

## Import BEAGLE Allelic R2 Files

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### Overview

This script will allow you to import a non-compressed Beagle .r2 file, which contains the allelic R<sup>2</sup> imputation score for every marker. Scores range from 0 to 1. For more information see:

<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\SVS\Import\

**Note:** The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between versions. The easiest way to locate this directory on your computer is to open SVS and select the **Tools >Open Folder > User Scripts Folder** menu option. If saved to the proper folder, this script will be accessible from the project navigator **Import** menu.

### Using the Script

1. From an open project select **Import >Import Scripts >Import BEAGLE Allelic R2 Files**.
2. Select the Beagle .r2 file(s) to import.

The resulting spreadsheets have one row per marker and one column containing the R<sup>2</sup> values. If multiple files are imported simultaneously, they are appended together. Applying a marker map to the R<sup>2</sup> spreadsheet will sort the markers and place them in genomic order. To apply a marker map go to **File > Apply Genetic Marker Map** from the R<sup>2</sup> spreadsheet.