## **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.

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59 E	「 🎛 😅 💵 👔 🗠 🥗 📕 🔠 🔟 🔐 🤾 🔀 了 ?							All: 472 x 52,891 Quant Pheno (Quantitative), 472 x 52,891					
Unsort		R	1	G	2		G	3	G	^			
Мар	Sample Label	Qı	iant Pheno	Hapma	p43437-BTA-	101873	ARS-BFGL-N	GS-16466	ARS-	B			
1	WG0099889-DNAD04_ANG000027	2	4.8389532585512			G_G		C_C					
2	WG0099889-DNAA02_ANG000008	2	1.7506929572886			G_G		C_T					
3	WG0099889-DNAA03_ANG000016	1	7.3037717691138			G_G		C_T					
4	WG0099889-DNAB03_ANG000017	2	6.6011234866098			G_G		C_C					
5	WG0099889-DNAB04_ANG000025	2	3.4778765840422			G_G		C_C					
6	WG0099889-DNAC02_ANG000010	2	7.0589945698839			G_G		C_C					
7	WG0099889-DNAC03_ANG000018	1	5.7245152305321			G_G		C_C					
8	WG0099889-DNAC04_ANG000026	6	.34720842916488			G_G		C_C					
9	WG0099889-DNAD02_ANG000011	2	3.8891657707582			G_G		C_C					
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	Genotype Data with Quantitative Phenotype - Sheet 1												

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

Genotype Data with Quantitative Phenotype - Sheet 1 [156]							-		×
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54	2 🚎 💵 🛃 🕍 🥗 💶 🗟 🔟	३१ 🗷	× 🖬 ?					All: • Active: •	472 x 52,891 472 x 52,890
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Мар	Sample Label	Q	uant Pheno	Hapma	p43437-BTA-1	01873	ARS-BFGL-NG	S-16466	ARS-B
1	WG0099889-DNAD04_ANG000027	2	4.8389532585512			G_G		C_C	
2	WG0099889-DNAA02_ANG000008	2	1.7506929572886	5		G_G		C_T	
3	WG0099889-DNAA03_ANG000016	1	7.3037717691138	3		G_G		C_T	
4	WG0099889-DNAB03_ANG000017	2	6.6011234866098	3		G_G		C_C	
5	WG0099889-DNAB04_ANG000025	2	3.4778765840422	2		G_G		C_C	
6	WG0099889-DNAC02_ANG000010	2	7.0589945698839	)		G_G		C_C	
7	WG0099889-DNAC03_ANG000018	1	5.7245152305321			G_G		C_C	
8	WG0099889-DNAC04_ANG000026	6	.34720842916488	3		G_G		C_C	
9	WG0099889-DNAD02_ANG000011	2	3.8891657707582	2		G_G		C_C	~
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		Genotyp	e Data with Quantita	ative Phenot	type - Sheet 1				

- 3. Select Scripts >Create Pseudo Marker Mapped Spreadsheet.
- 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.

Genotype Data with Quantitative Phenotype - Mapped Sheet 1 [159]								_		×	
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54 <b>t</b>	2 📪 🕕 😭 🎟 🔛 🔤 🗰 💙		🗟 🛱 🗷	X	<b>D</b> 7	?			All: 4 Active: 4	72 x 52, 72 x 52,	,891 ,890
Unsort		R	1		G	2		<b>G</b> 3		G	^
Мар	Sample Label	Qu	uant Pheno		Hapn	map43437-E	3TA-101873	ARS-BFGL-NG	S-16466	ARS-	
	Chromosome					1		1			
	Position					0		1			
1	WG0099889-DNAD04_ANG000027	2	4.838953258	5512			G_G		C_C		
2	WG0099889-DNAA02_ANG000008	2	1.750692957	2886			G_G		C_T		
3	WG0099889-DNAA03_ANG000016	1	7.303771769	1138			G_G		C_T		
4	WG0099889-DNAB03_ANG000017	2	6.601123486	6098			G_G		C_C		
5	WG0099889-DNAB04_ANG000025	2	3.477876584	0422			G_G		C_C		
6	WG0099889-DNAC02_ANG000010	2	7.058994569	8839			G_G		C_C		
7	WG0099889-DNAC03_ANG000018	1	5.724515230	5321			G_G		C_C		
C			2472004204	C 400			~ ~		~ ~	>	~
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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]								- 🗆	×	<	
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All: 472 x 52,8 All: 472 x 52,										,891 ,891	
Unsort		R	1	G	2		<b>G</b> 3		G	^	
Мар	Sample Label		Quant Pheno	Ha	pmap43437-B	TA-101873	ARS-BFGL-N	GS-16466	ARS	-	
	Chromosome				1		1				
	Position				0		1				
1	WG0099889-DNAD04_ANG000027		24.8389532585512	2		G_G		C_C			
2	WG0099889-DNAA02_ANG000008		21.7506929572886	5		G_G		C_T			
3	WG0099889-DNAA03_ANG000016		17.3037717691138	3		G_G		C_T			
4	WG0099889-DNAB03_ANG000017		26.6011234866098	3		G_G		C_C			
5	WG0099889-DNAB04_ANG000025		23.4778765840422	2		G_G		C_C			
6	WG0099889-DNAC02_ANG000010		27.0589945698839	9		G_G		C_C			
7	WG0099889-DNAC03_ANG000018		15.7245152305321			G_G		C_C			
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	Genotype Data with Quantitative Phenotype - Mapped Sheet 1										