18-Jan-21
ASB Standard 139, Reporting DNA Conclusions

#	Section	Type of Comment	Comments	Proposed Resolution	Final Resolution
30	General	T/E		The standard does not mention conclusions for samples that may involve contamination. There are laboratories that allow for interpretation when a sample is known to be contaminated. The standard needs to address this situation. Statements can be added to section 4.3.	Reject: This is being addressed by other documents in process and is out of scope for this document.
81			The document does not give a clear presentation or explanation of the conclusions offered. What is the place of this document within the context of a larger reporting standard? Additional comments have been submitted.		Reject: No recommendation is being offered. Please refer to the scope of this document.
82			The document is so vague that I cannot vote for it.		Reject: No recommendation is being offered to address the statement that this document is vague.
16	Foreword	E	The document applies to human DNA testing, it does not apply to non-human DNA testing (such as wildlife)	Add the word 'human', such as "This standard defines the required components for reporting human autosomal STR….'	Accept
53	Foreword	E	"accessible, high quality forensic-based"	insert hyphen, comma, and "and": "accessible, high-quality, and forensic-based"	Reject: This is ASB boilerplate.
68	Forward	T	Standard is clearly written for human forensic comparisons, not for non-human taxonomic or population assignments, which also use STRs and haplotypes. The scope of the document should be clarified.	"This standard defines the required components for reporting human autosomal STR and haplotype DNA interpretations and conclusions"	Accept
69	Keywords	T	Standard is clearly written for human forensic comparisons, not for non-human taxonomic or population assignments, which also use STRs and haplotypes. The scope of the document should be clarified.	add "human" in front of DNA	Accept
70	Scope	T	Standard is clearly written for human forensic comparisons, not for non-human taxonomic or population assignments, which also use STRs and haplotypes. The scope of the document should be clarified.	This standard contains the reporting requirements for human autosomal STR and haplotype DNA conclusions for results obtained from evidentiary samples in forensic casework. This standard does not apply to paternity or any other biological relatedness conclusions, nor does it apply to conclusions for non-human DNA analyses.	Accept with modification: Word "human" added. The scope is clear as it written.
23	1	T	Scope is far too limited to provide any kind of real guidance to laboratories. Requirements for reporting conclusions unaccompanied by complete report drafting requirements are confusing and ineffectual. Other groups have issued standards for complete report requirements covering complete reporting requirements, including examination, testing, and interpretation of evidence as well as reporting of results. *See* Nat'l Commission on Forensic Science Recommendation to the AG Documentation, Case Record, and Report Contents ("Reports should clearly state: the purpose of the examination or testing; the method and materials used; a description or summary of the data or results; any conclusions derived from those data or results; any discordant results or conclusions; the estimated uncertainty and variability; and possible sources of error and limitations in the method, data, and conclusions.")	Scope should be expanded to cover all reporting elements.	Reject: These other parameters are covered under ANAB, ISO and QAS and this scope is limited to conclusions.
17	1 Scope	E	The document applies to human DNA testing, it does not apply to non-human DNA testing (such as wildlife)	Add the word 'human', such as "This standard contains the reporting requirements for human autosomal…"	Accept

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24	2	T	The informative references list is extremely limited and ultimately uninformative.	Expand the informative reference list to include documents like those produced by the National Forensic Science Commission's Views on Documentation, Case Record, and Report Contents or Recommendation on Documentation, Case Record, and Report Contents.	Accept. Added to Bibliography
19	3	T	There is no definition of "conditioned" although it is referred to as part of the definition of "assumed contributor". This is a term has long been linked with the binary RMP based interpretation of DNA profiles. It is not sufficient for modern probabilistic genoypting LRs. For example, the 2 suspect situation. It was not appropriate to "assume" a suspect, but it is perfectly appropriate to condition the LR on one of the suspects if that is the proposition of the other suspect	define "conditioned contributor": An individual whose DNA is not in dispute between the parties and is accounted for in both propositions of an LR.	Reject: term "conditioned contributor" is not used in this document therefore not included in section 3. "i.e. conditioned upon" was removed from 3.1.
25	3	T	Each of the definitions is poorly written and confusing. These should be carefully reexamined. Reference should be made to SWGDAM, the National Forensic Science Commission's documents, and learned treatises like John Butler's texts.	Reexamine all definitions for clarity and to avoid conflict with other standards.	Reject: This recommendation is not specific.
47	3	E/T	Several QAS terms have been redefined, switching the term defined with a key word in the definition. Is there a reason to change these definitions when they are routinely referenced for audit requirements for all DNA testing laboratories? Examples: evidentiary sample vs forensic sample, exclusionary conclusion, interpretive statement vs qualitative statement, statistical statement vs quantitative statement, unsuitable vs uninterpretable	Use the QAS definition unless there is a substantive clarification being added; if so, make the additional content supplementary to the QAS definition.	Reject: QAS definitions were considered and modified for the purpose of this standard.
26	3.1	T	The definition of assumed contributor is dangerously wrong. According to SWGDAM, an "assumed contributor" is "an individual whose DNA on an item of evidence is reasonably expected." SWGDAM separately defines conditional interpretations. Here, the standard collapses assumptions and conditional interpretations. This ellision creates space for problematic confusion by labs. Furthermore, at the current levels of sensitivity, assumed contributor definitions should account for conservatism around the sample type for which an assumption can be made. Assumed contributors should be confined to items like intimate sources such as underwear, samples collected from a known individual's body, or crime scene samples involving known individual's expected body fluids (i.e. a stabbing victim's blood).	Appropriately define "assumed contributor" by removing the clause following "or," and including conservatism around sample types for which assumptions will be made.	Reject: The definition is clear for the purpose of this document and how the term is used in this document.
48	3.1	E/T	QAS also defines intimate sample, which is more specific than the assumed contributor.	include this additional definition as sub-text to the assumed contributor definition.	Reject: The definition is broader whereas intimate samples would limit reasonable scenarios.
79	3 and 4.3.5		It would be helpful to define "legacy kit", which is mentioned in section 4.3.5.		Reject: This is an industry accepted term.
80	3 and 4.3.5		A definition for legacy kit should be included in the standard.		Reject: This is an industry accepted term.

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31	3.3 (now 3.4)	E	“These data may be compared to data from reference sample(s) in an attempt to identify the possible source of the evidentiary sample.” This sentence doesn’t add anything to the definition. These same conclusions apply to the association of unknown profiles where there is no known individual to compare to.	Consider removing the second sentence.	Accept with modification: First sentence was revised for clarity. The second sentence was deleted.
49	3.3 (now 3.4)	T	"in an attempt to identify the possible source of the evidentiary sample"- this definition is using source attribution as the intention of the comparison, but there are no requirements detailed in document for defining the premise of any source attribution statements.	Adopt the requirement from SWGDAM Interpretation Guidelines to establish criteria under which source attribution declarations aare based. Consider rewording the definition to defer from a source statement, since not all laboratories report source attribution statements.	Reject with modification: First sentence was revised for clarity. The second sentence was deleted. Source attribution is outside the scope of this document.
61	3.5, 3.6, 3.7 (now 3.6, 3.7, 3.8)	T	These definitions create the potential bias in favor of categorizing results as "inclusionary" or "uninformative". The definition for "exclusionary" requires a definitive exclusion ("a conclusion that eliminates....") while the definition for inclusionary conclusion is much less definitive ("an individual is a potential contributor (i.e., cannot be excluded)"). This standard theoretically would allow a lab to report any likelihood ratio result as inconclusive or inclusionary because, by definition, the LR statistic is probabilistic and does not support definitive statements, like that required by the definition of exclusion. At the very least, this warrants further discussion.	Eliminate in the uninformative definition that uninformative conclusions could result from statistical analyses that fail to provide sufficient support for an exclusion (and unfinrmative LR). If an LR is <1, it supports exclusion.	Reject: These definitions are appropriate for the use of this document.
32	3.7 (now 3.8)	T/E	The definition for inconclusive needs more distinction from the definition of uninformative. The sentence “This could also result from statistical analyses that fail to provide sufficient support for an inclusion or exclusion (e.g., an uninformative likelihood ratio)” incorrectly inflates these ideas. Uninformative LRs usually fall in a range where false positive results can occur. In these instances, a LR can be generated and the determination about a result can be made, but a laboratory is choosing not to based on uncertainty in the model.	The definition for inconclusive only needs the first sentence.	Accept with modification: This definition was updated by removing the last example.
71	3.7 (now 3.8)	T	Unclear what is an uninformative likelihood ratio e.g. A LR of 20?	Remove last sentence.	Accept with modification: This definition was updated by removing the last example.
27	3.9 (now 3.10)	T	The definition of "probative" is so vague as to be unhelpful. This term does so much work throughout the standard that its imprecision and subjectiveness are alarming.	Reevaluate the use of the term "probative" to determine the need for statistical conclusions, and redefine the term to provide some manner of objective criteria.	Accept with modification: Definition was updated for clarity.
33	3.9 (now 3.10)	T/E		Probative is not a scientific term. The use of probative is often associated with value, something the lab should not determine. Attorneys determine if evidence and its associated results are probative. Probative should be removed from the document.	Reject with modification: Definition was updated for clarity.
72	3.9 (now 3.10)	T	This is context dependent as provided to the laboratory and may change	Explanation required in report as to why evidence/exhibits examined or not examined	Reject: This is outside the scope of this document and it is not appropriate for conclusions.

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34	3.Ten (now 3.11)	E		For consistency “biological samples” should be changed to “evidentiary samples” as seen in the definition for reference sample.	Accept with modification: Definition was updated for clarity.
54	3.1 (ten) (now 3.11)	T	Modify reference data definition to include comparison to evidentiary data.	Data generated from a reference sample for purposes of comparison to data generated from evidentiary sample(s) or evidentiary data.	Accept with modification: Definition was updated for clarity.
35	3.11 (now 3.12)	T		Laboratories have been known to issue conclusions based on abandoned samples, where DNA is collected from an item used (i.e., cup, straw, gum, etc.) by a known individual. These samples are not direct reference samples but are linked to known individuals. Something needs to be added to this definition to cover for such samples or abandoned samples needs to be added as a term and included in the body of document. Discussion of abandoned samples can be added to section 4.2	Reject: This definition covers any sample used as a reference.
36	3.13 (now 3.14)	E/T	The definition for this term is not in line with the other defined conclusions given in the document. The definition is written in terms of support of a proposition which is not used in the definitions for inclusion, exclusion, or inconclusive. This definition is flawed in the sense that conclusions are not based on a single proposition. Propositions should be thought of in pairs. Can “A scenario” also be clarified as well? Our comment on the definition of inconclusive addresses a scenario where the potential for false positive LRs can lead to a numerical range where the data might not be trusted, but this may not be the only circumstance where such a conclusion can be drawn.	Consider the following edit, “A conclusion where a comparison is determined to have no value even if there is support of an inclusion or exclusion; a statement of uninformative is determined by the laboratory and can apply to inconclusive conclusions as well.”	Reject with modification: Definition was updated for clarity.
55	3.14 (now 3.15)	E	Rephrase example portion of definition for "unsuitable for comparison" definition.	"...but not limited to, poor quality and/or limited data,..."	Reject: This is the same definition as in published ANSI/ASB Standard 040.
13	4	Technical	Section 4 does not require laboratories to have a policy requiring analysts to report exculpatory, impeachment, or mitigation evidence pursuant to Brady v. Maryland, 373 U.S. 83 (1963). Duties imposed by Brady and other laws mandating the disclosure of evidence material to the defense have been extended to forensic laboratories. Brady evidence may include problems in sampling, full profiles belonging to unknown contributors, deviations from standard operating procedures, instruments failing to perform as expected in controls, and the detection of contamination	4.X: The laboratory shall have a policy requiring analysts to report exculpatory, impeachment, or mitigation evidence pursuant to Brady v. Maryland, 373 U.S. 83 (1963) and any other applicable law.. Examples of information that should be reported include identified profiles belonging to unknown contributors, deviations from standard operating procedures, instruments not performing as expected, known contamination events, analyst misconduct, irregularities encountered, problems encountered in sampling, and any other event that may impact the reliability or meaning of the reported results.	Accept with modification: Section 4.6 was added to this report. It now reads: "Every report shall include a statement indicating that the report does not contain all of the documentation associated with the work performed. NOTE In order to understand and evaluate all the work performed a review of the case record is required."

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14	4	Technical	Section 4 does not prevent laboratories from using descriptive terms that may lead a lay audience to infer the presence or absence of some analytical conclusion, despite the absence of any performed analysis. Stated otherwise, descriptive terms should only be used when supported by data from validated analytical methods. For example, the terminology “sperm fraction” implies the detection of spermatozoa, and may be employed in cases where there is no detected DNA, where the “sperm fraction” is carryover from the “epithelial fraction”, and/or no serology has been performed. A legal or lay audience may misinterpret the meaning of “sperm fraction” to imply that sperm was detected in these cases.	4.X: The laboratory report shall not employ descriptive terminology that may lead a lay audience to infer the presence or absence of some analytical result despite the absence of any performed analysis. Any descriptive terminology used in the report must be supported by data from validated analytical methods.	Accept with modification. An additional sentence was added to 4.1 requiring the need for supporting validation studies. An additional sentence was also added to 4.2.1 regarding term definitions.
28	4	T	Include NCFS Recommendation regarding documentation of any analysis conducted.	Records should be created contemporaneous with the examination of evidence and the technical review that, along with the FSSPs’ [Forensic Science Service Provider] quality management system documents relating to the forensic work performed, would allow another analyst or scientist, with proper training and experience, to understand and evaluate all the work performed and independently analyze and interpret the data and draw conclusions. See National Commission on Forensic Science, Recommendation to the Attorney General, Documentation, Case Record and Report Contents. Adopted 2016.	Accept: Added to Bibliography
29	4	T	Currently, the standard merely states that the laboratory "shall have a protocol for reporting conclusions." However, the remainder of Section 4 includes no real requirements describing what that protocol should include or require. Speciify more detailed requirements for any report generated by analysis.	Reference the ASTM E620 report on Standard Practice for Reporting Opinions of Scientific or Technical Experts. See ASTM Committee Report E620-18, Published April 2018	Accept with modification: Suggested reference added to the Bibliography section.
62	4	T	There is uncertainty inherent in any scientific conclusion. Yet this standard does not require the reporting of uncertainty with inclusionary conclusions. There are also limitations to what a conclusion means. For instance, 4.3.4 rightly requires a laboratory to report the "limitations of lineage testing for haplotype testing inclusions…." A laboratory should report the limitations of the conclusion/	Include requirement that a laboratory include a statement of associated uncertainty and limitations for all inclusionary conclusions.	Reject: Required limitations are delineated in the requirements throughout the document.
12	4.1	Technical	Section 4.1 does not require laboratories to have a policy requiring analysts to report conclusions in a manner that is accessible and comprehensible to a legal or lay audience. By definition, a forensic biologist is not merely a scientist, but a specialized expert who must communicate scientific knowledge to stakeholders in the legal system.	4.1.4 The laboratory shall have a policy requiring analysts to report conclusions in a manner that is accessible and comprehensible to a legal or lay audience.	Reject: Laboratories write reports using industry accepted terminology.
37	4.1.1	E		Probative should not be used here. Consider using relevant or informative. For the second sentence the following edit can be used “An example of a statement of inclusion…”	Reject: This is an industry accepted term.
56	4.1.1	E	"and therefore statistical"	insert when: "and therefore when statistical"	Accept
73	4.1.1	T	Implies conclusions are considered probative without statistical analysis. Is this through visual comparison? Data/results should be transparent and not hidden. Also context dependent.	All results should be revealed in the report together with context provided to the laboratory	Reject: This is covered under section 4.2 and 4.3.

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38	4.1.2	E		This statement demonstrates why probative should not be used. The standard requires a statistical statement irrespective of the number of alleles detected. As a person of interest's alleles decrease in a mixture, there is a greater opportunity that a "probative" piece of evidence can become uninformative, inconclusive, or exclusionary. The idea of who may see these results as probative may change. Another word needs to be used in the place of probative in this statement.	Reject: This is an industry accepted term.
74	4.1.2, 4.1.3 and 4.2.1	T	Unclear as to meaning of these sections and appear contradictory. What is difference between probative inclusion and inconclusive if only one allele designated?	Laboratories should define in their reports when and how reported DNA profiles meet quality and reporting guidelines	Reject: This is outside the scope of this standard.
39	4.1.3	E		This statement should be written without the use of probative. Consider the following edit "The laboratory shall define circumstances where inclusive interpretive (qualitative) evaluations can be used in place of statistical evaluations. The inclusion of an individual on her own clothing, or the habitual driver's DNA on a vehicle steering wheel, are examples of a statement of inclusion that may not be considered informative and may not require a statistical statement."	Reject: This is an industry accepted term.
57	4.1.3	E	"and therefore statistical"	insert when: "and therefore when statistical"	Accept
58	4.1.3	E	Remove comma preceding "or" and the comma after "wheel".	"...clothing or the habitual driver's DNA on a vehicle steering wheel are..."	Accept
3	4.2.1	T	We state "all." I think that taking the rest of this document on board this would require a statistics for any sample that produced some alleles in at least one profile. Do we really want to insist on this amount of work? Can we get away with insisting on statistics from a representative sample of the most probative amplifications. For example if we had three swabs from one item, three extracts, three amplifications and we had already stated "exclusion" where appropriate can we run a statistic on the most probative amplification (and if there are multiple profiles either the most probative profile or done as replicates)	4.2.1 All evidentiary samples tested shall have an interpretive and/or comparative conclusionary statement in the report, as applicable. A statistical analysis shall be given for a representative sample of the most probative amplification(s) from the most evidentiary and probabative samples. Probative amplifications from the same extract should be run as replicates or the most probative profile selected.	Reject: It is not appropriate for a scientist to make a determination as to which sample is more relevant in the greater context of the case, and is contradictory to section 4.1.2.
40	4.2.1	T/E		Are comparative and conclusionary statements the same? Based on the definition for conclusionary statement they are. If the terms are meant to be different than comparative statement should be defined in section 3.	Accept. See 3.2 term and definition for "comparative statement" added.
63	4.2.1	E	Within NOTE 1 a reference is made re: gender. Gender is considered more of a social aspect rather than biological	Rephrase to state biological sex of the contributor	Accept
41	4.2.1 Note 2	T/E		Please clarify if note two is an extension of note one and applies to interpretive statements of evidence only. If not provide an example where statistical statements may apply (possibly haplotype testing).	Reject: Note 1 and note 2 are separate notes. The full conclusion would need to be the same.
65	4.3.1	T	Why is it necessary to state the number of contributors in the report? This is not required in the QAS. We currently do not do this as the information would increase the complexity of the report (for understanding purposes) and isn't needed for the contributor to understand the information.	Remove this requirement or make it optional.	Reject: It is critical for the readers of the report to have this information. The number of contributors is an assumption that could affect reported conclusions and be significant for circumstances of a case.

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20	4.3.2	T	6 lines of this paragraph give examples of when someone may be "assumed" and they are all linked to a contributor being linked to an evidence item such as body, clothing, touching or owning an item and so on. None of this may be relevant in an LR where the defense can choose their proposition that might be based on the presence of a contributor for any reason. The last two lines that say conditioning may be performed hardly covers the distinction between traditional assuming and what is invovled in LR propositions	This document needs to discuss the differences between assuming someone and conditioning. It is true that conditioning requires assuming a donor is present (in both propositions) but not all assuming is the same as conditioning	Accept with modification: This section was updated to refer to assumed/conditioned and assuming/conditioning.
75	4.3.2	T	Contributors should only be assumed if data supports this. Partial representation of an assumed contributor makes confusing genotype percentages when the genotype is not observed in the DNA profile. Contaminated evidentiary samples with staff DNA are quality failures and should not be reported with evidentiary value.	All components of an assumed contributor should be represented in the evidence DNA profile or otherwise accounted. Contaminated results should not be reported as evidentiary value but noted in report as quality failure.	Accept with modification: This section was updated to refer to assumed/conditioned and assuming/conditioning. Also see bibliography section #4.
4	4.3.2	T	reading this I become uncertain what to do with two POI. Imagine P1 and P2 are both included individually and together. It is best practice to assume P1 when interpreting P2.	4.3.2 Any assumed contributor(s) used in the interpretation of the data. Examples of possible scenarios where a contributor to a DNA mixture may be assumed include the individual whose body was swabbed for the collection of possible deposited biological fluids (e.g., vaginal swab, breast swab, bitemark swab, oral swab, penile swab), consensual sexual partner, individuals known to have worn, touched or handled an item (e.g., clothing, bedding, steering wheel of car), or contamination events having a known source (e.g., staff involved in evidence handling, collection or testing), and other included POI. Other case scenarios may involve the evaluation of data by conditioning (i.e., assuming) the analysis on other profile(s) and may be performed as needed.	Accept: "person(s) of interest" spelled out was added to this section per this recommendation.
42	4.3.3	E		Consider a substitute for probative in this statement.	Reject: Probative is a standard and widely used industry term.
43	4.3.3	T/E	Statements of inclusion can at times be masked as exclusionary statements.	An additional sentence should be added to 4.3.3 that reads “Examples of inclusionary language include phrases such as is included, cannot be excluded, is a contributor.”	Reject: The suggested alternatives are well understood in the discipline.
59	4.3.3	E	Remove comma preceding "with".	Any statements of inclusion with associated statistical statements in support of the probative inclusions.	Accept
5	4.3.4	T	We use the words "same paternal lineage." At some level all men are from the same paternal lineage and these words will lead to plausible courtroom discussion of how this is limited at all. Even if we change to "close paternal relatives" we are in trouble. In fact there is some probability that any man at some number of meioses distance is IBD and this will not fit well into a simple clause. One lab uses "males of the same paternal lineage (e.g. fathers, sons, and brothers, paternal grandfathers and uncles) may share the same Y-STR profile" and that therefore "the POI and potentially his paternal male relatives"	NOTE Haplotype testing is limited in that two specimens that exhibit the same haplotype may have originated from either a common individual source, from many individuals with a close paternal (Y-STR) relationship...	Accept
9	4.3.4	T	We need to avoid the implication that the propositions should be Hp: The donor to the stain is the POI or a close paternal relative Ha: The donor to the stain is a person unrelated to the POI.	Insert in the 4.2 series: the propositions considered in lineage marker work (if single source) should be Hp: the POI is the donor to the stain Ha: The POI is not the donor to this stain	Reject: This is outside the scope of the document as this document does not provide suggestions on how to set the propositions.

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76	4.3.4	T	Limitations of trace DNA not in this section	Limitations of trace DNA should be expalined in report: that the type of cell from which the DNA derived and when it was deposited is unknown and because the test is sensitive it is common to encounter mixtures but it is unknown if any DNA is relevant to the case	Reject: This is the activity level proposition.
1	4.3.5	T	This makes it sound like every report conclusion must also contain the number of loci used (or not used) in the interpretation in that reported conclusion. This is unecessarily burdensome and could be confusing to the reader of a report.	Make an allowance that this information may clearly reside in the exam documentation/notes instead of the report with a reference on the report of where to find that information.	Reject: This requirement is only in effect when the number of loci used is less than the number available in the kit.
6	4.3.5	T	There is not actually a rigorous requirement that two compared samples can only be interpreted at loci that they have in common. It is possible to compare two samples that share no loci at all via an intermediate sample that shares with both. This can be done without a rigorous assumption that all three come from the same donor.	Only those loci present in both the evidentiary and reference data, or connected via intermediary samples by appropriate statistical methods, shall be used in interpretation and statistical calculations	Accept with modification: Last sentence was added to this section.
8	4.3.5	T	I think, read pedantically, this asks us to list for each profile those loci that are degraded either to below the AT or to some other criterion (say below the ST if using CPI). This could become very tedious.	Move 4.3.5 from the 4.3 series to the 4.2 series	Reject: That is more appropriately under 4.3.
50	4.3.5	T	Requirement details reporting limitation on number of loci used, but QAS also requires reporting the loci used (not just those not used in statistic).	Add requirement per QAS to address the following: "Documenting of the genetic loci and assumptions used for statistical calculations, at a minimum, in the case notes."	Reject: This document is about reporting conclusions and not what should be reported in case notes.
66	4.3.5	T	Is this referring to locations removed as well as partial profiles. Again, why does this need to be included in the report. It again adds unnecessary infromation to the report when it isn't needed and makes it more difficult for the contributor to understand the report.	Require that it be included in the casefile, but not in the report.	Reject: The recommendation is the exception not the rule.
77	4.3.5	T	Unclear regarding legacy kits. Usually these are SNPs and are not STR loci.	Clarify regarding legacy kits	Reject: This is standard language in the forensic DNA testing community.
78	4.3.6	T	All evidence tested should have transparent results. The 'Note' is confusing.	All testing and data obtained should be disclosed. Omit 'Note'.	Reject: First recommendation is covered in section 4.2. The note is an illustrative example that is helpful to readers.
2	4.3.7	T/E	Unclear whether there is a typo here or if the intent was to report the reason data is INTERPRETABLE? I assume it was meant to be UNINTERPRETABLE?	Change the word interpretable to uninterpretable.	Accept
7	4.3.7	T	Can we also avoid any implication that the propositions should be Hp: Mr POI or a member of the paternal lineage Ha: A person unrelated to the POI. These are not the propositions that are or should be assessed.	remove 4.3.7	Reject with modification: Typo was corrected and the last word now reads "uninterpretable".
10	4.3.7	E	Last word in the sentence has what appears to be a typographical error	Change last word to "uninterpretable"	Accept
18	4.3.7	E	interpretable should be "uninterpretable"	insert 'un'	Accept
21	4.3.7	T	I think this should be reasons why something is "uninterpretable", as it reads we have to state why we can use data	change to uninterpretable	Accept
51	4.3.7	E	4.3 states the subpoints are aspects that shall be stated in the conclusions. "4.3.7 The reason(s) any DNA data, or minor components of mixed data, were deemed interpretable." Should this say **un**interpretable? Why would the lab need to specify why each sample is suitable in the report, if they have an SOP for reporting that details the requirements for suitability? 4.3.8 details stating the reason for no conclusions, so the intent of this standard is unclear.	Suggest moving reasons for suitability to criteria to evaluate in the intepretation SOP; inherent to reporting the conclusion is that these criteria were satisfied.	Reject with modification: Typo was corrected and the last word now reads "uninterpretable".

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64	4.3.7	T	It is unclear if there is a typo in this sentence - should it read "…were deemed **un**interpretable"? If it is correct as stated, please include an example.	Please include an example if this is correctly stated.	Reject with modification: Typo was corrected and the last word now reads "uninterpretable".
67	4.3.7	T	Is this referring to looking under the AT to determine number of contributors? This again creates undo complication in the report that will make it more difficult for the contributor to understand. We really need to keep in mind who recieves the report and what information they need.	Remove this requirement or make it optional.	Reject with modification: Typo was corrected and the last word now reads "uninterpretable".
22	4.3.8	T	Assuming 4.3.7 is "uninterpretable" this statement seems to be saying the same thing. In any case, perhaps the term "definitive conclusion" should be looked at. We give a statistic because of uncertainty in the inclusion, so how can any conclusion be "definitive"	Consider the term "definitive" and maek difference between 4.3.7 and 4.3.8 more clear	Reject: 4.3.7 is referring to interpretations and section 4.3.8 is referring to comparisons (comparisons are covered in ANSI/Standard 040 - added to the bibliography).
44	4.3.8	T/E	The standard does not provide a good explanation of the circumstances that lead to an uninformative or inconclusive conclusion and this needs to be added.	Additional information and examples need to be added to this standard. This section should explain the difference between inconclusive and uninformative and how an inconclusive result can fall within an uninformative range of data. Examples of scenarios should be added to 4.3.8 similar to standard 4.4.2 which describes evidence samples that can be used as reference samples or standard 4.3.2 which provides examples of scenarios where contributors to a DNA mixture can be assumed.	Reject: The circumstances that lead to an uninformative or inconclusive conclusion are out of the scope of this document. See ANSI/ASB Standards 020 and 040 added to the bibliography.
11	4.5	E	How will private laboratories that don't have CODIS access meet this requirement? We generate the data and reports but the client labs review the data and ultimately decide what will be uploaded. Adding to the complexity, many of our clients have different thresholds as far as what they consider a CODIS eligible profile especially with STRmix data and we are not always privy to their profile eligibility requirements.	Private laboratories instead could include a disclaimer statement in all reports directing the reader to the client lab (or whomever is taking ownership for CODIS upload as this task is also sometimes outsourced) for verification of profile CODIS uploads.	Reject: CODIS is listed as an example.
15	4.5	Technical	Requirement 4.5 should require that documentation mentioning DNA databases be separated from any report regarding analytical results. The mention of CODIS or DNA databases may have significant legal implications and is likely inadmissible at court. Any documentation regarding the entry or non-entry of the profile should be separated from the laboratory report. There should be separate standard mandating notification of relevant stakeholders that the profile was entered into a searchable database.	4.5: A laboratory report that provides analytical results shall not include any reference to whether DNA data will be entered into whether DNA data will be entered, or will not be entered, into a searchable database for the purpose of generating investigative leads (e.g., CODIS).	Reject: This is important information for the end-user.
45	4.5	T/E		The disposition of a DNA profile is not relevant to a conclusion being offered on the profile. The mention of database entry may be a requirement of general report writing, but it is not a requirement of reporting a conclusion of inclusion, exclusion, uninformative, or inconclusive. 4.5 should be removed from the document.	Reject: This is important information for the end-user.
52	4.5	E/T	"4.5 A statement shall be included in the report regarding whether DNA data will be entered, or will not be entered, into a searchable database for the purpose of generating investigative leads (e.g., CODIS)." Private labs that are implementing these standards do not submit to CODIS, nor have the eligibility to do so. Some submitters do request a note to detail the results will be considered for CODIS by the submitting agency- that is the extent we could comment on.	Suggest revision of this requirement to detail "as applicable for CODIS submitting laboratories".	Reject: CODIS is listed as an example. Some laboratories utilize other searchable databases.

#	Section	Type of Comment	Comments	Proposed Resolution	Final Resolution
60	5	T	Provide example report wording.	Add an additional section with example report wording for laboratories to be upon.	Reject: This is beyond the scope of this document.
46	Bibliography	T	A number of expected sources are not referenced. Were these sources considered in the draft preparation, or should they be at this time?	FBI QAS, ISO17025 (has report requirements), SWGDAM Mitochondrial DNA Analysis Interpretation Guidelines, Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios	Accept with modification: Published and accessible documents were added to this bibliography.
	Bibliography		The bibliography in Annex A is a bit weak and could include references to articles in peer-reviewed journals on report writing and conclusions		Accept with modification: Published and accessible documents were added to this bibliography.