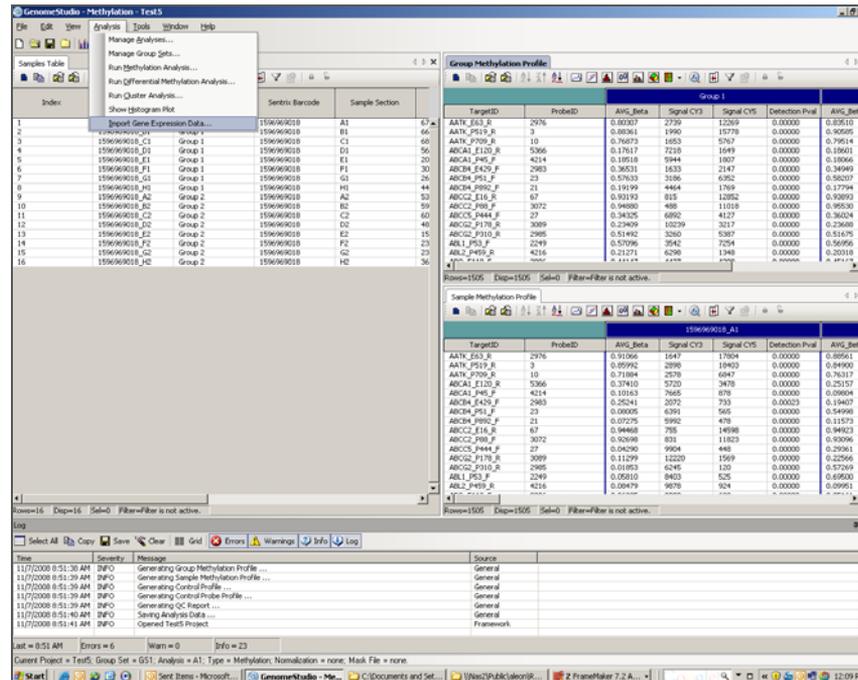
GenomeStudio gene expression data tables can be exported from the GenomeStudio Gene Expression Module and saved as tab-delimited (*.txt) data files for use with the GenomeStudio Methylation Module.

In order to perform a comparison between gene expression and methylation data, the sample names in the methylation project must match the sample names in the gene expression data file.

To import gene expression data from the GenomeStudio Gene Expression Module into the GenomeStudio Methylation Module, identify a gene expression data file in tab-delimited (*.txt) format that you want to import into the GenomeStudio Methylation Module. Prepare a gene lookup table if the identification of probes in the expression file is different from the TargetID used in the Methylation manifest. The first column in the Lookup table should be a Gene Expression unique probe identifier, and the second column should be a corresponding Methylation probe identifier.

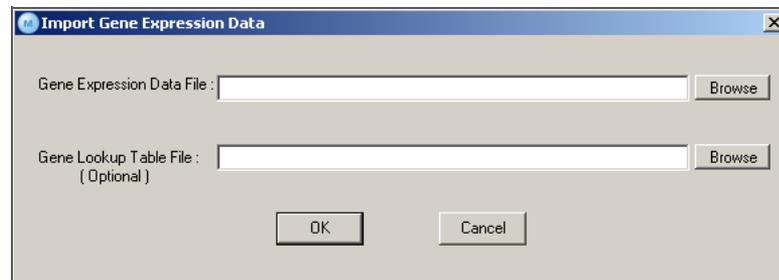
- 1 In the main menu, select **Analysis | Import Gene Expression Data**.

Figure 43 Importing Gene Expression Data



The Import Gene Expression Data dialog box opens.

Figure 44 Import Gene Expression dialog box



- Select the gene expression data file you want to analyze, and the lookup table, if needed.

Figure 45 Gene Expression Data File

TargetID	Brain.AVG_Signal	Breast.AVG_Signal	Liver.AVG_Signal	Heart.AVG_Signal	Kidney.AVG_Signal	Lung.AVG_Signal
ILMN_1762337	98.95413	108.5103	95.85145	93.28889	124.6891	114.5275
ILMN_2055271	112.0628	117.0071	115.1417	117.4529	109.9491	117.2788
ILMN_1736007	96.89695	98.57251	142.9353	91.0173	87.11807	87.98552
ILMN_2383229	96.48362	98.56734	4782.95	89.83987	396.887	97.29855
ILMN_1806310	97.08807	100.5675	6966.042	97.8418	509.048	95.76498
ILMN_1779670	83.30599	96.09895	431.351	77.80032	87.34923	76.60777
ILMN_1653355	112.248	115.6957	106.6967	102.8025	101.3124	103.6764
ILMN_1717783	63.4287	61.32037	68.86966	59.83905	61.57442	53.85741
ILMN_1705025	109.8561	98.5584	108.889	94.75819	81.96016	95.91678
ILMN_1814316	94.27387	97.90201	89.81	493.3497	93.10749	90.39512
ILMN_2359168	65.04059	67.44859	64.348	380.0492	70.78035	63.00218
ILMN_1731507	71.10106	67.54734	61.63067	201.356	60.55729	61.05072
ILMN_1787689	88.13202	103.3775	81.43134	82.88962	86.8854	86.68428
ILMN_3241953	261.1921	139.1634	562.7615	111.4282	282.4939	344.0719
ILMN_1745607	4631.445	8745.028	7006.131	5582.64	8155.205	13181.94
ILMN_2136495	88.29322	64.32262	61.65227	62.5661	59.70939	59.73615
ILMN_1668111	95.25826	95.07387	95.4987	96.20078	90.25865	88.72461
ILMN_2295559	95.97375	82.49684	87.66605	91.83961	91.59325	91.77586
ILMN_1735045	476.8448	603.2748	94.34424	497.9468	241.1429	299.802

Figure 46 Lookup Table

GeneExpression	Methylation
ILMN_1709541	cg00000292
ILMN_1674460	cg00000292
ILMN_1770052	cg00000292
ILMN_1788281	cg00000292
ILMN_1783120	cg00002426
ILMN_1777263	cg00003994
ILMN_1798076	cg00005847
ILMN_2344047	cg00006414
ILMN_1799717	cg00006414
ILMN_1697817	cg00007981
ILMN_1744432	cg00008493
ILMN_2094061	cg00008713
ILMN_1652309	cg00009407
ILMN_2401927	cg00009407
ILMN_1805011	cg00010193
ILMN_1785336	cg00011459

- Click OK.

A new combined Methylation and Gene Expression Analysis table is generated, which contains beta values and intensity values for each CpG locus with corresponding expression data.

Figure 47 Combined Methylation and Gene Expression Analysis Table

TargetID	R Pearson	R2	Rs Spearman	Hela 1		
				AVG_Beta	AVG_Signal	AVG_E
cq00000292	0.58324	0.34017	0.76923	0.90948	162	0.870
cq00003994	-0.14073	0.01980	0.00000	0.02954	86	0.786
cq00005847	0.06317	0.00399	0.16783	0.82306	79	0.517
cq00006414	0.12931	0.01672	0.67832	0.04111	83	0.234
cq00007981	-0.61701	0.38070	-0.38462	0.02767	4175	0.870
cq00008493	-0.32599	0.10627	-0.41259	0.96297	92	0.946
cq00008713	-0.00605	0.00004	0.04196	0.03384	78	0.031
cq00009407	-0.10572	0.01118	-0.17483	0.00912	165	0.029
cq00010193	-0.14852	0.02206	-0.27273	0.55399	82	0.587
cq00012199	0.02258	0.00051	0.11189	0.01475	87	0.203
cq00012386	-0.02916	0.00085	-0.20280	0.02058	101	0.038
cq00012792	0.27459	0.07540	0.48252	0.04001	73	0.030
cq00013618	0.44223	0.19557	0.52448	0.46156	526	0.192
cq00014085	-0.39313	0.15455	-0.43357	0.03065	1112	0.032
cq00015770	-0.36414	0.13260	-0.09091	0.62826	86	0.877
cq00016968	0.16853	0.02840	0.23776	0.50104	96	0.866
cq00019495	0.26613	0.07082	0.27972	0.10770	105	0.679
cq00020533	-0.04250	0.00181	-0.04895	0.52855	100	0.846
cq00021527	-0.13321	0.01775	-0.06993	0.02218	77	0.016
cq00022606	0.20880	0.04360	0.27972	0.04300	94	0.589
cq00022866	0.47121	0.22204	0.48951	0.83007	81	0.312
cq00024396	0.30924	0.09563	0.26573	0.09231	92	0.552
cq00024812	-0.03734	0.00139	0.30769	0.02789	96	0.040
cq00025138	-0.12428	0.01545	-0.24476	0.01668	101	0.296
cq00025991	-0.05527	0.00305	-0.04196	0.51679	78	0.728
cq00027083	-0.84939	0.72147	-0.38462	0.97858	107	0.972
cq00027674	-0.07709	0.00594	-0.09790	0.38435	96	0.566
cq00029826	-0.02992	0.00090	0.11888	0.08751	66	0.100
cq00029931	0.08327	0.00693	0.41259	0.01598	115	0.036
cq00030047	0.07627	0.00582	0.38462	0.91696	197	0.908

Rows=24593 Disp=24593 Sel=1 Filter=Filter is not active.

If a gene is represented by two or more CpG loci, each locus is displayed on a separate row; however, expression data is identical for all loci from the same gene.

Visualize the Correlation of Methylation and Expression Levels Data

Use the line plot to visually analyze the correlation of methylation and expression levels in your data.

- ▶ In the main toolbar, select  **Histogram Plot**.



NOTE

This plot can be toggled between a line plot and a histogram plot. The line plot displays by default.

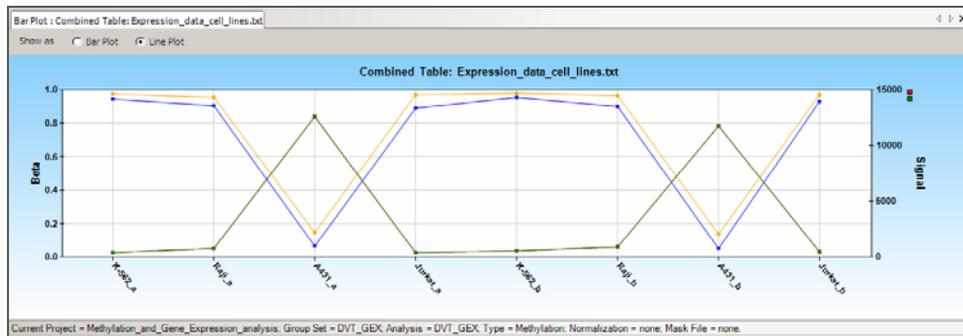
A new window with a double Y axis opens.



NOTE

In order to take advantage of the selection synchronization features of the table and the plot, you may need to dock the combined table in a new window. Docking the combined table in a different window allows you to view the combined table and the comparison histogram plot simultaneously.

Figure 48 Line Plot



The left axis displays the beta value for selected CpG locus (or multiple loci). The right axis displays intensity values for the corresponding gene.

User Interface Reference

Introduction	60
Detachable Docking Windows	61
Main Window Menus	91
Context Menus	94



Introduction

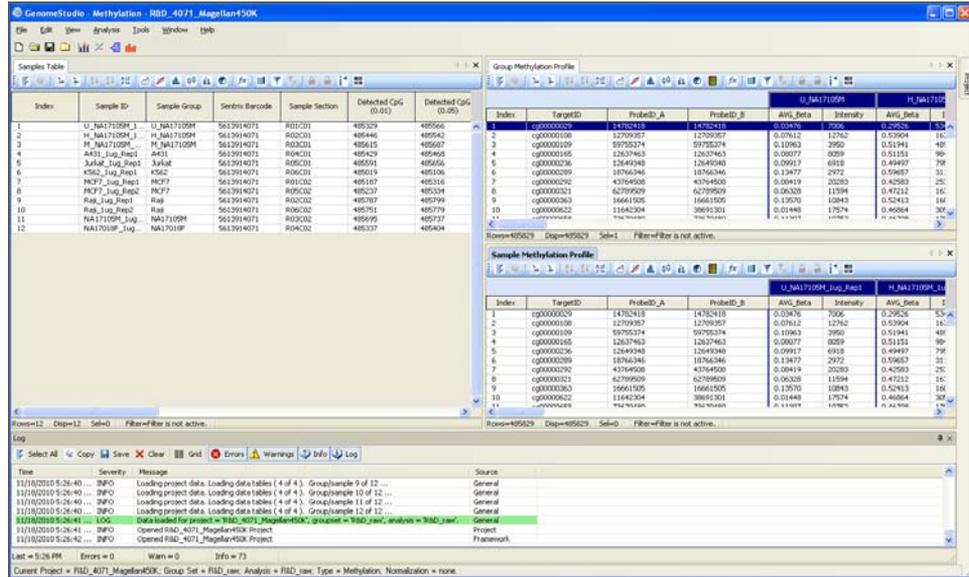
This chapter includes descriptions of the detachable docking windows, main window menus, and context menus available in the GenomeStudio Methylation Module.

Detachable Docking Windows

Detachable docking windows provide a flexible way to customize GenomeStudio's user interface to suit your analysis needs.

Figure 49 shows the default window configuration of the GenomeStudio Methylation Module.

Figure 49 Methylation Module Main Screen, Default View



The following sections describe each of the Methylation Module's detachable docking windows.

Control Probe Profile Table

Under normal experimental conditions, the signal intensities from negative controls can vary from approximately 100 to 1000 units. Since these controls are sample-dependent, a dramatic increase in these counts may indicate poor DNA template quality prior to the bisulfite conversion step. This is evident in the controls dashboard for Infinium Methylation.



NOTE

For more information about the Infinium Methylation Controls Dashboard, see "Infinium Methylation Controls Dashboard" on page 63.

For background normalization, the average intensity of all negative control bead types is subtracted from the average intensity of the analytical bead types. Therefore, increases in signal intensity of the negative controls may result in a smaller number of detected loci.

Figure 50 shows an example of a Control Probe Profile table.

Figure 50 Control Probe Profile Table

Index	TargetID	ProbeID	Signal_Grn	Signal_Red	Detection Pval	S
1	BISULFITE CONVERSION	4670278	10347	1413	0.00000	10
2	BISULFITE CONVERSION	4670484	665	1003	0.00493	70
3	BISULFITE CONVERSION	5270706	12136	1407	0.00000	10
4	BISULFITE CONVERSION	5290048	782	962	0.00019	78
5	EXTENSION	360446	1274	28517	0.00000	13
6	EXTENSION	520537	1456	47248	0.00000	13
7	EXTENSION	1190050	23262	2424	0.00000	31
8	EXTENSION	2630184	39334	1858	0.00000	44
9	HYBRIDIZATION	2450040	7845	1029	0.00000	74
10	HYBRIDIZATION	5690072	30327	1381	0.00000	33
11	HYBRIDIZATION	5690110	16513	750	0.00000	18
12	NEGATIVE	50110	633	833	0.49588	66
13	NEGATIVE	360079	675	770	0.60136	77
14	NEGATIVE	430114	679	689	0.89189	70
15	NEGATIVE	460494	766	807	0.08506	82
16	NEGATIVE	540577	709	715	0.69989	73
17	NEGATIVE	610692	721	807	0.21208	74
18	NEGATIVE	610706	713	738	0.57163	72
19	NEGATIVE	670750	694	778	0.46546	73
20	NEGATIVE	1190458	668	860	0.21208	75
21	NEGATIVE	1500059	695	736	0.66822	66
22	NEGATIVE	1500167	658	779	0.64008	80
23	NEGATIVE	1500398	614	800	0.74258	65
24	NEGATIVE	1660097	685	815	0.32890	83
25	NEGATIVE	1770019	690	785	0.45032	74
26	NEGATIVE	1940364	554	745	0.98277	68

The annotation columns of the Control Probe Profile table are listed and described in Table 8.

Table 8 Control Probe Profile Table

Column	Description	Type	Visible by Default?
Columns			
Index	Unique identifier for each sample	integer	Y
TargetID	Identifies the probe name. Also used as a key column for data import.	string	Y
ProbeID	Illumina identifier for probe sequence.	integer	Y
Subcolumns			
Signal CY3	[GoldenGate assays only] Intensity of the target in the green (Cy3) channel.	float	Y
Signal CY5	[GoldenGate assays only] Intensity of the target in the red (Cy5) channel.	float	Y
Signal_Grn	[Infinium assays only] Intensity of the target in the green channel.	float	Y
Signal_Red	[Infinium assays only] Intensity of the target in the red channel.	float	Y
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls.	float	Y

Table 8 Control Probe Profile Table (Continued)

Column	Description	Type	Visible by Default?
AVG_Signal	[GoldenGate assays only] Average intensity of the bead type/target in the group.	float	N
NARRAYS	[GoldenGate assays only] Number of samples in the group.	integer	N
ARRAY_STDEV	[GoldenGate assays only] Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample).	string	N
Avg_NBEADS	Average number of beads per bead type representing probes for the gene.	integer	N
BEAD_STDERR	Standard error associated with bead-to-bead variability for the target.	float	N

Infinium Methylation Controls Dashboard

If you have a project with Infinium data, you can view Infinium Methylation Controls in GenomeStudio by going to **Analysis | View Controls Dashboard**.



NOTE

Infinium Methylation Controls are available for Infinium Methylation projects only. For information about GoldenGate controls, see “GoldenGate Methylation Control Summary Graph” on page 70.

The following sections include descriptions of the Infinium Methylation Controls:

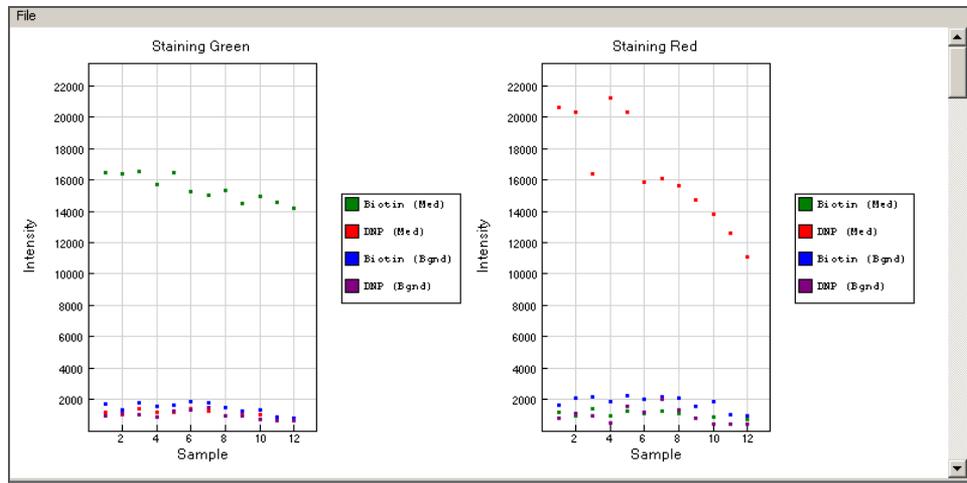
- ▶ *Staining Controls*
- ▶ *Extension Controls*
- ▶ *Hybridization Controls*
- ▶ *Target Removal Controls*
- ▶ *Bisulfite Conversion Controls*
- ▶ *G/T Mismatch Controls (HumanMethylation27)*
- ▶ *Specificity Controls*
- ▶ *Negative Controls*
- ▶ *Non-polymorphic Controls*

Staining Controls

Staining controls are used to examine the efficiency of the staining step in both the red and green channels. These controls are independent of the hybridization and extension step.

The performance of the staining controls should be monitored in both the red channel and the green channel.

Figure 51 Staining Controls

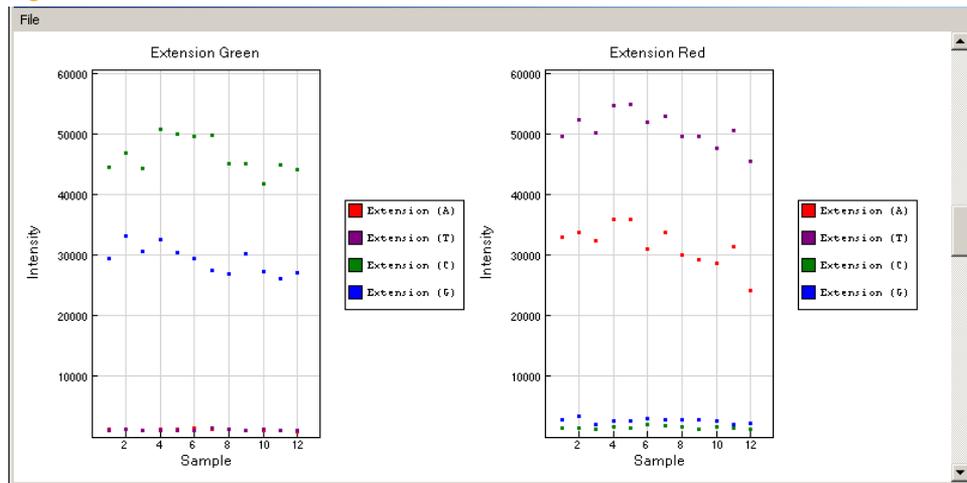


Extension Controls

Extension controls test the extension efficiency of A, T, C, and G nucleotides from a hairpin probe, and are therefore sample-independent.

The performance of the extension controls should be monitored in the red (A,T) and green (C,G) channels.

Figure 52 Extension Controls



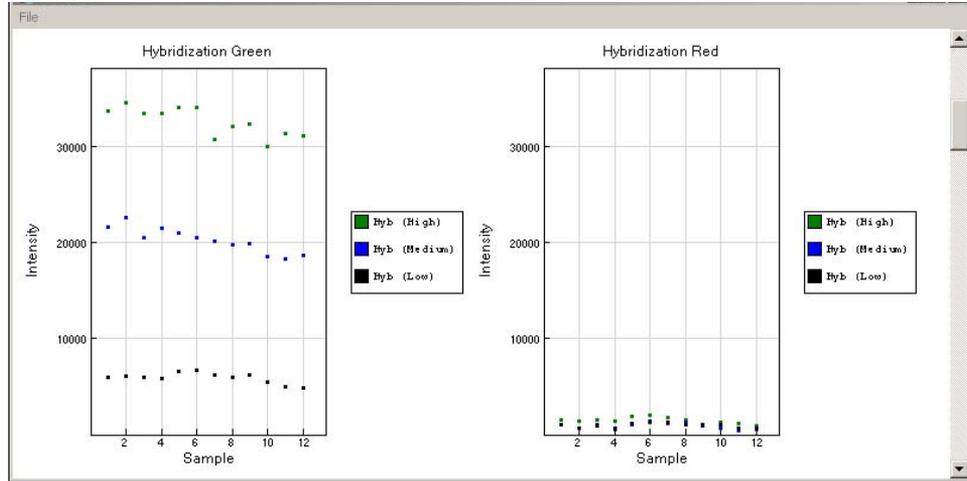
Hybridization Controls

Hybridization controls test the overall performance of the Infinium Assay using synthetic targets instead of amplified DNA. These synthetic targets complement the sequence on the array perfectly, allowing the probe to extend on the synthetic target as a template.

Synthetic targets are present in the hybridization buffer (RA1) at three levels, monitoring the response from high-concentration (5 pM), medium concentration (1 pM), and low-concentration (0.2 pM) targets. All bead type IDs should result in signal with various intensities, corresponding to the concentrations of the initial synthetic targets.

The performance of the hybridization controls should be monitored only in the green channel.

Figure 53 Hybridization Controls



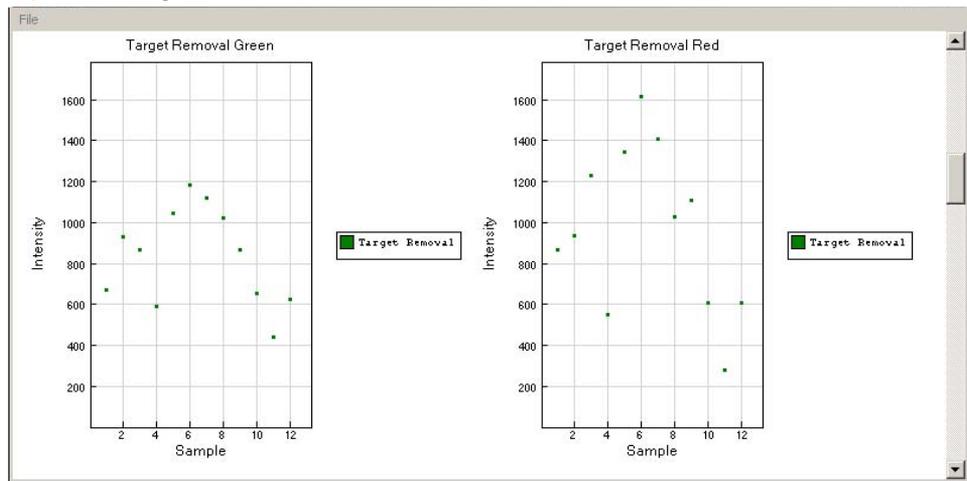
Target Removal Controls

Target removal controls test the efficiency of the stripping step after the extension reaction. In contrast to allele-specific extension, the control oligos are extended using the probe sequence as a template. This process generates labeled targets. The probe sequences are designed such that extension from the probe does not occur.

All target removal controls should result in low signal compared to the hybridization controls, indicating that the targets were removed efficiently after extension. Target removal controls are present in the hybridization buffer RA1.

The performance of the target removal controls should be monitored only in the green channel.

Figure 54 Target Removal Controls



Bisulfite Conversion Controls

These controls assess the efficiency of bisulfite conversion of the genomic DNA. The Infinium Methylation probes query a [C/T] polymorphism created by bisulfite conversion of non-CpG cytosines in the genome.

HumanMethylation27

Bisulfite conversion controls assess the efficiency of bisulfite conversion of the genomic DNA. The Infinium Methylation probes query a [C/T] polymorphism created by bisulfite conversion of the Hind III site [AAGCTT]. If the bisulfite conversion reaction is successful, the "C" (Converted) probes match the converted sequence and get extended. If the sample has unconverted DNA, the "U" (Unconverted) probes get extended.

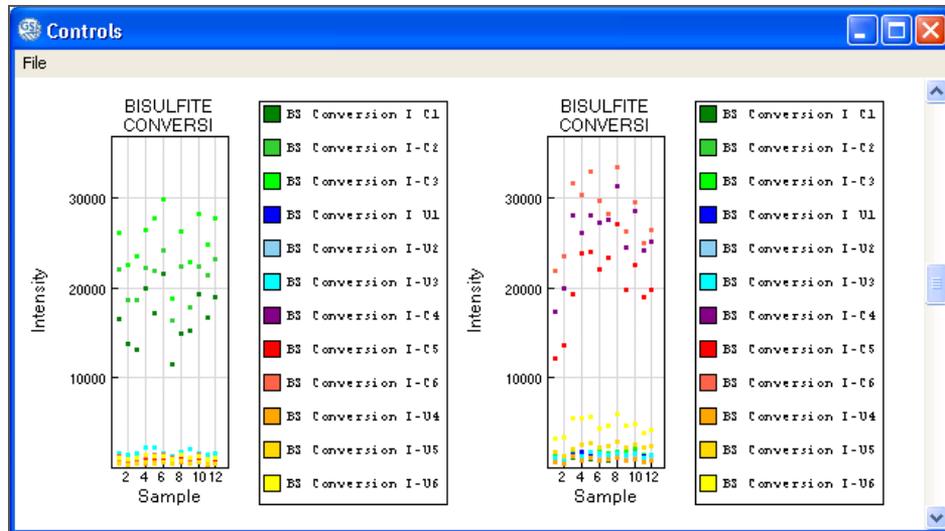
The performance of the bisulfite conversion controls should be monitored only in the green channel.

HumanMethylation450

► Bisulfite Conversion I

These controls use Infinium I probe design and allele-specific single base extension to monitor efficiency of bisulfite conversion. If the bisulfite conversion reaction was successful, the "C" (Converted) probes will match the converted sequence and get extended. If the sample has unconverted DNA, the "U" (Unconverted) probes will get extended. There are no underlying C bases in the primer landing sites, except for the query site itself. Performance of bisulfite conversion controls C1, C2 and C3 should be monitored in the Green channel, and controls C4, C5 and C6 should be monitored in Red channel.

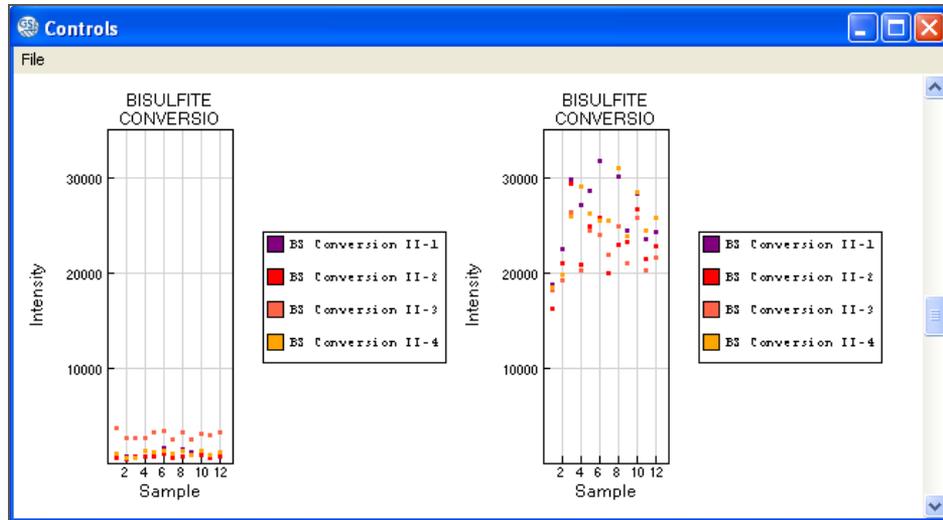
Figure 55 Bisulfite Conversion I Controls



► Bisulfite Conversion II

These controls use Infinium II probe design and single base extension to monitor efficiency of bisulfite conversion. If the bisulfite conversion reaction was successful, the "A" base will get incorporated and the probe will have intensity in the Red channel. If the sample has unconverted DNA, the "G" base will get incorporated across the unconverted cytosine, and the probe will have elevated signal in the Green channel.

Figure 56 Bisulfite Conversion II Controls

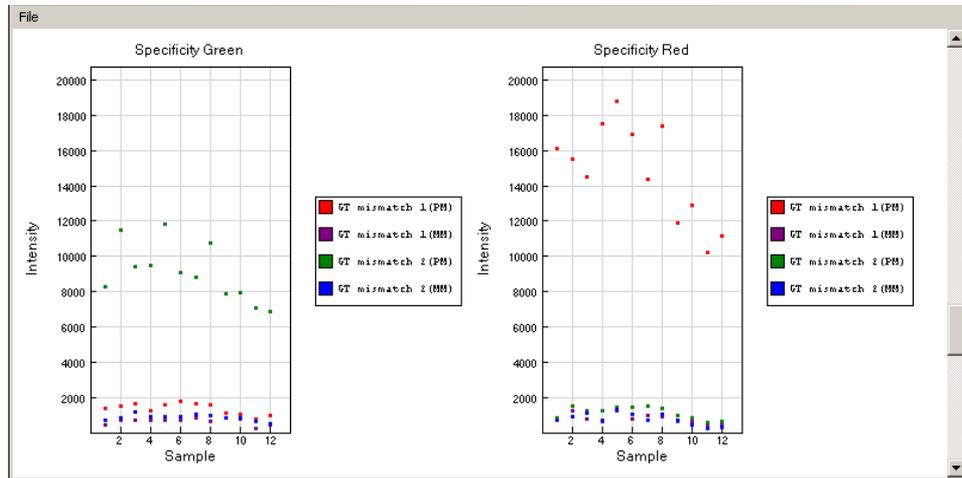


G/T Mismatch Controls (HumanMethylation27)

G/T mismatch controls check for non-specific detection of methylation signal over unmethylated background. Specificity controls are designed against non-polymorphic T sites. PM controls correspond to A/T perfect match and should give high signal. MM controls correspond to G/T mismatch and should give low signal.

The performance of the nonspecific binding controls should be monitored in both the green channel and the red channel.

Figure 57 G/T Mismatch Controls



Specificity Controls

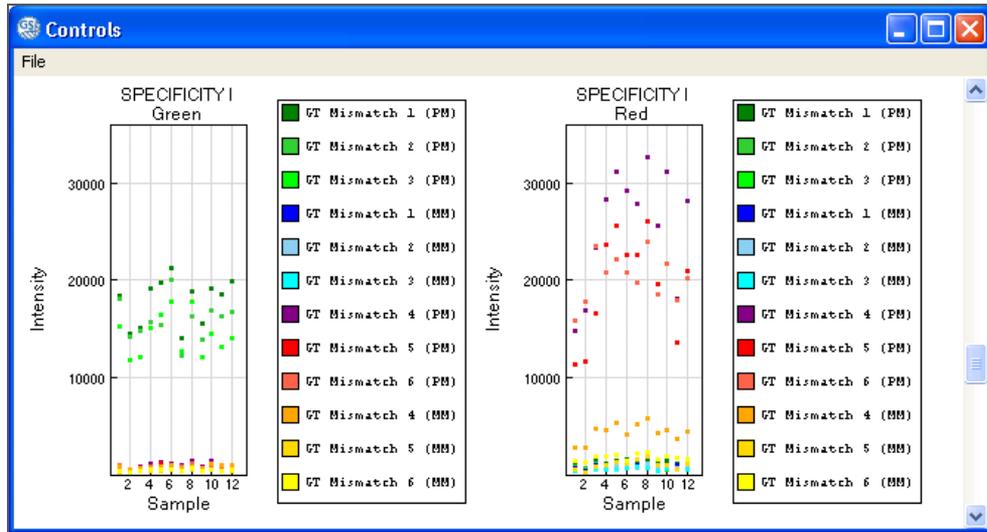
Specificity controls are designed to monitor potential non-specific primer extension for Infinium I and Infinium II assay probes. Specificity controls are designed against non-polymorphic T sites.

► Specificity I

These controls are designed to monitor allele-specific extension for Infinium I probes. The methylation status of a particular cytosine is carried out following bisulfite treatment of DNA by using query probes for unmethylated and methylated state of each CpG locus. In assay oligo design, the A/T match corresponds to the

unmethylated status of the interrogated C, and G/C match corresponds to the methylated status of C. G/T mismatch controls check for non-specific detection of methylation signal over unmethylated background. PM controls correspond to A/T perfect match and should give high signal. MM controls correspond to G/T mismatch and should give low signal. Performance of GT Mismatch controls should be monitored in both green and red channels. Controls dashboard table lists expected outcome for controls probes.

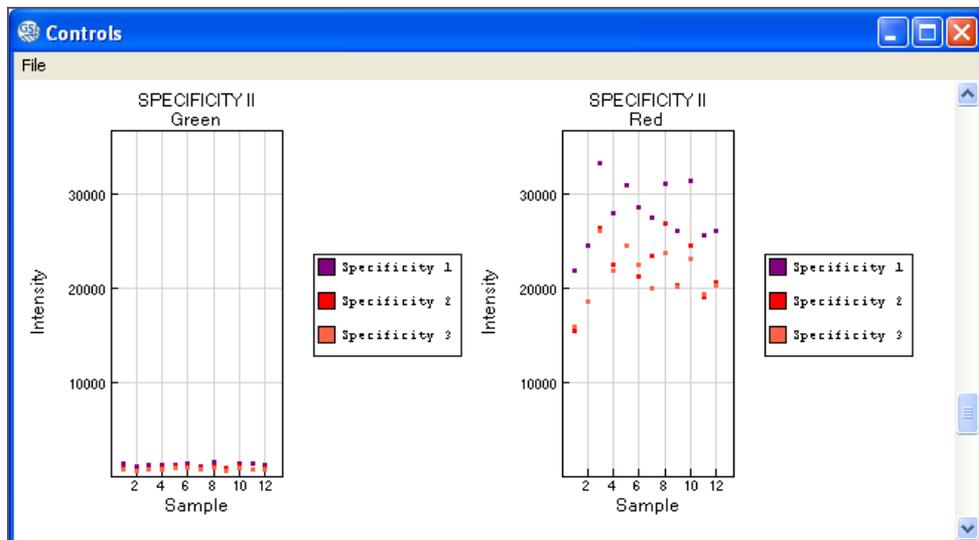
Figure 58 Specificity I Controls



► Specificity II

These controls are designed to monitor extension specificity for Infinium II probes and check for potential non-specific detection of methylation signal over unmethylated background. Specificity II probes should incorporate the "A" base across the non-polymorphic T and have intensity in the Red channel. In case of non-specific incorporation of the "G" base, the probe will have elevated signal in the Green channel.

Figure 59 Specificity II Controls

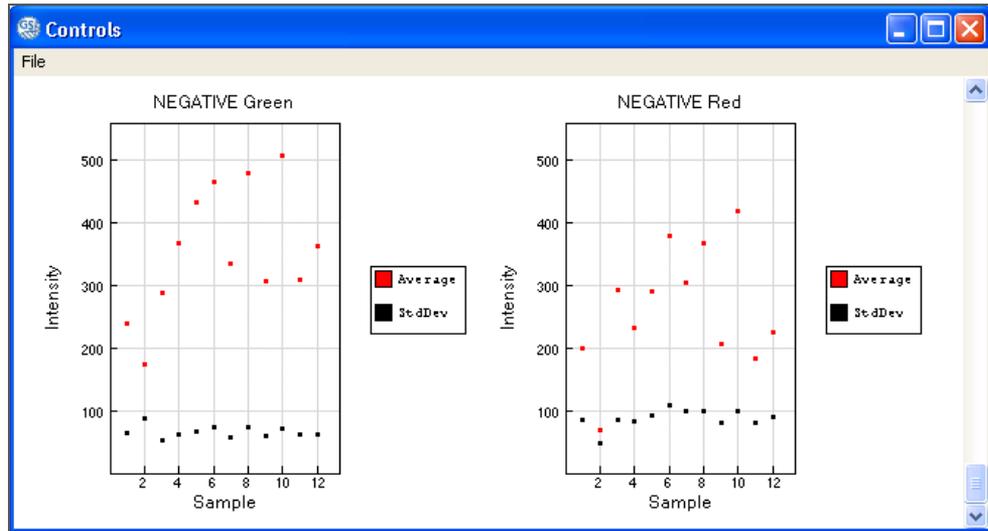


Negative Controls

Negative controls target bisulfite-converted sequences that do not contain CpG dinucleotides. Assay probes are randomly permuted and should not hybridize to the DNA template. The mean signal of these probes defines the system background.

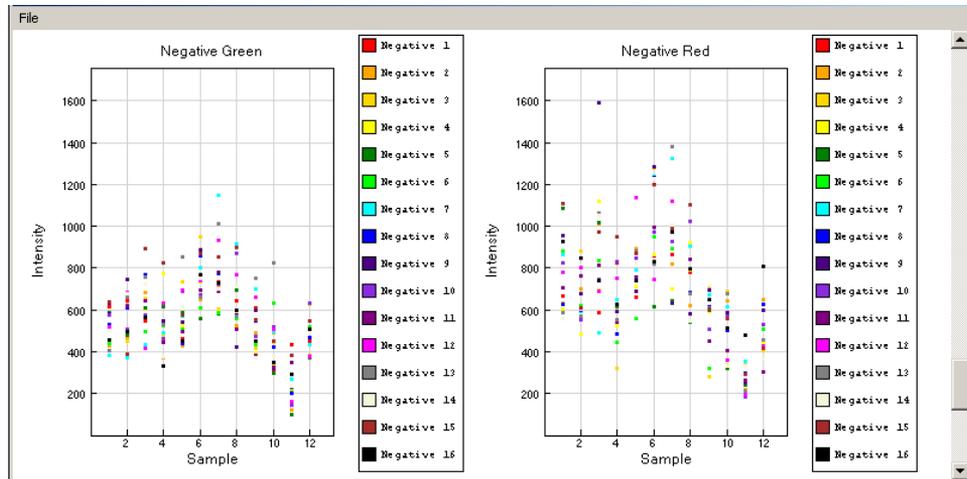
The performance of the negative controls should be monitored in both the green channel and the red channel.

Figure 60 Negative Controls - Infinium Human Methylation 450



The graph displays average and standard deviation of 600 negative controls.

Figure 61 Negative Controls - Infinium Human Methylation 27

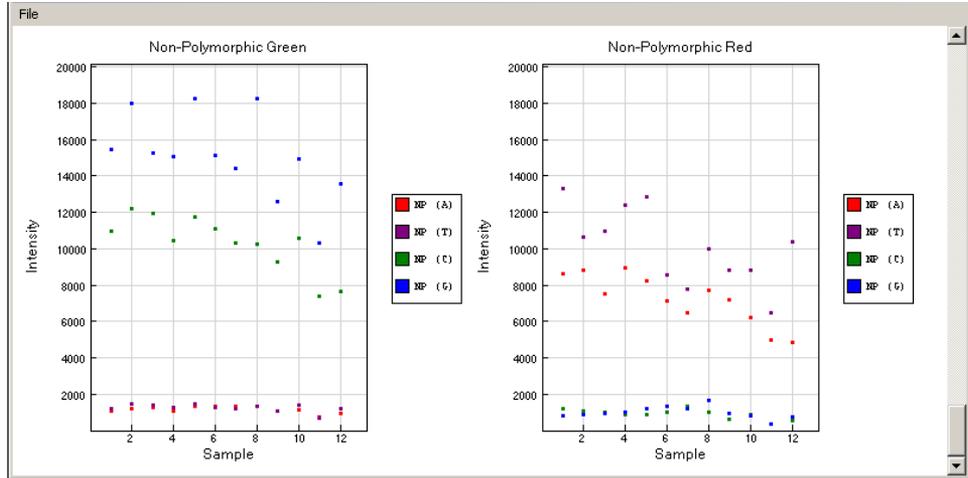


Non-polymorphic Controls

Non-polymorphic controls test the overall performance of the assay, from amplification to detection, by querying a particular base in a non-polymorphic region of the genome. They let you compare assay performance across different samples.

One non-polymorphic control has been designed for each of the four nucleotides (A, T, C, and G).

Figure 62 Non-polymorphic Controls

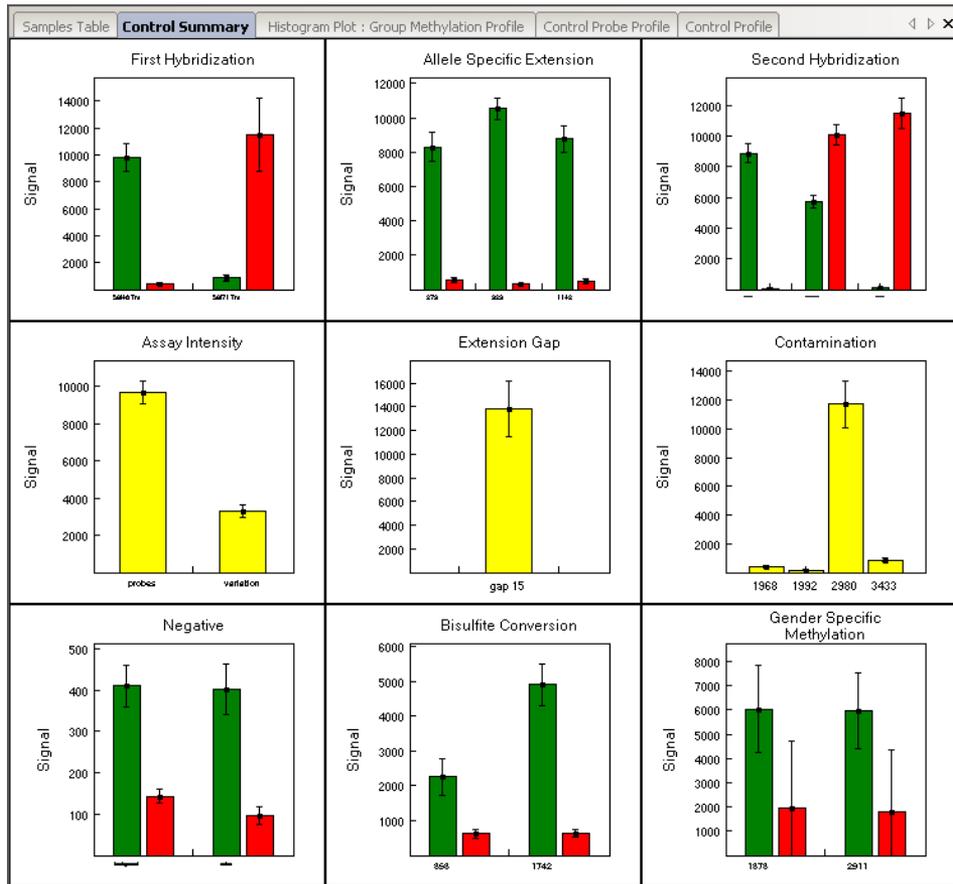


GoldenGate Methylation Control Summary Graph

Figure 63 shows an example of a control summary graph.

The control summary graph is available for GoldenGate Methylation projects only. For information about Infinium controls, see “Infinium Methylation Controls Dashboard” on page 63.

Figure 63 Control Summary Graph

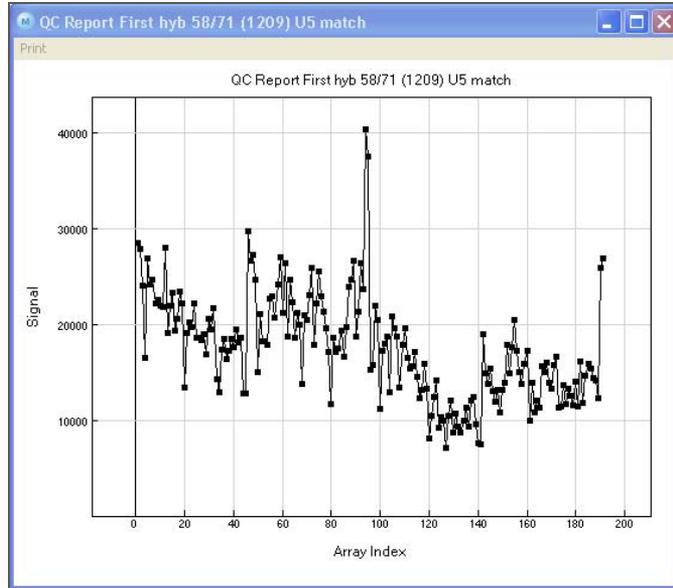


The graphs listed in Table 9 are components of the GoldenGate Assay control summary graph.

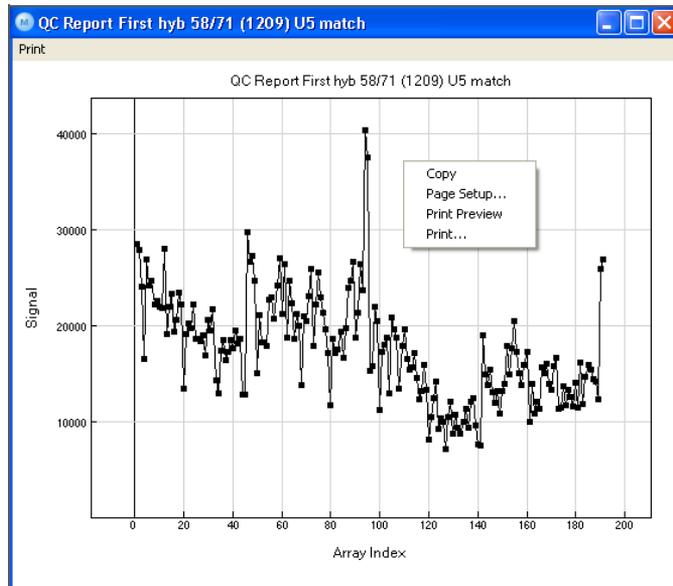
Table 9 GoldenGate Assay Control Summary Graph

Graph Name	Description
Second Hybridization	The second hybridization controls test the hybridization of single-stranded assay products to IllumiCode Sequences on the array beads.
Negative	Negative controls define the methylation assay background. LSO probes can hybridize to bisulfite-converted DNA. ASO (allele-specific oligo) sequences are randomly permuted and should not hybridize to the DNA template. As a result, an amplifiable target should not be formed, and the signal from these IllumiCodes should be low.
Contamination	The PCR contamination detection controls are divided into four types. Only one type is added to each oligo pool for the OMA tube. When a single OMA is run, only one contamination control type should have high signal. If two or more contamination control types have high signal, significant contamination may have occurred.
Assay Intensity	Assay intensity shows average signal intensity for all assay probes on an array.
First Hybridization	The first hybridization controls test the specificity of annealing ASOs with different T_m to the same DNA locus.
Extension Gap	The extension gap control tests the efficiency of extending 15 bases from the 3' end of the allele-specific oligo to the 5' end of the locus-specific oligo.
Allele-Specific Extension	The allele-specific extension controls test the extension efficiency of properly matched versus mismatched ASOs.
Gender-Specific Methylation	Methylation gender controls are designed against X-linked genes. Cy3 and Cy5 signal should be detected in females, and only Cy3 signal should be detected in males.
Bisulfite Conversion	Bisulfite conversion controls test for the presence of unconverted genomic DNA in assay samples.

- 1 To view secondary graph(s), click on a data point in any of the graphs. Each point in the secondary graph represents a sample.

Figure 64 First Hybridization Secondary Graph

- 2 To copy, change the page setup, or see a print preview, right-click on any graph to use the context menu.
- 3 To print the graph, do one of the following:
 - Right-click and use the context menu
 - Click **Print** in the upper left-hand corner of the menu bar.

Figure 65 Control Summary Context Menu

Group Methylation Profile Table

Figure 66 shows an example of a Group Methylation Profile table.

Figure 66 Group Methylation Profile Table

Index	TargetID	ProbeID_A	ProbeID_B	AVG_Beta	Intensity	AV
1	cg00000029	14782418	14782418	0.03476	7006	0.25
2	cg00000108	12709357	12709357	0.07612	12762	0.53
3	cg00000109	59755374	59755374	0.10963	3950	0.51
4	cg00000165	12637463	12637463	0.08077	8059	0.51
5	cg00000236	12649348	12649348	0.09917	6918	0.45
6	cg00000289	18766346	18766346	0.13477	2972	0.55
7	cg00000292	43764508	43764508	0.08419	20283	0.42
8	cg00000321	62789509	62789509	0.06328	11594	0.47
9	cg00000363	16661505	16661505	0.13570	10843	0.52
10	cg00000622	11642304	38691301	0.01448	17574	0.46
11	cg00000658	73670480	73670480	0.11307	10752	0.46
12	cg00000714	31749374	31749374	0.11639	24396	0.45
13	cg00000721	28657361	28657361	0.06439	7184	0.50
14	cg00000734	31689396	31689396	0.10846	13573	0.56
15	cg00000769	36699489	29771340	0.02858	20157	0.51
16	cg00000807	61697410	61697410	0.12373	16355	0.53
17	cg00000884	59727471	59727471	0.07148	5160	0.56
18	cg00000905	26622384	26622384	0.10952	10035	0.46
19	cg00000924	23801481	23801481	0.10910	14529	0.45
20	cg00000948	31633318	31633318	0.21820	15468	0.60
21	cg00000957	65648367	36743439	0.13282	24257	0.45
22	cg00001099	22750474	22750474	0.03304	15941	0.35
23	cg00001245	68626314	31783436	0.04364	16833	0.55
24	cg00001249	14610435	14610435	0.05042	14278	0.43
25	cg00001261	24724406	53655485	0.19752	29902	0.52
26	cg00001269	15671426	15671426	0.04913	14473	0.46
27	cg00001340	11722421	53758324	0.25061	37837	0.51

The columns and subcolumns available in the Group Methylation Profile Table depend on the assay used in the current project. Table 10 includes information about the columns and subcolumns available in the Group Methylation Profile Table for the Infinium HD Assay.

Table 10 Group Methylation Profile Table, Infinium HD Assay

Column	Description	Type	Visible by Default?
Columns			
Target_ID	Identifies the probe name. Also used as a key column for data import. Probes are named as follows: <ul style="list-style-type: none"> cg# represents CpG loci ch# represents non-CpG loci rs# represents SNP assays* (not affected by DNA methylation) 	string	Y
ProbeID_A	Illumina identifier for the probe sequence of Probe A	integer	Y
ProbeID_B	Illumina identifier for the probe sequence of Probe B	integer	Y
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ILMNSTRAND	Illumina strand (TOP or BOT)	string	N

Table 10 Group Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
ADDRESSA_ID	Address of probe A	integer	N
ALLELEA_PROBESEQ	Sequence for probe A	string	N
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N
INFINIUM_DESIGNTYPE	Defines Assay type - Infinium I or Infinium II	string	N
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
FORWARD_SEQUENCE	Sequence (in 5'-3' orientation) flanking query site	string	N
GENOMEBUILD	Genome build on which the forward sequence is based	integer	N
CHR	Chromosome on which the target locus is located, Genome build 37	integer	N
MAPINFO	Genomic position of C in CG dinucleotide, Genome build 37	integer	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
CHROMOSOME_36	Chromosome on which the target locus is located, Genome build 36	integer	N
COORDINATE_36	Genomic position of C in CG dinucleotide, Genome build 36	integer	N
STRAND	Design strand	string	N
PROBE_SNPs	Assays with SNPs present within probe >10bp from query site	string	N
PROBE_SNPS_10	Assays with SNPs present within probe ≤10bp from query site (HM27 carryover or recently discovered)	string	N
RANDOM_LOCI	Loci which were chosen randomly in the design process	string	N
METHYL27LOCI	Present or absent on HumanMethylation27 array	string	N
UCSCREFGENE_NAME	Gene name (UCSC)	string	N

Table 10 Group Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
UCSCREFGENE_ACCESSION	Accession number (UCSC)	string	N
UCSCREFGENE_GROUP	Gene region feature category (UCSC)	string	N
UCSCCPGISLANDS_NAME	CpG island name (UCSC)	string	N
Relation_to_UCSC_CpG_Island	Relationship to Canonical CpG Island: Shores - 0-2 kb from CpG island; Shelves - 2-4 kb from CpG island	string	N
PHANTOM	FANTOM-derived promoter	string	N
DMR	Differentially methylated region (experimentally determined)	string	N
ENHANCER	Enhancer element (informatically-determined)	string	N
HMM_ISLAND	Hidden Markov Model Island	string	N
REGULATORYFEATURE_NAME	Regulatory feature (informatically determined)	string	N
REGULATORYFEATURE_GROUP	Regulatory feature category	string	N
DHS	DNase hypersensitive site (experimentally determined)	string	N
Subcolumns			
AVG_Beta	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
MIN_Beta	Minimum methylation level (beta) of the CpG locus in the group of samples	float	N
MAX_Beta	Maximum methylation level (beta) of the CpG locus in the group of samples	float	N
NARRAYS	Number of samples in the group	integer	N
ARRAY_STDEV	Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample)	float	N
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N

Table 10 Group Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N
Signal_A	Signal intensity of the unmethylated (A) probe	integer	N
Signal_B	Signal intensity of the methylated (B) probe	integer	N
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N

* SNP assays can be used for sample identification and tracking. They should be excluded for differential methylation analysis.

Table 10 includes information about the columns and subcolumns available in the Group Methylation Profile Table for the Infinium Assay.

Table 11 Group Methylation Profile Table, Infinium Assay

Column	Description	Type	Visible by Default?
Columns			
Target_ID	Identifies the probe name. Also used as a key column for data import	string	Y
ProbeID_A	Illumina identifier for the probe sequence of Probe A	integer	Y
ProbeID_B	Illumina identifier for the probe sequence of Probe B	integer	Y
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ILMNSTRAND	Illumina strand (TOP or BOT)	string	N
ADDRESSA_ID	Address of probe A	integer	N
ALLELEA_PROBESEQ	Sequence for probe A	string	N
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N

Table 11 Group Methylation Profile Table, Infinium Assay (Continued)

Column	Description	Type	Visible by Default?
GENOMBUILD	Genome build	integer	N
CHR	Chromosome on which the target locus is located	integer	N
MAPINFO	Genomic position of C in CG dinucleotide	integer	N
PLOIDY	Ploidy type	string	N
SPECIES	Species	string	N
SOURCE	Genomic position source	string	N
SOURCEVERSION	Source version	float	N
SOURCESTRAND	Illumina strand orientation for source sequence	string	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
TOPGENOMICSEQ	Top sequence (reported regardless of whether TOP or BOT sequence is used for design)	string	N
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
TSS_COORDINATE	Transcription start site genomic coordinate	integer	N
GENE_STRAND	Gene strand	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N
SYMBOL	RefSeq gene symbol	string	N
SYNONYM	Gene synonyms	string	N
ACCESSION	Gene accession (of the longest transcript)	string	N
GID	RefSeq entry identifier (GI number)	string	N
ANNOTATION	Gene annotation from the NCBI database	string	N
PRODUCT	Gene product description from the NCBI database	string	N
DISTANCE_TO_TSS	Distance of CG dinucleotide to transcription start site	integer	N

Table 11 Group Methylation Profile Table, Infinium Assay (Continued)

Column	Description	Type	Visible by Default?
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
CPG_ISLAND_LOCATION	CpG island coordinates from the NCBI database	string	N
MIR_CPG_ISLAND	Chromosome start-end of upstream CpG island from a microRNA	string	N
MIR_NAMES	Name of microRNA near locus	string	N
Subcolumns			
AVG_Beta	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
MIN_Beta	Minimum methylation level (beta) of the CpG locus in the group of samples	float	N
MAX_Beta	Maximum methylation level (beta) of the CpG locus in the group of samples	float	N
NARRAYS	Number of samples in the group	integer	N
ARRAY_STDEV	Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample)	float	N
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N
Signal_A	Signal intensity of the unmethylated (A) probe	integer	N
Signal_B	Signal intensity of the methylated (B) probe	integer	N
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N

Table 12 includes information about the columns and subcolumns available in the Group Methylation Profile Table for the GoldenGate Assay.

Table 12 Group Methylation Profile Table, GoldenGate Assay

Column	Description	Type	Visible by Default?
Columns			
Index	Unique identifier for each sample	integer	Y
Target_ID	Identifies the probe name. Also used as a key column for data import	string	Y
ProbeID_A	Illumina identifier for probe sequence A	integer	Y
ProbeID_B	Illumina identifier for the probe sequence B	integer	Y
Group 1	The group to which this sample has been assigned	N/A	Y
Group 2	The group to which this sample has been assigned	N/A	Y
SEARCH_KEY	Gene identifier provided by the customer (for the DASL Assay). Generally equivalent to SYMBOL (for Direct Hyb)	string	N
PROBE_ID	Illumina identifier for probe sequence	integer	N
GID	RefSeq entry identifier (GI number)	string	N
ACCESSION	RefSeq entry (NM or XM number)	string	N
SYMBOL	Gene name as reported in RefSeq	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N
CHROMOSOME	Chromosome on which the target locus is located	string	N
REFSEQ	RefSeq version	string	N
CPG_COORDINATE	Chromosome coordinate of C in CpG locus	string	N
DIST_TO_TSS	Distance from Transcription Start Site in bp (optional)	string	N
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
INPUT_SEQUENCE	Original sequence of the region covered by assay probes	string	N
SYNONYM	Other names for the same gene (aliases)	string	N

Table 12 Group Methylation Profile Table, GoldenGate Assay (Continued)

Column	Description	Type	Visible by Default?
ANNOTATION	Gene description from NCBI RefSeq	string	N
PRODUCT	Protein name from NCBI	string	N
CG_NO	Unique CpG locus identifier from the Illumina CG database	string	N
Subcolumns			
AVG_Beta	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Signal CY3	Signal intensity in the green channel	integer	Y
Signal CY5	Signal intensity in the red channel	integer	Y
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	Y
MIN_Beta	Minimum methylation level (beta) of the CpG locus in the group of samples	float	N
MAX_Beta	Maximum methylation level (beta) of the CpG locus in the group of samples	float	N
NARRAYS	Number of samples in the group	integer	N
ARRAY_STDEV	Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample)	float	N
Avg_NBEADS	Average number of beads per bead type	float	N
BEAD_STERR	Average standard error associated with bead-to-bead variability	float	N

Sample Methylation Profile Table

Figure 67 shows an example of a Sample Methylation Profile table.

Figure 67 Sample Methylation Profile Table

Index	TargetID	ProbeID_A	ProbeID_B	AVG_Beta	Intensity	AV
1	cg00000029	14782418	14782418	0.03476	7006	0.25
2	cg00000108	12709357	12709357	0.07612	12762	0.53
3	cg00000109	59755374	59755374	0.10963	3950	0.51
4	cg00000165	12637463	12637463	0.08077	8059	0.51
5	cg00000236	12649348	12649348	0.09917	6918	0.45
6	cg00000289	18766346	18766346	0.13477	2972	0.55
7	cg00000292	43764508	43764508	0.08419	20283	0.42
8	cg00000321	62789509	62789509	0.06328	11594	0.47
9	cg00000363	16661505	16661505	0.13570	10843	0.52
10	cg00000622	11642304	38691301	0.01448	17574	0.46
11	cg00000658	73670480	73670480	0.11307	10752	0.46
12	cg00000714	31749374	31749374	0.11639	24396	0.45
13	cg00000721	28657361	28657361	0.06439	7184	0.50
14	cg00000734	31689396	31689396	0.10846	13573	0.56
15	cg00000769	36699489	29771340	0.02858	20157	0.51
16	cg00000807	61697410	61697410	0.12373	16355	0.55
17	cg00000884	59727471	59727471	0.07148	5160	0.56
18	cg00000905	26622384	26622384	0.10952	10035	0.46
19	cg00000924	23801481	23801481	0.10910	14529	0.45
20	cg00000948	31633318	31633318	0.21820	15468	0.60
21	cg00000957	65648367	36743439	0.13282	24257	0.45
22	cg00001099	22750474	22750474	0.03304	15941	0.35
23	cg00001245	68626314	31783436	0.04364	16833	0.55
24	cg00001249	14610435	14610435	0.05042	14278	0.43
25	cg00001261	24724406	53655485	0.19752	29902	0.52
26	cg00001269	15671426	15671426	0.04913	14473	0.46
27	cg00001340	11722421	53758324	0.25961	37837	0.51

The columns and subcolumns available in the Sample Methylation Profile Table depend on the assay used in the current project. Table 13 includes information about the columns and subcolumns available in the Sample Methylation Profile Table for the Infinium HD Assay.

Table 13 Sample Methylation Profile Table, Infinium HD Assay

Column	Description	Type	Visible by Default?
Columns			
TARGETID	Identifies the probe name. Also used as a key column for data import. Probes are named as follows: <ul style="list-style-type: none"> cg# represents CpG loci ch# represents non-CpG loci rs# represents SNP assays* (not affected by DNA methylation) 	string	Y
PROBEID_A	Illumina identifier for probe sequence A	integer	Y
PROBEID_B	Illumina identifier for probe sequence B	integer	Y
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ADDRESSA_ID	Address of probe A	integer	N

Table 13 Sample Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
ALLELEA_PROBESEQ	Sequence for probe A	string	N
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N
INFINIUM_DESIGNTYPE	Defines Assay type - Infinium I or Infinium II	string	N
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
FORWARD_SEQUENCE	Sequence (in 5'-3' orientation) flanking query site	string	N
GENOMEBUILD	Genome build on which the forward sequence is based	integer	N
CHR	Chromosome on which the target locus is located, Genome build 37	integer	N
MAPINFO	Genomic position of C in CG dinucleotide, Genome build 37	integer	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
CHROMOSOME_36	Chromosome on which the target locus is located, Genome build 36	integer	N
COORDINATE_36	Genomic position of C in CG dinucleotide, Genome build 36	integer	N
STRAND	Design strand	string	N
PROBE_SNPs	Assays with SNPs present within probe >10bp from query site	string	N
PROBE_SNPS_10	Assays with SNPs present within probe ≤10bp from query site (HM27 carryover or recently discovered)	string	N
RANDOM_LOCI	Loci which were chosen randomly in the design process	string	N
METHYL27LOCI	Present or absent on HumanMethylation27 array	string	N
UCSCREFGENE_NAME	Gene name (UCSC)	string	N
UCSCREFGENE_ACCESSION	Accession number (UCSC)	string	N

Table 13 Sample Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
UCSCREFGENE_GROUP	Gene region feature category (UCSC)	string	N
UCSCCPGISLAND_S_NAME	CpG island name (UCSC)	string	N
Relation_to_UCSC_CpG_Island	Relationship to Canonical CpG Island: Shores - 0-2 kb from CpG island; Shelves - 2-4 kb from CpG island	string	N
PHANTOM	FANTOM-derived promoter	string	N
DMR	Differentially methylated region (experimentally determined)	string	N
ENHANCER	Enhancer element (informatically-determined)	string	N
HMM_ISLAND	Hidden Markov Model Island	string	N
REGULATORYFEATURE_NAME	Regulatory feature (informatically determined)	string	N
REGULATORYFEATURE_GROUP	Regulatory feature category	string	N
DHS	DNase hypersensitive site (experimentally determined)	string	N
Subcolumns			
AVG_BETA	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N
Signal_A	Intensity of the unmethylated (A) probe	integer	N
Signal_B	Intensity of the methylated (B) probe	integer	N

Table 13 Sample Methylation Profile Table, Infinium HD Assay (Continued)

Column	Description	Type	Visible by Default?
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N

* SNP assays can be used for sample identification and tracking. They should be excluded for differential methylation analysis.

Table 13 includes information about the columns and subcolumns available in the Sample Methylation Profile Table for the Infinium Assay.

Table 14 Sample Methylation Profile Table, Infinium Assay

Column	Description	Type	Visible by Default?
Columns			
TARGETID	Identifies the probe name. Also used as a key column for data import	string	Y
PROBEID_A	Illumina identifier for probe sequence A	integer	Y
PROBEID_B	Illumina identifier for probe sequence B	integer	Y
SYMBOL	Gene symbol	string	Y
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ILMNSTRAND	Illumina strand (TOP or BOT)	string	N
ADDRESSA_ID	Address of probe A	integer	N
ALLELEA_PROBESEQ	Sequence for probe A	string	N
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N
GENOME BUILD	Genome build	integer	N
CHR	Chromosome on which the target locus is located	integer	N
MAPINFO	Genomic position of C in CG dinucleotide	integer	N
PLOIDY	Ploidy type	string	N
SPECIES	Species	string	N

Table 14 Sample Methylation Profile Table, Infinium Assay (Continued)

Column	Description	Type	Visible by Default?
SOURCE	Genomic position source	string	N
SOURCEVERSION	Source version	float	N
SOURCESTRAND	Illumina strand orientation for source sequence	string	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
TOPGENOMICSEQ	Top sequence (reported regardless of whether TOP or BOT sequence is used for design)	string	N
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
TSS_COORDINATE	Transcription start site genomic coordinate	integer	N
GENE_STRAND	Gene strand	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N
SYNONYM	Gene synonyms	string	N
ACCESSION	Gene accession (of the longest transcript)	string	N
GID	RefSeq entry identifier (GI number)	string	N
ANNOTATION	Gene annotation from the NCBI database	string	N
PRODUCT	Gene product description from the NCBI database	string	N
DISTANCE_TO_TSS	Distance of CG dinucleotide to transcription start site	integer	N
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
CPG_ISLAND_LOCATION	CpG island coordinates from the NCBI database	string	N
MIR_CPG_ISLAND	Chromosome start-end of upstream CpG island from a microRNA	string	N
MIR_NAMES	Name of microRNA near locus	string	N
Subcolumns			
AVG_BETA	Methylation level (beta) of the CpG locus in the group of samples	float	Y

Table 14 Sample Methylation Profile Table, Infinium Assay (Continued)

Column	Description	Type	Visible by Default?
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N
Red	Intensity of the unmethylated (A) probe	integer	N
Green	Intensity of the methylated (B) probe	integer	N
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N

Table 15 includes information about the columns and subcolumns available in the Sample Methylation Profile Table for the GoldenGate Assay.

Table 15 Sample Methylation Profile Table, GoldenGate Assay

Column	Description	Type	Visible by Default?
Columns			
TargetID	Identifies the probe name. Also used as a key column for data import	string	Y
ProbeID	Illumina identifier for probe sequence	integer	Y
SEARCH_KEY	Gene identifier provided by the customer (for the DASL Assay). Generally equivalent to SYMBOL (for Direct Hyb)	string	N
PROBE_ID	Illumina identifier for probe sequence	integer	N
GID	RefSeq entry identifier (GI number)	string	N
ACCESSION	RefSeq entry (NM or XM number)	string	N
SYMBOL	Gene name as reported in RefSeq	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N

Table 15 Sample Methylation Profile Table, GoldenGate Assay (Continued)

Column	Description	Type	Visible by Default?
CHROMOSOME	Chromosome on which the target locus is located	string	N
REFSEQ	RefSeq version	string	N
CPG_COORDINATE	Chromosome coordinate of C in the CpG locus	string	N
DIST_TO_TSS	Distance from Transcription Start Site in bp (optional)	string	N
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
INPUT_SEQUENCE	Original sequence of the region covered by assay probes	string	N
SYNONYM	Other names for the same gene (aliases)	string	N
ANNOTATION	Gene description from NCBI RefSeq	string	N
PRODUCT	Protein name from NCBI	string	N
CG_NO	Unique CpG locus identifier from the Illumina CG database	string	N
Subcolumns			
AVG_Beta	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Signal CY3	Signal intensity in the green channel	integer	Y
Signal CY5	Signal intensity in the red channel	integer	Y
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	Y
NARRAYS	Number of samples in the group	integer	N
ARRAY_STDEV	Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample)	float	N
Avg_NBEADS	Average number of beads per bead type	float	N
BEAD_STERR	Average standard error associated with bead-to-bead variability	float	N

Samples Table

Figure 68 shows an example of a Samples table.

Figure 68 Samples Table

Index	Sample ID	Sample Group	Sentrix Barcode	Sample Section	f
1	1596969018_A1	Group 1	1596969018	A1	679
2	1596969018_B1	Group 1	1596969018	B1	667
3	1596969018_C1	Group 1	1596969018	C1	685
4	1596969018_D1	Group 1	1596969018	D1	563
5	1596969018_E1	Group 1	1596969018	E1	205
6	1596969018_F1	Group 1	1596969018	F1	305
7	1596969018_G1	Group 1	1596969018	G1	262
8	1596969018_H1	Group 1	1596969018	H1	444
9	1596969018_A2	Group 2	1596969018	A2	532
10	1596969018_B2	Group 2	1596969018	B2	592
11	1596969018_C2	Group 2	1596969018	C2	602
12	1596969018_D2	Group 2	1596969018	D2	488
13	1596969018_E2	Group 2	1596969018	E2	156
14	1596969018_F2	Group 2	1596969018	F2	239
15	1596969018_G2	Group 2	1596969018	G2	236
16	1596969018_H2	Group 2	1596969018	H2	363

The columns and subcolumns available in the Samples Table depend on the assay used in the current project. Table 16 includes information about columns and subcolumns available in the Samples Table for the Infinium Assays.

Table 16 Samples Table, Infinium Assay

Column	Description	Type	Visible by Default?
Index	The row index of the sample	integer	Y
Sample ID	The sample identifier	string	Y
Sample Group	The sample group	string	Y
Sentrix Barcode	The barcode number of the Sentrix Array Product to which this sample was hybridized	string	Y
Sample Section	Position of the sample in the array	string	Y

Table 16 Samples Table, Infinium Assay (Continued)

Column	Description	Type	Visible by Default?
Detected Genes (0.01)	Number of CpG sites on the array detected with a p-value of 0.01	integer	Y
Detected Genes (0.05)	Number of CpG sites on the array detected with a p-value of 0.05	integer	Y
Signal Average GRN	Average intensity in the green channel	integer	Y
Signal Average RED	Average intensity in the red channel	integer	Y
Signal P05 GRN	The 5th percentile of intensity in the green channel	integer	Y
Signal P05 RED	The 5th percentile of intensity in the red channel	integer	Y
Signal P25 GRN	The 25th percentile of intensity in the green channel	integer	Y
Signal P25 RED	The 25th percentile of intensity in the red channel	integer	Y
Signal P50 GRN	The 50th percentile of intensity in the green channel	integer	Y
Signal P50 RED	The 50th percentile of intensity in the red channel	integer	Y
Signal P75 GRN	The 75th percentile of intensity in the green channel	integer	Y
Signal P75 RED	The 75th percentile of intensity in the red channel	integer	Y
Signal P95 GRN	The 95th percentile of intensity in the green channel	integer	Y
Signal P95 RED	The 95th percentile of intensity in the red channel	integer	Y

Table 17 includes information about columns and subcolumns available in the Samples Table for the GoldenGate assay.

Table 17 Samples Table, GoldenGate Assay

Column	Description	Type	Visible by Default?
Index	The row index of the sample	integer	Y
Sample ID	The sample identifier	string	Y
Sample Group	The sample group	string	Y

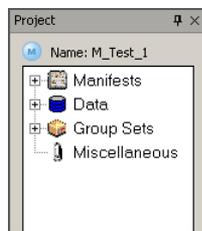
Table 17 Samples Table, GoldenGate Assay (Continued)

Column	Description	Type	Visible by Default?
Sentrix Barcode	The barcode number of the Sentrix Array Product to which this sample was hybridized	string	Y
Sample Section	Position of the sample in the array	string	Y
p05 Grn	The 5th percentile of intensity in the green (Cy3) channel	integer	Y
p50 Grn	The 50th percentile of intensity in the green (Cy3) channel	integer	Y
p95 Grn	The 95th percentile of intensity in the green (Cy3) channel	integer	Y
p05 Red	The 5th percentile of intensity in the red (Cy5) channel	integer	Y
p50 Red	The 50th percentile of intensity in the red (Cy5) channel	integer	Y
p95 Red	The 95th percentile of intensity in the red (Cy5) channel	integer	Y

Project Window

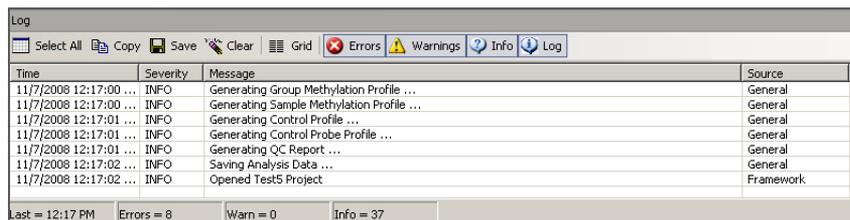
Figure 69 shows an example of a Project window.

The Project window identifies the manifest(s) loaded for your project and has a data section that identifies all of the Sentrix Array Product barcodes used in your project. You can expand a barcode and view the samples loaded on that Sentrix array product.

Figure 69 Project Window

Log Window

The Log window is a simple console which provides feedback on GenomeStudio processes. The Log window displays errors in **red**.

Figure 70 Log Window

Main Window Menus

Table 18 lists the selections available from the GenomeStudio Methylation Module's main window menu (and corresponding toolbar buttons).

Table 18 Main Menu Elements and Functions

Selection	Function	Toolbar Button (if used)
File Menu		
New Project	Opens a new project.	
Open Project	Opens a previously-saved project.	
Save Project	Saves all current information in this project, so you can return to it later.	
Save Project Copy As	Displays the Save Project Copy As dialog box, which allows you to specify a file name for and a location where to save a copy of the current project.	
Close Project	Closes the current project and returns you to the start window of the Methylation module.	
Manage Project Data	Opens the GenomeStudio Project Wizard - Project Data Selection dialog box, from which you can specify the array products to include in your project.	
Page Setup	Opens the Windows Page Setup dialog box, which you can use to set up the page properties and configure the printer properties.	
Print Preview	Opens the Print Preview window, which you can use to preview how the selected graph will print.	
Print	Displays the print dialog box. Use this dialog box to select options for printing the currently displayed graph.	
Recent Project	Allows you to select a project you recently worked on.	
Exit	Closes GenomeStudio.	
Edit Menu		
Cut	Cuts the current selection.	
Copy	Copies the current selection to the clipboard.	
Paste	Pastes the current selection from the clipboard.	
Delete	Deletes the current selection.	
Select All	Selects all rows in the current table.	
View Menu		

Table 18 Main Menu Elements and Functions (Continued)

Selection	Function	Toolbar Button (if used)
Save Default View	Allows you to save the default view of the open project.	
Restore Default View	Allows you to use a previously-saved default view.	
Save Custom View	Allows you to save a custom view of the open project.	
Load Custom View	Allows you to load a previously-saved custom view of a project.	
Log	Shows or hides the Log window.	
Project	Shows or hides the Project window.	
Analysis Menu		
Manage Analyses	Displays the GenomeStudio Manage Analyses dialog box, from which you can specify variables for this analysis.	
Manage Groupsets	Displays the GenomeStudio Project Wizard - Groupset Definition dialog box, from which you can manage your groups and groupsets.	
Run Methylation Analysis	Performs methylation analysis for the current experiment.	
Run Differential Methylation Analysis	Performs differential methylation analysis for the current experiment.	
Run Cluster Analysis	Creates a dendrogram for the current experiment.	
Show Histogram Plot	Creates a histogram plot for the current experiment.	
Reports	Displays the GenomeStudio Gene Expression Reports dialog box, which allows you to create a Final Report or a Custom Report.	
View Image	Displays the GenomeStudio View Image dialog box, which allows you to select Illumina products to view.	
View Marked Items in Web Browser	Displays the GenomeStudio Gene Expression Web Browser dialog box, which allows you to select columns and subcolumns from the current project to view in a web browser.	
View Controls Dashboard	Displays the Controls dialog box, which displays the available controls.	

Table 18 Main Menu Elements and Functions (Continued)

Selection	Function	Toolbar Button (if used)
Import Gene Expression Data	Displays the Import Gene Expression Data dialog box, from which you can specify a gene expression data file, and an optional gene lookup table.	
Tools Menu		
Options	<ul style="list-style-type: none"> • Project—Displays the Project Properties window in which you can make changes to project settings. • GenomeStudio—Opens the GenomeStudio Options window in which you can select GenomeStudio options, including the maximum number of project files and display attributes such as font name, size, and style. • Module—Displays the module Properties window, from which you can select file-based storage or memory-based storage. 	
Run Script	Allows you to run GenomeStudio scripts to automate selected tasks.	
Show Genome Viewer	Displays the Illumina Genome Viewer.	
Window Menu		
This menu is populated with the currently available windows. There are check marks next to the currently-displayed windows.		
Help Menu		
About GenomeStudio	Displays the GenomeStudio About dialog box, which contains: <ul style="list-style-type: none"> • Version information for the GenomeStudio Framework and any installed GenomeStudio modules • GenomeStudio copyright information • Software copyright notice 	
How to add documentation	Provides information about how to add user documentation to the Help menu.	

Context Menus

Table 19 lists GenomeStudio Methylation Module context menu elements and descriptions.

Table 19 Context Menu Elements and Functions

Element	Description
Histogram Plot: Group Methylation Profile Window	Properties —Displays the Plot Settings dialog box, from which you can alter the visual properties of the histogram plot.
	Clear Selected Values —Clears selected values from the histogram plot.
	Copy As —Copies the histogram plot to the clipboard as one of the following file types: Bitmap, JPEG, PNG, GIF, or TIFF.
Other Tabbed Windows	Show Only Selected Rows —Shows only selected rows.
	Configure Marks —Allows you to configure the properties of your marks.
	Mark Selected Rows <Add New> —Creates a new mark and marks selected rows.
	Select Marked Rows —Selects marked rows.
Tabs	Clear marks <All> —Clears all marks.
	Close —Closes the active window.
	Prominent —Brings the active window to the front.
	Rebalance —Rebalances all windows.
	Move to Next Tab Group —Moves the active window from its current tab group to the next tab group.
	Move to Previous Tab Group —Moves the active window from its current tab group to the previous tab group.
Project Window	Tear Away —Displays the active window in a separate browser.
	Export Project —Exports a project.
	Expand All —Expands all project repositories in the Project window.
	Collapse All —Collapses all project repositories in the Project window.
	Style —Selects a style for your project. Available project styles include: <ul style="list-style-type: none"> • Standard • Plain • Explorer • Navigator • Group • Office Light • Office Dark

Table 19 Context Menu Elements and Functions

Element	Description
Log Window	Log —Hides the Log window.
	Project —Hides the Project window.
	Show All —Shows the Log and Project windows.
	Hide All —Hides the Log and Project windows.

Sample Sheet Format

Introduction	98
Data Section	99
Sample Sheet Template	100
Sample Sheet Examples	101



Introduction

The sample sheet is a comma delimited text file (*.csv). It is divided into sections, indicated by lines with the section name enclosed by square brackets. The Data section is the only required section. You can also include a Header section, or other user-defined sections.

You must use a sample sheet if you plan to import gene expression data for correlation analysis. For more information about gene expression and methylation correlation analysis, see Chapter 5, *Comparing Methylation and Gene Expression Data*.

Data Section

The first row of the Data section must indicate the column names of the data to follow. The columns can be in arbitrary order, and additional user-defined columns can be included in the file.

Table 20 Data Section, Required and Optional Columns

Column	Description	Optional (O) or Required (R)
Sample_Name	Name of the sample (used only for display in the table). GenomeStudio assigns a default sample name, concatenating the SAM serial number and row/column designation Example: S12345	O
Sample_Well	The well within the sample plate for this sample (used only for display in the table) Example: A01	O
Sample_Plate	The barcode of the sample plate for this sample (used only for display in the table) Example: XXXXXXXXX-BCD	O
Sample_Group	User-specified name of the sample group Note: If Sample_Group is missing, GenomeStudio creates one group with the name "Default Group." Example: Group_1	R
Pool_ID	Name of the OMA Example: GS0007054-OMA	R
Sentrix_ID	SAM or BeadChip ID Example: 1167988	R
Sentrix_Position	For SAMs, the SAM sample to which the sample is hybridized. For BeadChips, the section to which the sample is hybridized. Example: R001_C001 (for a SAM), or A1 (for a BeadChip)	R



NOTES

- Your sample sheet header may contain any information you choose.
- Your sample sheet may contain any number of columns.
- Your sample sheet must be in comma-delimited (*.csv) file format.

Sample Sheet Template

You can download a template for a methylation sample sheet from iCom. Log into your iCom account from the Illumina home page, <http://www.illumina.com>.

Sample Sheet Examples

The following are example sample sheets for Infinium Methylation and GoldenGate Methylation.

Figure 71 Example Sample Sheet, Infinium Human Methylation 450

[Header]						
Investigator Name	Scientist					
Project Name	Methylation 450K Test					
Experiment Name	R&D_Alpha_Test					
Date	20-Sep-10					
[Data]						
Sample_Name	Sample_Well	Sample_Plate	Sample_Group	Pool_ID	Sentrix_ID	Sentrix_Position
U_NA17105M_1ug_Rep1			U_NA17105M		5613914071	R01C01
H_NA17105M_1ug_Rep1			H_NA17105M		5613914071	R02C01
M_NA17105M_1ug_Rep1			M_NA17105M		5613914071	R03C01
A431_1ug_Rep1			A431		5613914071	R04C01
Jurkat_1ug_Rep1			Jurkat		5613914071	R05C01
K562_1ug_Rep1			K562		5613914071	R06C01
MCF7_1ug_Rep1			MCF7		5613914071	R01C02
Raji_1ug_Rep1			Raji		5613914071	R02C02
NA17105M_1ug_Rep1			NA17105M		5613914071	R03C02
NA17018F_1ug_Rep1			NA17018F		5613914071	R04C02
MCF7_1ug_Rep2			MCF7		5613914071	R05C02
Raji_1ug_Rep2			Raji		5613914071	R06C02

Figure 72 Example Sample Sheet, Infinium Human Methylation 27

[Header]						
Investigator Name	Scientist					
Project Name	Infinium Methylation					
Experiment Name	Test					
Date	1/23/2007					
[Data]						
Sample_Name	Sample_Well	Sample_Plate	Sample_Group	Pool_ID	Sentrix_ID	Sentrix_Position
A341_a	A01	Test	A341_a		4098906047	A
NA10924_b	B01	Test	NA10924_b		4098906047	B
Jurkat_a	C01	Test	Jurkat_a		4098906047	C
NA10923_b	D01	Test	NA10923_b		4098906047	D
K562_a	E01	Test	K562_a		4098906047	E
Raji_b	F01	Test	Raji_b		4098906047	F
Raji_a	G01	Test	Raji_a		4098906047	G
K562_b	H01	Test	K562_b		4098906047	H
NA10923_a	A02	Test	NA10923_a		4098906047	I
Jurkat_b	B02	Test	Jurkat_b		4098906047	J
NA10924_a	C02	Test	NA10924_a		4098906047	K
A431_b	D02	Test	A431_b		4098906047	L

Figure 73 Example Sample Sheet, GoldenGate Methylation

[Header]						
Investigator Name	Scientist					
Project Name	Methylation					
Experiment Name	Methylation experiment					
Date	8/11/2006					
[Data]						
Sample_Name	Sample_Well	Sample_Plate	Sample_Group	Pool_ID	Sentrix_ID	Sentrix_Position
Sample_1	A01	Plate1	Group_1	GS0007001-OMA	1234567890	R001_C001
Sample_2	A02	Plate1	Group_2	GS0007001-OMA	1234567890	R001_C002
Sample_3	A03	Plate1	Group_3	GS0007001-OMA	1234567890	R001_C003
Sample_4	A04	Plate1	Group_4	GS0007001-OMA	1234567890	R001_C004
Sample_5	A05	Plate1	Group_5	GS0007001-OMA	1234567890	R001_C005
Sample_6	A06	Plate1	Group_6	GS0007001-OMA	1234567890	R001_C006
Sample_7	A07	Plate1	Group_7	GS0007001-OMA	1234567890	R001_C007
Sample_8	A08	Plate1	Group_8	GS0007001-OMA	1234567890	R001_C008
Sample_9	A09	Plate1	Group_9	GS0007001-OMA	1234567890	R001_C009
Sample_10	A10	Plate1	Group_10	GS0007001-OMA	1234567890	R001_C010
Sample_11	A11	Plate1	Group_11	GS0007001-OMA	1234567890	R001_C011
Sample_12	A12	Plate1	Group_12	GS0007001-OMA	1234567890	R001_C012
Sample_13	B01	Plate1	Group_1	GS0007001-OMA	1234567890	R002_C001
Sample_14	B02	Plate1	Group_2	GS0007001-OMA	1234567890	R002_C002
Sample_15	B03	Plate1	Group_3	GS0007001-OMA	1234567890	R002_C003
Sample_16	B04	Plate1	Group_4	GS0007001-OMA	1234567890	R002_C004
Sample_17	B05	Plate1	Group_5	GS0007001-OMA	1234567890	R002_C005
Sample_18	B06	Plate1	Group_6	GS0007001-OMA	1234567890	R002_C006
Sample_19	B07	Plate1	Group_7	GS0007001-OMA	1234567890	R002_C007
Sample_20	B08	Plate1	Group_8	GS0007001-OMA	1234567890	R002_C008
Sample_21	B09	Plate1	Group_9	GS0007001-OMA	1234567890	R002_C009
Sample_22	B10	Plate1	Group_10	GS0007001-OMA	1234567890	R002_C010
Sample_23	B11	Plate1	Group_11	GS0007001-OMA	1234567890	R002_C011
Sample_24	B12	Plate1	Group_12	GS0007001-OMA	1234567890	R002_C012
Sample_25	C01	Plate1	Group_1	GS0007001-OMA	1234567890	R003_C001
Sample_26	C02	Plate1	Group_2	GS0007001-OMA	1234567890	R003_C002
Sample_27	C03	Plate1	Group_3	GS0007001-OMA	1234567890	R003_C003
Sample_28	C04	Plate1	Group_4	GS0007001-OMA	1234567890	R003_C004
Sample_29	C05	Plate1	Group_5	GS0007001-OMA	1234567890	R003_C005
Sample_30	C06	Plate1	Group_6	GS0007001-OMA	1234567890	R003_C006
Sample_31	C07	Plate1	Group_7	GS0007001-OMA	1234567890	R003_C007
Sample_32	C08	Plate1	Group_8	GS0007001-OMA	1234567890	R003_C008
Sample_33	C09	Plate1	Group_9	GS0007001-OMA	1234567890	R003_C009
Sample_34	C10	Plate1	Group_10	GS0007001-OMA	1234567890	R003_C010
Sample_35	C11	Plate1	Group_11	GS0007001-OMA	1234567890	R003_C011
Sample_36	C12	Plate1	Group_12	GS0007001-OMA	1234567890	R003_C012
Sample_37	D01	Plate1	Group_1	GS0007001-OMA	1234567890	R004_C001
Sample_38	D02	Plate1	Group_2	GS0007001-OMA	1234567890	R004_C002
Sample_39	D03	Plate1	Group_3	GS0007001-OMA	1234567890	R004_C003

Technical Assistance

For technical assistance, contact Illumina Customer Support.

Table 21 Illumina General Contact Information

Illumina Website	http://www.illumina.com
Email	techsupport@illumina.com

Table 22 Illumina Customer Support Telephone Numbers

Region	Contact Number
North America toll-free	1.800.809.ILMN (1.800.809.4566)
United Kingdom toll-free	0800.917.0041
Germany toll-free	0800.180.8994
Netherlands toll-free	0800.0223859
France toll-free	0800.911850
Other European time zones	+44.1799.534000
Other regions and locations	1.858.202.ILMN (1.858.202.4566)

MSDSs

Material safety data sheets (MSDSs) are available on the Illumina website at <http://www.illumina.com/msds>.

Product Documentation

If you require additional product documentation, you can obtain PDFs from the Illumina website. Go to <http://www.illumina.com/support/documentation.ilmn>. When you click on a link, you will be asked to log in to iCom. After you log in, you can view or save the PDF. To register for an iCom account, please visit <https://icom.illumina.com/Account/Register>.

