Illumina Multiple Final Report File Import

Author: Greta Peterson and Hauwa Yusuf, Golden Helix, Inc.

Overview

This script is designed to automate the import and merging of multiple Illumina Final Report files.

Recommended Directory Location

Save the script to the following directory:

*..\Application Data\Golden Helix SVS\UserScripts\SVS\Import\Illumina\

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 project navigator's **Import > Illumina** menu.

Using the Script

 From the project navigator, choose Import >Illumina >Illumina Multiple Final Report File Import. Select the appropriate files, the file delimiter and indicate how the files are grouped. Enter your preferred Dataset Name and whether to keep or remove the intermediate spreadsheets. Then click Next >.

🕈 Illumina Multi File Import Wrapp	er	? <mark>×</mark>
Choose the Illumina Final Report Files to import		
FinalReportFile1.txt FinalReportFile2.txt		Add Directory
Select file delimiter:	Tab delimited	•
Indicate how files are grouped:	By SNP	
	By Sample	
Dataset name	Illumina Final Report Files	
Remove Intermediate Spreadsheets?	Yes	
	© No	
NOTE: It is assumed that all final report files are in the same format, column order, grouping, delimiter, etc. If this is not the case results cannot be guaranteed. NOTE: It is assumed that all final report files are in the same format, column order, grouping, delimiter, etc. If this is not the case results cannot be guaranteed. Next > Cancel		

2. On the next dialog select the column that represents your sample and SNP IDs and Click **OK**.

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Select a sample id column: Select a SNP id column:	Sample ID
ОК	Cancel

3. On the next dialog select which fields from the file to import. If you are importing any of the Allele fields you can also pre-filter the data by GC score at the top of the dialog.

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]			
	Use GC Score threshold	No			
	Enter GC Score Threshold	0			
	Alleles Forward	No			
	Alleles AB	No			
	Alleles Top	Yes 🔻			
	x	No			
	Y	No			
	B Allele Freq	Yes 🔻			
	Log R Ratio	Yes 🔻			
	OK Cancel				

4. Click **OK** to import and merge the files.