

Add Gene Names to Marker Map

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Overview

Adds the associated gene name(s) to each marker in a marker map.

Recommended Directory Location

Save the script to the following directory:

`*..\Application Data\Golden Helix SVS\UserScripts\SVS\Tools\`

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

Using the Script

1. Go to **Tools > Add Gene Names to Marker Map**.
2. Select the marker map in the marker maps folder that you want gene names added to.
3. Select the Gene Track from which the gene names will be obtained.
IMPORTANT: Make sure that the gene track uses the same reference build as the marker map. i.e. For an Affymetrix marker map version 30 use a gene track from the NCBI_36 build. For Affymetrix marker map version 31, use a gene track from the GRCh_37 build.
4. Select the gene name conflict resolution. This is the criteria used when there is more than one gene name associated with the marker's chromosome and position. The options are:
 - First: Use the first gene name in the list of gene names
 - Last: Use the last gene name in the list of gene names
 - Shortest: Use the shortest gene name
 - Longest: Use the longest gene name
 - All: Report all gene names
5. Click **OK** and the script will run. When the script completes successfully a message will be displayed indicating that a new marker map was created and saved in the marker maps folder. This new marker map will be immediately available for use.

To apply this marker map, open a spreadsheet and go to **File > Apply Marker Map**.