

Activate or Inactivate based on Genomic Position

Author: Autumn Laughbaum, Golden Helix, Inc.

Overview

This function activate or inactivate markers in the current spreadsheet based on existence in another spreadsheet's marker map or existence in an existing marker map file, or both. Matching is done based only on chromosome and position information from both sources and not on marker labels.

Recommended Directory Location

Save the script to the following directory:

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

Note: The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between XP, Vista, Windows7&8. 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 spreadsheet **Select** menu.

Using the Script

1. From a marker mapped spreadsheet, choose **Select >Activate or Inactivate based on Genomic Position**.
2. There are two options for the filtering criteria:
 - a. **Use another spreadsheet's attached marker map as criteria:** This would be applicable if, for example, you have data from two separate sources where markers are labeled differently (For one set markers are labeled with RS IDs and for the second set chr:position is used) and you would like to only look at markers in common between the two sets.
 - b. **Use a marker map file as criteria:** With this option you could select a marker map file directly instead of needing it applied to a separate spreadsheet. The marker map file must be saved in your User Marker Maps Folder to be accessible by this script. You can find this location by going to **Tools > Open Folder > Marker Maps Folder** from SVS.
- [**NOTE:** You could also apply both of these filters. In that case the second map and marker map file would both be included for activation/inactivation.]
3. Output Options:
 - a. You can choose to Activate or Inactivate markers that pass the specifications.
 - b. You can optionally create a subset spreadsheet.

Geno - Mapped Sheet 1 - Sheet 10 [84]

All: 100 x 5,001
Active: 100 x 1,974

Unsort		G 1	G 2	G 3	G 4	G 5	G 6	G 7	G 8	G ^
Map	Sample	Marker1	Marker2	Marker3	Marker4	Marker5	Marker6	Marker7	Marker8	
1	Sample1	C_C	A_A	G_T	C_C	A_C	C_C	T_T	C_G	
2	Sample2	C_G	A_A	G_T	C_C	?_?	C_C	G_T	G_G	
3	Sample3	C_G	A_A	?_?	C_C	A_A	C_C	G_T	C_G	
4	Sample4	C_C	?_?	G_G	C_C	C_C	C_C	G_T	C_C	
5	Sample5	C_G	A_A	G_T	C_C	C_C	C_C	T_T	C_C	
6	Sample6							?_?	C_C	
7	Sample7							G_G	C_C	
8	Sample8							G_T	C_G	
9	Sample9							T_T	C_C	
10	Sample10							?_?	C_C	
11	Sample11							G_T	G_G	
12	Sample12							G_G	G_G	
13	Sample13							G_T	C_G	

SVS Information

Filtering based on genomic position using genomic positions in spreadsheet
RefSeq Genes, UCSC Annotations - Row Subset [74]

1974 Columns Activated in spreadsheet

OK

The log message will appear as above, stating the selecting filtering options and the number of rows or columns that passed the criteria.