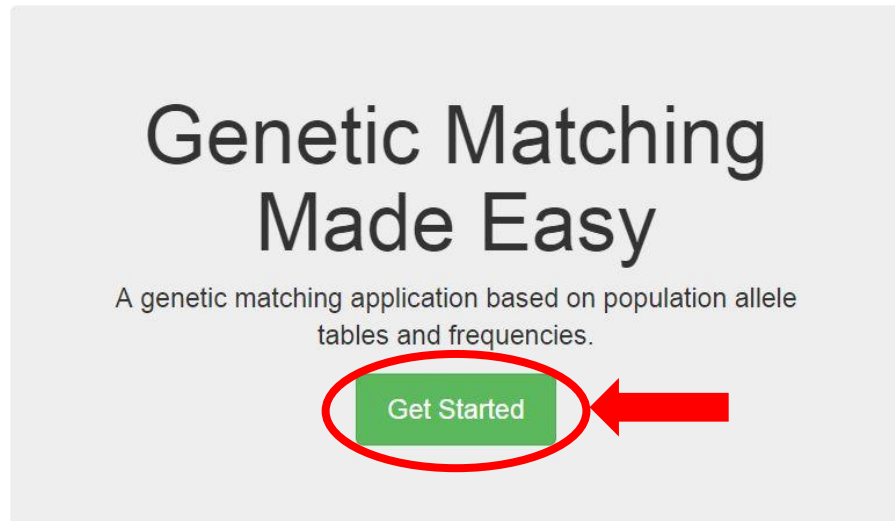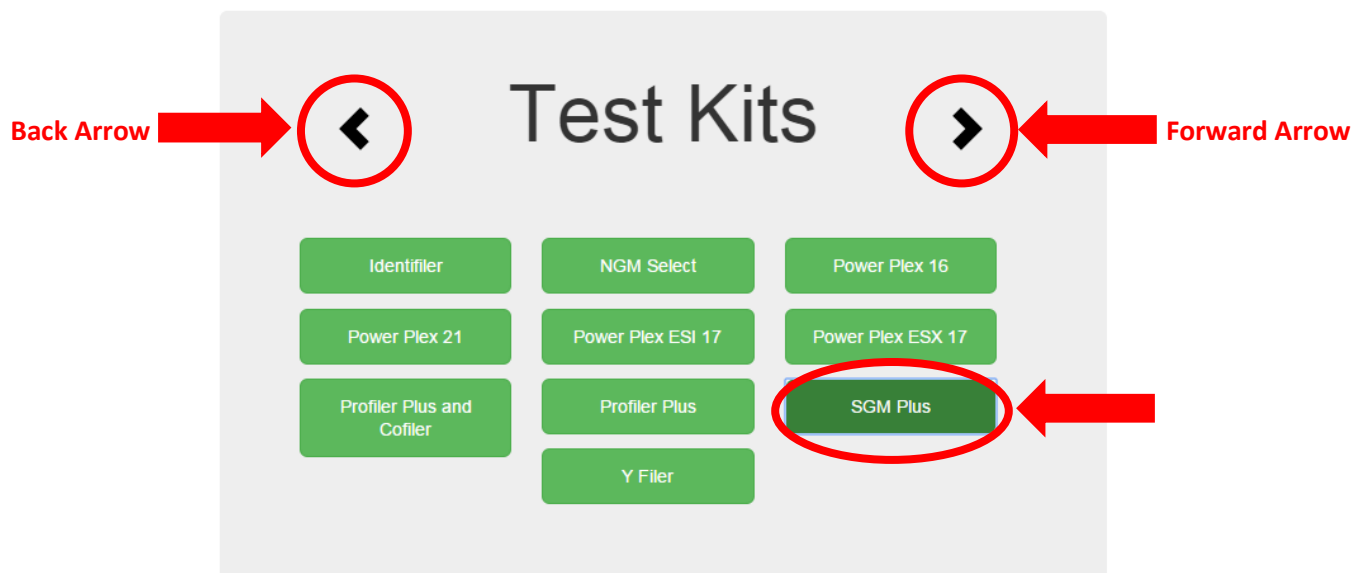# Statopus Tutorial

**Step 1:** Click the "Get Started" button to start the program.

Step 2: Choose the test kit used on the genetic profile by clicking on the button containing the correct test kit name. In the example below, the SGM Plus test kit was chosen

After you have selected the test kit, click the forward arrow to move on.

At any time in the process, you can click the back arrow to return to previous screens.

If you're working from a GeneMapper electropherogram like the one pictured below, often the test kit name can be found under the "Panel" heading.
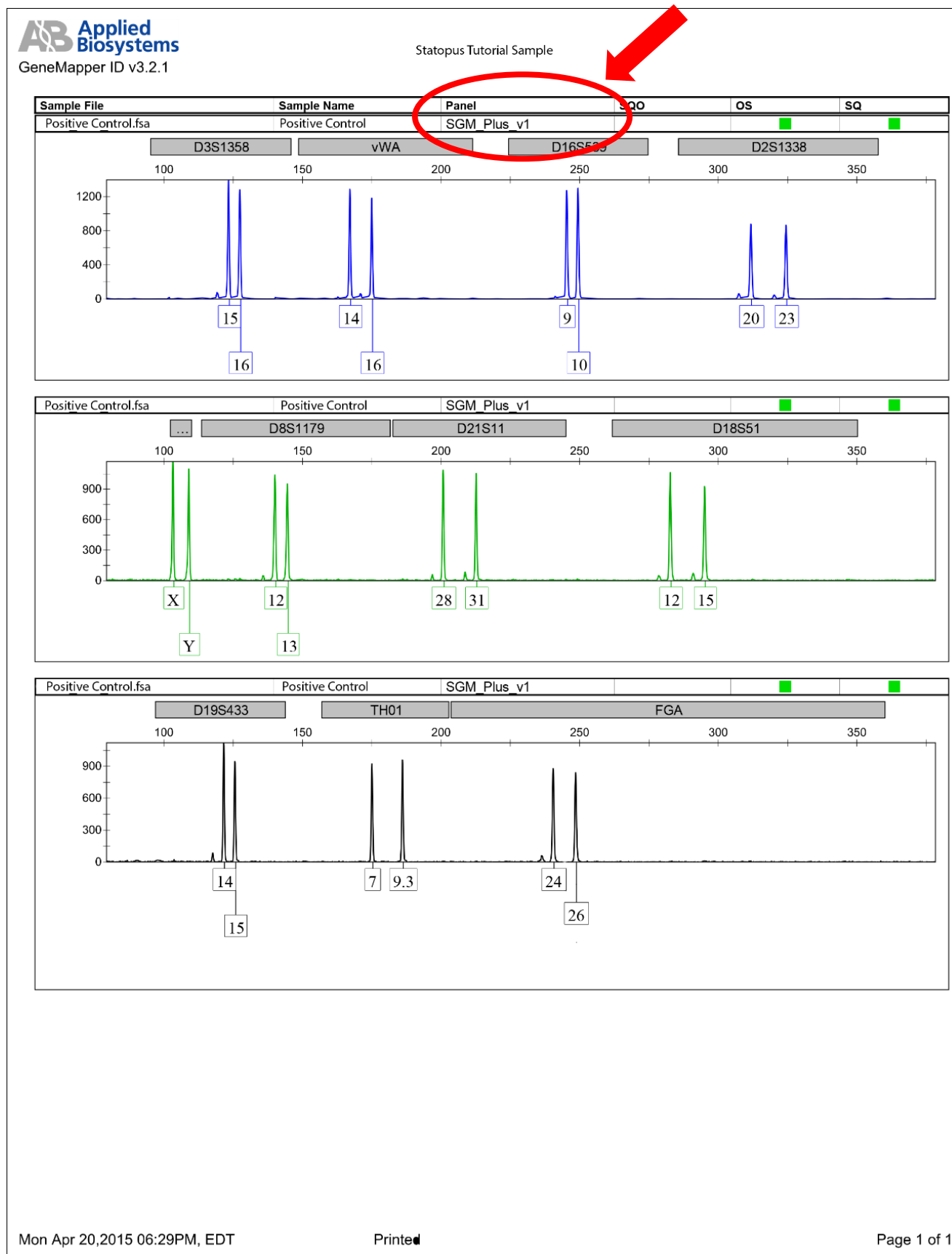
Step 3: Enter the genetic profile by clicking on a locus button. The set of possible alleles will appear beneath the "Alleles" heading and you can click on each allele button that corresponds to the genetic profile.

For example, looking at the first row of our example electropherogram, we can see that locus D3S1358 has an allele peak for 15 and 16, so we click on the 15 button and the 16 button as seen in the screenshot above.
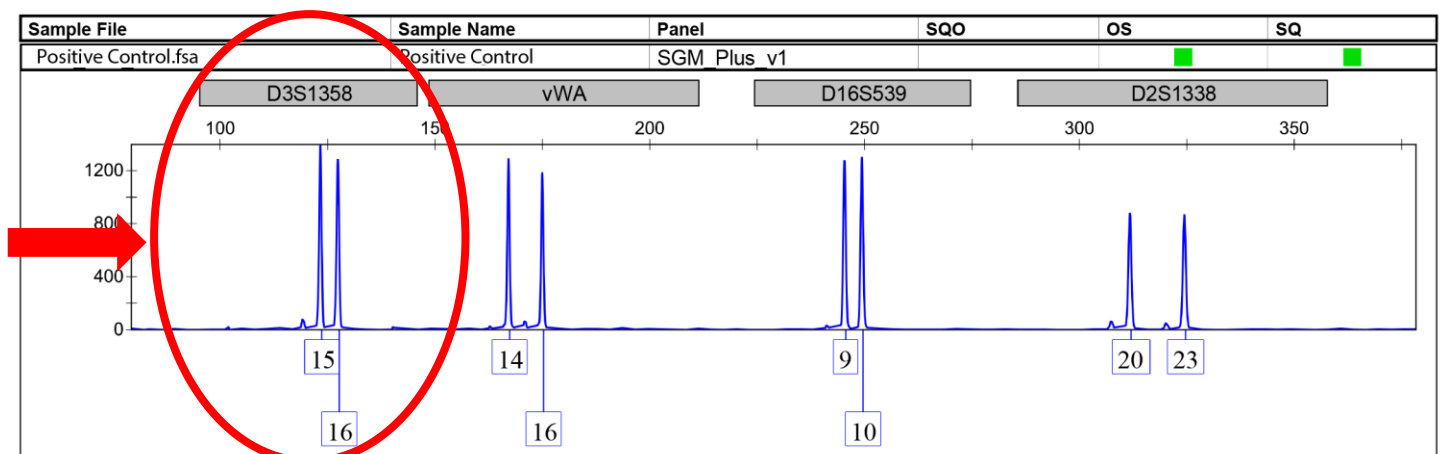
The next locus is vWA so we click on the "vWA" locus button to have its possible alleles appear. Our graph shows 14 and 16 alleles for vWA, so we click on the 14 and 16 buttons.
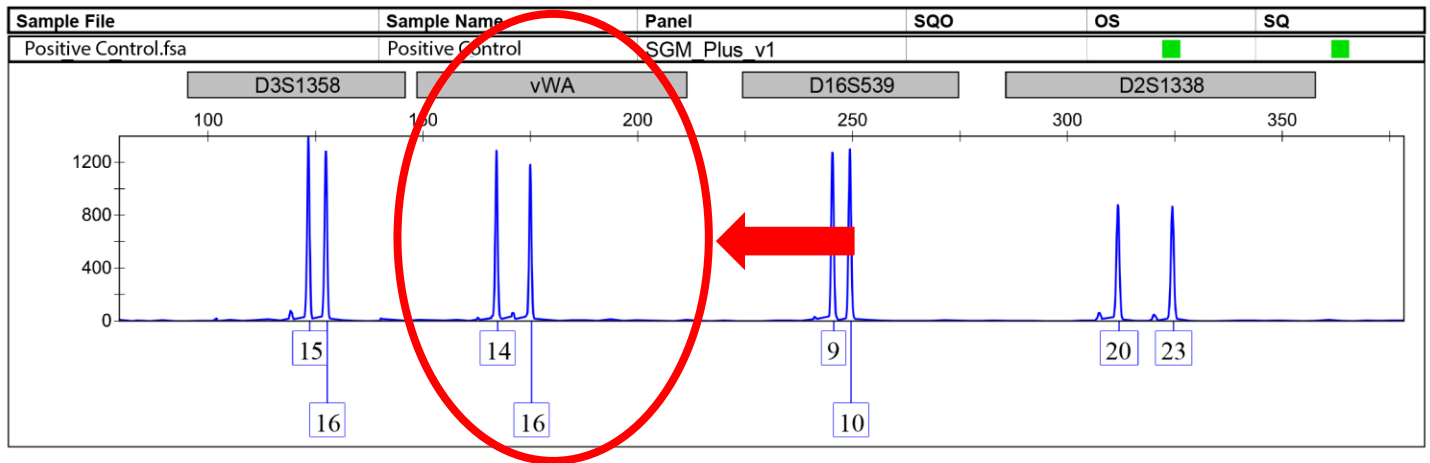
This process is repeated for each locus. Zero or more alleles can be chosen at each locus. Once all the alleles are input, click the forward arrow.
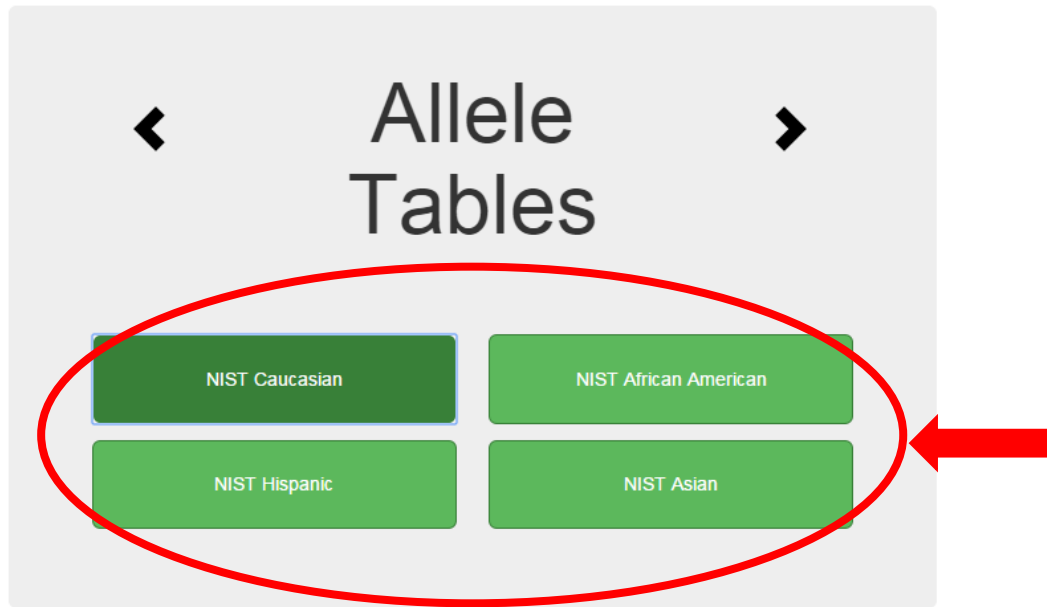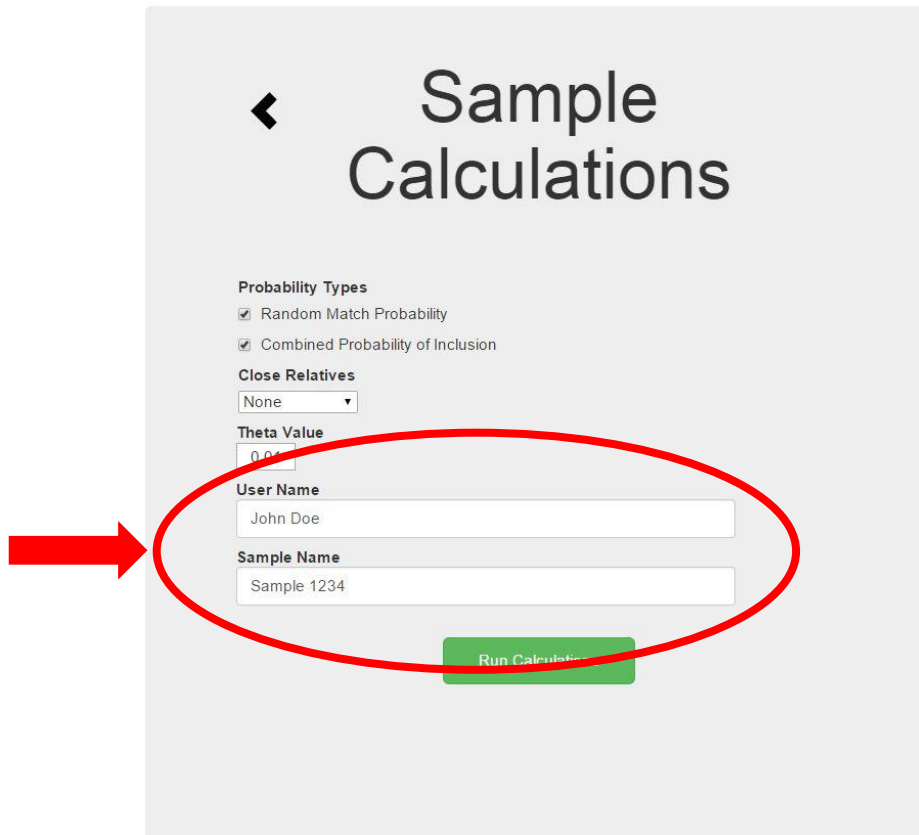
Step 4: Select one or more populations by clicking on the population buttons. For more information on populations, see the Statopus User Manual.

Step 5: Choose the statistics you would like run on the genetic profile by clicking on the checkbox next to each statistic name. If you want the probability involving close relative, choose the relation from the "Close Relatives" dropdown box. The theta value can be altered from its default value of 0.01. (For more information on each calculation, close relative calculations, and the theta value, see the Statopus User Manual.)

If desired, you can enter a user name and/or a sample name which will appear on the output screen along with the statistical results.
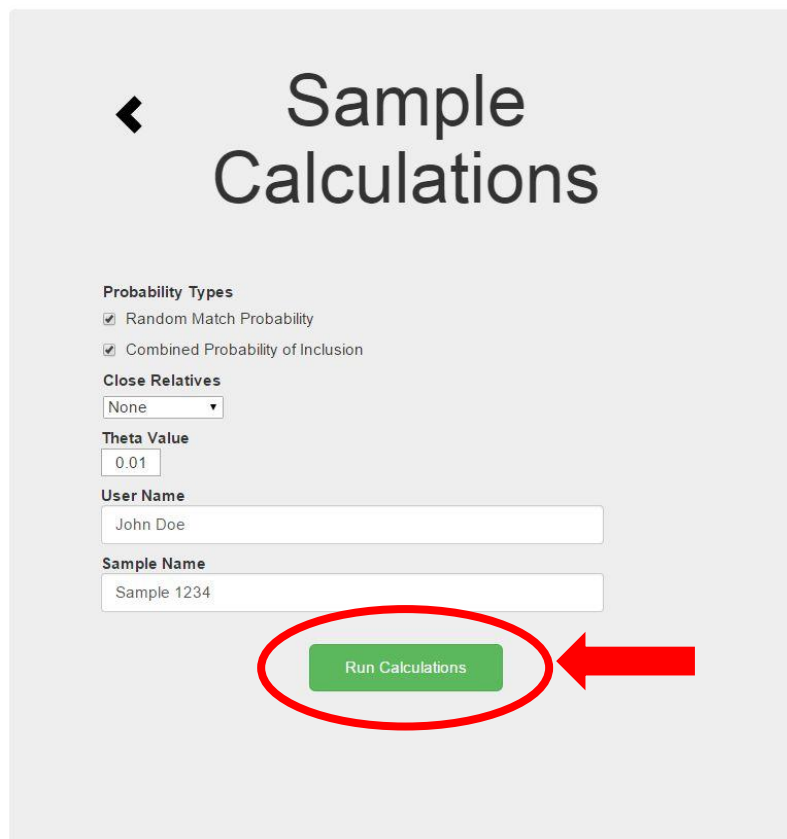
Step 6: Click the "Run Calculations" button to get the results of each statistic chosen.

Step 7: On the output screen, there will be a heading stating the test kit used, user name, and sample name, as well as a timestamp for when the output was generated.

Sample Results

Heading

Test Kit: SGM Plus

User Name: John Doe

Sample Name: Sample 1234

Date: Thu Apr 30 2015 14:57:44 GMT-0400 (Eastern Daylight Time)

RMP		NIST Caucasian	
Total Frequency		1.836e-14	
	Loci Freq.	Allele	Allele Freq.
D3S1358	1.287e-1	15	0.27285
		16	0.23823
vWA	3.690e-2	14	0.09280
		16	0.20083
D16S539	1.199e-2	9	0.10665
		10	0.05679
D2S1338	3.262e-2	20	0.15651
		23	0.10526
D8S1179	1.094e-1	12	0.16759
		13	0.32964
D21S11	2.271e-2	28	0.15928
		31	0.07202
D18S51	3.831e-2	12	0.11357
		15	0.17036
D19S433	1.120e-1	14	0.36150
		15	0.15651
TH01	1.324e-1	7	0.19391
		9.3	0.34488
FGA	7.000e-3	24	0.13435
		26	0.02632

CPI		NIST Caucasian	
Total Frequency		1.132e-10	

Below the heading will be separate tables for each statistic chosen on the Sample Calculations screen containing statistical results for each locus as well as the result for the entire genetic profile.

Sample Results

Test Kit: SGM Plus

User Name: John Doe

Sample Name: Sample 1234

Date: Thu Apr 30 2015 14:57:44 GMT-0400 (Eastern Daylight Time)

Result for entire profile

Results for Each locus

RMP		NIST Caucasian	
Total Frequency		1.836e-14	
	Loci Freq.	Allele	Allele Freq.
D3S1358	1.287e-1	15	0.27285
		16	0.23823
vWA	3.690e-2	14	0.09280
		16	0.20083
D16S539	1.199e-2	9	0.10665
		10	0.05679
D2S1338	3.262e-2	20	0.15651
		23	0.10526
D8S1179	1.094e-1	12	0.16759
		13	0.32964
D21S11	2.271e-2	28	0.15928
		31	0.07202
D18S51	3.831e-2	12	0.11357
		15	0.17036
D19S433	1.120e-1	14	0.36150
		15	0.15651
TH01	1.324e-1	7	0.19391
		9.3	0.34488
FGA	7.000e-3	24	0.13435
		26	0.02632

CPI	NIST Caucasian
Total Frequency	1.132e-10

To save or print your results, use your internet browser's save and print options.