

## Recode Affymetrix Genotypes

**Author: Jesse Dupre, Golden Helix, Inc.**

### Overview

This script will look at an open spreadsheet of Affymetrix genotype data and recode the genotypes from A's and B's to A's, G's, T's, and C's. The script uses Affymetrix annotations files to recode the genotype calls; if the spreadsheet contains SNPs that are not present in the selected annotations files, the SNPs will remain encoded with the general A/B alleles. Supported SNP sets include 10k, 100k, 500k, 5.0, and 6.0.

### Recommended Directory Location

A good directory location for saving this script at would be:

**C:/HelixTree/scriptsHT/user/Spreadsheet/Edit/.**

When saved to this folder, the script will be accessible from the spreadsheet edit menu.

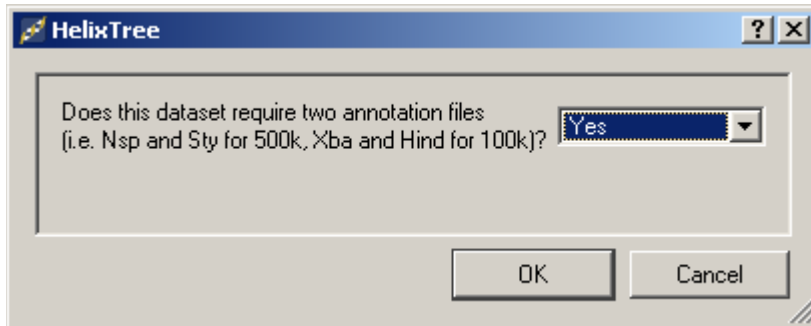
### Using the Script

Open a spreadsheet containing Affymetrix genotype data.

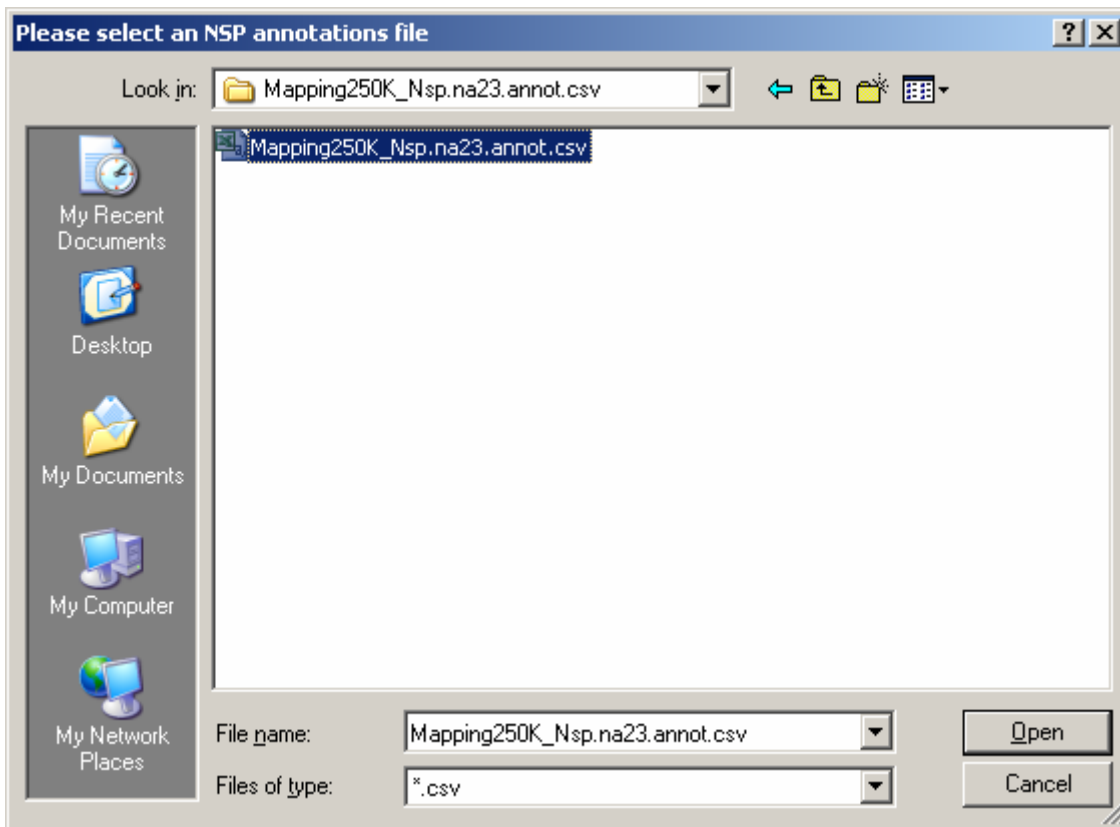
Unsort	Labels	G 1	G 2	G 3	G
		SNP_A-1855402	SNP_A-4249904	SNP_A-2174835	SNP_
1	NA10851_Sty-NA10851_Nsp	B_B	B_B	A_A	
2	NA10855_Sty-NA10855_Nsp	B_B	B_B	A_A	
3	NA10863_Sty-NA10863_Nsp	B_B	B_B	A_A	
4	NA11831_Sty-NA11831_Nsp	B_B	B_B	A_A	
5	NA11832_Sty-NA11832_Nsp	B_B	B_B	A_A	
6	NA12056_Sty-NA12056_Nsp	B_B	B_B	A_A	
7	NA12057_Sty-NA12057_Nsp	B_B	B_B	A_A	
8	NA12234_Sty-NA12234_Nsp	A_B	A_B	A_B	
9	NA12264_Sty-NA12264_Nsp	B_B	B_B	A_A	
10	NA12707_Sty-NA12707_Nsp	B_B	B_B	A_A	
11	NA12716_Sty-NA12716_Nsp				

Select the Recode Affy Genotypes script from the spreadsheet menu location where it was stored. Or, from the project viewer, select **Tools->Run Script** to open a dialog to browse for the script location.

You will be asked if the dataset will require two annotation files, which would be the case if you were analyzing the full 100k and 500k array sets. If you have SNPs from both arrays, select **Yes**. If you only have data from one of the 50k or 250k arrays, or if you have 10k, 5.0, or 6.0 data, select **No**.



You will be prompted for the location of the annotations files that should be used in the conversion -- these must be the raw Affymetrix annotation csv files. If you selected that the dataset requires two annotation files, you must select the locations of both. If you selected that the dataset does not require more than one annotation file, select the annotations file that is applicable for your dataset.



When the conversion has completed, a message box will appear stating the success of the conversion and the number of columns that were unable to be converted.

