Importing Copy Number Data

This tutorial uses a spreadsheet generated after data import, but we will illustrate the steps used to import the data in this section.

- Select Copy Number from the Workflows drop-down menu
- Select Import Samples from the Copy Number workflow

The import dialog will open (Figure 1).

🧐 Import Copy Number Samples	\times						
Specify Data Type							
Import Allele Intensity (This option requires "Create copy number from intensities")							
Import from Affymetrix CEL files							
O Import from Affymetrix Axiom Summary File							
Import Copy Number or Log Ratio (These options do not need "Create copy number from intensities")							
O Import from Agilent data							
O Load a project following Illumina GenomeStudio export							
O Import Illumina Final Report Text File							
O Import from NimbleGen Pair or CGH Data Summary files							
O Open existing file							
O Open existing project							
OK Cance	1						

Figure 3. Viewing the Import Copy Number Samples dialog

For Affymetrix arrays, Partek Genomics Suite can import CEL files with allele intensity values and calculate copy number estimates from these intensities. For Agilent, Illumina, NimbleGen, or Affymetrix .CHP files, Partek Genomics Suite can import files containing calculated copy numbers or log ratios.

For this tutorial, we will not be importing CEL files.

• Select Cancel to close the import dialog

Later sections of this tutorial will address starting with copy number or log ratios and performing GC wave correction on Affymetrix CEL files.

We can now open the tutorial data file.

- Download the zipped tutorial data folder Overlapping Copy Number with LOH
- · Unzip the files to an accessible directory
- Select File from the main menu
- Select Open...
- Select the file IC_Intensities_SNP6.fmt

The spreadsheet will open in the Analysis tab (Figure 2).

Partek Genomics Suite - 1 (IC_Intensities_SNP6 File Edit Tenneform View Cast Filter Tenneform	6) ale Wiadaw Custom Hala								– 🗆 X	
File Edit Transform View Star Filter 100	ois <u>w</u> indow <u>C</u> astorn <u>H</u> eip								Workflows Copy Number ~	
Analysis $ imes$									Copy Number ×	
	= 📣 🌆 🔵 🔻	0							└─ Import	
									Import samples	
1 (IC_Intensities_SNP6)								Add Sample Attributes		
	0riginal File	3. Tumor	4. SubjectID	5. Gender	6. Scan Date	7. AFFX-5Q-123	8. AFFX-5Q-456	9. AFFX-5Q-7	View Sample Information	
1.	IC_151N.CE IC_151N.CEL L.pimg	N	151	Female	07/27/07	1.58375	0.945171	2.48301	Choose Sample ID Column	
									Create Copy Number (from Allele Intensities Only)	
2.	IC 151T FF.IC 151T FF.CEL	т	151	Female	07/27/07	1.75068	0.918597	2.79518	> QA/QC	
	CEL.pimg								> Copy Number Analysis	
									> Visualization	
3.	IC_201N.CE IC_201N.CEL L.pimg	N	201	Female	07/28/07	2.14467	0.99283	2.9318	> Biological Interpretation	
									> Genomic Integration	
4.	IC 201T FF.IC 201T FF.CEL	т	201	Female	07/27/07	1.73562	0.866369	2.52811		
	CEL.pimg									
5.	IC_22N.CEL. IC_22N.CEL pima	N	22	Female	07/27/07	2.20981	1.11565	2.98037		
6.	IC 22T FF. IC 22T FF.CEL	т	22	Female	07/27/07	1.88953	1.07794	2.62485		
	CEL.pimg				1.1					
7.	IC_258N.CE IC_258N.CEL L.pimg	N	258	Female	07/27/07	1.89186	1.08757	2.85029		
8.	IC_258T_FF.IC_258T_FF.CEL	т	258	Female	07/27/07	2.06851	1.19668	2.92442		
	CEL.pimg									
Rover: 20 Columns: 2765697										

Figure 4. Viewing the tutorial data set spreadsheet

This spreadsheet was generated from the import of SNP6 CEL files and shows all 20 samples on rows. Columns 1-6 describe the samples with information such as file names, Subject ID, Gender, etc. The other columns are individual markers from the microarray with the log2 normalized intensities associated with each marker (marker labels are column headers). Opening the *IC_Intensities_SNP6.fmt* file is equivalent to importing the 20 sample files and adding sample attributes.

« Copy Number Analysis Exploring the data with PCA »

Additional Assistance

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



Your Rating: ☆☆☆☆☆ Results: ★★★★ 34 rates