Rename Genotypes

Author: Autumn Laughbaum, Golden Helix, Inc.

Overview

This script scans the genotypic columns to find all existing genotypes, and then prompts for replacements. The resulting spreadsheet has the same dimensions with the appropriate genotype substitutions.

Recommended Directory Location

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

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 **Edit >Recode** submenu.

Using the Script

1. Open a spreadsheet that contains several genotypic columns and choose **Edit >Recode >Rename Genotypes**
2. The script will scan all active genotypic columns in the spreadsheet. This step may take some time.
3. Enter a genotype replacement after each genotype in the list of the genotypes found. Click **OK**.

The resulting spreadsheet will be a child node of the original spreadsheet and will contain the same active dimensions. All genotypic columns have the appropriate genotype substitutions.