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.

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 RMP statistic. An exception to this requirement is when an assumed contributor is present in an intimate item (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, 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 DNA 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 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 ____(Container __) and slides prepared from Items ___ (Container __) 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 ___ this/these sample(s) is/are not being amplified. . No further analysis was performed on Item ___.*

5.4 Single Source Profiles

5.4.1 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.*

5.4.2 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.*

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

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

5.5 Mixtures

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

5.5.2 Mixtures with a Single Major Contributor (Distinguishable)

5.5.2.1 Known Reference Sample(s) Included: *The major contributor profile matches/is consistent with the DNA profile obtained from ______ (Item__).* See 5.4.4 for use of "matches/consistent with."

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

5.5.2.3 Known Reference Sample Assumed: *Assuming that _____,the donor of the known sample (Item __), is one of the sources of the DNA from this profile obtained from ____ Item (__), then the other component matches/is consistent with the profile obtained from the ______ (Item ___).*

5.5.2.4 Contribution to Overall Mixture:

5.5.2.4.1 Cannot exclude from the mixture: *The DNA profile(s) obtained from _________ (Item(s) ____) cannot be excluded as a contributor/as contributors to the mixture.*

5.5.2.4.2 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.*

5.5.3 Mixtures with Multiple Major Profile (Distinguishable):

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

5.5.3.2 Cannot exclude from the multiple major profile: *The DNA profile(s) obtained from ________ (Item_) cannot be excluded as a contributor/as contributors to the multiple major profile of this mixture.*

5.5.3.3 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 __) cannot be excluded as a contributor to the minor component of the mixture.*

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

5.5.4 Mixtures with No Major Contributor (Indistinguishable Mixture):

5.5.4.1 Cannot exclude from mixture: *The DNA profile(s) obtained from ______ (Item__) cannot be excluded as a contributor to/as contributors to the mixture.*

5.5.4.2 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.*

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

5.6 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 complexity and/or insufficient quality of recovered DNA.*

5.6.1 If the minor component is inconclusive; the known reference sample(s) may only be compared against the major contributor profile. The report wording will be the same as single source profile wording for both included and excluded reference samples with the qualifying, major contributor being added. For a two person mixture: "*Remaining minor contributor cannot be conclusively interpreted due to an insufficient amount of genetic data."* For a greater than 2 person mixture: *"Additional genetic data was detected, but cannot be conclusively interpreted due to complexity and/or insufficient quality of genetic data."*

5.7 No DNA Profile – When no alleles are detected above the analytical threshold: *No DNA profile was obtained from ______ (Item__).*

5.8 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.*

5.9 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.

5.10 Associations to Employees/Vendors/Batched Cases

5.10.1 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.

5.10.2 Forensic Scientists shall report exclusions to known reference samples in the case. (Refer to **5.3** and **5.4**.)

5.10.2.1 DNA Forensic Scientist who worked the case: *...State Crime Laboratory Forensic Scientist (name) who performed the DNA analysis on this item of evidence...*

5.10.2.2 Forensic Scientist or Field Agent previously involved with the item: *...State Crime Laboratory Forensic Scientist/Agent ________. This* *scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis...*

5.10.2.3 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…*

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

5.11 Random Match Probability Statistics

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

5.11.1 When Random Match Probability statistics have been generated for a profile, the following statement shall be used:

The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with/cannot be excluded from the DNA profile obtained from the ____ is approximately:
1 in _____ in the Caucasian population,
1 in _____ in the African American population, and
1 in _____ in the Hispanic population, using the population databases generated by NIST.

If the statistics are not generated for all loci "consistent with" shall be used. Cannot be excluded shall be used for indistinguishable mixtures.

5.11.2 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.*

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

5.12.1 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.

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

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

6.0 Limitations – N/A

7.0 Safety – N/A

8.0 References

Forensic Biology Section Procedure for Analysis and Interpretation using Fusion 6C

Forensic Biology Section Procedure for CODIS

9.0 Records – N/A

10.0 Attachments – N/A

Revision History

Effective Date	Version Number	Reason
01/03/2013	1	Original Document
02/01/2013	2	Added 5.2.6 to add statement to report for cases with evidence worked prior to 01/03/2013
03/08/2013	3	Definitions – clarified CPE and CPI; 5.2.4 – clarified when statement is added to report; 5.4 - Note – reworded statement to read # contributors; 5.4.1.2 – changed “predominant profile” to “predominant DNA profile”
05/30/2013	4	5.2.6 – added option for situation where comparisons cannot be made
09/13/2013	5	3.0 – updated definition for reference standard; 5.1 – removed “victim” wording; 5.2.6, 5.3.2 – clarified wording; 5.10 – clarified note when statement would be used; 5.11 – clarified notification report wording; 5.11.3 - added wording for one-time searches
09/25/2013	6	Header – added issuing authority titles; 5.11.3 – clarified wording; 5.11.4 – added wording for Notification of CODIS entry
12/18/2013	7	5.1 – changed wording to generate pop clock in all RMP cases; 5.14.1.1 – combined 5.14.1.1 and 5.14.1.2 for RMP stats
04/18/2014	8	3.0 – removed definitions, added references; 5.1 – removed population clock (added to statistics procedure); 5.2.1 – removed predominant profile; 5.3.2 – removed; 5.5.2, 5.14 – clarified wording; 5.14.1.1 – added requirement for all population groups; 5.14.2.2 – reworded for clarity
08/29/2014	9	5.2.6 – removed phone number; 5.2.7 – added wording for standards not suitable for comparison purposes

02/27/2015	10	5.4.1.1 – added “DNA”; 5.4.1.2 – changed wording for consistency; 5.10 – reworded to make consistent throughout section reporting; 5.12 – clarified wording; 5.14.2.2 – changed word for consistency
12/28/2015	11	5.2.7 – clarified wording; 5.2.8 – added extraction wording; 5.2.9 – updated report header and disposition note wording; 5.3 – added wording for assumed contributor to profile; 5.4 – removed Note; 5.4.1 – clarified wording for inclusion or exclusion; 5.4.2 – clarified wording for multiple major; 5.5 – added inconclusive wording and removed un-interpretable wording; 5.9, 5.15.3 - removed limited wording; 5.12.1 - clarified Note; 5.13.1 – added wording to contact NCSCL; 5.16.1.1 – removed world’s population reference; 8.0 – updated reference
12/20/2016	12	1.0, 2.0 – updated name of amplification kit; 3.0 – moved definition to section list; 5.1 – remove CPI; 5.2.2 – added wording for swabbing/cutting from item; 5.2.4 – changed to major; 5.2.4, 5.2.5 - added Y-STR loci; 5.2.6, 5.2.7 – wording change; 5.2.9 – changed loci; 5.2.10 – changed wording to clarify; 5.3 – added wording for quant results; 5.4.3 – added exclusion wording; 5.5.1, 5.5.3 – changed to major; 5.5.1.3 – added known reference assumed wording; 5.5.4 – added deduced contributor wording; 5.6 – combined statements, added comparison of samples with inconclusive minor; 5.12 remove presence of male wording; 5.14 – remove CODIS wording (moved to a CODIS procedure); 5.11 – changed wording to reflect major and NIST database, removed CPI wording; 8.0 – updated references
03/23/2018	13	5.1, 5.3 – added wording to allow qualifying words and removal of redundant phrasing from reporting statements; 5.2.5 – added allowance for male presence based on quant results; 5.2.9 – added wording for contamination of negative control; 5.4.4 – clarified wording for when match/consistent with is used; 5.5.1 – added primary mixture statement, removed below; 5.5.2.4.2 – changed predominant to major; 5.5.3.1, 5.4.8.1 – removed primary statement (under 5.5.1); 5.6 – clarified wording for inconclusive statement; 5.9 – clarified when comparison from previous submission is to be performed; 5.11.1 – added wording for cannot be excluded; 5.12 – added CODIS statement wording
01/25/2019	14	5.2.3 – changed naming of fractions in differential extraction; 5.2.7 – added wording for outsourced data CODIS hit reporting; 5.2.9 – added wording for previous interpretation cases; 5.2.11 – add wording for cases where only standards are worked; 5.2.14 – added wording for container for slides; 5.6 – clarified wording