Import Minimac Output

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Overview

This script will import Minimac info and dose files with phased genotype dosages which are output from running the Minimac software. For more information on Minimac see:

http://genome.sph.umich.edu/wiki/Minimac

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 Minimac Output**

2. Select the *.info file(s) and optionally the *.dosage file(s). If dosage files are imported, the markers can be filtered based on R^2 values.

Two spreadsheets are created, one for the info file and the other containing the dosage data.