Calculate Alt Read Ratio between Two Spreadsheets
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Overview

This tool calculates the ratio of alternate read given an alternate read and reference read spreadsheet. The resulting spreadsheet contains the per-cell ratio as (Alt Depth)/(Alt Depth + Ref Depth) and can be used for filtering purposes with Set Genotypes to No-Call.

Recommended Directory Location

Save the script to the following directory:
For SVS 8.0.0+
..\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\DNA_Seq*

For SVS 7.7.8 and earlier releases
..\Application Data\Golden Helix SVS\User Scripts\Spreadsheet\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 go to **Tools > Open Folder > User Scripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet's **DNA-Seq** or **Quality Assurance** menu depending on the version of SVS being used.

Using the Script

1. From a spreadsheet containing numeric read counts for the alternate allele, choose (for SVS 7)
   Quality Assurance >Calculate Alt Read Ratio between Two Spreadsheets
   or choose (for SVS8)
   DNA-Seq > Calculate Alt Read Ratio between Two Spreadsheets
2. In the prompt, choose the spreadsheet containing numeric read counts for the reference allele.

The resulting spreadsheet contains the percentage of alternate reads over total reads (alt + ref) for each spreadsheet cell (sample-marker pair).
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