EXHIBIT C

Procedures for the Interpretation of DNA Typing Results from the AmpF*l*STR® Identifiler® Plus and MiniFiler™ PCR Amplification Kits

1 Scope

These procedures describe the methods by which DNA typing results are verified and interpreted for forensic comparison purposes. The DNA typing results from the AmpF*l*STR® Identifiler® Plus and MiniFiler™ PCR Amplification Kits are obtained from the appropriate DNA typing software (e.g., ABI GeneMapper™ *ID*).

2 Background

Upon completion of the technical aspects of DNA analysis, the DNA typing results must be verified and interpreted by an Examiner. The verification of the accuracy of the DNA typing results involves a review of peak designations and other information generated by the appropriate DNA typing software, as well as an evaluation of quality controls. Based on this assessment, the Examiner performs interpretations, makes comparisons among samples (where appropriate), and draws conclusions that are captured for documentation and communication purposes within a FBI Laboratory Report.

The DNA typing results are derived through application of the appropriate DNA typing software during and after capillary electrophoresis (CE) of fluorescently-labeled amplification products that are generated for each specimen using the AmpF*l*STR® Identifiler® Plus Amplification Kit[1] and, where appropriate, the MiniFiler™ Amplification Kit. The Identifiler® Plus (27 cycles) Amplification Kit is used for the amplification of all sample types; however, bones and teeth may be amplified using Identifiler® Plus (28 cycles) Amplification Kit. The MiniFiler™ Amplification Kit is generally employed when the initial typing of the sample indicates degraded DNA.

Following amplification, CE is conducted using the ABI 3130xl Genetic Analyzer (3130xl). For each specimen, the appropriate software translates fluorescence intensity data collected by the genetic analyzer into electropherograms, and then labels any detected peaks with such descriptors as size (in base-pairs, or bp) and peak height (in relative fluorescence units, or RFU). Then, using AmpF*l*STR® Allelic Ladders for reference, the software labels peaks that meet certain criteria with allelic designations.

To ensure the accuracy of these computer-generated allele designations, the Examiner must verify that appropriate genotyping parameters (i.e., the GeneScan®-500 LIZ Internal Size Standard and appropriate allelic ladder) were used by the software and that the correct genotyping results were obtained for a known, positive control sample. Additionally, if genotyping results from more than one amplification kit are available for a given specimen, the Examiner must confirm the

[1] It is noted that the nDNAU has validated the Identifiler® Plus Amplification Kit using thermocycling parameters with both 27 cycles and 28 cycles. The interpretation of the results from these two methods is distinguished by using the terms "Identifiler® Plus (27 cycles)" and "Identifiler® Plus (28 cycles)."

the report:

> *"Nuclear DNA analyses were initiated on specimen Q1. Nuclear DNA and/or serological examinations were discontinued on the submitted item(s) per communication with Special Agent Smith on July 20, 2010 due to a plea agreement."*

7.9 Application of Population Frequency Data (Appendix A) to Probative[81] Inclusionary DNA Typing Results[82]

7.9.1 No random match probabilities[83] are calculated for exclusionary or inconclusive conclusions.[84]

7.9.2 Random match probabilities must only be calculated for Q specimen(s) if the DNA typing result of a Q specimen matches that of a reference specimen (e.g., K specimen or Q specimen of established origin[85]) and the match is determined by the Examiner to be probative (e.g., the victim's DNA typing results present on clothing recovered from a suspect).

7.9.3 Composite DNA profiles for forensic samples should be used for matching/statistical purposes. To reasonably ensure that a DNA profile compiled from genetic information derived from separate extractions, amplifications, and/or injections has arisen from the same individual, the resultant DNA profile must 1) be compiled from different items from a common source (e.g., replicate vaginal swabs), multiple cuttings of the same evidentiary stain, or cuttings from different stains of the same grouping on a given evidence item and 2) demonstrate concordance at the appropriate loci.

7.9.4 Random match probabilities and combined probabilities of inclusion[86] are calculated using four general United States population groups (i.e., African-American, Caucasian,

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[81] Because not all match conclusions are informative, a random match probability may not be calculated for all conclusions. For example, matching the source of a known (K) specimen to DNA isolated from a body sample (e.g., vaginal swab, oral, swab, thigh swab) and/or clothing recovered from that person is expected and need not be statistically represented. Similarly, matches to a common donor across multiple stains from the same item, or to multiple stains across evidentiary items of similar origin (i.e., a shirt and pants recovered from the same gym bag), that yield more common random match probabilities need not be calculated or reported.

[82] The sex typing results from the amelogenin locus are not included in the random match probability calculations.

[83] As used here, random match probability is defined as the chance of selecting a biologically unrelated individual at random having an STR profile matching the DNA obtained from the questioned specimen. The uncertainty associated with a random match probability calculated using any of the FBI databases in Appendix A has been empirically demonstrated to be less than about 10-fold in either direction (i.e., for a random match probability estimate of 1 in 10 million, the true frequency of that profile can be confidently expected to be between 1 in 1 million and 1 in 100 million). This confidence interval is taken from the 1996 National Research Council report entitled "The Evaluation of Forensic DNA Evidence" (page 33) and is based on published data assembled from around the world by the FBI.

[84] Any triallelic locus must not be included in the statistical calculations.

[85] A Q specimen of established origin may be used as a reference sample and is referred to as an "alternate known" (i.e., a DNA typing result obtained from blood on the clothing of a victim known to have been bleeding, an item of personal effect). The alternate known DNA profile may be obtained as a single-source or as a major contributor typing result.

[86] All random match probabilities and combined probabilities of inclusion must be reported as fractions truncated to two significant figures. For example, 1 in 13,400 is truncated to 1 in 13,000; 1 in 54,700,000 is truncated to 1 in 54,000,000, or 1 in 54 million; 1 in 3,750,000,000 is truncated to 1 in 3,700,000,000, or 1 in 3.7 billion.