



Methylation Custom Output Report Plug-in v2.0.0 for the GenomeStudio™ Methylation Module

1. General Information

The Illumina GenomeStudio Methylation Custom Output Report Plug-in is a software plug-in that works with Illumina's GenomeStudio Methylation Module v1.0 and above. This plug-in allows you to create input files for downstream applications and analysis, and gives you the option to configure report parameters such as output columns and sample display (rows or columns).

Using the Methylation Custom Output Report Plug-in, you can also create input files for use with mQTL (Methylation Quantitative Trait Loci) tools such as the Merlin Input Report and the PLINK Input Report. This document provides information about downloading, installing, and using the Methylation Custom Output Report Plug-in.

2. Version History

Build	Date
v2.0.0, Initial release	April 10, 2009

3. Downloading and Installing the Methylation Custom Output Report Plug-in

Perform the following steps to install the Methylation Custom Output Report Plug-in on your computer:

1. Download the Methylation Custom Output Report Plug-in setup program (*.msi) from the [illumina•connect](#) website or the GenomeStudio Portal.
2. Run the Methylation Custom Output Report Plug-in setup program.

The Methylation Custom Output Report Plug-in is installed on your computer.

4. Using the Methylation Custom Output Report Plug-in

1. Open a methylation project using the GenomeStudio Methylation Module.
2. In the main menu, select **Analysis | Reports**.
3. The GenomeStudio Methylation Reports dialog box appears.
4. In the GenomeStudio Methylation Reports dialog box, select **Custom Report** and choose **Methylation Custom Output Report** from the dropdown menu.
5. [Optional] Browse to your config file and adjust the algorithm input parameters. The table on the next page of this document includes descriptions of the input parameters.
6. Click **OK** to start the report. A progress bar shows the status of the report. When the report has finished processing, a dialog box asking "Would you like to view this report?" appears.
7. Click **Yes** to display a text file showing the location of the output file.

Note: The report output file may be too large to display in your default text file viewer. If this is the case, you can open the report output file using WordPad.



5. Adjusting the Parameters

The Methylation Custom Output Report format can be changed via an editable configuration file. When you install the Custom Output Report Plug-in, the config file is installed on your computer in the following location:

C:\Program Files\Illumina\GenomeStudio\Modules\BSM3\ReportPlugins\
MethylationCustomOutputReport\

Note: When you modify and save the default config file, changes are preserved for future sessions.

The following table contains configuration settings for Methylation Custom Output Reports.

Parameter Name	Description	Default Value	Mandatory
AnnotationFileColumns	Columns to be included in the tab-delimited annotation file	TargetID, SYMBOL, CHR, MAPINFO, GENE_STRAND	Yes
CreateAnnotationFile	If set to true, creates a separate annotation file in addition to the matrix format data file	True	Yes
DataTableName	Name of the data table to use	Sample Methylation Profile	Yes
DataTableColumns	Columns to be included in comma-delimited report; the first entry should be an ID column, such as Target_ID	TargetID,AVG_Beta	Yes
SamplesInRows	For output with samples in rows, set to true; for samples in columns, set to false	True	Yes
TabDelimited	For tab-delimited output, set to true; for comma-delimited, set to false	True	Yes

6. Technical Support

Direct questions about installing and using the Methylation Custom Output Report Plug-in to Illumina Technical Support at techsupport@illumina.com, 1.800.809.4566 (toll-free), or +1.858.202.4566 (outside North America).

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