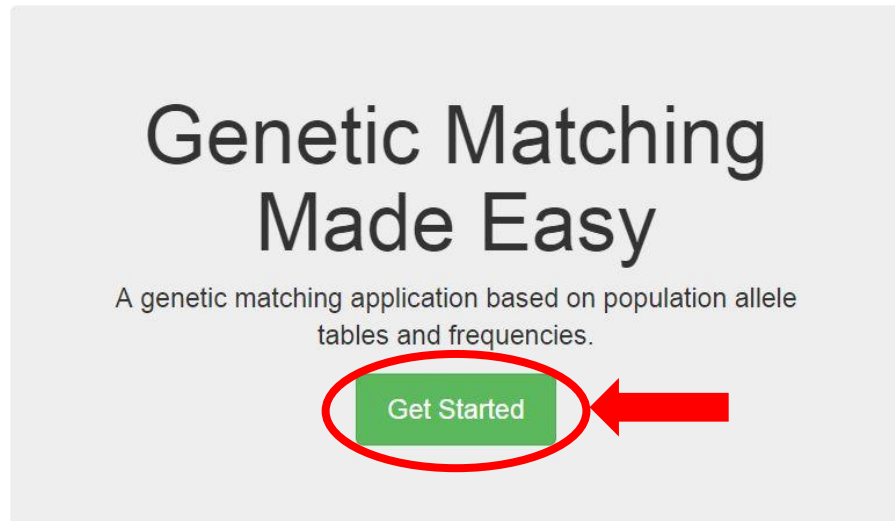
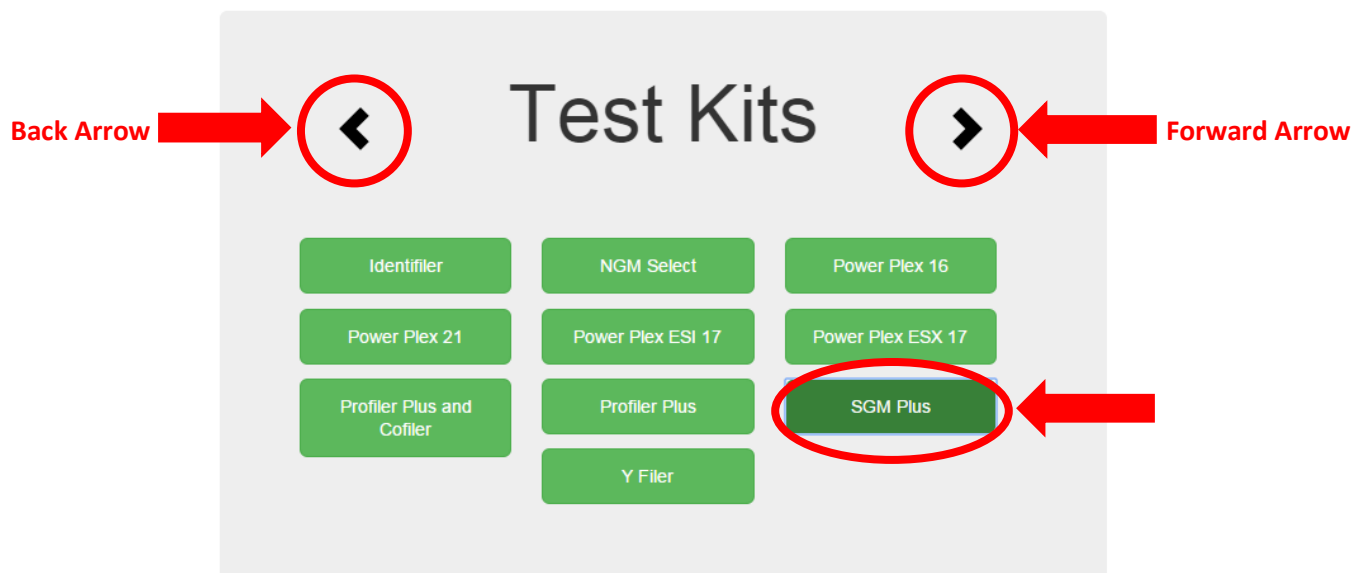


Statopus Tutorial

Step 1: Click the “Get Started” button to start the program.



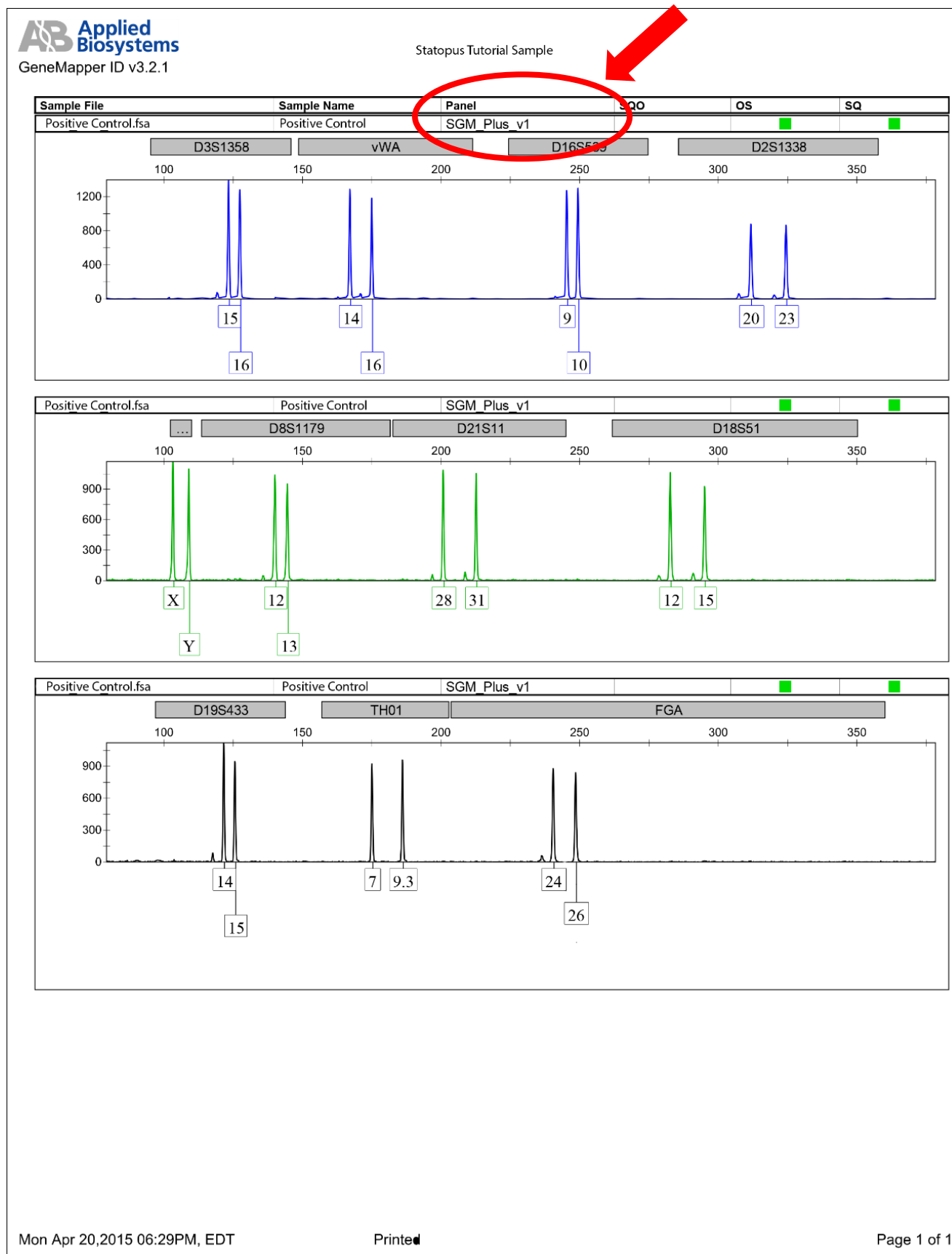
Step 2: Choose the test kit used on the genetic profile by clicking on the button containing the correct test kit name. In the example below, the SGM Plus test kit was chosen



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.

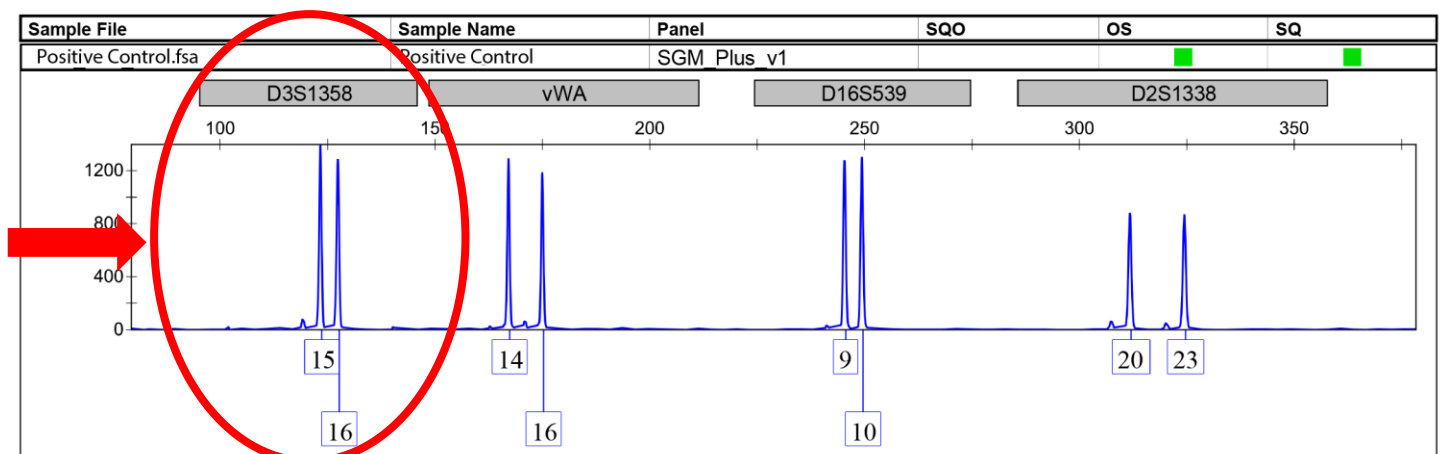
If you're working from a GeneMapper electropherogram like the one pictured below, often the test kit name can be found under the "Panel" heading.



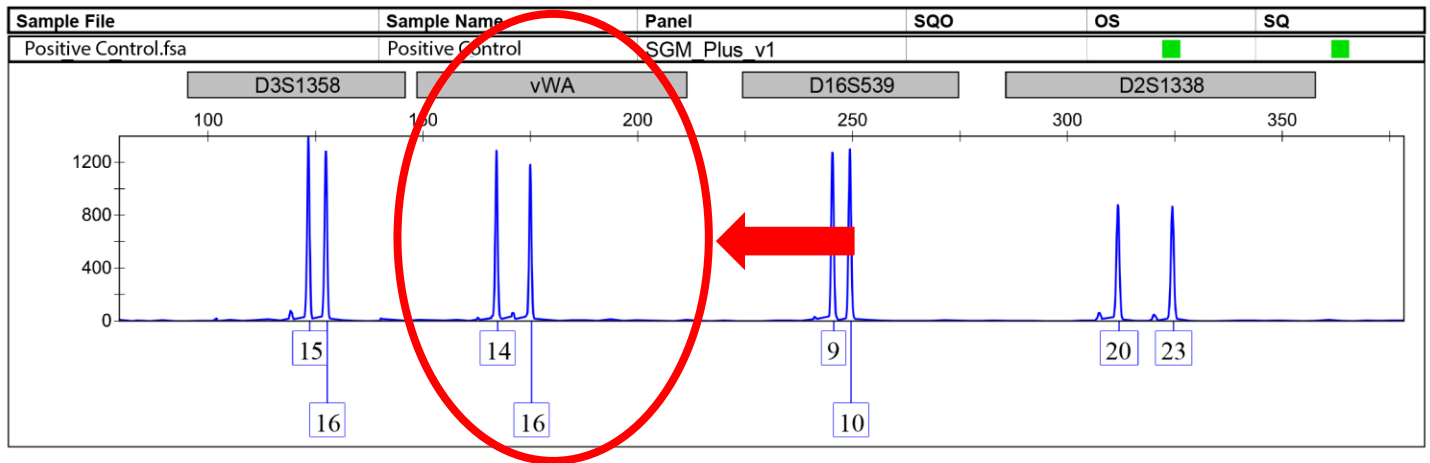
Step 3: Enter the genetic profile by clicking on a locus button. The set of possible alleles will appear beneath the “Alleles” heading and you can click on each allele button that corresponds to the genetic profile.



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.



<

Loci

>

D3S1358

vWA

D16S539

D2S1338

D8S1179

D21S11

D18S51

D19S433

TH01

FGA

Alleles

11

12

13

14

15

16

17

18

19

20

21

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.

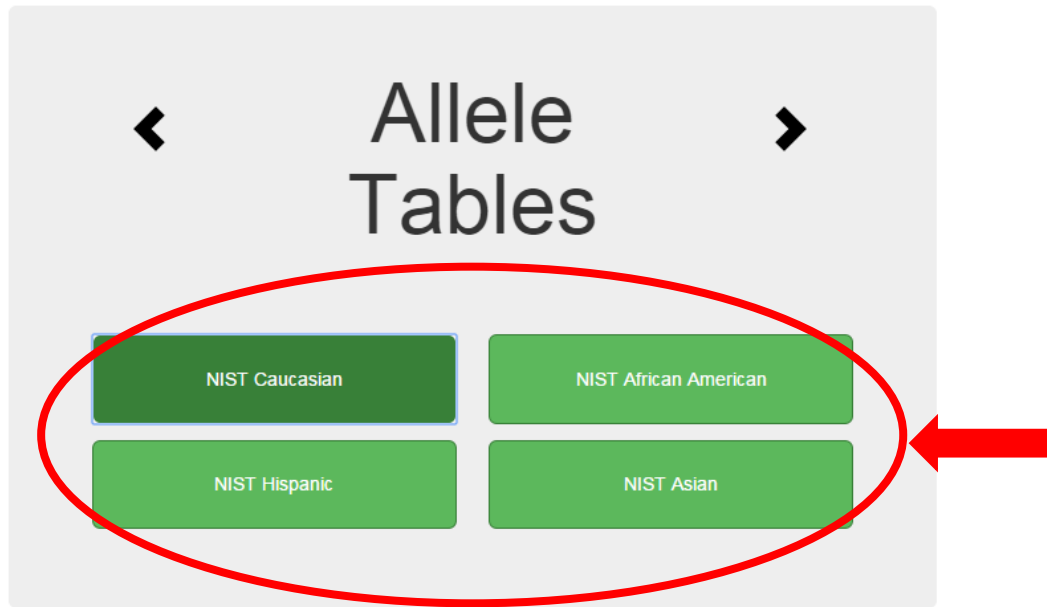
<

Loci

>

Forward Arrow

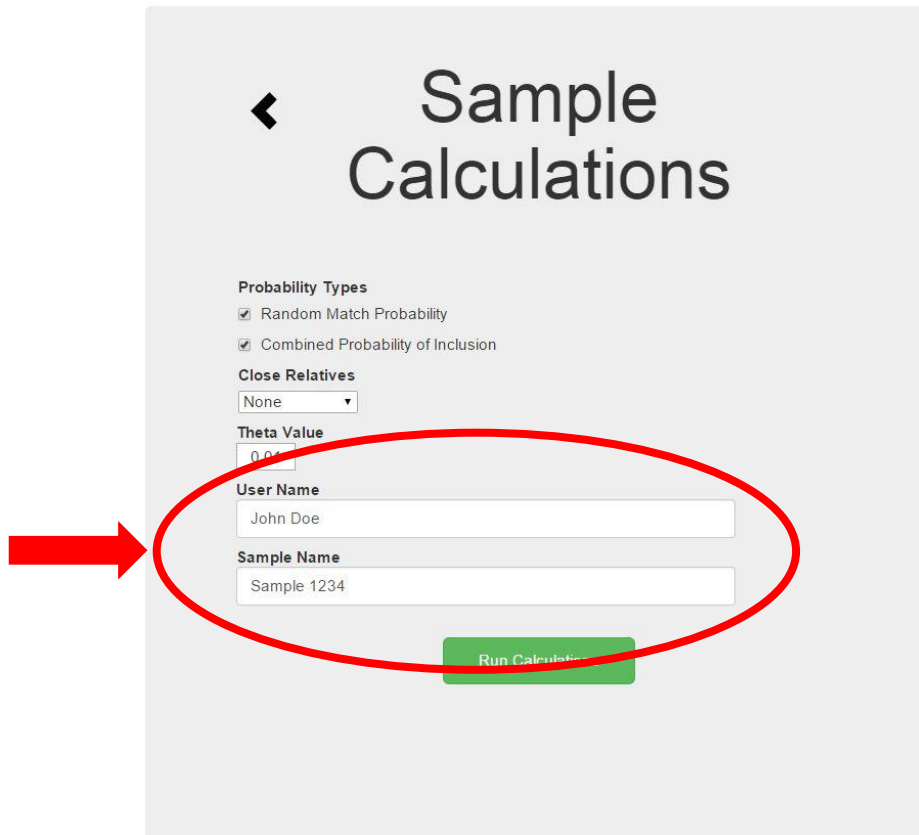
Step 4: Select one or more populations by clicking on the population buttons. For more information on populations, see the Statopus User Manual.



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.)

The screenshot shows a web interface titled "Sample Calculations" with a left navigation arrow. Below the title is a form with several sections. The "Probability Types" section has two checked checkboxes: "Random Match Probability" and "Combined Probability of Inclusion". The "Close Relatives" section has a dropdown menu currently set to "None". Below this is a "Theta Value" section with a text input field containing "0.01". Further down are two text input fields: "User Name" (containing "John Doe") and "Sample Name" (containing "Sample 1234"). At the bottom is a green button labeled "Run Calculations". A red oval is drawn around the "Probability Types" and "Close Relatives" sections. A red arrow points from the left edge of the oval towards the left side of the screen.

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.



Sample Calculations

Probability Types

- ☒ Random Match Probability
- ☒ Combined Probability of Inclusion

Close Relatives

None

Theta Value

0.01

User Name

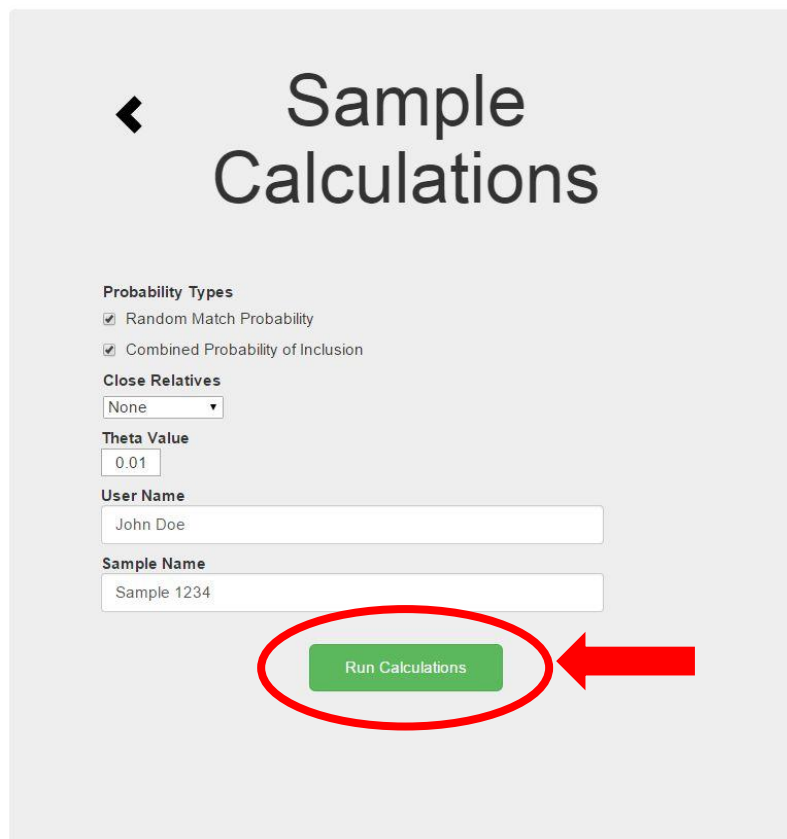
John Doe

Sample Name

Sample 1234

Run Calculations

Step 6: Click the “Run Calculations” button to get the results of each statistic chosen.



Sample Calculations

Probability Types

- ☒ Random Match Probability
- ☒ Combined Probability of Inclusion

Close Relatives

None

Theta Value

0.01

User Name

John Doe

Sample Name

Sample 1234

Run Calculations

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)

Results for Each locus

| RMP | NIST Caucasian | | |
|-----------------|----------------|--------|--------------|
| Total Frequency | 1.836e-14 | | |
| | Loci Freq. | Allele | Allele Freq. |
| D3S1338 | 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 |

Result for entire profile

| CPI | NIST Caucasian |
|-----------------|----------------|
| Total Frequency | 1.132e-10 |

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