FBS22 – STR Statistical Calculations Guidelines

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1. Scope

1.1. This procedure outlines the guidelines used to calculate the frequency of occurrence of single source and mixture evidence profiles employing AmpF*l*STR® Identifiler® Plus STR loci utilizing the Applied Biosystems®/Life Technologies® population database information.

2. Background

2.1. These practices set forth the FSL FBU's approach for conducting and documenting statistical analyses of evidence profiles in conformance with the requirements of the Department of Forensic Sciences (DFS) *Forensic Science Laboratory* (FSL) *Quality Assurance Manual*, the accreditation standards under ISO/IEC 17025:2005, and the supplemental standards set by the FSL's accrediting body, as well as guidance provided in the *Scientific Working Group on DNA Analysis Methods (SWGDAM) Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Laboratories* and the Federal Bureau of Investigation *Quality Assurance Standards (QAS) for Forensic DNA Testing Laboratories*.

2.2. In 2000 the DNA Advisory Board stated "When a comparison of DNA profiles derived from evidence and reference samples fails to exclude an individual(s) as a contributor(s) of the evidence sample, statistical assessment and/or probabilistic reasoning are used to evaluate the significance of the association. Proper statistical inference requires careful formulation of the questions to be answered, including, in this instance, the requirements of the legal system.

Inference must take into account how and what data were collected, which, in turn, determine how the data are analyzed and interpreted."

2.3. Statistical calculations are generated using allele frequencies of the STR loci in the AmpF*l*STR® Identifiler® Plus kit obtained from the validated Applied Biosystems®/Life Technologies® population database (see Appendix A).

2.3.1. Before a statistical calculation is performed, using the guidelines set forth in *FBS21 – Identifiler® Plus Interpretation Guidelines*, the DNA profile will be evaluated on a locus by locus basis to determine (1) suitability for interpretation and (2) suitability for inclusion in a statistical calculation(s).

2.3.2. After this determination has been made, comparisons to known/reference samples for the purpose of determining inclusion or exclusion are made.

2.3.3. A statistical calculation will be conducted to assess the significance of the finding only when the relevant person cannot be excluded as a possible contributor of, or to, a probative evidence profile generated from the genetic material. The calculation will provide an approximate frequency of the profile in three population groups – African American, U.S. Caucasians and U.S. Hispanics.

2.3.4. The statistical approach that is applied will depend on the circumstances of the case and the criterion addressed in this document.

2.3.4.1. It is understood that other methods for calculating frequency of occurrence of DNA testing results, particularly for mixture profiles, exist.

2.3.4.2. This laboratory does not conduct criminal paternity/relationship type statistics at this time. When the need arises for this type of calculation, a recommendation for outsourcing will be made.

2.3.4.3. This laboratory does not calculate relatedness statistics. In the event that a generated profile is suspected to have originated from a relative of the contributor and a DNA profile for comparisons cannot be obtained from that relative, a recommendation for outsourcing such calculations will be made.

3. Safety

3.1. Not applicable

4. Materials Required

4.1. Identifiler Plus Statistics Calculation Worksheet
4.2. Identifiler Plus CPI Mixture Statistics Calculation Worksheet

5. Standards and Controls

5.1. Not applicable

6. Calibration

6.1. Not applicable

7. Procedures

7.1. Significant Statistics Terminology

7.1.1. *Allele Frequency*: A frequency calculated by counting the number of times the allele is observed in the database of 2n, where n is the number of individuals in the database and 2n is the number of alleles counted. The allele frequency calculations relied upon by this laboratory can be found in Appendix A. For the population groups used by this laboratory, n is as follows: African American, n = 357; U.S. Caucasian, n = 349; and U.S. Hispanic, n = 290. Of note, should use of another racial/ethnic population group be relevant (e.g., the relevant person for a probative profile is Vietnamese-American), upon request, when allele frequency data is available, and with approval of the Technical Leader, that data may also be used for calculation and reporting purposes.

7.1.1.1. *Minimum Allele Frequency*: The frequency of 5/2n used for any allele that was observed less than five times when generating the population database. A minimum allele frequency is also used with approval of the Technical Leader when an allele not listed in Appendix A is encountered during casework (e.g., for a microvariant or variant allele). The minimum allele frequencies for the population groups used by this laboratory are as follows: African American, 0.0070; U.S. Caucasian, n = 0.0072; and U.S. Hispanic, n = 0.0086.

7.1.2. *Combined Probability of Inclusion (CPI)*: The portion of unrelated individuals in a defined population group that can be included as potential contributors to a DNA mixture result.

7.1.3. *Deconvolution*: Separation of contributors to a mixed DNA profile based on quantitative peak height information and any underlying assumptions.

7.1.4. *Deduced*: Inference of a foreign contributor's DNA profile after taking into consideration the contribution of a known/assumed contributor's DNA profile based on quantitative peak height information. Foreign contributor profiles may be deduced from intimate samples.

7.1.5. *Genotype*: The genetic makeup of an individual, specifically their STR profile at a locus or their STR profile at all loci.

7.1.6. *Hardy-Weinberg Equilibrium*: An underlying theoretical concept of population genetics that states allele and genotype frequencies in a population will remain constant from generation to generation in the absence of evolutionary influences.

7.1.7. *Heterozygous*: A typing result is heterozygous if it exhibits two different alleles at a particular locus, usually manifested as two distinct peaks for a locus in an electropherogram (one allele is inherited paternally and the other maternally).

7.1.8. *Homozygous*: A typing result is homozygous if it exhibits one detectable allele at a particular locus, usually manifested as a single distinct peak for a locus in an electropherogram. In this instance the same allele has been inherited from the father and the mother.

7.1.9. *Major Contributor(s)*: An individual(s) whose DNA profile(s) can account for the predominance of the DNA in a mixed profile.

7.1.10. *Minor Contributor(s)*: An individual(s) whose DNA profile(s) can account for the lesser portion of the DNA in a mixed profile.

7.1.11. *Probability of Identity (P_I)*: The probability that two unrelated individuals share a genotype. The P_I for a locus equals the sum of the squares of the probabilities of all possible genotypes at a locus. The P_I for the Identifiler® Plus® kit is calculated by multiplying all kit loci P_I values.

7.1.12. *Product Rule*: A calculation made by multiplying each individual STR genotype frequency together. The product rule may be used when all loci have been inherited independently of the other loci used in the calculation. This independence is assumed if the loci are on different chromosomes or are more than 50cM apart on the same chromosome.

7.1.13. *Random Match Probability*: The estimated frequency at which a particular evidence STR profile would be expected to occur in a defined population group (i.e., the probability of randomly selecting an unrelated individual from a population group who could be a potential contributor to an evidentiary profile).

7.1.13.1. *Modified Random Match Probability*: A term used in forensic biology when a random match probability is calculated for a component of a mixture to ensure the assumption of the number of unrelated contributors is included in the reported calculation statement.

7.1.14. *Restricted*: Refers to a statistical approach conditioned on the number of contributors and with consideration of quantitative peak height information and inference of contributor mixture ratios. This is used to limit the genotypic combinations of possible contributors.

7.1.15. *Stochastic Threshold (ST)*: The peak height below which the second allele of a heterozygous pair may not be detected. The ST can be used as an indicator of the potential allelic drop-out given that alleles detected below this threshold may be missing their sister allele. If the alleles are above this threshold, generally both sister alleles can be presumed to be present; however, when the majority of other loci have alleles below the stochastic threshold, it can be an indication that DNA from a low level donor may have dropped out completely. The stochastic threshold is based on internal validation studies and is set at 200 relative fluorescence units (rfus) for the Identifiler® Plus testing conducted by this laboratory.

7.1.16. *Unrestricted*: Refers to a statistical approach performed without consideration of quantitative peak height information and inference of contributor mixture ratios. For CPI, the number of contributors may or may not be considered/conditioned.

7.2. Random Match Probability (RMP) / Modified Random Match Probability (mRMP)

7.2.1. The genotype frequency for each locus will be calculated using the Hardy-Weinberg equilibrium formulas set forth in NRC II recommendation 4.1.

7.2.1.1. For a single contributor, when two alleles are detected at a locus, the genotypic frequency will be determined using the formula 2pq, where p represents the frequency of the 1st allele and q represents the frequency of the 2$^{nd.}$

7.2.1.2. For a single contributor, when one allele above the stochastic threshold is detected at a locus, the genotypic frequency will be determined using the formula $p^2 + p(1 - p)\theta$, where p represents the frequency of the allele and $\theta = 0.01$.

7.2.1.2.1. In simplest form, the genotype frequency for a homozygote is estimated as the square of the estimated allele frequency (p^2). NRC II recommendation 4.1 suggests using the aforementioned expression; as noted above, p represents the estimated allele frequency, while θ (theta) is a measure of potential population subdivision. Theta is also referred to as the inbreeding coefficient and its use makes a homozygous allele frequency more conservative.

7.2.1.2.2. A θ value of 0.01 will be used for routine casework since it is applicable for most situations. Upon approval of the Technical Leader, a θ value of 0.03 will be applied should genotype frequencies need to be generated for a smaller, isolated population (such as the Native American population).

7.2.1.3. For a single contributor, when one allele below the stochastic threshold is detected at a locus, the genotypic frequency will be determined using the formula 2p, where p represents the frequency of the observed allele. This formula will be used to take the potential for allele drop-out into account.

7.2.1.4. For a mixture, when discernment of one genotype for a major or minor contributor at a locus is not possible and an obligate allele for the contributor can be determined, the locus genotypic frequency will be represented using the formula 2p. This formula allows for genotype uncertainty/multiple potential contributor genotypes (e.g., 11,14; 13,14; and 14, ---).

7.2.1.5. As set forth in *FBS21 – Identifiler® Plus Interpretation Guidelines*, when applicable, a locus will be deemed inconclusive for inclusion in the statistical calculation.

7.2.1.6. No genotypic frequency will be generated for a tri-allelic contributor profile at a locus. This result will be deemed inconclusive for statistical calculation purposes.

7.2.2. A random match probability (RMP) will be calculated for full and partial single source profiles using the product rule.

7.2.2.1. A random match probability calculation may also be conducted when a complete major contributor profile can be fully deconvolved from a mixture profile or deduced from an intimate sample mixture profile.

7.2.3. A modified random match probability (mRMP) will be calculated using the product rule for major and/or minor mixture profile components that can be deconvolved or deduced.

7.2.3.1. The assumptions made in order to calculate the mRMP statistic(s) for a profile (e.g., number of contributors, assumed known(s)) will be reported as part of the statistical statement.

7.3. Combined Probability of Inclusion (CPI)

7.3.1. The probability of inclusion (P(I)) for each locus will be calculated using the formula $\{(p_1+p_2+\ldots p_n)^2+ \theta[p_1(1-p_1)+p_2(1-p_2)+\ldots+p_n(1-p_n)]\}$, where p_1 represents the frequency of the first allele detected, p_2 represents the frequency of the second allele detected, and so on, and where $\theta = 0.01$.

7.3.1.1. A θ value of 0.01 will be used for routine casework since it is applicable for most situations. Upon approval of the Technical Leader, a θ value of 0.03 will be applied should genotype frequencies need to be generated for a smaller, isolated population (such as the Native American population).

7.3.2. A combined probability of inclusion (CPI) will be calculated using the product rule and reported as 1/CPI.

7.3.3. Only those loci with no indication of allelic dropout and with all alleles above the stochastic threshold may be included in the CPI calculation. No assumptions are made regarding the potential number of contributors to the mixture profile.

7.3.4. A combined probability of inclusion (CPI) will be calculated using the loci deemed suitable for use in comparisons and the statistical calculation for the following types of profiles:

7.3.4.1. Two person mixture profiles deemed indistinguishable.

7.3.4.2. Two indistinguishable major contributors to a mixture profile of three individuals with an "ultra-minor contributor": (where the minor contributor alleles drop below stochastic and/or analytical threshold and a major contributor is, or both major contributors are, deemed probative). This restriction on CPI calculation will be included in the report statement.

7.3.4.3. A three person mixture profile with two indistinguishable minor contributors and a deconvolved major contributor profile. In this instance, a CPI will be conducted on the full profile to assess to significance of the minor contributors to the mixture.

7.3.4.4. A three person mixture profile with two indistinguishable major contributors and a single minor contributor profile. In this instance, a CPI will be conducted on the full profile to assess to significance of the minor contributor to the mixture.

7.3.4.5. Any other mixture profiles meeting the criteria for a CPI calculation.

7.4. Reporting of Statistics

7.4.1. Refer to *FBS23 – FBU Report Wording Guidelines* for specifics regarding statements used in *FBU Reports of Examination*.

7.4.2. The laboratory will perform a statistical analysis in support of all reported inclusions that are determined to be relevant in the context of a case (i.e., are deemed probative) and will maintain the corresponding paperwork in the case file.

7.4.2.1. When multiple stains/samples from the same item yield typing results that are consistent with originating from a common source(s) but have varying levels of discrimination, only the most informative statistic (i.e., the one with the highest discrimination potential) will be included in the FBU Report of Examination.

7.4.2.2. In most instances, detection of an individual's genotype on a sample obtained from their own body (i.e., an intimate sample) is considered non-probative and a statistic will typically not be calculated.

7.4.2.3. When a differential extraction has been performed on a sample and a single source profile has been obtained from the sperm fraction, a mixture result in the epithelial fraction that includes only the sperm donor profile and the epithelial cell donor's profile is considered non-probative. Accordingly, a statistic will typically not be calculated.

8. Sampling

8.1. Not applicable

9. Calculations

9.1. Calculations are conducted as described in Section 7. by entering the appropriate profile genotype information into the applicable statistics calculation worksheet.

10. Uncertainty of Measurement

10.1. When quantitative results are obtained, and the significance of the value may impact the report, the uncertainty of measurement must be determined. The method used to determine the estimation of uncertainty can be found in the *FSL Quality Assurance Manual – Estimation of Uncertainty of Measurement.*

10.2. NRC II states the following: "It is probably safe to assume that within a race, the uncertainty of a value calculated from adequate databases (at least several hundred persons) by the product rule is within a factor of about 10 above and below the true value."

11. Limitations

11.1. Any statistical calculation generated from STR DNA testing results is simply an estimate of the frequency of occurrence of that profile/profile component in the specified population group. It is not possible to generate a precise value.

11.2. As mentioned above, there are many methods for assessing the statistical significance of a DNA typing result. The methods employed by this laboratory are not all encompassing, nor are they intended to be.

12. Documentation

12.1. Sample-specific Identifiler Plus Statistics Calculation Worksheet(s), as needed

12.2. Sample-specific Identifiler Plus CPI Mixture Statistics Calculation Worksheet, as needed

12.3. FBU Report of Examination

13. References

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13.6. *Quality Assurance Standards for Forensic DNA Testing Laboratories*, Federal Bureau of Investigation (current revision).

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13.9. National Research Council. *The Evaluation of Forensic DNA Evidence*, Washington, DC: Academy Press, 1996. *(colloquially referred to as "NRC II")*

13.10. Ruitberg, C.M., Reeder, D.J., Butler, J.M. (2001). STR BASE: A short tandem repeat DNA database for the human identity testing community. *Nucleic Acid Research*, 29(1).

13.11. Stivers, D.N., and Chakraborty, R. (1997). A test of allelic independence based on distributions of allele size differences at microsatellite loci. *Human Heredity*, 47: 66-75.

13.12. *ISO/IEC 17025 General Requirements for the Competence of testing and Calibration Laboratories*, International Organization for Standardization, Geneva, Switzerland (current revision).

13.13. *Forensic Quality Services Supplemental Requirements for Forensic Testing Including FBI QAS*, FQS ANSI-ASQ Accreditation Board, Tampa, FL (current revision).

13.14. *Forensic Science Laboratory Quality Assurance Manual* (current revision)

13.15. DFS Departmental Operations Manual (current revision)

13.16. FSL Laboratory Operations Manual (current revision)

13.17. AmpF*l*STR® Identifiler Plus® PCR Amplification Kit User Guide. Rev. E. Life Technologies Corporation. 2014.

13.18. SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories (current revision).

13.19. STRBase (2015). http://www.cstl.nist.gov/strbase/ (accessed January 22, 2015).

APPENDIX A

The AmpF/STR® Identifiler® Kit, prior to the addition of the D8S1179 degenerate primer, was used to generate the population data provided below. Samples were collected from individuals throughout the United States with no geographical preference.

- For the African-American population: 357 samples were provided by the Kentucky State Police and the Federal Bureau of Investigation.
- For the U.S. Caucasian population: 349 samples were provided by the Kentucky State Police and the Federal Bureau of Investigation.
- For the U.S. Hispanic population: 290 samples were provided by the Minnesota Bureau of Criminal Apprehension/Memorial Blood Center of Minneapolis and the Federal Bureau of Investigation.

The following table shows the AmpF/STR® Identifiler® Plus Kit allele frequencies in the African American, U.S. Caucasian and U.S. Hispanic populations:

CSF1PO			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
6	0.0070	0.0072	0.0086
7	0.0462	0.0072	0.0086
8	0.0756	0.0072	0.0086
9	0.0378	0.0172	0.0086
10	0.2787	0.2421	0.2310
11	0.2059	0.3181	0.2828
11.3	0.0070	0.0072	0.0086
12	0.2913	0.3281	0.3966
13	0.0532	0.0731	0.0638
14	0.0098	0.0143	0.0086
15	0.0070	0.0072	0.0086
D2S1338			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
15	0.0070	0.0072	0.0086
16	0.5320	0.0473	0.0241
17	0.1078	0.1734	0.2121
18	0.0560	0.0630	0.0414
19	0.1415	0.1375	0.2276
20	0.0602	0.1461	0.1379
21	0.1401	0.0258	0.0259
22	0.1317	0.0401	0.0741
23	0.1078	0.1146	0.1136
24	0.0980	0.1175	0.0845
25	0.0812	0.1060	0.0517
26	0.0196	0.0272	0.0086
27	0.0070	0.0072	0.0086
28	0.0070	0.0072	0.0086

D3S1358			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
11	0.0070	0.0072	0.0086
12	0.0070	0.0072	0.0086
13	0.0070	0.0072	0.0086
14	0.1204	0.1576	0.0741
15	0.3053	0.2536	0.3914
15.2	0.0070	0.0072	0.0086
16	0.2857	0.2278	0.2672
17	0.1947	0.1819	0.1603
18	0.0672	0.1648	0.0897
19	0.0084	0.0100	0.0103
20	0.0070	0.0072	0.0086
D5S818			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
7	0.0070	0.0072	0.0672
8	0.0546	0.0072	0.0086
9	0.0168	0.0415	0.0517
10	0.0672	0.0544	0.0517
11	0.2549	0.3926	0.3914
12	0.3641	0.3524	0.2931
13	0.2157	0.1547	0.1259
14	0.0238	0.0072	0.0086
15	0.0070	0.0072	0.0086
16	0.0070	0.0072	0.0086
17	0.0070	0.0072	0.0086
D7S820			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
6	0.0070	0.0070	0.0086
7	0.0070	0.0129	0.0172
8	0.1877	0.1648	0.1172
9	0.1373	0.1762	0.0621
10	0.3445	0.2722	0.2741
11	0.1989	0.1805	0.2879
12	0.1078	0.1476	0.2017
13	0.0154	0.0372	0.0345
14	0.0070	0.0072	0.0086
15	0.0070	0.0072	0.0086
D8S1179			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
8	0.0070	0.0229	0.0086
9	0.0070	0.0115	0.0086
10	0.0238	0.0974	0.0845
11	0.0392	0.0602	0.0586
12	0.1331	0.1404	0.1207
13	0.2325	0.3252	0.3293
14	0.3011	0.2135	0.2621
15	0.2017	0.0989	0.1086
16	0.0462	0.0272	0.0241
17	0.0112	0.0072	0.0086
18	0.0070	0.0072	0.0086
19	0.0070	0.0072	0.0086

D13S317			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
8	0.0308	0.1218	0.0966
9	0.0252	0.0774	0.2172
10	0.0378	0.0444	0.0914
11	0.2451	0.2980	0.2310
12	0.4622	0.3080	0.2086
13	0.1541	0.1117	0.1017
14	0.0434	0.0372	0.0534
15	0.0070	0.0072	0.0086
D16S539			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
5	0.0070	0.0072	0.0086
8	0.0322	0.0172	0.0172
9	0.1905	0.1046	0.0931
10	0.1092	0.0559	0.1569
11	0.3151	0.3195	0.3017
12	0.1877	0.3023	0.2948
13	0.1485	0.1676	0.1155
14	0.0154	0.0301	0.0207
15	0.0070	0.0072	0.0086
D18S51			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
7	0.0070	0.0072	0.0086
9	0.0070	0.0072	0.0086
10	0.0070	0.0086	0.0086
10.2	0.0070	0.0072	0.0086
11	0.0070	0.0115	0.0121
12	0.0700	0.1390	0.1034
13	0.0434	0.1218	0.1448
13.2	0.0070	0.0072	0.0086
14	0.0686	0.1676	0.1552
14.2	0.0070	0.0072	0.0086
15	0.1947	0.1361	0.1655
16	0.1653	0.1361	0.1172
17	0.1821	0.1232	0.1414
18	0.1190	0.0774	0.0672
19	0.0602	0.0444	0.0414
20	0.0490	0.0172	0.0224
21	0.0210	0.0100	0.0103
22	0.0070	0.0072	0.0086
23	0.0070	0.0072	0.0086
24	0.0070	0.0072	0.0086
25	0.0070	0.0072	0.0086
26	0.0070	0.0072	0.0086
27	0.0070	0.0072	0.0086

D19S433			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
9	0.0070	0.0072	0.0086
10	0.0154	0.0072	0.0086
11	0.0714	0.0072	0.0086
11.2	0.0070	0.0072	0.0086
12	0.1078	0.0774	0.0621
12.2	0.0630	0.0072	0.0190
13	0.2983	0.2894	0.1603
13.2	0.0574	0.0172	0.0862
14	0.2101	0.3410	0.3172
14.2	0.0420	0.0086	0.0500
15	0.0476	0.1576	0.1345
15.2	0.0336	0.0272	0.0879
16	0.0238	0.0415	0.0431
16.2	0.0238	0.0172	0.0293
17	0.0070	0.0072	0.0086
17.2	0.0070	0.0072	0.0086
18.2	0.0070	0.0072	0.0086
D21S11			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
24	0.0070	0.0072	0.0086
24.2	0.0070	0.0072	0.0086
24.3	0.0070	0.0072	0.0086
25	0.0070	0.0072	0.0086
25.2	0.0070	0.0072	0.0086
26	0.0070	0.0072	0.0086
27	0.0504	0.0458	0.0121
28	0.2297	0.1676	0.0914
28.2	0.0070	0.0072	0.0086
29	0.1933	0.2049	0.2121
29.2	0.0070	0.0072	0.0086
29.3	0.0070	0.0072	0.0086
30	0.1723	0.2521	0.2931
30.2	0.0140	0.0330	0.0293
31	0.0798	0.0716	0.0672
31.2	0.0798	0.0946	0.0862
32	0.0112	0.0143	0.0155
32.2	0.0588	0.0716	0.1293
33	0.0070	0.0072	0.0086
33.2	0.0378	0.0330	0.0414
34	0.0126	0.0072	0.0086
34.1	0.0070	0.0072	0.0086
34.2	0.0070	0.0072	0.0086
35	0.0294	0.0072	0.0086
35.1	0.0070	0.0072	0.0086
35.2	0.0070	0.0072	0.0086
36	0.0084	0.0072	0.0086
37	0.0070	0.0072	0.0086
38	0.0070	0.0072	0.0086

FGA			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
16	0.0070	0.0072	0.0086
16.1	0.0070	0.0072	0.0086
17	0.0070	0.0072	0.0086
17.2	0.0070	0.0072	0.0086
18	0.0070	0.0272	0.0086
18.2	0.014	0.0072	0.0086
19	0.0672	0.0616	0.0707
19.2	0.0070	0.0072	0.0086
20	0.0700	0.1390	0.0741
20.2	0.007	0.0072	0.0086
21	0.1289	0.1691	0.1466
21.2	0.0070	0.0072	0.0086
22	0.2157	0.1691	0.1724
22.2	0.0070	0.0129	0.0086
22.3	0.0070	0.0072	0.0086
23	0.1499	0.1519	0.1190
23.2	0.0070	0.0072	0.0086
24	0.1751	0.1375	0.1534
24.2	0.0070	0.0072	0.0086
25	0.0798	0.0860	0.1414
26	0.0350	0.0272	0.0690
26.2	0.0070	0.0072	0.0086
27	0.0182	0.0072	0.0241
28	0.0140	0.0072	0.0086
29	0.0070	0.0072	0.0086
30	0.0070	0.0072	0.0086
30.2	0.0070	0.0072	0.0086
31.2	0.0070	0.0072	0.0086
32.2	0.0070	0.0072	0.0086
33.2	0.0070	0.0072	0.0086
34.2	0.0070	0.0072	0.0086
42.2	0.0070	0.0072	0.0086
43.2	0.0070	0.0072	0.0086
44.2	0.0070	0.0072	0.0086
45.2	0.0070	0.0072	0.0086
46.2	0.0070	0.0072	0.0086
47.2	0.0070	0.0072	0.0086
48.2	0.0070	0.0072	0.0086
50.2	0.0070	0.0072	0.0086
51.2	0.0070	0.0072	0.0086
TH01			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
4	0.0070	0.0072	0.0086
5	0.0070	0.0072	0.0086
6	0.1106	0.2049	0.2276
7	0.4286	0.2178	0.3362
8	0.2073	0.1146	0.0845
8.3	0.0070	0.0072	0.0086
9	0.1232	0.1619	0.1414
9.3	0.1162	0.2908	0.2034
10	0.0098	0.0072	0.0086
11	0.0070	0.0072	0.0086
13.3	0.0070	0.0072	0.0086

TPOX			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
6	0.0672	0.0072	0.0086
7	0.0224	0.0072	0.0086
8	0.3613	0.5330	0.4966
9	0.2115	0.1160	0.0724
10	0.0924	0.0430	0.0466
11	0.2143	0.2593	0.2724
12	0.0308	0.0473	0.1052
13	0.0070	0.0072	0.0086
vWA			
Allele	**African-American**	**U.S. Caucasian**	**U.S. Hispanic**
11	0.0070	0.0072	0.0086
12	0.0070	0.0072	0.0086
13	0.0126	0.0072	0.0086
14	0.0714	0.0931	0.0690
15	0.2003	0.1132	0.1000
16	0.2675	0.2335	0.3431
17	0.2059	0.2450	0.2155
18	0.1471	0.2249	0.1845
19	0.0672	0.0831	0.0707
20	0.0196	0.0115	0.0138
21	0.0070	0.0072	0.0086
22	0.0070	0.0072	0.0086
23	0.0070	0.0072	0.0086
24	0.0070	0.0072	0.0086

In addition to the alleles that were observed and recorded in the Applied Biosystems databases, other alleles have been published or reported to Applied Biosystems by other laboratories (see STRbase at http://www.cstl.nist.gov/strbase/var_tab.htm; accessed January 22, 2015)

The minimum allele frequency (5/2n) is listed in the above table for alleles occurring in low frequency as recommended in NRCII. The probability of identity (P_I) value is the probability that two individuals selected at random will have an identical AmpF*l*STR® Identifiler® Plus Kit genotype. The P_I values are as follows:

African-American 1.31×10^{-18}

U.S. Caucasian 5.01×10^{-18}

U.S. Hispanic 7.65×10^{-18}