Deviation Request Form (DRF)

Directions: The Initiator will complete Sections A through C. Additional continuation pages can be included if necessary.

Initiator	MJ DeHaan	**Date**	12/3/2020

A. Requested deviation applies to (Technical Procedure – include specific section):

Forensic Biology Procedure for Casework Report Writing Section 5.12.8

B. Requested deviation:

Replace <1 with <0.001. Remainder of section remains the same.

C. Necessity for the deviation:

To reflect changes in the interpretation and analysis procedure.

D. Technical review and Authorization (to be completed by the Quality Manager and/or Technical Leader)
Comments(to include merits and impacts):

Approved	☑	Yes	☐	No	Duration	until next version
Signature	Mackenzie DeHaan Digitally signed by Mackenzie DeHaan DN: C=US, OU=Forensic Biology, O=NCSCL, CN=Mackenzie DeHaan, E=mdehaan@ncdoj.gov Reason: I have reviewed this document Location: Date: 2020-12-03 14:16:56 Foxit PhantomPDF Version: 9.3.0				Date	12/3/2020

E. Quality Assurance Authorization (to be completed by the Quality Manager, Forensic Scientist Manager or designee)

Acceptable within general QA guidelines and good laboratory practice?	☑	Yes	☐	No
Significant negative impact to Crime Laboratory Quality System?	☐	Yes	☑	No

Restrictions/limitations:

☑	Authorized	☐	Rejected	Signature	Jody H. West Digitally signed by Jody H. West DN: cn=Jody H. West, o=DOJ, ou=State Crime Laboratory, email=jwest@ncdoj.gov, c=US Date: 2020.12.03 14:37:35 -05'00'	Date	12/3/2020

Deviation Request Form (DRF)

Directions: The Initiator will complete Sections A through C. Additional continuation pages can be included if necessary.

Initiator	MJ DeHaan	**Date**	08/25/2020

A. Requested deviation applies to (Technical Procedure – include specific section):

Procedure for Casework Report Writing_multiple sections

B. Requested deviation:

See attached

C. Necessity for the deviation:

To clarify reporting for cases using STRmix software

D. Technical review and Authorization (to be completed by the Quality Manager and/or Technical Leader)
Comments(to include merits and impacts):

Approved	☑	Yes	☐	No	Duration	until next version	
Signature	Mackenzie DeHaan Digitally signed by Mackenzie DeHaan DN: C=US, OU=Forensic Biology, O=NCSCL, CN=Mackenzie DeHaan, E=mdehaan@ncdoj.gov Reason: I have reviewed this document Location: Date: 2020-08-25 11:46:45 Foxit PhantomPDF Version: 9.3.0				Date	08/25/2020	

E. Quality Assurance Authorization (to be completed by the Quality Manager, Forensic Scientist Manager or designee)

Acceptable within general QA guidelines and good laboratory practice?	☑	Yes	☐	No
Significant negative impact to Crime Laboratory Quality System?	☐	Yes	☑	No

Restrictions/limitations:

DRF will be effective on 8/31/2020.

☑	Authorized	☐	Rejected	Signature	Jody H. West Digitally signed by Jody H. West DN: cn=Jody H. West, o=DOJ, ou=State Crime Laboratory, email=jwest@ncdoj.gov, c=US Date: 2020.08.25 11:35:32 -04'00'	Date	8/25/20

Form approved for use by: Timothy G. Suggs Digitally signed by Timothy G. Suggs DN: cn=Timothy G. Suggs, o=North Carolina State Crime Laboratory, ou=Quality Manager, email=tsuggs@ncdoj.gov, c=US Date: 2014.12.19 09:01:52 -05'00'

DRF_Casework Report Writing_08252020

5.6.1 Change wording: *The DNA profile obtained from___ (Item __) is being interpreted as a single source profile. The DNA profile obtained from ___ (Item __) is included as a possible contributor to this profile. The DNA profile(s) obtained from ___ (Item(s)__) is/are excluded as a contributor to this profile.*

Remove 5.6.4, 5.7.2, 5.7.3

5.7.4.1 Re-numbered as 5.7.2, 5.7.4.2 becomes 5.7.3

Add 5.7.4 No conclusion: *No conclusion can be rendered as to the contribution of the DNA profile obtained from ___ (Item__) due to insufficient quality or due to an inconclusive likelihood ratio result.*

Add new 5.12.5 The statement will be added to the report to inform which contributor gave the highest LR from the summary of contributors. *The statistical calculations best fit the DNA profile obtained from ___ (Item__) as contributor __ in this mixture profile.*

5.12.7 update wording to between 0.001 and 1000

Procedure for Casework Report Writing

1.0 Purpose – The purpose of this document is to provide casework report writing guidelines for DNA results when using the PowerPlex® Fusion 6C amplification kit.

2.0 Scope – This document applies to casework analysts and trainees in the Forensic Biology Section who are qualified to use the PowerPlex® Fusion 6C amplification kit.

3.0 Definitions - See Section Definition list

4.0 Equipment, Materials and Reagents – N/A

5.0 Procedure

5.1 Introduction - General reporting guidelines are provided throughout this procedure, and *most* reporting scenarios will fall within the provisions of this procedure. However, unique case circumstances may warrant the use of reporting language beyond those provided herein.

Wording used in reports may be modified with documented approval from the DNA Technical Leader. Forensic Scientists shall provide the DNA Technical Leader with the requested wording. The DNA Technical Leader shall then reply in writing with an approval or denial of the request. This correspondence shall be placed in the FA Case Record Object Repository. Adding qualifying words (e.g fraction 1, fraction 2, sperm, non-sperm, major, male) may be done without documented approval. Wording can be combined from statements contained in this procedure, including those under different reporting blocks (e.g. single source and mixture).

The results statements shall reflect only work that is performed. Portions of the statements listed in the reporting guidelines may be omitted if not reflective of testing actually performed. For reports where statements are being combined from multiple reporting statements, redundant phrasing (e.g. evidence descriptions) may be omitted as long as the reports reflect all interpretation and conclusions.

All inclusionary statements when compared to a reference sample shall be accompanied by the appropriate statistic. An exception to this requirement is when a sample has been conditioned using a known reference profile (e.g., vaginal swab).

5.2 General Principles

5.2.1 If a profile is determined to be partial (whether a single source, mixture, evidentiary or reference), the word partial shall be used to qualify the result. NOTE: Comparisons between partial reference profiles and evidentiary profiles can be made only for the loci at which results exist in the partial reference profile.

5.2.2 The following statement shall be entered into the Results area when cuttings/swabbings are taken and no chemical analysis for body fluid identification is preformed: “No chemical analysis for body fluid identification was performed on ___ (Item ___); however, a swabbing (or cutting) (sub-item, if applicable) was taken for DNA analysis.”

5.2.3 If a differential extraction is performed and no body fluid testing was performed on the item, fraction 1 and fraction 2 shall be used to qualify the results of the reported fractions. Non-sperm and sperm may still be used to qualify the fractions if body fluid testing had been previously performed on the item.

5.2.4 If a single source or single major unknown profile is obtained and a Y is present at Amelogenin and/or information is present at DYS570, DYS576, or DYS391, such profiles shall be qualified as male in the report.

5.2.5 If a Y is present at Amelogenin and/or information is present at DYS391, DYS570, or DYS576 in a mixture and no inclusionary statement to a male reference standard has been made, the overall mixture shall be qualified as having a male contributor: *This mixture contains at least one male contributor.* This statement may also be added if no information is present for the Y at Amelogenin or DYS391, DYS570, DYS576 and a male quantification value is obtained.

5.2.6 If multiple unknown profiles are present within a case, they should be qualified numerically. For example: first unknown (male), second unknown (male), etc.

5.2.7 For cases where the report is being written pursuant to receipt of a standard from a CODIS hit from a case that was worked by a vendor laboratory and the data was accepted for upload, the following statement shall be added to the report:

"This case was previously analyzed and reported by a laboratory other than the NC SCL. Comparisons will only be made to the item listed below. For further information, please do not hesitate to contact the reporting Forensic Scientist or the Forensic Scientist Manager of the Forensic Biology Section at the North Carolina State Crime Laboratory."

5.2.8 For cases where evidence was analyzed prior to January 1, 2017 and a request is made to make additional comparisons, the following statement shall be added to the report if comparisons cannot be made to all of the originally analyzed items/portions of items:

"Due to procedure changes, comparisons to evidence analyzed before this date can be made only for those DNA profiles generated from the items listed below. For further information, please do not hesitate to contact the Forensic Scientist or the Forensic Scientist Manager of the Forensic Biology Section at the North Carolina State Crime Laboratory."

5.2.9 For cases when previous interpretation was performed and additional standards have been submitted for additional comparisons with no additional analysis performed on the questioned items, the wording used shall be that of the original report where the unknown was interpreted.

5.2.10 If DNA standards (to include alternate standards) are not suitable for comparison purposes (e.g., due to degradation, presence of a mixture, or if no DNA present), then the following statement shall be used in the report: "no DNA profile suitable for comparison purposes was obtained from ____ (Item ___); therefore, additional DNA standard(s) from ____(name) need to be obtained and submitted."

5.2.11 If the results of a sample cannot be reported due to the contamination of the associated control, then the following statement shall be used in the report: "Examination of

____(Item ___) revealed that the associated negative control was contaminated. In such cases it is not possible for this laboratory to render any conclusion with regard to the interpretation of the associated sample." This statement shall only be used after documented consultation with the Forensic Biology Technical Leader.

5.2.12 If only DNA reference standards are analyzed in a case, the following statement shall be used in the report: "A DNA profile was generated from the known standard(s) from ___ (Item(s) __) for comparison purposes only."

5.2.13 The Results of Examination and Conclusions section of each report shall contain a paragraph that details which items were extracted and specifies what methodology/technology was used. The report shall contain the following statement (or equivalent): "DNA extractions were performed on Item(s) _____, as well as on the known DNA standards from _____ (Item(s)). These extracts were then quantitated, and applicable samples were amplified and tested with the DNA genetic markers CSF1PO, FGA, TH01, TPOX, vWA, D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, Penta D, Penta E and SE33 as well as Amelogenin, DYS391, DYS570, and DYS576."

5.2.14 If STRmix was used to aid interpretation or to perform statistical calculations the report shall contain the following statement (or equivalent): "STRmix™ interpretational software was used to aid in the analysis of DNA profiles obtained and to generate statistical calculations, using the population databases generated by NIST."

5.2.15 If additional standards have been requested, but not received and the results reported could be affected by the lack of standard (e.g. no victim standard and intimate sample is an indistinguishable mixture) then the following statement can be added to the report: "The known reference sample from ___ was requested and not received. Additional interpretation of ___ (Item __) may be possible once the requested standard is received and analyzed."

5.2.16 If standards have been requested but not received and the lack of a standard affects the disposition of the case (e.g. transfer for YSTR testing), then the following statement can be added to the report: "The known reference sample from ___ was requested and not received. Once the sample becomes available, it, along with Item/Container, may be submitted for additional (YSTR) analysis."

5.2.17 The report section for disposition shall have the header changed to read "Disposition" and shall contain the following statement (or equivalent):

Note: DNA extracts from Items ____(FA Identifier) and slides prepared from Items ___ (FA Identifier) are being returned along with the items of evidence in this case.

5.3 Reporting Quantification Results

When samples are not amplified due to the quantification results, the following statement shall be added to the report as applicable: Based on *quantification results from Item ___ an insufficient amount of (male) DNA was detected, therefore this/these sample(s) is/are not being amplified. . No further analysis was performed on Item(s) ___.* Or *Based on quantification results obtained*

*from samples/items analyzed as a part of this case, Item(s) __ is/are not being amplified. No further analysis was performed on Item(s)__.*When samples are being retained for YSTR testing due to quantification results, the following statement shall be added to the report*: The DNA extracts from Items ___ are being retained for YSTR testing.*

5.4 **No DNA Profile -** When no alleles are detected above the analytical threshold: *No DNA profile was obtained from _____(Item ___).*

5.5 **No interpretable DNA Profile –** When the DNA profile is uninterpretable: The DNA profile obtained from ___ (Item __) is uninterpretable due to complexity of the mixture/due to limited data obtained. This profile is not suitable for interpretation or comparisons."

5.6 Single Source Profiles

5.6.1 Matches and Exclusions: *A DNA profile was obtained from _____ (Item__) that matches the DNA profile obtained from _____ (Item__). The DNA profile(s) obtained from _____ (Item(s)__) is excluded as a contributor to this profile*.

5.6.2 An assumed contributor (i.e., victim or elimination reference standard profile) matches an intimate item: *The DNA profile obtained from ____ (Item __) is no different from that of the victim/subject (Item __) and the DNA profile obtained from____ (Item__) is excluded as a contributor to this profile*.

5.6.3 Known reference sample excluded (unknown profile): *The DNA profile obtained from ____ (Item __) is from an unknown contributor.*

5.6.4 Matches and Consistent With: If a single genotype option is allowed for statistical calculations at all loci the word ***MATCHES*** shall be used. If additional genotype options are allowed, the phrase ***IS CONSISTENT WITH*** shall be used.

5.7 Mixtures

5.7.1 **Primary statement:** *The DNA profile obtained from ___ (Item __) is being interpreted as a mixture of (#) contributors.*

5.7.2 Mixtures with a Single Major Contributor (Distinguishable)

5.7.2.1 Known Reference Sample(s) Included: *The major contributor profile matches/is consistent with the DNA profile obtained from _____ (Item__).* See 5.6.4 for use of "matches/consistent with."

5.7.2.2 Known Reference Sample(s) Excluded (i.e., unknown profile): *The major profile(s) is from an unknown contributor.*

5.7.2.3 Known Reference Sample Assumed: _____, the donor of the known sample (Item __) is assumed as being a contributor of DNA from the profile obtained from ___ (Item __). *The other component matches/is consistent with the profile obtained from the _____ (Item ___).*

5.7.2.4 Contribution to Overall Mixture:

5.7.2.4.1 Cannot exclude from the mixture: *The DNA profile(s) obtained from _____ (Item(s) ____) is included as a possible contributor(s) to the mixture.*

5.7.2.4.2 Excluded from the mixture (including the major profile): *The DNA profile(s) obtained from _____ (Item_) is/are excluded as a contributor/as contributors to the mixture.*

5.7.3 Mixtures with Multiple Major Profile (Distinguishable):

5.7.3.1 Primary statement: *This mixture contains a multiple major profile.*

5.7.3.2 Cannot exclude from the multiple major profile: *The DNA profile(s) obtained from _____ (Item_) are included as a possible contributor/as contributors to the multiple major profile of this mixture.*

5.7.3.3 Excluded from the multiple major profile but not excluded from the minor component: *The DNA profile from ____ (Item__) is excluded as a contributor to the multiple major profile of the mixture. However, the DNA profile from _____ (Item __) is included as a possible contributor to the minor component of the mixture.*

5.7.3.4 Excluded from the overall mixture: *The DNA profile(s) obtained from _____ (Item __) is/are excluded as a contributor/contributors to the mixture.*

5.7.4 Mixtures with No Major Contributor (Indistinguishable Mixture):

5.7.4.1 Cannot exclude from mixture: *The DNA profile(s) obtained from _____ (Item__) is/are included as a possible contributor to/as contributors to the mixture.*

5.7.4.2 Excluded from the mixture: *The DNA profile(s) obtained from _____ (Item__) is/are excluded as a contributor to/are excluded as contributors to the mixture.*

5.7.5 Derived (Minor) Contributor of Mixture - *The DNA profile obtained from ___ (Item __) matches/is consistent with the derived/minor DNA profile obtained from ____ (Item __).*

5.8 Inconclusive Profiles/Component – for DNA profiles and/or components of profiles obtained from Items whose results are not suitable for comparison, the following statement shall be used: *"The DNA profile obtained from ____ (Item ___) is inconclusive due to insufficient quality of recovered DNA. No comparisons to reference profiles for either inclusion or exclusion can be performed."*

5.9 Additional Alleles – When additional alleles are present in an interpretable mixture that cannot be attributed to any of the known reference standards provided: *Additional DNA was present which cannot be accounted for by the standard(s) submitted.*

5.10 Comparisons Across Multiple Submissions – Unless necessary for clarification, there will be no repeated comparisons between items of evidence and reference standards already established in prior case records/submissions. Once an individual's contribution or exclusion has been

determined and reported, it need not be reiterated in subsequent case records/reports. Additionally, it need not be reiterated if no DNA profile or no interpretable profile was obtained previously.

5.11 Associations to Employees/Vendors/Batched Cases

5.11.1 Forensic Scientists shall follow the reporting guidelines already provided in this document and modify the positive association (i.e., match, consistent with, cannot be excluded) based upon the categories below.

5.11.2 Forensic Scientists shall report exclusions to known reference samples in the case.

5.11.2.1 **DNA Forensic Scientist who worked the case:** *…State Crime Laboratory Forensic Scientist who performed the DNA analysis on this item of evidence...*

5.11.2.2 **Forensic Scientist or Field Agent previously involved with the item:** *…a State Crime Laboratory Forensic Scientist/Agent who performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis...*

5.11.2.3 **State Crime Laboratory Employee, Vendor or Visitor not involved with the item:** *…State Crime Laboratory (employee, vendor, visitor) _____. This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion…*

5.11.2.4 **Sample in a batched case:** *…State Laboratory item number _____ which was analyzed along with items of evidence in this case…*

5.12 Likelihood Ratio Statistics

5.12.1 Likelihood ratio (LR) statistics will be generated on samples whose profiles yield an inclusionary interpretation to a reference sample. STRmix will be used to generate all LR results.

5.12.2 The population group with the lowest 99% lower bound HPD result will be used for reporting.

5.12.3 Statements may be adjusted to account for the total number of contributors in a profile or to account for the contributors used in the proposition setting.

5.12.4 The propositions considered in the LR calculations will be reported:

Given the evidence, the following propositions were considered for the statistical calculation.
Hypothesis 1 (H1): The evidence originated from ___ and ____ OR
Hypothesis 2 (H2): The evidence originated from ___ and an unknown, unrelated individual.

5.12.5 If the LR >1000, supporting inclusion, then the following will be reported: The (mixture) DNA profile obtained from ___ (Item__) is at least ___ times more likely if it originated from ___ (Item __) (H1) than if it originated from an unknown, unrelated individual (H2).

5.12.6 Conditioned: If the LR >1000, supporting inclusion, then the following will be reported: The mixture DNA profile obtained from ___ (Item __) is at least ___ times more likely if it originated from (assumed contributor) and ___ (Item __) (H1) than if it originated from (assumed contributor) and an unknown, unrelated individual (H2).

5.12.7 If the LR = between 1 and 1000, then the following will be reported: An uninformative likelihood ratio was obtained for the comparison of ___ (Item__) to the DNA profile obtained ___ (Item __).

5.12.8 If the LR <1, supporting exclusion, then the following will be reported: The (mixture) DNA profile is at least __ times more likely if it originated from an unknown, unrelated individual (H2) than if it originated from ___ (Item _) (H1).

5.12.9 If the included contributors cannot be included in the mixture together (i.e., multiple reference profiles gave the highest LR as the same component) the following statement will be added to the report: However, ___ (Item _) and ___ (Item __) cannot both be included in the mixture together.

Note: Qualifiers such as partial, major, derived, non-sperm fraction or sperm fraction, fraction 1, fraction 2, etc. shall be used as appropriate in the statistical statements.

5.12.10 If no statistical data is generated, the following statement shall be used: *No population frequency data were generated for the contribution of the DNA profile from _____ (Item) to this item.*

5.13 CODIS Statements: When profiles are to be entered/searched in the CODIS database, the following statements shall be added to the report as applicable.

5.13.1 The profile(s) from Item(s) ___ have been entered into the Combined DNA Index System (CODIS) in accordance with state and national regulations, where regular searches will be performed. Notification will be issued if there is a hit in the database or if the profile(s) is/are removed from CODIS at any time in the future.

5.13.2 The DNA profile(s) from Item(s)__ will no longer be routinely queried against the CODIS (Combined DNA Index System) Database.

5.13.3 No profiles will be routinely queried against the CODIS (Combined DNA Index System) Database.

5.13.4 Based on the information provided upon submission, no DNA profile(s) developed in this case will be routinely queried against the CODIS (Combined DNA Index System) Database. If additional investigative information is obtained, please contact the laboratory for further evaluation.

6.0 Limitations – N/A

7.0 Safety – N/A

8.0 References

Forensic Biology Section STR Interpretation Procedure

Forensic Biology Section Procedure for CODIS

9.0 Records – N/A

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
07/01/2020	16	Removed previous version history; 5.1 remove – RMP, update wording; 5.2.9 – add wording for no additional analysis; 5.2.11 – update naming; 5.2.14 – add wording to document STRmix usage; 5.2.17 – updated wording; 5.4 – move from 5.7; 5.5- add uninterpretable wording; 5.6.4 – remove RMP; 5.7.2.4.1, 5.7.3, 5.7.4, 5.8 – update report wording; 5.11 – remove name; 5.12 – update stats to Likelihood ratio; 8.0 update references