

Alternate Allele Frequency

Author: Mike Thiesen, Golden Helix, Inc.

Overview

This script calculates the percentage of alternate alleles over all samples for each variant. The spreadsheet is expected to have samples as rows and a marker map applied to its columns. The marker map must contain a reference base field.

The resulting spreadsheet has variants as rows and the marker map applied rowwise. The spreadsheet has columns containing the reference count, alternate allele, alternate allele frequency, reference allele count and alternate allele count. Optionally, an annotation probe track (IDF) can be created.

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 a marker mapped spreadsheet containing genotypic columns. Make sure that the marker map contains the reference base.
2. Select **Scripts >Alternate Allele Frequency**.
3. Choose the correct **Reference Allele Field**. If you would like to save as an annotation track, Check **Save to IDF** and enter a file name, track name and build information. See Figure 1.

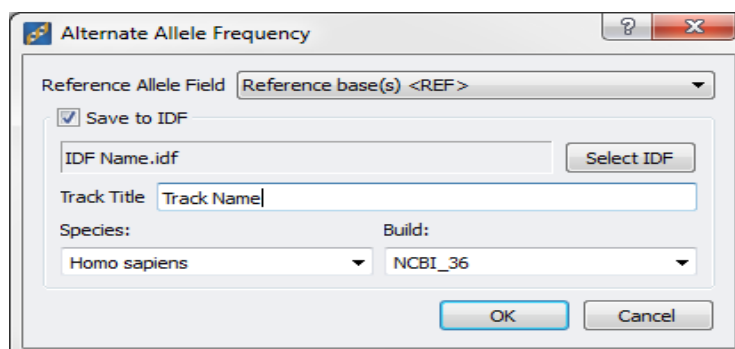


Figure 1: Alternate Allele Frequency Options