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

Report Wizard - Report Type		
Genotyping Report What type of report would you lik	eto generate?	
	marmina	
○ Final Report	O Locus Summary	
O DNA Report	○ Locus x DNA	
Custom Report		
Partek Report Plugin 2.17 by Pa	rtek from Partek Jac	
	itek from Partek, inc. v	
2. 2. □		
Export Options	^	
Annotation	Full	
AnnotationName	Human2M	
LaunchPartek	False	
SampleInformation	Full	
Туре	Illumina Copy Number Analysis	
Plugin Information		
Company	Partek, Inc.	
Url	http://www.partek.com/	
AnnotationName		
Annotation Name		
Cancel	< Back Next > Finish	

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 recommend 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)

Report Wizard - Destination	
Genotyping Report Where would you like to save your report?	illumına [®]
Output Path C:\customer test\lllumina GT example	V Browse
Report Name ExampleData	
Cancel < Back	Next > Finish

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)

le Edit Transform View Stat Filter	Tools Window	Custom Help						Workflows Copy Number
nalysis X								Copy Number
) 🧀 🗔 🛼 🛛 😆	🚝 🕁 📕	Q						> Import > QA/QC
1 (ExampleData_Genotype.txt)	Current Selection	n 0.106807					^	PCA Scatter Plot
2 (ExampleData_LogRRatio.bd) 3 (ExampleData_BAlleleFrequency.bd)	47. Type	48. Patient	49. rs10000092	50. rs1000055	51. rs100016	52. rs10003241		Sample Histogram
	1. Normal	P1	0.033319	0.106807	-0.117791	0.0163548		Chromosome View
	2. Normal	P2	0.164973	0.0381008	0.11794	0.0227506		✓ Copy Number Analysis
	3. Normal	P3	-0.164161	0.204304	0.0262853	-0.0584011		Detect Amplifications and Deletions
	4. Tumor	P1	-0.0341615	-0.748419	-0.107591	0.192407		· · · · · · · · · · · · · · · · · · ·
	5. Tumor	P2	0.010441	0.0364552	-0.131737	-0.167845		Analyze Detected Segments
	6. Tumor	P3	-0.0332311	0.167897	0.178929	-0.0298281		View Detected Regions
								Create Region List
								Find Overlapping Genes
								Overlap with Known SNPs

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.

