# Export BEAGLECALL Allele Signals

**Author:** Christophe Lambert, Golden Helix, Inc.

## Overview

This script will run from a marker-mapped spreadsheet with rows as sample pairs and columns with allele intensities. There will be two rows for each sample, one with A intensities and one with B intensities. You could obtain this spreadsheet (or two spreadsheets in the Affymetrix 500K array scenario) by checking the appropriate output options during the CEL import process. If you import CEL files from the 500K array, you will need to transpose the NSP and STY Quantile Normalized spreadsheets, then merge and apply a marker map to the merged spreadsheet. For any other array you will still need to transpose and apply a marker map. The script will then prompt the user for an output directory and export the allele signals for all chromosomes suitable for BEAGLECALL. [**Note**: BEAGLECALL does not work on male X or on Y.]

http://www.stat.auckland.ac.nz/~bbrowning/beagle/beagle.html

## Recommended Directory Location

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

**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 select the **Tools >Open Folder > UserScripts Folder** menu option. If saved to the proper folder, this script will be accessible from the spreadsheet **File** menu.

## Using the Script

Use on data from the Affymetrix 500K array:

1. Open the **Quantile Normalized – NSP** and the **Quantile Normalized – STY** spreadsheets generated during the CEL file import process.
2. Transpose each spreadsheet by selecting **Edit > Transpose Spreadsheet**.
3. Now merge these spreadsheets by choosing **File > Join or Merge Spreadsheets** from one spreadsheet' menu bar and when prompted, select the other in the merge options window.
4. If a marker map is not applied during the import, apply a marker map. **File > Apply Genetic Marker Map**. Choose the appropriate map. Also you should inactive the non-autosomal markers. **Select >Activate by Chromosomes** and uncheck **X**.

Use on data from other arrays:

5. Open the **Quantile Normalized** spreadsheet generated during the CEL file import process.
6. Transpose the spreadsheet by selecting **Edit > Transpose Spreadsheet**.
7. Now apply a marker map. **File > Apply Genetic Marker Map**. Choose the appropriate map. Also you should inactive the non-autosomal markers. **Select >Activate by Chromosomes** and uncheck **X**.

Your spreadsheet should look similar to Figure 1.

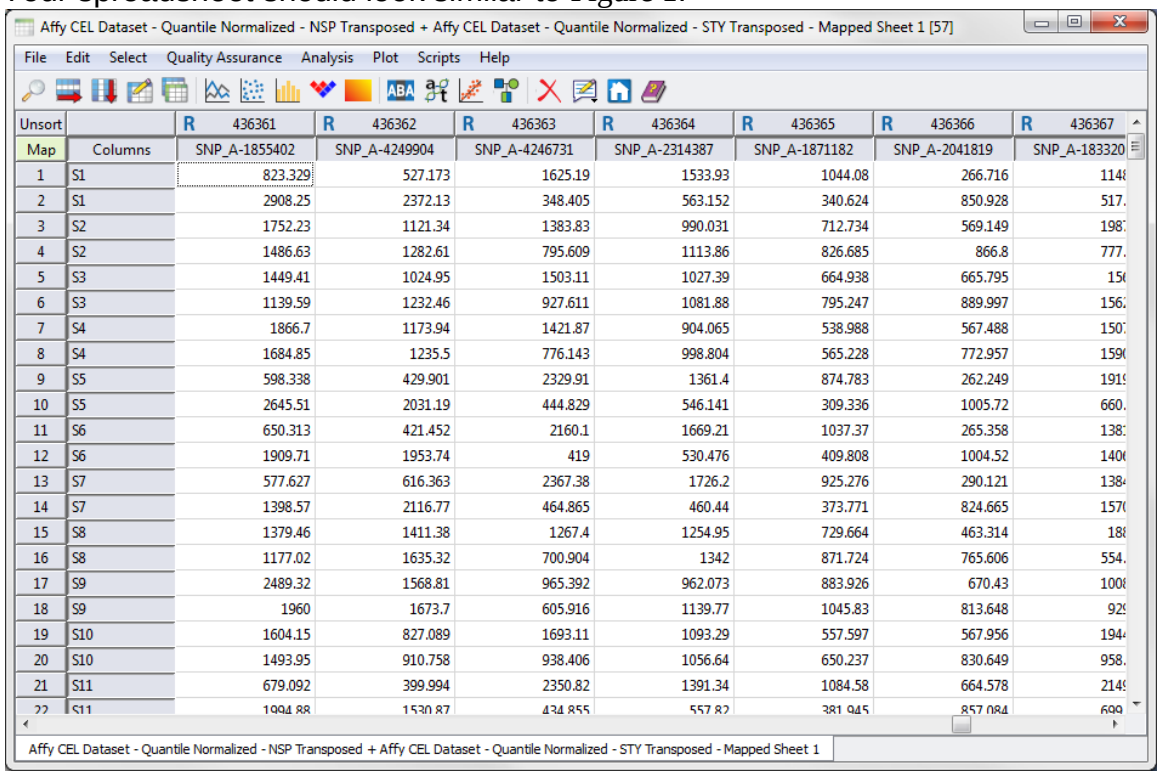


**Figure 1 Transposed, Merged and Mapped Allele Frequency Spreadsheet**

8. Now run the script. **File >Export BEAGLECALL Allele Signals**.
9. Give the file a name, browse to a folder where you want the file saved, and click **Save**.

Upon completion, 22 separate .signals files will saved in the folder you indicated, assuming the file you began with consisted of data from all chromosomes.