Using Partek's Report Plug-in for Illumina's GenomeStudio to Export Methylation Data

This tutorial describes how to export methylation data using Partek's Report Plug-in for the Illumina® GenomeStudio Methylation Module for use in Partek® Genomics Suite™.

The GenomeStudio plug-in exports your data into a project that Partek can directly open. It is the fastest and most consistent way to get fully annotated Illumina methylation data into Partek.

If you don't have access to GenomeStudio, you can import a Final Report from GenomeStudio, but it requires manual work and may not include annotations. See the *Importing Final Report from BeadStudio's Gene Expression Module* tutorial for more information.

Installing the Plug-in

- Download the plug-in from the Illumina's GenomeStudio portal
- Extract the **PartekReport.Methylation.dll** file from the distributed zip file
- Move the **DLL** file into *GenomeStudio's Methylation Module's report plug-in folder* (create the folder if it does not exist) **C:/Program Files/Illumina/GenomeStudio/Modules/BSM3/ReportPlugins/PartekReport** (Figure 1)

Note: If you have old versions of the plug-in, please remove them from the GenomeStudio folder hierarchy.
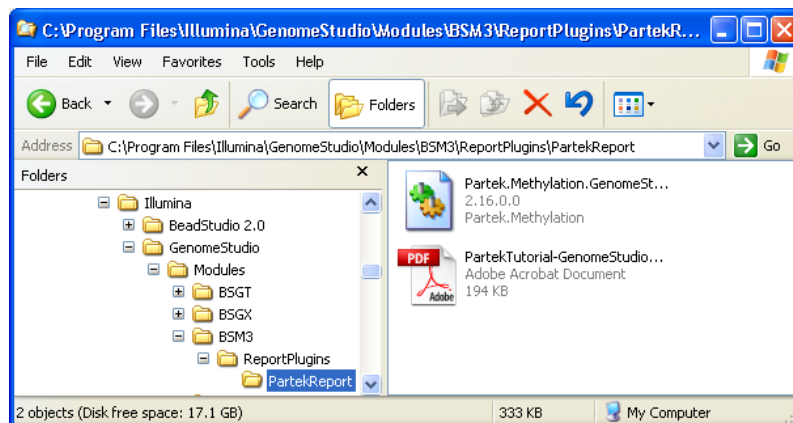

Figure 1: Placing the Partek Report DLL in the appropriate directory

Exporting from GenomeStudio

- Select **Analysis > Reports…** from the main menu
- Select **Custom Report**
- Choose **Partek Report Plug-in** from the list of custom plug-ins (Figure 2)
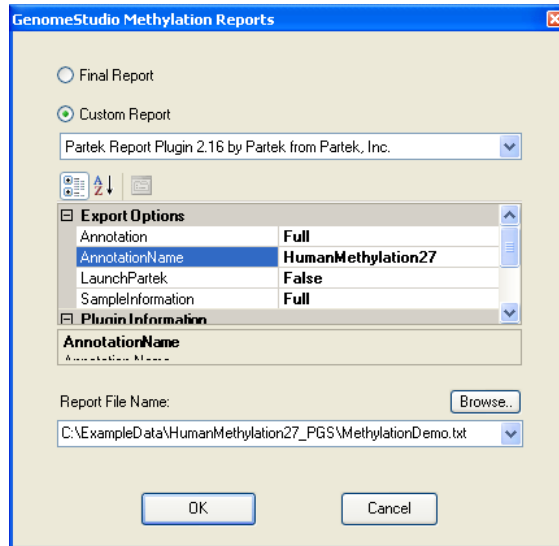- Configure the export options based on the information below

Figure 2: Configuring the GenomeStudio Methylation Report dialog

Export Options

Annotation	The level of detail you would like your exported annotation to have. *Minimal* will contain the required information to do data analysis, and *Full* will contain everything from GenomeStudio.
AnnotationName	This should be equivalent to the name of the bgx file you imported the data with. If you don't know this information, you should use something unique to your data set.
LaunchPartek	After the plug-in has completed exporting, you can launch Partek GS afterward. If Partek is not already running, it will start.
SampleInformation	The level of detail you would like your exported sample information to have. If you have entered data from your experiment into the samples table, you should select *Full*.

Table 1: Export options

- It is **strongly recommended** to put the exported files in their own folder, since this allows you to move the folder instead of all the files individually
- Select **OK** to start the export process

The result of the export process is a project file (.ppj), which you can open directly in Partek. The project file will open the beta and signal intensities data, and associate the annotation information to the intensities file. All intensities are log transformed. The markers that you have just created data for are described in the annotation information. The plug-in also creates a manifest file describing the files and date of creation.
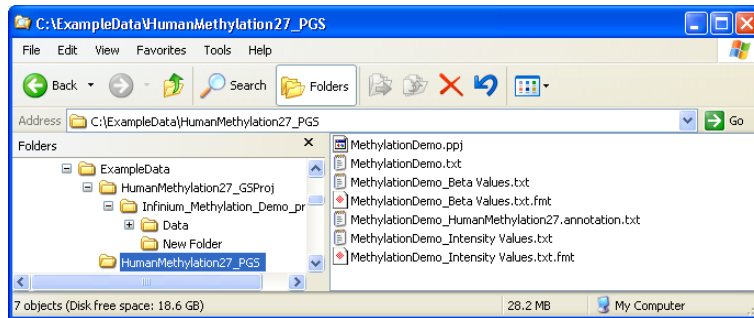

Figure 3: Exported files from the GenomeStudio project

Opening the Project in Partek® Genomic Suite™

Note: If you selected the **LaunchPartek** option on the report dialog (Figure 2), this step has already been completed.
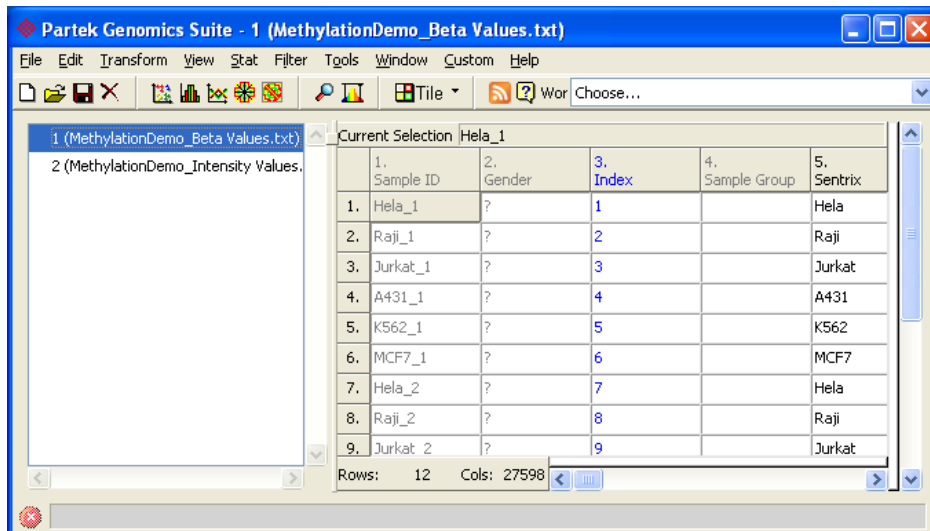

Figure 4: Open the new project in Partek

- On the main menu, select **File > Load Project**
- You should see a *BetaValues* spreadsheet and an *Intensities* data file

Frequently Asked Questions

Q: Why doesn't the Partek plug-in appear in my list of custom plug-ins?

> **A:** You have placed the DLL file in the incorrect location. GenomeStudio opens error dialogs if a plug-in is faulty, so if you receive no errors then it did not find the file.

Q: After I open my project in Partek my annotations are missing or the annotations are incorrect. Is the annotation corrupted?

> **A:** If you use the same name as a previously created annotation, Partek will not overwrite existing annotation references. You will need to manually change the annotation links in your file, or update the File Manager so all files use your new annotation. For more information, please see the **Associating a Spreadsheet with an Annotation File** document on our tutorials website.

Q: Why does my data look different than in GenomeStudio?

> **A:** Your data is automatically normalized for analysis in Partek. The data will be shifted such that the lowest value is 1 and the $\log_2$ taken. To avoid shifting the data you should not use background correction when creating your project in GenomeStudio. This results in negative intensities in your data and creates problems for various normalization procedures.

End of Tutorial

This is the end of Illumina data import tutorial. If you need additional assistance with this data set, you can call our technical support staff at +1-314-878-2329 or email support@partek.com.