

## Export BEAGLECALL Allele Signals

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### 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's 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 inactivate 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.

Map	Columns	R 436361	R 436362	R 436363	R 436364	R 436365	R 436366	R 436367
1	S1	823.329	527.173	1625.19	1533.93	1044.08	266.716	1144
2	S1	2908.25	2372.13	348.405	563.152	340.624	850.928	517
3	S2	1752.23	1121.34	1383.83	990.031	712.734	569.149	198
4	S2	1486.63	1282.61	795.609	1113.86	826.685	866.8	777
5	S3	1449.41	1024.95	1503.11	1027.39	664.938	665.795	150
6	S3	1139.59	1232.46	927.611	1081.88	795.247	889.997	156
7	S4	1866.7	1173.94	1421.87	904.065	538.988	567.488	150
8	S4	1684.85	1235.5	776.143	998.804	565.228	772.957	159
9	S5	598.338	429.901	2329.91	1361.4	874.783	262.249	191
10	S5	2645.51	2031.19	444.829	546.141	309.336	1005.72	660
11	S6	650.313	421.452	2160.1	1669.21	1037.37	265.358	138
12	S6	1909.71	1953.74	419	530.476	409.808	1004.52	140
13	S7	577.627	616.363	2367.38	1726.2	925.276	290.121	138
14	S7	1398.57	2116.77	464.865	460.44	373.771	824.665	157
15	S8	1379.46	1411.38	1267.4	1254.95	729.664	463.314	18
16	S8	1177.02	1635.32	700.904	1342	871.724	765.606	554
17	S9	2489.32	1568.81	965.392	962.073	883.926	670.43	100
18	S9	1960	1673.7	605.916	1139.77	1045.83	813.648	92
19	S10	1604.15	827.089	1693.11	1093.29	557.597	567.956	194
20	S10	1493.95	910.758	938.406	1056.64	650.237	830.649	958
21	S11	679.092	399.994	2350.82	1391.34	1084.58	664.578	214
22	S11	1004.88	1530.87	434.855	557.82	381.045	857.084	600

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 be saved in the folder you indicated, assuming the file you began with consisted of data from all chromosomes.