

## MAF Filtering on Recoded Spreadsheet

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### Overview

This script calculates minor allele frequency (MAF) on recoded data created by Recode Genotypes with X Chromosome Adjustment.

This script requires a marker mapped spreadsheet with several integer columns and a binary or categorical Sex column. If the Sex column is binary, 0 represents Males and 1 represents Females. The first letter of the value in a categorical column is used, i.e. both male and M could represent a male sample.

### Recommended Directory Location

Save the script to the following directory:

\*..\Application Data\Golden Helix  
SVS\UserScripts\Spreadsheet\Genotype\Quality\_Assurance

**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's **Genotype > Quality Assurance and Utilities** submenu.

### Using the Script

1. Open a spreadsheet containing several mapped integer columns and a sex column (created by Recode Genotypes with X Chromosome Adjustment).
2. Choose **Genotype > Quality Assurance and Utilities > MAF Filtering on Recoded Spreadsheet**.
3. Enter an appropriate MAF threshold and direction. Then choose a binary or categorical Sex column and specify any additional chromosomes (default X) that should be adjusted. Click **OK**.

A detailed results spreadsheet is created as a child node of the original spreadsheet. This results spreadsheet had a column contain the calculated MAF and a binary column indicating whether or not the column was inactivated (or passed the threshold).