MIP CN Transformation

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Overview

This script creates 5 transposed spreadsheets, one for each column imported from the MIP Array copy number text file: **Copy A**, **Copy B**, **CopyNumber**, **AlleleRatio**, and **AllelicDifference**

Recommended Directory Location

Save the script to the following directory:
*..**\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Edit**

Note: The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between XP and Vista. The easiest way to locate this directory on your computer is to open SVS and go to **Tools >Open Folder > UserScripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Edit** menu.

Importing Affymetrix MIP Copy Number Data and Applying Marker Map

Before you can run this script you'll need to import your Affymetrix MIP copy number data. This file comes as a standard text file and can be imported using the Text Importer in SVS. To do this:

1. Open an existing project or create a new one.
2. Go to **Import >Text**.
3. Select the **MIP Copy Number text file** and choose **Tab Delimited** for file format.
4. Under the **Advanced Options** tab you need to insert **NA** as a **Custom encoding** for missing values (Figure 1). Click **OK** to finish.
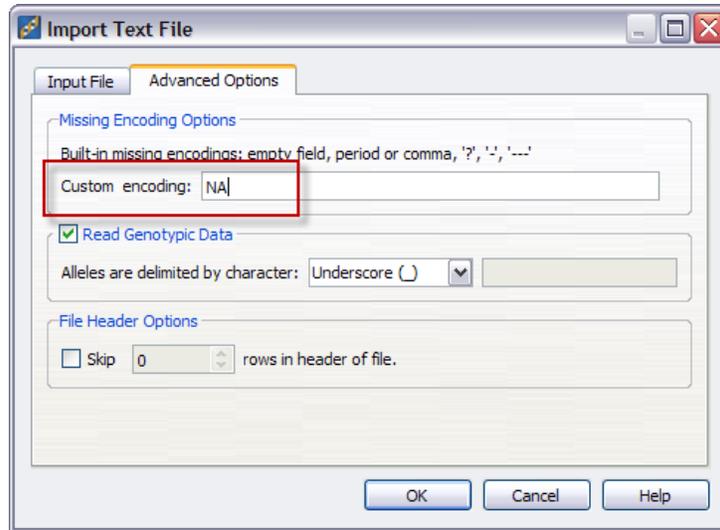
Figure 1: MIP data uses 'NA' as the encoding for missing data.
This needs to be specified in the Import Text File Dialog.

The spreadsheet created upon import should have sample identifiers as column headers and MIP probes as rows, where there are different columns of data for each sample, these columns could be: **Copy A**, **Copy B**, **CopyNumber**, **AlleleRatio**, and **AllelicDifference** (Figure 2).

Figure 2: MIP Copy number spreadsheet.

5. Before using the script you will need to apply a MIP Array marker map to the spreadsheet. If you have not already done so, you can download the MIP Marker Map.dsm file from the same web page as the MIP CN Data Transformation script.

   Save the MIP **Marker Map.dsm** file in your Marker Maps directory. To get to this

directory go to the **Project Navigator** and select **Tools >Genetic Marker Maps** and then click the **View MarkerMaps Folder** button.

6. To apply the marker map, from the **MIP Copy Number Dataset** spreadsheet, select **File >Apply Genetic Marker Map**. Select the **MIP Marker** Map. Make sure to choose **Row Labels** under **Marker Names Are**. Click **OK** to finish.

    You'll be asked which map fields (or annotations) you would like to see by default. Select all and click **OK**.

When the software is finished applying the marker map, you will get a new spreadsheet denoted as a green icon in the Project Navigator. There will also be a green **Map** button in the upper-left hand corner of the spreadsheet itself. Click this button if you wish to see the annotations for a given marker.

Using the Script

1. From the mapped **MIP Copy Number Dataset** spreadsheet, select **Edit >MIP CN Transformation**.

Upon completion, five new spreadsheets will be created.