

Creating Copy Number from Allele Intensities

- [Create Copy Number from Pairs](#)
- [Create Copy Number from Reference Baseline](#)

The first step in analyzing Affymetrix intensity data is to estimate the number of copies of each marker (allele).

- Select **Create Copy Number (from Allele Intensities Only)**

This launches the *Copy Number Creation* dialog (Figure 1).

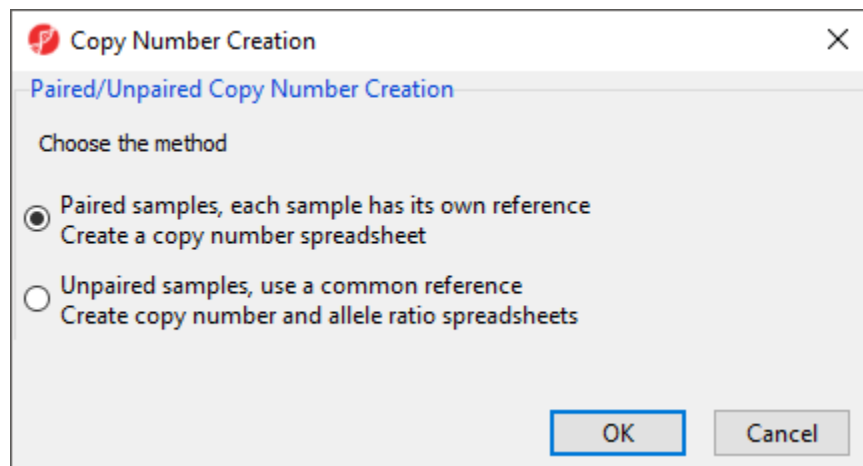


Figure 5. Choosing paired samples or unpaired samples

Choosing *Paired samples* assumes that each sample has its own reference sample with a common sample ID and generates a copy number spreadsheet. Choosing *Unpaired samples* uses a common reference, either a single sample or a group of samples, to create both a copy number spreadsheet and an allele ratio spreadsheet.

Create Copy Number from Pairs

In this tutorial, we have paired tumor-normal samples and thus can use the *Paired samples* option.

- Select **Paired samples**
- Select **OK**

The next dialog, *Create Copy Number from Pairs*, asks you to choose the column shared by each pair and the column that identifies the baseline category (Figure 2).

Create Copy Number from Pairs (Spreadsheet 1)

Identify the baseline samples

Column: 3. Tumor

Baseline category: N

Match the sample pairs

Column: 4. SubjectID

Result file

IC_Intensities_SNP6_pairedcopynumber.fmt

Browse...

OK Cancel

Figure 6. Creating copy number from pairs

- Select **3. Tumor** for *Column*
- Select **N** for *Baseline category*
- Select **4. SubjectID** for the *Column* to match sample pairs
- Select **OK**

This will pair samples based on *4. SubjectID*, and set the baseline sample as the sample in the pair with a value of *N* in the *3. Tumor* column. The spreadsheet produced (Figure 3) has a row for each tumor sample. In this tutorial, columns 7+ include copy number estimates for each marker. Column 1-6 are identical to the source spreadsheet.

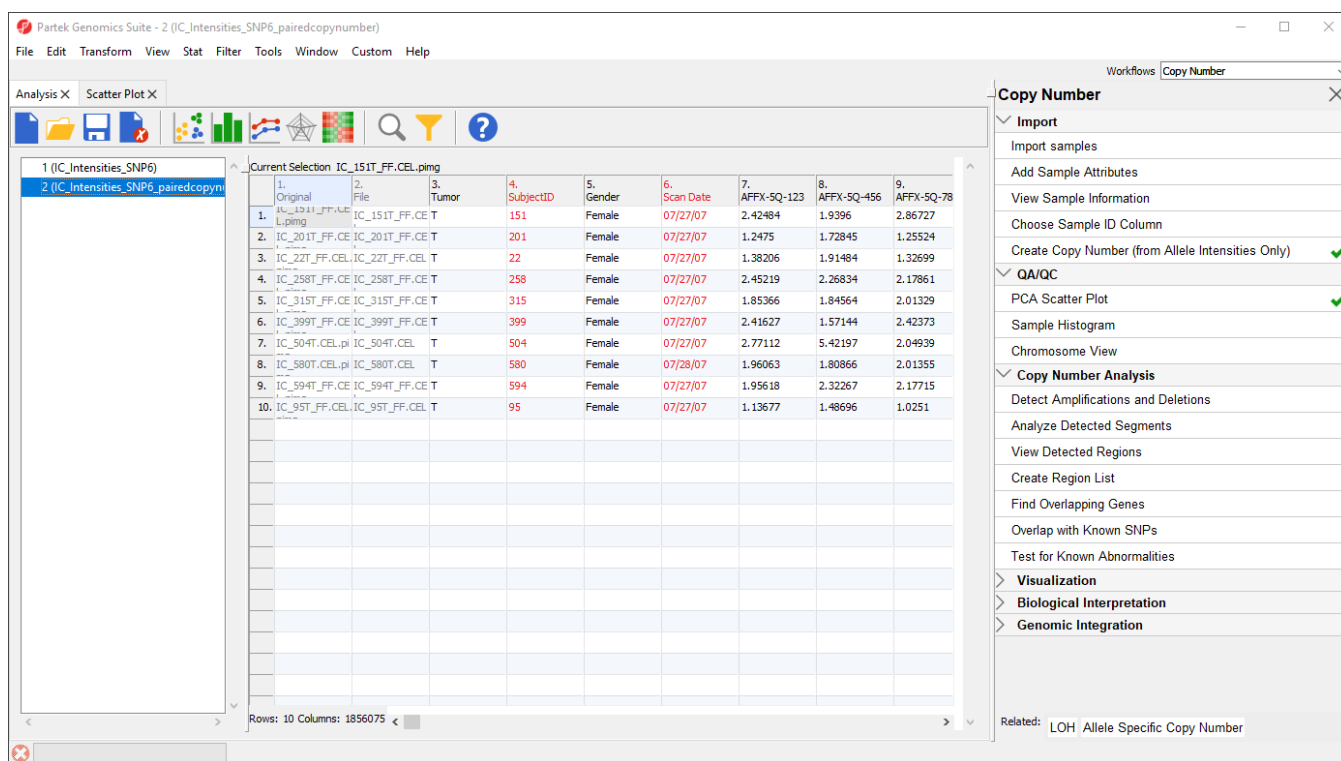



Figure 7. Viewing the paired copy number spreadsheet

Create Copy Number from Reference Baseline

Alternatively, if paired samples are not available or appropriate, the *Unpaired samples* option can be selected in the *Copy Number Creation* dialog (Figure 1). Selecting this option opens the *Unpaired Copy Number* dialog (Figure 4).


Unpaired Copy Number
✕

This operation will analyze the intensity spreadsheet to generate a copy number spreadsheet and allele ratio spreadsheet.

Specify a reference to use when creating copy number

☒ Use an existing reference file (.cnmodel)

Browse...

☐ Use Partek distributed baseline
 ?

☐ Use all samples in the spreadsheet

Spreadsheet

1 (IC_Intensities_SNP6) ▾

☐ Use only reference samples from spreadsheet

Spreadsheet

1 (IC_Intensities_SNP6) ▾

 Reference column

3. Tumor ▾

 Reference value

N ▾

Results

Specify the output files that will be created when creating copy number and allele ratio from spreadsheet "1 (IC_Intensities_SNP6)"

Copy number result

Browse...
?

Allele ratio result

Browse...
?

OK
Cancel




Figure 8. Viewing the unpaired copy number dialog

There are several options for creating a reference baseline. First, you can use an existing reference file. These may be distributed by the manufacturer of your array, such as Affymetrix or Illumina, or previously created using Partek Genomics Suite from a set of normal samples. Second, you can use the reference file distributed by Partek. Third, you can choose all the samples from a separately imported spreadsheet. Fourth, you can choose a subset of the samples within the current spreadsheet to pool to create a reference.

In each case, every sample in your spreadsheet will be compared to the referece and two spreadsheets will be generated, a copy number spreadsheet and an allele ratio spreadsheet.

For more information about using unpaired samples in copy number calculations, please consult our [Unpaired Copy Number Estimation](#) white paper.

[« Exploring the data with PCA](#) [Detecting regions with copy number variation »](#)

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