6.1 Responsibility:

DNA Section Personnel.

6.2 DNA Report Templates:

Note: The DNA Report Template is located in the controlled Current NUC Report Templates folder on the S: Drive.

6.2.1 Nuclear DNA Reports: Formerly, there were multiple types of DNA reports. Currently, all DNA reports are called DNA Reports. “Supplemental” and “Amended” may be added to this title as appropriate.

6.2.2 Mitochondrial DNA (mtDNA) Reports: mtDNA report statements are incorporated in the DNA Report Template. See mtDNA SOP-43 for guidelines on mtDNA report writing.

6.2.3 Supplemental Report Numbering: Supplemental reports for each report heading are numbered independently of each other. For example:

DNA Report
Supplemental DNA Report
Supplemental DNA Report II
Amended DNA Report

6.2.4 Statistics Templates

Note: See DNA SOPs 21, 25, 39, and 40 for single source and mixture profile interpretations and statistic details.

6.2.4.1 Statistics are calculated and documented for case files using STRmix (single source and mixture STR profiles), DNA QR-44 (match probability of parentage), Y-Mix and YHRD, (Y-STR profiles), PopStats with DNA QR-46 (probability of kinship), and DNA QRs-307 and 318 (for deconvolution). When applicable, the Excel workbooks containing these listed quality records are found on the S: Drive.

6.2.4.2 Frequency data to calculate the statistical weight of DNA matches may be derived from the following databases:

CODIS Popstats Database
Y-Chromosome STR Haplotype Reference Database (yhrd.org)

Per specific requests, with TL and DD/AD approval, other peer reviewed databases may be used.

6.2.5 GlobalFiler, Fusion 6C and ID/IDP Conclusion Statements:

Note: If multiple amplification kits are reported out together, specify kit name in conclusion statements.

6.2.5.1 Elimination through STRmix: The following statements will be used when the LR calculated through STRmix is less than 1:

6.2.5.1.1 Single source profiles: "The results are consistent with the DNA profile from item #xx originating from a single (add if can determine: male/female) individual. The results do not support the hypothesis that John Doe is the source of this profile. Assuming one individual, John Doe is eliminated as the source of the DNA profile from item #xx."

6.2.5.1.2 Mixture profiles: "The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). The results do not support the hypothesis that John Doe is a contributor to this profile. Assuming xx contributors, John Doe is eliminated as a contributor to the DNA profile from item #xx."

6.2.5.2 Elimination without using STRmix: The following statements will be used when an individual is eliminated visually by an analyst, without running STRmix software:

6.2.5.2.1 Single Source: "The results are consistent with the DNA profile from item #xx originating from a single (add if can determine: male/female) individual. Jane Doe is eliminated as the source of the DNA profile from item #xx."

6.2.5.2.2 Mixture profiles (profile not too complex to run through STRmix): "The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). Jane Doe is eliminated as a contributor to the DNA profile from item #xx."

6.2.5.3 Inconclusive through STRmix: The following statements will be used when the LR calculated through STRmix is ≥ 1 but less than 10,000 for Fusion 6C, and ≥ 1 but less than 1,000 for GlobalFiler and ID/IDP:

6.2.5.3.1 Single source profiles: "The results are consistent with the DNA profile from item #xx originating from a single (add if can determine: male/female) individual. Assuming one individual, given the low likelihood ratio(s) calculated, the results are inconclusive as to whether John Doe could be the source of the DNA profile from item #xx."

6.2.5.3.2 Mixture profiles: “The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). Assuming xx contributors, given the low likelihood ratio(s) calculated, the results are inconclusive as to whether John Doe could be a contributor to the DNA profile from item #xx.”

6.2.5.4 Other conclusions without running STRmix:

6.2.5.4.1 The following statement will be used when the DNA profile is a mixture too complex for STRmix deconvolution: “The results indicate that the DNA profile from item #xx is a mixture that is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #xx, no comparisons will be made.”

6.2.5.4.2 The following statement will be used when the profile has limited data detected to run STRmix software, and the profile does not warrant an elimination conclusion: “Due to limited data detected from item #xx, the comparison to John Doe is inconclusive.”

6.2.5.5 Positive associations (i.e. LR’s higher than the laboratory’s inconclusive zone) as determined through STRmix:

Note: The lowest calculated likelihood ratio HPD lower bound on the STRmix report, ceilinged at 100 billion, will be reported out. The following statement will be used when LR ≥ 10,000 for Fusion 6C and LR ≥ 1,000 for GlobalFiler and ID/IDP:

6.2.5.5.1 Single source profiles: “The results are consistent with the DNA profile from item #xx originating from a single (add if can determine: male/female) individual. Assuming one individual, the DNA profile from item #xx is at least xx times more likely to occur if it originated from John Doe than if it originated from an unknown individual.”

6.2.5.5.1.1 For samples that are identical (same data all above the stochastic threshold regardless of injection) to one another, there is no need to run STRmix again. The same LR may be reported as follows:

“The results from items #xx, #yy, and #zz are identical to the results from item #aa. Therefore, assuming one individual, the DNA profile(s) from item(s) #xx, #yy, and #zz is/are at least xx times more likely to occur if it/they originated from Joe Smith than if it/they originated from an unknown individual.”

6.2.5.5.2 Mixture profiles (without conditioning): “The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). Assuming xx contributors, the DNA profile obtained from item #xx is at least xx times more likely to occur if it originated from John Doe and xx unknown individual(s) than if it originated from xx unknown individuals."

6.2.5.5.3 Mixture profiles (with conditioning): "The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). Jane Doe is assumed to be a contributor to the DNA profile from item #xx." Assuming xx contributors, where Jane Doe is one of the contributors, the DNA profile obtained from item #xx is at least xx times more likely to occur if it originated from John Smith, (and) Jane Doe (and xx unknown individual(s)) than if it originated from Jane Doe and xx unknown individual(s)."

6.2.5.6 The following statement will be used when assuming a known to a single source profile "The results are consistent with the DNA profile from item #xx originating from a single (male/female) individual. J. Doe is assumed to be the source of the DNA profile from item #xx."

6.2.5.7 Statement when conditioning a laboratory staff member:

"The results are consistent with the DNA profile from item #xx being a mixture of xx contributors (add if can determine: with (at least) xx of them being male). The results are consistent with a laboratory staff member being a contributor to the DNA profile from item #xx. Assuming xx contributors, where the laboratory staff member is one of the contributors, the DNA profile obtained from item #xx is at least xx times more likely to occur if it originated from John Smith, (and) the laboratory staff member (and xx unknown individual(s)) than if it originated from the laboratory staff member and xx unknown individual(s)."

6.2.6 Report wording for clear major in 5+ person mixtures.

6.2.6.1 Consistent with source wording: "The results are consistent with the DNA profile from item #xx being a mixture. A major (male/female) profile was deduced from item #xx. The results are consistent with J. Doe being the source of the major profile deduced from item #xx. The major profile deduced from item #xx is at least xx times more likely to occur if it originated from J. Doe than if it originated from an unknown individual.

6.2.6.2 Eliminated as source wording: "The results are consistent with the DNA profile from item #xx being a mixture. A major (male/female) profile was deduced from item #xx. J. Smith is eliminated as the source of the major profile deduced from item #xx."

6.2.6.3 Wording for full profile with major component deduced: "The results are consistent with the DNA profile from item #xx being a mixture of (at least) five contributors (with at least xx of them being male). This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #xx, no comparisons to the minor alleles present in the profile will be made."

6.2.7 Y-STR Conclusion Statements:

Note: The statistic being reported is the highest figure (most common) from the African American, Caucasian, or Hispanic population with 95% confidence interval already applied. Loci not used in statistical calculations will be noted through a footnote designation (Locus not used for statistics) in the allele table, located in the appendix of the report.

Note: If multiple amplification kits are reported out together, specify kit name in conclusion statements.

Note: Wherever a mixture statement specifies "xx" contributors, know that for Yfiler profiles, "xx" cannot exceed 2 contributors, based upon our validations.

6.2.7.1 Single-source profiles with full detection at all loci with results: "The results are consistent with the DNA profile from item #xx originating from a single male lineage. The results are consistent with John Doe (or another member of the same male lineage) being the source of the DNA profile from item #xx. The expected frequency of individuals who could be the source of the DNA profile from item #xx is less than 1 in xx in the general male population."

6.2.7.2 Single-source profiles with partial detection at all loci with results: "The results are consistent with the DNA profile from item #xx originating from a single male lineage. John Doe (or another member of the same male lineage) cannot be eliminated as the source of the DNA profile from item #xx. The expected frequency of individuals who could be the source of the DNA profile from item #xx (at loci…/ at all loci tested except…) is less than 1 in xx general male population."

6.2.7.3 Mixture profiles with full detection at all loci with results: "The results are consistent with item #xx being a mixture of xx male lineages. John Doe (or another member of the same male lineage) is included as a potential contributor to the DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the DNA profile item #xx is less than 1 in xx in the general male population."

6.2.7.4 Mixture profiles with partial detection at loci with results: "The results are consistent with item #xx being a mixture of xx male lineages. John Doe (or another member of the same male lineage) cannot be eliminated as a potential contributor to the DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the DNA profile from item #xx (at loci…/ at all loci tested except…) is less than 1 in xx in the general male population."

6.2.7.4.1 Deconvolution of major contributor: "The results are consistent with item #xx being a mixture of xx male lineages. A major profile was deduced from item #xx. The results are consistent with John Doe (or another member of the same male lineage) being the source of the major DNA profile deduced from item #xx. The expected frequency of individuals who could be the source the major DNA profile from item #xx is less than 1 in xx in the general male population."

6.2.7.5 Elimination from Y–STR profiles:

6.2.7.5.1 Single Source Profiles: "The results are consistent with the DNA profile from item #xx originating from a single male lineage. J. Doe is eliminated as the source of the DNA profile from item #xx."

6.2.7.5.2 Mixture Profiles: "The results are consistent with item #xx being a mixture of (at least) xx male lineages. J. Doe is eliminated as a contributor to the DNA profile from item #xx." If deconvolution: John Doe is eliminated as the source of the major DNA profile deduced from item #xx.

6.2.7.6 If limited data is detected from an item for a comparison, report as follows: "Due to limited data detected from item #xx, the comparison to J. Doe is inconclusive."

6.2.7.7 Mixture too complex (more than 3 lineages for Yfiler Plus, and more than 2 lineages for Yfiler): "Due to the complexity of the DNA profile from item #xx, the comparison to J. Smith is inconclusive."

6.2.8 Statistics statement for paternity (RMNE): "The expected frequency of males who could be the father of NAME is less than 1 in xx in the general population."

6.2.8.1 Statistics statement for Kinship analysis: see DNA SOP-25 Kinship Analysis.

6.2.9 Conclusion Templates:

6.2.9.1 The following footnote will be used when STRmix was used to calculate LR: "Profile analyzed and comparison made using STRmix™ analysis software."

6.2.9.2 The following statement shall be used when a profile is a 5 person mixture, too complex for STRmix interpretation, but case information indicates assuming individual(s) will be appropriate and could therefore make the mixture interpretable: "Item #xx could potentially be interpreted with STRmix if elimination known(s) are submitted."

Note: This statement is not warranted with every 5 person mixture. An example of an exception: A weapon possession case with evidence not being touched by a victim, etc. Case scenario should determine utilization of this wording.

6.2.9.3 Statement stating that a known is assumed as a contributor to a profile shall be stated prior to any statistical statements involving that assumption.

6.2.9.4 Analysts should combine like conclusions and/or separate those conclusions from the number of contributor's statement as warranted, making statements grammatically correct while increasing ease of interpretation for our clients.

6.2.10 Additional Report Phrasing: The following are commonly used in DNA Reports; however, this is not an exhaustive list of all possible remarks or report wording allowed by the DNA Section. All buttons in the DNA Report Buttons tab or More DNA Report Buttons tab in the DNA Report Document located on the S: Drive are approved wording. Any variation or additions to these phrases are allowed with TL approval.

6.2.10.1 Evidence disposition: The following statements will be used, depending on how the evidence is disposed:

6.2.10.1.1 For evidence consumed in testing: "Item #xx was consumed in testing." For DNA extracts consumed in testing: "The DNA extract from item #xx was consumed in testing."

6.2.10.1.2 Item #xx (or a sample from item #xx) was retained at the laboratory. For reports containing new questioned sample testing, with those extracts being retained at the laboratory, an additional statement will be added to the remarks section: "Any remaining DNA extracts are retained at the laboratory." There is no need to list the item numbers of these extracts, nor a need to list them in the Evidence Description section.

6.2.10.1.3 Item #xx was returned to the submitting agency.

6.2.10.1.4 Item #xx was forwarded to the xx Unit of the laboratory.

6.2.10.1.5 If only empty packaging for a known sample is being returned, with the testable portion of that known sample being retained at the laboratory, analysts shall use the following statement: "The testable portion from item #xx was retained at the laboratory. Item #xx was returned to the submitting agency."

6.2.10.2 If trace materials (that could be tested) were noted in a physical examination worksheet, and not reported on in a separate Forensic Biology Report, those findings must be noted in the "Remarks" section of the DNA report.

6.2.10.2.1 Trace materials only noted, as appropriate: "Hair-like fibers and other trace materials were noted on item #xx but not collected."

6.2.10.2.2 Trace materials collected and returned to original packaging: "Hair-like fibers and other trace material were collected from item #xx and returned to the submission packaging."

6.2.10.2.3 There is no need to report out trace material on cigarette/tobacco material.

6.2.10.2.4 When an evidence description is used, it is not necessary to carry forward the "container". For example, Submission #001: Box "with stained knife"; item #001-001: stain on knife. The box that the knife was submitted in does not have to continue in the description.

6.2.10.3 For cases in which a sample was entered into CODIS, the "Remarks" section will state that the submitting agency will be notified of any positive CODIS associations.

6.2.10.4 Items listed in the under "Evidence Description", but not tested, shall be noted as such in the "Remarks" section.

6.2.10.5 Any request for appropriate known samples shall be noted in the "Remarks" section.

6.2.10.6 If the Quantifiler-Trio results dictate that additional male-specific testing may be beneficial to the client if a known sample is submitted, this shall be noted in the "Remarks" section, so long as controls are still present to perform this testing.

6.2.10.7 Any testing results from Kastle-Meyer (KM) (whether sent to DNA or not sent to DNA), are reported out. For blood screening testing not reported by FB: "A screening test for the presence of blood was performed on (additional) (stains located on) item #1. …

6.2.10.7.1 Positive: Blood was indicated (on the (additional) stains) with this test."

6.2.10.7.2 Negative: Blood was not indicated (on the (additional) stains) with this test."

6.2.10.7.3 Inconclusive: Due to indeterminate results and/or substrate interference, this testing was determined to be inconclusive."

6.2.10.8 Notes of non-blood like stains, dirt, grass, etc. are not reported out, but noted on worksheets.

6.2.10.9 KM Testing Reporting Summary:

In Testing Summary Table AND in Conclusions Section	Stain KM tested, collected, and tested for DNA or collected, tested, and retained for possible DNA testing
In Conclusions Section	Stain KM tested, but not collected for DNA
In Remarks Section	Reddish-brown stains noted on worksheets, but not tested

6.2.10.10 Stop at Quantitation statement (property crimes): When no DNA has been detected in quantitation, report in Remarks section: "Since no human DNA was detected from item #xx using the Quantifiler Trio DNA quantitation method, no further testing has been performed." This will be noted in the "Testing Summary" table, under a "Halted after Quantitation" column.

6.2.10.11 Reporting out items that underwent the Male Screen procedure:

6.2.10.11.1 In the "Conclusions" section, the actual male screen procedure will be reported out as follows: All to start with "A screening test for the presence of male DNA was performed on item #xx. …

6.2.10.11.1.1 Positive screen: Male DNA was detected with this test."

6.2.10.11.1.2 Negative screen: Male DNA was not detected with this test."

6.2.10.11.1.3 Inconclusive result (insufficient human DNA detected): Due to the low quantity of total human DNA, this testing was determined to be inconclusive."

6.2.10.11.1.4 Inconclusive result (Microcon failure): Due to indeterminate results, this testing was determined to be inconclusive."

6.2.10.11.2 All male screen procedure results will also be summarized in the "Testing Summary" table as follows:

TESTING SUMMARY

Item #	Screening	Profile Obtained[1]	Type	CODIS Entry
		GF		
1-1	Male DNA (-)			
1-2	Male DNA (+)	Yes	Male	Yes – CT and National
1-3	Male DNA (inc)	Yes	Female	No - Not Appropriate

[1] GF = GlobalFiler STR DNA amplification kit

6.2.10.11.3 Halt at quant statements for casework questioned samples that previously tested positive or inconclusive through the male screen procedure, and not being amplified after EZ1 extraction (to be reported in remarks section):

6.2.10.11.3.1 No male DNA detected: "Since no (male) DNA was detected from item #xx using the Quantifiler Trio DNA Quantitation method, no further testing has been performed."

6.2.10.11.3.2 Sufficient male DNA detected for male-specific testing only, known from suspect is not in-house: "Male DNA was indicated in item #xx with high levels of total human DNA compared to male DNA, therefore no further testing has been performed. Additional male-specific testing may be performed if a known sample from a/the suspect is submitted."

6.2.10.11.3.3 Sufficient male DNA detected for testing, but more probative/positive samples in case amplified: "Sufficient male DNA on item #xx was detected, but no further testing was performed at this time."

6.2.10.11.4 Additional statement to be added to "Remarks" section when sexual assault kits have items not tested: "Further examination on item #xx may be conducted upon request."

6.2.11 Additional DNA Report Sections

6.2.11.1 Evidence Description: Exhaustive list of all items of evidence pertaining to report.

6.2.11.1.1 Multiple cuttings of a singular item taken for different purposes may be listed under parent item, so long as all different purposes are listed on report. For example vaginal swabs from a sexual assault kit (#001-002-02) may have a Y-screen cutting, a cutting for DNA testing, and a cutting for additional serological testing. Notation for and fractions of a differential extraction would be off of this item. The Y-screen result will be listed for #001-002-02, and the "Remarks" section note will that item #001-002-02 was retained at the laboratory for further serological testing. For example:

EVIDENCE DESCRIPTION

#001-002-02	Vaginal swabs[1]
#001-002-02A	Vaginal swabs, EF
#001-002-02B	Vaginal swabs, SF

[1] A differential extraction was performed, separating the DNA extracted from this item into an epithelial-rich fraction (EF) and a sperm-rich fraction (SF). Detection of some DNA from one fraction in the other may occur due to incomplete separation.

TESTING SUMMARY

Item #	Screening	Profile Obtained[1]	CODIS Entry
		GF	
001-002-02	Male DNA(+)		
001-002-02A		Yes	No - Not Appropriate
001-002-02B		Yes	Yes - CT and National

[1] GF = GlobalFiler STR DNA amplification kit

REMARKS

Item #001-002-02 was retained at the laboratory. Additional serological testing may be conducted upon request.

6.2.11.2 Testing Summary: Contains table documenting any items tested, which, if any, DNA profiles were obtained for that item (or if the sample was halted at quantitation), information regarding CODIS entries for appropriate samples, and when applicable, details regarding previously tested samples and screening test results (including blood and male DNA). If the DNA Report does not have a conclusions summary table, the type of DNA profile (single source or mixture), will also be documented in the testing summary. For example:

TESTING SUMMARY

Item #	Screening	Profile Obtained[1]	Type	CODIS Entry
		GF		
1S1	▨	Yes	Mixture	Yes - CT and National
1S3	Blood(+)	Yes	Male	No - Not Appropriate

[1]GF = GlobalFiler STR DNA amplification kit

6.2.11.3 Conclusions Summary: Contains table documenting items that had profile results, the description of that evidence, the type of DNA profile (single source or mixture), and conclusions to all knowns associated in the case. For example:

CONCLUSIONS SUMMARY

Item #	Description	Type	J. Doe (#2)	J. Smith (#3)
1S1	Swabbing – Steering Wheel	Mixture	Assumed	Included
1S3	Cutting – Cigarette Butt	Female	Consistent with Source	Eliminated

6.2.11.4 Appendix: Contains all DNA profiles in appropriate allele tables.

6.2.12 Report templates for CT DSS reporting results generated by outsourcing labs:

6.2.12.1 Report statements for single-source profiles (if STRmix is not being run by outsourcing vendor):

a. “The results are consistent with NAME being the source of the DNA profile from item #xx. The expected frequency of individuals who could be the source of the DNA profile from item #xx is less than 1 in xx in the general population.” Note: The statistic being reported is the highest figure (most common point estimate) from the African American, Caucasian, or Hispanic populations.

b. “NAME cannot be eliminated as the source of the DNA profile from item #xx. The expected frequency of individuals who could be the source of the DNA profile from item #xx (at loci…/ at all loci tested except…) is less than 1 in xx in the general population.”

6.2.12.2 Report statements for mixture profiles (if STRmix is not being run by outsourcing vendor):

a. "The results are consistent with item #xx being a mixture. NAME is included as a potential contributor to the DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the DNA profile (at loci…/ at all loci tested except…) from item #xx is less than 1 in xx in the general population."

b. "The results are consistent with item #xx being a mixture. NAME cannot be eliminated as a potential contributor to the DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the DNA profile from item #xx (at loci…/ at all loci tested except…) is less than 1 in xx in the general population."

c. <u>Assumed 2-person mixture (major)</u>: "The results are consistent with item #xx being a mixture. Assuming two contributors to the mixture, a major profile was deduced. The results are consistent with NAME being the source of the major profile deduced from item #xx. The expected frequency of individuals who could be the source of the major DNA profile deduced from item #xx is less than 1 in xx in the general population."

d. <u>Assumed 2-person mixture (minor)</u>: "The results are consistent with item #xx being a mixture. Assuming two contributors to the mixture, a minor profile was deduced. The results are consistent with NAME being the source of the minor profile deduced from item #xx. The expected frequency of individuals who could be the source of the minor DNA profile deduced from item #xx is less than 1 in xx in the general population."

e. <u>3 & 4 person mixtures with deduced major:</u> "The results are consistent with item #xx being a mixture. A major profile was deduced. The results are consistent with NAME being the source of the major DNA profile from item #xx. The expected frequency of individuals who could be the source of the major DNA profile deduced from item #xx is less than 1 in xx in the general population."

6.2.12.3 F6C report statement for mixture profiles when using the restricted CPI calculation: "The results are consistent with item #xx being a mixture. A major DNA mixture profile was detected. NAME is included as a potential contributor to the major DNA mixture profile from item #xx. The expected frequency of individuals who could be a contributor to the major DNA mixture profile deduced from item #xx is less than 1 in xx in the general population."

6.2.12.4 Report wording for 5+ person mixtures:

6.2.12.4.1 No clear major: "The results are consistent with item #xx being a mixture of 5 contributors (with at least xx of them being male). This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #xx, no comparisons will be made."

6.2.12.4.2 >5 person mixtures: “The results are consistent with item #xx being a mixture of at least 5 contributors (with at least xx of them being male). This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #xx, no comparisons will be made.”

6.2.12.4.3 Deduced major portion of profile: “The results are consistent with the DNA profile from item #xx being a mixture. A major (male/female) profile was deduced from item #xx. J. Smith is eliminated as the source of the major profile deduced from item #xx.”

6.2.12.4.4 Full profile with deduced major: “The results are consistent with the DNA profile from item #xx being a mixture of five contributors (with at least xx of them being male). This profile is too complex for STRmix interpretation. Due to the complexity of the DNA profile from item #xx, no comparisons to the minor alleles present in the profile will be made.”

6.2.13 Amended report letter (sample):

Date

Asst. State's Attorney
Hartford State's Attorney's Office
101 Lafayette St.
Hartford, CT 06106

RE: Connecticut DESPP, Division of Scientific Services, Case ID, Police Department Case #.

Dear Ms. Attorney:

During a review of the supplemental DNA report dated xx-xx-xx for the above case a typographical error was noted.

In section 3 the second to last sentence should read:
Item #1 was returned to the appropriate submitting agency.

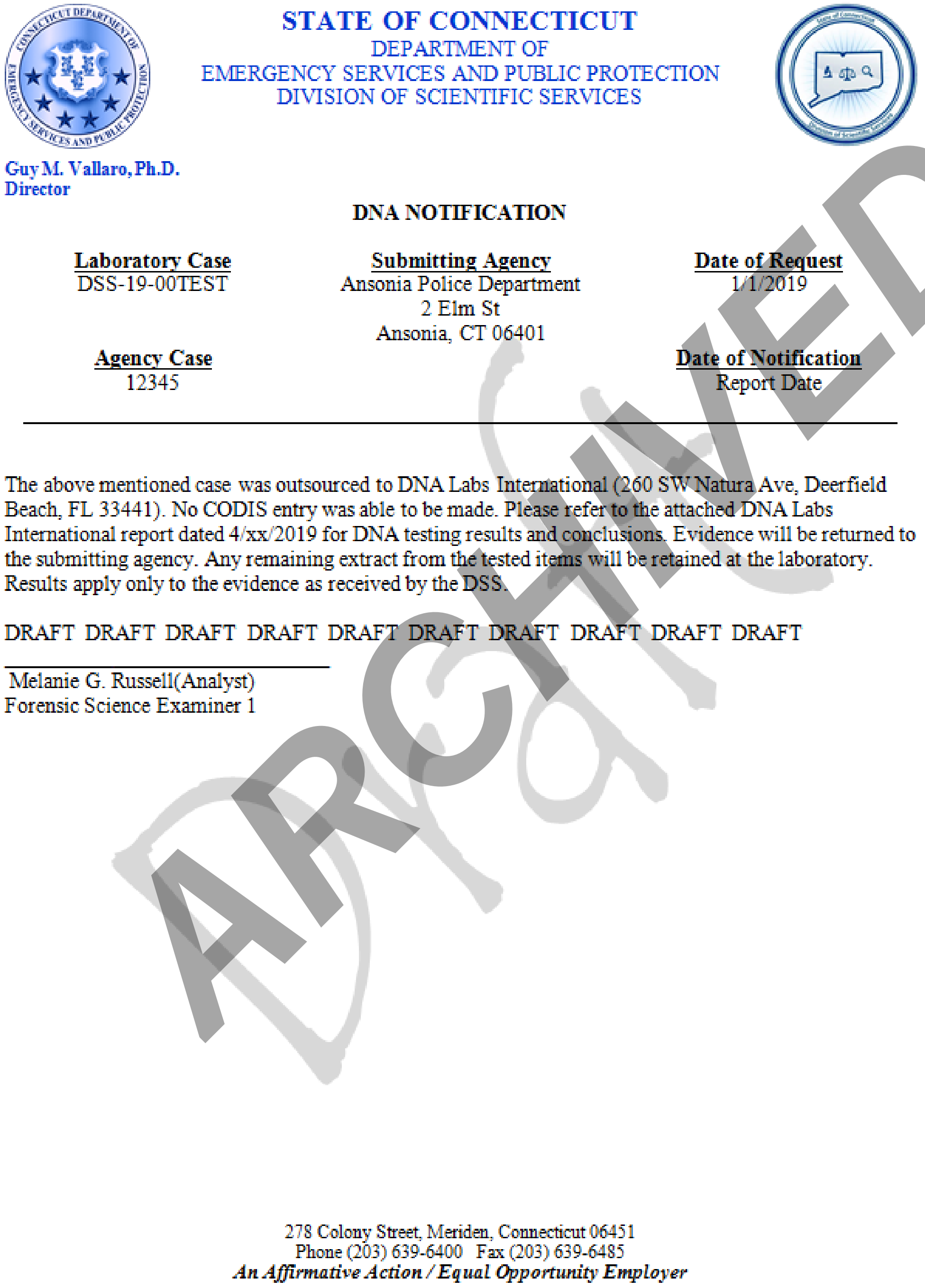
Enclosed is an amended copy of the report. Please forward this information to the appropriate individual(s).

Thank you for your attention in this matter.

Sincerely,

____
Analyst
Forensic Science Examiner

6.2.14 No Ownership Notifications



STATE OF CONNECTICUT
DEPARTMENT OF
EMERGENCY SERVICES AND PUBLIC PROTECTION
DIVISION OF SCIENTIFIC SERVICES

Guy M. Vallaro, Ph.D.
Director

DNA NOTIFICATION

Laboratory Case
DSS-19-00TEST

Submitting Agency
Ansonia Police Department
2 Elm St
Ansonia, CT 06401

Date of Request
1/1/2019

Agency Case
12345

Date of Notification
Report Date

The above mentioned case was outsourced to DNA Labs International (260 SW Natura Ave, Deerfield Beach, FL 33441). No CODIS entry was able to be made. Please refer to the attached DNA Labs International report dated 4/xx/2019 for DNA testing results and conclusions. Evidence will be returned to the submitting agency. Any remaining extract from the tested items will be retained at the laboratory. Results apply only to the evidence as received by the DSS.

DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT

Melanie G. Russell(Analyst)
Forensic Science Examiner 1

278 Colony Street, Meriden, Connecticut 06451
Phone (203) 639-6400 Fax (203) 639-6485
An Affirmative Action / Equal Opportunity Employer

6.3 List of Critical Reagents and Equipment

All critical reagents will be appropriately tested to ensure proper performance prior to their use in casework samples. See SOP-8 for QC testing.

6.3.1 Critical reagent chemicals and solutions:

Anode Buffer Container
Cathode Buffer Container
dH_2O (used for sample prep through amplification)
Dithiothreitol (DTT)
Extraction Buffer
Formamide
PCIA (Phenol/Chloroform/Isoamyl Alcohol 25:24:1 v/v)
Prep-N-Go solution
TE Buffer

6.3.2 Critical Enzymes/Biologicals/Kits:

Proteinase K
Quantifiler Trio Kits
Primer Sets (if not as part of an assembled kit)
Allelic Ladders (if not as part of an assembled kit)
EZ1 Extraction Kits
Yfiler Plus Kits
GeneScan^{TM} -600 LIZ^{TM}
POP-4
GlobalFiler Amplification Kits
GlobalFiler Express Amplification Kits
cRNA

6.3.3 Evaluation and testing of critical reagents and solutions Refer to DNA SOP-8.

6.3.4 Critical Instruments: those requiring an annual performance check prior to use. Below is a list of what is included as a critical instrument.

Note: Refer to DNA SOP-9 for performance check information on the below listed equipment.

Thermometers that are traceable to national or international standard(s)
Balance/Scales
Incubators/heat blocks used in analytical procedures

Thermal cyclers
Thermal cycler temperature-verification system
  Note: this instrument is not currently in use due to an outside vendor conducting performance checks of thermal cyclers (see DNA SOP-9)
Real-Time PCR Instruments
Robotic Systems (EZ1, etc.)
Electrophoresis detection systems (Genetic Analyzers)
Pipettes
Centrifuges

6.4 General Chemical Inventory

6.4.1 Dry Chemicals:

Dithiothreitol (DTT)
Dryrite
Ethylenediaminetetraacetic acid disodium, dihydrate (EDTA)
Potassium Chloride
Sodium Chloride
Sodium Dodecyl Sulfate (lauryl sulfate)
Sodium Hydroxide
TRIS, ULtraPure Grade
TRIS Hydrochloride
TRIS-base (hydroxymethyl amino methane)

6.4.2 Liquid Chemicals:

Ethanol, Reagent
Hydrogen Peroxide
pH Buffer (4.00, 7.00 & 10.00)
Proprietary Solvent, anhydrous
Sodium Hypochlorite (bleach)
Hydrochloric acid
Conditioning Reagent

6.4.3 Enzymes/Biologicals:

DS-36 Matrix Standard (Dye Set J6)