

Export BEAGLECALL Genotype Probabilities

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Overview

You can use this script on a marker mapped spreadsheet that has rows as samples and genotype columns. Upon completion, 23 separate .gprobs files will be created, one for each active chromosome in the marker mapped spreadsheet.

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

Recommended Directory Location

Save the script to the following directory:

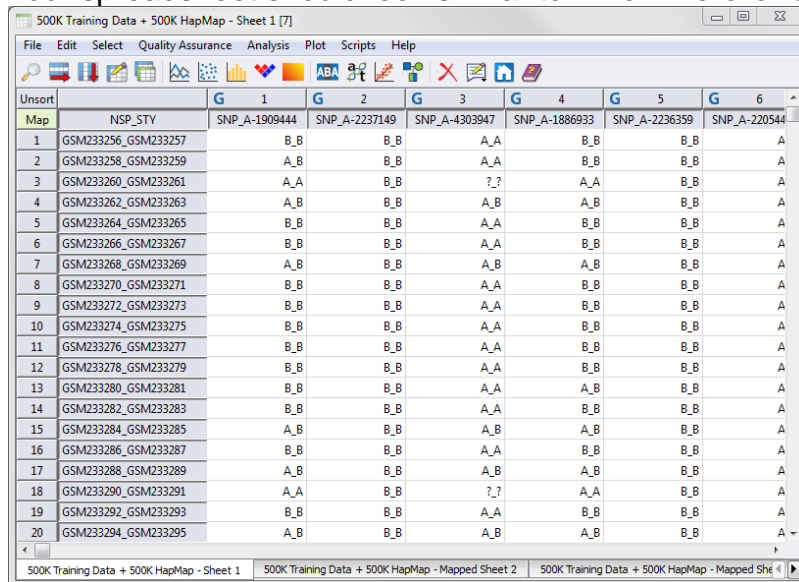
*..\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\File\

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

1. Open the marker mapped spreadsheet that matches the previous description.

Your spreadsheet should look similar to **Error! Reference source not found..**



The screenshot shows a spreadsheet titled "500K Training Data + 500K HapMap - Sheet 1 [7]". The spreadsheet has columns for "Map", "NSP_STY", and six chromosomes labeled "G 1" through "G 6". The rows represent 20 samples, each with a unique ID in the "NSP_STY" column and genotype calls in the "G" columns. The genotype calls are two-letter codes (e.g., "B_B", "A_A", "A_B", "B_B", "?_?") representing the alleles at each SNP position.

Map	NSP_STY	G 1	G 2	G 3	G 4	G 5	G 6
1	GSM233256_GSM233257	B_B	B_B	A_A	B_B	B_B	A
2	GSM233258_GSM233259	A_B	B_B	A_A	B_B	B_B	A
3	GSM233260_GSM233261	A_A	B_B	?_?	A_A	B_B	A
4	GSM233262_GSM233263	A_B	B_B	A_B	A_B	B_B	A
5	GSM233264_GSM233265	B_B	B_B	A_A	B_B	B_B	A
6	GSM233266_GSM233267	B_B	B_B	A_A	B_B	B_B	A
7	GSM233268_GSM233269	A_B	B_B	A_B	A_B	B_B	A
8	GSM233270_GSM233271	B_B	B_B	A_A	B_B	B_B	A
9	GSM233272_GSM233273	B_B	B_B	A_A	B_B	B_B	A
10	GSM233274_GSM233275	B_B	B_B	A_A	B_B	B_B	A
11	GSM233276_GSM233277	B_B	B_B	A_A	B_B	B_B	A
12	GSM233278_GSM233279	B_B	B_B	A_A	B_B	B_B	A
13	GSM233280_GSM233281	B_B	B_B	A_A	A_B	B_B	A
14	GSM233282_GSM233283	B_B	B_B	A_A	B_B	B_B	A
15	GSM233284_GSM233285	A_B	B_B	A_B	A_B	B_B	A
16	GSM233286_GSM233287	B_B	B_B	A_A	B_B	B_B	A
17	GSM233288_GSM233289	A_B	B_B	A_B	A_B	B_B	A
18	GSM233290_GSM233291	A_A	B_B	?_?	A_A	B_B	A
19	GSM233292_GSM233293	B_B	B_B	A_A	B_B	B_B	A
20	GSM233294_GSM233295	A_B	B_B	A_B	A_B	B_B	A

Figure 1 Genotype Spreadsheet

2. To run the script, choose **File >Export BEAGLECALL Allele Signals**.
3. Give the file a name, browse to a folder where you want the file saved, and click **Save**.

Upon completion, a separate .gprobs file for each active chromosome is saved in the specified folder.