Build Variant Spreadsheet

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Overview

This tool builds a variant spreadsheet based on a probe track and region definition selected by the user. By default, the entire track is included in the output spreadsheet.

Recommended Directory Location

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

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 go to **Tools >Open Folder > UserScripts Folder**. If saved to the proper folder, this script will be accessible from the project navigator's **Tools** menu.

Region Definition

Leaving the default * in the region definition text box will result in the entire annotation track being included in the spreadsheet. A smaller region can be defined as a single chromosome, a region within a chromosome, several chromosomes or a region that spans several chromosomes. 'Chr' or 'chr' may be included before the chromosome. The examples below are all accepted as region definition input.

- Chr1, chr1, 1
- Chr1:1-10000, 1:10000-99999
- chr1-10, 1-10
- Chr5:12345-X:99999, 1:1-10:99999, 10:11111-X

Using the Script

1. Open a project and choose **Tools >Build Variant Spreadsheet**.
2. Choose an annotation track and a region as described above. Click **OK**.
3. In the next dialog, choose the following:
   - How to define column headers, either Chr:Pos or categorical field in track.
   - Optionally flip alleles based on strand field (strand values of '-', 'bot', 'minus' result in the alleles being flipped).
   - Choose whether alleles are found in one field in track or two fields
     - If one field, choose field and allele delimiter
     - If two fields, choose reference and alternate allele fields

The resulting spreadsheet has two rows, one containing the homozygous reference call and another containing the homozygous alternate call.