

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. Unsigned, electronic versions of final reports are located on the U: drive in the "CASEREPORTS" folder.

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: Formerly, Mitochondrial DNA Reports were separate from Nuclear DNA Reports. The mtDNA report statements have been incorporated into the DNA Report Template. See mtDNA SOP-10 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 4, 5, 21, 25, and 31 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), DNA QR-43 (Y-STR profiles), DNA QR-46 (probability of kinship), and DNA QRs-307e-i (from the F6C deconvolution workbook). 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

National Y-STR Database (<https://usystrdatabase.org/>)

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

6.2.5 Fusion 6C and ID/IDP 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 two 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.”

6.2.5.1.2 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 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 on the STRmix advanced report, ceilinged at 100 billion, will be reported out. The following statement will be used when $LR \geq 10,000$ for Fusion 6C and $LR \geq 1,000$ for 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 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 Laboratory Staff Member being a contributor to the DNA profile from item xx. Assuming xx contributors, where 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) Laboratory Staff Member (and xx unknown individual(s)) than if it originated from Laboratory Staff Member and xx unknown individual(s).”
- 6.2.6 Report wording for clear major in 5+ person mixtures.
- 6.2.6.1 5 person mixture wording: The results are consistent with item #xx being a mixture of 5 contributors (with at least xx of them being male).
- 6.2.6.2 >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).
- 6.2.6.3 Consistent with source wording: “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.

6.2.6.4 Eliminated as source wording: “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. Due to the complexity of the DNA profile from item #xx, no comparisons will be made as to whether J. Smith could be a minor contributor to the mixture.”

6.2.7 Yfiler:

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.

6.2.7.1 Single-source profiles with full detection at all loci with results: “The results are consistent with the Yfiler DNA profile from item #xx originating from a single male individual. The results are consistent with John Doe (or another member of the same paternal lineage) being the source of the (Yfiler) DNA profile from item #xx. The expected frequency of individuals who could be the source of the (Yfiler) 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 Yfiler DNA profile from item #xx originating from a single male individual. John Doe (or another member of the same paternal lineage) cannot be eliminated as the source of the (Yfiler) DNA profile from item #xx. The expected frequency of individuals who could be the source of the (Yfiler) 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 two male contributors. John Doe (or another member of the same paternal lineage) is included as a potential contributor to the (Yfiler) DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the (Yfiler) 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 two male contributors. John Doe (or another member of the same paternal lineage) cannot be eliminated as a potential contributor to the (Yfiler) DNA profile from item #xx. The expected frequency of individuals who could be a contributor to the (Yfiler) 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 Yfiler deconvolution of major contributor: The Yfiler results are consistent with item #xx being a mixture of two male contributors. A major profile was deduced from item # XX. The results are consistent with John Doe (or another member of the same paternal lineage) being the source of the major Yfiler DNA profile deduced from item #XX. The expected frequency of individuals (at loci.../at all loci except...) who could be the source the (Yfiler) DNA profile is less than 1 in XX in the general male population.
- 6.2.7.5 Elimination from Yfiler profiles
- 6.2.7.5.1 Single Source Profiles: “The results are consistent with the Yfiler DNA profile from item #xx originating from a single male individual. 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 two male contributors (or at least three male contributors). 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 Yfiler DNA profile deduced from item #XX.
- 6.2.7.6 If limited data is detected from an item for a Yfiler 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: “Due to the complexity of the Yfiler 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 SOP 25.
- 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 Item #xx was consumed in testing.
- 6.2.10.1.2 Item #xx (or a sample from item #xx) was retained at the laboratory.
- 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 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.
- 6.2.10.3 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 Staining noted on the evidence examination worksheets, but not tested, shall be noted in the “Remarks” section.
- 6.2.10.7 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.
- 6.2.10.8 For blood screening testing not reported by FB: A screening test for the presence of blood was performed on additional stains located on item #X. Blood was not detected on the additional stains with this test. Or Blood was indicated on the additional stains with this test. To be noted in the “Conclusions” section.
- 6.2.10.8.1 Notes of non-blood like stains, dirt, grass, etc. are not reported out, but noted on worksheets.
- 6.2.10.8.2 Any testing results from Kastle-Meyer (KM) (whether sent to DNA or not sent to DNA), are reported out.
- 6.2.10.8.3 If “other BLS” are noted on worksheets, then this information is reported so that the user of the report is apprised of the potential additional testing.
- 6.2.10.9 A screening test for the presence of male DNA was performed on item #xx. Male DNA was/was not detected with this test.

TESTING SUMMARY

Item #	Screening	Profile Obtained ¹	Type	CODIS Entry
		F6C		
1S1	Male DNA (-)	Yes	Mixture	Yes - CT and National

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1S2	Male DNA (+)	Yes	Male	No - Not Appropriate
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¹F6C = Fusion 6C STR DNA amplification kit

6.2.11 Additional DNA Report Sections

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

6.2.11.2 Testing Summary: Contains table documenting any items tested, which, if any, DNA profile was obtained for that item, information regarding CODIS entries for appropriate samples, and when applicable, details regarding previously tested samples and screening test results. If the DNA Report does not have any reference samples, 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
		F6C		
1S1		Yes	Mixture	Yes - CT and National
1S3	Blood(+)	Yes	Male	No - Not Appropriate

¹F6C = Fusion 6C 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

Fusion 6C (F6C):

6.2.12.1 F6C report statements for single-source profiles:

- 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 (at loci.../ at all loci tested except...) 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 F6C report statements for mixture profiles:

- 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. Assumed 2-person mixture (major): The results are consistent with item #xx being a mixture. Assuming two contributors to the mixture, a major profile was deduced at loci x,y, and z. The results are consistent with NAME being the source of the major profile deduced from item #. The expected frequency of individuals who could be the source of the major DNA profile deduced from item #xx (at loci.../ at all loci tested except...) is less than 1 in xx in the general population.
- d. Assumed 2-person mixture(minor): The results are consistent with item #xx is a mixture. Assuming two contributors to the mixture, a minor profile was deduced at loci x,y, and z. 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 item #xx (at loci.../ at all loci tested except...) is less than 1 in xx in the general population.”

e. 3 & 4 person mixtures with deduced major: The results are consistent with item #xx is a mixture. A major profile was deduced at loci x,y, and z. 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 (at loci.../ at all loci tested except...) 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:

a. The results are consistent with item #xx being a mixture. A major DNA mixture profile was detected at loci x,y and z. NAME is included as a potential contributor to the major DNA mixture profile from item #. The expected frequency of individuals who could be a contributor to the major DNA mixture profile deduced from item #xx (at loci.../ at all loci tested except...) is less than 1 in xx in the general population.”

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

6.2.12.4.1 The results are consistent with item #xx being a mixture of 5 contributors (with at least xx of them being male).

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).

6.2.12.4.3 Consistent with source wording: “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 expected frequency of individuals who could be the source of the major DNA profile deduced from item #xx (at loci.../ at all loci tested except...) is less than 1 in xx in the general population.”

6.2.12.4.4 Eliminated as source wording: “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. Due to the complexity of the DNA profile from item #xx, no comparisons will be made as to whether J. Smith could be a minor contributor to the mixture.”

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

6.3 STR Stutter Data

Note: Please see DNA SOP-29 for Fusion 6C Stutter Data

6.3.1a Identifier Stutter Values

<u>Locus</u>	<u>Parent allele</u>	<u>Threshold %</u>
D8S1179	to 11.3	10
	12 +	12
D21S11	to 27.3	10
	28 – 31.3	12
	32 +	13
D7S820	all	10
CSF1PO	all	10
D3S1358	to 14.3	10
	15 +	12
TH01	all	10
D13S317	to 13.3	10
	14 +	12
D16S539	to 11.3	10
	12 +	12
D2S1338	all	12
D19S433	to 13.3	10
	14-15.1	12
	15.2 +	15
vWA	to 15.3	10
	16 +	12

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TPOX	all	10
D18S51	to 14.3	10
	15 – 16.3	12
	17 +	14
D5S818	to 12.3	10
	13 +	12
FGA	to 22.3	10
	23 +	12
FGA (Extended)	30.2+	18

6.3.1b Identifier Plus Stutter Values:

N – 1 Repeat			N + 1 Repeat		
Locus	Parent Allele	Threshold %	Parent allele	Threshold %	
D8S1179	to 9.3	8	all	2.0	
	10 – 12.3	10			
	13 - 16	12			
	16.1+	14			
D21S11	to 27.3	10	all	2.0	
	28 – 32.3	12			
	33 – 35.3	13			
	36	14			
D7S820	to 9.3	8	all	2.0	
	10 – 13.3	10			
	14+	12			
CSF1PO	to 9.3	8	all	2.0	
	10 – 12.3	10			
	13+	12			
D3S1358	to 14.3	10	all	3.5	
	15 – 17.3	12			
	18+	14			

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TH01	to 7.3	5	all	2.0
	8+	7		
D13S317	to 9.3	7	all	3.0
	10 – 11.3	10		
	12+	12		
D16S539	to 9.3	8	all	2.0
	10 – 11.3	10		
	12 – 12.3	12		
	13+	14		
D2S1338	to 16.3	10	all	2.0
	17 – 23.3	12		
	24+	15		
D19S433	to 13	10	all	2.0
D19S433	13.1 – 14.3	12		
	15+	15		
vWA	to 14.3	10	all	2.0
	15 – 17.3	12		
	18+	15		
TPOX	to 10.3	8	all	2.0
	11+	10		
D18S51	to 10.3	8	all	3.0
	11 - 13	10		
	13.1 - 15	12		
	15.1 - 18	15		
	18.1+	18		
D5S818	to 9.3	10	all	3.0
	10 – 13.3	12		
	14	14		
FGA	to 18.3	10	all	2.0
	19 – 23.3	12		
	24 – 32.2	15		
	32.3+	18		

6.3.2 Yfiler Stutter Values:

**State of Connecticut Department of Emergency Services and Public Protection
Division of Scientific Services**

Documents outside of Qualtrax are considered uncontrolled.

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Locus	Parent Allele	Threshold %
DYS456	to 14	10
	14.1 - 17	13
	17.1 +	14
DYS389I	to 13.3	10
	14+	12
DYS390	to 23	10
	23.1 +	12
DYS389II	to 26.3	12
	27 - 29	14
	29.1 +	16
DYS458	to 15.3	10
	16 - 18	12
	18.1 +	14
DYS19	to 15.3	10
	16 - 18	12
	18.1 +	14
n-2 bases	all	14
n+2 bases	all	2.5
DYS385	to 13	10
	13.1 - 15	12
	15.1 - 19	15
	19.1 +	18
DYS393	to 10	10
	10.1 - 13	12
	13.1 - 15	14
	15.1 +	15
DYS391	to 11	10
	11.1 +	12
DYS439	to 10.3	10
	11 +	12

DYS635		to 20	10
		20.1 +	12
DYS392		to 12	12
		12.1 - 13	14
		13.1 +	18
n+3 bases		all	10
GATA H4		to 11	10
		11.1 - 12	12
		12.1 +	14
DYS437		to 14.3	9
		15 +	11
DYS438		to 12	5
		12.1 +	6
DYS448		all	7

6.4 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.

6.4.1 Critical reagent chemicals and solutions:

dH₂O (used for sample prep through amplification)
Extraction Buffer
Dithiothreitol (DTT)
Formamide
CE Buffer

6.4.2 Critical Enzymes/Biologicals/Kits:

Proteinase K
Quantifiler Trio Kit
Amplitaq Gold Polymerase (if not as part of an assembled kit)
Primer Sets (if not as part of an assembled kit)
Allelic Ladders (if not as part of an assembled kit)
EZ1 Extraction Kits

Yfiler Kit
GeneScan-500LIZ
Pop-4
Fusion 6C Amplification Kits
WEN ILS500
cRNA

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

6.4.4 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 above listed equipment. Refer to mtDNA SOP-12 for Agilent Bioanalyzer. Refer to mtDNA SOP-1 for mtDNA Critical Reagents.

Thermometers that are traceable to national or international standard(s)

Balance/Scales

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 SOP-9)

Real-Time PCR Instruments

Electrophoresis Detection Systems (Agilent Bioanalyzers-mtDNA)

Robotic Systems (Biomek, EZ1, etc.)

Genetic Analyzers

Pipettes

Centrifuges

6.5 General Chemical Inventory

6.5.1 Dry Chemicals:

Dithiothreitol (DTT)

Dryite

(EDTA) Ethylenediaminetetraacetic acid disodium, dihydrate

Potassium Chloride

Sodium Chloride

Sodium Dodecyl Sulfate (lauryl sulfate)

Sodium Hydroxide

TRIS, ULtraPure Grade

TRIS Hydrochloride
TRIS-base (hydroxymethyl amino methane)

6.5.2 Liquid Chemicals:

Ethanol, Reagent
Hydrogen Peroxide
pH Buffer (4.00, 7.00 & 10.00)
Proprietary Solvent, anhydrous
Sodium Hypochlorite (bleach)
CE 10X Buffer (stock)
Hydrochloric acid

6.5.3 Enzymes/Biologicals:

ABI 3130 Matrix Standards
AmpliTaQ Gold
Proteinase K

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