Import Genotype Data

This user guide describes how to export copy number and genotype data using Partek's Report Plug-in for Illumina GenomeStudio Genotype Module for use in Partek Genome Suite. The GenomeStudio plug-in lets you export data into a project that can be opened in Partek Genome Suite open directly. It is the fastest and most consistent way to get fully annotated Illumina gene expression data into Partek.

- Partek Genotype plug-in installation
- Export report from GenomeStudio
- Open project in Partek Genomics Suite

Partek Genotype plug-in installation

Download the plug-in zip file, unzip the file, there is a folder called **PartekReport** which contains two .dll files --**Partek.Common.dll** and **Partek. GeneExpression.GenomeStudio.dll**, move the **PartekReport** folder to

C:\Program Files \Illumina\GenomeStudio 2.0\Modules\BSGT\ReportPlugins, if there is no **ReportPlugins** folder in **BSGT** folder, create one, the path and folder names have to be exactly match one described above (Figure 1).

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

Export report from GenomeStudio

In GenomeStudio genotype project:

- Choose **Analysis > Reports>Report Wizard** from the main menu
- Select **Custom Report** and choose **Partek Report Plug-in** from the drop-down list
- Specify *AnnotationName*, do NOT include **<>** in the name, you can the same name as the .bgx file you imported the ddata with, or a unique name to your dataset

Figure 4. Configuring the GenomeStudio copy number report dialog

- Leave all the others as default value (Figure 2) click **Next**

- Specify the report file name, we recoommend to put the exported files in their own folder, which allows you to move thefolder instead of all the files individually.
- Click **Finish** (Figure 3)

Figure 5. Specify output folder and file name

The output generate 9 files in the folder including a project file (.ppj), annotation file, summary file and 3 sets of Partek spreadshet file-- each spreadsheet consists of 2 files.

Open project in Partek Genomics Suite

To open the report, launch Partek Genomics Suite, choose **File > Open Project**, browse to the .ppj file to open. There will be three spreadsheets opened (Figure 4)
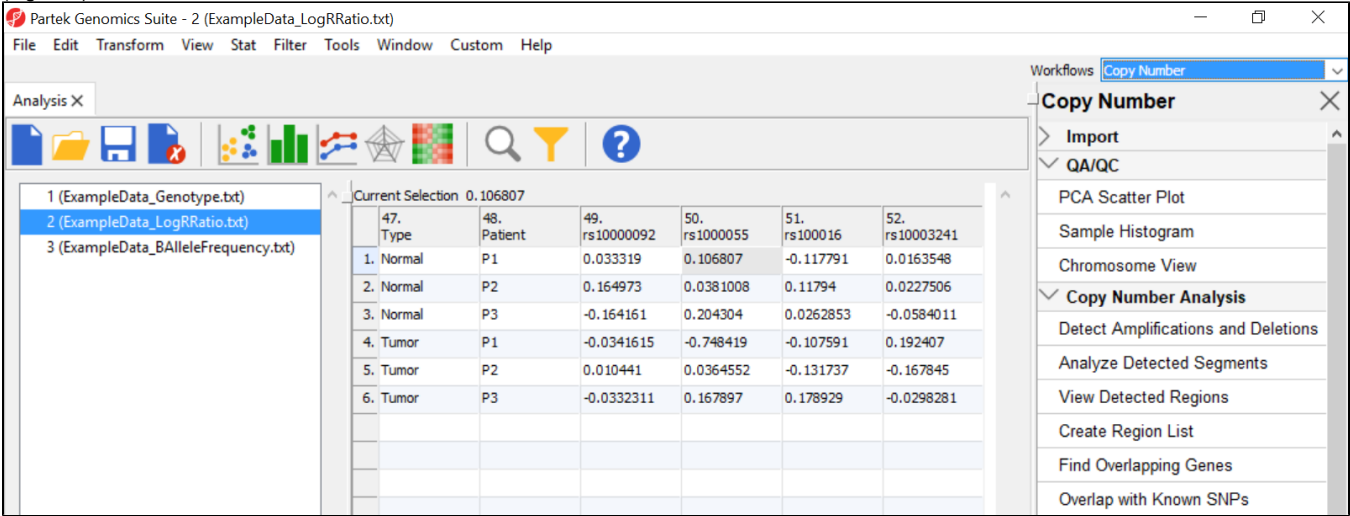

Figure 6. Open project in Partek Genomics Suite

Spreadsheet 1 contains genotype calls, spreadsheet 2 contains log R ratio which is copy number in log scale, spreadsheet 3 contains B allele frequency.

To do copy number analysis, select spreadsheet 2 log R ratio, choose Copy number workflow, start from QA/QC section. Genotype spreadsheet will be used for Association and LOH workflow.

Your Rating: ☆☆☆☆☆   Results: ★★★★⯪ 33 rates