# 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.

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 or could be 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 may 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. If RMP statistics are generated, denote that the NIST population frequencies were used. The population group with the lowest RMP result will be reported (not all three population group results).

**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** If not listed under items created/separated header, then the report section for disposition 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 obtained, no further analysis was*

*performed on the sample(s) taken from Item(s) ___. "Sample(s*)" may be removed if the statement is reporting the results from a fraction or an already sub-itemed piece of evidence where the result can be applied to the whole.
The following statement will be added to the report if additional testing is possible. These situations include sample selection after quant where samples remain that meet threshold (e.g., F1 samples where F2 were amplified) or additional samples/areas in case could be tested (e.g., additional KM+ samples not previously extracted). Situations where the statement is not to be added to the report include no samples exceed quantitation threshold for amplification, no extract remains for testing (e.g., shell casings), or all swabs underwent DNA testing. *Additional testing may be possible for certain items in this case. If additional analysis is required, contact the analyst for sample evaluation.*
When samples are being retained for YSTR testing due to quantification results, the following statement shall be added to the report unless documented in the report disposition*: The DNA extracts/lysates 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." The portion suitable to the profile being interpreted will be used for reporting and the other statement will be removed.

**5.6** **Interpretable DNA Profiles –** the following statements shall be used in the reporting of interpretable profiles.

**5.6.1** **Number of contributor statement:** *The DNA profile obtained from __ (Item _) is being interpreted as a single source profile/mixture of (#) contributors*.

**5.6.2** **Interpretable/Inconclusive components:** *This mixture contains _ interpretable components. Component __ is inconclusive due to an insufficient quality of recovered DNA. No comparisons to reference profiles for either inclusion or exclusion can be performed to this component/these components.*

**5.6.3** **Reference profile included:** *The DNA profile(s) obtained from __ (Item _) is/are included as a contributor(s) __ (and __ if required) of this mixture.*

**5.6.4** **Reference profile excluded:** *The DNA profile(s) obtained from __ (Item _) is/are excluded as a contributor to this profile/the interpretable component(s).*

**5.6.5** **Unknown profile**: *The DNA profile obtained from ____ (Item __) is from an unknown contributor.* For a mixture profile, the following wording may be added to the reporting statements: *containing at least one male profile.*

**5.6.6** **Bone sample in UHR case:** Report as unknown profile – *The DNA profile obtained from ____ (Item __) is from an unknown (male) contributor.*

**5.6.7** **Known Reference Sample Assumed:** *The interpretation of this profile/mixture is being conditioned using the DNA profile obtained from ___ (Item __) as contributor one.*

**5.6.8** **Inconclusive Likelihood Ratio (LR )to interpretable component:** Report as "no conclusion can be rendered as to the contribution of __ to the interpretable component(s) of the mixture due to an inconclusive likelihood ratio result." Inconclusive LR to inconclusive component: Report "excluded as a contributor to the interpretable component(s) of the mixture."

**5.6.9** **Inconclusive:** *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.*

**5.6.10** **Additional Comparisons –** When additional interpretable contributors are present in a 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.* When contributor one is the conditioned reference and the other contributors are inconclusive: *Due to the quality of the profile, no future comparisons to this item will be performed.*

**5.7** **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.

**5.8** **Associations to Employees/Vendors/Batched Cases**

**5.8.1** 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.

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

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

**5.8.2.2** **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...*

**5.8.2.3** **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…*

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

**5.9** **Likelihood Ratio Statistics**

**5.9.1** 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.

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

**5.9.3** 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.

**5.9.4** The propositions considered in the LR calculations will be reported for inclusions or if requested for inconclusive results:

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.

**5.9.5** A statement shall be added to the report to inform which contributor gave the highest LR from the summary of contributors. This statement is not needed for items that give an inconclusive or exclusionary LR result. *The statistical calculations best fit the DNA profile obtained from __( Item _) as contributor _ in this mixture profile.* If possible, the best fit statement will be incorporated into the results statements for the comparisons.

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

**5.9.7** Conditioned: If the LR >1000, supporting inclusion, then the following will be reported: *The mixture DNA profile obtained from ___ (Item __) is approximately ___ 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).*

**5.9.8** If the LR is between 1e-3 and 1e3, then the LR statistics will be included in the case notes, but not reported unless specifically requested. If requested, the following will be reported: *An uninformative likelihood ratio was obtained for the comparison of ___ (Item__) to the DNA profile obtained ___ (Item __).* This wording may be omitted if the no conclusion results statement is being reported for this profile.

**5.9.9** If the LR <1e-3, supporting exclusion, the LR statistics will be included in the case notes, but not reported unless specifically requested. If requested, then the following will be reported: *The (mixture) DNA profile is approximately __ times more likely if it originated from an unknown, unrelated individual (H2) than if it originated from ___ (Item _) (H1).* The resultant statistical value will be adjusted to be consistent with the proposition statement.

**5.9.10** 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.

**5.9.11** 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.* To accurately reflect the analysis, "reported" may replace "generated" in the reporting statement based on the testing performed in the case record.

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

**5.10.1** 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.

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

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

**5.10.4** 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.

**5.10.5** For entry of YSTR profiles that do not have an associated autosomal profile, the following statement shall be used: "The YSTR profile(s) from Items __ have been entered into the Combined DNA Index System (CODIS) in accordance with state and national regulations. No profiles will be routinely queried against the CODIS Database at this time. Notification will be issued if the profile(s) is/are queried, if there is a hit in the database, or if the profile(s) is/are removed from CODIS at any time in the future.

**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 |
| 05/24/2024 | 19 | 5.3 Updated stop at quant statement wording; 5.6.6 – add UHR bone sample wording; 5.6.7 – updated conditioning statement; 5.6.9 – added wording for samples with no additional comparisons; 5.9.11 added reporting option for statement |