Create Pseudo Marker Mapped Spreadsheet

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Overview

From a non-marker mapped spreadsheet this script creates a new marker mapped spreadsheet with a pseudo marker map containing chromosome 1, positions 1 - # Active Columns or Active Rows. If it is desired to skip mapping certain columns (or rows), first inactivate these columns (or rows) in your non-marker-mapped spreadsheet.

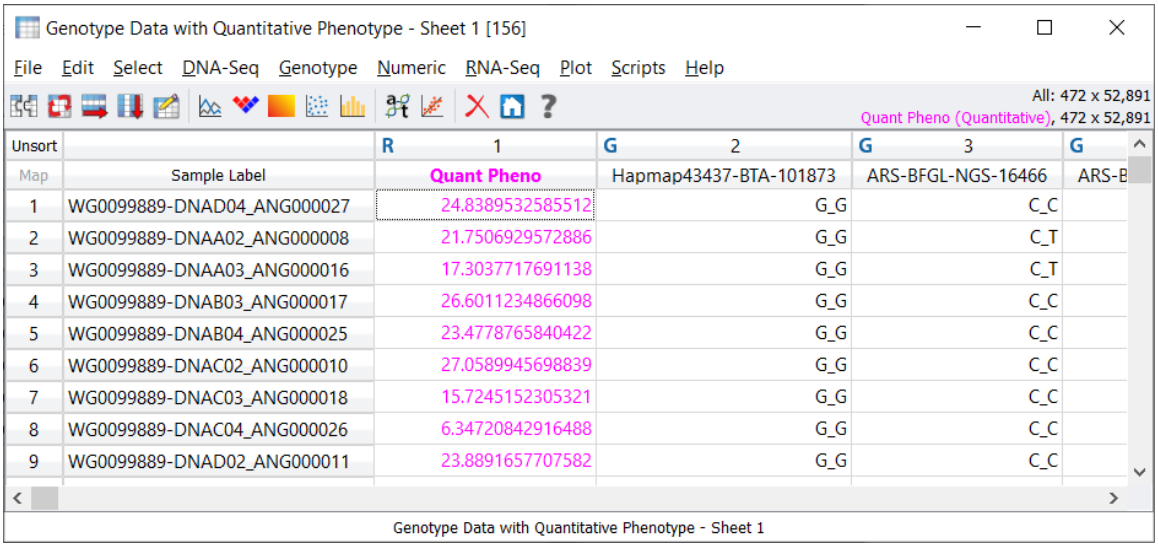
Recommended Directory Location

Save the script to the following directory:
*..**\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Scripts**

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 **Tools >Open Folder > UserScripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Scripts** menu.

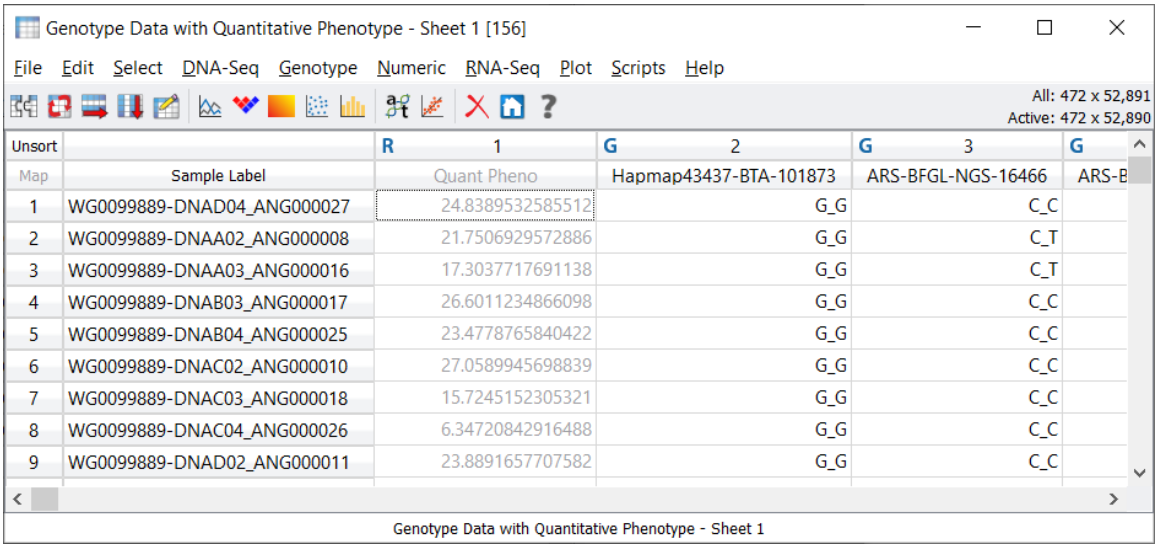
Using the Script

1. Open the non-marker mapped spreadsheet.

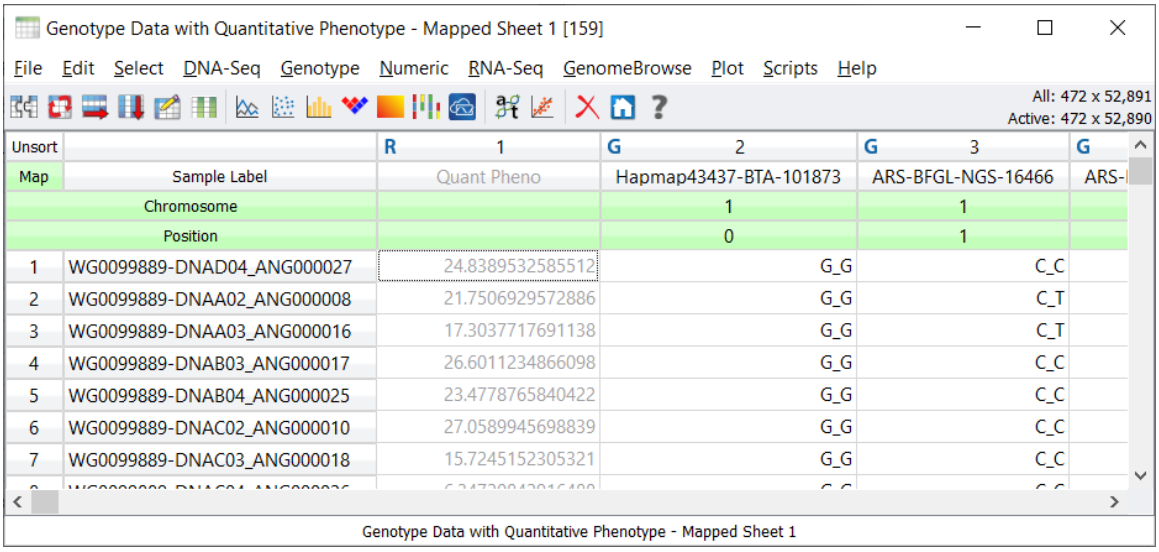


Unsort		R 1	G 2	G 3	G
Map	Sample Label	Quant Pheno	Hapmap43437-BTA-101873	ARS-BFGL-NGS-16466	ARS-B
1	WG0099889-DNAD04_ANG000027	24.8389532585512	G_G	C_C	
2	WG0099889-DNAA02_ANG000008	21.7506929572886	G_G	C_T	
3	WG0099889-DNAA03_ANG000016	17.3037717691138	G_G	C_T	
4	WG0099889-DNAB03_ANG000017	26.6011234866098	G_G	C_C	
5	WG0099889-DNAB04_ANG000025	23.4778765840422	G_G	C_C	
6	WG0099889-DNAC02_ANG000010	27.0589945698839	G_G	C_C	
7	WG0099889-DNAC03_ANG000018	15.7245152305321	G_G	C_C	
8	WG0099889-DNAC04_ANG000026	6.34720842916488	G_G	C_C	
9	WG0099889-DNAD02_ANG000011	23.8891657707582	G_G	C_C	

2. Inactivate any columns (or rows) you wish to remain unmapped.

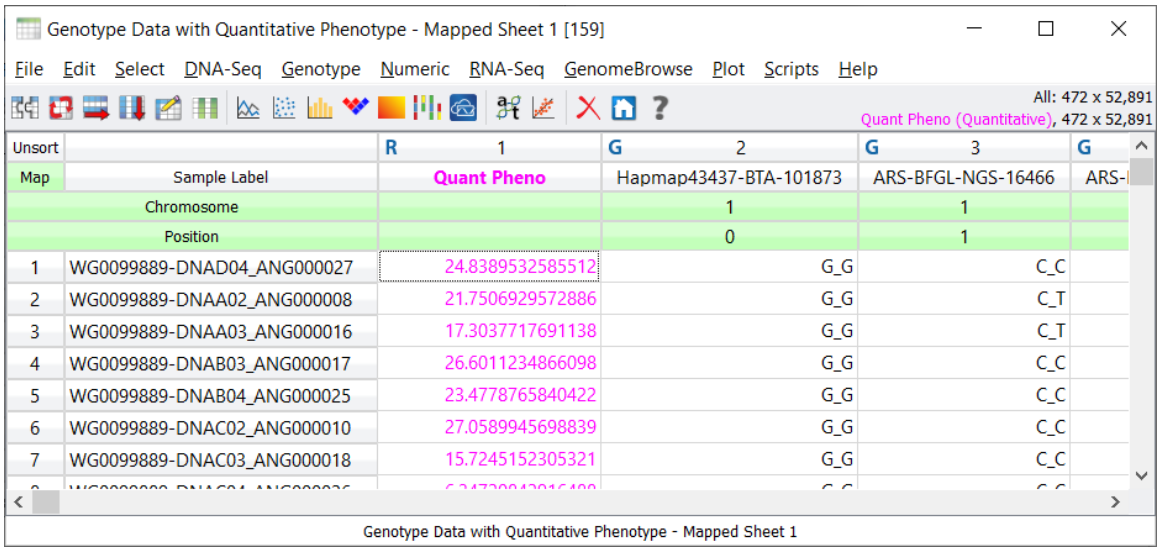


3. Select **Scripts >Create Pseudo Marker Mapped Spreadsheet**.
4. Choose whether you want to create the genetic marker map based on **Active Column Headers** or **Active Row Labels**. For the example above, Active Column Headers would be appropriate.
5. Click **OK**. A new marker mapped spreadsheet with a pseudo marker map containing chromosome 1, positions 1 - #Active Columns or Active Rows will result.



6. In the new spreadsheet, re-activate (or make dependent) all columns (or rows) for which mapping was skipped over.

The final result will look like your original spreadsheet with the proper columns (or rows) containing the pseudo marker map.


Genotype Data with Quantitative Phenotype - Mapped Sheet 1 [159]
File Edit Select DNA-Seq Genotype Numeric RNA-Seq GenomeBrowse Plot Scripts Help
All: 472 x 52,891
Quant Pheno (Quantitative), 472 x 52,891
Unsort
R 1
G 2
G 3
G
Map
Sample Label
Quant Pheno
Hapmap43437-BTA-101873
ARS-BFGL-NGS-16466
ARS-
Chromosome
1
1
Position
0
1
1 WG0099889-DNAD04_ANG000027 24.8389532585512 G_G C_C
2 WG0099889-DNAA02_ANG000008 21.7506929572886 G_G C_T
3 WG0099889-DNAA03_ANG000016 17.3037717691138 G_G C_T
4 WG0099889-DNAB03_ANG000017 26.6011234866098 G_G C_C
5 WG0099889-DNAB04_ANG000025 23.4778765840422 G_G C_C
6 WG0099889-DNAC02_ANG000010 27.0589945698839 G_G C_C
7 WG0099889-DNAC03_ANG000018 15.7245152305321 G_G C_C
Genotype Data with Quantitative Phenotype - Mapped Sheet 1