IN THE UNITED STATES DISTRICT COURT FOR THE DISTRICT OF NEW MEXICO

UNITED STATES OF AMERICA, CR No. 10-2734 JCH

Plaintiff, vs.

JOHN CHARLES McCLUSKEY

Defendant

# (CORRECTED) SUPPLEMENTAL MEMORANDUM IN SUPPORT OF MOTION TO EXCLUDE DNA TEST RESULTS AND REQUEST FOR DAUBERT HEARING

COMES NOW, Defendant John Charles McCluskey, by and through his counsel of record, Michael Burt and Theresa Duncan, pursuant to Federal Rules of Evidence Sections 104(a), 402, 403, 702, 901(b)(9), and the Fifth, Sixth, and Eighth Amendments to the United States Constitution, and submits this supplemental memorandum in support of his motion to exclude certain expert testimony derived from a DNA testing kit and a presumptive blood test that the government proposes to introduce in the upcoming trial. [Doc. 422]. This corrected supplemental memorandum is the same as Doc. 441, expect that pages 149-162 of that document have been edited to add correct citations and Exhibit numbers and to correct typographical and other errors . The grounds for his original motion were: (1) there is no reliable scientific basis for this proposed testimony, and thus the testimonyis inadmissible under *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993) and *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 119 S.Ct. 1167, 143 L.Ed.2d 238 (1999); (2) the testimony is inadmissible under the 2000 amendments to Rule 702 in that (a) the testimony is not based upon sufficient facts or data, (b) the testimony is not the product of reliable principles and methods, and (c) the government’s DNA technicians have not applied the principles and methods reliably to the facts of the case; (3) numerous statistical flaws render the DNA evidence in this case inadmissible under Rules 402, 403, and 702, as well as under D*aubert* and the due process, fair trial, and cruel and unusual provisions of the Fifth, Sixth, and Eighth amendments to the Constitution; (4)

the failure to applyreliable scientific procedure, as outlined in numerous protocols, renders any DNA test results inadmissible under Rule 702; (5) the presumptive blood test is unreliable and its results are irrelevant and substantially more prejudicial than probative and, (6) Rule 901(b)(9) requires that an adequate foundation be laid before any of the government’s computer generated DNA evidence is admitted into evidence.

The defendant has previouslyfiled a supplemental memorandum addressing the admissibility of the presumptive blood test results. [Doc. 424]. This memorandum will address the admissibility of the government’s DNA evidence and is based on the attached Memorandum of Points and Authorities, the motions to exclude DNA and serology evidence previously filed herein [Docs. 422, 424], the lodged Exhibits contained on a CD to be filed manually, and any oral and documentary evidence and argument as may be produced at the hearing on said motion.

Dated: May 9, 2012

Respectfully submitted,

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IN THE UNITED STATES DISTRICT COURT FOR THE DISTRICT OF NEW MEXICO

UNITED STATES OF AMERICA,

Plaintiff, vs.

JOHN CHARLES McCLUSKEY,

Defendant

CR No. 10-2734 JCH

**MEMORANDUM IN SUPPORT OF MOTION TO EXCLUDE DNA TEST RESULTS AND REQUEST FOR DAUBERT HEARING**

# Statement of Facts and Threshold Objections

This motion addresses the admissibility of expert testimony based on testing and analysis of certain DNA samples extracted and chemically multiplied from a number of items the government deems relevant in this case.

In recent years, DNA testing techniques have evolved rapidly, from RFLP testing, to DQ Alpha testing, to Polymarker testing, to D1S80 testing, and most recently, to STR testing using commercially available “kits.” STR testing is the only testing used in this case. The “Identifiler PCR Amplification Kit” used in this case employed technology and test procedures substantially different from previous DNA testing methods.1

1 To greatly simplify an extremely complex subject, the DQ Alpha and Polymarker test kits used for a number of years employed a methodology which determines the sequence of a section of DNA by a method called reverse dot blot hybridization. The D1S80 kit, as well as the earliest used RFLP method, determined the length of a section of DNA by a method called gel electrophoresis. In all three of these methods, the lab technician makes a purported match by visually inspecting and comparing either the blue dots produced by the DQ Alpha or Polymarker test kits or the gel typing bands produced in RFLP and D1S80 testing. In contrast, short tandem repeat (STR) testing of DNA fragments using the Identifiler kit is fully automated and is done on a sophisticated typing machine (the 3130 Genetic Analyzer), which employs a complex proprietary software package (GenoMapper ID), and a completely different technology called capillary electrophoresis. The only similarity with the older methodology is that like the D1S80 kit, as well as the earliest used RFLP method, STR testing determines only the length of a section of DNA, not the sequence of the DNA. The implications of this limitation are explored fully

The procedural background and the particular expert conclusions at issue in the present motion are as follows.

On June 30, 2011, the Court entered a preliminary discovery order consistent with D.N.M.LR-Cr. 16.1. [Doc. 203.] Under that Order, Mr. McCluskey is deemed to have requested discovery under Fed. R. Crim. P. 16 unless he filed a waiver within seven days from the entry of the Order. [*Id*.] Mr. McCluskey did not file a waiver. On September 9, 2011, this Court entered a Scheduling Order which set January 20, 2012 as the “[d]eadline for government to complete all summaries and provide all reports on all experts, with all foundational data to be disclosed by February 17, 2012.” [Doc. 220, p.1]. The Court set March 30, 2012 as the “[d]eadline for defense *Daubert* motions directed at government experts.” (Id.). 2

On January 30, 2012, the government filed a four page Notice of Intention To Offer Expert Testimony [Doc. 261]. This Notice concedes that the Notice itself does not comply with Rule 16(a)(1)(G), or this Court’s Scheduling Order, for it explicitly states that “the United States will provide the experts’ credentials, summaries, and reports as separate discovery, and foundational information at a later time...” (Id.). The Notice purports to be only a “list of experts and the subject area of their expected testimony.” (Id.) The list includes the names of fifteen named experts in fourteen different areas of forensic science. The list does not constitute “a written summary of testimony...[which] describe[s] the witness’s opinions, the bases and reasons for those opinions, and the witness’s qualifications.” Federal Rule of Criminal Procedure, Rule 16(a)(1)(G). Instead, for each expert the Notice lists certain broad subject matters, and then indicates that the expert’s testimony “will include discussion of” that broad topic, without indicating what that discussion will consist of. For example, with respect to the firearm examiner’s testimony at issue in the present motion, the notice merely states that the United

below.

2 The Court has since extended the deadline to April 22, 2012, and has granted permission

for the filing of this supplemental memorandum. [Docs. 416, 428].

States gives notice that it intends to introduce certain expert testimony, including the testimony of :

Carrie Zais, Forensic Scientist, New Mexico Department of Public Safety Forensic Laboratory. Testimony will include the analysis of the serology/DNA.

[Doc. 261, p. 2-3].

On January 30, 2012, Mr. McCluskey filed a Motion to Compel Production of Expert Disclosures in Compliance with Rules 16(a)(1)(G) and this Court's Scheduling Order, for Depositions of Government Experts Pursuant to Rules 2, 16(a)(2), and 57, and for Adjustment of Scheduling Order. [Doc. 292]. In response to the motion, the government indicated that “[t]he United States will agree to provide to Defendant and this Court a further summary under Rules 702, 703, or 705 of the Federal Rules of Evidence of evidence it intends to present during its case-in-chief pursuant to Rule 16(a)(1)(G).” [Doc. 332, p. 50]. The government also indicated that depositions of the government’s experts was unnecessary because “numerous Daubert motions presumably will be heard by this Court wherein the experts for the Government will testify, as well as being available to testify at trial and subject to cross-examination.” (Id.)

On March 30, 2012, over two months after the Court’s January 20, 2012, deadline, the government filed a Supplemental Notice of Intent to Offer Expert Testimony. [Doc. 383]. The Supplemental Notice lists eleven expert witnesses.3

The summary with respect to the DNA examiner’s testimony is as follows: The United States intends to call Supervising Forensic Scientist, New

Mexico Department of Public Safety Forensic Laboratory, Carrie Zais, who is

3 Four witnesses listed in the original notice (Dr. Nadia Granger, Dr. Lee M. Blum, Dan Wright, and Andrew Armstong) are not listed in the supplemental notice. In conversation with counsel following the last court appearance on April 3, 2012, the government clarified that the government did not intend to call these four witnesses. The government indicated agreement to Mr. McCluskey’s position that he reserves the right to file *Daubert* or other motions challenging the admissibility of these four witnesses should the government change its position.

specialized in serology and DNA analysis, to testify about the DNA analysis she conducted in this case. Ms. Zais is expected to testify regarding her expert opinions and specialized knowledge in determining the numerous conclusions she discusses within her report, provided to defense on December 23, 2010 (bates range 1327-1328; 1396-1397; 1586-1589; 1655-1661; 1761-1763), February 24,

2011 (bates range 2346-2354; 2546-2549; 3015-3020); and October 5, 2011 (bates range 3898-99). The basis and reasons for her opinion, and her qualifications have been provided as discovery to Defendant and his counsel.

Foundational data was disclosed on February 16, 2012, which included approximately 70 pages of methodology, testing analysis, results, notes, and national match detail report. Ms. Zais, as Supervising Forensic Scientist, Advanced, at the laboratory, is expected to discuss her forensic DNA analyst experience dating back to 2002, as well as the hundreds of cases she has been involved in, which she relied upon in this case to determine that, among the numerous conclusions she made, DNA from Defendant was found within the Haases pickup truck. She is expected to testify regarding the strict chain of custody involved in blood samples, the lab control which are in place to protect the integrity of the samples, and the peer review process which follows the analysis of these samples and subsequent comparison.

Qualified as an expert numerous times in various courts, Ms. Zais is also expected to testify as to receiving standards for Defendant, Casslyn welch, Tracy Province, Gary Haas, and Linda Haas. She is expected to testify regarding her analysis and comparison of samples collected into evidence to those of the five standards she obtained. She will testify as to the numerous conclusions she found,

based on her expert opinion, specialized knowledge as a forensic scientist and DNA analyst, her training and professional experience. Ms. Zais is also expected to testify regarding the use of Phenolphthalein to confirm the presence of blood in the pickup truck.4

[Doc. 386, p. 4-5].

The supplemental notice, like the original notice, does not constitute “a written summary of testimony...[which] describe[s] the witness’s opinions, the bases and reasons for those opinions, and the witness’s qualifications.” Federal Rule of Criminal Procedure, Rule 16(a)(1)(G). Saying that “ [s]he will testify as to the numerous conclusions she found”, does not tell us what those conclusions are. Saying that her opinions will be “ based on her expert opinion, specialized knowledge as a forensic scientist and DNA analyst, her training and professional experience” does not begin to describe “the bases and reasons for those opinions.”

The referenced reports provided on December 23, 2010 (bates range 1327-1328; 1396-

1397; 1586-1589; 1655-1661; 1761-1763), February 24, 2011 (bates range 2346-2354; 2546-

2549; 3015-3020); and October 5, 2011 (bates range 3898-99), the non-duplicative portions of which are included on the Exhibit CD as Exhibit 1, set forth the specific opinions that are challenged in this memorandum on Rule 702, *Daubert,* and other grounds are as follows:

# Report of August 30, 2010

* 1. “Blood was indicated on items L1, L2, L3, L4, L5, L6, L7, L8, L9, L12, L12, SR1A, and SR1B.”; 5
  2. “A partial unknown male DNA profile was obtained from 4-d (at 10 of 15 loci). The

4 Ms. Zais’s testimony regarding the use of Phenolphthalein to confirm the presence of blood in the pickup truck” is the subject of a separate memorandum filed as Doc. 424.

source of item v-5 (Gary Haas secondary standard) is eliminated as a source of the DNA profile identified on item 4-d.”;

* 1. “The unknown female DNA profile identified on 26b is consistent with the unknown female DNA profile identified on item v-3 (Linda Haas secondary standard).”;
  2. “The unknown male DNA profile identified on items 13, L1, L2, L3, L4, L5, L7, L8, L9 and L12 is consistent with the unknown male DNA profile identified on item v-5 (Gary Haas secondary standard).”;
  3. “A DNA mixture of two or more individuals was obtained from item L6. A major unknown DNA profile was resolved from this mixture and is consistent with the unknown DNA profile identified on item v-5 (Gary Haas secondary standard)”;

# Report of September 30, 2010

* 1. “Blood was indicated on items 1B22A, 1B22B, 1B22C, 1B23B, 1B39A, and 1B39A-

1.”; 6

* 1. “A DNA mixture of two or more individuals was obtained from items 1B22A,

1B22B, 1B22C, and 1B39A. To a reasonable degree of scientific certainty, John McCluskey is the source of the major DNA profile resolved from these mixtures. ”;

* 1. “A DNA mixture of two or more individuals was obtained from item 1B22D. John McCluskey and Casslyn Mae Welch cannot be eliminated as possible contributors to this DNA mixture. Tracy Province, the source of item v-3 (Linda Haas secondary standard), and the source of item v-5 (Gary Haas secondary standard) are eliminated as contributors to this DNA mixture.”;
  2. “A partial DNA profile was obtained from item 1B23B (at 11 of the 15 loci). To a reasonable degree of scientific certainty, Tracy Province is the source of this partial DNA

profile.”;

* 1. “Tracy Province cannot be eliminated as a possible source of the partial DNA profile identified on item 4-d.”;
  2. “Casslyn Mae Welch cannot be eliminated as a possible contributor to the DNA mixture identified on item L6.”;
  3. “John McCluskey cannot be eliminated as a possible contributor to the DNA mixture identified on item L13.”;

# Report of December 22, 2010

* 1. “Blood was indicated on items 1B14C, 1B57, 1B58, 1B72B, R-1, R-6, and T-7A.”; 7
  2. “To a reasonable degree of scientific certainty, John McCluskey is the source of the DNA identified on items 1B13 and 1B14C.”;
  3. “A partial DNA mixture of two or more individuals was obtained from item 1B43 (at 13 of 15 loci). Casslyn Mae Welch cannot be eliminated as a possible contributor to this DNA mixture.”;
  4. “To a reasonable degree of scientific certainty, Casslyn Mae Welch is the source of the DNA identified on item 1B57.”;
  5. “A DNA mixture of two or more individuals was obtained from item 1B72A, John McCluskey cannot be eliminated as a possible contributor to this DNA mixture.”;
  6. “A DNA mixture of two or more individuals was obtained from item 1B72B. John McCluskey cannot be eliminated as a possible contributor to this DNA mixture.”;
  7. “A DNA mixture of two or more individuals was obtained from item 31a. To a reasonable degree of scientific certainty, John McCluskey is the source of the major DNA profile resolved in this mixture.”;
  8. “A DNA mixture of two or more individuals was obtained frm item 31e. Tracy

Province, John McCluskey, the contributor of item v-3 (Linda Haas secondary standard), and the contributor of item v-5 (Gary Haas secondary standard) cannot be eliminated as contributors to this DNA mixture.”;

* 1. “A DNA mixture of two or more individuals was obtained from item 31g. To a reasonable degree of scientific certainty, John McCluskey is the source of the major DNA profile resolved from this mixture.”;
  2. “A DNA mixture of two or more individuals was obtained from R-6. The contributor of item v-3 (Linda Haas secondary standard) and the contributor if item v-5 (Gary Haas secondary standard) cannot be eliminated as possible contributors to this DNA mixture.”;
  3. To a reasonable degree of scientific certainty, Tracy Province is the source of the DNA identified on item T-7A.”; and

# Report of April 27, 2011

* 1. “Blood was indicated on item 1B22E. To a reasonable degree of scientific certainty, John McCluskey is the source of the DNA identified on item 1B22E.”

Based on these reports and on voluminous foundational material disclosed to counsel on February 14, 2012 and April 20, 2012, it is apparent that the government proposes to have its DNA analyst render an opinion that Mr. McCluskey is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B22A, 1B22B, 1B22C, 1B39A , 1B13, 1B14C, 31a, 31g, and 1B22E to the exclusion of all other people in the world. The government also proposes to have its DNA analyst render an opinion that Mr. Province is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B23B and item T-7A to the exclusion of all other people in the world, and that Ms. Welch is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B57 to the exclusion of all other people in the world. See, National Academy of Sciences, National Research Council, Committee on Identifying the Needs of the Forensic Science Community, Strengthening Forensic Science in the United States: A Path Forward ( 2009) ("NAS 2009 Report") at 43 (“[A] conclusion of individualization implies that

the evidence originated from that source, to the exclusion of all other possible sources.”). 8 The government also seeks to have its DNA analyst testify that Mr. McCluskey “cannot be eliminated”as a “possible”contributor to the mixed or single DNA profile in evidentiary items 1

8 The NAS 2009 Report, written by a group of distinguished scientists and other scholars on a Committee chaired by Harry T. Edwards, Judge, United States Court of Appeals for the District of Columbia Circuit, is discussed in more detail below. Ross Zumwalt, Chief Medical Examiner, Office of the Medical Examiner of the State of New Mexico, was also on the Committee. Because of the importance of the NAS 2009 Report to this motion it is being provided to the Court in its entirety as Exhibit 4 to defendant’s motion to exclude firearms evidence, incorporated herein by reference. As the Court is probably aware, the NAS is generally considered the most prestigious scientific organization in the United States, "election to the Academy is considered one of the highest honors that can be accorded a scientist or engineer," and it holds a charter "to 'investigate, examine, experiment, and report upon any subject of science or art' whenever called upon to do so by any department of the government." Reports published by the NAS's research arm, the National Research Council, "provide a public service by working outside the framework of government to ensure independent advice on matters of science, technology, and medicine. They enlist committees of the nation's top scientists, engineers, and other experts, all of whom volunteer their time to study specific concerns. The results of their deliberations have inspired some of America's most significant and lasting efforts to improve the health, education, and welfare of the population." See *About the NAS*, [http://www.nasonline.org/site/PageServer?](http://www.nasonline.org/site/PageServer) pagename=ABOUT\_main\_page. The NAS 2009 Report , therefore, constitutes an assessment not by individual scientists or scholars but by a scientific institution, the first such assessment of forensic science evidence by a mainstream scientific institution of any kind.

The NAS has published two prior books on the admissibility of DNA evidence. See,

National Research Council, DNA Technology in Forensic Science (1992)(hereinafter “NRC I”); National Research Council, The Evaluation of Forensic DNA Evidence (1996)(hereinafter "NRC II"). Both are available online a[t http://books.nap.edu/openbook.](http://books.nap.edu/openbook)

As Mr. McCluskey has previously pointed out, when the NAS speaks, courts listen. See e.g, Melendez-Diaz v. Massachusetts, U.S. , 129 S.Ct. 2527, 2536, 2537, 174 L.Ed.2d 314 (2009)(quoting the NAS 2009 Report for the propositions that "[f]orensic evidence is not uniquely immune from the risk of manipulation", and that " ‘[t]he forensic science system, encompassing both research and practice, has serious problems that can only be addressed by a national commitment to overhaul the current structure that supports the forensic science community in this country.'" ); *United States v. Davis*, 602 F.Supp.2d 658, 663 n.2 (D.Md.2009)(“The NRC II is widely regarded as one of the definitive publications on the use of DNA evidence in the field of forensics.”); *United States v. Peters*, 1995 U.S. Dist. LEXIS 20950

\* 43 n. 15 (D. N.M. 1995)(NRC I “contains an authoritative discussion of many of the issues involved in this case.”), aff'd, 133 F.3d 933 (10th Cir. 1998) (unpub.).

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B22D, L13, 1 B72A, 1B72B, and 31e, that Mr. Province “cannot be eliminated”as a “possible”contributor to the mixed or single DNA profile in evidentiary items 4-d, 31e, and that Ms. Welch “cannot be eliminated”as a “possible”contributor to the mixed or single DNA profile in evidentiary items 1B22D, L6, and 1B43, and that Gary and Linda Haas “cannot be eliminated”as a “possible”contributor to the mixed or single DNA profile in evidentiary items 31e and R6. Finally, the government also seeks to have its DNA analyst testify that the mixed or single DNA profile in evidentiary item 26b is “consistent with” the unknown female DNA profile in the secondary DNA standard of Linda Haas, and that “the mixed or single DNA profile in evidentiary item 13, L1, L2, L3, L4, L5, L6, L7, L8,L9, and L12 is "consistent with" the unknown male DNA profile in the secondary DNA standard of Gary Haas.

Unusually, and, as discussed below, in direct violation of the NMDPS’s own DNA protocol, the DNA reports in this case set forth very few random match probability frequencies. Of the 41 evidentiary samples enumerated above, “probability of inclusion frequencies” are given for only 9 samples. For sample 1B22D, where it is concluded that neither Mr. McCluskey nor Ms. Welch can be eliminated as “possible” contributors to the mixture, it is stated in the report of September 30, 2010, that the following probability of inclusion frequencies exist (at 5 of the 15 loci):

African American 1 in 44 individuals

Apache 1 in 85 individuals

Caucasian 1 in 12 individuals

Navajo 1 in 161 individuals

Southwest Hispanic 1 in 64 individuals.

For sample 4d, where it is concluded that Mr. Province cannot be eliminated as a “possible” contributor, it is stated in the report of September 30, 2010, that the following probability of inclusion frequencies exist (at 7 of the 15 loci):

African American 1 in 2.665 trillion individuals

Apache 1 in 47.15 billion individuals

Caucasian 1 in 12.15 billion individuals

Navajo 1 in 184.4 billion individuals Southwest Hispanic 1 in 45.17 billion individuals.

For sample L6d, where it is concluded that a “major” unknown DNA profile was resolved from this mixture that is “consistent with” the DNA profile of Gary Haas, it is stated in the report of September 30, 2010, that the following probability of inclusion frequencies exist (at 13 of the 15 loci):

African American 1 in 26.18 million individuals

Apache 1 in 4.396 million individuals

Caucasian 1 in 2.879 million individuals

Navajo 1 in 35.17 million individuals Southwest Hispanic 1 in 42.77 million individuals.

For sample L13, where it is concluded that Mr. McCluskey cannot be eliminated as a “possible” contributor to the mixture, it is stated in the report of September 30, 2010, that the following probability of inclusion frequencies exist (at 15 of the 15 loci):

African American 1 in 5.47 trillion individuals

Apache 1 in 4.773 billion individuals

Caucasian 1 in 18.8 billion individuals

Navajo 1 in 17.74 billion individuals

Southwest Hispanic 1 in 174. 2 billion individuals.

For sample 1B43, where it is concluded that Ms. Welch cannot be eliminated as a “possible” contributor to the mixture, it is stated in the report of December 22, 2010, that the following probability of inclusion frequencies exist (at 7 of the 15 loci):

African American 1 in 212 million individuals

Apache 1 in 2.74 billion individuals

Caucasian 1 in 12.84 million individuals

Navajo 1 in 12.16 billion individuals Southwest Hispanic 1 in 382.1 million individuals.

For sample 1B72A, where it is concluded that Mr. McCluskey cannot be eliminated as a “possible” contributor to the mixture, it is stated in the report of December 22, 2010, that the following probability of inclusion frequencies exist (at 11 of the 15 loci):

African American 1 in 299,800 individuals

Apache 1 in 2307 individuals

Caucasian 1 in 44,580 individuals

Navajo 1 in 5,118 individuals

Southwest Hispanic 1 in 42,520 individuals.

For sample 1B72B, where it is concluded that Mr. McCluskey cannot be eliminated as a “possible” contributor to the mixture, it is stated in the report of December 22, 2010, that the following probability of inclusion frequencies exist (at 13 of the 15 loci):

African American 1 in 61,390 individuals

Apache 1 in 4221 individuals

Caucasian 1 in 9268 individuals

Navajo 1 in 1635 individuals

Southwest Hispanic 1 in 17,130 individuals.

For sample 31e, where it is concluded that neither Mr. McCluskey, nor Mr. Province,nor Gary and Linda Haas can be eliminated as a “possible” contributor to the mixture, it is stated in the report of December 22, 2010, that the following probability of inclusion frequencies exist (at 5 of the 15 loci):

African American 1 in 58 individuals

Apache 1 in 5 individuals

Caucasian 1 in 21 individuals

Navajo 1 in 5 individuals

Southwest Hispanic 1 in 24 individuals.

For sample R6, where it is concluded that neither Gary nor Linda Haas can be eliminated as a “possible” contributor to the mixture, it is stated in the report of December 22, 2010, that the following probability of inclusion frequencies exist (at 15 of the 15 loci):

African American 1 in 2.028 billion individuals

Apache 1 in 12.29 million individuals

Caucasian 1 in 203.1 million individuals.

Navajo 1 in 29.71 million individuals. Southwest Hispanic 1 in 1.055 billion individuals.

Finally, the DNA reports set forth that no human DNA was detected on item G2, 1B23A and g-1, 1B58, G18, that human DNA was detected on items v-1, 31f, 34a, 34c, and 34d; however, not in sufficient quantity for further DNA analysis, that no DNA profile was obtained from items 4c, 11, and 28, that no interpretable DNA was obtained from items 17, SR1A, 1B39A-1, and that the mixtures obtained from item 31b, 31d, and 34b were suitable for elimination purposes only. As an initial threshold objection, Mr. McCluskey asserts that these inclusive results are not relevant and are therefore inadmissible under Rule 402 (“Evidence which is not relevant is not admissible.”). See, *United States v. Holloway*, 971 F.2d 675, 680 (11th Cir. 1992)(“ Inconclusive tests are not material...”); *Commonwealth v. Curnin*, 409 Mass. 218, 222 n. 7, 565 N.E.2d 440 (1991) (“In certain circumstances, the results of a DNA test may be inconclusive. If so, the consequences of the test are inadmissible.”); *Commonwealth v.*

*Buckman*, 461 Mass. 24, 34, 957 N.E.2d 1089 (2011)(same).

Mr. McCluskey also objects on relevancy grounds to the conclusion that “to a reasonable

degree of scientific certainty, John McCluskey is the source of the DNA identified on items 1B13 and 1B14C. (Exh. 1, Report of December 22, 2010). Item 1B13 (a baseball cap) and 1B14 (blue jeans) were found in Mr. McCluskey’s possession when he was arrested. Neither item tested positive for the presence of blood. The fact that Mr. McCluskey’s DNA was allegedly found in items of his clothing is hardly surprising and does not have “any tendency to make the existence of any fact that is of consequence to the determination of the action more or less probable than it would be without the evidence.” Fed. Rules of Evidence, Rule 401.

The remainder of this memorandum is devoted to demonstrating that the DNA evidence outlined above is prohibited by *Daubert v. Merrell Dow Pharmaceutical*, 509 U.S. 579 (1993) and the Federal Rules of Evidence.

# ARGUMENT

# Introduction.

“The past two-and-a-half decades have seen tremendous growth in the use of DNA evidence in crime scene investigations as well as paternity and genetic genealogy testing.” John M. Butler, Fundamentals of Forensic DNA Typing (2010)(“hereinafter, “Butler,

Fundamentals”), p. 5. 9 However, as with all of the forensic sciences, “[i]t is important to keep in mind that forensic DNA tests must be performed carefully in order to obtain reliable results.” (Id. at 7). Stringent standards and precise protocols must be “faithfully followed by forensic DNA laboratories to help maintain a high level of quality in the data obtained” and “information

9 Dr. John Butler is currently a National Institute of Standards and Technology Fellow and Group Leader of Applied Genetics in the Biochemical Science Division at NIST. He is a regular invited guest of the FBI’s Scientific Working Group on DNA Analysis Methods (SWGDAM) and a member of the Department of Defense Quality Assurance Oversight Committee for DNA Analysis. In addition to the book quoted in the text he is the author of numerous published articles and three other books on forensic STR testing. See, John M. Butler, Forensic DNA Typing, First Edition: Biology & Technology Behind STR Markers (1st ed.

2001); John M. Butler, Forensic DNA Typing, Second Edition: Biology, Technology, and Genetics of STR Markers (2nd ed. 2005); John M. Butler, Advanced Topics in Forensic DNA Typing: Methodology (1st ed. 2012).

produced as part of a forensic examination must be reliable and able to hold up in court under rigorous scrutiny.” (Id.)

The NAS 2009 Report reminds us:

Among existing forensic methods, only nuclear DNA analysis has been rigorously shown to have the capacity to consistently, and with a high degree of certainty, demonstrate a connection between an evidentiary sample and a specific individual or source. Indeed, DNA testing has been used to exonerate persons who were convicted as a result of the misapplication of other forensic science evidence.58 However, this does not mean that DNA evidence is always unassailable in the courtroom. There may be problems in a particular case with how the DNA was collected, examined in the laboratory, or interpreted, such as when there are mixed samples, limited amounts of DNA, or biases due to the statistical interpretation of data from partial profiles.

(NAS 2009 Report, p. 100)

The reason why DNA evidence must be subjected to rigorous scrutiny is obvious but bears emphasis. “Testimony from forensic DNA analysts can be overwhelming to jury members—who often have limited exposure to the concepts of biology, genetics, and the technology used to generate DNA profiles.” John M. Butler, Advanced Topics in Forensic DNA Typing: Methodology (1st ed. 2012)(hereinafter “Butler, Advanced Topics”), p. 542. “ There is a considerable aura to DNA evidence. Because of this aura it is vital that weak evidence is correctly represented as weak or not presented at all. ” Id.(internal quotation omitted).

Thus, a *Daubert* hearing is particularly important in DNA cases. See *McDaniel v. Brown*,

U.S. , 130 S.Ct. 665, 675, 175 L.Ed.2d 582 (2010) (“Given the persuasiveness of [DNA] evidence in the eyes of the jury, it is important that it be presented in a fair and reliable manner.”) Because DNA evidence, surrounded as it is by a media-inspired aura of infallibility, by its very nature will be particularly compelling to lay jurors, and because DNA typing is used in the present capital case for purposes of identifying perpetrators of particularly serious crimes, extreme circumspection in evaluating the techniques and protocols of DNA typing is mandated. As was stated in *United States v. Chischilly*, 30 F.3d 1144, 1156 (9th Cir. 1994),

Notwithstanding *Daubert's* express preference for exposing novel scientific theories and methodologies to the glare of the adversarial process, Daubert enjoins watchful assessment of the risk that a jury would assign undue

weight to DNA profiling statistics even after hearing appellant's opposing evidence, the testimony of Government witnesses under vigorous

cross-examination and the careful instructions of the district court on burdens of proof. Of particular concern is where the Government seeks to present probability testimony derived from statistical analysis, the third main phase of DNA profiling. Numerous hazards attend the courtroom presentation of statistical evidence of any sort. Accordingly, Rule 403 requires judicial vigilance against the risk that such evidence will inordinately distract the jury from or skew its perception of other, potentially exculpatory evidence lacking not so much probative force as scientific gloss.

See also, *Government of Virgin Islands v. Byers*, 941 F. Supp. 513, 527 (D. P.R.1996) (“For the lay person...it is easy to conceive that th[e] same science that can reveal the genetic secrets of the living, the dead, and the yet unborn is potent enough to solve the most perplexing crime. There is something very primal about DNA and genetic science that lends itself to a posture of ‘mythic infallibility.’”). *See also, People v. Venegas*, 18 Cal.4th 47, 81-84 (1998) (noting “DNA evidence is different,” and that “[t]his is an instance in which the method of scientific proof is so impenetrable that it would . . . ‘assume a posture of mystic infallibility in the eyes of a jury’”).

In addition, because DNA typing methodologies for use in the forensic arena are rapidly evolving at a rate that generally outpaces the ability of appellate courts to review the changes, keen attention to the issues that have been decided and those that are still unresolved is required.10

10 For instance, although the Tenth Circuit held in *United States v. Davis,* 40 F.3d 1069 (10th Cir.1994) that the district court did not abuse its discretion in *admitting* the RFLP DNA testing results in that case, it further held in *Attorney General of Oklahoma v. Tyson Foods, Inc.* 565 F.3d 769, 781 (10th Cir. 2009) that the district court did not abuse its discretion in using a *Daubert* analysis to give no weight to PCR DNA testing results in that case because the district court’s decision arose “ out of the novelty of its application to an entirely new area, which required the development of primers that had not been identified previously. Thus, the court looked to other indications of reliability, including those enumerated by the *Daubert* Court, but could find none In addition, the record casts further doubt on Dr. Harwood's methodology,

suggesting other procedural flaws.” Neither the Tenth Circuit nor any other federal court has passed on the particular combination of DNA methodologies employed in this case (Identifiler/Real Time Quantification/3130 Genetic Analyzer), and of course no court has passed on whether these methodologies were correctly applied in Mr. McCluskey’s case, a determination required by amended Rule 702 as well as by *Davis* and *Tyson Foods,* as discussed below.

Unfortunately, jurors’ heavy reliance on DNA experts can be woefully misplaced because DNA test samples are subject to misinterpretation, faulty analysis, mislabeling, contamination, and other serious deficiencies. See NAS 2009 Report, p. 47 (“[A]lthough DNA analysis is considered the most reliable forensic tool available today, laboratories nonetheless can make errors working with either nuclear DNA or mtDNA—errors such as mislabeling samples, losing samples, or misinterpreting the data.”). Also, the tests themselves may be unreliable, skewed or misinterpreted by human error. As was stated in *United States v. Bentham*, 414 F.Supp.2d 472, 473 (S.D.N.Y.2006), “[f]alse positives-that is, inaccurate incriminating test results-are endemic to much of what passes for ‘forensic science.’...Even the ‘gold standard’ of forensic testing, DNA tests, may, because of human error, prove fallible.” Consequently, the court must exercise its gate-keeping function under *Daubert* to ensure that such unreliable evidence does not reach the jury.

Countless cases have now demonstrated that despite its widespread use, DNA evidence is by no means failsafe. In fact, when DNA testing was first introduced, experts argued that a false match (a test result that incriminated an innocent defendant) was impossible. See, William C. Thompson, Franco Taroni, & Colin G.G. Aitkin, *How the Probability of a False Positive Affects the Value of DNA Evidence*, 48 J. FORENSIC SCI. 1, 2 (2003) [hereinafter “Thompson, False Positive”]. “This claim is now broadly recognized as wrong in principle , and it has repeatedly proven wrong in practice.” (Id. at 2). False matches and flawed DNA test results can cause wrongful convictions of innocent people, and DNA evidence has been called into question or proven faulty in several cases around the country.11 Understanding why and how this occurs

11 *See,* e.g., Butler, Fundamentals at 292 ( examining scandals at the FBI and Houston Police Department DNA Units and pointing out that “unfortunately errors in data interpretation by the HPD laboratory led to the false conviction and incarceration of a young man accused of a 1998 rape.”); NAS 2009 Report, p. 132 (“Although DNA laboratories are expected to conduct their examinations under stringent quality controlled environments, errors do occasionally occur. They usually involve situations in which interpretational ambiguities occur or in which samples were inappropriately processed and/or contaminated in the laboratory. Errors also can occur when there are limited amounts of DNA, which limits the amount of test information and

requires a brief description of the theory of forensic DNA testing and its associated safeguards and problems.

# General Principles of DNA Analysis.

# The Theory of Forensic DNA Testing.

At the outset it is worth noting a few basic principles of forensic DNA analysis. See, Butler, Fundamentals at pp. 6-7. First, with the exception of identical twins, the genome (i.e., the complete genetic composition) of each individual is unique and is inherited from an individual’s parents with one half coming from the mother and one-half from the father. “However, to limit the expense and time of testing, forensic DNA analysis only examines a small subset of genetic variation within the human genome in order to differentiate among individuals. Out of the more

than 6 billion nucleotides present in the diploid human genome, fewer than 4000 nucleotides, or 0.0006% of the material, are examined from highly variable and nondescript regions. By way of comparison, if each nucleotide were 1 inch (2.5 cm) in length, the nuclear DNA in a single cell would be more than 100,000 miles (160,000 km) long — yet forensic DNA tests only examine about 300 feet (90 m) of this information. Because only a fraction of the available DNA information is examined, statistical calculations are performed to estimate the occurrence of a random match based on measured frequencies of particular genetic attributes among unrelated individuals.” (Id.)

Forensic laboratories typically “type” samples using commercial test kits that can detect genetic characteristics (called alleles) at various loci (locations) on the human genome. The test

increases the chance of misinterpretation.”); William C. Thompson, *The Potential For Error In Forensic DNA Testing* (2008)(hereinafter, “Thompson, Potential For Error”), <http://www.councilforresponsiblegenetics.org/pagedocuments/h4t5eoyuzi.pdf>; William C. Thompson, *Tarnish on the ‘Gold Standard;’ Understanding Recent Problems in Forensic Testing*, CHAMPION, Feb. 2006, at pp. 10-12 [hereafter “ Thompson, Tarnish on the Gold Standard”]; Adam Liptak, *You Think DNA Evidence is Foolproof? Try Again*, N.Y. TIMES, Mar. 16, 2003. For sources documenting errors in DNA testing, *see* “Scientific Testimony: DNA Testing Problems”, <http://www.scientific.org/DNAProblems/DNA-Problems.htm>(last visited 05/04/12).

kits used in the United States generally examine the 13 STR loci selected by the FBI for CODIS, the national DNA database. Some of the newer test kits such as the Identifiler kit used in this case also examine two additional STR loci. 12 At each STR locus, there are a number of different alleles (generally between 6 and 18) that a person might have. Each person inherits two of these alleles, one from each parent. Numbers are used to identify the alleles and the pair of alleles at a particular locus constitutes a genotype. Hence, one person can have a genotype (for a locus called D3S1358) of “14,15;” while another person has the genotype “16,17.” The complete set

of alleles detected at all loci for a given sample is called a DNA profile. When describing DNA profiles, people sometimes mention the number of loci they encompass. See, Thompson, Potential For Error at 3.

The resulting DNA profile for a sample, which is a combination of individual

STR genotypes, is compared to other samples. In the case of a forensic investigation, these other samples would include known reference samples such as those taken from the victim or suspects, which are compared to the crime scene evidence. “If there is no match between the questioned forensic sample and the known sample, then the samples may be considered to have originated from different sources.” (Butler, Fundamentals, p. 7). Importantly, “[i]n forensic DNA typing, if *any* STR locus fails to match when comparing the genotypes between two or more samples, then the profiles between the questioned and reference sample will be declared a non-match, *regardless of how many other loci match*.” (Butler, Fundamentals at 221 (emphasis added); See also John Butler, Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers (2nd ed. 2005)("[i]n forensic DNA typing, if any *one* STR locus fails to match when comparing the genotypes between two or more samples, then the profiles between the questioned and reference

12 To put the limited nature of a DNA analysis of only 13 or 15 STR loci into perspective, Dr. Butler notes that “more than 20,000 tetranucleotide STR repeats have been located throughout the human genome. However, when the core STR loci that are widely used today were selected back in the mid-1990s, only a handful of STR loci were known and characterized.” Butler, Fundamentals at 148.

sample will be declared a non-match, regardless of how many other loci match."(emphasis added), p. 386.

“ If a match or ‘ inclusion’ results, then an estimate is made of the rarity of the obtained DNA profile by comparing it to a population database, which is a collection of DNA profiles obtained from unrelated individuals of a particular ethnic group. For example, due to minor

genetic differences between the groups, African Americans and Caucasians have different population databases for comparison purposes .... Finally a case report is generated. This report

typically includes the random match probability (i.e., an estimate of the rarity of the observed DNA profile) for the match in question. This random match probability is the chance that a randomly selected individual from a population will have an identical STR profile or combination of genotypes at the DNA markers tested.” Butler, Fundamentals at p. 7.

# Overview of the DNA Testing Process. 13

1. **Sample Collection and Characterization**

Law enforcement personnel who collect and submit crime scene evidence for DNA analysis must carefully collect, package and seal the evidence and then arrange for its secure delivery to a DNA laboratory. “The importance of proper DNA evidence collection cannot be overemphasized. If the DNA sample is contaminated from the start, obtaining unambiguous information becomes a challenge at best and an important investigation can be compromised.” (Butler, Fundamentals, p. 80-81). “ Regardless of the method of collecting a DNA sample from a reference or crime scene source, it is imperative that the collection material be DNA-free prior to

13 Unless otherwise indicated, all of the information provided in Sections B. 2-4 and C. comes from United States Department of Justice, Office of the Inspector General, The FBI DNA Laboratory: A Review of Protocol and Practice Vulnerabilities (May 2004), available at [http://www.usdoj.gov/oig/special/0405/final.pdf.](http://www.usdoj.gov/oig/special/0405/final.pdf) and included on the Exhibit CD as Exhibit 2.

use.” (Butler, Advanced Topics, p.467). 14

In this case, the DNA analyst’s notes indicate that all of the evidentiary samples were delivered in sealed envelopes. However, there is a notation for samples 4-c and 4-d that “[c]igarette butt is covered in a clear, oily solution (it was reported to have brake fluid spilled on it after law enforcement confiscation).” (Discovery, 6778). Moreover, it is noted with respect to several samples that prior to the bags being sealed the items in the bag had undergone some type of chemical testing by either crime scene investigators or latent fingerprint (LP) examiners, as follows: L-1 (“dark blue/black staining...previously processed with amido black LP staining”), L- 4 (“dark brownish/black staining”), L13 (dark blue staining on most of swab...previously processed with amido black LP staining”), 13 (“moderate amount of black staining...previously examined for LP”), SR1A (“large amount of brownish/ blackish staining throughout ...note: previusly examined for LP”); SR1B (same), 14 (“moderate amount of black and purplish staining...previously examined for LP”) , 1B22 (various areas of pinkish staining...previously examined for LP”), 1B23 (small amount of pinkish staining...previously examined for LP”), T- 7A (“spot on right front leg-positive for blood w/hemastix [by crime scene examiner’”), 1B9A (same), 1B14C (same), 1 B57 (same), 1B21 (moderate amount of pinkish staining throughout...previously examined for LP”), 31a-31g (gray brown, or blue staining), 34a-34f

14 Dr. Butler describes in his book how

For over 15 years investigators in Europe chased what was popularly referred to as the “German phantom,” a supposed serial offender whose DNA profile was continually appearing in a variety of crimes In 2008, the “offender”

was discovered to be an elderly lady who worked for a manufacturer packaging DNA collection swabs. In placing the swabs in their packages, she had inadvertantly contaminated some of them with her own DNA, which when used for the purpose of crime scene investigation revealed her DNA profile rather than biological material from the crime scene.

(Butler, Advanced Topics, p. 470.)

(orangish brown, black/grey, blue, or grey staining), 1B 14 (“large amount of brownish staining”). (Discovery 6433-6436, 6466-6469 6660-6661, 6778-6779, 6795).

The impact of other forensic examiners having prior access to DNA samples is explained by Dr. Butler:

Brushes used to dust for fingerprints can cross-contaminate samples if precautions are not taken by the crime scene investigator (van Oorschot et al. 2005). One study found that out of 51 used latent fingerprint brushes tested a full or partial DNA profile was obtained 86% of the time (Proff et al. 2006). Some secondary transfer with contaminated fingerprint brushes was also demonstrated. Thus, changing brushes after investigating crime scenes or a thorough decontamination procedure for brushes after use is recommended (Proff et al.

2006). Another illustration of potential contamination during other forensic examinations is with firearms examinations, which should be conducted after DNA collection if possible. Alternatively, the firearm examiners need to wear gloves, masks, and other personal protective equipment in order to protect the evidence from contamination. In all cases, it is beneficial to have DNA profiles from latent print and firearms examiners on file as part of the staff elimination database (see Chapter 4). In addition, prior to utilizing chemicals for presumptive testing, it is best to evaluate potential impact on obtaining successful results with downstream DNA testing.

(Butler, Advanced Topics, p. 18)

It does not appear that any of these precautions were followed in this case.

In any event, upon receipt of the evidence, a DNA analyst first determines if the evidence might provide DNA by visually examining it for indications of body fluid stains, and then performing testing to determine whether specific body fluids that might contain DNA are present. Here, as more fully explained in Doc. 424, the analyst used only presumptive tests for the presence of blood and is now claiming that such tests “confirm” the presence of blood.

# Extraction

When possible, a DNA analyst extracts only a portion of the stains on the evidence and saves the remainder in case future testing is necessary. See, Butler, Fundamentals, p. 89 (“Every effort should be made to avoid completely consuming or destroying evidence so that a portion is available for future testing if needed.”). Generally, stains on fabric are cut out of the item and the DNA is extracted from the cuttings. If the stains are on a hard object, such as a knife or a steering wheel, some of the dried body fluid is removed from the object with a cotton swab

(known as swabbing an item) and the DNA is extracted from the cotton swab. In this case, the vast majority of the DNA evidence was collected on cotton swabs, and although it is not entirely clear for many samples whether the analyst consumed the whole swab or the whole stain in testing she did note for samples L1, L2, L3, , L5, L6, L7, L8, L9, L12 that “all of stain...collected for DNA testing”whereas for sample L 4 and L13 she noted that “½ of stain collected for DNA testing.” (Discovery 6779, 6841-6842). It thus appears that at least as to samples L1, L2, L3, L5, L6, L7, L8, L9, L12, and possibly as to other samples, the analyst has deprived Mr. McCluskey of his ability to extract and re-test these samples in their original state, contrary to the procedure she followed with respect to samples L4 and L 13, and contrary to widely accepted protocols and other recommendations addressing the issue of retesting.15

15 The FBI’s Quality Assurance Standards for Forensic DNA Testing Laboratories (eff.

July 1, 2009)(Exh. 3, Exhibit CD), <http://www.fbi.gov/about-us/lab/codis/qas_testlab.pdf> provides in Standard 7.2 that “[w]here possible, the laboratory shall retain or return a portion of the evidence sample or extract.” Standard 7.3 provides that “[t]he laboratory shall have and follow a documented policy for the disposition of evidence that includes a policy on sample consumption.” Numerous other organizations have also addressed this issue. See, American Bar Association, Criminal Justice Standards on DNA Evidence, Standard 3.4(a) (approved by the American Bar Association, House of Delegates, August 7, 2006) (counseling that "[w]hen possible, a portion of the DNA evidence tested and, when possible, a portion of any extract from the DNA evidence should be preserved for further testing"); National Research Council, The Evaluation of Forensic DNA Evidence, p. 88, (1996) (recommending that "[w]henever feasible, forensic samples should be divided into two or more parts at the earliest practicable stage and the unused parts retained to permit additional tests"); National Institute of Justice, National Commission on the Future of DNA Evidence, Postconviction DNA Testing: Recommendations for Handling Requests pp. 24, 63, (Sept.1999), http:// [www.](http://www/) ncjrs. org/ pdffiles 1/ nij/ 177626. pdf, (recommending that samples be split whenever possible before and during the testing process).

"The rationale for this preference is manifest: the preservation of a sample for retesting

provides a means to challenge the reliability of an adverse test result by attempting to replicate the result in a subsequent test in the event there is a dispute as to the adequacy of the testing procedures employed in the initial test." *Thompson v. State*, 395 Md. 240, 254, 909 A.2d 1035 (Md.2006). Here, the utilization of all of the stains in testing samples L1, L2, L3, L5, L6, L7, L8, L9, L12 has destroyed Mr. McCluskey’s ability to retest these samples. For that reason, as well as many others to be discussed below, no government DNA evidence should be allowed in this case. See, *Arizona v. Youngblood*, (1988) 488 U.S. 51 [109 S.Ct. 333, 102 L.Ed.2d 281,

*California v. Trombetta*, (1984) 467 U.S. 479 [104 S.Ct. 2528, 81 L.Ed.2d 413]; *United States v.*

The process used to extract the DNA varies depending on the organic source of the stain and the material containing the stain. However, it is generally accepted that “[m]ost standard procedures for extracting DNA from forensic substrates involve manipulations that expose the sample to potential contamination.” D. Moss, et. al., *An Easily Automated, Closed-Tube Forensic DNA Extraction Procedure Using a Thermostable Proteinase*, Int J Legal Med (2003) 117: 340–349. 16 Therefore,

All samples must be carefully handled regardless of the DNA extraction method to avoid sample-to-sample contamination or introduction of extraneous DNA. The extraction process is probably where the DNA sample is more susceptible to contamination in the laboratory than at any other time in the forensic DNA analysis process. For this reason, laboratories usually process

the evidence samples at separate times and sometimes even different locations from the reference samples.

(Butler, Fundamentals, p. 101)

In this case, all samples except samples L1, L4, and L 13 were subjected to an automated extraction procedure using a Maxwell 16 Robotic System. 17 Sample L1, L4, and L13 were

*Bohl*, 25 F.3d 904, 910 (10th Cir.1994) (bad faith requirement in discovery and applies only where "the exculpatory value of the evidence is indeterminate and all that can be confirmed is that the evidence was ‘potentially useful' for the defense"). See also, Seth F. Kreimer & David Rudovsky, *Double Helix, Double Blind: Factual Innocence and Postconviction DNA Testing*, 151 U. Pa. L. Rev. 547, 587 (2002) ("In an era of universal use of DNA evidence to both implicate and exonerate criminal suspects, it would be disingenuous for the prosecutor to claim that anything short of truly accidental loss was not strong evidence of bad faith.")

16 “Further studies have shown that a significant portion (20-76%) of the DNA that is collected by a cotton cloth/swab stick is lost during the extraction phase.” R. van Oorschot, *Are You Collecting All the Available DNA from Touched Objects*, 1239 International Congress Series 1239 (2003) 803, 804)

17 Curiously, an internal audit provided to the defense in discovery and dated October 20, 2010 checks as not applicable two items on the FBI’s Quality Assurance Standards Audit For Forensic DNA Testing Laboratories Form:

6.1.4 If a robotic workstation is used to carry out DNA extraction, quantification, PCR setup, and/or amplification in a single room, has the laboratory validated the analytical process in accordance with Standard 8 ?

a. If the robot performs analysis through amplification, is the robot housed in a separate room from that used for initial evidence examinations

originally subjected to a manual (Chelex) extraction procedure and then to a second extraction procedure using the Maxwell 16. The NMDPS Serology/DNA/ Databasing Quality Manual classifies the Maxwell 16 as a “critical DNA instrument”, which means that “[r]outine maintenance shall be established ...to include preventative maintenance performed by the manufacturer..and at least annually, a performance check must be conducted and documented...and approved by the DNA Technical Leader prior to the instruments use in casework or databasing.” (NM DPS Serology/DNA/Databasing Quality Manual (eff. 6/23/10), Ex. 4 , Section 16.4) 18 The Manual also purports to establish “special precautions” to prevent contamination of the robot, but these are no more than vague statements, such as “[c]are must be taken to avoid splashes, spills or other potential contamination issues” and “[r]obotic surfaces will be cleaned with...ethanol.” (Exh.3, Sec. 4, p. 5).

An external audit provided to the defense in discovery and conducted on May 16-17, 2011 states that

The Maxwell 16 robotic instruments had no preventive maintenance in 2010. The NM DPS Biology Quality Manual states preventive maintenance will be conducted annually by an outside provider. The auditors read a memo stating that the annual maintenance on the Maxwell 16 robotic instruments was not performed because the laboratory did not have a service contract to do so.

A memorandum provided in discovery dated July 20, 2011 and signed by Quality Assurance Manager Adam Pasternick and DNA Technical Leader Jennifer Otto indicates that in

The auditor, DNA Technical Leader Jennifer Otto, checked “N/A” next to these items and wrote “6.1.4 and 6.1.4a are marked NA because the laboratory does not use a robotic workstation for extraction through amplification.” She also checked these items “N/A” in an internal audit conducted on October 20, 2011. The records in this case indicate otherwise.

18 The defense has been provided three versions of this Manual, each with a different effective date. The Manuals are included on the Exhibit CD as Exhibit 4 (eff. 6/13/10), Exhibit 5 (eff. 10/13/10), and Exhibit 6 (eff. 4/1/11). The defense has also been provided with two versions of the NM DPS’s Serology/DNA SOP, referenced below. The SOPs are included on the Exhibit CD as Exhibit 7 (eff. 7/1/10) and Exhibit 8 (eff. 4/1/11). For the most part, and unless otherwise noted, the various versions contain identical language, so citations will usually be to the earliest version.

response to this audit finding, the NM DPS simply changed its protocol:

Since funding currently and in the future is questionable for instrument service contracts, the Biology Quality Manual will be changed to reflect that although the lab will strive to obtain preventative maintenance for instrumentation whenever possible, the Biology section will no longer be required to have annual preventative maintenance if circumstances/funding will not allow such action and since preventative maintenance is not currently a [FBI]QAS standard.

There are also other issues concerning the extraction process. For the most part, the evidentiary samples were not processed “at separate times *and* ...even different locations from the reference samples.” (Butler, Fundamentals, p. 101)(emphasis added). The NMDPS Manual only requires that “[e]vidence samples are extracted at a separate time *or* space from reference samples.” (Exh. 3, Sec.4, p. 3)(emphasis added). Similarly, the NM DPS’s Serology/DNA SOP states that “DNA extractions of known and questioned samples are performed at different times *and/or* different locations (*or* instruments). When possible, questioned samples should be extracted before known samples. Extractions of potentially high and low DNA containing samples are also performed separately in time *or* location (*or* instruments).” Exh.6, at 6-1 (emphasis added).

Here, samples L1, L4, and L 13 were extracted on August 9, 2010 at 7:55 a.m. On the same date, at 9:20 a.m., apparently in the same place, the Haas reference samples were extracted. On August 17, 2010, at 7:20 a.m., again apparently in the same place, the Haas reference samples were extracted a second time. On the same date, at 10:00 a.m., again apparently in the same place, samples SR1A and SR1B were extracted. On August 20, 2010, again apparently in the same place, samples L2, L3, L5, L7, L8, L9, and L 12 were extracted *after* the reference sample of Gary Haas had already been extracted. On August 30, 2010, the analyst concluded that these samples were “consistent with” the reference sample for Gary Haas.

Similarly, on September 13, 2010, at 11:10 a.m. the analyst extracted samples 1B22A- 1B22D, 1B23A-1B23B, and 1B3939A-1B39A-1. On the same date, at 12:55 p.m., apparently at the same place, she extracted the reference samples for McCluskey, Province, and Welch. She extracted all other samples in the case, in the same place, after these reference samples had

already been extracted.

# Quantitation

After extraction, the sample is quantitated to determine the amount of human DNA, if any, present in the sample. Quantitation of DNA is a quality assurance step to ensure that there is enough DNA in a forensic sample to give optimal results based on the specifications noted for each amplification kit used. The Quality Assurance Standards for Forensic DNA Testing Laboratories issued by the FBI, states under Standard 9.4: “ The laboratory shall quantify the amount of human DNA in forensic samples prior to nuclear DNA amplification”. (Exh. 3)

Correct quantitation is a critical step in the analysis because it is generally understood by DNA experts that “[u]sing samples with either more or less than the optimum amount will produce unreliable results.” *United States v. Davis*, 602 F.Supp.2d 658 (D.Md.2009). “[C]ommercial STR typing kits work best with an input DNA template of around 1 ng. [of human DNA.]” (Butler, Fundamentals, p. 112). As explained by Dr. Butler,

Determination of the amount of DNA in a sample is *essential* for most PCR- based assays because a narrow concentration range works best with multiplex short tandem repeat (STR) typing. Typically 0.5 to 2.0 ng of input human DNA is optimal with current commercial STR kits.

Too much DNA results in overblown electropherograms that make interpretation of results more challenging and time consuming to review. Too little DNA can result in loss of alleles due to stochastic amplification and failure to equally sample the STR alleles present in the sample.

(Butler, Fundamentals, p. 111)(emphasis added) 19

19 The recommended amount of input DNA varies from kit to kit and from laboratory to laboratory based on the results of developmental and internal validation studies. The manufacturer of the Identifiler Kit recommends, based on its own developmental validation, that “[t]he amount of input DNA added to the AmpFlSTR Identifiler PCR Amplification kit should be between 0.5 and 1.25 ng.” Applied Biosystems, Identifiler PCR Amplification Kit User’s Manual (20 ), p. 4-31, available at <http://www3.appliedbiosystems.com/cms/groups>

/applied\_markets\_support/documents/generaldocuments/cms\_041201.pdf. However, the manufacturer is quick to add that “[i]ndividual laboratories may find it useful to determine an appropriate minimum peak height threshold based on their own results and

instruments using low amounts of input DNA.” (Id.).

Dr. Butler further explains the term “stochastic fluctuation”:

Forensic DNA specimens often possess low levels of DNA. When amplifying very low levels of DNA template, a phenomenon known as *stochastic fluctuation* can occur. Stochastic effects, which are an unequal sampling of the two alleles present from a heterozygous individual, result when only a few DNA molecules are used to initiate PCR. PCR reactions involving DNA template levels below approximately 100 pg of DNA, or about 17 diploid copies of genomic DNA, have been shown to exhibit allele dropout. False homozygosity results if one of the alleles fails to be detected.

(Butler, Fundamentals, p. 68)20

The NM DPS’s internal validation on this issue (called a “sensitivity study”) was very limited: “The AmpFlSTR Identifiler positive control was amplified using 0.1, 0.25, 0.5, and 1.0 ng.” (Quantifiler Internal Validation, CD Exhibit 9, p. 376). Based on this limited testing, it was concluded that

(Id.)

The 0.25 and 0.1 ng. samples exhibited stochastic PCR effects resulting in imbalance in fluorescent signal between the two allele peaks of some heterozygous loci. The manufacturer's recommended amount of input DNA with the AmpFlSTR Identifiler kit is between 0.5 and 1.25 ng. The data support this input DNA range. Samples containing less than 0.5 ng. DNA were successfully typed. The manufacturer suggests individual laboratories determine an appropriate minimum peak height threshold for interpretation based on their own results and instruments. In order to avoid or minimize stochastic effects, the minimum peak height threshold for interpretation with the AmpFlSTR Identifiler kit is 300 RFU when utilizing 310 Genetic Analyzer #2. Peaks between 150 and 300 RFU may be interpreted with caution at the analyst's discretion.

Despite this conclusion, which does not appear to be supported by the data as to the

samples being “successfully” typed below 0.5 ng, the Lab’s DNA SOP instructs that in preparation for amplification, “[a]dd approximately 1-2 ng (Identifiler)...of target sample DNA to the appropriate amplification tubes...” (Exh. 7, p. 9-4). The SOP goes on to recommend, based on a follow-up validation of the 3130 Genetic Analyzer, that the minimum peak height threshold be lowered to 100 RFU. (Id. at 15-5).

20 “False homozygosity” can lead directly to false incrimination. For instance, the analyst claims that Mr. McCluskey is the “source” of what she terms a “major” DNA profile in a mixture of DNA obtained from a swab of the Haas pickup truck steering wheel (item 31a) and gear shifter (31g). For these samples, the “major” profiles (assuming such can be discerned) typed as a homozygote (two of the same alleles at a single locus which are displayed as a single peak) for loci D7S820 (10, 10), D3S1358 (17, 17), D16S539 (12, 12), D21S1338 (23, 23), D19S433 (14, 14), vWA (16, 16),TPOX (8, 8), and D5S818 (13, 13). Mr. McCluskey is also a homozygote at

In this case, the method of quantitation used is called Real-Time PCR (q PCR) which is performed through the use of either of two kits sold by Applied Biosystems, the Quantifiler Human DNA Quantification Kit and the Quantifiler Duo DNA Quantification Kit. Both kits are relatively new, having replaced a prior kit known as the Quantiblot Kit, which was phased out by Applied Biosystems in 2006. Importantly, although Dr, Butler acknowledges that quantitation is an “essential”part of the testing process, he also admits that for a variety of technical reasons these newer kits “are usually not perfect and represent a ‘ballpark-park figure’”. (Butler, Advanced Topics, p. 64.) He concludes that “[m]ost DNA quantitation measurements are precise within a factor of two” and he strongly suggests that “replicate qPCR testing is advisable to strengthen reliabiliy in correlating DNA quantitation results with expected STR typing performance.” (Id. p. 58, 64.). No such replicate qPCR testing was performed in this case.

Morever, the NM DPS SOP requires that in performing qPCR testing the analyst must use the Human DNA Standard supplied by Applied Biosystems, which serves as the foundation for the quantitation computation. (Exh. 7, p. 8-2) One published study on the reliability of the Quantifiler Kit has demonstrated that when the Applied Biosystems Human DNA Standard is used in the testing, the kit erroneously and consistently *overestimates* the amount of human DNA in a sample by large amounts as compared to the Quantiblot kit. *See*, I. Koukoulas et al., *Quantifiler: Observations of Relevance to Forensic Casework*, 53 J. Forensic Sci. 135, 137 (2008)(“This would lead to less DNA being added to a subsequent PCR reaction for STR analysis which may result in lower peak heights for amplified DNA, and at the extreme, stochastic effects.”)(Exhibit 10, Exhibit CD). For example, for one sample, the Quantiblot kit estimated the DNA concentration of the sample as 0.25 ng/ul, while the Quantifiler estimated the

these loci. But what if the evidence samples was actually a 10, 12 at D7S820, or a 17,18 at D3S1358, etc., but because of “stochastic fluctuation,” the 12 allele at at D7S820 or the 18 allele at D3S1358 simply dropped out of the profile. In this scenario, and recalling that Mr.

McCluskey would be falsely included as a possible donor to the sample when in fact he would have been excluded if the 12 or the 18 allele had not dropped out.

concentration of the sample as 4.0 ng/ul. For another sample, the Quantiblot kit estimated the DNA concentration of the sample as 0.125 ng/ul, while the Quantifiler estimated the concentration of the sample as 2.0 ng/ul. (Id.) Several other samples demonstrated similarly large variability. The authors note that “[t]he amount of DNA in casework samples was overestimated (in 99% of samples) when the QF kit was used with the QF standard compared to when using the Promega standard instead...” (Id. at 137)(parenthetical in original). The authors trace part of the problem to the Applied Biosytems standard that is used in the kit and they note “multiple observations throughout our validation indicating that the QF standard was not supplied at the specified concentration”, and that Applied Biosystems has “expressed their concern about the variability observed between the QuantifilerTM kits and are conducting further tests.” (Id. t 136, 138)

In a study funded by the National Institute of Justice, the National Forensic Science Technology Center has replicated findings of the Koukoulas study with respect to the Quantifiler Duo DNA Quantification Kit, finding that “[i]n general, Applied Biosystems quantitation standards showed the greatest variability over time and between lot numbers.” Robert O’Brien and Debra Figarelli, *Do You Know How Much DNA You Really Have ?*, available at [www.nfstc.org/?dl\_id=217](http://www.nfstc.org/?dl_id=217) (Exhibit 11, Exhibit CD). This study concludes:

Low copy number (LCN) samples have been defined as those containing 200 picograms of DNA or less. There are also restrictions for entering LCN analysis results into CODIS. This makes it very important that laboratories’ quantitation methods are accurate and reliable to ensure that they know how much of a sample they are working with. Accurate quantitation results will also allow a laboratory to choose the best analysis method for characterization....

Even though qPCR is considered an estimate, the accuracy of the results are very important. LCN analysis is being defined by the quantity of DNA, and there are restrictions regarding the upload of LCN DNA profiles into CODIS. Laboratories should take steps to ensure the quantitation results are accurate; if they do not, they may inadvertently perform LCN analysis, since the true quantity of DNA is not known.

(Exh. 11)

The steps recommended to ensure that quantitation results are accurate with the use of the

quantification kits are as follows:

1. Using the NIST SRM 2372 standard to determine the accuracy of the quantitation results. The NIST SRM 2372 standard should be diluted so it falls within the dynamic range of the slope. These dilutions should be made periodically to ensure that the diluted NIST samples are accurate.
2. Based on validation studies, an acceptable range for the Y-intercept should be determined. A correction factor can then be applied to curves whose Y-intercept falls outside of this range. This validation should be repeated if any changes are made to the instrument during preventative maintenance or if any changes to the optics or chemistry are made.
3. Validation studies should not only be based on the NIST SRM 2372 results but should also be based on the RFUvalues that are observed when the manufacturer’s suggested target amount (usually 1ng/ìl) of DNA is amplified. Laboratories should also set an acceptable RFU range when this amount of DNA is amplified.
4. Laboratories should validate the length of time a diluted standard maintains its accuracy to ensure that over time the accuracy is not drifting. This will also help to ensure that the laboratory is not needlessly wasting time and money by consistently making new standard curves.

(Exh.11)

So far as the defense is aware, none of these procedures were employed in this case. The NM DPS SOP states that “[t]he dynamic range for quantitation as determined by Quantifiler Duo, Quantifiler Human and Quantifiler Y is used to estimate the amount of template DNA. This range is 50.0 ng/ul down to 0.023 ng/ul. Quantitation values that are greater than 50.0 ng/ul are not reliable and should be interpreted with caution. At the analysts discretion the sample can be diluted and re-quantitated. *Quantitation values that are less than 0.023 ng/ul are not reliable and should be interpreted with caution.”* (Exh.7, p. 8-8)(emphasis added).

The italicized sentence makes no sense. If quantitation values that are less than 0.023 ng/ul “are not reliable”, then why should they be interpreted at all ? In this case, for example, the range for quantitation for the samples tested varies from a low of 0.0215 ng/ul for sample 1 B23B (swab of stain of bottom of S & W handgun) to a high of 38.7 ng/ul for sample 1B14C (swab of shirt seized at time of Mr. McCluskey’s arrest). Several of the evidentiary samples are very near the “unreliable” threshold of 0.023 ng/ul identified in the SOP: 4d (0.0662 ng/ul), 26b (0.0711 ng/ul), L2 (0.0432 ng/ul), L3 (0.0906 ng/ul), L 5 (.0298 ng/ul ), 1B 22A (.0768 ng/ul ),

1B22 D (.0670 ng/ul), 1 B43 (0.0663 ng/ul), 31d (0.0682 ng/ul), and 34b (0.0277 ng/ul), highlighting the critical need to accurately estimate the quantification values. If, as the Koukoulas study shows, the Quantifiler estimates can be off by as much as 3.75 ng, how can the estimates derived from this kit be used to accurately assess whether the quantitation values are below the reliability threshold of 0.023 ng/ul ? They cannot.

In this case, the analyst specifically identifies sample 1B23B as containing approximately 215 picograms of total input amount of DNA and as therefore being a “LCN” sample, which means a “Low Copy Number” sample. (Discovery, p. 6688).21 Yet she concludes in her report of September 30 , 2010, without any mention of the fact that this is a LCN sample, that “to a reasonable degree of scientific certainty, Tracy Province is the source of this partial DNA profile.” How is this an interpretation made “with caution” ?

The NM DPS SOP states:

21 The NMDPS SOP states that when the range of quantitation as determined by the Quantifiler kits is between 0.05 ng to 0.25ng (250 picograms), “[a] sample in this range is considered LCN.” (Exh. 7, p. 8-9) The fact that both the analyst and the protocol acknowledge that at least one of the samples in this case is an LCN sample distinguishes this case from two other federal capital cases involving LCN DNA admissibility challenges where the government’s expert constructed elaborate semantic and other arguments to deny that any of the samples at issue were in fact LCN samples. See, *United States v. Davis*, 602 F.Supp.2d 658 (D.Md.2009); *United States v. Williams*, 2009 WL 1704986 (C.D.Cal. Jun 17, 2009).

# LOW COPY NUMBER (LCN) SAMPLES

Validation studies for both Identifiler and Yfiler STR kits have demonstrated a range of total input amounts of DNA where amplification

stochastic effects are observed. For Identifiler, samples with a total input amount of DNA less than 250 picograms (0.25ng) demonstrate stochastic effects and should be evaluated and interpreted with caution. For Yfiler, samples with a total input amount of DNA less than 100 picograms (0.1ng) demonstrate stochastic effects and should be evaluated and interpreted with caution. Per CODIS rules, any sample amplified at these amounts or less and injected on a genetic analyzer for 10 seconds is not eligible for entry into CODIS. If the sample is of good enough quality at a 5 second injection for entry into CODIS, the analyst should print the electropherograms from both the 5 and 10 second injections and include both in the case file for review. The 5 second injection can be used for CODIS entry and the 10 second injection for interpretation on the report.

(Exh. 7, p. 13-9)

To the contrary, “low copy number” (LCN) DNA typing is an STR methodology that has not yet been validated as reliable and that the FBI and the United States Department of Justice claims is not in fact generally accepted as reliable by the forensic community.22 As the name

22 On February 17, 2006, in the District of Columbia case of *United States v. Jenkins*, Crim. Action No. F320-00, the United States Attorney’s Office raised an objection to the defense use of the low copy methodology and informed the court that “after consulting with some [FBI] folks down in Quantico, I was told that there is this new methodology known as low copy...and that procedure has not gained general acceptance yet in the scientific community...[and] my understanding is not only is it something that the FBI at this stage doesn’t do but,...[t]hey won’t even run the profile through CODIS because they don’t accept the results from low copy.” (Transcript of Proceedings of February 17, 2006)(Exhibit 12 on CD).

The low copy technique originated in the United Kingdom. In 2007, an Irish court, using a *Daubert* analysis, and after conducting an extensive evidentiary hearing, ruled the low copy technique unreliable. *See*, *Queen v Hoey*, [2007] NICC 49 (Exhibit 13 on CD). See also, NAS 2009 Report at 131 (“If insufficient nuclear DNA is present for STR testing, or if the existing nuclear DNA is degraded, two options potentially are available. One technique amplifies the amount of DNA available, *although this technique is not widely available in U.S. forensic laboratories*. A second alternative is to sequence mitochondrial DNA (mtDNA).”)(emphasis added); See also, van Daal, A, *LCN DNA Analysis: Limitations Prevent General Acceptance*, Profiles in DNA (2010), available a[t http://www.promega.com/resources/articles/profiles-in-dna](http://www.promega.com/resources/articles/profiles-in-dna)

/lcn-dna-analysis-limitations-prevent-general-acceptance/ (“In summary, the lack of reproducibility and other issues surrounding current LCN typing demonstrate a lack of scientific reliability and thus acceptability. The practice of further splitting already low amounts of DNA template is questionable. In order for the forensic community to generate reliable results from these low-level samples, significant improvements to the current LCN methods must be made.”)

implies, low copy number is usually associated with a low amount of DNA . “The method is typically associated with an elevated PCR cycle number 23, but it is important to realize that the effects may occur at 28 PCR cycles, typically with a major/minor mixture where the minor component alleles are subject to drop-out and may be the same size as stutter alleles. There are a number of caveats associated with LCN reporting. LCN alleles are not necessarily category A (unambiguous). Therefore, LCN mixture analysis will have to allow for stochastic events

(drop-out, heterozygous imbalance and contamination)” P. Gill, et al., *DNA Commission of the International Society of Forensic Genetics: Recommendations on the Interpretation of Mixtures,* 160 Forensic Science International (2006), 90–101.24 *See also*, C. Peel & P. Gill, *Attribution of DNA Profiles to Body Fluid Stains*, International Congress Series 1261 (2004) 53– 55 (“It has also been shown that a full profile can be recovered from secondary transfer of epithelial cells (from one individual to another and subsequently to an object) at 28 cycles. This sensitivity increases the chance of detecting extraneous cells deposited in an event unrelated to a crime by the standard processing of body fluid stains. Precautions taken in the reporting of LCN cases may therefore be applicable to all cases involving low levels of DNA, such as minute blood stains on touched objects, even when amplified using standard 28 cycle profiling techniques.”).

Dr. Butler explains some of the “caveats associated with LCN reporting” that Gill

23 The PCR process is explained below. Quite unusually, neither the number of PCR cycles utilized in this case, nor many other important parameters of the testing are documented in the bench notes.

24 Peter Gill, a UK Forensic Science Service scientist, is the main proponent of the LCN technique. Even he admits in his article that “[t]he operational definition of low copy number PCR is the manifestation of stochastic effects leading to allelic imbalance, drop-out and increased prevalence of laboratory-based contamination. Consequently, the conventional rules of heterozygous balance and other characteristics of DNA profiling do not apply in the same way.” *See also*, R. Kobayashi et al., *the Risk of Missing One Allele with Very Low DNA Quantities Using PCR*, International Congress Series 1261 (2004), 634–636, 635 (“To obtain the correct genotype, it is necessary to use 100 pg of DNA as a template. When the quantity of extracted DNA is unknown and this quantity could be high enough to give a PCR product, but insufficient for a reliable genotyping, it is very difficult to determine genotypes correctly.”)

euphemistically refers to in his article. He explains that:

The number of PCR cycles is often increased to improve the amplification yield from samples containing extremely low levels of DNA template. For example, by increasing the PCR cycle number from 28 to 34, many more copies of DNA molecules are being generated. With 100% efficiency, 67 million copies of a target sequence are produced with 28 cycles while 4 billion copies are generated with 34 cycles (see Table 7.1). This increase in PCR amplification cycles enables STR typing to routinely obtain results with samples containing less than 100 pg of DNA template. However, application of LCN results should be approached with caution due to the possibilities of allele dropout, allele drop-in, and increased risks of collection-based and laboratory-based contamination.

(Butler, Fundamentals, p. 330-331).

He continues:

Trying to generate a reliable STR profile with only a few cells from a biological sample is similar to looking for an object in the mud or trying to decipher the image in a fuzzy photograph. Since the sensitivity of the STR typing assay is turned up so high, it is often not immediately clear if you have a reliable result or even a probative one.

When LCN testing is performed at least three artifacts typically arise:

* 1. additional alleles are often observed from sporadic contamination in what is referred to as “allele drop-in,” (2) “allele dropout” is common where an allele fails to amplify due to stochastic effects, and

(3) stutter product amounts are enhanced so that they are often higher than the typical 5-10% of the nominal allele. Heterozygote peak imbalance is typically exacerbated due to stochastic PCR amplification, where one of the alleles is amplified by chance during the early rounds of PCR in a preferential fashion. Allele dropout can be thought of as an extreme form of heterozygote peak imbalance.

(*Id*.)

Most of the evidentiary samples in this case are complex mixtures of two or more

individuals. Dr. Bruce Budowle, the FBI’s retired lead forensic DNA scientist, has flatly declared that “[m]ixture analyses and confirmation of a mixture are not reliable with LCN typing, because

...imbalance of heterozygote alleles, increased production of stutter products, and allele drop-in can occur.” B. Budowle, *Low Copy Number - Consideration and Caution*, Presentation at the Genetic Identity Conference Proceedings, 12th International Symposium on Human Identification-2001, available a[t http://www.promega.com/~/media/files/resources](http://www.promega.com/%7E/media/files/resources)

/conference%20proceedings/ishi%2012/oral%20presentations/budowle.pdf?la=en. Dr. Butler agrees: “In practice many LCN profiles are mixtures and difficult to interpret reliably due to the issues of allele dropout and drop-in described above.” (Butler, Fundamentals, p. 333). See also, Budowle, B., Eisenberg, A.J. and van Daal, A., *Validity of low copy number typing and applications to forensic science*, 50 Croat. Med. J. 207–17 (2009)(“While LCN typing is appropriate for identification of missing persons and human remains and for developing investigative leads, caution should be taken with its use in other endeavors until developments are made that overcome the vagaries of LCN typing. A more in-depth evaluation by the greater scientific community is warranted.”), available at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2702736> /?tool=pubmed; Budowle, B., *Low Copy Number Typing Still Lacks Robustness and Reliability*, Profiles in DNA (2010)(“LCN typing has not been well developed and applied appropriately. Moreover, the validation studies do not comport with protocols, assumptions for calculating the weight of the evidence are in question, and the scientific literature recommendations are not necessarily in concert with practices. Substantially more work is needed before the conditions are known under which LCN

typing should be used for reliable identification purposes.”), available at <http://www.promega.com/resources/articles/profiles-in-dna/low-copy-number-typing-still-lacks-r> obustness-and-reliability.

It is also important to point out that, as demonstrated above, the values stated for the Quantifiler kits are only a “ball park estimate” of the *total* amount of input DNA in a sample and do not, for mixed samples , reflect the input DNA for each component of the mixture. Thus, the fact that a Quantifiler calculation indicates that 1.0 ng of total input DNA is being used does not address the issue of whether any component of a mixture is below the reliability threshold. As Dr. Butler points out, “[w]hen mixtures are observed at low DNA amounts, the individual components to the mixture will be even lower in amount and the stochastic effects become worse making it extremely challenging to recover the correct profile of the original contributors to the

mixture. In these situations where the full profile cannot be recovered even with replication and consensus, statistical methods accounting for allele drop-out are an option.” (Butler, Advanced Topics, supra.) However, “the probability of drop-out is not routinely used by forensic laboratories as of early 2011.” (Id.). This statistical method was not used in this case.

As indicated above, allelic dropout can lead to inaccurate typing and false incrimination, and it is for this reason that Mr. McCluskey challenges the Quantifiler quantitation technique and typing methodology in this case, which by definition is a low copy number case at least as to sample 1 B23B, and as to all samples that are close in quantitation value to the 0.023 ng/ul reliability cutoff established in the SOP, including samples 4d (0.0662 ng/ul), 26b (0.0711 ng/ul), L2 (0.0432 ng/ul), L3 (0.0906 ng/ul), L 5 (.0298 ng/ul ), 1B 22A (.0768 ng/ul ), 1B22 D (.0670

ng/ul), 1 B43 (0.0663 ng/ul), 31d (0.0682 ng/ul), and 34b (0.0277 ng/ul) .

Further, because of the unreliability of the Quantifiler kits , and the fact that most of the samples in this case are mixtures “of two or more individuals”, all of the samples should be treated as low copy samples and excluded from evidence. For example, sample 31a, a “touch DNA” sample from the Haas pickup truck steering wheel was quantitated using the Quantifiler kit and the results indicated a 1.73 ng/ul concentration of human and higher primate DNA contributed by “two or more individuals”. 25 Similarly, sample 31g, a “touch DNA” sample

25 The NM DPS protocol states: “The QuantifilerTM Human DNA Quantitation Kit is designed to quantify the total amount of amplifiable human (and higher primate) DNA in a sample.” (Exh. 7, p. 8-1). The fact that the kit also quantitates non-human DNA naturally gives rise to the question of whether other sources of non-human DNA may be contributing to the quantitation results, particularly as it relates to bacteria and yeast, which are ubiquitous in crime scene evidentiary samples. The FBI’s Quality Assurance Standard 8.2. provides that “[d]evelopmental validation shall precede the use of a novel methodology for forensic DNA analysis” and that developmental validation studies “shall include, where applicable,... species specificity.” Applied Biosystem’s developmental validation is summarized in the Quantifiler Human DNA Quantitation Kit User’s Manual, available a[t http://www3.appliedbiosystems.com/](http://www3.appliedbiosystems.com/) cms/groups/applied\_markets\_support/documents/generaldocuments/cms\_041395.pdf. It states at page 6-14 that the company tested the kit with only “53 bacterial species and one yeast species.” Although the company concluded that “[t]he Quantifiler Human Kit and the Quantifiler Y kit did not detect DNA from any of the bacterial or yeast species *tested*”, Mr. McCleskey argues that

from the Haas pickup gear shifter was quantitated using the Quantifiler kit and the results indicated a 0.918 ng/ul concentration of human and higher primate DNA contributed by “two or more individuals”. Given that the Koukoulas study demonstrated that the Quantifiler kit overestimates quantitaation by as much as 3.75 ng, and the fact that we do not know how many persons or non-persons contributed to the total DNA content of these or any other samples 26 , and in what proportions, how can we have any assurance that the DNA of any particular human contributor is in the sample in a quantity greater than the 0.023 ng/ul reliability threshold set forth in the SOP ? The answer is that we cannot have any such assurance and that the testing results are therefore unreliable and inadmissible.

Further, although, as indicated in footnote 22, the FBI, the Department of Justice, scientists, as well as at least one court, have determined that the low copy number technique is not reliable enough for court use, even the proponents of this technique do not endorse it unless stringent guidelines are followed. These specific guidelines, discussed below, were not followed in this case and thus regardless of the reliability of the technique when proper protocols are followed, the DNA testing in this case, performed on samples that were quantitated with unreliable kits, is inadmissible under Rules 403, 702, and *Daubert*.

# Amplification

Once the DNA is extracted from the evidence and quantitated, it undergoes a process

there is too much of an analytical gap from this limited data to any stronger conclusion than what is stated in the SOP: “"The QuantifilerTM Human DNA Quantitation Kit *is designed to quantify* the total amount of amplifiable human (and higher primate) DNA in a sample." (emphasis added). It may be “designed for” this purpose, but there is insufficient evidence to support any conclusion that the kit does not quantitate any bacterial or yeast, or other non- primate DNA other than for those species specifically tested.

26Numerous samples in this case have quantitation values equal to or below the two examples cited in the text: v5 (0.235), 13 (0.703), L1 (0.680), L4 (1.720), L7 (0.130), L8 (1.730),

L9 (0.122), L12 (0.478), L13 (0.382), SR1B (0.174), 1B22B (0.331), 1B22C (0.200), 1B39A

(0.345), 1B13 (1.11), 1B57 (1.170), 1B72A(0.277), 1B72B (0.870), 31b (0.108), 31c (0.261),

31e (0.124), R6 (0.143), T7A (0.296), T11x (0.659), 1B22E (0. 862).

known as polymerase chain reaction (PCR), which is also referred to as amplification, described more fully below. The process is performed in a machine called a thermal cycler, which sends the sample through a series of steps and cycles, usually 28, but sometimes more. This process, often analogized as biological photocopying, allows scientists to make copies of specific chromosomal segments. The amplification process gives forensic scientists the ability to analyze DNA samples smaller than RFLP samples, and has allowed DNA analysis to become a much more useful tool for forensic scientists.

PCR is a method for obtaining testable DNA from minuscule samples. PCR is not a genetic test, “but merely a tool to increase the amount of genetic material to be tested.” W.C. Thompson *Guide to Forensic DNA Evidence*, in EXPERT EVIDENCE: A PRACTITIONER’S GUIDE TO LAW, SCIENCE AND THE FJC MANUAL 215 (1997). *See also*, *United States v. Hicks*, 103 F.3d 837, 845 (9th Cir. 1996) (“The PCR method itself is not a genetic test; it is a mere amplification technique.”); *United States v. Davis*, 602 F.Supp.2d 658, 665 (D.Md. 2009)(“PCR, a sample preparation technique, is a laboratory process for copying a short segment of DNA millions of times.”); *United States v. Morrow*, 374 F.Supp.2d 51, 57 (D.D.C.2005)(“PCR is not itself a method of DNA typing, but is instead a technique of sample preparation. PCR is a laboratory process for copying a short segment of DNA millions of times, thereby replicating the natural DNA duplication process.”).

Dr. Butler cautions:

The sensitivity of PCR necessitates constant vigilance on the part of the laboratory staff to ensure that contamination does not affect DNA typing results. Contamination of PCR reactions is always a concern because the technique is very sensitive to low amounts of DNA. A scientist setting up the PCR reaction can inadvertently add his or her own DNA to the reaction if he or she is not careful. Likewise, the police officer or crime scene technician collecting the evidence can contaminate the sample if proper care is not taken.

(Butler, Fundamentals, p. 141). “It is well-documented that DNA contamination on items used at both the crime scene and within the forensic laboratory can result in DNA profiles that may incorrectly implicate individuals or make evidence meaningless.” K. Shaw, et al., *Comparison of*

*the Effects of Sterilisation Techniques on Subsequent DNA Profiling*, 122 Int J Legal Med (2008), 29–33.

In amplification, extracted DNA is added to chemical reagents and heated, causing the two strands that compose the DNA molecule (they resemble two sides of a “ladder,”) to separate.

Each of the two strands then can be used as a template to make (or synthesize) a new double-stranded DNA molecule.

The reagents in which the DNA is heated contain markers that identify the starting and ending points of the DNA fragment that is duplicated. The markers also are called primers because they prime (or stimulate) the synthesis reaction. Primers are short synthetic pieces of DNA designed to match the regions of human DNA which are highly variable. As the DNA and chemicals begin to cool, the primers attach to the single-stranded DNA. The primers contain fluorescent labels so that they may be detected by lasers later in the testing process.

Once the primers have bound to the beginning and end of the segment being copied, individual building blocks of DNA from the reagents fill in the rest of the empty spots on the single-strand.

The heating and cooling of the DNA is accomplished by a machine called a thermal cycler, in which a tray of capped tubes containing the DNA and chemical reagents are placed. The thermal cycler can be programmed to heat and cool repeatedly for specific amounts of time. At the end of many repetitions, millions of copies of the original DNA section are created.

Any DNA present in a tube when the amplification process begins, whether from evidence or introduced through contamination, will be amplified. To ensure that the DNA profile generated from the amplified DNA is representative of the DNA from the evidence sample and not from contamination, and to verify that the testing process is accurate, DNA protocols require forensic DNA scientists to analyze a series of control samples. For each batch of samples processed, at least one positive control, one negative control, and one reagent blank are analyzed along with the DNA samples. The positive control tube contains the reagents

necessary for amplification plus DNA from a source for which the DNA profile is known. Since the scientists know the correct test results for the positive control, it allows them to determine the accuracy and performance of the amplification and analysis processes. The negative control tube contains all of the reagents used for amplification. The reagent blank contains all of the reagents used to process an item of evidence from extraction through electrophoresis. DNA from the evidence is not added to these controls, though their contents are amplified. The purpose of the negative control and the reagent blank is to reveal any contamination that is present in the reagents or introduced during the testing process.

“However, because PCR contamination can be tube specific, negative controls analyzed with a batch of samples cannot provide complete confidence that the associated batch of extracted casework material is contaminant free.” (Butler, Fundamentals, p. 153. *See also*, Trevor Howitt, *Ensuring the Integrity of Results: A Continuing Challenge in Forensic DNA Analysis*, Oral Presentation of the Genetic Identity Conference Proceedings, 14th International Symposium on Human Identification - 2003, available at <http://www.promega.com/geneticidproc>

/ussymp14proc/oralpresentations/Howitt.pdf) (“It is impossible to carry out QC checks on individual items of consumables, such as tubes, tips and other components, to guarantee that they are DNA-free prior to use, because once they have been QC tested they are discarded. However, QC testing of a sample of components from a batch can help provide some indication as to the general batch quality. Even so, it will only show whether gross systematic contamination is present and it cannot provide a guarantee that sporadic contamination events have not occurred.”).27 Here, all of the samples were tested in batches, with samples both from this case

27 “It should also be emphasized that critical consumables used at each stage in the collection and processing of samples need to be considered, and not just those used within the testing laboratory. It is essential therefore that the kits used by the police at scenes of crime to recover DNA evidence and those utilized for the collection of reference samples from suspects and victims are also manufactured in DNA-free conditions and subjected to appropriate

QC-testing.” (*Id.*) *See also*, Butler, Advanced Topics, Ch. 4)(“Contamination of PCR consumables (tubes and other plastic-ware) can be a concern due to the high sensitivity of the

and other cases.

The use of traditional controls is especially ineffective in low copy situations. As Dr. Gill explains, “[w]ithin the context of LCN, we have shown that the negative control does not act as indicator of minor contamination within associated processed samples of the same batch. This is because the method is sensitive enough to detect a single molecule of DNA. By definition, one molecule cannot affect more than one tube hence the negative control cannot operate in the traditional sense. Conversely, casework samples could be affected by laboratory-based contaminants that do not appear in the negative control.” *See*, P. Gill, et al., *An Investigation of the Rigor of Interpretation Rules for STRs Derived From Less Than 100 pg of DNA*, 112 Forensic Science International 17, 22.

In this case, negative, positive, and reagent blank controls were used and there were some problems. First, in numerous situations where two negative controls were run at the same time, the analyst only printed one of the two results, noting “not printed; only optimal data used/ printing.” (See e.g. Discovery, p. 6445, 6478, 6674, 6699, 6834, 6849). If the “non-optimal” data indicates that the controls failed then these results should be printed and produced to the parties and the Court.

The negative and reagent controls used with the running of numerous samples on August

technique.”); L. Gefredis, et al., *The Detection and Treatment of Consumable Contamination*, Oral Presentation of the Genetic Identity Conference Proceedings, 18th International Symposium on Human Identification - 2007, available at <http://www.promega.com/geneticidproc>

/ussymp18proc/abstracts/Abstract11Gefrides.pdf. (“[U]unknown profiles are sometimes attributed to consumables used in DNA extraction or amplification procedures. It may be impossible to track a consumable profile back to an individual consumable or manufacturer”); Jeannie Tamariz, *The Application of Ultraviolet Irradiation to Exogenous Sources of DNA in Plasticware and Water for the Amplification of Low Copy Number DNA*, Proceedings of the American Society of Forensic Sciences, Vol. XII, Feb. 2006, available at [http://www.aafs.org/pdf/Seattleabstracts06.pdf.](http://www.aafs.org/pdf/Seattleabstracts06.pdf) (“Using High Sensitivity Forensic STR PCR DNA typing methods, it was determined that contamination of presumably sterile plastic ware and water can be present in low concentrations not previously detected by standard PCR methods.”)

19, 2010 show a peak at the D3S1358 locus, and the reagent blank also shows a peak at D7S820. (Discovery, p. 6809, 6811) The second reagent blank run the same date with a 10 second injection time still showed a peak at the D3S1358 locus. (Discovery, p. 6816) A third run of a reagent blank with a 10 second injection time still showed a peak at the D3S1358 locus. A fourth run of a reagent blank with a 10 second injection time still showed a peak at the D3S1358 locus, and a peak at vWA. (Discovery, 6824) Finally, a sixth run of a reagent blank at 10 seconds showed no peaks. (Discovery, p. 6831). A reagent control and negative control used with the running of samples on August 24, 2010 show a peak at the D3S1358 locus. (Discovery, p. 6853, 6864). There should have been no peaks at all in these samples.

Negative and reagent controls used with the running of numerous samples on September 22, 2010 show a peak at the D3S1358 locus. (Discovery, p. 6678, 6692). Another reagent blank run on the same date shows no peaks at this locus. (Discovery, p. 6696). Negative and reagent controls used with the running of numerous samples on November 3, 2010 show a peak at the D3S1358 locus, and the reagent control also shows peaks at CSF1P0, THO1, and D2S1138. (Discovery, p. 6449, 6457). A negative control used with the running of numerous samples on November 10, 2010 show a peak at the D3S1358 locus (Discovery, p. 6464). No reagent blank was run with the case sample (T-7A) run on that date. (Discovery 6460). A negative control used with the running of numerous samples on December 13, 2010 shows peaks at the D871179, CSFIPO, D3S1358, D2S1138, D19S443, D5S818 loci (Discovery, p. 6482). There are

numerous other such examples throughout the case file.

The National Research Council, in its first book on forensic DNA typing (“NRC I”),

, spells out the implications of finding contamination in the controls :

As with contamination due to handling, carryover contamination can be signaled by the appearance of product in blank controls and of mixed or inappropriate types in samples and positive controls. Such controls should be used rigorously. *Moreover, it should be remembered that the controls are useful for monitoring general contamination in the laboratory, not the accuracy of a particular experiment. If a blank control is positive in one experiment, it indicates a potential problem not just for that experiment, but for any*

(NRC I, p. 67)

*experiment performed at about the same time—even in a laboratory contaminated with PCR carryover, blank controls do not necessarily become contaminated on every occasion. It will be wise to repeat all work with samples that have never been exposed to the PCR-typing laboratory.*28

The NMDPS has detailed procedures in its SOP for setting up and conducting PCR amplification and for protecting against the ever present danger of contamination. Whether these procedures were followed cannot be determined from the documentation provided. Therefore an evidentiary hearing is requested to assess whether the analyst in this case followed laboratory and industry protocols. The issue of contamination is explored in more detail below.

# Short Tandem Repeat (STR) Analysis.

After amplification is complete, the DNA is analyzed using a machine (the 3130 Genetic Analyzer) that separates the DNA fragments present in the sample. This process is known as capillary electrophoresis. Special software (Genemapper ID) then measures the length of the DNA fragments, determines the alleles that correspond to the fragments, and compiles a DNA profile for the sample.

As the name implies, short tandem repeat (STR) analysis is a method of determining an individual’s DNA profile by counting the number of times a small DNA sequence (short tandem repeat unit) is repeated at a specific chromosomal location. STR analysis consists of three processes: amplification, electrophoresis, and interpretation. By this process, the length of a DNA strand is estimated (measured in basepairs), but not its sequence (the particular arrangement of the ACTG building blocks of the DNA molecule).

Amplification has already been described. In general, electrophoresis is performed by adding DNA to one end of a piece of gelatinous material which contains tiny holes that allows

28 This passage also illustrates why retesting the sample is not the cure-all for all problems created by faulty DNA laboratory work. If an evidence sample became contaminated by the lab, then retesting a contaminated sample obviously does not ensure a correct result.

the material to function as a molecular sieve. An electric current is applied across the material, causing the DNA fragments to move. Since it is easier for smaller fragments to move through the material, the smaller fragments move farther than the larger fragments. As a result, at the end of electrophoresis the DNA fragments are sorted by size. The size of the DNA fragments is determined by comparing the distance each fragment moved to the distances moved by the fragments of known size.

# Capillary Electrophoresis.

The principles described above also apply to capillary electrophoresis, a form of electrophoresis employed by the NMDPS Laboratory in this case. Its distinguishing characteristic is that the electrophoresis occurs inside a capillary tube (a very thin glass tube, comparable to a human hair) with a sieving material inside, rather than on a piece of gelatinous material. Capillary electrophoresis is an automated process that analyzes many DNA samples and requires minimal involvement by DNA scientists after the initial set-up procedures are completed and quality control procedures are maintained. These procedures include cleaning and calibrating the electrophoresis machine (3130 Genetic Analyzer) and preparing the amplified DNA for analysis.

To prepare amplified DNA for capillary electrophoresis, the DNA scientist:

* + Places a sufficient number of empty tubes in a rack;
  + Adds water for dilution and internal size standard29 to each of the empty tubes;
  + Adds an appropriate amount of one of the following to the tubes containing the internal size standard:
    - amplified DNA from known samples, unknown or evidentiary samples, or the positive control;
    - amplified negative control or reagent blank; or

29 The internal size standard contains DNA fragments of known sizes that provide reference points for determining the length of the sample’s DNA fragments.

* + - an allelic ladder,30 which contains the more common alleles in the general population for specific chromosomal locations; and
  + Seals the tubes with soft rubber caps.

Once the tubes are sealed, the rack is ready to be placed on the capillary electrophoresis machine. A sample list is prepared which identifies the location of each sample on the rack and makes it possible for the machine’s computer to locate a specific sample. An injection list is also prepared which tells the computer the order in which the samples are to be analyzed. The capillary electrophoresis machine has a probe that punctures the soft rubber caps on the tubes and withdraws a specific amount of sample. The sample is drawn up into the capillary tube (referred to as injecting the sample) where the electrophoresis is completed.

As mentioned previously, the primers used during amplification contain fluorescent markers that allow the DNA fragments to be detected by lasers. The manufacturer of the capillary electrophoresis machine has developed proprietary software to display the test results and to aid in their interpretation. Using this software, the capillary electrophoresis machine determines the size of the DNA fragments in a sample based on the information detected by the lasers. The machine and the software then represent the lengths of the various fragments as peaks on a graph.

When the predecessor of the 3130 Genetic Analyzer (the ABI 310) was first released in the mid-1990s, sample processing was performed in two steps by two different software programs: GeneScan and Genotyper. Data viewed in GeneScan is the raw, unanalyzed, collection data that reflects everything the laser detects, including interference that is common in electrophoresis instruments . Genotyper allows forensic scientists to take GeneScan data and display it in a format that conceals background noise and peripheral information, and to focus their review on the results of the control and evidence samples. Distinguishing what in fact is

30 Allelic ladders are used like molecular rulers to help “measure” the lengths of the fragments in the reference and evidentiary samples.

“noise” and what are the results of the sample is a major challenge in STR analysis. These older programs have now been replaced by a software package called

GeneMapper ID that combines the functions of GeneScan and Genotyper with additional quality scores for the data. “ Bins”’ and “ panels” are created by the user or provided by the STR kit manufacturer that enable the electrophoretic peaks to be designed as STR alleles for each tested locus.

The earlier STR typing kits that were used with the hardware and software were designed to type some or all of the “core” thirteen loci that were chosen by the FBI at an STR project meeting in November 1997, to be the basis of the future CODIS national DNA database.

The 13 CODIS core loci are: CSF1PO, FGA, TH01, TPOX, VWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, and D21S11. (Butler, Fundamentals, p. 154-155). The

the Identifiler kit, released in 2001, allows typing of these two loci, as well as two others (D2S1338 , D 19S433), and permits gender determination through typing of Amelogenin. All of the STR typing kits share certain limitations. As summarized by Dr. Butler:

1. Less discrimination power per locus compared to VNTRs due to a smaller number of alleles and less heterozygosity per locus.
2. The possibility of contamination from stray DNA is increased because of the PCR amplification process.
3. Expensive equipment required for detection.
4. Stutter products and unbalanced peak heights may occur and make the interpretation of mixtures more difficult.
5. Data interpretation must account for artifacts such as dye blob, electrophoretic spikes, etc.

(Butler, Fundamentals, p. 67)

To determine whether alleles and genotypes at the loci in Identifiler are present, the analyst examines the peaks that have been called and based on experience and laboratory

protocol may or may not edit the calls made by the software. Decisions to edit a

software-designated peak supposedly come from an understanding of biological or instrumental artifacts . 31 Any editing of the data is supposed to be documented either in an analyst’s case notes or in comments made in the electronic or paper printouts of the STR data. An allele table is usually created from the edited allele calls, but no such table was prepared in this case . (Butler, Fundamentals, pp. 211-212).

As Dr. Butler points out:

While STR allele calls may be made in an automated fashion with data analysis software, the resulting genotype information needs to be manually examined by experienced analysts. Data analysis and review are essential for

confirming STR results prior to making final reports. Software algorithms follow set parameters and criteria and hence can never be as effective at making difficult calls as a

trained analyst. *Strict guidelines for data interpretation should be in place to avoid problems with individual bias when the data is reviewed*.

(Butler, Fundamentals, p. 213)(emphasis added). See also, Krane, et. al, *Sequential Unmasking: A Means of Minimizing Observer Effects in Forensic DNA Interpretation*, J Forensic Sci, July 2008, Vol. 53, No. 4, p. 1006 (“The interpretation of an evidentiary DNA profile should not be influenced by information about a suspect’s DNA profile Each item of evidence must be

interpreted independently of other items of evidence or reference samples. Yet forensic analysts are commonly aware of submitted reference profiles when interpreting DNA test results, creating the opportunity for a confirmatory bias, despite the best intentions of the analyst This bias can

result in false inclusions under not uncommon conditions of ambiguity encountered in actual casework. It can also render currently used frequency statistics or likelihood ratios misleading. These problems can be minimized by preventing analysts from knowing the profile of submitted references (i.e., known samples) when interpreting testing results from evidentiary (i.e., unknown

31 “During polymerase chain reaction (PCR) amplification of short tandem repeat (STR) alleles, a number of artifacts can arise that may interfere with the clear interpretation and genotyping of the alleles present in the DNA template. These artifacts include stutter products and non-nucleotide addition. Other factors that impact STR typing...includ[e] microvariants, tri- allelic patterns, allelic dropout, and mutations...” John Butler, Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers (2nd ed. 2005), p. 123.

or questioned) samples.”)

The strict guideline suggested by Dr. Butler and recommenced by Dr. Krane and his co- authors is set forth in the NM DPS SOP:

When the DNA results clearly demonstrate that an evidence sample contains a mixture of DNA the profile will be carefully examined to determine if the profile consists of two or more individuals, if a major profile can be

determined, if a minor profile can be determined, or what are the possible genotypes of contributors, etc.

*standards*. However, NM-DPS does not make assumptions regarding the possible number of contributors to a mixture profile for statistical analysis. *After the questioned mixture profile has been examined* a determination must be made as to whether or not the reference standards analyzed could be contributors to this mixture. This is done by comparing the DNA alleles detected from the standards, at each locus, with those of the evidence.....

If the mixture consists of identifiable, distinct major and minor profiles, then conclusions may be made regarding the separate major and minor DNA profiles. *This examination should be done without prior consideration of known samples*. Some loci may have stutter peaks that may create doubt as to the definite profile of a minor contributor(s). Inconclusive loci are not included in the

interpretation, except for elimination and are not included in the statistical calculation. Whether or not a dissected into individual contributors will affect the interpretation of the mixture

profile.

(Exh. 7, p. 13-11)(emphasis added)

Unfortunately, this guideline was not followed in this case. The discovery reflects that on August 19, 2010, at 7:54 a.m, the analyst typed the reference samples for Gary and Linda Haas, and then printed out the results. (Discovery 6829-6830). The only evidentiary samples typed before this time were samples L1, L4, L13,4-c, 4-d, 11, 13, 17, 26b, 28, SR1A, and SR1B.(Discovery 6777-6829). All other samples were typed and interpreted only after the analyst already knew the profiles for the decedents.

The discovery also reflects that on September 22, 2010, at 3:04 p.m., the analyst typed the reference samples for Mr. McCluskey, Mr. Province, and Ms Welch, and then printed out the electropherogram showing the results. (Discovery 6693-6695). The analyst thereafter typed and interpreted numerous samples *after she had already learned the DNA profiles for the reference samples*. Included in the samples she typed and interpreted after she learned the results on these reference samples are samples 1B22C, 1B39A, 4d, L6, L13, SR1B, and all the evidentiary samples listed in the reports of December 22, 2010, and April 27, 2011. Because the analyst did

not follow an important aspect of her own protocol, Mr. McCluskey asks that the results of any tests she interpreted after she learned the DNA profilesof the reference sample not be permitted.

# 5. Matching and Statistical Analysis.

In the typical case, an analyst then compares the peaks and labels from known and questioned samples to determine whether the samples have the same alleles.

A complication arises if the sample is a mixture, as it frequently is in cases involving commonly touched articles such as steering wheels, clothing, etc. “These mixtures can be challenging to interpret and depending on the alleles present in the profile, the individual components may never be unambiguously separated. In addition, partial profiles where entire loci have dropped out sometimes occur due to the presence of degraded DNA or polymerase chain reaction ( PCR ) inhibitors.” John M. Butler, Forensic DNA Typing, Second Edition : Biology, Technology, and Genetics of STR Markers, p. 519. As pointed out above, “[w]hen mixtures are observed at low DNA amounts, the individual components to the mixture will be even lower in amount and the stochastic effects become worse making it extremely challenging to recover the correct profile of the original contributors to the mixture. In these situations where the full profile cannot be recovered even with replication and consensus, statistical methods accounting for allele drop-out are an option.” (Butler, Advanced Topics, supra.) However, “the probability of drop-out is not routinely used by forensic laboratories as of early 2011.” (Id.). This statistical method was not used in this case.

If a match or “ inclusion” results, then an estimate is made of the rarity of the obtained DNA profile by comparing it to a population database, which is a collection of DNA

profiles obtained from unrelated individuals of a particular ethnic group. (Butler, Fundamentals,

p. 9). “Since we do not have the luxury of access to DNA profiles of everyone living on planet Earth, we must use smaller population data sets to extrapolate the possibility of a random match. To estimate this match probability, allele frequencies are collected from various ethnic/racial

sample sets. Based on their allele frequencies from validated databases, population genetic principles are applied to infer how reasonable it is that a random, unrelated individual could have contributed the DNA profile in question. (Id. at 229).

By counting the number of times alleles occur at a particular location in racial groups, the analyst determines the likelihood that two random individuals from that group would have the same alleles at that location. The analyst then determines the likelihood that random individuals would have the same alleles at all the locations that matched. The analyst may come up with a frequency estimate that only one individual in millions or billions would randomly match in the same way. (*Ibid*.)

When more than one locus is tested, as in the Identifiler kit used in this case, technicians conduct the initial frequency calculation for the alleles at each gene or marker. The frequencies for each gene are then multiplied together using the Product Rule, and an overall frequency emerges. This “random match probability,” represents “the theoretical likelihood that a randomly selected person from the general population (or from the population of a certain large ethnic or racial group) would genetically match the trace evidence as well as the defendant.” (Koehler, J. J.,. *DNA Matches and Statistics: Important Questions, Surprising Answers* (1993) 76 Judicature, 222-229, at p. 224.).

The validity of using the Product Rule rests on a number of assumptions. First, that the population studied engages in random mating--that mates are not chosen based on their genotype at the markers used in DNA testing. NRC II at 90. If the alleles of a gene are subject to random mating, then the alleles should be in what is called Hardy-Weinberg (HW) equilibrium. A population is in HW equilibrium if the actual observations of each genotype are consistent with that expected under the HW test. (*Id*. at 91-92). A population will not be in equilibrium if the occurrence of a particular genotype in a population is significantly different than expected after statistical analysis. The lack of equilibrium indicates that there is some substructure to the population so that the alleles of a given gene are not assorting independently from generation to

generation.

When, as in this case, analysts test multiple genes, they must also assume that the loci are independent or in “linkage equilibrium” (NRC II, *supra*, at p. 106). Only if the loci are independent will the frequency of a multi-locus genotype be equivalent to the product of the genotype at each locus (*Ibid*).

In sum, STR DNA typing requires three major steps, each of which is subject to detailed and multi-layered protocols and procedures the correct application of which iss criticaal to avoid unreliable results. *First*, a sample containing human DNA is extracted from a forensic sample and the quantity of DNA is determined. *Second,* the DNA is amplified using PCR. *Third*, the amplified sample is then typed for alleles at specific loci. Once the sample has been typed, the results are compared to known samples of DNA, which have also been typed at the same loci, using the same techniques. If there is a reported match, then, using a database of genotype frequencies, the analyst determines the random match probability that the known sample and unknown sample are from the same source.

Finally, every DNA test includes procedural controls to guard against faulty results due to contamination or mislabeling of a DNA sample or due to the complications arising from mixtures, degradation, etc. *Contamination* occurs when an alternate source of DNA is added to the original sample and can result in a false match because the test will reveal alleles other than those originally present. *Mislabeling* occurs when a DNA sample is wrongly identified and may result in a false match because the test literally tests another person’s DNA. Administered *correctly*, a control should reveal if the sample was contaminated or mislabeled. Absent a proper control, determining whether the test is accurate is impossible. But even the use of routine controls does not guarantee reliabiliity.

# Standards Governing Forensic DNA Analysis.

The creation of national standards for DNA analysis played a pivotal role in establishing the integrity of the DNA testing process. As Dr. Butler explains,

Any scientific test which results in information that may lead to the loss of liberty for an individual accused of a crime needs to be performed with utmost care. DNA typing is no exception. It is a multi-step, technical process that needs to be performed by qualified and effectively trained personnel to ensure that accurate results are obtained and interpreted correctly. When the process is conducted properly, DNA testing is a capable investigative tool for the law enforcement community with results that stand up to legal scrutiny in court. When laboratories do not follow validated protocols or have not had adequately trained personnel, problems have arisen in the past.

John M. Butler, Fundamentals, p. 291.

In its second report on forensic DNA testing, the National Research Council specifically recommended that “Laboratories should adhere to high quality standards (such as those defined by TWGDAM and the DNA Advisory Board) and make every effort to be accredited for DNA work (by such organizations as ASCLD-LAB).” (NRC II Report, p. 4 Recommendation 3.1).

Following the issuance of this report in 1996, it was generally accepted among reputable scientists and courts that these standards define correct scientific methodology for purposes of establishing the validity and reliability of DNA testing results, and for purposes of Rule 702. *See, United States v. Martinez*, 3 F. 3d 1191, 1197(8th Cir. 1993) (“A number of courts have required that the trial court...inquire into whether the expert properly performed the techniques involved in creating the DNA profile); *United States v. Morrow*, 374 F. Supp. 2d 51 (D.D.C. 2005) (“Of course, the admission of such evidence will be contingent upon a showing by the government that the techniques, methods, and practices used in the testing in this case, as well as the expert’s qualifications, met with the generally accepted and established protocols”). See also, *United States v. Davis*, 40 F.3d 1069, 1074 n.6 (10th Cir.1994)(“If the offering party does not follow [ DNA] protocol, the scientific evidence may not be relevant under *Daubert 's* second prong because improperly applied science cannot assist the trier of fact.”); *United States v.*

*Coronado-Cervantes*, 912 F.Supp. 497, 500 (D.N.M.1996)(The Tenth Circuit in *Davis* “has intimated that under *Daubert's* ‘relevance’ prong, it may be necessary to inquire into whether standard protocol, in the DNA context, was followed in a particular case In the absence of clear

directive from the Tenth Circuit, this Court finds that under Daubert's second ‘relevance’ prong, compliance with standard protocol in applying the RFLP technique is essential and goes to admissibility, rather than merely to the weight of DNA evidence as urged by the government.

This is so because failure to follow standard protocol in applying the RFLP technique may yield an unacceptably high risk of false positive error.”) Cf., *United States v. Wright*, 215 F. 3d 1020, 1027 (9th Cir. 2000) (“Wright does not contend that the correct testing procedures were disregarded in this particular case”). Unlike in *Wright*, Mr. McCluskey does contend, as outlined above and throughout this motion, that the correct testing procedures and protocols were disregarded in this particular case. It is therefore important for the court to understand the generally accepted and established procedures and protocols in the field.

# Sources of DNA Standards.

Forensic DNA laboratories, particularly those like the NM DPS DNA Laboratory participating in the FBI’s Combined DNA Index System (CODIS),32 have relied upon two primary sources of operational standards since the first forensic DNA laboratories were established in the late 1980s: 1) the Technical Working Group on DNA Analysis Methods (TWGDAM); and 2) the DNA Advisory Board.

TWGDAM was established in 1989 with representatives from 12 federal, state, and local laboratories, and focused specifically on the development of forensic DNA methods. Later that same year, TWGDAM developed and published in the Crime Laboratory Digest33 a set of quality

32 CODIS is a national DNA information repository that allows public laboratories across the country to store and compare DNA profiles from crime scene evidence, from convicted offenders, and from unidentified remains.

33 The Crime Laboratory Digest was superseded by Forensic Science Communications in April of 1999. Forensic Science Communications is a forensic science journal published quarterly in January, April, July, and October by FBI Laboratory personnel.

guidelines for forensic DNA laboratories.34 TWGDAM expanded these guidelines in 1991 and in 1995.35 In addition, TWGDAM worked with the National Institute of Standards and Technology (NIST) to develop model reference material that laboratories across the country could use to gauge the reliability of their equipment and DNA testing processes. In January 1999, TWGDAM was renamed the Scientific Working Group on DNA Analysis Methods (SWGDAM), and in that capacity produced additional guidance for the forensic community, including guidelines for data interpretation36, training, quality assurance, and health and safety audits.

While no formal legal authority was granted to TWGDAM and SWGDAM,

the guidelines they produced were accepted by the Laboratory Accreditation Board of the American Society of Crime Laboratory Directors as the benchmark for DNA laboratory accreditation. Further, when Congress authorized the creation of CODIS in the DNA Identification Act of 1994,37 it provided that the guidelines issued by TWGDAM would be deemed to be national standards until the FBI issued its own standards pursuant to the Act.

The second source of DNA standards is the FBI DNA Advisory Board (Board). In the

34 Technical Working Group on DNA Analysis Methods, “Guidelines for a quality assurance program for DNA restriction fragment length polymorphism analysis,” Crime Laboratory Digest, Vol. 16, 1989, pp. 40–59.

35 Technical Working Group on DNA Analysis Methods, “Guidelines for a quality assurance program for DNA analysis,” Crime Laboratory Digest, Vol. 18, 1991, pp.

* 1. ;Technical Working Group on DNA Analysis Methods, “Guidelines for a quality assurance program for DNA analysis,” Crime Laboratory Digest, Vol. 22, 1995, pp. 21–43.

36 Scientific Working Group on DNA Analysis Methods (SWGDAM), Short Tandem Repeat (STR) Interpretation Guidelines, Forensic Science Communications, Volume 2, No. 3, July 2002, available a[t http://www.fbi.gov/hq/lab/fsc/backissu/july2000/strig.htm.](http://www.fbi.gov/hq/lab/fsc/backissu/july2000/strig.htm) The current SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories were approved by SWGDAM on January 10, 2010 and are included on the Exhibit CD as Exhibit 14.

37 Section 210301 to 210306 of Title XXI of Pub. L. 103-322, September 13, 1994, 108 Stat. 2065.

DNA Identification Act, Congress required that the FBI establish an advisory board to develop national quality assurance standards governing all CODIS participants.38 As a result, the FBI established the Board, which was formally constituted on March 10, 1995. Its members were appointed by the FBI Director based upon nominations from a variety of forensic and science organizations, and included forensic scientists from state, local, and private forensic laboratories; molecular and population geneticists; a NIST scientist; a quality control specialist; an ethicist; and a judge. The Board’s mission was to develop and revise, as necessary, standards for quality assurance, including proficiency testing standards for laboratories and analysts that examine DNA.

The Board fulfilled its mission with the submission to the FBI Director of quality assurance standards for two types of DNA laboratories:

* + - Quality Assurance Standards for Forensic DNA Testing Laboratories (Forensic Standards), effective October 1998. 39
    - Quality Assurance Standards for Convicted Offender DNA Databasing Laboratories (Offender Standards), effective April 1999. 40

# Overview of Applicable DNA Standards

At present, at least three sets of standards govern the DNA activities of the NM DPS

38 42 U.S.C. § 14131(a)(1).

39 DNA Advisory Board, Quality Assurance Standards for Forensic DNA Testing Laboratories (July 1998), available at <http://www.fbi.gov/hq/lab/fsc/backissu/july2000>

/codispre.htm. A more current version of these standards, adopted July 1, 2009, are included on the Exhibit CD as Exhibit 3. An even more current version, effective September 1, 2011, is available a[t http://www.fbi.gov](http://www.fbi.gov/) [http://www.fbi.gov](http://www.fbi.gov/) [http://www.fbi.gov/about-us/lab/codis.](http://www.fbi.gov/about-us/lab/codis)

These latest standards post-dated the testing in this case.

40 DNA Advisory Board, Quality Assurance Standards for Convicted Offender DNA Databasing Laboratories (April 1999), available at <http://www.fbi.gov/hq/lab/fsc>

/backissu/july2000/codispre.htm. A newer version of these standards, effective July 1, 2009, is available a[t http://www.fbi.gov/about-us/lab/codis/qas\_databaselabs.](http://www.fbi.gov/about-us/lab/codis/qas_databaselabs)

Crime Laboratory: 1) Quality Assurance Standards; 2) Accreditation Standards; and 3) New Mexico law. These standards are interrelated: to comply with the Quality Assurance Standards, a laboratory is supposed to pursue accreditation actively; to become accredited, a laboratory must demonstrate compliance with the Quality Assurance Standards; and to comply with some state’s laws (e.g. Maryland) a DNA laboratory must be accredited. Because these standards play such a critical role in defining correct scientific procedure in forensic DNA analysis, each of the standards is described below.

# Quality assurance standards

Quality Assurance Standards consist of two sets of standards: 1) Forensic Standards that govern the activities of DNA laboratories that analyze crime scene evidence, and 2) Offender Standards that govern the activities of DNA laboratories that analyze samples from convicted offenders. The Forensic Standards contain 155 requirements organized under 15 headings, and the Offender Standards contain 136 requirements also organized under 15 headings.41

The key categories of requirements addressed in the two sets of Standards, which correspond to section headings in the Standards, are the following:

* + - Quality Assurance Program: written guidelines should be adopted and should contain the required categories of standards.
    - Organization and Management: key roles and duties should be described in writing, as should the interrelation between the personnel involved in DNA analysis.
    - Personnel: personnel filling key roles should be properly educated, trained, and should perform duties appropriate to their position.
    - Facilities: the design of the laboratory should ensure security and minimize contamination.

41 A high degree of overlap exists between the two sets of standards. A total of 119 requirements are shared (identical or similar), 36 requirements are unique to the Forensic Standards, and 17 requirements are unique to the Offender Standards.

* + - Evidence Control (Forensic Standards only) and Sample Control (Offender Standards only): to ensure the integrity of evidence and of offender samples, and their proper disposition, the laboratory should have a documented control system and adequate implementing procedures.
    - Validation: the laboratory should demonstrate that its analysts are capable of using certain equipment and methods properly.
    - Analytical Procedures: every procedure used by the laboratory in DNA analysis should be described in detail in writing and formally approved by laboratory management.
    - Equipment Calibration and Maintenance: the laboratory should establish a written program for ensuring that equipment used for DNA analysis receives regular calibration and maintenance in accordance with recognized national standards.
    - Reports: the laboratory should have written guidelines for maintaining documentation that supports reported conclusions regarding case evidence. Reports should describe with specificity the information collected and written policies should exist to govern the release of such information.
    - Review: administrative and technical reviews should be conducted of all reports and supporting documentation for all evidence. The testimony of analysts in court should also be reviewed.
    - Proficiency Testing: scientists performing DNA analysis should complete an external proficiency test (a test from an outside agency or commercial test provider that measures an analyst’s skill in performing DNA analysis correctly) every 180 days, which should be reviewed and documented.
    - Corrective Action: written procedures should exist governing a laboratory’s documentation and resolution of errors made during proficiency testing and DNA analysis.
    - Audits: the laboratory should undergo an audit every year, and at least every other year

this audit should be conducted by an external entity.

* + - Safety: the laboratory should have and follow a written environmental health and safety plan.
    - Subcontractor of Analytical Testing for Which Validated Procedures Exist: a laboratory making use of a subcontractor for any part of the DNA analysis process should establish certain specified controls to ensure the integrity of the subcontractor’s work and results.

According to documents provided to the defense in discovery and the ASCLD/Lab’s website, the NM DPS Sante Fe Laboratory was granted its current accreditation on December 10, 2009. The Laboratory was thus accredited when it performed the analysis and wrote the reports in this case. It also appears that at the time of the testing in this case the Laboratory had in effect a Serology/DNA/Databasing Quality Manual (eff. 6/23/10) (Exhibit 4), as well as a Serology/DNA SOP (eff. 7/1/10). (Exhibit 7).

Each one of these documents is voluminous and contains general guidelines on all phases of laboratory management and DNA analysis. For instance, the Serology/DNA SOP contains general guidelines for conducting STR DNA analysis, including PCR Laboratory procedural safeguards, sterilization procedures, extraction, quantitation, preparation of reagents for STR analysis, PCR setup and amplification procedures, instrument setup, sample preparation, capillary electrophoresis procedures, data analysis procedures, etc. In the Serology/DNA/Databasing Quality Manual, general guidelines are provided on a variety of topics, including validation procedures, analytical procedures, equipment calibration and maintenance, documentation of case records, measurement traceability, validation of test procedures, evidence handling, standards and controls, calibration and maintenance of equipment, proficiency testing, etc.

Mr. McCluskey has documented above some of the ways these standards were not followed in this particular case. It is anticipated that at the hearing of this motion both sides will reference these documents in an attempt to show that correct scientific procedures were or were

not followed in this case. At this juncture, it is important to point out that the mere existence of these manuals does not show that the laboratory followed correct scientific procedures. The FBI- DNA Laboratory has much more detailed SOP manuals than the NM DPS DNA Laboratory. Yet the existence of those manuals did not prevent widespread fraud and forensic incompetence by one of its DNA examiners as revealed in Exhibit 2, the report of the Office of the Inspector General, The FBI DNA Laboratory: A Review of Protocol and Practice Vulnerabilities (May 2004). 42 That report traces the FBI’s problems to a variety of defects in the protocols themselves, including: (1) protocols that lack sufficient detail; (2) protocols that fail to inform the exercise of staff discretion; (3) protocols that fail to ensure the precision of note taking; and (4) outdated protocols. (*Id*. pp. 77-112). Regarding the FBI’s Short Tandem Repeat Analysis Protocol, which is similar but more detailed than the NM DPS STR SOP, the OIG found that of the 46 sections within this document, 19 were vulnerable, including :

* Guidelines for Control Samples
* Extraction (includes a total of 10 sections)
* Amplification
* STR Typing: Setting up a Run
* GeneScan Analysis
* Interpretation of Control Samples
* Laboratory Set-up (includes a total of 4 sections) (*Id*. at 79).

As indicated, one major flaw found in the protocols was a lack of sufficient detail.

42 Nor was this an isolated incident. As pointed out in the NAS 2009 Report at page 193- 194: “Well-publicized problems in large crime laboratories have uncovered systematic deficiencies in quality control Despite important movement in recent years toward developing

and implementing quality control measures in the forensic science disciplines, a lack of uniform and mandatory quality assurance procedures, combined with some highly publicized problems involving large crime laboratories, has led to heightened attention to efforts to remedy uneven quality among laboratories through the imposition of standards and best practices.”

Concerning this defect, the OIG wrote:

[W]e consider this vulnerability to be the most significant of the ones we identified and the most important indicator of the DNAUI’s susceptibility to inadvertent noncompliance. Protocols that lack essential detail can create a work environment that encourages use of disparate and unproven laboratory practices. When laboratory staff members must rely on ad hoc verbal cues from their peers to complete their duties, the risk increases that they will deviate from the practices that are necessary to generate valid and reliable testing results. In addition, protocols that lack essential detail can foster a perception among staff members that the protocols are not authoritative and can be disregarded, even though they should serve as the DNAUI’s primary source of instruction.

(*Id.* at 81)

The Court is urged to read this document in its entirety before it entertains any argument that the mere existence of the NM DPS’s SOP and Quality Manual shows that the analyst following correct scientific procedure in this case. As was pointed out in the NAS 2009 Report (pp.47-48):

[A]lthough DNA analysis is considered the most reliable forensic tool available today, laboratories nonetheless can make errors working with either nuclear DNA or mtDNA—errors such as mislabeling samples, losing samples, or misinterpreting the data.

Standard setting, accreditation of laboratories, and certification of individuals aim to address many of these problems, and although many laboratories have excellent training and quality control programs, even accredited laboratories make mistakes. Furthermore, accreditation is a voluntary program,

except in a few jurisdictions in which it is required (New York, Oklahoma, and Texas).

# Accreditation and certification standards

The primary accreditation or certification entities for forensic and offender DNA laboratories are the American Society of Crime Laboratory Directors – Laboratory Accreditation Board (ASCLD-LAB) and the National Forensic Science Technology Center (NFSTC). Both groups draw upon the requirements set forth in the Forensic and Offender Standards for their evaluation of a public DNA laboratory’s operations. 43

43 In addition, The International Organization for Standardization (ISO) issues guidance documents on a variety of topics. ISO 17025:2005 entitled General Requirements for

the Competence of Testing and Calibration Laboratories is the standard to which

While TWGDAM/SWGDAM and the Board were pivotal in creating standards for DNA laboratories, they lacked the means to enforce them. To compensate for this shortcoming, the Board adopted an “Accreditation Premise” which set forth the Board’s expectation that standards compliance would be assured through the process of accreditation. Accrediting organizations would need to adopt and hold laboratories accountable for compliance with the Board’s standards. The Board acknowledged that a weakness in this approach was the lack of any enforceable requirement that laboratories be accredited, even for CODIS participation. In an attempt to address this problem, the Board passed a resolution in February 1999 stating that unaccredited laboratories should seek accreditation “with all deliberate speed.” In addition, this language was used in the preface to the Forensic and Offender Standards to emphasize the importance of accreditation.

Compliance with DNA-related standards is an issue systematically examined by the United States Department of Justice, Office of Inspector General (OIG). In 1999, the OIG performed an audit of CODIS to determine the extent of state and local CODIS participation and

many DNA testing laboratories seek to be accredited to by accrediting organizations, such as ASCLD/LAB or NFSTC. (Butler, Fundamentals, p. 293). The NM DPS Sante Fe

laboratory was granted accreditation under ISO 17025:2005. As discussed below, one important requirement for ASCLD/LAB accreditation under ISO 17025:2005 is standard 5.4.6.2 which requires that “[t]esting laboratories shall have and apply procedures for estimating uncertainty of measurement.” As Dr. Butler observes, “[w]ith the adoption of ISO 17025 by many forensic laboratories, analysts have to face the concept of measurement uncertainty...Measurement uncertainty exists with DNA testing particularly during the DNA quantitation and STR allele sizing steps. With appropriate validation studies, variation that does exist can be understood so that experiments performed may yield reliable results.” (Butler, Advanced Topics, supra). Here, the defense has been provided in discovery with a 2010 internal audit (Exhibit 15) and a 2011 internal audit (Exhibit 15), both of which contain the notation: “Is the lab conformant with ASCLD/LAB uncertainty policy ?”. The defense has been provided with no documents indicating that the laboratory has such procedures or that the analyst applied such procedures in this case.

to verify compliance with the FBI’s quality assurance standards and national index requirements. In the report summarizing its findings,44 while the OIG noted that all audited laboratories had complied with the Forensic and Offender Standards’ annual audit requirement, weaknesses were noted with some of the external audits: 1) audit findings were not binding on the laboratories (they could disregard them if they wanted); 2) although accreditation and certification agencies had the authority to ensure a laboratory took appropriate corrective action, accreditation or certification audits did not typically focus on compliance with the quality assurance standards; and 3) laboratory audits were not always performed consistently.

In response to the OIG’s findings and recommendations, the FBI created a standardized DNA audit guide (Guide) with input from the Board, ASCLD-LAB, and NFSTC to ensure that auditors of local, state, and federal DNA laboratories are thorough and interpret the Quality Assurance Standards consistently.45 The FBI offers Guide training for auditors, including those representing accrediting and certifying organizations such as ASCLD-LAB and NFSTC. For an audit to fulfill the Quality Assurance Standards’ external audit requirement, it must be conducted in accordance with the Guide and by an auditor trained in its use. However, as the OIG has noted in Exhibit 2, “as this report details, even with these precautions, internal control weaknesses are not always uncovered in quality assurance audits. In fact, weaknesses in DNAUI procedures and protocols allowed a technician routinely to disregard required steps in the analysis of DNA, even while the Unit received clean audit reports from both internal and

44 The OIG audit report, The Combined DNA Index System, Report No. 01-26, was issued in September 2001 and is available a[t http://www.justice.gov/oig/reports/FBI](http://www.justice.gov/oig/reports/FBI)

/a0126/final.pdf. The NM DPS Sante Fe Laboratory was not included in the audit and the OIG has not subsequently audited the lab.

45 Federal Bureau of Investigation, *Quality Assurance Audit for Forensic DNA and Convicted Offender DNA Databasing Laboratories*, Forensic Science Communications, July 2004, Volume 6, Number 3, available a[t http://www.fbi.gov/about-us/lab](http://www.fbi.gov/about-us/lab)

/forensic-science-communications/fsc/july2004. The more current versions of these standards are available a[t http://www.fbi.gov/about-us/lab/codis.](http://www.fbi.gov/about-us/lab/codis)

external auditors and while the Unit was accredited by ASCLD-LAB.” (Exhibit 2, p. 21).

# New Mexico law

In New Mexico, the only statutory provision which addresses the standards to be employed by DNA testing laboratories is § 29-16-4 of the DNA Identification Act, which governs CODIS database identifications and provides that “[p]rocedures used for DNA testing shall be compatible with the procedures the federal bureau of investigation has specified, including comparable test procedures, laboratory equipment, supplies and computer software. Procedures used shall meet or exceed the provisions of the federal DNA Identification Act of 1994 regarding minimum standards for state participation in CODIS, including minimum standards for the acceptance, security and dissemination of DNA records.”

The New Mexico DNA Oversight Committee established by N.M. Stat. § 29-16-5 merely adopts rules and procedures regarding the administration and operation of the state’s DNA CODIS identification system, including the missing persons DNA identification program, and the sex offender DNA identification system. The Committee is comprised of nine members, none of whom are required to be technically trained in forensic DNA analysis and include

the secretary of corrections or as designee, the attorney general or as designee, the president of the district attorneys association or designee.

The rules adopted by the Oversight Committee are included on the Exhibit CD as Exhibit 16. As can be seen, they are geared solely to regulating the CODIS identification system, although they do importantly provide that “[s]amples shall be handled, examined, and processed one at a time to avoid possible cross-contamination from another sample or from the examiner”, and that “[f]ive percent of all samples tested shall consist of samples with a known DNA profile and shall be presented to the analyzing laboratory in a ‘blind’ fashion to ensure proficiency and to act as a quality assurance measure. Results of these analyses are to be evaluated with the corresponding offender or arrestee samples. Should any resultant ‘blind’ sample's DNA profile not match the expected known result for that sample, an error rate is to be

calculated by the administrative center and be presented to the analyzing laboratory and to the oversight committee.” There are no accreditation or licensing requirements even for CODIS laboratories. The analyst in this case was not certified by any regulatory agency.

By contrast, the Maryland Legislature has embraced the accreditation and certification requirements wholeheartedly. Unlike any other state, as of 2007, Maryland includes forensic laboratories within the meaning of the term, “health care facilities,” thus subjecting such laboratories to stringent licensing and accreditation standards. *See*, MD Code, Health - General,

§ 19-2301 et. seq.

MD Code, Health - General, § 17-2A-02 provides that “[t]he Secretary shall adopt regulations that set standards and requirements for forensic laboratories,” that “[t]he regulations shall contain the standards and requirements that the Secretary considers necessary to assure the citizens of the State that forensic laboratories provide safe, reliable, and accurate services,” and that “[t]he regulations shall:...[r]equire the director of a forensic laboratory to establish and administer an ongoing quality assurance program using standards acceptable to the Secretary.”

MD ADC 29.05.01.01-1 incorporates into Maryland law both the Quality Assurance Standards for Forensic DNA Testing Laboratories (October 1, 1998) and the Quality Assurance Standards for Convicted Offender DNA Databasing Laboratories (April 1, 1999).

MD ADC 29.05.01.03 provides: “The Director [of the Department of State Police Crime Laboratory] shall:...[e]nsure compatibility with Federal Bureau of Investigation and CODIS requirements as well as the DAB Standards, including the use of: (a) Comparable test procedures, (b) Quality assurance, proficiency tests, and audits, (c) Laboratory equipment, [and]

1. Computer software and hardware.”

MD ADC 29.05.01.09 provides: “Blood, body fluid, or tissue samples shall be analyzed according to State Police protocol and standard operating procedures by personnel qualified under the DAB Standards.”

MD ADC 29.05.01.10 provides in part: “Any procedure adopted by the Director shall

include quality assurance guidelines to ensure that DNA identification records meet standards and audit requirements for laboratories that submit DNA records for inclusion in the Statewide DNA Data Base System and CODIS.”

Finally, MD Code, Courts and Judicial Proceedings, § 10-915, provides that DNA evidence is inadmissible absent proof that “ the analysis of genetic loci has been validated by standards established by TWGDAM or the DNA Advisory Board.”

Again, as emphasized by the OIG, even if it was shown that the laboratory in this case was accreditated and the analyst who performed the testing was certified, the mere existence of or compliance with accreditation or licensing standards is not enough to ensure that a DNA laboratory is following reliable scientific protocols in a particular case. (Exhibit 2, p. 21).

1. **The Potential for and Occurrence of Error**. As pointed out above, the NAS 2009 Report concluded:

Although DNA laboratories are expected to conduct their examinations under stringent quality controlled environments, errors do occasionally occur. They usually involve situations in which interpretational ambiguities occur or in which samples were inappropriately processed and/or contaminated in the laboratory. Errors also can occur when there are limited amounts of DNA, which limits the amount of test information and increases the chance of misinterpretation.

(NAS 2009 Report, p. 132)

Errors resulting from mislabeled or contaminated DNA samples “appear to be chronic and occur even at the best DNA labs.” (Thompson, *Tarnish on the Gold Standard, supra*, at p. 11.) Significant errors have been documented in California, Maryland, Minnesota, Nevada, North Carolina, Pennsylvania, Texas, and Washington.46 There are documented errors even by

46 *See*, *e.g.,* Phoebe Zerwick, DNA Mislabeled in Murder Case, Winston-Salem J., (Aug. 28, 2005); Mixed Results; Forensics, Right or Wrong, Often Impresses Jurors, Winston-Salem J., (Aug. 29, 2005); Thompson, *supra*, at p.10-11; Ruth Teuchroeb, Rare Look Inside State Crime Labs Reveals Recurring DNA Test Problems, Seattle-Post Intelligencer (7/22/2004) (hereinafter “Teuchroeb”).

California’s supposedly premier DNA Laboratory, the CAL-DOJ Laboratory.47

Many errors are traced to DNA laboratories that are overworked and undersupervised.48 Labs often have caseloads that vastly exceed their capabilities, leading analysts to rush test results. (Bureau of Justice Statistics, Survey of DNA Crime Laboratories, 2001, (2002) at p. 2. [“Some labs have become high-tech sweatshops...”]; Thompson, *supra*, at p.12.) In 2004, the Chicago Tribune reported that “evidence of problems ranging from negligence to outright deception has been uncovered at crime labs in at least 17 states.” (Maurice Possley, Steve Mills, & Flynn McRoberts, *Scandal Touches Even Elite Labs; Flawed Work, Resistance to Scrutiny Seen Across U.S*., Chicago Tribune (Oct. 21, 2004.). The chances for sample switching and contamination errors increase significantly in laboratories such as the NMDPS DNA Unit that process evidence samples from different cases in the same analytical run in order to save time and money. *See* generally, A.D. Kloosterman, *Credibility of Forensic DNA Typing is Driven By Stringent Quality Standards*, Accred. Qual. Assur. (2001) 6:409–414 (“Sample mix-up and contamination of forensic evidence are the most serious concerns throughout the laboratory

47 *See*, United States Department of Justice, Office of the Inspector General, Audit Report No. 01-26, The Combined DNA Index System, September 2001, [http://www.usdoj.gov/oig/reports/FBI/a0126/final.pdf,](http://www.usdoj.gov/oig/reports/FBI/a0126/final.pdf) p. 25 (“The California Department of Justice, Berkeley DNA Laboratory, Berkeley, California [Berkeley Laboratory], inadvertently uploaded 2 inappropriate profiles to the national index out of the 50 forensic profiles we evaluated. These profiles matched the DNA profiles of crime victims. In addition, the laboratory uploaded one incomplete and one inaccurate profile to the national index. The incomplete profile was not tested at one of the NDIS-required loci. Laboratory officials stated that the incomplete profile was an oversight and that they were in the process of testing the required locus for the profile. The inaccurate profile included an extra value at one locus. Laboratory officials explained that the extra value was for a nondiagnostic result and should not have been included in the uploaded profile. The laboratory corrected the uploaded profile by removing the extra value.”).

48 Garrett E. Land, Judicial Assessment or Judicial Notice? An Evaluation of the Admissibility Standards for DNA Evidence and Proposed Solutions to Repress the Current Efforts to Expand Forensic DNA Capabilities, 9 J. Med. & L. 95, 98 (2005); J. Herbie DiFonzo, *The Crimes of Crime Labs*, 34 Hofstra L. Rev. 1, 2 (2005) (hereinafter “DiFonzo”).

process.”).49

Even in the best-run lab under the best of conditions, a test of an uncontaminated, properly labeled DNA sample may result in a false positive, because DNA analysts have substantial leeway to make subjective judgments during the STR testing process. See generally, Erin Murphy, *The Art in the Science of DNA: A Layperson’s Guide to the Subjectivity Inherent in Forensic DNA Typing*, 58 Emory L.J. 489 (2008) An analyst testing a sample with DNA from more than one contributor must make judgments about which alleles are from a primary contributor, whether any contributors share alleles, and whether unexpected alleles are from an alternate contributor or other sources. The analyst may create a false profile based on a combination of alleles from two contributors, or exclude the actual perpetrator from the test result. A test may show fewer that the expected number of alleles and an analyst may be forced to simply guess whether all alleles have been detected or not. Or a test may show more than the expected number of alleles, possibly indicating a flaw in the testing process, or the misreading of the test by the automated software, or any number of other random factors.

Thus, the room for human error is heightened with each opportunity for subjective judgment. Interpretation “guidelines” are of little help in addressing the issue, because the “guidelines” themselves are too loose to provide any real guidance. For instance, the crucial issue of how an analyst should go about making a match is left to this vague language: “When a DNA profile generated from an evidence sample is different from that of a standard

(a known individual), then it is concluded that the known individual is eliminated as a source of the DNA identified from the evidence. When a DNA profile generated from an evidence sample exhibits the same genotype as from a known individuals DNA, then it is concluded that

49 The NMDPS’s DNA Unit has a policy of documenting every incident of DNA contamination within the Unit. See , SOP, Section 16.1. Although defense counsel has received no such reports from the government as *Brady* material, it is hard to believe that such reports do not exist, as in counsel’s experience contamination reports of this type are widespread in forensic DNA labs. Mr. McCluskey hereby moves for disclosure of any such reports under *Brady*.

this individual cannot be eliminated as a source of the DNA identified from the evidence.” (SOP, Exh.7, p. 13-10). What does “different” mean, and by what qualitative or quantitative standards is such a difference judged? The SOP never says. Even more ludicrous is the “standard” for deciphering mixtures: “If the mixture consists of identifiable, distinct major and minor profiles, then conclusions may be made regarding the separate major and minor DNA profiles.” (Id. at 13-11) How does one go about determining whether a profile is “distinct” enough to be able to discern a “major” profile ? The mixture interpretation guideline goes on:

If there are alleles of the standard DNA profile that are not in the mixture, then this person is eliminated as a contributor to the DNA identified in this mixture. Of course, there is always a possibility that one’s DNA at one or more loci may be present in trace amounts as to not be detectable (i.e., stochastic effects, inhibition, allelic dropout at longer loci, etc.). The analyst should indicate on the electropherogram if they suspect allelic dropout or other factors affecting the DNA results may be present, and how those results may affect the interpretation and statistics of that sample. Extreme care should be taken in determining an individual is eliminated when limited DNA data is available for comparison.

In other words, there is a preference against eliminating a suspect’s profile when “limited” DNA is available (whatever that means), and even if there are alleles of the standard DNA profile that are not in the mixture, this might not be enough of a “difference” to exclude a person, where the analyst, in her “discretion”, indicates that there is a “possibility” that “one’s DNA at one or more loci may be present in trace amounts as to not be detectable (i.e., stochastic effects, inhibition, allelic dropout at longer loci, etc.)”.

This is the vague and elastic standard under which the analyst concluded, “to a reasonable degree of scientific certainty”, that Tracy Province was the source of the Low copy number 1B23B sample. Yet a comparison with the DNA results for this sample with that of Province reveals that the analyst typed the evidence sample as a 9, 9 at the TPOX locus, and did not call a peak in the 11 position because it was well below the 100 RFU cutoff set by the lab’s validation study.. Province is a 9, 11 at this locus. If, as the analyst concluded, the evidence sample is a 9, 9 at the locus and Province is a 9,11, then wasn’t this a enough of a difference to exclude him ? The answer is that under the amorphous standard set out above, the analyst is

given liberty to conclude that because of the “possibility” that the peak in the 11 position might in fact be an allele (even though the lab’s interpretation guidelines prohibit the analst from so concluding), he is not excluded. This is one of several examples from this case that illustrates how much play there is in the interpretive “guidelines”.

Moreover, as pointed out in the NAS 2009 Report at page 8, “[t]he findings of forensic science experts are vulnerable to cognitive and contextual bias.” Many analysts were trained as law enforcement officers and many public labs are closely aligned with police departments.

Analysts may be privy to details of the prosecution’s theory of the case and the expected outcome of the test. Thus they may consider information outside the realm of scientific knowledge, and unconsciously tilt their findings to support the prosecution’s theory. For instance, in this case, the analyst submitted her August 30, 2010 report which concluded that “[b]lood was indicated on ite[m] L1", yet her notes indicate "2 small cuttings collected of stain for pheno testing- 1 pheno negative and 1 pheno faint." [Discovery 6779]. She also submitted her report of September 30, 2010 which concluded, “to a reasonable degree of scientific certainty”, that Mr. Province was the source of the low copy 1B23 sample, yet nowhere in her report does she even mention that this is a LCN sample, or the dangers that might present. This is a person who is indeed unconsciously tilting her findings to support the prosecution’s theory, for as the FBI’s former chief DNA analyst has concluded, “the limitations and vagaries of LCN typing should be documented and made available (in the report or in an accompanying document) so all involved in the investigative and legal process are aware of the limitations that may impact the significance in a specific case result. Publicizing the potential of the application of LCN typing without describing its limitations is not a responsible role for the forensic scientist to take.” Budowle, B., Eisenberg, A.J. and van Daal, A., *Validity of low copy number typing and applications to forensic science*, 50 Croat. Med. J. 207, 215 (2009). The point is that in the hands of an irresponsible forensic analyst, vague and elastic interpretation guidelines become dangerous and make it especially important to heed the type of sequential masking

guideline discussed above.

In this case, when the analyst knew the DNA profiles of both the decedents and the suspects well before she typed and interpreted many of the evidence samples, the biasing effect of such information on any interpretative analysis conducted after such knowledge was gained cannot be underestimated. Indeed, it is just such information from a computer match that the FBI claims was the reason that three senior FBI fingerprint experts were led to a fingerprint misidentification in the infamous Brandon Mayfield case. *See*, Robert B. Stacey, Unit Chief, Quality Assurance and Training Unit, Federal Bureau of Investigation, *Report on the Erroneous Fingerprint Individualization in the Madrid Train Bombing Case*, Forensic Science Communication, Jan. 2005, Vol. 7, No. 1, available a[t http://www.fbi.gov/about-us/lab](http://www.fbi.gov/about-us/lab)

/forensic-science-communications/fsc/jan2005/special\_report/2005\_special\_report.htm. (“The power of the IAFIS match, coupled with the inherent pressure of working an extremely high-profile case, was thought to have influenced the initial examiner's judgment and

subsequent examination. Once the mind-set occurred with the initial examiner, the subsequent

examinations were tainted.”)

Worse yet, intentional falsification occurs in some cases. An analyst may “fak[e] test results to cover up errors arising from cross-contamination of DNA samples and sample

mix-ups.” (Thompson, *supra*, at 12.) Indeed, analysts have been “fired for scientific misconduct, and specifically for falsification of test results,” from laboratories operated by the FBI, the Chief Medical Examiner in New York City, the U.S. Army, and private enterprises. (*Ibid*.) A DNA analyst in the FBI laboratory failed to use proper controls and falsified laboratory reports, (*Ibid*.), “render[ing] over two years worth of her STR work scientifically invalid and unsuitable for use in court.” (United States Department of Justice, Office of the Inspector General, The FBI DNA Laboratory: A Review of Protocol and Practice Vulnerabilities (May 2004)[, http://www.usdoj.gov/oig/special/0405/final.pdf.).](http://www.usdoj.gov/oig/special/0405/final.pdf.))

The NAS 2009 Report notes at page 44-45:

Other scandals, such as one involving the Houston Crime Laboratory in 2003, highlight the sometimes blatant lack of proper education and training of forensic examiners. In the Houston case, several DNA experts went public with accusations that the DNA/Serology Unit of the Houston Police Department Crime Laboratory was performing grossly incompetent work and was presenting findings in a misleading manner designed to unfairly help prosecutors obtain convictions. An audit by the Texas Department of Public Safety confirmed serious inadequacies in the laboratory’s procedures, including “routine failure to run essential scientific controls, failure to take adequate measures to prevent contamination of samples, failure to adequately document work performed and results obtained, and routine failure to follow correct procedures for computing statistical frequencies.

With these principles and concerns in mind, the Court has the task of deciding the extent to which the DNA evidence in this capital case is admissible.

# The Government Must Show that its DNA Evidence is Admissible Pursuant to *Daubert* and Rule 702.

In this case, the government seeks to introduce DNA evidence extracted from cotton swabs and other evidence and quantitated using an unreliable kit, producing at least one and most likely many more LCN samples, a technique that is not considered generally reliable even in the forensic science community. As indicated, the Short Tandem Repeat (STR) testing in this case was derived from a commercially developed PCR testing kit (Identifiler) and complicated hardware (3130 Genetic Analyzer) and software (GeneMapper ID). The particular kit and methodologies used in this case are novel: they have never been reviewed for admissibility under *Daubert* or Rules 403 and 702 by the Tenth or any other Circuit . Even the best established DNA methods (those based on RFLP analysis) are sometimes misapplied and the testing results from such misapplication have been held to be inadmissible or entitled to no weight under *Daubert*. *See* e.g., *Attorney General of Oklahoma v. Tyson Foods, Inc.* 565 F.3d 769, 781 (10th Cir. 2009)(although PCR was well established as reliable, the district court did not abuse its discretion in using Daubert to give no weight to the PCR DNA testing results in that case because the district court’s decision arose “ out of the novelty of its application to an entirely new area, which required the development of primers that had not been identified previously.”); *People v. Venegas*, 18 Cal.4th 47 (1998) (reversal of rape conviction is required

for lack of compliance by the FBI with correct scientific procedures for determining the statistical probability of a random match in an RFLP case); *State v Schwartz* (1989, Minn) 447 NW2d 422, 426 (RFLP testing inadmissible because the testing laboratory failed to conform with appropriate quality control standards and guidelines regarding availability and independent validation of data and results.)(“[S]pecific DNA test results are only as reliable and accurate as the testing procedures used by the particular laboratory.”); *People v Castro* (1989) 144 Misc 2d 956, 545 NYS2d 985 (RFLP testing inadmissible because the testing laboratory failed to perform scientifically accepted procedures to resolve test result ambiguities and discrepancies possibly caused by contamination or degradation of a sample ). Cf., *Bryte v. Am. Household, Inc.*, 429 F. 3d 469 (4th Cir.2005)(arson expert’s opinion as to the cause of a fire was properly excluded under Rule 702 where the expert did not follow the standards of his profession.)

“It is by now well established that Fed.R.Evid. 702 imposes on a district court a gatekeeper obligation to ‘ensure that any and all scientific testimony or evidence admitted is not only relevant, but reliable.’ ” reliable.” *Dodge v. Cotter Corp.*, 328 F.3d 1212, 1221 (10th Cir.2003) (quoting *Daubert v. Merrell Dow Pharms., Inc.*, 509 U.S. 579, 589 (1993)). This function “requires the judge to assess the reasoning and methodology underlying the expert's opinion, and determine whether it is both scientifically valid and applicable to a particular set of facts.” (Id. at 1221) The Supreme Court has made clear that “where [expert] testimony's factual basis, data, principles, methods, or their application are called sufficiently into question ... the trial judge must determine whether the testimony has ‘a reliable basis in the knowledge and experience of [the relevant] discipline.’ ” *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 149, 119 S.Ct. 1167, 143 L.Ed.2d 238 (1999) (quoting Daubert, 509 U.S. at 592).

Generally, the district court should focus on an expert's methodology rather than the conclusions it generates. *Daubert*, 509 U.S. at 595, 113 S.Ct. 2786. However, an expert's conclusions are not immune from scrutiny: “A court may conclude that there is simply too great an analytical gap between the data and the opinion proffered.” *General Elec. Co. v. Joiner*, 522

U.S. 136, 146, 118 S.Ct. 512, 139 L.Ed.2d 508 (1997) ( “[N]othing in either *Daubert* or the Federal Rules of Evidence requires a district court to admit opinion evidence which is connected to existing data only by the ipse dixit of the expert.”); *Dodge v. Cotter Corp.*, 328 F.3d at 1222.

Under *Daubert*, “any step that renders the analysis unreliable ... renders the expert's testimony inadmissible. This is true whether the step completely changes a reliable methodology or merely misapplies that methodology. It is critical that the district court determine whether the evidence is genuinely scientific, as distinct from being unscientific speculation offered by a genuine scientist.” 328 F.3d at 1222 (internal quotations and citations omitted).

Though the district court has discretion in how it conducts the gatekeeper function, the Tenth Circuit has “ recognized that it has no discretion to avoid performing the gatekeeper function.” (Id. at 1223). “A natural requirement of the gatekeeper function is the creation of ‘a sufficiently developed record in order to allow a determination of whether the district court properly applied the relevant law.’” Id. at 1223, quoting *Goebel v. Denver & Rio Grande W.*

*R.R. Co.*, 215 F.3d 1083, 1087 (10th Cir.2000). See also, *Dodge v. Cotter Corp.*, 203 F.3d 1190,1200 n. 12 (10th Cir.2000) ( “ Dodge I ”)(urging the district court on remand to “vigilantly make detailed findings to fulfill the gatekeeper role crafted in Daubert ” to ensure that each “particular opinion is based on valid reasoning and reliable methodology”). Citing these cases, it was concluded in *United States v. Gomez-Paz*, 2011 WL 4345891 \* 5 (D. Colo. Sept. 16, 2011), that “[i]n the Tenth Circuit, determination of the sufficiency of the foundation under Rule 702 requires factual findings, preferably made after an evidentiary hearing.”

In reviewing the admissibility of DNA evidence in this case under *Daubert*, this court does not write on a blank slate. Several federal rulings on DNA evidence have helped establish the nature and scope of the issues reviewable under *Daubert*. *See generally, Daubert v. Merrell Dow Pharmeceuticals*, 43 F.3d 1311 (9th Cir. 1995) (“*Daubert II*”). *See also*, *Attorney General of Oklahoma v. Tyson Foods, Inc.* 565 F.3d 769 (10th Cir. 2009); *United States v. Trala*, 386 F.3d 536 (3rd Cir. 2004); *United States v. Wright*, 215 F.3d 1020 (9th Cir. 2000);*United States v.*

*Hicks*, 103 F.3d 837 (9th Cir. 1996); *United States v. Chischilly*, 30 F.3d 1144 (9th Cir. 1994); *United States v. Gipson*, 383 F. 3d 689 (8th Cir. 2004); *United States v. Martinez*, 3 F.3d 1191 (8th Cir. 1993); *United States v. Beasley*, 102 F.3d 1440 (8th Cir. 1996); *United States v. Bonds,* 12 F. 3d 540 (6th Cir. 1993); *United States v. Davis,* 40 F.3d 1069 (10th Cir. 1994); *United States v. Black Cloud*, 101 F.3d 1258 (8th Cir. 1996); *United States v. Williams*, 2009 WL 1704986 (C.D.Cal. Jun 17, 2009); *United States v. Davis*, 602 F.Supp.2d 658 (D.Md.2009); *United States v. Morrow*, 374 F. Supp. 2d 51 (D.D.C. 2005); *United States v. Beeler*, 62 F. Supp. 2d 136 (D. Me. 1999); *United States v. Cuff*, 37 F. Supp. 2d 279 (S.D. N.Y. 1999); *United States v. Shea*, 957 F.Supp. 331 (D.N.H. 1997); *United States v. Gaines*, 979 F. Supp.

1429 (S.D. Fla. 1997); *United States v. Lowe,* 954 F. Supp. 401 (D. Mass. 1996); *Government of the Virgin Islands and United States v. Byers,* 941 F. Supp. 513 (V.I. 1996); *United States v. Coronado-Cervantes*, 912 F. Supp. 497 (D. N.M. 1996); *Government of the Virgin Islands v.*

*Penn*, 838 F. Supp. 1054 (1993); *United States v. Peters*, 1995 U.S. Dist. LEXIS 20950 (D.

N.M. 1995), aff'd, 133 F.3d 933 (10th Cir. 1998) (unpub.); *United States v. Perry*, 1994 U.S. Dist. LEXIS 20463 (D. D.C. 1994).

One key point established by these cases is that forensic DNA testing requires a series of distinct steps, and that the methods employed at *each major step* are independently reviewable under *Daubert*; each step must be scientifically valid. *See United States v. Shea*, 957

1. Supp. 331, 337 (1997). For example, *Hicks, Chischilly, Byers*, *Shea*, *Gaines*, *Coronado- Cervantes*, and *Peters* identified three major steps in DNA tests that employ RFLP analysis50 and made it clear that failure to use a reliable method for any of these steps would preclude admissibility of the resulting evidence. For newer technologies, this court will need to identify the steps in the testing procedure and ascertain that a scientifically valid method is being used at

50 The steps were: (1) processing of the DNA samples to produce DNA prints, (2) comparison of the prints to determine whether there is a “match,” and (3) estimating the statistical significance of the match, i.e., probability of a match would be declared between samples from different people.

each step, particularly at critical steps (i.e., points where serious errors might occur).51 *See* e.g., *Murray v. State*, 692 So. 2d 157 (Fla. 1997)(trial judge failed to conduct requisite step-by-step inquiry set out in case law as to whether Polymerase Chain Reaction (PCR) method of DNA typing used by state's expert, or probability calculations used to report test results, were admissible; trial court improperly allowed DNA evidence to be admitted under faulty rationale that scientific principles underlying that evidence were more appropriately resolved by jury as matter of weight.)

Statistical computation will obviously be a critical step for every DNA testing procedure that purports to find a “match” between samples with respect to their genetic characteristics. The National Resource Council in its 1992 report, *DNA Technology in Forensic Science*, stated, “DNA ‘inclusions’ cannot be interpreted without knowledge of how often a match might be expected to occur in the general population.” In its 1996 report, *The Evaluation of Forensic DNA Evidence*, the National Resource Council posited, “[I]t would not be scientifically justifiable to speak of a match as proof of identity in the absence of underlying data that permit some reasonable estimate of how rare the matching characteristics actually are.” Speaking even more forcefully, the NAS 2009 Report concludes at page 184:

The concept of individualization is that an object found at a crime scene can be uniquely associated with one particular source. By acknowledging that there can be uncertainties in this process, the concept of “uniquely associated with” must be replaced with a probabilistic association, and other sources of the crime scene evidence cannot be completely discounted. The courts already have proven their ability to deal with some degree of uncertainty in individualizations, as demonstrated by the successful use of DNA analysis (with its small, but nonzero, error rate).

Scientific commentary has clarified the necessary elements of the statistical estimation procedure. In particular, it is now clear that no statistical procedure is acceptable unless it addresses the probability of two events that could cause a “match” to be reported between

51 For PCR-based forensic tests, for example, the scientific community considers sample collection and preservation against contamination to be a step that is critical to the overall reliability of the test results.

samples from different people: (1) a *coincidental match* between different individuals who happen to have the same genetic characteristics, and (2) a *false positive* (false match) due to laboratory error. The NAS 2009 Report is unequivocal on this point :

It is also important to note that errors and corresponding error rates can have more complex sources than can be accommodated within the simple framework presented above. For example, in the case of DNA analysis, a declaration that two samples match can be erroneous in at least two ways: The two samples might actually come from different individuals whose DNA appears to be the same within the discriminatory capability of the tests, or two different DNA profiles could be mistakenly determined to be matching. The probability of the former error is typically very low, while the probability of a false positive (different profiles wrongly determined to be matching) may be considerably higher. *Both sources of error need to be explored and quantified in order to arrive at reliable error rate estimates for DNA analysis.*

(NAS 2009 Report at 121)(emphasis added).

As indicated above, the probability of a coincidental match is typically estimated by determining the frequency of matching genetic characteristics (genotypes) in a suitable reference population (or populations). The probability of a false positive can be estimated by determining the laboratory’s or the profession’s rate of errors in blind proficiency tests.52 *See generally*, L. Mueller, *The DNA Controversy And NRC II*, in STATISTICAL METHODS IN THE HEALTH SCIENCES: GENETICS (M.E. Halloran & S. Geisser eds. (1999); D.H. Kaye, *DNA, NAS, NRC,*

*DAB, RFLP, PCR, and More: An Introduction to the Symposium on the 1996 NRC Report on Forensic DNA Evidence*, 37 JURIMETRICS 395 (1997); Jonathan Koehler, *Why DNA Likelihood Ratios Should Account For Error (Even When A National Research Council report Says They Should Not)*, 37 JURIMETRICS J. 425 (1997).

52 Mr. McCluskey has been given access to only five proficiency tests performed by the primary analyst and none by the peer reviewer. These five tests were completed on March 15, 2010, September 20, 2010, December 28, 2010, April 4, 2011, and October 11, 2011. None of them were blind and only the two most recent ones involved simple mixtures. Although no errors are apparent in these five tests, it must be stressed that even if no errors have been made yet, it does not mean that the analyst’s or the laboratory’s error rate is zero. *See* Jonathan Koehler, *Why DNA Likelihood Ratios Should Account For Error (Even When A National Research Council report Says They Should Not)*, 37 JURIMETRICS J. 425 (1997) .

Another critical step for every DNA testing procedure is the exact methodology used to determine the various DNA types within each testing system. *See* generally, *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 154 (1999) (“For one thing, and contrary to respondents’ suggestion, the specific issue before the court was not the reasonableness in general of a tire expert’s use of a visual and tactile inspection to determine whether overdeflection had caused the tire’s tread to separate from its steel-belted carcass. Rather, it was the reasonableness of using such an approach, along with Carlson’s particular method of analyzing the data thereby obtained, to draw a conclusion regarding the particular matter to which the expert testimony was directly relevant.) (emphasis added).

In *Attorney General of Oklahoma v. Tyson Foods, Inc.*, 565 F.3d 769, 781 (10th Cir.

2009), in concluding that the district court did not abuse its discretion in using a *Daubert* analysis to give no weight to PCR DNA testing results in that case, the Tenth Circuit did not focus on the reliability of PCR amplification in the abstract, but instead on the fact that the district court’s decision arose “ out of the novelty of its application to an entirely new area, which required the development of primers that had not been identified previously. Thus, the court looked to other indications of reliability, including those enumerated by the *Daubert* Court, but could find none In addition, the record casts further doubt on Dr. Harwood's

methodology, suggesting other procedural flaws.”

The Attorney General in that case argued “that *Daubert* should not have been used to assess the *application* of the experts' methodologies, but rather should have been used to assess *only* the *methodologies* upon which the doctors relied.” 565 F.3d at 779 (emphasis in original). The Tenth Circuit disagreed:

It is an elusive process to divine the difference between a methodology and what constitutes a change from that methodology; therefore, under *Daubert*, we simply hold that “ ‘any step that renders the analysis unreliable renders the expert's testimony inadmissible. This is true whether the step completely changes a reliable methodology or merely misapplies that methodology.’ ” *Mitchell v.*

*Gencorp Inc.*, 165 F.3d 778, 782 (10th Cir.1999) (quoting *In re Paoli R.R. Yard PCB Litig*., 35 F.3d 717, 745 (3d Cir.1994) (emphasis omitted))....

Moreover, when experts apply methodologies in novel ways, they may

arrive at conclusions that result in “ ‘too great an analytical gap between the data and the opinion proffered’ ” to be determined reliable (quoting Joiner, 522

U.S. at 147, 118 S.Ct. 512). In other words, as Tyson Foods argues, when experts employ established methods in their usual manner, a district court need not take issue under *Daubert*; however, where established methods are employed in new ways, a district court may require further indications of reliability.

In *People v. Venegas,* 18 Cal. 4th 47 (1998), the California Supreme Court’s discussion of general acceptance did not focus on a particular locus or even on a generic methodology such as RFLP, but rather on the “general scientific acceptance of the FBI’s RFLP methodology used in this case ” Concluding that the methodology used in the case met the *Frye* test of general

acceptance, the Court nonetheless concluded that the testing results were prejudicially admitted because the third prong of California’s version of *Frye* is a case-specific inquiry: Were the proper scientific procedures followed in the particular case? “The test's third prong does not

apply the *Frye* requirement of general scientific acceptance-it assumes the methodology and technique in question has already met that requirement. Instead, it inquires into the matter of whether the procedures actually utilized in the case were in compliance with that methodology and technique, as generally accepted by the scientific community. [Q]uestions concerning whether a laboratory has adopted correct, scientifically accepted procedures for [DNA testing] or determining a [profile] match depend almost entirely on the technical interpretations of experts. Consideration and affirmative resolution of those questions constitutes a prerequisite to admissibility under the third prong ” ( *Venegas*, supra, at pp. 78-81).

The focus on the specific methods and procedures used in the particular case is universal in *Daubert and Frye* litigation. As stated in *State v. Jackson*, 255 Neb. 68, 582 N. W. 2d 317, 325 (1998) a case in which the Nebraska Supreme Court ruled that the results of an unspecified STR procedure should not have been admitted absent a foundation that the lab had followed its own testing protocols, the admissibility of PCR- based testing methods is generally held to turn on the following issues: “(1) whether the witnesses on the DNA issue are experts in the relevant scientific fields, (2) whether the type of DNA testing used in the case under consideration is generally accepted by the relevant scientific communities, including the accompanying

statistical analysis; (3) whether the testing protocol used in the case under consideration is generally accepted as reliable if performed properly, (4) whether the test conducted properly followed the protocol; (5) whether DNA analysis evidence is more probative than prejudicial . .

. and (6) whether statistical probability evidence interpreting the DNA analysis results is more probative than prejudicial.”

Other courts have agreed with this approach. *See United States v. Beasley*, 102 F. 3d 1440, 1445 (8th Cir. 1996) (“[T]he PCR method of DNA typing using the DQ alpha Amplitype test kit and the Polymarker test kit has achieved general acceptance within the forensic science community.”); *United States v. Lowe*, 954 F. Supp. 401, 411 (D. Mass 1997) (Changes in the FBI’s RFLP methodology are significant enough to require *Daubert* analysis even though general RFLP methodology has already been ruled admissible); *United States v. Gaines*, 979 F. Supp. 1429,1437 (S.D. Fla 1997) (“For DQA1 and PM, the process used for determining a match involves the use of the reverse dot blot test. For D1S80 and Amelogenin, the process used is gel electrophoresis. Since the processes are different, they will be addressed separately.”); *Commonwealth v. Blasioli*, 552 Pa. 149, 1998 WL 313388 (1998) (“This Court has generally required that both the theory and technique underlying novel scientific evidence must be generally accepted.”); *Commonwealth v. Sok*, 425 Mass. 787, 683 N.E.2d 671,798 (1997) (“Here we are primarily concerned with whether the particular test kits were reliable when utilized by CBR.”); *State v. Harvey*, 151 N.J. 117, 699 A. 2d 596, 622-623 (1997) (“Proving general acceptance ‘entails the strict application of the scientific method, which requires an extraordinarily high level of proof based on prolonged , controlled, consistent, and validated experience.’ Here, the State’s burden is to prove that the polymarker test and the interpretation of its results are non-experimental, demonstrable techniques that the relevant scientific community widely, but perhaps not unanimously, accepts as reliable.”) ( acceptance of PM generally did not preclude challenge to dot -intensity analysis, as “ a court must examine each step of a scientific process or technique.”).

Of all the federal cases cited above, four have specifically upheld the admissibility of the Profiler Plus and/or Cofiler test kits and the 310 Genetic Analyzer, technology which was not used in this case. (*Gipson*, *Davis* (Maryland), *Morrow*, and *Trala*.) However, it is important to note that none of the cited cases addressed the low copy number technique used in this case, or the Quantifiler and Identifiler kits, or the 3130 Genetic Analyzer, or Genemapper ID, which *are* the methodologies at issue here, not STR typing in general, and certainly not PCR “testing” in general. Furthermore, no other case in the United States has addressed the admissibility of low copy number testing or of the other methodologies used in this case.53 Moreover, in addition to a

53 A nationwide Westlaw search of all state and federal cases reveals only one case where the issue of the admissibilty of low copy testing is addressed. *People v. Megnath*

27 Misc.3d 405, 898 N.Y.S.2d 408 (2010). That case, a trial court decision, was based on *Frye*, and erroneously concluded, contrary to all of the literature cited above, that low copy testing was generally accepted as reliable in the forensic scientific community and that it was not a novel technique within the scope of the *Frye* doctrine. Of course, *Daubert*, not *Frye,* governs this case*.* Only one other case even uses the term “low copy” in connection with forensic DNA testing.

That case, *United States v. McAllister*, 55 M.J. 270 (2001) did not address an admissibility question at all, but a defense funding request for an expert on PCR contamination. The court ruled that the expert should have been provided. One judge dissented and in the course of his dissent on the funding issue he dropped a footnote to describe the PCR process as follows:“‘PRC is very sensitive and can detect target sequences that are in extremely low copy number in a sample’”, quoting Griffiths et al., Modern Genetic Analysis 21 (W.H. Freeman and Co., New York (1999). *Daubert* was never mentioned and the case itself did not involve low copy number testing. As mentioned earlier, the *Davis* case in Maryland and the *Williams* case in California both concluded that no low copy testing had taken place in those cases, so the admissibility need not be addressed.

A nationwide Westlaw search of all state and federal cases reveals only six cases where the word Identifiler was used, all in California. Only one of the cases, *People v. Jackson*

163 Cal.App.4th 313 (2008), addressed the admissibility of the Identifiler kit under *Frye* and concluded that the challenge could not be sustained because defendant failed to show that the kit changed the methodology of the testing from prior approved methods. The Tenth Circuit explicitly rejected this approach in *Tyson Foods*, ruling that “any step that renders the analysis unreliable renders the expert's testimony inadmissible. This is true whether the step completely changes a reliable methodology or merely misapplies that methodology. ” 565 F.3d at 779. No cases have considered the admissibility of Quantifiler, the 3130 Genetic Analyzer, or Genemapper ID.

general challenge to the reliability of low copy number testing, Mr. McCluskey is also raising other reliability issues which are supported by recent literature that either did not exist or was not considered in the decided cases. Further, in *Morrow*, the court noted that “none of the Defendants have argued, to date, that PCR/STR testing is not generally reliable.” (374 F. Supp. at 51). Here, for reasons to be discussed below, Mr. McCluskey is rising this issue, and his arguments are based on some claims that are matters of first impression, including the issue of low copy testing, the failure to use sequencing instead of length-based testing, and certain statistical issues unique to this case.

Moreover, as noted above, the Court in *Morrow* also ruled that even accepting the general reliability of PCR/STR testing, “the admission of such evidence will be contingent upon a showing by the Government that the techniques, methods, and practices used in the testing in this case, as well as the expert’s qualifications, meet with the generally accepted and established protocols.” (Id. at 62). This is also the rule in the Tenth Circuit. See, *United States v. Davis*, 40 F.3d 1069, 1074 n.6 (10th Cir.1994)(“ If the offering party does not follow [ DNA] protocol, the scientific evidence may not be relevant under *Daubert 's* second prong because improperly applied science cannot assist the trier of fact.”); *United States v. Coronado-Cervantes*, 912 F.Supp. 497, 500 (D.N.M.1996)(“[T]this Court finds that under *Daubert's* second ‘relevance’ prong, compliance with standard protocol in applying the RFLP technique is essential and goes to admissibility, rather than merely to the weight of DNA evidence as urged by the government. This is so because failure to follow standard protocol in applying the RFLP technique may yield an unacceptably high risk of false positive error.”) *See also*, *United States v. Gipson*, 383 F. 3d 689, 696-697 n. 8 (8th Cir. 2004)(“[W]e reiterate that: “[I]n every case, of course, the reliability of the proffered test results may be challenged by showing that a scientifically sound methodology has been undercut by sloppy handling of the samples, failure to properly train those performing the testing, failure to follow the appropriate protocols, and the like.”), citing *United States v. Beasley*, 102 F.3d at 1448. *See also*, *Kumho Tire Co. v. Carmichael*, 526 U.S. at

150 (“[W]e can neither rule out, nor rule in, for all cases and for all time the applicability of the factors mentioned in *Daubert*, nor can we now do so for subsets of cases categorized by category of expert or by kind of evidence. Too much depends upon the particular circumstances of the particular case at issue.”); *United States v. Baines*, 573 F.3d 979 (10th Cir.2009)(same); *United States v. Prim*, 431 F. 3d 1147, 1152(9th Cir. 2005)("In accordance with *Kumho Tire*, the broad discretion and flexibility given to trial judges to determine how and to what degree [the *Daubert*] factors should be used to evaluate the reliability of expert testimony dictate a case-by-case review rather than a general pronouncement that in this Circuit [a well accepted

technique] is reliable.”); *Skidmore v. Precision Printing and Packaging, Inc.*, 188 F.3d 606, 618 (5th Cir.1999) (“Whether *Daubert's* suggested indicia of reliability apply to any given testimony depends on the nature of the issue at hand, the witness's particular expertise, and the subject of the testimony. It is a fact-specific inquiry.”)

# The Court Should Conduct A Hearing Under Rule 702 and *Daubert* to Determine Whether the Government’s Evidence Is Reliable And Whether All Steps of The DNA Typing Methodology Used In This Case Were Correctly Performed.

Under *Daubert* and amended Rule 702, expert testimony is admissible only if it will “assist the trier of fact to understand the evidence or to determine a fact in issue” and , further, only if : “(1) the testimony is based on sufficient facts or data, (2) the testimony is the product of *reliable* principles and methods, and (3) *the witness has applied the principles and methods reliably to the facts of the case.”* This “newly-expanded rule goes further than *Kumho* to ‘provide ... some general standards that the trial court *must* use to assess the reliability and helpfulness of proffered expert testimony.’” *Rudd v. General Motors Corp*., 127 F. Supp.2d 1330, 1336 (M.D.Ala.2001)(emphasis in original). *See also*, *United States v. Gomez-Paz*, 2011 WL 4345891 \* 5 n.11 (D.Colo. Sept.16, 2011)(“The current version of Rule 702, adopted in response to *Daubert*... expands the foundational requirements for expert testimony. In a sense, it shifts the analysis from being ‘expert centric’ to ‘opinion/testimony centric.’ ”); *United States v. Horn*, 5 F.Supp.2d 530, 554 (D.Md.,2002)(“Following the *Kumho Tire* decision and the

December 2000 changes to Rule 702, a detailed analysis of the factual sufficiency and reliability of the methodology underlying expert testimony is required for all scientific, technical or specialized evidence, not just ‘novel scientific’ evidence.”).

*Daubert*, Rule 702 and even *Frye* are all designed to “forestall the jury's uncritical acceptance of scientific evidence or technology that is so foreign to everyday experience as to be unusually difficult for laypersons to evaluate.” (*People v. Venegas*, *supra*, 18 Cal.4th at p.81.) DNA evidence involves “method[s] of scientific proof ... so impenetrable” that it “assume[s] a posture of mystic infallibility in the eyes of a jury.” (*Id*. at p. 83-84). *See also*, *United States v. Chischilly* 30 F. 3d. 1144 ,1156 (9th Cir. 1994) (“ *Daubert* enjoins watchful assessment of the risk that a jury would assign undue weight to DNA profiling statistics even after hearing appellant's opposing evidence, the testimony of Government witnesses under vigorous

cross-examination and the careful instructions of the district court on burdens of proof.”)

As outlined above, forensic STR DNA testing, and especially Identifiler and low copy number testing, is a complicated and highly technical procedure that requires a series of distinct steps and each step is typically governed by multi-faceted protocols. The methods, protocols and procedures employed *at each step* are subject to independent review under *Daubert and* Rule 702. Under *Daubert*, as supplemented by Rule 702, the “principle *and* methods” must be reliable, and the expert must have “ applied the principles and methods *reliably* to the facts of the case*”.* In other words, the Court first determines whether the principles and methods underlying low copy number testing are reliable. If the Court accepts the view of the FBI and others that this technique, especially as it applies to mixtures, is not reliable, then the evidence is inadmissible. But even if the Court rejects this argument, the Court still must consider whether the expert actually reliably applied the principles and methods of the technique in this case. *See*, *United States v. Davis*, 40 F.3d 1069, 1074 n.6 (10th Cir.1994)(“If the offering party does not follow [ DNA] protocol, the scientific evidence may not be relevant under *Daubert 's* second prong because improperly applied science cannot assist the trier of fact.”); *United States v.*

*Coronado-Cervantes*, 912 F.Supp. 497, 500 (D.N.M.1996)(The Tenth Circuit in *Davis* “has intimated that under *Daubert's* ‘relevance’ prong, it may be necessary to inquire into whether standard protocol, in the DNA context, was followed in a particular case In the absence of

clear directive from the Tenth Circuit, this Court finds that under Daubert's second ‘relevance’ prong, compliance with standard protocol in applying the RFLP technique is essential and goes to admissibility, rather than merely to the weight of DNA evidence as urged by the government. This is so because failure to follow standard protocol in applying the RFLP technique may yield an unacceptably high risk of false positive error.”), citing *United States v. Martinez*, 3 F.3d 1191 (8th Cir.1993). See also, *People v. Venegas*, 18 Cal 4th at 78 (“Due to the complexity of the DNA multisystem identification tests and the powerful impact that this evidence may have on a jury, satisfying *Frye* alone is insufficient to place this type of evidence before a jury without a preliminary critical examination of the actual testing procedures performed. ”). *See also*,

*United States v. Beasley* (8th Cir. 1996) 102 F.3d 1440,1448 (“In every case, of course, the reliability of the proffered test results may be challenged by showing that a scientifically sound methodology has been undercut by sloppy handling of the samples, failure to properly train those performing the testing, failure to follow the appropriate protocols, and the like.”); *State v. Jackson* (Neb. 1998) 255 Neb. 68, 582 N. W. 2d 317, 325(the results of STR testing should not have been admitted absent a foundation that the lab had followed its own testing protocols).

Importantly in this case, the “failure to follow the appropriate protocols” rubric of *Davis and Beasley* brings into play all of the quality assurance and other standards discussed above, including most especially in an Identifiler and low copy PCR case, the critical issue of contamination control, which the literature shows is the most serious concern with this technique. An illustrative case on this point is *People v. Reilly* (1987) Cal App 3d 1127, 1153, an early electrophoresis case decided long before the problems of PCR or low copy contamination were appreciated, yet the Court explained that even under the old methods of blood typing, issues of contamination could pose admissibility issues under a standard (prong

3) identical to the third prong of Rule 702:

“Essentially, this part of the *Kelly/Frye* standard insures that the technique was performed reliably in each particular case before the evidence can be put to the trier of fact. The fact that our courts impose this case-specific burden bolsters our conclusion that potentiallyunresolved questions of deterioration or contamination do not invalidate the technique as a whole. *Rather, if those questions are serious enough on the facts of a particular case, they can be addressed in the second phase (prong three) of Kelly/Frye* and, of course, before the trier of fact at trial should the evidence be ruled admissible.

Here, of course, the court is not faced with traditional blood typing, but with a highly sensitive PCR amplification technique that can pick up minute traces of contamination and amplify the contaminant a billion-fold. Contamination is the single greatest problem in the transfer of PCR and low copy technology to forensic testing. This is because the extraordinary ability of PCR to reproduce a single copy of DNA is also its greatest disadvantage. “PCR is not discriminating as to the source of the DNA it amplifies, and it can be exceedingly sensitive.” (NRC I at 65). “ Any procedure that uses PCR is susceptible to error caused by contamination leading to amplification of the wrong DNA.” (NRC II at 71) As the NRC I warns, “[e]ven the simple act of flipping the top of a plastic tube might aerosolize enough DNA to pose a problem.” (NRC I at 66.) According to the NRC II, “adherence to a standard QC program provides safeguards against these kinds of laboratory error.” (NRC II at 82). (*See also*, *Hughes v. State* (Miss. 1999) 735 So. 2d 238, 272 (“PCR is an amplification process; and, as such, contamination by foreign DNA is a critical issue.”); *Williams v. State*, (Md. 1996)342 Md. 724, 749 679 A.2d 1106 (“Possible contamination of samples is a major concern with the reliability of forensic use of PCR testing.”).

In light of the significant risk of contamination with Identifiler and the low copy number technique, if the Court does not rule the technique unreliable based on the literature and the *Hoey* case cited above, the court should conduct a Rule 702 hearing to determine whether the stringent contamination and other safeguards for this testing advocated by its proponents have been followed. Mr. McCluskey demonstrates above and throughout this memorandum that they

have not.

The prosecution must also satisfy *Daubert* and Rules 403 and 702 with regard to the statistical computations used in this case. *See*, *United States v. Chischilly* 30 F. 3d. 1144 ,1156 (9th Cir. 1994)(“Of particular concern is where the Government seeks to present probability testimony derived from statistical analysis, the third main phase of DNA profiling.”). *See also*, *United States v. Coronado-Cervantes*, 912 F.Supp. 499 (D.N.M.1996)(“There are two distinct processes involved in DNA profiling: (1) the Restriction Fragment Length Polymorphism (RFLP) analysis, which is the process by which a laboratory technician analyzes a DNA sample collected at the crime scene and compares its DNA profile with that of the suspect's; and (2) the methodology by which experts estimate the statistical probability of a coincidental match. The

Court finds that [*Daubert*] must be independently applied to each of the two processes involved in DNA profiling.”); *People v. Barney*, 8 Cal.App.4th 798, 817 (1992)(“[S]ince a match between two DNA samples means little without data on probability, the calculation of statistical probability is an integral part of the process and the underlying method of arriving at that calculation must pass muster....”) Thus, ensuring that a non-statistician crime lab technician employed correct statistical procedures is a prerequisite to admissibility under *Daubert* and Rule 702.

In *People v. Venegas*, *supra*, 18 Cal. 4th 47, the court considered the validity of the "floating bin method of calculation" used by the FBI in that case. The Court concluded that the trial court erred prejudicially when it failed to recognize that the FBI did not follow correct scientific procedures when it calculated a random-match probability of 1 in 65,000 under the “modified ceiling approach.” (*Id*. at p. 90-91.)

Here, with certain exceptions, the prosecution’s statistics are much less probative, as argued above. But the evidence is still statistical and as the Ninth Circuit stated in *United States*

*v. Chischilly*, “[n]umerous hazards attend the courtroom presentation of statistical evidence of any sort. Accordingly, Rule 403 requires judicial vigilance against the risk that such evidence

will inordinately distract the jury from or skew its perception of other, potentially exculpatory evidence lacking not so much probative force as scientific gloss.” 30 F. 3d at 1156. 54

As documented below, one important emerging statistical issue concerns the fact that Arizona’s CODIS system recently reported a significant number of 9, 10, and 11 loci matches in its relatively small database of 65,000 samples. The existence of these unexpected matches undermines the continuing validity of the government’s random match probability statistics. As discussed below, these findings warrant not only a Rule 702 hearing, but a general reliability hearing on this issue as well. Similarly, for the reasons discussed by the Court of Appeal in *People v. Pizarro* (2003) 110 Cal.App.4th 530*,* 601*,* the Court should conduct a hearing on the NM DPS’s mixture analysis in this case, which for all practical purposes is the same as the “dot blot intensity analysis” condemned as un-validated by the Court of Appeal in *Pizzaro*. Here, as

54 One state supreme court succinctly explained why judicial vigilance is necessary for DNA evidence: “DNA evidence is powerful evidence and for that reason material misrepresentations of its significance are apt to be prejudicial.” *Brown v. Commonwealth*, 313 S.W.3d 577, 617 (Ky. 2010). The court went on to accurately summarize the many ways in which this evidence gets either misrepresented by prosecutors or misunderstood by juries:

DNA analysts frequently express the significance of their results by observing that there is a 1 in X chance that a non-related member of the reference population selected at random would be a potential source of the evidentiary DNA sample. Apparently, this is not the same as saying that there is a 1 in X chance that the evidentiary sample came from someone other than the defendant. It is not the same as saying that there is a 1 in X chance that the defendant is not guilty. It is not the same as saying that there is a 1 in X chance that there exists another person who matches the defendant's profile. And it is not the same as saying that X people would have to be tested before one would expect to find another match.

Id. at 616, citing Jonathan J. Koehler, *Error and Exaggeration in the Presentation of DNA Evidence at Trial*, 34 Jurimetries Journal 21 (Fall 1993) and *McDaniel v. Brown*, –––U.S. ––––, 130 S.Ct. 665, 175 L.Ed.2d 582 (2010)( “[I]f a juror is told the probability a member of the general population would share the same DNA is 1 in 10,000 (random match probability), and he takes that to mean there is only a 1 in 10,000 chance that someone other than the defendant is the source of the DNA found at the crime scene (source probability), then he has succumbed to the prosecutor's fallacy.”).

will be demonstrated below, the technicians are subjectively manipulating and interpreting a complex mixture of peaks, not dot intensity, but the principle that this part of the process must be shown to be reliable, particularly in “low copy” cases, is the same.

In what follows, the defense will summarize other issues that should be the focus of an evidentiary hearing in this case. At the outset, however, the defense emphasizes the one overriding principle set forth in both *Chischilly* and *Venegas,* which is that the trial court must assume a very conservative stance in judging the admissibility of highly complex scientific evidence such as the DNA evidence offered in this case. *See United States v. Chischilly* 30 F. 3d. 1144 ,1156 (9th Cir. 1994); *People v. Venegas* (1998) 18 Cal.4th 47, 79, 81-84.

# The Government Bears the Burden of Showing That its Witnesses Are Qualified to Testify about Reliability, Methodology, and Statistical Issues.

David H. Kaye and George Sensabaugh’s, *Reference Guide on DNA Identification*, in Reference Manual on Scientific Evidence (3rd ed. 2011), p. 134, helpfully points out that

Human DNA identification can involve testimony about laboratory findings, about the statistical interpretation of those findings, and about the underlying principles of molecular biology. Consequently, expertise in several fields might be required to establish the admissibility of the evidence or to explain it adequately to the jury. The expert who is qualified to testify about laboratory techniques might not be qualified to testify about molecular biology, to make estimates of population frequencies, or to establish that an estimation procedure is valid evidence.

*Venegas* is instructive about the requirements for a qualified methodology witness. The Court states that proof is required that “the testifying expert understand the technique and its underlying theory, and be throughly familiar with the procedures that were in fact used in the case at bar to implement the technique.” 18 Cal. 4th at 81. The FBI agent who testified in *Venegas* was found to be qualified as to some issues, but not qualified as to others. *See*, Id. at 68.(“Lynch has a master's degree in cell biology. She worked from 1985 to 1989 as an examiner in the serology unit of the FBI laboratory in Washington D.C., then transferred to the DNA analysis unit where she was trained in laboratory techniques, molecular biology, and statistical calculations. The trial court ruled Lynch was qualified to testify as an expert on how the FBI

performs RFLP analysis, but not on the broader issue of whether there is general scientific acceptance of the statistical databases here in question. Lynch, it should be added, did not claim expert qualification in either population genetics or statistics.”)

The DNA forensic community itself has amplified on the *Venegas* requirement of “understand(ing) the technique and its underlying theory”. The community requires that all forensic DNA analysts “shall” have the following minimum requirements: (1) a BA/BS degree or its equivalent in biology, chemistry or forensic science-related area; (2) successful completion of graduate or undergraduate level course work covering the subject areas of biochemistry, genetics and molecular biology, as well as course work and/or training in statistics and population genetics as it applies to forensic DNA analysis; (3) a minimum of six months of forensic DNA laboratory experience, “including the successful analysis of a range of samples typically encountered in forensic case work prior to independent case work analysis using DNA technology”; and “successfully completing a qualifying test before beginning independent casework responsibilities.” and, (4) examiners shall undergo, at regular intervals not to exceed 180 days, external proficiency testing. Exhibit 3, *FBI Quality Assurance Standards for Forensic Dna Testing Laboratories*, Standard 5.4, Standard 3.1.1.11.These requirements apply not only to the analyst who does the DNA testing, but also to the technical reviewer, who is required by the DAB Guidelines to be “qualified” and to review all case files and reports “to ensure conclusions and supporting data are reasonable and within the constraints of scientific knowledge.” Id., p. 7, Standard 12.

Although not mandatory, the first NRC Report, strongly recommends that DNA analysts be certified by the American Board of Criminalists. *See*, NRC I at 109 (“Quality assurance programs in individual laboratories alone are insufficient to ensure high standards. External mechanisms are needed, to ensure adherence to the practices of quality assurance. Potential mechanisms include individual certification, laboratory accreditation, and state and federal regulation.”). The NAS 2009 Report goes further:

The certification of individuals complements the accreditation of laboratories for a total quality assurance program. In other realms of science and technology, professionals, including nurses, physicians, professional engineers, and some laboratorians, typically must be certified before they can practice. The same should be true for forensic scientists who practice and testify.

(NAS 2009 Report, p. 184)

The NM DPS Laboratory does not require its analysts to be certified. Documents provided to the defense concerning the analyst’s qualifications are included on the Exhibit CD as Exhibit 18. These documents show that the analyst, Carrie Zais, received a Bachelor of Arts degree in 2000, that she has been working at the NM DPS only since October 2007, and that she is not certified. An audit document indicates that from October 2009-October 2010 she was working in the capacity of “technical support personnel”, yet she states in her CV that from October 2007 to October 2010 she was employed as a “Forensic Scientist, Advanced” and that from October 2010 to the present she was employed as a “Supervising Forensic Scientist, Advanced.” She lists no specific training for the Identifiler kit of the 3130 Genetic Analyzer, although she does list one course for “Genemapper X”. She indicates that from October 2002 to October 2007 she worked at Orchid Cellmark doing “[n]o-suspect and [s]uspect casework.” (Exh. 18). As in *Venegas*, these qualifications may qualify her to testify to the procedures she used in this case , but they do not qualify her to testify about molecular biology, to make estimates of population frequencies, or to establish that a biological methodology or an estimation procedure is valid evidence or generally accepted..

In addition, the forensic DNA community requires that all DNA analysts adhere to rigorous continuing education requirements. *See* Exh, 3*,* FBI Quality Assurance Standards, Standard 5.1.3.1 (“The technical leader, casework CODIS administrator, and analyst(s) shall stay abreast of developments within the field of DNA typing by attending seminars, courses, professional meetings or documented training sessions/classes in relevant subject areas at least once each calendar year. A minimum of eight cumulative hours of continuing education are required annually and shall be documented.”) It is unclear from the documents provided whether

this requirement has been met.

The importance of the continuing education requirement cannot be overemphasized in the rapidly developing and ever-changing field of forensic DNA STR analysis. As the California Supreme Court emphasized in *People v. Soto* (1999) 21 Cal.4th 512, 540 n.31, “(i)n the context of rapidly changing technology, every effort should be made to base (decision) on the very latest scientific opinions...” . The Identifiler kit used in this case was not even introduced into the marketplace until 2001, and many of the scientific articles documenting the pitfalls of the kit are just now beginning to appear, as demonstrated below. Knowledge of the current state of this literature is obviously crucial in *Daubert* litigation, where an expert is being asked to opine on whether deviation from a relatively new and untested protocol has any significance on the result. In the words of the NRC II, a qualified analyst must have “a thorough understanding of the principles, use, and limitations of methods and procedures applied to the tests performed.” NRC II at 76 (emphasis added).

Finally, no discussion of lack of prong one or three qualifications would be complete without a discussion of bias. As indicated in NRC II, “(b)ias in forensic science usually leads to sins of omission rather than commission. Possibly exculpating evidence might be ignored or rejected. Contradictory test results or evidence of sample mixture may be discounted. Such bias is relatively easy to detect if test results are reviewed critically.” NRC II pg. 84-85. *See also*, *People v. Pizarro* (1992) 10 Cal.App.4th 57, 78 (“The only testimony regarding the procedures employed by the FBI in the present case was presented by an FBI agent who had been assigned to the DNA unit since its inception. Prior to admitting testimony as potentially damaging as DNA

forensic identification, the prosecutor should have been required to demonstrate through the testimony of at least one impartial expert witness that the protocols and/or procedure of the FBI were generally accepted within the scientific community as reliable.”).

# Numerous Statistical Flaws Render the DNA Evidence in this Case Inadmissible under Rules 402, 403, and 702, as Well as under D*aubert* and the Due Process, Fair Trial, and Cruel and Unusual Provisions of the Fifth, Sixth, and Eighth Amendments to the Constitution.

# Introduction.

John McCluskey brings the present motion to exclude any incriminating DNA test results under *Daubert v. Merrell Dow Pharmaceuticals*, 509 U.S. 579, 113 S.Ct. 2786, 125 L.Ed.2d 469 (1993), Federal Rules of Evidence 402, 403, and 702 , and under the Fifth, Sixth, and Eighth Amendments to the Constitution which, in death penalty cases, “places special constraints on the procedures used to convict an accused of a capital offense and sentence him to death” and “ requires a ‘greater degree of reliability’ when it is imposed.” *Murray v. Giarratano*, 492 U.S. 1, 8-9, 109 S.Ct. 2765, 106 L.Ed.2d 1 (1989) (internal citations omitted). *See also*, *Monge v.*

*California*, 524 U.S. 721, 732, 118 S.Ct. 2246, 141 L.Ed.2d 615 (1998) (observing that there is an “acute need for reliability in capital sentencing proceedings”); *Ege v. Yukins,* 485 F.3d 364 (6th Cir. 2007)(bitemark testimony which included unfounded statistical analysis was so unreliable that defendant's conviction violated due process)*;United States v. Green*, 405 F.Supp.2d 104, 109 (D.Mass.2005)(“While I recognize that the *Daubert-Kumho* standard does not require the illusory perfection of a television show (CSI, this wasn't), when liberty hangs in the balance-and, in the case of the defendants facing the death penalty, life itself-the standards should be higher than were met in this case...”). 55

55 It goes without saying that the rule that there must be a “greater degree of reliability” in the procedures used to convict an accused of a capital offense and sentence him to death does not apply to the admissibility of evidence used by the defendant in a sentencing phase to convince a jury not to sentence him to death. Under the Eighth Amendment, there is a “low threshold” standard for the admissibility of defense evidence, and “ ‘[v]irtually no limits are placed on the relevant mitigating evidence a capital defendant may introduce” at a penalty phase. *Tennard v.*

*Dretke*, 542 U.S. 274, 124 S.Ct. 2562, 159 L.Ed.2d 384 (2004). By bringing this motion, Mr. McCluskey does not in any way suggest what evidence may or may not be admissible at a sentencing phase should the case go that far. Consideration of that issue would be premature at this time, but Mr. McCluskey reserves the right to offer any and all mitigating evidence should

While Mr. McCluskey has a host of valid objections to how and by whom the DNA testing itself was conducted in this case, he focuses first not on the testing methodology, but on five specific objections which relate to the statistical aspects of the proposed testimony and bear special emphasis at the outset.

First, in the absence of scientifically reliable statistics, evidence that Mr. McCluskey’s, or his former co-defendants’, or the decedents’, DNA profile is “consistent with” the DNA profile of an evidentiary sample, or that such persons “cannot be eliminated” as a “possible” contributor to the sample is unreliable, speculative, irrelevant, and more prejudicial, misleading, and confusing than probative and thus any testimony about these particular samples is inadmissible under rules 402, 403, and 702, as well as under *Daubert* and the due process, fair trial, and cruel and unusual provisions of the fifth, sixth, and eighth amendments to the constitution.

Second, any testimony tracking the language of the reports summarized above about that Mr. McCluskey, or another person involved in this case, is the source of the DNA in any evidentiary sample is inadmissible under Rules 402, 403, and 702, as well as under D*aubert* and the due process, fair trial, and cruel and unusual provisions of the Fifth, Sixth, and Eighth Amendments to the Constitution because there is no reliable or generally accepted method for uniquely identifying a DNA sample to its source (“source attribution”).

Third, the probability of inclusion frequencies for samples 1B22d, 1B72B, and 31e are irrelevant, and more prejudicial, misleading, and confusing than probative and thus any testimony about these particular samples is inadmissible under rules 402, 403, and 702, as well as under *Daubert* and the due process, fair trial, and cruel and unusual provisions of the fifth, sixth, and eighth amendments to the constitution.

Fourth, the failure to include in the statistics any measure of laboratory error rate renders the testimony inadmissible.

Lastly, the improper restriction of the statistics to African Americans, Apaches,

the case reach a sentencing phase.

Caucasians, Navajos, and Southwestern Hispanics renders any statistical probability calculation inadmissible.

# In the Absence of Scientifically Reliable Statistics, Evidence That Mr. McCluskey’s, Or His Former Co-Defendants’, Or The

**Decedents’, DNA Profile Is “Consistent With” the DNA Profile of an Evidentiary Sample, or That Such Persons “Cannot Be Eliminated” as a “Possible” Contributor to the Sample is Is Unreliable, Speculative, Irrelevant, and More Prejudicial, Misleading, and Confusing than Probative and Thus Any Testimony about These Particular Samples Is Inadmissible under Rules 402, 403, and 702, as Well as under D*aubert* and the Due Process, Fair Trial, and Cruel and Unusual Provisions of the Fifth, Sixth, and Eighth Amendments to the Constitution.**

Evidence that Mr. McCluskey’s, or his former co-defendants, or the decedents, DNA profile is "consistent" with the DNA profile of evidentiary samples in this case, or that such persons “cannot be excluded” as a “possible” contributor to the DNA in a sample, is impossible to understand and evaluate without statistics. As Judge Vasquez explained in *United States v.*

*Coronado-Cervantes*, 912 F.Supp. 499, 500 (D.N.M.1996):

When the laboratory work is completed and a DNA profile from a suspect has been declared to match the DNA profile of the perpetrator, it means the suspect cannot be *excluded* as a possible contributor of the DNA found at the crime scene. Statistics must then be generated to give significance to the match by demonstrating how probable it is that a random match could occur, i.e., that the suspect's DNA profile and the perpetrator's DNA profile would match if they were not the same person.

As the California Supreme Court succinctly explained the issue, the value of such evidence depends on the statistical probability of finding a "consistent" profile in the general population:

A determination that the DNA profile of an evidentiary sample matches the profile of a suspect establishes that the two profiles are consistent, but the determination would be of little significance if the evidentiary profile also matched that of many or most other human beings. The evidentiary weight of the match with the suspect is therefore inversely dependent upon the statistical probability of a similar match with the profile of a person drawn at random from the relevant population.

*People v. Venegas*, 18 Cal.4th 47, 82, 954 P.2d 525, 548-9 (1998). See also, *United States v. Davis*, supra (Citing this passage from *Venegas*, “[t]he Court agrees that DNA evidence cannot be admitted in a vacuum; the Government must also present some additional information with

which a jury can accurately assess the significance of the consistency between a defendant’s DNA profile and that of the evidence.”)

As was held in *Davis*, to determine whether the DNA evidence in this case deserves great weight, little weight, or no weight at all, the jury must have statistical data on the probability of finding the "consistent" profile in relevant reference populations.56 "Without the probability assessment, the jury does not know what to make of the fact that the patterns match: the jury does not know whether the patterns are as common as pictures with two eyes, or as unique as the Mona Lisa." *United States v. Yee*, 134 F.R.D. 161, 181 (N.D. Ohio 1991), aff'd. sub nom. *United States v. Bonds*, 12 F.3d 540 (1993). *See also*, *United States v. Morrow*, 374 F.Supp.2d 51, 63 (D.D.C.2005)(“Without statistical data on the frequency of the matching characteristics in the relevant reference population ... the jury was left to speculate about the value of the DNA evidence.”).

In the vast majority of federal cases in which DNA evidence has been admitted, the evidence of a DNA match is accompanied by statistical information. *See*, e.g., *United States v. Wright*, 215 F. 3d 1020, 1025 (9th Cir. 2000)(“the probability that the DNA of a Black individual selected at random would match the DNA recovered from the crime scene was approximately one in 1.3 billion); *United States v. Davis*, 40 F.3d 1069, 1073 (10th Cir.1994)(RFLP expert “based her testimony on population genetics and stated that the frequency of such random matches among African–Americans to be 1 in 30,000 for Mr. Davis and 1 in 600,000 for Mr.

Reed.”); *United States v. Ewell*, 252 F.Supp.2d 104, 113 n. 12 (D.N.J.2003)("the probability of a random DNA match is one in 280 million"); *United States v. Gaines*, 979 F.Supp. 1429,

1431-32 (S.D. Fla. 1997) (probability of random match ranged from 1 in 6.1 million to 1 in 170

million); *United States v. Lowe*, 954 F.Supp. 401, 416-17, 420-21 (D.Mass.1996) (match

56 To illustrate the point, consider the value of evidence that a bloodstain at a crime scene and defendant’s blood are “consistent” in that both contain hemoglobin. Such evidence would be worthless for proving defendant was the blood donor because all human blood contains hemoglobin.

probability ranged from 1 in 11 billion for the Caucasian population to 1 in 810,000 for the same population);*United States v. Shea*, 957 F.Supp. 331, 335 (D.N.H.1997), aff'd, 159 F.3d 37

(1998), cert. denied, 526 U.S. 1077, 119 S.Ct. 1480, 143 L.Ed.2d 563 (1999)(probability of random match in Caucasian population was 1 in 200,000).

The necessity of using statistics to explain the value of DNA evidence has been widely acknowledged. As the Tenth Circuit has stated, “statistical probabilities are basic to DNA analysis and their use has been widely researched and discussed.” *United States v. Davis*, 40 F.3d 1069, 1075 (10th Cir.1994). A number of legal commentators have suggested that the admissibility of DNA evidence depends on having scientifically valid statistics on the frequency of the matching DNA profiles. *See* e.g. David L. Faigman, et al., 4 Mod. Sci. Evidence § 30:14 (201 edition)(“Unless some reasonable explanation accompanies testimony that two profiles match, it is surely arguable that the jury will have insufficient guidance to give the scientific evidence the weight it deserves.”); Kenneth S. Broun , 1 McCormick On Evidence, Sec. 210 (6th ed. 2006)("[W]ithout being informed of such background statistics, the jury is left to its own speculations").

Scientific experts have also declared that numbers are necessary to give meaning to DNA evidence. NRC I was adamant about the need to present statistics in connection with DNA evidence :

Interpreting a DNA typing analysis requires a valid scientific method for estimating the probability that a random person might by chance have matched the forensic sample at the sites of DNA variation examined. A judge or jury could appropriately weigh the significance of a DNA match between a defendant and a DNA sample if told, for example, that "the pattern in the forensic sample occurs with a probability that is not known exactly but is less than 1 in 1000"...To say that two patterns match, without providing any scientifically valid estimate (or, at least an upper bound) of the frequency with which such matches might occur by chance, is meaningless...DNA "inclusions" cannot be interpreted without knowledge of how often a match might be expected to occur in the general population.

NRC I, supra, at p. 74-75.

Like its predecessor, NRC II declared that "[i]t would not be scientifically justifiable to

speak of a match as proof of identity in the absence of underlying data that permit some reasonable estimate of how rare the matching characteristics actually are." Id. at p. 192. "Certainly, a judge's or juror's untutored impression of how unusual a DNA profile is could be very wrong. This possibility militates in favor of going beyond a simple statement of a match, to give the trier of fact some expert guidance about its probative value.". (Id. at p. 193) 57

The NAS 2009 Report specifically recognized the problem with the kinds of opinions being offered in this case:

The terminology used in reporting and testifying about the results of forensic science investigations must be standardized. Many terms are used by forensic scientists in scientific reports and in court testimony that describe findings, conclusions, and degrees of association between evidentiary material (e.g., hairs, fingerprints, fibers) and particular people or objects.

Such terms include, but are not limited to “match,” “consistent with,” “identical,” “similar in all respects tested,” and “cannot be excluded as the source of.” The use of such terms can and does have a profound effect on how the trier of fact in a criminal or civil matter perceives and evaluates scientific evidence.

(NAS 2009 Report, p. 21)

The Report concludes that “[t]he concept of individualization is that an object found at a crime scene can be uniquely associated with one particular source. By acknowledging that there can be uncertainties in this process, the concept of ‘uniquely associated with’ must be

replaced with a probabilistic association, and other sources of the crime scene evidence cannot be

57 NRC II discusses the use of *qualitative* terms such as "rare" or "extremely rare" to characterize DNA evidence. However, this discussion presumes that a scientifically valid quantitative estimate has actually been made. In other words, NRC II considers the possibility that an expert might use non-quantitative language to explain the statistical estimates to the jury. However, NRC II argues against the use of qualitative testimony in most cases on grounds that it is vague and subject to misinterpretation.

Except for strong claims of uniqueness, purely qualitative presentations suffer from ambiguity. Professional forecasters, physicians, science writers, students, and soldiers show high variability in translating verbal probability expressions to numerical expressions [citations omitted]. Judges and jurors are likely to show similar variability in interpreting the meaning of such verbal expressions. To help a court or jury to understand the importance of a match, most experts provide quantitative, rather than qualitative, estimates of the frequency of an incriminating profile in one or more races, or an upper bound on the frequency. (Id. at p. 195).

completely discounted.” *See also*, John Butler, Fundamentals, p. 230 ("Statistics attempt to provide meaning to the match.”).

Indeed, the NM DPS DNA/Serology SOP itself states: “Reports will contain a statement assessing whether particular individuals can or cannot be eliminated as possible contributors of the evidence. In cases where a particular person cannot be eliminated as a contributor of the DNA profile obtained from an evidence sample, the laboratory report shall contain a statement about the frequency of occurrence.” (Exh.7, p. 14-1)

Although the issue has not arisen in the Tenth Circuit, appellate courts in other jurisdictions have considered whether DNA evidence is admissible in the absence of statistical data. With very few exceptions, courts have required that statistics be presented as a condition of admissibility. For example, in *United States v. Porter*, 618 A.2d 629 (D.C. 1992) the Court of Appeals addressed the admissibility of evidence of a "match" between a suspect's DNA profile and an evidence sample profile. The Court of Appeals noted that, because a person's forensic DNA profile is made up only of a limited number of genetic markers out of the millions of DNA sequences in a person's entire DNA strand, it is possible for two people to coincidentally have the same profile. 618 A.2d at 632. Accordingly, the court held that DNA match evidence is not probative without an estimate of the chance that the match is merely coincidental. Because jurors lack the scientific knowledge to assess the likelihood of a coincidental match, DNA match "evidence is probative" only if accompanied by an accurate statistical estimate of the "probability of a coincidental match." 618 A.2d at 631. This estimate must be generally accepted within the scientific community pursuant to *Frye v. United States* as accurately expressing the statistical significance of the match. Id.

Numerous other courts agree. *See e.g.*, *State v. Wright*, 360 Mont. 246, 255, 253 P.3d 838, 844 (2011)(“Without reliable accompanying evidence as to the likelihood that other individuals in a given population could be a match (or could not be excluded as possible contributors), the jury has no way to evaluate the meaning of the result.”); *Commonwealth v.*

*Mattei*, 455 Mass. 840, 920 N.E.2d 845 (2010)(reversible error to admit expert testimony that the defendant could not be excluded as a potential source of DNA found at the crime scene unless there was accompanying testimony explaining the statistical significance of those non-exclusion results); *Deloney v. State*, 938 N.E.2d 724, 730 (Ind.App. 2010)(“DNA evidence that does not constitute a match or is not accompanied by statistical data regarding the probability of a defendant's contribution to a mixed sample is not relevant, Evid. R. 402, and should not be admitted.”); *People v. Coy*, 243 Mich. App. 283, 620 N.W.2d 888 (2000) (plain error to present a DNA match in a mixed stain without a qualitative or quantitative estimate of its significance); *Peters v. State*, 18 P.3d 1224 (Alaska Ct. App. 2001) (error to introduce "consistent with" testimony for mixed stains unaccompanied by any further indication of probative value) . 58

58 See also, *State v. Williams,* 574 N.W.2d 293, 298 (Iowa 1998) ("We agree with the NRC Report which stated ‘[t]o say that two [DNA] patterns match, without providing any scientific valid estimate . . . of the frequency with which such matches might occur by chance, is meaningless.’"); *Murray v. State*, 692 So. 2d 157, 162 (Fla. 1997)(fact that a DNA match is found may be meaningless without estimates demonstrating the significance of the match); *Hull*

*v. State*, 687 So.2d 708 (Miss. 1996) ("'the ultimate results of DNA testing would become a matter of speculation' without statistical evidence"); *State v. Carter*, 246 Neb. 953, 984, 524 N.W.2d 763, 783 (1994)("[W]e hold that evidence of a DNA match will not be admissible if it has not been accompanied by statistical probability evidence that has been calculated from a generally accepted method") *Nelson v. State*, 628 A.2d 69 76 (Del. 1993)(trial court's exclusion of match frequency "inherently inconsistent" with its admission of testimony of a match, because "without the necessary statistical calculations, the evidence of the match was 'meaningless' to the jury.");*State v. Cauthron*, 120 Wash. 2d 879, 907, 524 N.W.2d 763, 783, 846 P.2d 502, 516 (1993)("[T]estimony of a match in DNA samples, without the statistical background or probability estimates, is neither based on a generally accepted scientific theory nor helpful to the trier of fact."); *State v. Vandebogart*, 616 A.2d 483, 494 (N.H. 1992)("A match is virtually meaningless without a statistical probability expressing the frequency with which a match would occur."); *People v. Barney*, 8 Cal.App.4th 798, 817, 10 Cal.Rptr.2d 731, 742 (Cal.App. 1992)("The statistical calculation step is the pivotal element of DNA analysis, for the evidence means nothing without a determination of the statistical significance of a match of DNA patterns."); *Ex Parte Perry*, 586 So.2d 242, 254 (Ala. 1991)(“Stated simply, the evidence necessary to show a ‘match’ does not by itself indicate the frequency with which a given DNA pattern might occur statistically or might occur in a given population; to establish population frequency generally requires data on the relevant populations involved as well as data for the mathematical, statistical analysis.”); *Commonwealth v. Curnin*, 409 Mass. 218, 222 n. 7, 565

In the present case, as outlined above, no statistical estimates have been made with respect to many samples in this case. Consequently, there is no scientific basis for any claim about the probative value of the DNA evidence on these samples and no foundation for any expert testimony about these samples. In the absence of a scientifically valid statistical estimate, the value of the proposed testimony about these samples is entirely speculative.

Morever, the very form of the opinions stated in the reports about these samples (“consistent with”; “cannot be excluded as possible contributors”) should dictate their exclusion since they are framed in such speculative terms they cannot possibly assist the trier of fact. The Supreme Court held in *Daubert I*, 509 U.S. at 590-91, 113 S.Ct. at 2795- 96, that Rule 702 requires “the trial judge must ensure that any and all scientific testimony or evidence admitted is not only relevant, but reliable.” The Court also made clear that “Rule 702 further requires that the evidence or testimony ‘assist the trier of fact to understand the evidence or to determine a fact in issue.’ This condition goes primarily to relevance.” (Id. at 599). The Court also emphasized that the phrase “scientific ...knowledge” in Rule 702 “connotes more than subjective belief or unsupported speculation.” (Id. at 590)

Under this standard, the Ninth Circuit held in *Daubert v. Merrell Dow Pharm*., 43 F.3d 1311, 1313 (9th Cir.1995) (*Daubert II* ) that expert testimony offered to prove causation did not satisfy the relevance requirement because the evidence suggested only that use of the drug at issue "could possibly have caused plaintiffs' injuries," rather than "more likely than not" caused the injuries, i.e., that use of the drug more than doubled the likelihood the injuries would occur. 43 F.3d at 1320-22. The Court also held that "(f)ederal judges must... exclude proffered scientific evidence under Rules 702 and 403 unless they are convinced that it speaks clearly and directly to an issue in dispute in the case, and that it will not mislead the jury." Id. at 1321 n. 17.

N.E.2d 440 (1991)(in a criminal trial a trial court may “not permit the admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring.”)

Similarly, in *Hull v. Merck & Co., Inc.*, 758 F.2d 1474, 1477 (11th Cir.1985) (per curiam) the Eleventh Circuit found that admission of speculative and "potentially confusing testimony is at odds with the purposes of expert testimony as envisioned in Fed.R.Evid. 702."

In *Bryte v. Am. Household, Inc.*, 429 F.3d 469, (4th Cir. 2005) the Fourth Circuit reached the same result, ruling that an arson expert was properly prohibited from expressing an opinion as to the cause of a fire because he did not, consistent with the standards of his profession, exclude “[a]ll other reasonable origins and causes” . The court was guided by the principle that “*Daubert* aims to prevent expert speculation, and our review of the record convinces us that [the expert’s failure to address alternative explanations] cannot be reconciled with the reliability mandate.” (Id. at 477).

In *Heaps v. General Motors Corp.*, 2006 WL 2456231 (D.Md.2006), a district court has cited *Bryte* in support of a ruling that an expert’s speculative opinion is inadmissible under Rule 702: “the opinion offered by [the expert] is speculative. Instead of opining that the car's intermittent failure to start *is* indicative of a manufacturing defect, [the expert] opines that this condition "*can* be indicative of a defect in materials and workmanship." ...By merely opining that it is *possible* that Plaintiff's car is defective, [the expert] is engaging in speculation and conjecture with respect to whether the car is *in fact* defective. As a result, [the expert’s] opinion would not assist the trier of fact to understand the evidence in this case or to determine facts in issue.

Accordingly, this Court concludes that the opinion offered by [the expert] is inadmissable under Fed.R.Evid. 702.” *Heaps v. General Motors Corp.*, 2006 WL 2456231, \*5 (D.Md.2006).

Similarly, speculative opinions about the origin of DNA samples do not qualify as “scientific...knowledge” within the meaning of Rule 702 because “ the word ‘knowledge’ connotes more than subjective belief or unsupported speculation.” *Daubert v. Merrell Dow Pharm*., 509 U.S. at 590-91.

Numerous other courts have also prohibited speculative opinions in a variety of contexts, including speculative opinions by DNA experts. *See* e.g., *United States v. Frazier*, 387 F. 3d

1244, 1265 (11th Cir. 2004) (opinion of expert properly excluded where the "probability it expresses is unclear, imprecise, and ill defined."); *United States v. Natson*, 469 F.Supp.2d 1253, 1258 (M.D.Ga. 2007)(“The only conclusion that Weiss can reach from his testing is that the Defendant is ‘possibly’ the father. The possibility that Defendant is the father may be higher than others at 26 to 1, but it does not rise to any reasonable level of scientific certainty. It would be sheer speculation for a jury to determine from Weiss's testimony that Defendant is the father.

Therefore, the Court finds that the testimony is not relevant and would not assist the trier of fact. Accordingly, it is not admissible under Federal Rules of Evidence 702, 401, and 402.”); *United States v. Rutherford* (D. Neb. 2000) 104 F. Supp. 2d 1190 (testimony of handwriting expert that defendant "very probably" authored a document was too speculative to be admissible.)

In light of the speculative nature of the opinions being offered with respect to numerous samples, the probative value of his testimony is nonexistent. Furthermore, whatever slight probative value there is to such speculative testimony is clearly outweighed by the danger that the jury will place undue reliance on such speculation.

As described below, at least two district courts have excluded DNA evidence on Rule 403 grounds even where weak statistical evidence was offered in support of a DNA match. *See*, *United States v. Natson*, 469 F.Supp.2d 1253 (M.D.Ga. 2007); *United States v. Graves*, 465 F.Supp.2d 450, 459 (E.D.Pa. 2006). Here, the statistics are not just weak, they are non-existent.

There is thus even greater reason than there was in *Natson* and *Grave* to exclude the testimony under Rule 403. *See also*, *United States v. Shea*, 957 F.Supp. 331, 345-346 (D.N.H.1997) (“Random match probability estimates calculated with the product rule provide an important means of placing the significance of a DNA profile match in an appropriate context *When the*

*significance of a random match probability estimate is properly explained*, the probative value of the evidence is not substantially outweighed by the limited potential that jurors could be misled.”)(emphasis added); *Commonwealth v. Mattei*, 455 Mass. 840, 852, 920 N.E.2d 845 (Mass.2010)(“[A]dmitting evidence of a failure to exclude without accompanying evidence that

properly interprets that result creates a greater risk of misleading the jury and unfairly prejudicing the defendant than admission of a ‘match’ without accompanying statistics.”)..

Here, in the absence of scientifically reliable statistics, evidence that Mr. McCluskey’s, or his former co-defendants’, or the decedents’, DNA profile is “consistent with” the DNA profile of an evidentiary sample, or that such persons “cannot be eliminated” as a “possible” contributor to the sample is unreliable, speculative, irrelevant, and more prejudicial, misleading, and confusing than probative and thus any testimony about these particular samples is inadmissible under rules 402, 403, and 702, as well as under *Daubert* and the due process, fair trial, and cruel and unusual provisions of the fifth, sixth, and eighth amendments to the constitution.

# Expert Testimony That Mr. McCluskey, Or Another Person Involved In This Case, is the Source of the DNA In Any Evidentiary Sample is Impermissible Because Statistical Estimates Associated with the DNA Evidence - Not Inferences about the Meaning of Those Estimates and Ultimate Opinion Testimony - Are at the Core of DNA Match Evidence’s Admissibility and Presentation Before the Jury.

* + 1. **Introduction**.

As indicated above, it is apparent that the government proposes to have its DNA analyst render an opinion that Mr. McCluskey is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B22A, 1B22B, 1B22C, 1B39A , 1B13, 1B14C, 31a, 31g, and 1B22E to the exclusion of all other people in the world. The government also proposes to have its DNA analyst render an opinion that Mr. Province is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B23B and item T-7A to the exclusion of all other people in the world, and that Ms. Welch is the “source” of the “major” DNA mixed or single profile in evidentiary items 1B57 to the exclusion of all other people in the world. See, NAS 2009 Report at 43 (“[A] conclusion of individualization implies that the evidence originated from that source, to the exclusion of all other possible sources.”)

The government's request that its expert be allowed to opine that someone *is* the source of certain DNA evidence in this case to the exclusion of everyone else in the world should be summarily denied because such an opinion will not be helpful to the trier of fact, it does not

concern reliable “scientific, technical, or other specialized knowledge” within the meaning of Rule 702 and *Daubert*, and it is more prejudicial, misleading, and confusing than probative under Rule 403. Indeed, such an opinion is inherently unscientific because , as *Daubert* teaches, “there are no certainties in science”, and “scientists do not assert that they know what is immutably ‘true’-they are committed to searching for new, temporary, theories to explain, as best they can, phenomena”. (*Daubert*, supra, 509 U.S. at 590.) . See also NAS 2009 Report at 116 (“Scientific data and processes are subject to a variety of sources of error.”). Butler, Advanced Topics, supra (“Limitations exist in our ability to measure anything. We can never be 100% certain in science.”). Consequently, “DNA evidence of a ‘match’ is only admitted with statistical evidence of the probability of a coincidental match, not as a definitive statement.” *United States v. Green*, 405 F.Supp.2d 104, 109 n. 4 (D.Mass.2005).59 See also, *United States v. Williams*, 2010 WL 188233 \* 3 (E.D.Mich. 2010)(“DNA analysis, as with most scientific inquiries, is about probabilities, not absolutes.”)

Further, aided by reliable and admissible statistical analysis, it is up to the jury to decide whether anyone is in fact the person whose DNA was on certain objects or whether the fact that the person’s DNA profile is consistent with the crime scene profile is due to coincidence or some laboratory error. These ultimate issues are factual and legal, not scientific. As was stated by one

59 Like the government in this case, the government in *Green* proposed to have an expert (there, a firearm’s examiner) testify that evidence of a firearm match was to the exclusion of all other weapons in the world. Judge Gertner rejected the proposed testimony under *Daubert* and Rule 702: “I will not allow [a firearm’s examiner] to conclude that the shell casings come from a specific Hi Point pistol ‘to the exclusion of every other firearm in the world.’ That

conclusion-that there is a definitive match-stretches well beyond [the expert’s] data and methodology.” 405 F.Supp.2d at 109 n. 4 In so concluding, the judge specifically analogized firearm identification testimony to DNA testimony, and emphasized the point that even in DNA testing , experts are confined to providing statistics and are not allowed to attribute a DNA sample to its source. (Id. at n. 4). Five other district courts have followed *Green* on this point.

See, *United States v. Willock*, 696 F.Supp.2d 536 (D.Md.2010)(same); *United States v. Taylor*, 663 F.Supp.2d 1170 (D.N.M. 2009)(same); *United States v. Glynn*, 578 F. Supp 2d 567 (S.D.N.Y. 2008)(same); *United States v. Diaz*, 2007 WL 485967(N.D.Cal. 2007)(same); *United States v. Monteiro*, 407 F.Supp.2d 351(D. Mass. 2006) (same).

district court, “[e]vidence supplied by experts as to legal conclusions is not admissible, ‘nor indeed ‘evidence’ at all.” *Safeway, Inc. v. Sugarloaf Partnership, LLC.*423 F.Supp.2d 531, 539 (D.Md.2006) *See also*, *United States v. Cooper*, 482 F.3d 658, 664 (4th Cir. 2007)(“[T]he trial court must take care... not to encroach upon [the jury’s] fact-finding power.”); *Steele v. D.C. Tiger Market*, 854 A.2d 175, 181 (D.C. 2004)( "[E]xpert testimony is admissible to help the jury to do its work and not to do the jury's work for it."). Rules 403 and 702 “afford ample assurances against the admission of opinions which would merely tell the jury what result to reach...”. (Advisory Committee Notes to Rule 704).

The present argument (in contrast to others raised herein) does not seek to exclude the government's DNA evidence for the above-enumerated samples ; rather, it merely seeks to prevent the government from reporting the testing results in court in such a novel, prejudicial, and conclusory manner. Nor, given the clarity of the law and of the general view of scientists that a source attribution statement is legal and not scientific in nature, does Mr. McCluskey believe the Court should grant the government a *Daubert* hearing as to this issue. As the proponent of the scientific evidence, the government bears the burden to prove its proposed evidence is admissible. The government cannot carry its burden on this issue.

# The Vast Majority of Scientific and Legal Authorities Reject the Government Expert's Claimed Ability to Make a "Source Attribution" Statement on the Basis That Such an Inference Is Not Grounded in Reliable Science and must Be Left to Jurors Provided with the Tools of DNA Match Frequency Estimates.

As will be explored in more depth below, and as stated in the declaration of population geneticist Dr. Laurence D. Mueller, PhD (Exhibit CD, Exhibit 19)

Testimony that a particular person is the source of a DNA evidentiary sample is not based upon sufficient facts or data and is not the product of reliable scientific principles and methods. The usual assumption underlying this type of testimony is that source attribution is justified when the random match probability is greater than about 1 in 300 billion. However, the arguments I make below could be applied to any arbitrary limit chosen to declare source attribution. Ultimately, there is no scientific basis to support any quantitative limit as sufficient to declare uniqueness given our current empirical understanding of this problem.

As Dr. Mueller makes clear, the prevailing practice among scientists, endorsed as a legal matter in the numerous cases cited above, is to provide the best available probability statistics to jurors about how much weight to give to the reported DNA match, and to let the jurors make their own decisions. Indeed, most scientists consider testimony opining that a particular person is, as a matter of scientific expertise, the source of forensic DNA evidence to be a subjective, non-scientific opinion that must be avoided.

The government's request here relies upon the FBI's practice. At a 1997 conference, the FBI pronounced, "[t]he time for source attribution has come," and stated that henceforth its analysts would provide source attribution statements. The FBI reasoned that, "attorneys may question and judges may decide the weight of these determinations, but it is within the purview of the scientist to report and opine the identification." Jennifer A.L. Smith & Bruce Budowle, *Source Identification of Body Fluid Stains Using DNA Profiling*, available at <http://www.promega.de/geneticidproc/eusymp2proc/18.pdf.60> Because statistical "estimates ha[ve] approached the point where it is unlikely that two unrelated individuals carry the same type," Bruce Budowle, et al., *Source Attribution of a Forensic DNA Profile*, 2 Forensic Sci.

Communications1(July2000), available a[t http://www.fbi.gov/hq/lab/fsc/backissu/july2000](http://www.fbi.gov/hq/lab/fsc/backissu/july2000)

/source.htm (emphasis added), when the threshold [of 1 in 280 billion]61 is surpassed, a source

60 Shortly thereafter, the FBI published its position in its online journal. *See* Bruce Budowle, et al., Source Attribution of a Forensic DNA Profile, 2 Forensic Sci. Communications (July 2000), available a[t http://www.fbi.gov/about-us/lab/forensic-science-communications](http://www.fbi.gov/about-us/lab/forensic-science-communications)

/fsc/july2000/source.htm/backissu/july2000/source.htm; *See also Statistical and Population Genetics Issues Affecting the Evaluation of the Frequency of Occurrence of DNA Profiles Calculated From Pertinent Population Database(s)*, 2 Forensic Sci. Communications (July 2000), (endorsing source attribution statements if, unlike here, calculation accounts for all potential contributors, such as world population and relatives).

61 The FBI uses 280 billion because that figure was, at one time, one thousand times the population the U.S. population. The current population of the U.S. is 304,000 million; the current world population is 6.6 trillion. *See*[, http://www.census.gov/ipc/www](http://www.census.gov/ipc/www)

/idb/worldpopinfo.html.

attribution "statement will be used in FBI Laboratory reports replacing the statement which provided the actual probabilities associated with selecting an unrelated individual at random from the specific populations. The frequency calculations will be maintained in the case notes and will be provided, if needed for discovery purposes." FBI Laboratory, Short Tandem Repeat Analysis Protocol 10-10 (Apr. 1, 2002)

The FBI's policy position was immediately, and has since been consistently, assailed by the scientific community. 62 Forensic scientists and academicians note that the FBI's decision to infer source attribution from even small probabilities of coincidence cannot be a scientific opinion, as it requires a "leap of faith" and a (non-scientific) subjective belief in the accuracy of the statement. For instance, Dr. Norah Rudin and Keith Inman - each who worked with the California Department of Criminal Justice and are frequent collaborators with law enforcement laboratories - summarize the FBI's position and observe that “many laboratories have been understandably reluctant to make this leap. Opposition has also come from members of the academic statistical genetics community who argue that the FBI ‘identity calculation’ is incorrect and makes unwarranted assumptions, particularly about subpopulations and close relatives.” Norah Rudin & Keith Inman, An Introduction to Forensic DNA Analysis 151 (2d ed. 2002).

Rudin and Inman go on to distinguish the role of the scientist (in presenting the statistical estimates) and the fact finder (in inferring the evidentiary meaning of those estimates):

62 The FBI's policy is also inconsistent with both NRC reports that predated it and the one that followed it. Both pre-policy NRC reports put the question of source attribution outside the realm of scientists and question where and how the courts can draw the line to permit evidentiary arguments of uniqueness. *See* NRC I at 92 ("Regardless of the calculated frequency, an expert should - given the relatively small number of loci used and the available population data - avoid assertions in court that a particular genotype is unique in the population."); NRC II at 33, 92 (concluding that source attribution statements were subjective in nature and "outside our province" as "[t]here is no "bright-line" standard in law or science that can pick out exactly how small the probability of the existence of a given profile in more than one member of a population must be before assertions of uniqueness are justified").

It is the purview of the fact finder to draw inferences from circumstantial evidence, and, of course, potentially individualizing physical evidence is circumstantial evidence. However, there are pieces of information that only science can legitimately provide to the fact finder, such as population frequencies, transfer and persistence data, and limitations of the evidence and the test.

Keith Inman & Norah Rudin, Principles and Practice of Criminalistics: the Profession of Forensic Science (2001).

Forensic scientist Dr. John Buckleton - the Principal Scientist at ESR in New Zealand (the New Zealand equivalent of the FBI) and a frequent testifier and trainer in the United States - also discusses in his treatise whether science enables source attribution statements for DNA evidence. Like Rudin and Inman, Dr. Buckleton concludes that the expression of such an opinion is a "leap of faith" that goes beyond the bounds of science:

To conclude the same source from a probabilistic model, someone has to decide that the probability estimate produced by that model at this extreme end of extrapolation is sufficiently reliable that it can be trusted and the probability is sufficiently small that it can be ignored.

. . . [T]his [is] the "leap of faith."

John Buckleton, *Population Genetic Models*, in John Buckleton, Christopher M. Triggs & Simon Walsh, Eds., Forensic DNA Evidence Interpretation 105 (2005). After critiquing the FBI's policy, Dr. Buckleton, concludes:

[W]e would be unwise to conclude the same source because it is not our place to do so. If we do so, I would prefer the standard to be much higher than previously suggested AND I would like us to make transparent that we have subjectively decided to round a probability ESTIMATE off to zero. On balance I cannot *See* much positive coming from a policy of declaring a common source.

*Id*. at 109 (capitalization emphases in original).

On this question, practicing forensic scientists stand shoulder-to-shoulder with academic statisticians, knowledgeable about DNA forensics, who consider the government's proposed statement to be non-scientific and wrong. As just one example from the published literature,

some of the sharpest criticism of the FBI's presentation of source attribution testimony comes from Dr. Bruce Weir, a nationally recognized leader in applying statistical methods to forensic DNA, author of a leading treatise on statistical genetics, and the prosecution witness in the O. J. Simpson trial. Dr. Weir has written:

The FBI procedure (Budowle et al., 2000) rests on the probability of a DNA profile not occurring in a population, apart from the suspect…. There are two problems with this approach [internal citations omitted]. In the first place, all N profiles in a population are not independent and the (1 - P) to the N calculation ignores all the issues of conditional probabilities, population structure and relatedness discussed above. The more serious problem may be that of perception-there is quite a difference between telling a jury that the suspect has been identified by his DNA profile and telling them that there is a 1% chance someone else has this profile. *The absoluteness implied by statements of identity is not a statistical concept.*

Bruce Weir, *Forensics*, in D.J. Balding, M. Bishop & C. Cannings, Eds., *Handbook of Statistical Genetics* Vol. 2, 848-49 (2d ed. 2003) (emphasis added) .63 *See also*, A. Biederman, et al., *Decision Theoretic Properties of Forensic Identification: Underlying Logic and Argumentative Implications*, 171 Forensic Science International 120 (2008)(“Definite conclusions of identification cannot, however, be based on purely probabilistic schemes unless unrealistic assumptions are admitted. As a consequence, forensic identification is not, at present, considered as the result of a scientific process ). Actually, forensic identification requires a suppression of uncertainty that goes beyond that which is covered by actually available evidence.”); L.A. Foreman et al., *Interpreting DNA Evidence: A Review*, 71 Int'l Statistical Rev. 473-95 (2003) (discussing "questionable practice of source attribution 'with reasonable scientific certainty'") ;

D.J. Balding, *When Can a DNA Profile Be Regarded as Unique?*, 39 Sci. & Just. 257, 258-59

63 Dr. Weir also publicly criticized the FBI's 2000 Forensic Science Communications paper, noting that the FBI's source attribution policy insufficiently accounted for relatedness in populations. *See* Bruce S. Weir, *DNA Match and Profile Probabilities: Comment on Budowle et al. (2000) and Fung and Hu (2000)*, 3 Forensic Sci. Communications (Jan. 2001), available at [http://www.fbi.gov/about-us/lab/forensic-science-communications/fsc/jan2001/weir.htm.](http://www.fbi.gov/about-us/lab/forensic-science-communications/fsc/jan2001/weir.htm)

(1999) ("Although attractive in some respects, a practice of declaring uniqueness in court would lead to substantial difficulties Perhaps the most problematic assumption underlying the

calculation of a probability of uniqueness is the assumption that there is no evidence in favor of [the suspect] [I]t is usually not appropriate for the forensic scientist to pre-empt the jurors'

assessment of the non-scientific evidence.") .

Reputable scientists have pointed out that even in cases where the RMP is very small as in Mr. McCluskey’s case - scientific claims of "uniqueness" and "source attribution" are dubious because once a DNA profile is observed in an individual, the chances of a coincidental observation of the exact same profile increase dramatically given the genetic similarity between that individual and his relatives. The likelihood of brothers and other relatives sharing the same DNA profile will increase the more databases grow. *See* David J. Balding, Weight-of-Evidence for Forensic DNA Profiles 19 (2005) ("Any particular DNA profile is very rare, but once that profile is observed, it becomes more likely that other people, especially among the individual's relatives or ethnic group, also have it. What matters in practice for DNA profile evidence is not .

. . the overall frequency of the profile, but the probabilities of the other possible culprits having the profile given that the suspect has it.").

Some government experts have testified that they have never observed two unrelated individuals sharing the same genetic profile, and that it is nearly impossible for two or more people to share the same genetic profile at 9 or more loci. That testimony appears to be the result of the fact that the government has simply never searched its CODIS databases to look for coincidentally matching DNA profiles at large number of loci.

In 2001, the Arizona Department of Public Safety searched its convicted offender database as a quality control measure to determine if duplicate profiles existed in the database. The search uncovered not only duplicates, but at least one match, at 9 genetic locations, between

unrelated individuals.64 (Kathryn Troyer etal., *A Nine STR Locus Match Between Two Apparently Unrelated Individuals Using AmpflSTR Profile Plus and COfiler*, Promega 12th International Symposium (2001)(Exhibit 20 on CD). That 9-loci match was accompanied by an expected frequency of only one occurrence in a population over twice the size of the entire United States at the time the results were reported – and yet two identical profiles were observed in a small state offender database of just tens of thousands. (Id. at 2.) This coincidental match invited further exploration into the occurrence of coincidental matches among DNA profiles in DNA databases. In 2005, an Arizona court ordered the disclosure of a “match report” chronicling all matches in the same database in 2005, by then containing 65,493 profiles. That report revealed findings that, at first blush, appeared truly remarkable: 122 profiles matched at (exactly) 9 loci, an additional 20 matched at 10 loci, one pair matched at 11, and another at 12 out of a possible 13. (Arizona Department of Public Safety Crime Laboratory, 9+ Locus Match Summary Report (Oct.

2005)(Exhibit 21 on CD). 65 Random match probabilities for profiles of 9 and 10 genetic locations – that is, the likelihood that an unrelated person randomly selected from the population will match a given profile – have denominators well into the billions and far beyond. As Dr.

Laurence Mueller indicates in his declaration :

As I have written, a study of the Arizona offender databases of 65,000 people revealed 122 pairs of people that marched at nine STR loci and twenty pairs of people that match at ten STR loci, and one pair at eleven and twelve STR loci (Mueller, L.D., 2008, *Can simple population genetic models reconcile partial match frequencies observed in large forensic databases?* Journal of Genetics 87: 101-108). Only three of the nine loci match pairs have been checked carefully and one of them (a Caucasian and an African American) yields a random match probability of 1 in 110 billion. It seems almost certain that if all 122 pairs were checked the 1 in 300 billion figure would be exceeded for unrelated people. If matches were examined in a database like the FBI CODIS which now exceeds 6 million

64 Not only were the individuals unrelated, but they were of entirely different races – one was African-American, and the other was Caucasian.

65 According to the Arizona report, the eleven and twelve loci matches were between siblings.

profiles, it may even be possible to find a 13-locus match. For this reason, DNA profiles cannot be assumed to be unique, especially among relatives and therefore coincidental matches are possible and their probabilities need to be estimated.

(Exhibit 19).

Importantly, similar findings have been replicated in the Prince George County and Maryland state databases. In 2005, a Prince George County DNA analyst published a study that indicated that a search of the local database which consisted of only several hundred unrelated individuals revealed one individual who showed a high degree of similarity with a large number of unrelated profiles, matching at seven loci in two separate instances. The overall expected frequency of this profile was approximately 1 in 1 trillion. Julie Kempton, *Patterns of Allele Sharing in 13-Locus DNA Profiles of Siblings and Other Relatives*, Proceedings of the American Society of Forensic Sciences, Vol. XI, Feb. 2005 (Exhibit 22 on CD).

Based on these studies, on August 8, 2006, a state court judge in the Davis Maryland case ordered the Maryland State Police CODIS director to perform an “Arizona” search of DNA profiles by searching the Maryland DNA Database against itself and determine the number of pairs of profiles that match identically at 1-13 loci. On January 24, 2007, the court modified the order from 1-13 loci to 9-13 loci. On January 31, 2007, Maryland CODIS administrator Michelle Graves produced a declaration in the state court proceedings (Exhibit 23 on the CD) indicating the results of such a search:

21 candidate matches at 9 loci

3 candidate matches at 10 loci

1 candidate match at 11 loci

4 candidate matches at 12 loci

3 candidate matches at 13 loci

After the administrator refused to discuss these results with defense counsel, the state court ordered the administrator to answer specified questions, including: “[w]hat are the possible

explanations of the results of the search report for the numbers reported at 9, 10, 11, 12, and 13 loci and which, if any explanation does she believe is the most probable.” (Order of Judge Steven Platt, March 16, 2007, Exhibit 24 on the CD). Ms. Groves responded: “[t]he 3 ‘candidate matches’ at 13 loci are the 3 sets of confirmed identical twins present in our database. The most likely explanation for the ‘candidate matches’ at 9, 10, 11, and 12 loci are related family members. These ‘candidate matches’, however, cannot be interpreted since the Maryland State Police Forensic Sciences Division does not have access to the data, or the personnel necessary to research familial relations.” (Affidavit of Michelle Groves, March 12, 2007, Exhibit 25).

Howver, as Dr. Mueller points out in a declaration filed in the state court proceedings in response to the Grove affidavit, “research has suggested that relatives alone are not an adequate explanation of the matching patterns in offender databases. In particular, the Maryland search shows more matches at 12 loci than it does at 10 or 11 loci. This pattern would not be expected as a result of close relatives in the database.” (Declaration of Dr. Laurence Mueller, April 9, 2007, Exhibit 26 on the CD). Further, the Kempton study of the Prince George County database showed that “[t]he average number of identical loci (both alleles shared) in full siblings was 4.7, with a range of 1-9.” (Exhibit 26).

Besides the eleven and twelve loci matches between siblings in the Arizona database, scientists have generated large-scale simulations using the FBI's own data that demonstrate that siblings have perfectly matching DNA profiles across all thirteen CODIS loci with an average frequency of at least 3.0 per 459,361 pairs of siblings. *See* David R. Paoletti et al., *Empirical Analysis of the STR Profiles Resulting From Conceptual Mixtures*, 50 J. Forensic Sci., 1361-66 (Nov. 2005).66

What does this say about the claim of the DNA analyst in this case to be able to attribute t

66 This frequency suggests that some such pairs of perfectly matching siblings are likely to exist in large populations such as the general population of the United States and, eventually, in DNA profile databases that contain large numbers of close relatives.

a sample of DNA to its source based on statistical models ? While the numerous matches between unrelated individuals revealed in the Arizona and Maryland reports may appear highly improbable to the non-scientist, a closer, informed inspection demonstrates that the reported matches are not far out of synch with expectation. If the search process and likely existence of relatives in an offender database are taken into account statistically, the number of 9-12 loci matches discovered in the Arizona and Maryland databases is not remarkable at all, but just roughly what statisticians would expect to find in databases of those sizes.(*See* Charles Brenner, *Arizona DNA Database Matches*[, http://dnaview.com/ArizonaMatch.htm](http://dnaview.com/ArizonaMatch.htm) (Jan. 8, 2007).) The lesson from Arizona and Maryland is simple: The more comparisons that are made, the more likely it becomes that matches will be observed between profiles b”elonging to different individuals, despite RMPs that, to a non-statistician, suggest a match under any circumstances to be exceedingly improbable. In a DNA case ,the unexpected – finding a coincidental match – becomes the expected as the number of comparisons increases.

Finally, as Dr. Mueller states in his declaration, and as is discussed more fully below, “the assertion of source attribution ignores an important scientific aspect of DNA: the possibility of laboratory error.” (Exhibit 19). See also, NAS 2009 Report at 121 (“in the case of DNA analysis, a declaration that two samples match can be erroneous in at least two ways: The two samples might actually come from different individuals whose DNA appears to be the same within the discriminatory capability of the tests, or two different DNA profiles could be mistakenly determined to be matching. The probability of the former error is typically very low, while the probability of a false positive (different profiles wrongly determined to be matching) may be considerably higher. Both sources of error need to be explored and quantified in order to arrive at reliable error rate estimates for DNA analysis.”)

Given the chorus of concern among scientists - both practicing bench forensic scientists and genetic statisticians - that the inference of source attribution from small probabilities is a non-scientific endeavor, it is unsurprising that many government forensic laboratories in this

country have protocols different than the FBI's. For example, the highly respected Connecticut State Crime Laboratory, a regional partner with the FBI in DNA testing, will not issue source attribution statements. Rather, even in cases such as this one where the RMP is calculated to be 1 in 4.3 quadrillion , Connecticut will report the match probability as follows: "[T]he expected frequency of the observed DNA profile is less than 1 in 300 million." Department of Public Safety, Division of Scientific Services, Connecticut Forensic Laboratory, DNA Typing Methods, SOP 7-7.3 (Genotypic Frequency Ceiling) (March. 15, 2003). Similarly, the Orange County, California police crime lab would not testify to a source attribution statement about the evidence in this case; rather, that state laboratory would report that the estimated frequency is less than 1 in 10 trillion. Orange County Sheriff-coroner Department Forensic Science Services, Methods Manual, Version 2.1 44 (Population Frequency Estimation) . The Virginia state crime laboratory would report the RMP and state that the RMP exceeded the world population. Commonwealth of Virginia Department of Criminal Justice Services Division of Forensic Science, Fluorescent Detection PCR-based STR DNA Protocol (May 15, 2002) 11.4.3 . The Michigan state crime laboratory would simply report the RMP. Michigan State Police, Michigan State Police PCR Protocol, DNASOP 25, Page 5.7 (Standard DNA Calculations).

International common law jurisdictions also reject the use of source attribution statements. Cf. *Roper v. Simmons*, 543 U.S. 551, 125 S. Ct. 1183, 1198-1200 (2005) (looking to practices of foreign jurisdictions). For example, authors of the leading Canadian treatise on courtroom uses of forensic DNA, David Rose and Lisa Goos, an attorney and a government forensic scientist respectively, state that source attribution is a controversial method of reporting DNA matches that is not used in Canada:

The scientist may testify that, absent an identical twin, it can be concluded to a reasonable certainty that the evidence sample and the defendant sample are from the same person. This method of expression is controversial for the following reasons: it involves an inappropriate personal interpretation of the evidence which may tend to exaggerate the strength of the DNA evidence, and similarly cause the scientist to assess other pieces of evidence not necessary for an opinion regarding the DNA match or its significance.

David Rose & Lisa Goos, *DNA: A Practical Guide*, 5-16.1 (2004) (internal citations excluded). The Forensic Science Services in the United Kingdom - the founding and premier forensic DNA laboratory in the world - also does not offer source attribution statements in court. *See*, L.A. Foreman et al., *Interpreting DNA Evidence: A Review*, 71 Int'l Statistical Rev. 473-95 (2003) (“At the present time, it is the policy of the FSS in those cases where there is a match between two full SGMPlus profiles not to carry out a match probability calculation for unrelated people: instead the figure of one in a billion is given—whatever the ethnic group cited in the alternative proposition.”)

In the English case of *Doheny&Adams* [1997] 1 Cr. App. R. 369, after the scientist had reported a match probability of 1 in 27 million, the trial judge in summing up stated, “I should think there are not more than 27 million males in the United Kingdom which means that it is unique.” The appellate court mandated a number of recommendations for the reporting of DNAevidence, one of which was that it was not part of the scientist’s role to comment on the likelihood that it was the defendant who left the crime stain.

In short, the FBI's policy is anomalous. In contrast to the FBI, many other crime laboratories, forensic scientists, statisticians, molecular biologists, and legal commentators share the view that scientists should not make the inference that the suspect is the contributor of the DNA but, rather, leave it to the jury to either draw that inference if the proponent of the DNA evidence submits sufficient evidence or reject it. So too, this Court should reject the government's extraordinary request that its expert be permitted to give an opinion that a person is the source of any DNA sample in this case.The making or rejecting of that inference is the jury's role, not the expert's. *See also*, *Gant v. United States*, 518 A.2d 103, 110 (D.C. 1986) ("[T]he trial court also must prevent an expert witness from preempting the function of the jury.

Improper preemption can occur in two ways: when the witness speaks too directly to the ultimate issue (i.e., guilt or innocence) or speaks to matters in which the jury is just as competent as the expert to consider and weigh the evidence and draw the necessary conclusions.")

(quotations and citations omitted).

# This Court Should Preclude Expert Opinion Evidence That Concludes That Mr. McCluskey, Or Another Person Involved In This Case, Is the Sole Source of DNA Evidence Because its Probative Value Is Substantially Outweighed by its Prejudicial Effect And Such Testimony Would Violate the Right to Due Process.

Even if this Court rules that government testimony that someone is the sole source of DNA samples is not barred by the foregoing analysis, and finds the government has met its burden of admissibility under *Daubert*, the proposed expert opinion evidence should nonetheless be excluded because its probative value is substantially outweighed by the great potential for prejudice.

As indicated above,“ *Daubert* enjoins watchful assessment of the risk that a jury would assign undue weight to DNA profiling statistics even after hearing appellant's opposing evidence, the testimony of Government witnesses under vigorous cross-examination and the careful instructions of the district court on burdens of proof." *United States v. Chischilly*, 30 F.3d 1144, 1156 (9th Cir. 1994). As also pointed out, at least two district courts have excluded DNA evidence on Rule 403 grounds because of the danger of misinterpreting statistical evidence. *See*, *United States v. Natson*, 469 F.Supp.2d 1253 (M.D.Ga. 2007); *United States v. Graves*, 465 F.Supp.2d 450, 459 (E.D.Pa. 2006).

In *United States v. Porter* , 1991 WL 319015 (D.C. Super. 1991) Judge Kennedy explained that understanding the meaning of forensic DNA testing cannot be left to

cross-examination or competing experts, because juries will gravitate toward easy answers and absorb only the "bottom line" if given multiple ways of representing the significance of a DNA match:

It is almost certain that jurors would simply "jump" to the bottom line numbers without giving any meaningful consideration to any dispute over the principles, which underlie the methodology used to generate those numbers. To permit the fancy of jurors to operate in this manner is the antithesis of "due process."

1991 WL 319015 at \*27. To overcome this tendency, Judge Kennedy exhorted courts to

determine pre-trial whether the proffered DNA evidence can and will be reported in an manner that accurately reflects the significance of the evidence. Cf., *Ege v. Yukins,* 485 F.3d 364 (6th Cir. 2007)(bitemark testimony which included unfounded statistical analysis was so unreliable that defendant's conviction violated due process)

In the present case, even if the "source attribution" statement is found to be scientifically reliable by this Court, it will mislead jurors in precisely the way Judge Kennedy described. If history is any guide, jurors will disregard any statistics counsel for Mr. McCluskey or the government may adduce at trial about the possibility of a coincidental match and will instead fixate on the DNA examiner's much simpler statement that he is certain "to a reasonable degree of scientific certainty" that someone is the contributor of DNA samples . A source attribution statement by the government would effectively overwhelm attempts to challenge the expert's findings insofar as such challenges would have to delve into statistical matters that lack the same certainty and gravity with jurors. In a case like this, the government's expert opinion that someone is the source of the DNA could be dispositive - and dangerously so - in the eyes of jurors. *See*, *United States v. Green*, 405 F.Supp.2d 104, 117 (D.Mass.2005)(“[A] certain patina attaches to the testimony, running the risk that the jury, labeling it “scientific,” will give it more credence than it deserves. These concerns are especially present in the case at bar, where the ballistics testimony purports to conclude that the Hi Point weapon found at 6 Esmond Street was ‘the one’ that fired the shells found a year earlier, ‘to the exclusion of all other weapons in the world.’”); *Smith v. United States*, 389 A.2d 1356, 1359 (D.C. 1978) ("Because of the authoritative quality which surrounds expert opinion, courts must reject testimony which might be given undue deference by jurors and which could thereby usurp the truthseeking function of the jury.").

This Court should act cautiously and exercise its discretion to preclude the government's novel way of reporting the alleged DNA matchs in this case. Whatever additional probative value there may be in allowing the government to ignore the very small probabilities of a

coincidental match and make a source attribution statement, the tendency of such a statement to overshadow legitimate inquiries into the statistical probabilities of a coincidence having happened in this case is too prejudicial.

For the foregoing reasons, Mr. McCluskey respectfully requests that this Court preclude the government from presenting expert opinion evidence that anyone is the sole source of DNA samples in this case and asks this Court to limit government testimony about the results of its DNA testing to presentation of a reliable statistical probability figure.

# The Probability Of Inclusion Frequencies For Samples 1B22D, 1B72B, And 31e Are Irrelevant, and More Prejudicial, Misleading, and Confusing Than Probative and Thus Any Testimony About These Particular Samples is Inadmissible under Rules 402, 403, and 702, as Well as Under D*aubert* and the Due Process, Fair Trial, and Cruel and Unusual Provisions of the Fifth, Sixth, and Eighth Amendments to the Constitution

As summarized above, the few probability of inclusion frequencies reported by the analyst in this case are very high with respect to three samples: 1B22D(e.g, 1 in 12 Caucasians), 1B72B(e.g., 1 in 9268 Caucasians), and 31e (1 in 21 Caucasians) As stated in *United States v. Chischilly*, 30 F.3d 1144, 1156 (9th Cir. 1994), “ *Daubert* enjoins watchful assessment of the risk that a jury would assign undue weight to DNA profiling statistics even after hearing appellant's opposing evidence, the testimony of Government witnesses under vigorous cross-examination and the careful instructions of the district court on burdens of proof."). At least two district courts have excluded DNA evidence on Rule 403 grounds even where weak statistical evidence was offered in support of a DNA match. *See*, *United States v. Natson*, 469 F.Supp.2d 1253 (M.D.Ga. 2007)(DNA expert’s opinion that the Defendant was 26 times more likely to be the father of a fetus than a random person, and that there was a 96.30% probability that Defendant was the father “is not probative of any of the issues in the case, and insofar as his testimony may have some probative value, that probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, and the possibility of misleading the jury” where statistical computation fell below the 99.99 % significance level generally accepted by the scientific

community.).*United States v. Graves*, 465 F.Supp.2d 450, 459 (E.D.Pa. 2006)(“[E]ven with appropriate safeguards, the minimal probative value of the umbrella DNA evidence--in which half of the relevant population cannot be excluded as a contributor to the DNA sample--is substantially outweighed by the danger of unfair prejudice and confusion of the issues.”). Here, the statistics are not just weak, they are non-existent. There is thus even greater reason than there was in *Natson* and *Grave* to exclude the testimony under Rule 403.

# The Failure to Include in the Statistics Any Measure of Laboratory Error Rate Renders Any Statistical Probability Calculation Inadmissible.

The potential for false positives due to laboratory error in DNA testing is now beyond dispute. "Laboratory errors happen, even in the best laboratories and even when the analyst is certain that every precaution against error was taken." NRC 1 at 88-89. *See also, J.* Koehler, *DNA Matches and Statistics: Important Questions and Surprising Answers*, 76 Judicature, 222-229 (1993)("[B]ased on the little evidence available to date, a reasonable estimate of the

false positive error rate is 1-4 percent."); J. Koehler, *Error and Exaggeration in the Presentation of DNA Evidence*, 34 Jurimetrics Journal 21,t 26 (proficiency testing shows error rate of 1-4%); Donald Berry, *Comment*, 9 Stat. Sci. 252, 253 (1994)("Only the frequency and type of errors are at issue."); R.C. Lewontin, *Comment: The Use of DNA Profiles in Forensic Contexts*, 9 Stat. Sci. 259 (1994)(discussing sources of error); William C. Thompson, *Comment*, 9 Stat. Sci. 263, 265 (1994)(discussing data on laboratory error); *Cf.* Dan L. Burk, *DNA Identification: Possibilities and Pitfalls Revisited*, 31 Jurimetics 53, 80 ("Bald statements or broad hints that DNA testing is infallible...are not only irresponsible, they border on scientific fraud"). *See also*, Karl Reich, *Utilizing Proficiency Testing Survey Results in Forensic DNA Laboratories*, Abstracts of the Genetic Identity Conference Proceedings, 15th International Symposium on Human Identification - 2004, available at <http://www.promega.com/GENETICIDPROC/ussymp15proc/> posterpresentations/42Graffy-Boonlayangoor.pdf (“An analysis of the PTSR [Proficiency Testing Survey Results] for forensic DNA laboratories reveals that the error rate from forensic DNA

laboratories is much higher than for clinical laboratories. Here we summarize the results of EPT [external proficiency tests] from the College of American Pathologists (CAP) for Forensic DNA and Identity Testing from 1997-2003 and Collaborative Testing Service (CTS) from 2001-2003. The average percentage discrepancy reported among participant laboratories was 2.71% and 3.01%,respectively. This crude measure of the DNA analysis error rate clearly under-reports the true error rate for these laboratories.”)

Indeed, most experts have long believed that having an accurate estimate of the false positive rate is *more* important than having an accurate estimate of the probability of a coincidental match because the rate of false positives is likely to be much greater than the rate of coincidental matches.67 Paul J. Hagerman, *DNA Typing in the Forensic Arena*, 47 Am.J.Hum.Genet. 876 (high false positive rate makes probability of coincidental match irrelevant); Richard Lempert, *Some Caveats Concerning DNA As Criminal Identification Evidence: With Thanks to the Reverend Bayes*, 13 Cardozo L.Rev 303, 325 (the probability of a coincidental match between people who have the same DNA profile "is usually dwarfed by the probability of a false positive error"); Mueller, *The Use of DNA Typing in Forensic Science*, 3 Accountability in Research 55, 58 (exact probability of a coincidental match "should hardly matter" to jury given much greater likelihood of false positive); A.D. Kloosterman, *Credibility of Forensic DNA Typing is Driven By Stringent Quality Standards*, Accred. Qual. Assur. (2001) 6:409–414 (“When we take into account that the laboratory error rate can never be reduced to zero, it is plausible that the probability that an innocent person would match a crime stain with a frequency of, e.g., 1 in 1 billion is likely to be negligible compared to the probability that the match was induced by a crucial mistake in the laboratory such as a clerical error, contamination, swapping of samples, etc.”); Richard Ostrowski & Daniel Krane, *Unresolved Issues in Forensic*

67 By analogy, if one needed to estimate the amount of money a man was carrying, it would typically be more important to have accurate information on the number and denomination of bills in his wallet than on the number and denomination of coins in his pocket because the coins would represent only a small portion of his total money.

*Use of DNA Profiling*, 3 Accountability in Research 47 (1993).

A central premise of DNA appellate cases is that evidence of a DNA match is inadmissible unless accompanied by statistics that can tell the trier of fact what the match means. Now that the scientific community has recognized that error rates *must* be taken into account in order to make a meaningful evaluation of DNA evidence, the logic of those cases requires that juries be given statistics on the probability of laboratory error; without such statistics, evidence of a DNA match is inadmissible because it is impossible to evaluate.

The 1996 NRC Report recommends without persuasive analysis that the issue should be simply ignored *See*, Richard Lempert, *After the DNA Wars: Skirmishing With NRC II*, (1997) 37 Jurimetrics J. 439. But it would be absurd for courts to insist on valid quantitative estimates of the probability of a coincidental match, without also requiring valid estimates of the rate of false positives due to laboratory error, when the scientific community has determined that the latter is *more* important than the former to a rational evaluation of DNA evidence. If DNA evidence is "meaningless" without statistical estimates of the probability of a coincidental match, it is also "meaningless" without statistical estimates of the probability of a false positive.

Other experts have echoed this conclusion:

Statisticians and geneticists involved in the controversy over DNA testing have understandably been fascinated by and mostly written on disputes regarding the statistical and genetic issues that DNA identification raise, but laboratory error places the most serious limits on the evidentiary import of reported DNA matches. If justice is the mutual goal of those involved in the debates over DNA identifications--and I believe it is everyone's concern--the possibility of error must be honestly faced, and it must be incorporated into estimates of the incriminatory power of DNA matches.

Richard Lempert, *Comment: Theory and Practice in DNA Fingerprinting*, 9 Statistical Science 255, 257 (1994).Accord, Laurence D. Mueller, *The DNA Controversy And NRC II*, in Statistical Methods in the Health Sciences:Genetics, ME Halloran & S. Geiser (eds., 1999) pp.17-18; Jonathan Koehler, *Why DNA Likelihood Ratios Should Account For Error (Even When A National Research Council report Says they Should Not)* 37 Jurimetrics 425(1997), R. Lempert,

*After The DNA Wars: Skirmishing With NRC II*, 37 Jurimetrics 439(1997); William Thompson, *Accepting Lower Standards: The National Research Council’s Second Report On Forensic DNA Evidence*, 37 Jurimetrics J. 405-424 (1997); David Balding, *Errors and Misunderstanding In the Second NRC Report*, 37 Jurimetrics J. 469 (1997).

Finally, in 2009, the NAS saw the light and explicitly concluded in its influential and comprehensive study of the forensic sciences that:

It is also important to note that errors and corresponding error rates can have more complex sources than can be accommodated within the simple framework presented above. For example, in the case of DNA analysis, a declaration that two samples match can be erroneous in at least two ways: The two samples might actually come from different individuals whose DNA appears to be the same within the discriminatory capability of the tests, or two different DNA profiles could be mistakenly determined to be matching. The probability of the former error is typically very low, while the probability of a false positive (different profiles wrongly determined to be matching) may be considerably higher. Both sources of error need to be explored and quantified in order to arrive at reliable error rate estimates.

NAS 2009 Report at 121.

The NAS concluded that “[t]he estimation of such error rates requires rigorously developed and conducted scientific studies”, and that “[t]he assessment of the accuracy of the conclusions from forensic analyses and the estimation of relevant error rates are key components of the mission of forensic science.” (Id. at 122).

Even before that groundbreaking study, at least one court heeded the well-reasoned statistical arguments of the experts cited above. With respect to Dr. Koehler , who has written most prolifically on the issue, it is significant that the Mississippi Supreme Court has declared in *Watts v. State*, 733 So.2d 214, 224(1999) that “as... Dr. Koehler’s articles sugges[t], the introduction of statistical evidence can be meaningless without any evidence of the testing laboratory’s error rate.” The Court also described Dr. Koehler’s standing in the scientific community: “ Dr. Koehler, adjunct professor at the University of Texas School of Law and assistant professor at the University’s Business, is one of the leading authorities on the use (and misuse) of statistics in the presentation of DNA evidence.” Id at n. 2. In line with this opinion,

and the recent conclusions of the NAS 2009 Report, the Court should conclude that the failure of the government to include as part of its statistical computation an estimate of the lab error rate is a *Daubert* and Rule 702 violation, and renders the evidence more misleading than probative under Rule 403.

# The Improper Restriction of the Statistics to African Americans, Apaches, Caucasians, Navajos, and Southwestern Hispanics Renders Any Statistical Probability Calculation Inadmissible.

In a state such as New Mexico, where the minority population is substantially large and diverse, there can be no justification for restricting the statistical calculations to only five groups. This issue is addressed persuasively in *State v. Carter* (1994) 246 Neb. 953, 524 N.W. 2d 763 as follows:

As previously discussed and as Blake's testimony illustrates, all population groups share common PCR DQ Alpha genotypes. It is only the frequency with which these genotypes appear within the different racial or ethnic groups which varies. Since Blake concedes that an individual's race or ethnic background cannot be determined by his or her genotype, the logic of presenting limited statistical frequencies when the racial or ethnic background of the perpetrator is unknown is flawed. There is nothing in this method that accounts for the possibility that the perpetrator was of another racial or ethnic group such as Hispanic, Native American, or Asian. It is apparent that the statistical frequency evidence the jury heard in the present case was based on the assumption that the perpetrator was either black or Caucasian. To limit the statistical frequency evidence to two racial groups when the racial or ethnic background of the perpetrator is unknown is prejudicial under any circumstances; however, in the present case it was particularly offensive in light of the fact the defendant is a black man and his Caucasian friends (Hicks and Harpster) were excluded as possible suspects by PCR DNA tests. *See also*, *State v. Anderson,* 115 N.M. 433, 853 P.2d 135, 147 (N.M.App.1993) (court noted that the data base chosen depends on the ethnicity of the defendant and not necessarily the ethnicity of the perpetrator of the crime. It concluded that this method was misleading, because "[i]f, in fact, the crime was committed by someone of a different racial or ethnic database, then the appropriate subgroup, and thus the odds, would change, perhaps dramatically"); *People v. Pizarro,* 10 Cal.App.4th 57, 12 Cal.Rptr.2d 436, 459 (1992) (it is a "bootstrap argument" to assume relevancy of a data base simply because the suspect falls within that racial or ethnic group);

R.C. Lewontin, Letter, *Which Population?,* 52 Am.J.Hum. Genetics

205 (1993) (the relevant question is not the ethnicity of the defendant).

In *United States v. Peters*, 1995 U.S. Dist. LEXIS 20950 \* 122 (D. N.M. 1995), aff'd, 133 F.3d 933 (10th Cir. 1998) (unpub.), Judge Campos followed similar reasoning to conclude:

The NRC Report acknowledges the correctness of using frequencies that are based on the population of possible perpetrators, rather than on the population to which a particular suspect belongs. See, NRC Report, Pl. Ex. 38(b) at 85. Dr. Weir also recommends that "the frequency of a profile should be calculated with each database, and all results presented unless there is clear evidence that the crime was committed by a member of a particular racial group." Pl. Ex. 186 at 3. It is my understanding that the victim in this case was unable to see her attacker and has not clearly identified him as Navajo. Therefore it is appropriate to use all the FBI databases to calculate frequencies in addition to the FBI's American Indian database and the new Navajo database estimates.

The same reasoning should be applied in this case to prevent the government from limiting the statistical evidence to only five distinct groups, especially when, and notwithstanding *Peters*, two of those groups are defined as Apache and Navajo. In that regard, the United States government has presented expert testimony in another recent post-*Peters* criminal case involving the admissibility of DNA evidence that the expert “does not know whether statistical data exists for Native Americans, and the government implied that such data may not exist, arguing that the category ‘Native American’ is more ‘political’ than racial or ethnic in nature, noting the ability of each Native American tribe to determine who may be a member of the tribe.” *United States v.*

*Hair*, 2011 WL 333236 \* 6 (N.D.Okla. 2011(noting the inconsistency between the government’s position in that case and the one taken in *United States v. Coronado-Cervantes*, 912 F.Supp. 497, 500 (D.N.M.1996)). The government in this case should not be permitted to assert the exact opposite position that valid statistical data does exist for Native American tribes. See generally, *New Hampshire v. Maine*, 532 U.S. 742, 749, 121 S.Ct. 1808, 149 L.Ed.2d 968 (2001)

The MNDPS STR protocol states that “[t]he five population databases currently utilized for statistical calculations (African American, Caucasian, Southwest Hispanic, Apache and Navajo) with allelic frequencies of STR loci are those found in the FBI CODIS Popstats

program. Other databases are acceptable, as long as the appropriate statistical evaluations have been completed and show the database to be valid for use in forensic statistical calculations.” (Exhibit 7, p. 14-3). Here, it is necessary to use such databases in order not to mislead the jury. **68**

# The Failure to Apply Reliable Scientific Procedure As Outlined in the FBI Quality Assurance and SWGDAM STR Interpretation Guidelines, the NRC Reports, the Manufacturer’s Protocols, the Lab’s Own Protocols, the Forensic Literature, and Independent Audit Guidelines Renders Any DNA Test Results Inadmissible.

As pointed out above, the first issue the court needs to decide is whether the government can satisfy its burden to show that the Identifiler and low copy number DNA testing technique being offered in this case, along with its accompanying and varied hardware and software methods and statistical formulations is reliable “science” within the meaning of *Daubert*. Only if the Court so concludes is it necessary to go on and determine whether the experts have “applied the principles and method reliably to the facts of the case” under Rule 702. Mr. McCluskey turns to that issues now, but he urges the Court for all of the reasons stated above to rule that the Identifiler and low copy number technique, and the specific hardware and software methods and statistical techniques being offered in this case cannot survive *Daubert* scrutiny.

In turning to the issue of whether the experts have “applied the principles and method reliably to the facts of the case” under Rule 702 (i.e., whether they have applied reliable scientific procedure ), Mr. McCluskey begins by noting that the government’s burden under the cannot be satisfied by merely showing that a lab technician used the commercially distributed Identifiler

68 The Protocol misleadingly states that “[t]he five population databases currently utilized for statistical calculations (African American, Caucasian, Southwest Hispanic, Apache and Navajo) with allelic frequencies of STR loci are those found in the FBI CODIS Popstats program.” According to the President's DNA Initiative - DNA Analysts training website, the CODIS software, PopStats, has the following population databases: (1)African American; (2) Asian; (3) Caucasian; (4) Hispanic; and (5) Native American. Population Databases, available at [http://www.nfstc.org/pdi/Subject07/pdi\_s07\_m02\_01.htm.](http://www.nfstc.org/pdi/Subject07/pdi_s07_m02_01.htm)

and Quantifiler kits. The use of a commercially distributed standardized "kit" does not mean a laboratory employs adequate methods and controls to do reliable testing. Individual laboratory quality assurance and quality control measures are required, and many scientists, and the NRC itself, believe that additional scientific controls are necessary to make PCR based forensic testing reliable. The NRC I makes this point clear in its comments on Roche's DQ-alpha "kit":

One commercial kit for forensic PCR analysis has been marketed. Other such kits will probably be ready for commercial distribution soon. The committee sees a potential for introduction of unreliable kits and the misuse of kits. The existence of a kit suggests ease of use and low chance of technical error. The committee believes that nonexpert laboratories will run a significant chance of error using kits. We therefore recommend that a standing committee (discussed later in this chapter) consider the issue of regulatory approval of kits for commercial use in forensic DNA analysis. Even though no precedent exists for the regulation of tests in forensic DNA applications, we believe that it might be necessary for a government agency to test and approve kits for DNA analysis before their actual forensic use.

NRC I Report, at 69.

This recommendation, written in 1992, along with the committee’s other recommendation that the DNA labs themselves be subjected to state and federal regulations, have still not been acted upon in most states, although, as indicated above, Maryland recently became the sole exception. For the most part, however, the issue of determining “correct scientific procedures”, for the purpose of determining whether the expert has “applied the principles and method reliably to the facts of the case” under Rule 702 must be answered in reference to the DAB Guidelines, three National Research Council reports, the lab’s own protocols, the manufacturer’s User’s Manual, and the relevant scientific literature.

The task of assessing compliance with these standards may be made easier in this case by proof of independent audits conducted in accordance with DAB Guidelines. However, it is important to emphasize that it is the court’s roll to assess compliance with *Daubert and* Rule 702, not the auditor’s who are themselves affiliated with law enforcement. This observation is

particularly apt here, where the existing audit process is relatively superficial. *See*, NRC II at 77 (Laboratories that seek ASCLD-LAB accreditation “must submit all their documentation to an accreditation review team and must undergo a week-long site inspection by that team. The site inspection includes a critical evaluation of randomly selected case files to verify that the QC standards as documented are being met.”).

In addition, a review of the pertinent scientific literature discussed below reveals many emerging reliability problems with the Identifiler kits which have not been addressed by any existing laboratory or auditor. In what follows, the defense will briefly summarize some of the major failures of correct scientific procedure that are at issue in this case, although some of them have already been alluded to above, such as failure of properly use controls, the failure to follow the laboratories own protocol requirement that the evidence samples be typed and interpreted prior to the reference samples, and the failure to comply with ASCLD/LAB’s uncertainty of measurement policy. In doing so, however, the defense urges the Court to view the deficiencies not only individually, but also in combination. The defense’s position is that whether viewed singly or in combination, the following deficiencies require the exclusion of all DNA evidence under *Daubert* and Rule 702:

# Lack of certification of the analyst.

Summarizing existing professional standards requiring certification of analysts, the NAS 2009 Report concludes at page 208 :

The certification of individuals complements the accreditation of laboratories for a total quality assurance program. In other realms of science and technology, professionals, including nurses, physicians, professional engineers, and some laboratorians, typically must be certified before they can practice. The same should be true for forensic scientists who practice and testify. Although the accreditation process primarily addresses the management system, technical methods, and quality of the work of a laboratory (which includes the education and training of staff), certification is a process specifically designed to ensure the competency of the individual examiner.

For this reason, the failure of the analyst in this case to be certified is an important reason not to allow any DNA tyesting performed by her under Daubert and Rule 702. It must be remembered also that, according to the literature, the Identifiler and low copy number technique used in this case requires a great deal of experience and skill to obtain and interpret results.

Finally, there is the fact that this is a death penalty case, in which the highest standards of reliability are needed. For all of these reasons, the Court should rule that the government’s DNA test results are inadmissible because the analyst who performed the tests was not certified or otherwise licensed. *See*, *United States v. Green*, 405 F.Supp.2d 104, 109 (D. Mass. 2005)(lack of accreditation and certification were one of many reasons to limit testimony of ballistics expert)

# Lack of blind proficiency testing.

“Participation in a proficiency-testing program is an essential part of a successful laboratory’s quality assurance effort.” (Butler, Fundamentals, pp. 298-299). Although rather expensive and time consuming to arrange and conduct, “[a] blind external proficiency test is generally considered the most effective at monitoring a laboratory’s abilities...” (Id. at 298).

NRC I states that “ courts should require that a proponent of DNA typing evidence have appropriate accreditation--including documentation of external, blind proficiency testing (as well as other accreditation that might be mandated by government or come to be generally accepted in the profession)--for its evidence to be admissible.” NRC I at 106-107 The Report explains that

There is strong legal foundation for such a position. As a number of courts have correctly recognized, the admissibility of scientific evidence depends not just on a technology’s being sound in principle, but on the testing laboratory’s having applied it in the case at hand according to generally accepted standards.

*Id.* at 107.

The NAS 2009 Report states that “[a] particular need exists for routine, mandatory proficiency testing that emulates a realistic, representative cross-section of casework, for example, DNA proficiency testing.” (NAS 2009 Report, p. 25) p. 25.

Standard 13.1 of the FBI’s Quality Assurance Standards requires that each DNA analyst undergo an external proficiency test at least twice a year. (Exh. 3).

As pointed out above, the rules adopted by the New Mexico Oversight Committee provide that for CODIS (but not forensic testing examiners)

Five percent of all samples tested shall consist of samples with a known DNA profile and shall be presented to the analyzing laboratory in a ‘blind’ fashion to ensure proficiency and to act as a quality assurance measure. Results of these analyses are to be evaluated with the corresponding offender or arrestee samples. Should any resultant ‘blind’ sample's DNA profile not match the expected known result for that sample, an error rate is to be calculated by the administrative center and be presented to the analyzing laboratory and to the oversight committee.

The Maryland Legislature has recognized the importance of blind proficiency testing by providing in MD Code, Public Safety, § 2-507 that “At regular intervals not exceeding 180 days, the Crime Laboratory and each analyst who performs DNA analyses at the Crime Laboratory shall undergo external proficiency testing, including at least one external blind test, by a DNA proficiency testing program that meets the standards issued under: (1) § 1003 of the federal DNA Identification Act of 1994 (42 U.S.C. § 14131); or (2) the guidelines for a quality assurance program for DNA analysis, known as the ‘TWGDAM’ guidelines.”

In this case, although the NM DPS’s Serology/DNA/Databasing Quality Manual requires that each analyst “must be externally proficiency-tested semiannually”, there is no requirement that the testing be “blind”, as opposed to “open”. (Exh. 4, Sec. 11). As pointed out above, Mr.

McCluskey has been given access to only five proficiency tests performed by the primary analyst and none by the peer reviewer. These five tests were completed on March 15, 2010, September 20, 2010, December 28, 2010, April 4, 2011, and October 11, 2011. None of them were blind and only the two most recent ones involved simple mixtures. The testing in this case was conducted in August, September, and December, 2010, and in April 2011. Although no errors are apparent in these five tests, it must be stressed that even if no errors have been made yet, it does not mean that the analyst’s or the laboratory’s error rate is zero. *See* Jonathan Koehler, *Why*

*DNA Likelihood Ratios Should Account For Error (Even When A National Research Council report Says They Should Not)*, 37 JURIMETRICS J. 425 (1997).

As in other areas of forensic science, current proficiency testing programs are simply too lax to satisfy the requirements of correct scientific procedure. *See*, *United States v. Green*, 405 F.Supp.2d 104, 109 (D.Mass.2005)(“[W]hen liberty hangs in the balance-and, in the case of the defendants facing the death penalty, life itself-the standards should be higher than were met in this case, and than have been imposed across the country. The more courts admit this type of ... evidence without requiring documentation, proficiency testing, or evidence of reliability, the more sloppy practices will endure; we should require more.”); *United States v. Plaza* (E.D. Pa. 2001) 188 F. Supp. 2d. 549, 565 (E.D. Pa.2002); ("On the record made before me, the FBI examiners got very high proficiency grades, but the tests they took did not. The defense witnesses succeeded in raising real questions about the adequacy of the proficiency tests taken annually by certified FBI fingerprint examiners."); *United States v. Lewis* (S.D.W.Va 2002) 220 F.Supp.2d 548, 554 (“ There were aspects of Mr. Cawley's testimony that undermined his credibility. Mr.

Cawley testified that he achieved a 100% passage rate on the proficiency tests that he took and that all of his peers always passed their proficiency tests. Mr. Cawley said that his peers always agreed with each others' results and always got it right. Peer review in such a ‘Lake Woebegone’ environment is not meaningful.”)

# Lack of adequate internal and developmental validation.

One crucial requirement established by professional guidelines and standards is that forensic DNA tests must be developmentally validated through extensive empirical studies. *See*, SWGDAM Revised Validation Guidelines Standard 1.2.1 (“Developmental validation must precede the use of a novel methodology for forensic DNA analysis.”)69; DAB Standard 8.1( “The

69 The Revised Validation Standards were approved by SWGDAM July 10, 2003 and are available at <http://www.fbi.gov/hq/lab/fsc/backissu/july2004/standard/2004_03_standards02.htm> (Exhibit 20 herein). The Standards were revised yet again and are currently contained in the

laboratory shall use validated methods and procedures for forensic casework analysis. Novel

forensic DNA methodologies shall undergo developmental validation to ensure the accuracy, precision and reproducibility of the procedure.”); TWGDAM Guidelines 4.1.2 (“ Validation studies must have been conducted by the DNA laboratory or scientific community prior to the adoption of a procedure by the DNA laboratory.”).

According to NRC I, developmental validation is necessary to establish an objective and quantitative procedure for identifying the pattern of a sample and for declaring a match, to identify possible artifacts that could lead to incorrect interpretation if not recognized,70 to understand the limits of each DNA typing method for sensitivity to quantity, mixture,and contamination, to establish the statistical frequency of the genetic markers and the error rate of the procedure. NRC I at 52-55

TWGDAM Guideline 4.1.5.1 sets forth the minimal requirements which must be meet in order to satisfy the requirement of developmental validation, including studies in the following areas: standard specimen studies, consistency studies, population studies, reproducibility studies, mixed specimen studies, environmental studies, matrix studies, nonprobative evidence studies, nonhuman studies, minimum sample studies, and on-site evaluation studies. DAB Standard 8.1 contains a similar listing, as does Standard 2 of the Revised Guidelines.

The 1992 NRC Report also emphasizes that the key validating studies must not only be done but published and peer reviewed before a laboratory can claim that its methods are generally accepted.

If a new DNA typing method (or a substantial variation on an existing one) is to be used in court, publication and scientific scrutiny are very

FBI’s 2009 Quity Assurance Standards. (Exh. 3).

70 “Each DNA typing method must be rigorously characterized with respect to the type of possible artifacts, the conditions under which they are likely to occur, the scientific controls for detecting their occurrence, and the steps to be taken when they occur...” NRC 1 at 54.

important. Extensive empirical characterization must be undertaken. Results must be published in appropriate scientific journals. Publication is the mechanism that initiates the process of scientific confirmation and eventual acceptance or rejection of a method.

NRC 1 at 56; *See also*, TWGDAM Guideline 4.1.5.12 (“It is essential that the results of the developmental validation studies be shared as soon as possible with the scientific community through presentations at scientific/professional meetings. It is imperative that details of these studies be available for peer review through timely publications in scientific journals.”); DAB Guideline 8.1.4 (“The laboratory shall, whenever possible, select methods that have ben published by reputable technical organizations or in relevant scientific texts or journals.”); Revised Guidelines 1.2 (“Peer-reviewed publication of the underlying scientific principle(s) of a technology is required. Peer-reviewed publication of the results of developmental validation

studies is encouraged. However, technologies or procedures may be implemented without

peer-reviewed publication if the results of developmental studies have been disseminated to the scientific community for review and evaluation through multiple ways, such as presentation at a scientific meeting or publication in a technical manual.”) The existence of an “extensive literature in peer-reviewed journals” was key to the Supreme Court’s recent ruling in *People v. Soto*, 21 Cal. 4th at 540, that population substructure does not impact significantly upon DNA RFLP population frequency estimates.

A second fundamental requirement is internal validation, which requires that the laboratory gain “a solid base of experience in forensic application” before it uses a new DNA typing method. NRC I at 55; Revised Validation Guidelines 1.2.2 (“Internal validation is conducted by each forensic DNA testing laboratory and is the in-house demonstration of the reliability and limitations of the procedure. Prior to using a procedure for forensic applications, a laboratory must conduct internal validation studies.”); DAB Standard 8.1.3 (“Internal validation shall be performed and documented by the laboratory.”); TWGDAM Guideline 4.5 (“Prior to implementing a new DNA analysis procedure or an existing DNA procedure the forensic

laboratory must first demonstrate the reliability of the procedure in-house.”) According to NRC I, internal validation involves five separate steps:

1. familiarity with the system using fresh samples (i.e., fresh blood);
2. test marker “survival” in dried stains (i.e., blood);
3. test system on simulated samples that have been exposed to various environmental conditions;
4. establish “basic competence” in the use of the system by blind trials;
5. test the system on nonprobative evidence samples in which the origin is known, to check reliability.

The NRC I recommends that when a DNA technique is initially developed, all five steps should be carefully followed. *Id.* p. 55. It further recommends that as laboratories adopt a particular technique, “it will not always be necessary for them to repeat all the steps, but they must demonstrate familiarity and competence by following steps 1, 4, and 5.” *Id.*

The 1995 TWGDAM Guidelines are even more rigorous. Guideline 4.5 provides that internal validation “must” include the following:

* + 1. The method must be tested using known samples.
    2. If a modification which materially effects the results of an analysis has been made to an analytical procedure, the modified procedure must be compared to the original using identical samples.
    3. Precision (eg. Measurement of fragmented lengths) must be determined by repetitive analysis to establish criteria for matching.
    4. The laboratory must demonstrate that its procedures do not introduce contamination which would lead to errors in typing.
    5. The method must be tested using proficiency test samples. The proficiency test may be administered internally, externally, or collaboratively.

DAB Standard 8.1.3 also requires internal validation, and adds requirements not found in TWGDAM. For instance, Standard 8.1.3.1 requires that the “ procedure shall be tested using known and nonprobative evidence samples”, and that “(t)he laboratory shall monitor and document the reproducibility and precision of the procedure using human DNA controls.”

In this case, the burden should be on the government to show that both developmental and internal validation has been conducted for all techniques used, including mixture and “low copy” analysis. An evidentiary hearing is needed to resolve these issues.

# 4. Failure in a Identifiler and low copy number case to follow generally accepted methods for maintaining chain of custody and for preventing, detecting and eliminating PCR contamination.

Another requirement established in all the reports, guidelines, and standards is the absolute necessity of maintaining a proper chain of custody and controlling for the problem of contamination in any PCR testing, but most especially low copy testing. Forensic DNA testing based on the PCR technique is very different than RFLP testing in this regard. There is universal recognition in the scientific community that special and peculiarly difficult problems must be resolved if a reliable transfer of the extremely sensitive PCR technology from its present use in research laboratories and clinical (medical) diagnostic laboratories to the forensic arena is to be accomplished.

One point that emerges immediately in considering PCR- based forensic testing is that the scientific community has unequivocally warned about special dangers of sample contamination. These dangers embrace both the methods used for the initial collection, preservation, and handling of samples by crime scene technicians as well as the methods used for processing the samples in the laboratory. The NRC 1 Report expressed its most "serious concern" about the problem of "contamination of evidence samples with other human DNA," and warns that “

1. ven the simple act of flipping the top of a plastic tube might aerosolize enough DNA to pose a problem.” NRC 1 at 65 The Report goes on to underscore that reliable methods must be developed to prevent and control contamination problems unique to forensic PCR based testing in both the sample gathering and laboratory testing processes. NRC 1 at 66. The NRC II likewise warns that “any procedure that uses PCR methodology is susceptable to error by contamination” and that “(i)f the contaminating DNA is present at a level comparable to the target DNA, its amplification can confound the interpretation of typing results, possibly leading to an erroneous conclusion.” NRC II at 23. The NRC II is also emphatic that “ the integrity of the chain of custody is of paramount importance” , and that “(t)his means meticulous care, attention to detail, and through documentation of every step of the process, from collecting the evidence material to the final laboratory report.” Id. at 25; *See also*, TWGDAM Guideline 4.5.4(“The laboratory must demonstrate that its procedures do not introduce contamination which would lead to errors in typing.”); DAB Standard 6.1(“The laboratory shall have a facility that is designed to provide adequate security and minimize contamintion.”), Standard 7.1(“The laboratory shall have and follow a documented evidence control system to ensure the integrity of physical evidence. This system shall ensure that...the laboratory follows documented procedures that minimize loss, contamination, and/or deleterious change of evidence.”)

The NAS 2009 Report states that “DNA tests performed on a contaminated or otherwise compromised sample cannot be used reliably to identify or eliminate an individual as the perpetrator of a crime.” (NAS 2009 Report, p. 9).

Therefore, it must be emphasized that a *Daubert* inquiry concerning STR PCR- based testing must embrace the methods used by the crime scene investigators and laboratories for identifying, correcting, and preventing contamination in the collection, preservation, and handling of crime scene samples. In *Hicks*, the Ninth Circuit rejected this argument with respect to DQ Alpha PCR testing. 103 F. 3d at 846. But the greater sensitivity of STR testing, particularly “low copy” STR testing, calls for a different result, as the passage quoted above from

Dr. Butler’s book and other literature to be discussed below make clear.

Contamination is the single greatest problem in the transfer of PCR technology to forensic testing. This is because the extraordinary ability of PCR to reproduce a single copy of DNA is also its greatest disadvantage. "PCR is not discriminating as to the source of the DNA it amplifies, and it can be exceedingly sensitive." (NRC I at 65). “ Any procedure that uses PCR is susceptable to error caused by contamination leading to amplification of the wrong DNA.” (NRC II at 71)

Contamination can arise in a myriad of ways. The general categories of contamination outlined by the two NRC reports are:

# Contamination from handling in the field during collection, either by cross-contaminating samples with each other directly, cross-contaminating samples through DNA carry-over on evidence gathering instruments or the gatherer's clothing, mixing up samples, or inadvertent contribution from the biological products from the evidence gatherer him or herself (sweat, sneezing, dandruff, etc.).

“The important consequences of those sorts of contamination are that samples might appear to be mixtures from several persons and, in the worst case, that only the contaminating type might be detected. The concern is greater with PCR-based typing methods than with VNTR analysis because PCR can amplify very small amounts of DNA. A false match could occur if the genetic type of the contaminating materials by chance matched the genetic type of a principle (such as a suspect) in a case or worse, if the contaminant itself came from a suspect in the case.” (NRC II at 83).

In this case, the government should be required to show through the testimony of qualified experts that the NM DPS DNA lab and other law enforcement agencies involved in the processing of the DNA evidence had, and employed, a generally accepted method for the collection, preservation, and handling of the samples in this case. The integrity of the samples from the point in time of when they were collected to when they came into the lab’s hand’s up to

the point of testing remains a mystery that should be the subject of an evidentiary hearing. *See*, *State v. Morel*, 676 A.2d 1347, 1356 (R.I. 1996) (“In the preservation and testing of DNA evidence, careful attention and proper handling of the crime sample by police and scientists are crucial in defending chain-of-custody issues and in ensuring that laboratory mislabeling and inadvertent contamination have not occurred.”).

# In the laboratory, cross-contamination of samples to each other, or contamination emanating from the evidence handlers and their instruments, while samples are being manipulated, sorted, labeled, dried, cut, before, during, and after the DNA extraction and amplification process.

Although the NM DPS DNA SOP (Exhibit 7) recognizes that the sensitivity of PCR- based analysis, involving the amplification of minute quantities of DNA necessitates precautions to avoid contamination of samples yet to be amplified, it is expected that, *at best*, the analyst in this case will be able to testify that she followed the standard procedures outlined in the protocol for preventing of cross-contamination of samples to each other, or contamination emanating from the evidence handlers and their instruments, while samples are being manipulated, sorted, labeled, dried, cut, before, during, and after the DNA extraction and amplification process.

Those procedures appear to be confined to the “special precautions” outlined in the protocol: (1) Extractions and PCR set-up should be conducted within self-contained hoods; (2) Change gloves frequently. Prior to leaving the lab area, always remove gloves and wash hands;

(3) It is important that the DNA extraction of questioned samples be performed as a separate batch or set from the DNA extraction of known samples. This precaution will help prevent potential cross-contamination between evidence samples and reference samples; (4) Every sample analyzed shall be given a unique laboratory identification number that is carried throughout the entire analysis; (5) Whenever possible, extract samples containing high levels of DNA (whole blood, high sperm counts) separately from samples containing a low level of DNA (stamps, small bloodstains, low sperm counts, etc.) to minimize the potential for

sample-to-sample contamination; (6) Use disposable gloves at all times; (7) Clean scissors thoroughly with alcohol wipes or bleach, or use fresh scalpel blades after cutting each evidence sample; (8) Use a clean cutting surface for each piece of evidence; (9) Sterilize those solutions that can be heated in an autoclave without affecting their performance; (10) Use sterile disposable pipet tips and microcentrifuge tubes; (11) Always change pipet tips between handling each sample even when dispensing reagents; (12) Store reagents as small aliquots to minimize the number of times a given tube of reagent is opened. It is recommended that the small aliquots be retained until typing of the set of samples for which the aliquots were used is complete; (13) Centrifuge all tubes before opening them; (14) Include reagent blank controls with each set of DNA extractions; (15) Before and after setting up DNA extractions, clean all work surfaces thoroughly with a 10% dilution of bleach. In addition, using disposable bench paper prevents the accumulation of human DNA on permanent work surfaces; (16) Wear a dedicated lab coats for pre-amplification and post-amplification sample handling; (17) When possible, maintain a portion of the evidentiary sample for additional testing. If consuming an entire for analysis, first receive consent to do so from the State's Attorney (if assigned) or lead detective in the case; (18) Add the appropriate “blank” solution to the negative control (no DNA added) tube last, after all DNA samples have been added to the other tubes. This tube functions as a negative control for the PCR setup; and (19) Avoid touching the inside surface of the tube caps; (20) Change pipet tips after addition of each sample DNA to a PCR Reaction Mix; (21) Store the DNA Amplification Reagents in a refrigerator separate from evidentiary samples; (22) The work area for amplified DNA analysis is a physically separate area used only for those activities that involve the handling of amplified DNA; and (23) Amplified DNA or equipment and supplies used to handle amplified DNA should not be taken out of the amplified DNA work area, unless thoroughly cleaned with bleach solution; (24) dedicated equipment and supplies in the amplified DNA analysis room should never come in contact with unamplified samples; (25) exercise caution when opening tubes; (26) Use disposable bench paper to cover the work area used to

perform specimen preparation steps to prevent the accumulation of amplified DNA on permanent work surfaces. Diluted bleach should be used periodically to wash exposed work surfaces; and

1. Use the Thermal Cycler only for amplification and denaturation of amplified DNA for typing. Never use the Thermal Cycler for incubation of tubes containing unamplified DNA; (27) Store tubes of amplified DNA in the amplified DNA room, although amplified DNA and reagents may be stored in the same refrigerator. (SOP, Exhibit 7)

As impressive as this checklist appears to be, the question is not how long the list is, but whether it was followed in this case. We already know that although negative controls were used, the results of those controls were simply ignored when they showed the presence of DNA. We also know that the analyst did not maintain a portion of several samples for retesting. Whether the other parts of the protocol were or were not followed should be resolved at an evidentiary hearing.

More importantly, whatever the sufficiency of these procedures when they were adopted in 2003, in light of more recent scientific literature and the increased sensitivity of current STR tests, these procedures are no longer sufficient to address the danger of contamination, especially in cases like the present one involving low copy number testing.

As early as 2000, Dr. Gill’s study documented the insufficiency of even more rigorous controls in low copy cases. *See*, P. Gill, et al., *An Investigation of the Rigor of Interpretation Rules for STRs Derived From Less Than 100 pg of DNA*, 112 Forensic Science International 17, 22 (“DNA extractions were carried out in facilities designed to minimise the chance of laboratory contamination. We use a purpose built laboratory that is fitted with a HEPA filter and maintained under positive air pressure. There is restricted access; all operators wear disposable gowns and masks. All plastic-ware used was guaranteed DNA-free by manufacturers, and was treated with UVprior to use. *Nevertheless, negative controls still showed spurious alleles, albeit at low level. In the example shown in Table 1, 21 of 30 negative controls showed evidence of contamination.”*); Id. at 23-24 (“Within the context of LCN, we have shown that the negative

control does not act as indicator of minor contamination within associated processed samples of the same batch.This is because the method is sensitive enough to detect a single molecule of DNA. By definition, one molecule cannot affect more than one tube hence the negative control cannot operate in the traditional sense. Conversely, casework samples could be affected by laboratory-based contaminants that do not appear in the negative control.”).

Because of the “increased risks of laboratory-based contamination to consider in a LCN case, Gill and his co-authors, and others, have recommended additional precautions, including that “[d]uplication of every allele is demonstrated before reporting”, and that “[i]n the context of LCN, replication of extraction negative controls is recommended in order to determine if laboratory-based contaminants are reproducibly amplified.” (Id. at 25). In a subsequent article, Dr. Gill expanded on these requirements:

Because there is a serious possibility of transferring LCN DNA from a

modern source, to either minimize the chance of contamination or to identify an occurrence,we use the following guidelines:

* 1. DNA extractions and setting up PCR reactions are carried out in a dedicated laboratory.
  2. Personnel wear disposable laboratory coats, gloves, and face masks.
  3. Benches and equipment are frequently treated with bleach (or equivalent) and irradiated with Uvlight.
  4. PCR amplification is carried out in a separate laboratory or laboratory area.
  5. Negative controls are used with every test to demonstrate absence of contamination.
  6. PCR tests are duplicated wherever possible.

P. Gill, *Application of Low Copy Number DNA Profiling*, 42 Croatian Medical Journal

229 (2001), available at [http://www.cmj.hr/2001/42/3/11387628.pdf.](http://www.cmj.hr/2001/42/3/11387628.pdf) None of these stringent procedures were followed in this case.

Under these circumstances, and given that no other recommendations for low copy testing appear to have been followed, no DNA evidence should be permitted for any low copy samples.

Other parts of the protocol, even if followed, are similarly flawed. For instance, there is an emphasis on using disposable gloves and changing them frequently. However, it has been demonstrated that gloves themselves are a source of contamination and that gloves do not prevent “pass through contamination”. As demonstrated in M. Miguel Lorente, *Potential Contamination When Wearing Sterile Gloves During PCR Preparation: Pass-Through Contamination From Skin*, Proceedings of the American Academy of Forensic Sciences (Feb. 2003), p. 68, available a[t http://www.aafs.org/pdf/2003ChicagoProceedings.pdf](http://www.aafs.org/pdf/2003ChicagoProceedings.pdf) :

One vector for contamination is the gloves worn during experimentation. It is imperative to wear sterile gloves and change the gloves as needed. Clinical and epidemiological studies have demonstrated that bacterial and viral contamination can occur on the surface of sterile gloves after being worn for a period of time. Thus, DNA may get on gloves and be transferred during handling (i.e., cross contamination). It is also possible for DNA to leach from the user’s hand through the glove (i.e., pass through contamination). While contamination of this nature is not a routine concern, it may explain rare circumstances of undefined contamination....

[E]xperiments show that ...even after five minutes some DNA leached through the gloves, even in the apparent negative controls. These results are compatible with the clinical studies which have shown that after a time, even with careful washing, bacterial and virus contamination on the surface of the gloves can occur related to time and user.

This same study and others show that “even. careful washing” does not prevent DNA

contamination. *See also*, C. Nussbaumer, et al., *DNA-Typing of Sperm Collected From*

*Skin and Clothes After Washing*, Proceedings of the American Academy of Forensic Sciences (Feb. 2003), p. 69, available a[t http://www.aafs.org/pdf/2003ChicagoProceedings.pdf](http://www.aafs.org/pdf/2003ChicagoProceedings.pdf) (“The

results of DNA-typing of samples from ...experiment[s] show that neither showering nor laundering by washing machine removed all of the sperm cells. Most of the samples from the skin were typed successfully and even showed high amounts of male DNA. Similarly, most of the samples of laundry showed full DNA profiles of the sperm donor.”).

The FBI has demonstrated that DNA samples remain subject to successful DNA typing even after being exposed to household bleach. *See*, A. Isenberg, et al., *DNA Typing of a Polymerase Chain Reaction Amplified DlS80/Amelogenin Multiplex Using Capillary Electrophoresis and a Mixed Entangled Polymer Matrix*, 17 Electrophoresis 1505, 1508. (1996). There are also “reports of alcohol pre-treatments *enhancing* PCR yields.” D.McNevin, *Short Tandem Repeat (Str) Genotyping of Keratinised Hair Part 1. Review of Current Status and Knowledge Gaps*, 153 Forensic Science International 237 (2005)(emphasis added). Bleach and alcohol do not work.

The use of steam sterilization (autoclaving) to sterilize instruments and reagents is similarly a procedure that the forensic community itself has proven to be ineffective in controlling contamination. *See*, J. Sanderson, *The Effects of Steam Sterilization on DNA*, 1998 Promega Eighth International Symposium on Human Identification, available at

<http://www.promega.com/geneticidproc/ussymp8proc/ab38.html(>“The practice of autoclaving reagents and supplies used in aseptic protocols has been widely accepted within the scientific community. There has been a question however, as to whether steam sterilization destroys all possible contaminating DNA-especially sequences synthesized by the Polymerase Chain Reaction (PCR). It has been proposed that the high pressures involved in autoclaving simply scatters the DNA molecules randomly about the vessel they are contained within rather than breaking them down. To address this question, an experiment was performed to determine if DNA subjected to steam sterilization would be broken apart to the point where it was unsuitable for amplification ...These results prove amplified DNA products are more substantial than can be disposed of by autoclave sterlization.”). It is also apparent from the protocol itself that the NM

DPS DNA Laboratory does not follow the recommendations of the F.B.I. and others that DNA lab technicians should wear protective hair nets and face masks.

Most surprisingly, even the UV irradiation procedure recommended by Dr. Gill has been found to be ineffective in controlling PC contamination. *See*, K. Shaw, et al., *Comparison of the Effects of Sterilisation Techniques on Subsequent DNA Profiling*, 122 Int J Legal Med (2008) 29–33 (“Four sterilisation techniques (UV, gamma and beta radiation and ethylene oxide treatment) were examined for their potential to degrade contaminating DNA to such an extent that subsequent DNA profiling was impossible. This work indicated that the most successful technique to reduce DNA contamination was ethylene oxide treatment. Of the radiation techniques tested in this study, gamma was the most successful at eradicating DNA and UV radiation was the least.”)(“It is clear from this study that UV radiation, using the parameters specified here, does not degrade amplifiable DNA sufficiently, as full profiles were obtained from all samples.”)71

In sum, although there are issues to be resolved at an evidentiary hearing, the current scientific literature indicates quite clearly that the contamination controls in place at the NM DPS DNA Laboratory are insufficient to guard against the very real danger of contamination in a case involving samples of less than 100 picograms. Thus, even if the analyst testifies that she followed the laboratory’s contamination protocol, the DNA evidence in this case should be excluded under Rule 702.

71 *See also*, Jeannie Tamariz, *The Application of Ultraviolet Irradiation to Exogenous Sources of DNA in Plasticware and Water for the Amplification of Low Copy Number DNA*, Proceedings of the American Society of Forensic Sciences, Vol. XII, Feb. 2006, available at <http://www.aafs.org/pdf>/Seattleabstracts06.pdf (“Using High Sensitivity Forensic STR PCR DNA typing methods, it was deter, available at mined that contamination of presumably sterile plastic ware and water can be present in low concentrations not previously detected by standard PCR methods. One technique commonly used to eradicate the presence of DNA is ultraviolet irradiation...Overall, there was a decrease in concentration of DNA recovered as the duration of treatment increased. Nonetheless, following 45 minutes of irradiation of a PCR plate with 500 pg of DNA, 5.7 pg was still apparent.”)

# Contamination from contaminants in solutions, reagents, aerosols, water, and even in Taq DNA polymerase.

As the NRC I warns, "(e)ven the simple act of flipping the top of a plastic tube might aerosolize enough DNA to pose a problem." (NRC I at 66). The NRC II recommends that “ adherence to a standard QC program provides safeguards against these kinds of laboratory error.” (NRC II at 82). In this case, the NM DPS DNA Laboratory has some Quality Control (QC) language in its Quality Assurance Manual, outlining on paper an established QC program. The question to be resolved at an evidentiary hearing is whether the program was followed in this case. Of particular concern is whether the laboratory followed the FBI’s established protocol of quality control testing of several critical reagents, including the GS500 (ROX) standard, formamide, Performance Optimized Polymer (POP-4), and the Genetic Analyzer Buffer.

# PCR product carryover contamination - the contamination of evidence samples or reaction solutions with PCR products from prior amplifications.

“The most serious problem is contamination of evidence samples and reaction solutions with PCR products from prior amplifications.” (NRC I at 66). “ A false match can occur if the genetic type of a contaminant matches by chance the genetic type of a principle in the case; in the worst case, the contaminant originates from another party in the case.” (NRC II at 84).

One of the developers of the Cetus/Roche kit, Dr. Russell Higuchi, describes the phenomenon:

More unique to PCR is the possibility of carryover contamination from a completed PCR to another sample yet to be amplified. Because by the nature of PCR, PCR product will seed production of more PCR product, the sheer number of copies of PCR product after amplification can make the consequences of such contamination more dramatic. A typical PCR could have 1012 copies of an amplified gene. If a preparer inadvertently transfers, as before, 0.1 µl72 of PCR sample A into sample B, even though sample B has a relatively high concentration of human DNA, the number of copies of the target,

72 A µl is a microliter (one millionth of a liter).

single-locus gene that derive from sample A far outnumber the copies that actually stem from sample B. Thus, the DNA type obtained will be that of A and not B, and the relative amount of the B type is so small that it would not even show up in the test, eliminating the possibility that the presence of more than two alleles would flag the occurrence of the contamination.73

The NRC highlighted the problem of PCR carryover contamination as a key area of vulnerability, declaring "it has become clear that carryover products from one PCR reaction to another must also be eliminated." NRC 1 at 67. Accordingly, the NRC commented that “[m]ethods of detecting and preventing contamination from one PCR reaction to another in forensic laboratories are generally still in their early stages, and additional development should be encouraged.”

It is plain, however, that forensic PCR laboratories have not responded appropriately. For example, the NRC pointedly suggested that it would be a good idea to treat all evidence samples with uracil N-glycose (UNG) before amplification to destroy any PCR carryover from previous PCR reactions. *Id*. Clinical laboratories have followed up on this idea. *See*, H. Burkardt, Standardization and Quality Control of PCR Analysis, 38 Clin Chem Lab Med. 87 (2000)( finding that because of the failure to use chemical anti-contamimation controls like UNG, “(t)he first diagnostic results that were obtained by the new PCR technology were a disaster because of the high rate of false-positive tests created by contamination”).

As far as the defense is aware, forensic PCR laboratories, including the one which did the testing in this case, do not use UNG or any other chemical treatment to protect against carryover contamination.

The NRC II recommends among other precautions the maintenance of a one-way flow of material and the use of chemical sterilization precautions. The DAB Guidelines are clear on this

73 R. Higuchi and E.T. Blake, “PCR in Forensic Science, DNA Technology and Forensic Science,” 32 *Banbury Report*, Cold Spring Harbor Laboratory Press (1989), at page 275.

point. Standard 6.1.3 provides that “ The laboratory shall ensure that...amplified DNA is generated, processed and maintained in a room(s) separate from the evidence exzamination, DNA extraction and PCR setup area.” The Profiler Plus User’s Manual treats the threat of cross- contamination as so serious as to require four designated work areas. In this case, an evidentiary hearing is necessary to resolve how exactly the New Mexico’s DNA Laboratory guards against cross-over contamination. The contamination reports summarized above suggest that the contamination control in the laboratory is lax.

Many laboratories attempt to downplay the problem of contamination by claiming that there have not been any “outbreaks of contamination”, but only “isolated instances” or “excessive number of incidents of contamination.” as pointed out above, this attempt at downplaying the significance of the contamination problem is an approach that has been rejected as early as the first NRC report:

As with contamination due to handling, carryover contamination can be signaled by the appearance of product in blank controls and of mixed or inappropriate types in samples and positive controls. Such controls should be used rigorously. *Moreover, it should be remembered that the controls are useful for monitoring general contamination in the laboratory, not the accuracy of a particular experiment. If a blank control is positive in one experiment, it indicates a potential problem not just for that experiment, but for any experiment performed at about the same time—even in a laboratory contaminated with PCR carryover, blank controls do not necessarily become contaminated on every occasion. It will be wise to repeat all work with samples that have never been exposed to the PCR-typing laboratory.*

(NRC I, p. 67)

# Failure to follow any procedure to correct for the known fact that short tandem repeats can be the same length but different sequence.

The Identifiler kit types the length of a short tandem repeat, not its actual sequence. Yet as Dr. Butler explains in his book, it is being discovered with increasing frequency that certain STRs have the exact same length but in fact two different DNA sequences. As he explains,

Complex repeat sequences , such as those found in D21S11 , can contain variable repeat blocks in which the order is switched around for alleles that are the same length . For example , the STR locus D21S11 has four alleles that are all 210bp when amplified with the Identifiler kit (Appendix I) . While these alleles would be sized based on overall length to be “allele 30,", they contain repeat blocks of 4-6-CR-12 , 5-6-CR-11 , 6-5-CR-11 , and 6-6-CR-10 for the pattern

[TCTA ] - [ TCTG ] -constant region ( CR ) - [ TCTA ]. *In such cases , variant alleles would only be detectable with complete sequence analysis* .”

(J. Butler, Advanced Topics, p. 129 (emphasis added).

Dr. Butler’s “solution” to this problem is startling. He states:

It is important to realize that from an operational point of view internal allele variation is not significant . In the end a match is being made against many loci not just one , such as D21S11, with possible internal sequence variation.

Most of the STR loci used in human identity testing have not exhibited internal sequence variation, particularly the simple repeat loci TPOX, CSF1PO, D5S818, D16S539, TH01, D18S51, and D7S820. 74 Alleles are binned based on measured size with STR typing since *sequence analysis of individual alleles is too time consuming* and, because STR variation is primarily size-based, would *rarely* reveal additional information.

(Butler, Advanced Topics, p. 128 (emphasis added).

In other words, simply ignore the problem because the sequencing solution would be “too consuming” and would only “rarely” reveal additional information. That cannot be reliable

74 It is interested to note that in the 2005 edition of his book this sentence read: “Most of the STR loci used in human identity testing have not exhibited internal sequence variation, particularly the simple repeat loci *D8S1179, D3S1358, D21S1138, VWA* .” John Butler, Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers (2nd ed. 2005), p. 131-132 (emphasis added). In the 2012 edition the sentence was changed to read: “Most of the STR loci used in human identity testing have not exhibited internal sequence variation, particularly the simple repeat loci *TPOX, CSF1PO, D5S818, D16S539, TH01, D18S51, and D7S820*.” The sentence had to be changed because between 2005-2012, it was discovered that alleles at the D8S1179, D3S1358, D21S1138, VWA loci did exhibit internal sequence variation. The situation is a good illustration of how fluid our state of knowledge is about STRs, and how assertions being made by DNA experts rapidly become incorrect as new information is learned. As Butler acknowledged in his 2005 book, “we have listed the reference where each new allele ( and its sequence if published ) has been described . As more and more samples are analyzed using these STR loci , we recognize that new ( rare ) alleles will be discovered and that this list will quickly become outdated.” Butler, Forensic DNA Typing , p. 561- 562.

scientific procedure in a case in which the analyst is attributing DNA to a particular source, especially since most labs now routinely engage in mitochondrial DNA analysis, which utilizes sequencing analysis, and most especially in light of Dr. Butler’s own admonition that “[i]n forensic DNA typing, if any *one* STR locus fails to match when comparing the genotypes between two or more samples, then the profiles between the questioned and reference sample will be declared a non-match, *regardless of how many other loci match*.” John Butler, Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers (2nd ed. 2005), p. 386 (emphasis added).

In this case, the very problem Dr. Butler describes with respect to the D21S11 locus is present in multiple ways. According to Appendix I of Butler’s Advanced Topics book (pp. 551- 571), there are actually four “allele 30s” at this locus, all with the same length, but with different sequences, designated as 30a, 30b, 30c, and 30d. According to the government, Mr. McCluskey and the steering wheel and gearshift samples, as well as all other samples being matched to Mr. McCluskey, were typed as a 30, 31.2 at this locus. But the Identifiler kit only measures length, not sequence. What if Mr. McCluskey is a 30a, 31.2, or a 30b, 31.2, and the evidence samples are really a 30c, 31.2, or a 30d, 31.2 at this locus, or vise versa ? According to Dr. Butler’s interpretative rules, he would be excluded as the source of the sample, and the kits would have missed the exclusion. What does this do to the absoluteness of the source attribution statistics being offered in this case? What does it do to the underlying theory that the Identifiler kit an unambiguously discern a person’s alleles ?

Similarly, Tracy Province and the evidence samples he was matched to were typed as 29,

31.2 at the D21S11 locus. According to Appendix I, there are two “29 alleles”, 29a and 29b. Again, what if Tracy Province is a 29a, 31.2 at this locus and the samples he was matched to are a 29b, 31.2 , or vise versa ? Again, an exclusion is being missed and the data is being misleadingly presented in such a way as to suggest that the alleles can be unambiguously typed with the Identifiler kit, when in fact they cannot. The same problem exists for the samples

matched to Ms. Welch. She and the evidence samples she was matched to were typed as a 28,

33.2 at the D21S11 locus. According to Appendix I, there are two “28 alleles” (28a and 28b), and there are three “33.2 alleles” (33.2a, 33.2b, and 33.2 c.) The Identifiler kit treats them all the same, but they are not the same.

It is also important to recognize that this problem is not confined to D21S11, as Dr. Butler implies. Mr. McCluskey and the evidence samples matched to him typed (under the government’s view) as a 13, 14 at the D8S1179 locus. Appendix I of Dr. Butler’s book indicates that there are actually four “allele 13s”, 13a, 13b, 13c, and 13d. Same problem. At D371358, Mr. McCluskey and the evidence samples matched to him typed (under the government’s view) as a 17, 17. Appendix I of Dr. Butler’s book indicates that there are actually three “allele 17s”, 17a, 17b, and 17c. Same problem. At D21338, the government claims that Mr. McCluskey and the evidence samples to which he was matched both type as 23, 23. Appendix I of Dr. Butler’s book indicates that there are actually two “allele 23s”, 23a, and 23b. Same problem. At VWA, the locus Dr. Butler claimed in 2005 had not exhibited any internal sequence variation, the government claims that Mr. McCluskey and the evidence samples to which he was matched both type as 16, 16. Appendix I of Dr. Butler’s 2012 book indicates that there are actually two “allele 16s”, 16a, and 16b. Same problem. In all, this issue comes up for 5 of 15 loci typed for Mr.

McCluskey, for 4 of 15 loci typed for Mr. Province, for 4 of 15 loci typed for Ms. Welch, for 3 of 15 loci typed for Mr. Haas , and for 3 of 15 loci typed for Mrs. Haas . This hardly suggests a rare occurrence confined to D21S11.

Lastly, Dr. Butler states in his 2012 book, but not in is earlier book, that “[o]ver the past several years, work with mass spectrometry has demonstrated that same-size STR alleles with different internal sequences or alleles with sequence variation in the flanking region can be resolved from one another using a base composition approach.” (Butler, Advanced Topics, p.

128-129)(citing numerous studies). Thus, the technology exists to type STRs by sequence, and not length, but this technology is not being used because it is “too time consuming.” That may be

true, but in the meantime the DNA analyst in this case should not be able to assert or imply that the Identifiler kit can accurately and reliably discern alleles at the 15 loci tested.

This sequence vs. length problem would seem to deliver the knockout punch to the source attribution theory, as well as to the other astronomical numbers generated by the government, which fail to account for the statistical likelihood of a mistaken match based on the failure to recognize a sequence difference. Further, it calls into question the very reliability of the Identifiler kit. How can the government be telling a jury that nobody else in the world could have contributed the sample, when the DNA test it is using is leaving unresolved whether there is an exclusion, based on sequence differences, between the suspect and the evidence sample.

Although it may or may not be “too time consuming” to resolve this crucial issue, that is no excuse in a death penalty case. Because of this problem, the evidence should be ruled inadmissible under D*aubert* and Rule 702.

# Failure to follow any procedure to correct for the danger of primer binding site mutations.

Another disturbing feature of Applied Biosystems’ typing kits is that the results that are obtained from the kit can vary from the results obtained using competitor Promega kits. See, Butler, Advanced Topics, Ch.5) Thus, one piece of evidence analyzed with the Identifiler or Profiler Plus kit may have a different genetic profile than one analyzed with a Promega kit. If the Court follows the reasoning of some courts who hold that any kit that uses PCR or tests for STRs has already been validated for court use, then both results and both kits would be considered reliable since both use PCR and test at STR loci.. This is logically inconsistent and would lead to absurd results. For example, if one lab tested the evidence using a Promega kit and the results were inculpatory, and then another lab retested the same evidence with a Perkin Elmer kit and the results were exculpatory, then one expert would have to testify that both kits were reliable and generally accepted. This example illustrates the fallacy of the argument and the reasoning that STR based tests are interchangeable because they involve STR markers as a class or PCR as a

common element.

The inconsistency in test results between the two manufacturers is documented in the series of articles that began to appear in the late 1990s and have continued to this day. *See* e.g., David Parsons, *Resolution of a Typing Differance Between Perkin Elmer’s Profiler Plus Kit and Promega’s PowerPlex 1.1 Kit Using Sequence Analysis*, Tenth International Symposium On Human Identification(1999)(Two samples typed as a homozygous at vWA locus using Profiler Plus kit, but as heterozygous using Promega’s PowerPlex kit. A primer binding site mutation was suspected as the cause, but “(s)ince the sequence for the primers for the Profiler Plus are not published, the exact location of the mutation with respect to the primer cannot be known. If this mutation occurred in the priming region for Perkin Elmer’s Profiler Plus kit, it would provide the needed explanation for the observed results.”)75 ; C. Alves, et. al., *vWA STR Genotyping: Inconsistency Between Perkin Elmer’s Profiler Plus Kit And Promega’s Geneprint*, International Society for Forensic Haemogenitics, Eighteenth International Congress Abstracts, August 17-21, 1999, San Francisco, Ca., p. 30, (simultaneous study of vWA locus by the Perkin Elmer’s Profiler Plus Kit and the Promega Geneprint Kit produced an inconsistency between the genotyping in each kit: using Profiler Plus it was found to be 18, 18 and with Geneprint 16, 18. “Since primer sequences were not available from the manufacturers we could not sequence the corresponding regions. However, it is tempting to interpret the inconsistency as a result of a Perkin Elmer primer annealing failure The finding now reported evidences the need for

caution when comparing genotypes or gene frequencies made in amplicons and produced by different primers.”); M.C. Kline, et. al., *Nonamplification of a vWA Allele*, J. FORENSIC SCI. 1998 Jan., 43(1):250 (National Institute of Standards and Technology researcher documents same inconsistency and indicates that Perkin Elmer “is aware of the problem and they are actively

75[http://www.promega.com/~/media/files/resources/conference%20proceedings/ishi%2010/poster](http://www.promega.com/%7E/media/files/resources/conference%20proceedings/ishi%2010/poster)

%20abstracts/70parsons.pdf?la=en

pursuing an explanation for this allelic dropout by sequencing the sample”); S. Walsh, *Commentary on Kline, MC, Non-Amplification of a vWA Allele*, J. FORENSIC SCI. 1998 Sept., 43(5) 1103 (Perkin Elmer admits the problem exists, and claims it is caused by a flanking sequence mutation. “Our laboratory has observed flanking sequence mutations in several STR loci, including the vWA loci reported here, D16S539, and TPOX. Other laboratories have reported flanking sequence mutations at D13S317 and DS7820. Perkin Elmer admits that the problem will continue, but claims that it can be avoided by using Perkin Elmer products exclusively.”). *See also*, A. Amorim, et. al, *Genotyping Inconsistencies and Null Alleles Using AmpFLSTR Identifiler and Powerplex 16 Kits*, International Congress Series 1261 (2004) 176–178 (“A total of 22 inconsistencies between kits was observed (for D5S818, D8S1179, D16S539, FGA and VWA”; these findings “confirm the results from previous studies showing that a nonnegligible proportion of genotypic inconsistencies is expected to occur for any

PCR-based system when using different primer pairs.”). 76

In this case, using the Identifiler kit, the government claims that Mr. McCluskey and the samples to which he was matched are homozygote at loci DS7820 (10, 10), D3S1358 (17, 17), D16S539 (12, 12), D2S1338 (23, 23), D19S433 (14,14), vWA (16, 16), TPOX (8, 8), and

D5S818 (13,13). At all of these loci only a single peak shows up at each loci; e.g., at D5S818 ony a 13 peak is visible. But what if, because of this problem, Mr. McCluskey is actually a 13, 14, or a 13, 15 at this locus, and the evidence sample is in fact a 13, 13, or vise versa ? Once again, an exclusion is being missed. The same issue exists for Mr. Province (homozygote at 5 loci), Ms.

Welch (homozygote at 2 loci), Mr. Haas (homozygote at 6 loci), and Mrs. Haas (homozygote at 6 loci). So far as the defense is aware, the New Mexico’s Crime Laboratory has not adopted any of the remedies suggested in the scientific literature to address this problem. This stance cannot be considered reliable scientific procedure in view of the severity of this particular problem in this

76<http://www.isfg.org/files/dc16f182fbefb9ba18c36aff32e06c8f08fabcfa.03014961_3596>

15819513.pdf.

case.

# Failure to account for tri-allelic patterns.

A crucial assumption underlying the NM DPS’s mixture analysis in this case is that every individual only has two alleles at each DNA locus.

However, as Dr. Butler points out in his book, “[t]hree-banded or tri-allelic patterns are sometimes observed at a single locus in a multiplex STR profile . These extra peaks are not a result of a mixture but are reproducible artifacts of the sample The three peaks or bands seen at

a particular locus may or may not be equal in intensity . While the TPOX three-banded patterns reported by Grouse and co-workers ( 1999 ) were approximately equal in intensity ( similar to Figure 6 . 7a ), there are also occasions when tri-allelic patterns occur with peaks of unequal intensity More than 50 different tri-allelic patterns have been reported at all 13 CODIS STR

loci with most of them being seen at TPOX and FGA.” John M. Butler, Forensic DNA Typing, Second Edition: Biology, Technology, and Genetics of STR Markers (Academic Press, 2005), pp. 132-133. *See also*, Michelle Uithoven, The Success of the California DNA Data Bank and the Unusual Offender Profiles Seen, CAC News, Feb. 2005, available at <http://www.cacnews.org/pdfs/1st%20q%202005.pdf>(“Given the fact that an analyst working in the CAL-DNA Data Bank could analyze more than 1,000 profiles in one day, it is surprisingly common for an analyst to see a variety of genetic anomalies such as tri-alleles, microvariants, partial null alleles, and even complete null alleles. These types of profiles may be rare to a casework DNA analyst because they do not typically see the large number of profiles a Data Bank analyst does on a daily basis. Querying the CAL-DNA Data Bank has shown that there are

a total of 372 offender profiles that have a tri-allelic variant at one or more locus and that the four most common tri-allelic loci are TPOX, D18S51, D21S11 and D13S317.”)

So far as the defense is aware, New Mexico’s Crime Laboratory lab has not adopted any

remedy to correct this problem. This failure cannot be considered reliable scientific procedure in view of the severity of this particular problem in this case, where a complicated mixture is being interpreted.

# Use of a computer software program for calling alleles that has been shown to produce erroneous results.

Exhibit 27 is a July 2000 article from the FBI’s journal *Forensic Science Communications* entitled *Modification of the Stutter Position Label-Filtering Macro in the PE Biosystems Genotyper Version 2.5 Software Package: Resolution of Stutter Filter Backtalk*, which documents that researchers from the Oregon State police have found a major glitch in the Genotyper Software package used with the Profiler Plus kit. The glitch causes both the unmodified version of the software and Oregon’s modification of the software to make erroneous allele calls because of a software problem called “stutter filter backtalk”. The authors specifically recommend a proven protocol for correcting the problem.

In this case, it is unclear whether without a hearing whether the New Mexico’s Crime Laboratory is aware of this problem and took any specific steps to correct it, as other labs have done. The question at the evidentiary hearing will be whether the lab followed the recommended fix in this case. Manifestly, the failure to correct a software problem that causes erroneous allele calls cannot be correct or reliable scientific procedure.

# Failure to adhere to the FBI Quality Assurance And SWGDAM STR Interpretation Guidelines For Interpreting STR data and artifacts.

DAB Guideline 9.6 provides that “(t)he laboratory shall have and follow written general guidelines for the interpretation of data.” Exh. 3 at 20. The SWGDAM *Short Tandem Repeat Interpretation Guidelines* states that

Because forensic DNA typing characterizes STR loci using PCR and electrophoretic technologies, some data that result from this analytical scheme

may not represent actual alleles that originate in the sample. It is therefore necessary, before the STR typing results can be used for comparison purposes, to identify any potential non-allelic peaks. Non-allelic peaks may be PCR products (e.g., stutter, non-template dependent nucleotide

addition, and nonspecific amplification product), analytical artifacts (e.g., spikes and raised baseline), instrumental limitations (e.g., incomplete spectral separation resulting in pull-up or bleed-through), or may be introduced into the process (e.g., disassociated primer dye). Generally, non-allelic data such as stutter, non-template dependent nucleotide addition, disassociated dye, and incomplete spectral separation are reproducible; spikes and raised baseline are generally

non-reproducible.

(Exhibit 14, p. 5)

The Guidelines provide that a laboratory is required to establish “ criteria based on empirical data (obtained internally or externally), and specific to the amplification and detection systems used, to address the interpretation of non-allelic peaks.” (Id.)

An evidentiary hearing is needed to assess whether these guidelines have been followed in this case.

# Failure to adhere to other essential quality control testing.

The existing scientific literature suggests the urgent need for more rigorous quality control testing in cases involving the Identifiler and the 3130 Genetic Analyzer and other Applied Biosystems typing kits and Genetic Analyzers.

For example, Exhibit 28 is an article from the 2000 Promega Eleventh International Symposium on Human Identification entitled *Matrix Files: Problems and Solutions* which documents problems with bad matrix files which “can produce extraneous peaks in the STR electropherograms.”. The article suggests specific protocols to avoid these problems, including cleaning plates in 1 M sodium hydroxide, adjusting volumes of DNA template and reagents, creation of new matrices, and tracking of plates and cassettes. The NM DPS DNA Laboratory should be shown to be in compliance with these standards in order to negate the possibility that the matrices themselves are causing false peaks.

Similarly, Exhibit 29 is a September 2000 article in the Journal of Forensic Sciences entitled *Detection and Correction of a Migration Anomaly on a 310 Genetic Analyzer* which documents “erroneous allele calls by Genotyper software due to retarded migration” caused by an eroded connector for the cathode mounted on the heat plate assembly of the 310 Genetic

Analyzer. The study “warrants additional quality measures during STR analysis on the 310 GA, particularly for analysis of forensic evidence samples where the quantity of sample can be limited.”

Exhibit 30 is a 2001 Journal of Forensic Science article entitled *Evaluation of Capillary Electrophoresis Performance Through Resolution Measurements* stating that “(t)he quality of the reagents used in CE [capillary electrophoresis] can drastically affect resolution”, and recommending that quality assurance program include routine “resolution testing”to provide “an evaluation of the health of the capillary electrophoresis system.”

Exhibit 31 is an article entitled *ABI Prism® 3100 Genetic Analyzer Instrument to Instrument Variation*, in the Abstracts of the Genetic Identity Conference Proceedings, 16th International Symposium on Human Identification - 2005, which demonstrated that “the same amplified product run on different ABI 3100 Genetic Analyzers produced noticeably different peak heights for the same alleles”, that “ average peak height intensities for entire samples or across allelic ladder alleles varies as much as two fold across the 11 genetic analyzers”, and that “the relative instrument intensity tended to correlate with instrument age, but not specifically with laser age."

Exhibit 32 is an article entitled *Differences in Electropherogram Peak Heights Reported by Different Versions of the Genescan® Software*, in the Abstracts of the Genetic Identity Conference Proceedings, 14th International Symposium on Human Identification - 2003, which reports that the instrument's three different smoothing options “have been known to result in significant differences in the peak heights that are reported”, that “[i]mprovements in the underlying algorithm of the most recent version of the software also result in significant and somewhat predictable differences in peak height values”, and that “[l]aboratories that have performed validation studies using older versions of GeneScan® should either reanalyze the data generated in those validation studies with the newest version of the software or otherwise take into consideration the systematically higher peak height values obtained as they begin following

the recommendation of the manufacturer and use the new algorithm."

Exhibit 33 is an article entitled *Addressing Ambient Temperature Variation Effects on Sizing Precision of AmpFlSTR® Profiler Plus™ Alleles Detected on the ABI Prism® 310 Genetic Analyzer* in Forensic Science Communications, January 2003,Volume 5, Number 1, which documents that that “ [o]ne critical factor affecting precision is the electrophoresis running temperature”, that “[c]hanges in running temperature affect the viscosity of the polymer matrix and the sieving of DNA fragments”, that “it can also affect DNA secondary conformation”, that . [b]ecause the entire length of the capillary on the 310 Genetic Analyzer is not insulated, ambient temperature fluctuations that occur can affect the run temperature, at least in the exposed portions of the capillary”, that “[t]he manufacturer recommends that the ambient temperature not vary by more than ±2ºC during a run” , and that “periodic runs have shown losses in precision, presumably due to fluctuations in ambient temperature."

These studies demonstrate conclusively that Applied Biosystems’s DNA typing kits and their associated software are extremely temperamental instruments that requires many quality control measures to ensure accuracy and reliability. In this case, an evidentiary hearing is necessary to ascertain if any of these quality control measures were utilized. The failure to adhere to these measures should render the evidence unreliable and inadmissible under Rule 702 (3).

# M. Rule 901(b)(9) Requires That an Adequate Foundation Be Laid Before Any of the Government’s Computer Generated DNA Evidence Is Admitted into Evidence

This motion began with a brief description of the complexities inherent in the hardware and software programs used to generate the electropherograms that serve as the foundation for the expert opinions at issue in this motion. While the computer technology itself is highly complicated and subject to numerous pitfalls, the structure of the DNA expert’s testimony in this case can be very simply described: the analyst utilizes computer technology to produce labelled peaks that the analyst then relies upon and interprets to declare a match. In that sense, the

government's evidence utilizes true "black box" technology: the technician feeds the sample in and the computer, through some mysterious process, transforms the sample into peaks on a printout. The computer even labels the alleles for the analyst. The expert is using those peaks and the labelled alleles as the basis for her opinions in this case.

Rule 901(b)(9) of the Federal Rules of Evidence provides that authentication or identification of a process or system requires "[e]vidence describing a process or system used to produce a result and showing that the process or system produces an accurate result." The advisory committee notes to rule 901(b)(9) provide that the rule "is designed for situations in which the accuracy of a result is dependent upon a process or system which produces it." The notes also suggest that the rule is particularly adapted to such "recent developments" as the computer. Therefore, the federal rule dictates that the inquiry into basic foundational admissibility requires sufficient evidence to authenticate both the accuracy of the image and the reliability of the machine producing the image. *See*, C. Mueller & L. Kirkpatrick, 5 Federal Evidence (3d ed. 2007) § 9.20 (“The Rule speaks in generic terms, as if only the process or system itself must be described and in effect validated, but the authentication of particular evidence generated or collected by means of a process or system also requires specific proof indicating that the underlying method was properly followed or put into execution in the particular case.”)

Several factors that establish authentication under rule 901 of the Federal Rules of Evidence have been identified. "This standard can generally be satisfied by evidence that (1) the computer equipment is accepted in the field as standard and competent and was in good working order, (2) qualified computer operators were employed, (3) proper procedures were followed in connection with the input and output of information, (4) a reliable software program was utilized,

(5) the equipment was programmed and operated correctly, and (6) the exhibit is properly identified as the output in question." C. Mueller & L. Kirkpatrick, 5 Federal Evidence (3d ed. 2007) § 9.20 (citing other commentators); E. Weinreb, *“Counselor, Proceed With Caution”:The*

*Use of Integrated Evidence Presentation Systems and Computer-Generated Evidence in the Courtroom*," 23 Cardozo L. Rev. 393, 410 (2001) (citing same factors); *See*, *State v. Swinton*, 268 Conn. 781, 847 A.2d 921(2004)("We agree that ‘[r]eliability must be the watchword' in determining the admissibility of computer generated evidence;... and we conclude that these six factors adequately refine our requirement ... that, in order to lay a proper foundation for computer generated evidence, there must be ‘testimony by a person with some degree of computer expertise, who has sufficient knowledge to be examined and cross-examined about the functioning of the computer.'... In addition to the reliability of the evidence itself, what must be established is the reliability of the procedures involved, as defense counsel must have the opportunity to cross-examine the witness as to the methods used.")(extensive discussion); *Commercial Union Ins. Co. v. Boston* Edison Co., 412 Mass. 545, 549, 591 N.E.2d 165 (1992) (conditioning admissibility on sufficient showing that: "[1] the computer is functioning properly;

[2] the input and underlying equations are sufficiently complete and accurate [and disclosed to the opposing party, so that they may challenge them]; and [3] the program is generally accepted by the appropriate community of scientists"); *Kudlacek v. Fiat S.p.A.*, 244 Neb. 822, 843, 509 N.W.2d 603 (1994) (same); *State v. Clark*, 101 Ohio App.3d 389, 416, 655 N.E.2d 795 (1995) (same), aff'd, 75 Ohio St.3d 412, 662 N.E.2d 362 (1996); *Clark v. Cantrell*, 339 S.C. 369, 384, 529 S.E.2d 528 (2000) (holding computer generated evidence admissible where it is [1] authentic under state equivalent to federal rule 901[b][9], [2] relevant under state evidence rules, [3] a "fair and accurate representation of the evidence to which it relates" and [4] its probative value substantially outweighs dangers of its admission).

As these cases illustrate, courts are beginning to carefully scrutinize black box computer evidence. Construing a state equivalent of Rule 901(b)(9) in light of confrontation and fair trial concerns, the Connecticut Supreme Court has conducted an extensive review of the authorities on this issue in *State v. Swinton*, 268 Conn. 781, 847 A.2d 921(2004). The Court concluded, in line with the many other state and federal decisions reviewed, that trial courts must

“take the time to ensure that basic foundational requirements are met, particularly because the potential mischief caused by a standard that is too lax would be great.” (Id. at 818-819).

The “potential mischief” referred to by the Court was described as follows:

We are cognizant of the strong impact that computer generated evidence may have on juries. "Part of the mystique of computers is the aura of reliability that computers share with other forms of scientific and technical evidence. The impact that scientific evidence has on juries has been an issue in the criminal justice system for some time and in various contexts. As one juror

explained after a recent trial, ‘You can’t argue with science.’”

Id. at 819 n. 32, quoting R. Garcia, *“'Garbage In, Gospel Out”: Criminal Discovery, Computer Reliability, and the Constitution*, 38 UCLA L. Rev. 1043, 10917 (1991).

Quoting the same article, the Court continued:

Although computer systems raise serious reliability issues, the reported cases do not adequately reflect this reality." R. Garcia, *" 'Garbage In, Gospel Out': Criminal Discovery, Computer Reliability, and the Constitution,"* 38 UCLA L. Rev. 1043, 1087 (1991). “Why do the reported cases fail to adequately expose the serious reliability issues raised by computerized information? Many people, including defense attorneys, prosecutors, judges, and juries, do not understand computers. As a result, people tend to suspend their healthy common sense skepticism when they deal with information technology. Computers make it possible to do some things that could not be done without computers. The mere fact that computers can do some things at all tends to mask the issue of whether the computers can do it well. The 'gee whiz' quality of computers may conceal the underlying frailties of the systems.” *Id*., at 1090.

*Id.* at 808 n. 25

The “underlying frailties” of computer generated evidence are summarized by the Court as follows:

We note that "[r]eliability problems may arise through or in: (1) the underlying information itself; (2) entering the information into the computer; (3) the computer hardware; (4) the computer software (the programs or instructions that tell the computer what to do); (5) the execution of the instructions, which transforms the information in

some way--for example, by calculating numbers, sorting names, or storing information and retrieving it later; (6) the output (the information as produced by the computer in a useful form, such as a printout of tax return information, a transcript of a recorded conversation, or an animated graphics simulation); (7) the security system that is used to control access to the computer; and (8) user errors, which may arise at any stage." R. Garcia, *" 'Garbage In, Gospel Out': Criminal Discovery, Computer Reliability, and the Constitution*," 38 UCLA L. Rev. 1043, 1073 (1991); *See also* K. Butera, *Seeing is Believing: A Practitioner's Guide to the Admissibility of Demonstrative Computer Evidence,* 46 Clev. St. L. Rev. 511, 525 (1998) (proper authentication requires that reliability of computer process and accuracy of results be subject to scrutiny).

The Fourth Circuit has spoken to this issue in *United States v. Washington*, 498 F. 3d 225 (4th Cir. 2007), a driving under the influence case in which the appellant claimed that the raw data generated by the forensic lab's diagnostic machines and relied on by a toxicologist to give his testimony amounted to testimonial hearsay statements of the lab technicians who operated the machines. As a result, appellant claimed that the toxicologist’s testimony was not admissible, as Washington had a right to confront the technicians and cross-examine them by reason of the Sixth Amendment's Confrontation Clause. While rejecting the confrontation clause claim, the court address the protection afforded by Rule 901(b)(9):

Any concerns about the reliability of such machine-generated information is addressed through the process of authentication not by hearsayor Confrontation Clause analysis. When information provided by machines is mainly a product of “mechanical measurement or manipulation of data by well-accepted scientific or mathematical techniques,” 4 Mueller & Kirkpatrick, supra § 380, at 65, reliability concerns are addressed by requiring the proponent to show that the machine and its functions are reliable, that it was correctly adjusted or calibrated, and that the data (in this case, the blood) put into the machine was accurate (i.e., that the blood put into the machine was the defendant's). In other words, a foundation must be established for the information through authentication, which Federal Rule of Evidence 901(b)(9) allows such proof to be authenticated byevidence “describing [the] process or system used to produce [the] result” and showing it “produces an accurate result.”

For reasons already discussed in connection with Mr. McCluskey’s *Daubert* claims, the reliability problems identified by the court in *Swinton* and alluded to in *Washington* are not

theoretical in this case. Nor, as in *Washington*, is the Court dealing with a technology like the one at issue there (“headspace gas chromatography” for drug testing) which the court felt involved “mechanical measurement or manipulation of data by well-accepted scientific or mathematical techniques” . Instead, the Court is dealing with an emerging technology that has already shown its propensity for glitches and reliability problems.

Because of the complexity of the computer systems at issue, and their inherent limitations and flaws, as explicated in a growing body of scientific literature, and because of the serious stakes in this case, this Court should require strict adherence to Rule 901(b)(9), as well as the other rules and principles set forth in this motion.

# CONCLUSION

For all of the foregoing reasons, this Court should grant an evidentiary hearing in this matter and then rule that: (1) there is no reliable scientific basis for the government’s proposed DNA testimony, and thus the testimony is inadmissible under *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993) and *Kumho Tire Co. v. Carmichael*, 526 U.S. 137,

119 S.Ct. 1167, 143 L.Ed.2d 238 (1999); (2) the testimony is inadmissible under the 2000 amendments to Rule 702 in that (a) the testimony is not based upon sufficient facts or data, (b) the testimony is not the product of reliable principles and methods, and (c) the government’s DNA technicians have not applied the principles and methods reliably to the facts of the case; (3) numerous statistical flaws render the DNA evidence in this case inadmissible under rules 402, 403, and 702, as well as under D*aubert* and the due process, fair trial, and cruel and unusual provisions of the Fifth, Sixth, and Eighth amendments to the Constitution; (4) the failure to apply reliable scientific procedure as outlined in numerous protocols renders any DNA test results inadmissible under Rule 702; and/or (5) Rule 901(b)(9) requires that an adequate foundation be laid before any of the government's computer generated DNA evidence is admitted into evidence.

Dated: May 10, 2012 Respectfully submitted,

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Attorneys for Defendant John McCluskey

# CERTIFICATE OF CONFERENCE

I hereby certify that on April 22, 2012, I contacted Assistant United States Attorney Linda Mott to determine the government's position on this motion. Ms. Mott advised that the government is opposed to the motion.

/s/ Michael N. Burt

Michael N. Burt

# CERTIFICATE OF SERVICE

I hereby certify that on May 10, 2012, a true and accurate copy of the foregoing pleading was emailed to counsel of record by CM/ECF.

/s/ Michael N. Burt

Michael N. Burt