

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).

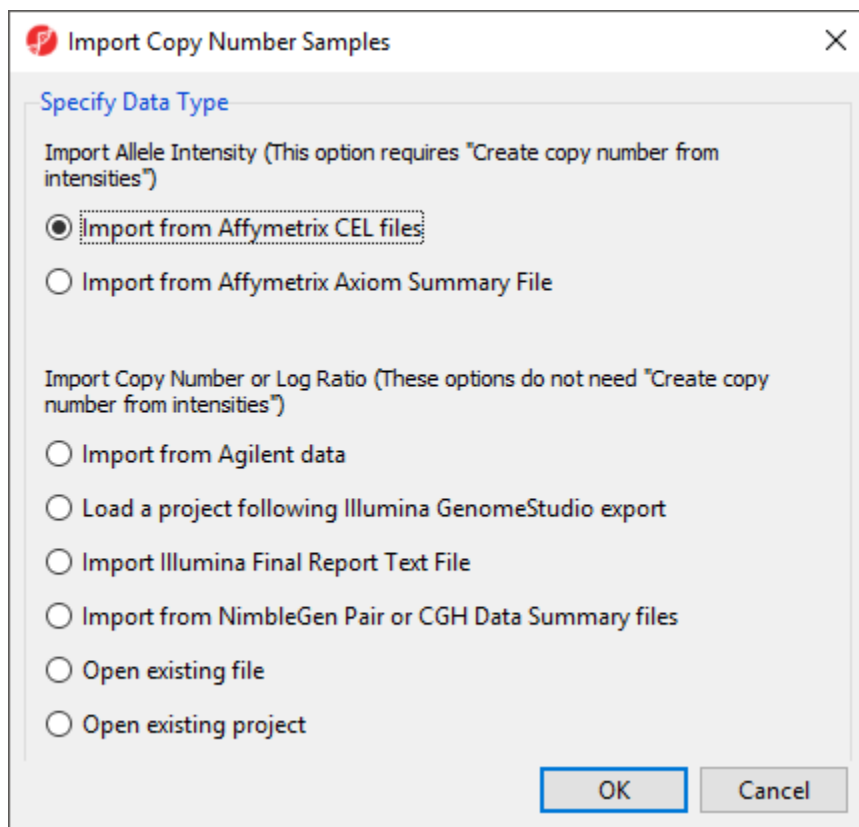


Figure 3. Viewing the Import Copy Number Samples dialog

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).

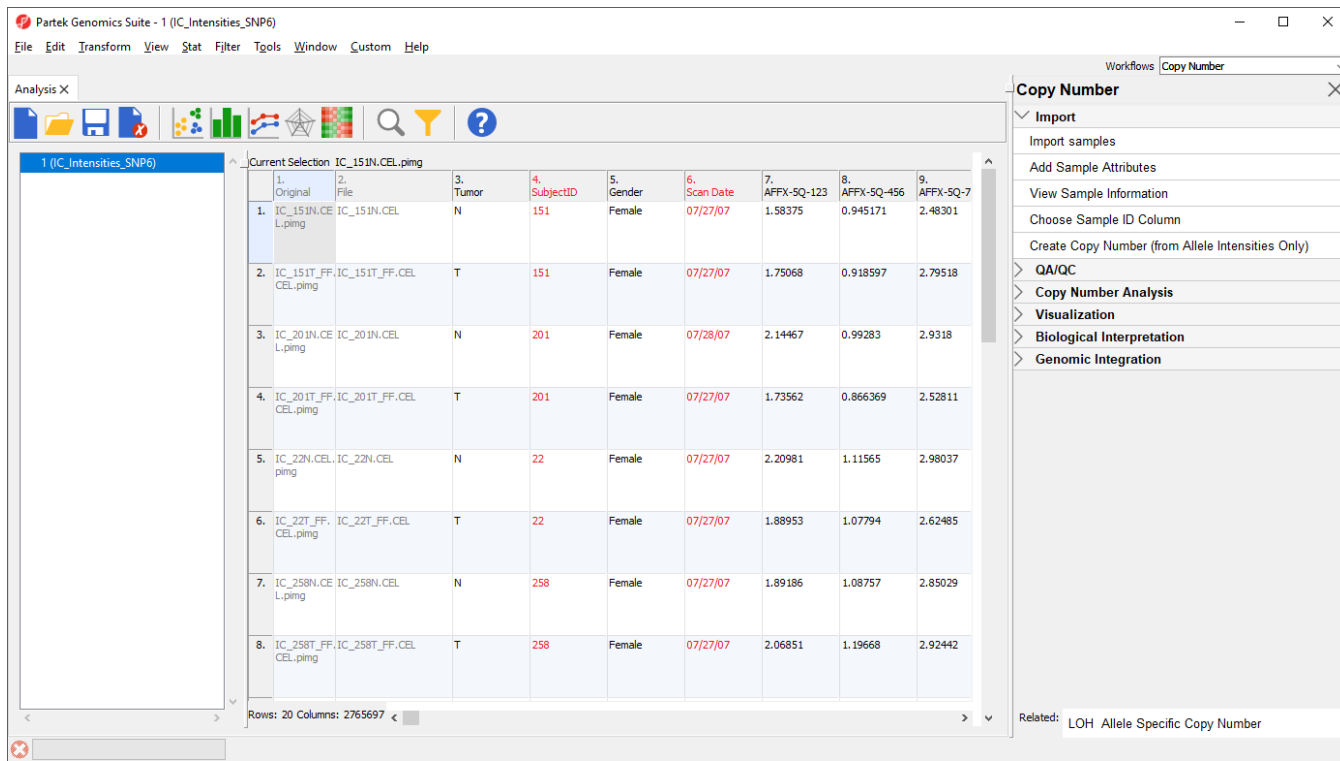


Figure 4. Viewing the tutorial data set spreadsheet

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

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