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1 [The R.M.C. 803 session was called to order at 0902,  
2 08 December 2021.]

3 MJ [COL ACOSTA]: The commission is called to order.

4 Government, please account for who is present for the  
5 United States.

6 TC [MR. MILLER]: Again, good morning, Your Honor. These  
7 proceedings are being transmitted via CCTV to the locations in  
8 the United States pursuant to your order. Present for the  
9 United States, as identified on previous detailing memo,  
10 myself, Mark Miller; Mr. John Wells; Lieutenant Commander  
11 Cherie Jolly; Lieutenant Commander Keven Schreiber; Major  
12 Michael Ross.

13 Also present are Mr. Forrest Parker Smith, Ms. Joleen  
14 Sanders, Master Sergeant Laura Speranza, and Staff Sergeant  
15 Carlos Salazar, and our interpreter, [REDACTED]

16 Seated in the back of the courtroom, specialist --  
17 Supervisory Special Agent and Case Agent Luke Hardison of the  
18 FBI; his assistant, Kymberleigh Albites; Frederic Gallun of  
19 the FBI OGC; Audra O'Brien, also of the OGC; and Lisa  
20 Grossweiler, and Mr. Giusti is also here. Thank you, Your  
21 Honor.

22 All persons have the necessary clearances.

23 MJ [COL ACOSTA]: All right. Defense?

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1 LDC [MR. NATALE]: Good morning, Your Honor. Anthony  
2 Natale on behalf of Mr. al Nashiri. All the people I'm going  
3 to list have all of the proper clearances to be present for  
4 all of the sessions that we have.

5 Along with myself is Captain Mizer, Ms. Carmon,  
6 Ms. Morgan. Mr. Dolphin is here today. I am sure that at  
7 some point Ms. Janes, Mr. Hoffmann, Mr. Roy will all be  
8 present. As always, we will have our interpreter here.

9 In the RHR, we plan to have Commander Piette; however,  
10 he is presently getting his COVID test. So he will be coming  
11 in later, and he is the only one that we anticipate who will  
12 be in there. He's taking the COVID test with the hopes and  
13 expectation that he will be able to be here in person.

14 MJ [COL ACOSTA]: So he's not going to remain up there for  
15 next week? He's ----

16 LDC [MR. NATALE]: At this point he is not, and we're  
17 hoping to plan that he will actually be here, sir.

18 MJ [COL ACOSTA]: All right. Does Mr. Nashiri consent to  
19 him not being present in the RHR during this time period?

20 LDC [MR. NATALE]: Yes, Your Honor. We've discussed that.  
21 He understands what roles we have, and he understands the  
22 circumstances, and he has no problem with that.

23 MJ [COL ACOSTA]: All right. I'm going to address it very

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1 briefly with Mr. Nashiri at this time.

2 LDC [MR. NATALE]: Absolutely, sir.

3 MJ [COL ACOSTA]: Thank you, Mr. Natale.

4 Mr. Nashiri, Lieutenant -- or, pardon me, Commander  
5 Piette is -- was normally present in the Remote Hearing Room  
6 where he could see and hear everything and communicate with  
7 your other counsel here during the previous sessions. Right  
8 now he is not present in there, and we're about to begin  
9 another session this morning.

10 Do you consent to him not being present and able to  
11 communicate with your co-counsel during this session?

12 ACC [MR. AL NASHIRI]: [Waves hand.]

13 MJ [COL ACOSTA]: Okay.

14 DDC [CAPT MIZER]: And, Judge, could I just address the  
15 use of the RHR next week?

16 MJ [COL ACOSTA]: Yes, Captain Mizer. You can come up to  
17 the podium, please, just so you can take your mask off and I  
18 can hear you a little better and you don't have to stand up  
19 crooked over the desk.

20 DDC [CAPT MIZER]: Thank you, Judge. Good morning.

21 MJ [COL ACOSTA]: Good morning.

22 DDC [CAPT MIZER]: I think, as you know, there's been some  
23 back-and-forth as to what the RHR is going to be used for

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1 during this hearing. I mean, I think that it started out with  
2 both parties at an 802 saying that the RHR wasn't going to be  
3 used. Then the government said that it was going to be used.  
4 And I think we're back now to that it's not going to be used.

5 As you know, we left Commander Piette behind to ----

6 MJ [COL ACOSTA]: To conduct potentially the  
7 cross-examination of the government witness that is located --  
8 that was going to testify from the RHR?

9 DDC [CAPT MIZER]: Yes, Judge. And if this sounds like a  
10 complaint, it's not. This is litigation; things move around.  
11 But we would like a commitment that if I put him on a plane --  
12 he's out getting a COVID test now -- on Saturday, that next  
13 week the RHR is not going to have witnesses in it that I need  
14 to leave someone there for. That's it.

15 We can shut down the RHR, save Uncle Sam/the taxpayers  
16 money, and give those folks up there probably a much-needed  
17 rest. But we need to have that clarified ----

18 MJ [COL ACOSTA]: I'm --

19 DDC [CAPT MIZER]: ---- before I get him on a plane.

20 MJ [COL ACOSTA]: Mr. Miller is already moving.

21 Mr. Miller.

22 TC [MR. MILLER]: Yes, it is. Litigation is moving, Your  
23 Honor.

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1 MJ [COL ACOSTA]: Yes.

2 TC [MR. MILLER]: The -- I think, as the government  
3 indicated previously, the RHR will be used for one witness  
4 next Monday. We anticipate it will be open. And so I don't  
5 know what sort of decision -- how that affects their decision,  
6 but we will have a witness ----

7 MJ [COL ACOSTA]: Well, as they previously stated, if  
8 you're going to have a witness testifying from there, they  
9 wanted their attorney there ----

10 TC [MR. MILLER]: Correct. I understand.

11 MJ [COL ACOSTA]: ---- to view him in person and  
12 cross-examine him in person. But now your witness is going to  
13 be ----

14 TC [MR. MILLER]: Right.

15 MJ [COL ACOSTA]: ---- there on Monday?

16 TC [MR. MILLER]: Right.

17 MJ [COL ACOSTA]: And testify from there?

18 TC [MR. MILLER]: I can make that commitment.

19 MJ [COL ACOSTA]: Okay.

20 TC [MR. MILLER]: That's definitely going to happen.

21 DDC [CAPT MIZER]: That's good enough for us, Judge.

22 MJ [COL ACOSTA]: Okay.

23 DDC [CAPT MIZER]: We'll have Commander Piette there.

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1 MJ [COL ACOSTA]: All right.

2 TC [MR. MILLER]: Thank you, Your Honor.

3 MJ [COL ACOSTA]: And if you're not going to fly  
4 Commander Piette down, I would authorize one of your  
5 paralegals or whoever to go communicate with him that they  
6 can -- that he doesn't need to go get tested today just  
7 because of the -- like all of you, I've had numerous versions  
8 of that test, and the one that he's going to get is the least  
9 pleasant of the bunch, so ----

10 DDC [CAPT MIZER]: Aye, sir. We'll send the paralegal in  
11 the office to do that now.

12 MJ [COL ACOSTA]: Okay. Thank you.

13 DDC [CAPT MIZER]: Thank you.

14 MJ [COL ACOSTA]: All right. We're here today to hear the  
15 defense Daubert challenge to the DNA testing. Government, do  
16 you agree it's your burden?

17 ATC [MAJ ROSS]: Yes, sir.

18 MJ [COL ACOSTA]: Are you prepared to proceed?

19 ATC [MAJ ROSS]: We are, sir.

20 MJ [COL ACOSTA]: Do the parties consent to my considering  
21 of your motions, the attachments thereto, the evidence I'm  
22 going to receive in today's hearing, and the argument of  
23 counsel in resolving this issue?

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1 ATC [MAJ ROSS]: Yes, sir.

2 DC [MS. CARMON]: Yes, Your Honor.

3 MJ [COL ACOSTA]: Government, you may proceed.

4 ATC [MAJ ROSS]: The government will call Alan Giusti to  
5 the stand.

6 Before you sit, if you would please raise your right  
7 hand.

8 **ALAN GIUSTI, civilian, was called as a witness for the**  
9 **prosecution, was sworn, and testified as follows:**

10 ATC [MAJ ROSS]: Please have a seat and remove your mask.

11 WIT: Thank you.

12 **DIRECT EXAMINATION**

13 **Questions by the Assistant Trial Counsel [MAJ ROSS]:**

14 Q. Mr. Giusti, you're a forensic scientist at the FBI; is  
15 that correct?

16 A. Yes, a forensic examiner in the DNA Casework Unit.

17 Q. And you performed analysis in -- analysis in this case  
18 against the accused, Mr. Nashiri; is that correct?

19 A. Yes, I have.

20 Q. And, in fact, you testified yesterday in this  
21 courtroom, correct?

22 A. Yes, I did.

23 Q. And you provided your qualifications to the -- to the

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1 court?

2 A. Yes.

3 ATC [MAJ ROSS]: Your Honor, at this time we would move to  
4 qualify him as an expert in forensic DNA analysis. We can go  
5 through those qualifications again, if you'd like, though.

6 DC [MS. CARMON]: No objection, Your Honor.

7 MJ [COL ACOSTA]: He is so recognized. You may proceed.

8 Q. Are you familiar with PCR/STR methodology of forensic  
9 DNA analysis?

10 A. Yes, I am. PCR/STR is -- basically describes the  
11 process and the types of DNA regions that we analyze.

12 So PCR stands for polymerase chain reaction, and it's  
13 a chemical reaction that takes place in a test tube and it  
14 essentially mimics what happens in living organisms in that it  
15 creates new DNA in a test tube.

16 STR stands for short tandem repeat, and that describes  
17 the regions of DNA that we specifically look at when we  
18 develop DNA profiles.

19 And a short tandem repeat, just to give a little  
20 background, you can kind of think of it like boxcars in a  
21 train. It's a stretch of DNA or it's a piece of DNA that has  
22 repeating units and those units are four units in length, so  
23 four base pairs, which is the building block of DNA.

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1           So those units repeat one after another, and they vary  
2 from person to person and even within a person, so you get  
3 different length fragments of DNA at an STR region. So a DNA  
4 profile is a collection of multiple STR -- excuse me --  
5 regions that vary in length both within a person and between  
6 individuals. So it's -- they're very useful for telling  
7 people apart or distinguishing individuals.

8           The only individuals that have the same STR profile  
9 would be identical twins because they come from the same  
10 fertilized egg.

11          Q. When was this process started to be used by the FBI?  
12 When did the FBI start to use this process?

13          A. Well, we went online for casework in January of 1999.  
14 The science really developed in the early '90s when these STR  
15 regions were discovered and characterized. And then there was  
16 about a, you know, slightly less than ten-year process where  
17 the STR regions were chosen for forensic usage.

18          The kits that you heard about yesterday were developed  
19 so that we could look at more than one STR at a time, and they  
20 go -- went through a validation process to make sure they were  
21 reliable and sound and robust when we finally applied them to  
22 forensic evidence or cases.

23          Q. You said validation process. What does that mean?

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1 A. Well, validation is a -- is a very general or broad  
2 term that describes everything that has to be done before a  
3 forensic test can go online. And for forensic DNA tests,  
4 there are very specific requirements that have to be followed  
5 to validate a new technique.

6 So you have to demonstrate many different aspects of  
7 it that show it is reproducible, reliable, that it provides  
8 consistent results, that it works on forensic samples that  
9 have been damaged by the environment, say. There's a whole  
10 array of parameters that you have to look at to validate a new  
11 test, especially a new STR-based test.

12 Q. Who does the validation?

13 A. Initially, it was done by the -- well, for our  
14 process, it was done by the Forensic Science Research Unit  
15 that was located at Quantico.

16 Q. And that's with the FBI?

17 A. Yes. That's -- I'm sorry, yes. That's the FBI.

18 So the first set of validations for the STR approach  
19 was validated by our research unit. As time has gone on,  
20 they've continued to do validations, but different units have  
21 been involved.

22 Right now, we have a unit called the DNA Support Unit  
23 whose sole function is to validate new technologies, to handle

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1 the quality control issues for DNA testing, and also manage  
2 the quality assurance program. Those are all three very large  
3 undertakings, so the caseworking unit really can't do them  
4 anymore, so we have a separate unit to do that.

5 Q. Can you describe the FBI's validation process as it  
6 specifically pertains to the PCR/STR methodology of forensic  
7 DNA analysis?

8 A. Yes. The -- I think it was mentioned yesterday that  
9 there are standards that are administered by the FBI Director  
10 called quality assurance standards for forensic DNA testing.  
11 And those actually came out of the original 1994 DNA  
12 Identification Act. And there's a history of what happened.  
13 There was originally a DNA advisory board that came up with  
14 these guidelines and they are now managed, if you will, by  
15 that organization called SWGDAM, Scientific Working Group on  
16 DNA Analysis Methods.

17 Those standards have existed in some form even before  
18 the current version and standards -- well, when they were  
19 TWGDAM, which was the predecessor or precursor to SWGDAM, they  
20 were guidelines, but they were guidelines that were followed  
21 by pretty much every forensic lab that was validating new  
22 technologies, and they specified what had to be looked at or  
23 tested before you could bring on a new PCR/STR-based test.

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1 Q. How long did the FBI's validation process for this  
2 methodology last?

3 A. It went through -- it went through several phases. It  
4 probably, I would estimate, maybe took about three and a half  
5 to four years. Part of it involved selecting -- and this is,  
6 again, before we knew what we were -- you know, what kind of  
7 tests we were going to do. It was a matter of choosing which  
8 STR markers that we were going to look at, which ones were the  
9 most useful for forensic purposes.

10 Once those were chosen, they were tested by multiple  
11 forensic science laboratories around the country, and that was  
12 called a -- that was like a CODIS, or Combined DNA Index  
13 System, working group. They were trying to form a consensus  
14 in the community as to which ones we would look at.

15 Then when it came to the internal validation, that was  
16 done by our research unit, and they began to look at things  
17 like changing the parameters for the PCR-based test.

18 Q. When you say ----

19 A. I'm sorry.

20 Q. Let me interrupt you. What do you mean by changing  
21 the parameters of the test?

22 A. Well, one of the things that goes into develop -- and  
23 I -- I should back up a little more. There are two types of

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1 validation. There's developmental validation and internal  
2 validation. Developmental validation is what you do to  
3 literally develop the test to make sure that it is ready to go  
4 and that it is behaving, again, robustly and reliably. That  
5 involves, as I say, many different components but one of them  
6 is changing the parameters.

7           So the company that makes the kits that we use --  
8 you've heard about Profiler Plus, that's one of them -- they  
9 have a recommended set of conditions, basically chemical  
10 components that go into it. Part of our developmental  
11 validation was to modify those to use twice the amount of  
12 magnesium, for example, or half the amount of magnesium. All  
13 of these things were done to see if we could improve -- well,  
14 potentially improve, or at least to see how they would impact  
15 the PCR process.

16           So we tested out all the different parameters that go  
17 into the PCR -- the reaction, the chemical reaction where DNA  
18 is made, so that was a big part of it. We also looked at the  
19 sensitivity. You know, how -- how little DNA could you test  
20 to see -- and still get a viable profile.

21           Q. What were your results in that regard?

22           A. Well, the -- in our -- with our validation study, the  
23 sensitivity under the current -- or the approach that we were

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1 using when we went -- went online with casework is -- and it's  
2 in our publication, is that we were able to detect full DNA  
3 profiles from as little as 78 picograms of DNA.

4           And just to get into a little technology or jargon  
5 here, you've heard about a nanogram as being the target amount  
6 of DNA for PCR as being the ideal target, and certainly it is  
7 a good target. That represents one one-billionth of a gram.  
8 A picogram is three -- three magnitude -- three -- is a  
9 thousandfold less. So a picogram is a trillionth of a gram.  
10 So instead of saying .078 nanograms, I'm going to move the  
11 decimal point and say 78 picograms. But that's really what  
12 we're talking about, is obtaining a full DNA profile from as  
13 little as 78 picograms of DNA, of human DNA.

14           Q. Now, does that mean you can't test anything  
15 below .78 picograms?

16           A. No. At the -- you know, at the -- at the end of all  
17 of this, we discovered that you can analyze any amount of DNA  
18 that you obtain from an item, from a sample. But a big part  
19 of the validation is understanding what will happen to the DNA  
20 profile when you use less and less DNA. So our validation  
21 looked at that parameter.

22           So we could start with, you know, the manufacturer's  
23 target of 1 nanogram, and then we took it down because, from

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1 evidence, you never know how much DNA you're going to get. So  
2 we wanted to know if we only got a small amount of DNA, what  
3 kind of DNA profile would we get and what characteristics  
4 would it have, based upon the amount of DNA.

5 Q. Is there a minimal amount of DNA needed to undergo  
6 forensic DNA analysis in the FBI Lab?

7 A. Not for us. I would say a theoretical minimum would  
8 be you'd have to have at least one cell worth of DNA, but  
9 that's a really very, very small amount.

10 Q. And that's -- you make that statement pursuant to  
11 your -- the validation process?

12 A. As to the amount of DNA that we have?

13 Q. As to the fact that there's no minimal amount needed  
14 to test.

15 A. Correct. As part of our validation we -- I call it  
16 stress tested the system. We decided -- you know, we made  
17 sure that we understood what would happen if you didn't have  
18 the optimal amount of DNA, what kind of DNA profiles would you  
19 get. So that was before we went into casework and amplified  
20 as much or as little DNA as we got from evidence, we knew what  
21 to expect from our validation studies.

22 Q. Now, does this analysis apply only to single-source  
23 samples, or what about mixed samples?

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1 A. It also applies to mixed samples. So, again, whether  
2 we have a single-source sample or a mixture of DNA, if there  
3 is human DNA present, we will subject it to our standard  
4 analytical process.

5 And because of -- again, I'm going to sound like a  
6 broken record here -- because of our validation studies, we  
7 know what to expect from a mixture of DNAs, even if some, say  
8 one component is -- you know, is a -- is a -- is a large -- a  
9 major donor or the major component and if there's a minor  
10 component. We've done those studies as part of our validation  
11 as well.

12 So, again, regardless of the amount of DNA, we've  
13 looked at these variations to see how they behave.

14 Q. Now, you testified that you can get a full DNA profile  
15 with as little as .78 picograms. Why would you submit  
16 anything less than that for forensic DNA analysis?

17 A. Well, just -- I'm sorry. Just to correct, it was  
18 78 picograms or .078 nanograms.

19 I'm sorry. Why would we submit less than that?

20 Q. If you had less than that, why would you submit it for  
21 testing?

22 A. Because that was a situation where we obtained a  
23 full -- a full DNA profile. Even if we have less than that

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1 78 picograms, we might still get a partial DNA profile or some  
2 information.

3           And, you know, for -- for a DNA examiner like myself,  
4 I -- I compare it -- I compare it to physical characteristics.  
5 If you can get any information from S -- any number of STR  
6 regions, whether it's one, five, nine, or 13, or up to 20  
7 or -- well, we use 21 now, but if you can get any information,  
8 it's like getting a physical characteristic of a person.

9           If you get 21 characteristics, you can develop a very  
10 good picture of a person. If you had three, like brown hair,  
11 brown eyes, and white skin, not very useful, but it still  
12 rules out some people. So it is still useful information;  
13 it's just not as distinguishing or as discriminating.

14           So we will test any amount of DNA to try to get some  
15 information from the sample.

16           Q. You mentioned partial profile. What's that?

17           A. Well, a partial profile, there's a couple of different  
18 explanations for it, but in general, it would be if you have  
19 either less than a full set of your -- of your STR markers.  
20 So in the case of -- when we went online actually by summer of  
21 1999, we were looking at 13. Now we look at 21. So a full  
22 DNA profile would be either 13 at the time or 21 now.  
23 Anything less than that would be considered a partial profile.

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1           It also refers to the results at a -- at a single STR  
2 region. And I'll probably talk more about that, but it has to  
3 do with you may not always get the full profile at a single  
4 STR region if you don't have enough DNA. So you'll have --  
5 you'll be missing one of the results. And we also call that a  
6 partial profile. So I'll try to keep them, you know, distinct  
7 but there are two definitions, really.

8           Q. Now, if you're unable to get results at specific loci  
9 on the profile, you get a partial profile, does that undermine  
10 the results that you got at the -- the results for the loci  
11 you did get a result for?

12          A. No, not at all. As I said, it's -- it can be a result  
13 of not having enough DNA. It could be that the DNA was broken  
14 down by environmental factors and some of the STR regions were  
15 lost.

16           So the nice thing about these -- these kits, these --  
17 we call them multiplex because they had multiple STR regions.  
18 You can still get individual results at some of the STR  
19 regions and maybe not at the others, but each individual  
20 result is considered reliable.

21          Q. Now, are the same loci -- loci tested each time?

22          A. Yes. That's a -- depending on the -- the test we're  
23 doing or when, you know, when we're doing the test, but we

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1 always use the same STR loci. So originally we had a set of  
2 13, and those came out of some of the studies that were done  
3 in the '90s to determine which STR regions were going to go  
4 into the national database. Because we -- we wanted to -- we  
5 needed to have everybody using the same set of markers, or STR  
6 loci, so we could compare across the country.

7           If the FBI chose 13, you know, say -- I'll screw it  
8 up -- but just 13 random loci, and California chose 13  
9 different ones, and New York chose, you know, 13 different  
10 ones, we wouldn't be able to compare data. We wouldn't be  
11 able to see if somebody in California also committed a crime  
12 in New York or anywhere else. So that standardization was  
13 designed to make sure we could compare nationwide. And that's  
14 continued throughout the last, what, 21 years since this has  
15 gone online.

16           So we've added more STR loci to make the test more  
17 powerful, but we still have it set up so that we can all  
18 cross-compare our data, and that's how the national database is  
19 able to work.

20           Q. Why those specific loci?

21           A. Well, they were chosen because -- or they've been  
22 chosen because they are very robust, which is one thing we  
23 look for. Again, forensic samples can be challenging. The

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1 DNA may have been affected by environmental factors or treated  
2 with, you know, harsh chemicals, things like that.

3 We wanted STR loci that would routinely -- routinely  
4 amplify, would give us a result when we -- when we did the  
5 amplification process. And we also wanted ones that were  
6 sufficiently discriminating so that ones that had enough  
7 variety in their -- the types of versions or alleles that you  
8 could get so that you could more easily tell people apart.

9 I'm trying to -- you know, an example, if -- if blood  
10 types were an STR region, you've got, you know, basically A,  
11 B, and O. That's not very useful. If you only have those  
12 three, it's not very useful for telling people apart. So we  
13 want STR regions that have a lot of different possibilities or  
14 different alleles, if you will, so that they can be used to  
15 tell people apart.

16 Q. Now, the loci that you test for, do those code for  
17 physical characteristics in a human being?

18 A. No. In fact, that was one of the requirements for  
19 selecting these loci, that they not have any biological  
20 function in humans because when a gene or a region of DNA has  
21 a biological function, there can be -- I'm trying to think of  
22 the best way to put it.

23 They won't separate or they won't segregate -- they

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1 may not segregate randomly, and part of the -- ultimately,  
2 part of the way we can do calculations or statistics is that  
3 the results from STR regions will assort randomly without  
4 regard to what they are. If they had to -- if they had a  
5 function, it might drive -- it might drive them in a certain  
6 direction that would not be random.

7           So it's -- it's -- I guess a way to describe it is  
8 like some genes are -- are harmful to humans. I'm trying --  
9 I'm thinking like sickle cell anemia is a blood disorder  
10 predominantly found in African Americans, or actually started  
11 out in Africa. But people with that -- you know, with two of  
12 those genes, I think -- I'm a little fuzzy on that -- but  
13 it has a negative effect on them. It can -- I guess it can  
14 actually lead to death. So that gene, the evolutionary  
15 pressure is negative. You know, it's like -- you know, it  
16 tends to kill people off. Or cancer genes are another  
17 example.

18           STR regions don't do anything, so as humans breed and  
19 make more humans, there's not going to be any direction in  
20 which the STRs go. They're not going to go all toward, you  
21 know, say, like Type A and avoid Type B. It's going to be an  
22 equal mix, say, of A and B.

23           Q. The validation studies that you talked about at the

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1 FBI, were those studies published?

2 A. Yes, they were.

3 Q. Were they subject to peer review?

4 A. Yes. They were published in the Journal of Forensic  
5 Sciences in 2001, and they were subjected to -- subjected to  
6 peer review by outside scientists before they were published.

7 Q. Now, the PCR/STR process, how prevalent is this in the  
8 forensic science community?

9 A. It's pretty much the dominant form of DNA testing  
10 worldwide. It is used throughout the United -- pretty much  
11 any country that does forensic DNA testing, and also, say, you  
12 know, kinship or parentage testing is using the PCR/STR  
13 process.

14 Q. And the process has been tested, just to be clear?

15 A. Yes. Yes.

16 Q. And it's been subject to peer review?

17 A. Yes.

18 Q. Extensive peer review?

19 A. Yes, very much so.

20 Q. And does it have a known or potential error rate?

21 A. We -- we have not calculated an error rate for it.

22 And part of the reason for that is that -- well, it has to do  
23 with sort of the definition of an error rate, at least as --

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1 as it can be applied to forensic DNA analysis, and  
2 unfortunately, today's situation provides a good example.

3           You've heard that some of the rapid COVID tests have  
4 a percentage of false negatives and false positives, and that  
5 is simply because of the nature of the test. So the -- if  
6 it's, say, you know, 2 percent give false positives and  
7 5 percent give false negatives, that's simply from the nature  
8 of the test. There's no way to engineer that out.

9           With forensic DNA testing, we build controls and  
10 checkpoints into every -- every test we do. And if a mistake  
11 happens -- and errors and mistakes do happen, because you're  
12 dealing with humans.

13           MJ [COL ACOSTA]: Can you please stop for a second.

14           WIT: Sure.

15           **[Public address announcement.]**

16           MJ [COL ACOSTA]: I've stopped the proceedings just  
17 because there's a speaker going on the outside. It's making  
18 it hard for people to hear, including myself.

19           All right. You may proceed.

20           WIT: Thank you, Your Honor.

21           A. So as I said, errors can occur. Anytime humans are  
22 involved, mistakes can happen. And instruments can fail,  
23 things like that. So there are errors that can happen during

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1 forensic DNA testing, but because of our checkpoints, we  
2 are -- you know, there -- those -- those checkpoints or  
3 assessments are designed to catch when a mistake happens. And  
4 if it's something inherent in the system, a bad piece of  
5 equipment or, you know, somebody's not, you know, heating  
6 something for long enough, we correct that.

7           So we don't expect to have an -- an inherent error  
8 rate associated with our test. So, you know, the -- it was  
9 actually a subject in the 1996 NRC report that talked about  
10 error rates and essentially that report did not have a good  
11 method for calculating error rate. They simply felt that the  
12 analyst should acknowledge errors and demonstrate how to  
13 correct -- how to correct those in the future.

14         Q. Were you in court when Dr. Reich talked about the  
15 steps of PCR/STR?

16         A. Yes, I was.

17         Q. Did he accurately describe those steps?

18         A. Yes.

19         Q. I'd like to ask you about step 3, the quantitation  
20 step. Could you please describe that step.

21         A. Yes. As Dr. Reich described, it is basically the step  
22 where you determine how much DNA do you have in your samples,  
23 whether it's known reference samples or evidence samples.

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1 It's important to know how much DNA you have for a number of  
2 reasons, one of which being you want to make sure you put the  
3 right amount of DNA into the amplification step which comes  
4 next. So it's a -- it's an important checkpoint during the  
5 analysis.

6 Q. Now, how much do you -- how much of the sample do you  
7 use to establish quantitation?

8 A. At the time these samples were tested, we actually  
9 used one-tenth of the sample. So we had roughly 20  
10 microliters of sample, and we would take 2 microliters or  
11 one-tenth and put that into the quantitation process.

12 MJ [COL ACOSTA]: Can you repeat that, please?

13 WIT: Yes.

14 A. We would use one-tenth of the sample for the  
15 quantitation step. So if we had roughly 20 microliters of our  
16 evidence, purified evidence DNA, or any DNA, also from knowns,  
17 we would take one-tenth of that or 2 microliters and use that  
18 for quantitation.

19 Q. Why one-tenth?

20 A. Because based upon the quantitation process we were  
21 using, we determined that was adequate to get an assessment as  
22 to how much DNA there was.

23 Q. And that was determined during the validation process?

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1 A. Yes, it was.

2 Q. And that's contained in your standard protocols?

3 A. Yes, it is.

4 Q. What is a slot blot?

5 A. A slot blot was the -- pretty much almost original  
6 method for determining the amount of DNA that you had in a  
7 sample. And the process was -- was actually very quite  
8 simple. You would take a piece of nylon membrane that had  
9 the -- that would bind DNA, so it was very good at -- if DNA  
10 came into contact with it, the DNA would stick there and  
11 stay -- stay stuck.

12 So what you do is you have a -- like a plastic block  
13 that has little channels or like sort of narrow oval-shaped  
14 channels in it, and you would add on the outside known  
15 standards or known amounts of DNA. So these were your -- this  
16 was like your DNA ruler, and you would have, like,  
17 20 nanograms, which is a lot of DNA, and it would range down  
18 to 0.1 nanograms, or 100 picograms, of DNA, which would be the  
19 lowest amount.

20 In between you had, I think, four other rows or  
21 columns with -- that you could put samples in, and you would  
22 take that 2 microliters of DNA from your evidence or your  
23 known sample and squirt it in. And then you would add some

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1 more liquid. The DNA would bind. You would fix the DNA.

2           Once that was done, you would take that membrane, that  
3 plastic membrane with your DNA stuck to it, and you would  
4 treat it with a DNA probe. And we call it a probe because it  
5 would have either a radioactive atom attached to it or later  
6 on, which was much safer, we would add a chemiluminescent dye  
7 to it. And chemiluminescence is just -- it's like what  
8 fireflies have. That's bioluminescence, but it's a chemical  
9 that when you treat it it will give off light and expose film,  
10 which is I where I'm going with this.

11           So you would add this DNA probe. If there was DNA in  
12 any of those slots, and there should be in your standards, the  
13 probe would bind. You would wash off the rest of the unused  
14 probe. You would take that nylon membrane and put it up  
15 against a piece of x-ray film and you would let it expose for  
16 an appropriate period of time.

17           Then you develop the film just like they do in --  
18 well, they used to do in the hospitals before they went  
19 digital. But they would develop the film, and you would end  
20 up with an x-ray image of the exposed film showing how intense  
21 the probe had bound and, therefore, how much DNA you had. The  
22 stronger the intensity of the -- the signal or image, the more  
23 DNA you had. And the weaker -- or the less DNA you had, the

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1 weaker the intensity of the image would be.

2           So you'd end up with a -- like a little grid with  
3 these narrow oval bands, we'd call them. We would compare  
4 them to the known standards, and that's how we would determine  
5 how much DNA we had in our samples.

6           Q. Did the slot blot undergo your validation process at  
7 the FBI?

8           A. Yes, it did.

9           Q. How prevalent was its use at the time, specifically in  
10 the early 2000s?

11          A. It was -- it was the only method that we used for  
12 quantitation. And I believe from other publications I saw,  
13 you know, that it was -- it was common to other forensic labs,  
14 to use it for determining the amount of DNA.

15          Q. You mentioned other publications. This slot blot was  
16 subject to peer review as well?

17          A. Yes. The process -- there were -- there were  
18 different versions of the slot blot, but they were -- there  
19 were several publications that talked about the development of  
20 the slot blot assay that were published in peer-reviewed  
21 journals.

22          Q. Is it reliable?

23          A. Oh, very much so.

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1 Q. Was it reliable in the early 2000s?

2 A. Yes.

3 Q. Is it reliable today?

4 A. If somebody wanted to use it and the materials  
5 existed, they could. Yeah, it would still be reliable.

6 Q. Are there new procedures used today?

7 A. Yes. There are procedures now that are much -- much  
8 more precise than the slot blot. The slot blot gives you an  
9 estimate of the amount of DNA. Well, pretty much every  
10 process gives you an estimate, but there is a technology now  
11 that uses a different form of PCR, actually, that gives you a  
12 more accurate determination of the quantitation of -- or the  
13 amount of DNA. And you can also get more information from  
14 this newer type of testing procedure.

15 So that's why we've -- I want to say it was 2007, we  
16 switched to the newer type of quantitation process and  
17 continue to use an even newer version today.

18 Q. Tell me about amplification.

19 A. Well, as you heard, amplification is the process where  
20 you make more copies of your STR regions. It is -- again,  
21 it's a chemical process. It mimics what living organisms do  
22 when they make DNA. But with amplification, as we use it,  
23 it's not copying the entire human genome, if you will.

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1           By way of background, a human being -- a single human  
2 cell is made up of about 3 billion units. I mean, that's a  
3 tremendous amount of DNA. We only care about, at least in  
4 forensics, we only care about these 13 or 15 or 21, whatever,  
5 STR regions. It's a very small component of that -- that  
6 entire mass of human DNA.

7           So in amplification, we create the chemical conditions  
8 that allow us to target the STR regions of interest and  
9 amplify them. So what the amplification process does is it --  
10 you take your DNA, you add your chemical components. One of  
11 them are the -- the kits, these amplifier -- these, like,  
12 Profiler Plus or multiplex kits, and then you put them in an  
13 instrument called a thermal cycler, which is a  
14 computer-controlled heat block, really.

15           And what it does is it -- it will go through what's  
16 called a cycle, and it will raise the temperature. It will --  
17 which means it opens the DNA up. DNA is double-stranded; it  
18 goes single-stranded. These -- you lower the temperature a  
19 little bit. Primers, really short pieces of DNA, that will  
20 target just the STR regions, go in and they bind, and they  
21 form a short double-stranded region of DNA. And then you add  
22 chemicals that will make more DNA.

23           So after one cycle you've targeted 13 or 21 or however

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1 many STR regions. So one cycle will essentially double the  
2 amount of DNA from those STR regions. So if you had one copy  
3 of human DNA in that test tube, you would have, at the end of  
4 one cycle you would have two copies just of your STR regions.  
5 So that would be one cycle.

6           You repeat that a number of times. Every cycle  
7 doubles the amount. So you go from one to two, two to four.  
8 By the time you finish, and we routinely use 28 cycles, you've  
9 done 2 to the 28th amplification of your STR region. I think  
10 that's somewhere close to a billion-fold. I think it's  
11 several hundred million, but it's a huge number. So even if  
12 you started with one copy of an STR region, you'd have close  
13 to a billion copies at the end of your amplification process.

14       Q. You said 28 cycles?

15       A. That's currently what -- well, that's what we used  
16 initially and that's actually currently what we use now.

17       Q. Now, how do you ensure that whoever is running these  
18 tests does 28 and not 27 or 29?

19       A. Well, I mentioned it uses the -- the thermal cycler,  
20 as I said, is basically a computer-controlled or heat --  
21 heating block. When you come up with the conditions for  
22 amplification that you want to run through -- you know, you  
23 want to run, you can actually program that into the thermal

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1 cyclers and save the program. So that once you've done that  
2 the next person, or whoever else wants to amplify using that  
3 thermal cycler pulls up the correct program and it goes  
4 through the exact same parameters every time. It's actually  
5 one of the ways we standardize the process so there is no  
6 variation.

7 Q. You mentioned the Profiler Plus kit.

8 A. Yes.

9 Q. Who makes that kit?

10 A. Well, it's not made anymore. At the time it was made  
11 by a company called Applied Biosystems. Yeah. I think  
12 they're now owned by a company called Thermo Fisher. But in  
13 the late '90s, early 2000s, it was Applied Biosystems.

14 Q. How many labs use those kits?

15 A. I don't really know. I mean, at the time there were  
16 two corporations that were making these multiplex kits. One  
17 was Applied Biosystem. The other was called Promega. And  
18 they both had different kits that contained the same 13 or  
19 more STR loci. So it really depended on what the lab had  
20 validated.

21 We validated the Applied Biosystem kits, which were  
22 Profiler Plus, and then the other one was called COfiler.  
23 Other labs, I believe, used Promega kits. If I remember

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1 correctly, I think the Virginia Department of Forensic  
2 Sciences used Promega kits at the time.

3           So it didn't matter which kit you used as long as you  
4 validated it -- validated it for your protocols.

5           Q. Now, you said these kits underwent the FBI validation  
6 process. Do they also have to go through a manufacturer's  
7 validation process?

8           A. Yes. The manufacturers themselves went through a  
9 developmental validation step. Again, many of the things I  
10 mentioned before about developmental validation were first  
11 done by the corporations, because creating a multiplex kit  
12 takes a lot of work, and most -- and a forensic lab, really  
13 even one like us that has a research unit, would be hard  
14 pressed to do that.

15           So the companies would come up with these kits, but  
16 they would do the developmental validation. And, in fact,  
17 Applied Biosystems did, and they also published their findings  
18 in a peer-reviewed scientific journal.

19           Q. Let's move on to the next step, electrophoresis. If  
20 you could, just give a brief description of that process  
21 again.

22           A. Sure. Briefly, the electrophoresis process is where  
23 the STR fragments get separated according to length. So I

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1 mentioned before that STR regions vary by length. Some are  
2 long, some are short.

3           When you finish the amplification step, you've got a  
4 test tube with this, you know, billion-fold amplification of  
5 potentially 13 STR regions. Well, they're all mixed together.  
6 You can't tell the length in that test tube. So the way you  
7 separate them is to subject them to electrophoresis.

8           And what you do, and what we did in this case, was you  
9 take that tube with the amplified DNA. You inject a small  
10 portion of it -- the instrument does what's called an --  
11 electrokinetic injection. What it means is it uses  
12 electricity to get -- to pull DNA into a very thin glass tube  
13 called a capillary. Now, that thin glass tube is filled with  
14 a very viscous liquid. It's not quite gelatinous, but it's  
15 very, very thick and gooey.

16           And that liquid will allow smaller pieces of DNA, or  
17 shorter fragments, to run faster through it. They can wiggle  
18 their way through faster. And wiggle is actually pretty close  
19 to what happens. Longer pieces of DNA can't wiggle as  
20 quickly. They move more slowly.

21           So all of those fragments start out in one test tube.  
22 They start to get separated according to their length. So the  
23 shorter fragments are running faster. The longer fragments

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1 are running behind. And ultimately they pass by a camera that  
2 has -- it's a special type of camera. And those DNA fragments  
3 also have a chemical dye, a fluorescent dye attached to them.  
4 As they go by the camera, they get hit with a laser, and the  
5 camera captures the light giving off those fragments.

6 So now you're -- this is called raw data. So you're  
7 collecting all of this data as your fragments go by the  
8 camera. Then there's a software application that will analyze  
9 that and prepare essentially a picture of the DNA profile from  
10 that collection of -- of STR loci.

11 Q. What is an electropherogram?

12 A. An electropherogram is the name of the plot or diagram  
13 of the DNA profile that you get. So, as I said, when the  
14 camera catches these fragments going by a -- a little window,  
15 it's capturing that data and it's saying, okay, this is a  
16 small fragment. I'm going to put it -- I'm going to graph it  
17 here, and here's a slightly longer fragment.

18 And it will create a graph -- kind of looks like an  
19 EKG printout, really, of a line with little peaks that  
20 represent the STR fragments. That final printout is called an  
21 electropherogram.

22 Q. What do the peaks represent?

23 A. The peaks represent the -- the results for the STR

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1 loci. So I think I -- I can't remember if I used the word  
2 "allele" before, but the STR loci can have either one or two  
3 copies -- actually, I think Dr. Reich mentioned that -- that  
4 you can get -- you know, you get a copy from your mother and  
5 one of your father. They can be different lengths. And so  
6 for that STR region, you'd have two peaks or two alleles,  
7 types, forms is another -- you know, another word -- other  
8 words that can be used.

9           If you got both the same from your mother and father,  
10 you'd have one peak, but it would be taller than, say -- you  
11 know, it would be -- it would be taller because you'd have two  
12 copies stacked on top of each other.

13           Q. You said the term "allele." Just to be clear, what is  
14 an allele?

15           A. An allele is a term -- it's a -- it's a genetic term  
16 and it means just the form or type at a particular DNA --  
17 usually at a gene, but also at an STR locus.

18           So when I -- you know, if I were to say you've got two  
19 peaks at a particular STR locus, that would also be called two  
20 alleles. So you'd have -- and the alleles will have -- so  
21 I'll use those peaks and alleles maybe interchangeably, but  
22 the alleles simply represent the result at that -- at a  
23 particular STR locus, and each locus will have its own peaks

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1 or its own alleles associated with it.

2 Q. Now, there are numeric values associated with a loci.  
3 What are those -- for example, 13, 15; 11, 11. What do those  
4 numeric values represent?

5 A. They're very basic. They actually represent the  
6 number of boxcars that I mentioned earlier on. So when I said  
7 an STR region has repeating units or repeating chunks of DNA,  
8 the number of repeats that are detected based on the length  
9 are the number.

10 So if I have a fragment of DNA that has ten copies  
11 repeating one after another like ten boxcars, we'd call that  
12 an allele, 10. That's a 10. That peak is given -- it's 10  
13 because it has ten boxcars in the middle of it. If it were  
14 11, it would have one more. If it was 11, 14, that would mean  
15 you had one fragment that -- fragment, STR fragment or piece  
16 of DNA that had 11 boxcars and the other one had 14. So it's  
17 a really very basic designation for the result.

18 Q. You mentioned the height of these peaks. How is the  
19 height relevant?

20 A. The height is a representation or is an indicator of  
21 how much DNA you have and also a little bit the quality of the  
22 DNA you have. So if you start with a pristine DNA sample,  
23 like a known sample, whether you collect a cheek swab or blood

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1 from anybody, you purify the DNA. That should be, you know,  
2 near-perfect DNA.

3           So if you amplify that -- you know, say, you put a  
4 target amount of DNA in, so you amplify a certain amount,  
5 maybe, you know, the optimal amount, you will get a DNA  
6 profile. And because the DNA was good quality and there was a  
7 lot of it, you will get peaks or alleles that have a certain  
8 height, and they're going to be -- tend to be pretty tall.  
9 And that indicates I've got high-quality DNA, I started with  
10 a -- a lot of DNA, and it amplified well.

11           So the taller the peak, the better the quality of the  
12 DNA. And also, the starting amount of DNA can be assessed  
13 from the -- from the heights of those peaks.

14           Q. What is a mixed sample?

15           A. A mixed sample is simply a sample that has DNA from  
16 more than one individual present. I mean, they're very common  
17 in forensic specimens. So you may have mixed blood stains.  
18 You could have, say, blood and semen stains. You can have an  
19 item that's been handled by several people who will leave DNA  
20 behind in the form of skin cells. Any one of those will give  
21 you a mixed DNA -- can be considered a mixed DNA sample.

22           Q. How do you interpret the results of a mixed sample?

23           A. Based upon our protocol, we will look at the number of

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1 peaks or number of alleles that we see at the STR regions, at  
2 the STR loci. Generally, you will see one or two -- if it's  
3 from a single person, you'll see a single peak or you'll see  
4 two peaks.

5           If you see three peaks or more at more than two  
6 regions, because there are some -- some mutations that can  
7 occur where you see a three-peak pattern in a single person,  
8 but if you see more than three peaks or more across the DNA  
9 profile -- and in our protocol, it's two or more. We say at  
10 least two, if not more -- we would call that a mixed DNA  
11 profile.

12       Q. So y'all have protocols in place to interpret these?

13       A. Yes. Yes. Part of our -- part of our standard  
14 operating protocol is -- has an interpretation section.

15       Q. How do we know those protocols are reliable?

16       A. They -- well, first of all, they were developed from  
17 the validated test -- the validated procedures that we came up  
18 with from our research unit. They've also gone through both  
19 internal audits and external audits.

20           So our protocols, as part of our accreditation  
21 process, get reviewed by outside auditors or assessors to make  
22 sure that they meet, well, many standards, both the quality  
23 assurance standards, the FBI quality -- FBI quality assurance

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1 standards, and also standards by our accrediting body.

2 Q. Have there been any changes to the protocols since the  
3 items in this case were tested?

4 A. Yes. Our technology has changed and improved greatly  
5 over the last 22 years.

6 Q. Do those changes affect the reliability of the  
7 protocols in place at the time?

8 A. No. At the -- any protocol that we used in casework  
9 at any given time had been validated and it had been approved.  
10 As we've made changes, there was always another round of  
11 validation. So, again, now our DNA Support Unit will do  
12 another round of validation, they will generate another  
13 protocol. We will do internal validation to test it out in  
14 casework before it goes online.

15 So any protocol that we -- and we do all that before  
16 we ever use it on casework, so any protocol we've used on  
17 casework has gone through the validation and approval process.

18 Q. What happens after you develop a profile?

19 A. Well, after a profile is developed, it's my job to  
20 interpret that profile, so to look at the DNA profile, look at  
21 the electropherograms, and make an assessment as to what --  
22 the nature of that profile. Is it single source? Is it a  
23 mixture? How strong are the results? All of these things

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1 that -- that I need to do to ultimately interpret that profile  
2 to come to some conclusion as to the nature of the profile and  
3 what possible DNA sources might be in that.

4           And then ultimately, if I have a known sample, after  
5 I've looked at the evidence sample -- because that's another  
6 one of our rules, you have to look at the evidence DNA before  
7 you do any comparisons -- then if I have a known sample, I  
8 will do a comparison to the -- to the evidence profile.

9           Q. Why do you look at the evidence before you do any  
10 comparisons?

11          A. Well, it's actually a requirement -- it's a  
12 requirement, according to the quality assurance standards and  
13 many other recommendations. The reason is to avoid -- avoid  
14 developing any bias.

15                So if I were to look at, say, a known DNA profile  
16 before I looked at the evidence, I might see certain things in  
17 that known sample, and say, oh, yeah, I see them in the  
18 unknown sample. He must be there in or, you know, she must be  
19 in there.

20                But if I look at the evidence profile first, I can  
21 say, okay, it's single source or it's a mixture. This  
22 appears -- you know, looks like it might have two  
23 contributors, three contributors, whatever. I will assess it,

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1 it looks like it may have a major contributor or it may be an  
2 indistinguishable mixture, all of these ways to sort of  
3 characterize that profile.

4 I have to take it as is before I do any comparison so  
5 I don't bias myself, like I'm looking for person A, you know,  
6 in -- in that profile. It's a way to say, okay, here's what's  
7 going on with this profile. Now let me look at my known DNA  
8 profile and say could this person be a potential contributor?

9 Q. Are you familiar with the term "random-match  
10 probability"?

11 A. Yes, I am.

12 Q. What does that term mean?

13 A. Random-match probability is a statistical calculation  
14 that we -- we -- that is used in forensic science. And what  
15 it says -- well, the reason we calculate any probability or  
16 calculate any statistic is, not only is it a requirement, but  
17 DNA is not absolute identification. You know, we cannot ever  
18 say this person is the source of that DNA absolutely. There  
19 is always a possibility that a random unrelated person could  
20 have the same DNA profile as that observed in the evidence.

21 And so we, as the -- as the examiner, as the forensic  
22 scientist, we need to provide that statistic, which is  
23 essentially saying if John Doe is not the contributor of this

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1 DNA, if he is not the one who left this DNA, then the  
2 probability that a random unrelated person could also have  
3 that DNA profile is 1 in -- and that's the random-match  
4 probability. It could be 1 in 100, 1 in 1,000, 1 in  
5 10 trillion. It all depends on how much information you have  
6 in the DNA profile from the item of evidence.

7 Q. How do you go about calculating that figure?

8 A. We use it -- it's -- we derive the -- we calculate it  
9 using the information from the evidence -- evidence's DNA  
10 profile. So depending on how many STR regions that -- that I  
11 have -- that I have in my profile, each one is considered an  
12 independent event. And this is -- you know, some people have  
13 described it like rolling dice or lottery ticket numbers, but  
14 what we do is to calculate the random-match probability for  
15 each STR region we have.

16 So, you know, a way to describe it is let's say you've  
17 got six -- six dice. You roll the first one, you get a five.  
18 Well, you had a one-out-of-six probability of getting that  
19 one, of getting a five. You roll the next one, you get a two.  
20 Same thing, one out of six. You do that six times, and  
21 whatever you get from those dice, you can multiply them  
22 together. So it would be one-six times one-six times one-six,  
23 and I don't know what that is, but it's a fairly small number.

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1           We do the same thing with DNA profiles. We will  
2 calculate a random-match probability using established genetic  
3 equations for each STR locus, and then multiply them all  
4 together, and that's called the product rule which is another  
5 established genetic principle, and we calculate the overall  
6 random-match probability for the entire DNA profile.

7           So the overall probability -- random-match probability  
8 is based on the individual random-match probabilities for each  
9 result in that DNA profile, each STR region that I have from  
10 that profile.

11          Q. You said these equations are established. Established  
12 by who?

13          A. Well, the -- the individual -- the individual locus  
14 calculation actually comes from a genetic principle called the  
15 Hardy-Weinberg equilibrium, and it's called the Hardy-Weinberg  
16 equation. And actually, it was a concept that was developed  
17 by two scientists independently. I think George Hardy was a  
18 mathematician in England. And I can't remember Weinberg's  
19 first name, but I think -- but I think he was -- is German,  
20 and I forget his specialty.

21           But anyway, they looked at the behavior of genetic  
22 markers, and they came up with this calculation to say if  
23 they -- or this -- this -- this phenomenon. And basically it

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1 says if genetic markers behave independently, if those alleles  
2 assort randomly, with no regard to each other, you can  
3 multiply them together to calculate a random-match  
4 probability.

5           And the product rule came out -- came from an  
6 extension of that. I -- I'm not sure who developed that. But  
7 basically it said that if you have multiple independent  
8 events, like multiple STR regions that don't interact with  
9 each other genetically, that they just randomly behave, you  
10 can multiply them all together to come up with a random-match  
11 probability.

12           Q. Now, is this defined in terms of random-match  
13 probability of the world, a specific geographic region, an  
14 ethnic group? How is that defined?

15           A. It -- it can vary. We actually -- when we started,  
16 when we developed our test, we decided to create population  
17 databases that were a general representation of the -- of the  
18 U.S. population. So we have a population database for African  
19 Americans, for Caucasians, for Southeastern Hispanic, and  
20 Southwestern Hispanic.

21           And, you know, a population database is simply a table  
22 of fractions that indicates four, if you have -- so for a  
23 given population and a given STR locus, all the different

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1 possibilities. So if at, let's say, STR locus 1 you have 10  
2 forms, 10 types, or 10 alleles, we calculate the frequency for  
3 each one of those, 10 through -- say 10 through 20. Those  
4 frequencies are plugged into the Hardy-Weinberg equation and  
5 ultimately they get all multiplied together.

6 So these population databases -- databases allow us to  
7 predict the occurrence of any possible genotype or STR type  
8 that we observe.

9 Q. You mentioned ethnic groups that the FBI has a  
10 database -- database figures on.

11 A. Yes.

12 Q. Do you have figures for the Asian population?

13 A. We do not, no.

14 Q. Do you have figures for any type of Middle  
15 Eastern-specific population?

16 A. No, we do not.

17 Q. Are you familiar with the NRC?

18 A. Yes, the National Research Council.

19 Q. Do they have any guidance on what to do in this, in  
20 that -- in a situation where a potential suspect is not a  
21 member of any group that you have information on?

22 A. Sure. There's a lot of history with it, but without  
23 getting into the history, eventually -- there was a report

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1 that Dr. Reich mentioned, NRC-I, and it was the first report  
2 that looked at forensic DNA testing.

3           And this NRC, this National Research Council, is a  
4 collection of generally experts in the field, esteemed  
5 scientists, who independently review the -- the nature of the  
6 science. Well, in 1992, they issued a report, but their  
7 recommendations for statistics were not well -- well, my  
8 opinion, and pretty much everybody in the forensic community  
9 did not agree with them, and even -- even population  
10 geneticists wrote papers saying this is not a valid approach  
11 that they were suggesting.

12           So the National Research Council formed another  
13 committee that published a second document in 1996. I believe  
14 it's called The Evaluation of Forensic DNA Statistics or it --  
15 it really specifically dealt with statistical issues.

16           So that 1996 report -- and in between 1992 and 1996,  
17 scientists, including the FBI, were looking at various  
18 populations. We were studying all the available populations  
19 that we could get our hands on, to see how did these -- at the  
20 time it was the pre-STR type of DNA testing, but how did these  
21 DNA markers behave in different populations, so within a major  
22 racial group, between major racial groups.

23           We generated -- labs generated a ton of data. And

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1 ultimately the 1996 NRC report reviewed that. And they said  
2 if you don't have the specific database for an individual, a  
3 subject in a case, you should provide statistics based on all  
4 those available, to give a range of values.

5           So it's a way of providing a range of values that can  
6 estimate the random-match probability for different racial or  
7 ethnic groups to give context to the rarity or maybe common --  
8 you know, commonness of a DNA profile. So that became -- that  
9 became the pretty much standard approach used by forensic  
10 laboratories.

11           Q. If an individual who is a suspect or even charged with  
12 a crime is not a member of the group for which you have  
13 information or data on, how is that relevant?

14           A. It -- I mean, it -- it may or may not be relevant.  
15 There are differences between generally major -- you know,  
16 we -- even in the four that we've studied, and actually we  
17 also have several Native American databases that we use.

18           Part of our studies indicated that between major  
19 racial or significant ethnic groups, there is more variation.  
20 So a DNA profile will tend to look -- have a different  
21 random-match probability generally by a factor of ten but  
22 sometimes more, say between Caucasian and African American.

23           So if you have that kind of variation between, you

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1 know, major racial or ethnic groups, like South -- or for us,  
2 I would say Southeastern Hispanic, Southwestern Hispanic are  
3 more sort of geographical ethnic groups. If you have more  
4 variation between those, then by providing all four  
5 random-match probabilities, the goal is to provide some range  
6 or context for the profile you get from the item of evidence.

7           If the person who may be a contributor to that  
8 evidence is from a different racial or ethnic group, that --  
9 we may not have the best estimation for that racial or ethnic  
10 group, but we do have a range of values. And we know that  
11 generally the range doesn't vary by much more than a factor of  
12 a hundred.

13           Q. So you say generally between racial groups the number  
14 you get doesn't vary by a factor of a hundred. Can you  
15 explain that, please.

16           A. Sure. What that means is that if you were to have a  
17 DNA profile and you calculated the random-match probability  
18 and it was one in a billion in Caucasians, if you would do --  
19 if you were to run that same profile into an African American  
20 population, it may come back as low as one in 10 million, or  
21 it could be as rare as one in 100 billion. You know, there  
22 could be that kind of factor of a hundred variation.

23           But the relevant thing from our -- you know, from --

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1 as an analyst's point of view is that a rare profile does not  
2 become a common profile. So you may have a frequency or a  
3 probability of one in a billion. It may go down to one in  
4 10 million, but that's still a very small number.

5 So that's why we provide those four -- you know, use  
6 the four databases to say, yes, you can have a range of  
7 values, but this profile is either very common, which can  
8 happen when we have very little information, or it's still  
9 going to be rare.

10 Q. I'd like to ask you to switch gears a little bit and  
11 ask you about allele dropout. What is allele dropout?

12 A. Allele dropout is a phenomenon that occurs as you  
13 amplify smaller and smaller amounts of DNA, or less and less  
14 DNA. So, as I say, you know, we -- we try -- we try to use  
15 one nanogram of DNA as our target if we have that. But as you  
16 attempt to amplify less and less DNA, you may not get a full  
17 profile.

18 And I think I mentioned earlier one of the other  
19 definitions of partial profile was you may lose an allele from  
20 an STR locus. So, for example, if you have an STR locus and  
21 it's supposed to be -- you know, that person has an 11, 14, if  
22 you have a small amount of DNA, even during the amplification,  
23 you might lose one of those alleles. You might -- or you

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1 won't see it.

2           So when you look at the electropherogram, the 14 might  
3 not be visible or the 11 might not be visible because there  
4 was not enough starting DNA to adequately amplify to give a  
5 result. So when that happens, we call that allele dropout.

6           Q. Does your SOP with the FBI account for that?

7           A. Yes, it does. As I mentioned before, our  
8 interpretation rules address how to deal with low-level DNA  
9 samples, and our validation studies also examined that so that  
10 we would have the thresholds that we do.

11          Q. Are you familiar with the term "stochastic threshold"?

12          A. Yes. Stochastic is an adjective basically that means  
13 random or unexplainable event. And what it really tends to  
14 mean is -- mean is that under certain circumstances you can  
15 have something randomly happen during a process that you  
16 cannot predict, so it's an unpredictable random event.

17                 And allele dropout actually is a stochastic effect  
18 because, you know, when you start with your DNA, you have a  
19 certain amount of DNA. But if one -- and -- you know, say  
20 we'll focus on one STR region, and if there's supposed to be  
21 two peaks or two alleles, a stochastic effect would be the  
22 dropping out of one.

23                 So, in other words, one allele is amplifying, you

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1 know, okay, is just fine. The other one doesn't amplify as  
2 well. That's a random stochastic event. So when that  
3 happens, that kind of event is called a stochastic event.

4 A stochastic threshold is something that we determine  
5 during validation that tells us for DNA alleles or peaks in a  
6 profile of a certain height, if they're above this height,  
7 then we are -- we consider them reliable and -- and accurate.  
8 But below a certain height, we have to account for these  
9 random stochastic events like allele dropout.

10 Q. So if it's below the height, what do you do?

11 A. We -- we -- well, I don't want to say we -- we don't  
12 interpret it differently, but we do -- we look at them  
13 differently. So we look at them and we have to account for  
14 all the things that could happen when you don't have enough  
15 DNA.

16 So my interpretation would take that into account and  
17 I would say, you know, let's say I see at a particular STR  
18 region, I see one peak but it's below my threshold. That  
19 tells me, it's like I don't think that's a single-peak  
20 profile. It could be, but it could also be that I'm missing  
21 one. So that height lets me know when I have to be more  
22 critical in my interpretation.

23 Q. Would that lead to an inconclusive result?

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1           A. For us, yes, inconclusive is when something falls  
2 below our stochastic threshold and we do not -- we don't use  
3 inconclusive results for calculating a random-match  
4 probability. Now, we can -- we can use those results, and  
5 it's in our protocol, to exclude someone.

6           So if I have results that are below my stochastic  
7 threshold, I'll still compare them if I have a known sample.  
8 And if those results exclude that person, I will use them to  
9 exclude. And that's a process we've had since we started  
10 doing DNA. If we have information, even if it doesn't meet  
11 our best threshold, if it excludes an individual, we will use  
12 it to exclude.

13          Q. What is allele stacking?

14          A. Allele stacking, I think I -- I think I mentioned  
15 earlier when we were talking about peaks that are the same --  
16 the same allele. So, again, for example, you get -- at a  
17 particular STR region, you get an 11 from your mother and an  
18 11 from your father. They're going to stack, so you're going  
19 to get a taller peak.

20          That can also happen in mixtures. So if you have a  
21 mixture of DNA -- and let's say I've got a two-person mixture,  
22 and Person A at a particular locus has an 11, 14. And Person  
23 B has a 14, 18. I'm going to see three peaks at that STR

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1 locus. I'm going to see an 11, I'm going to see a 14, and if  
2 it's a one-to-one mixture, I'm going to see a 14 that's  
3 generally twice as tall as the 11, and I'm going to see an 18  
4 that's probably about the same height as an 11, so it will  
5 look like a little mountain range almost.

6 When you have a mixture and the people in the mixture  
7 share results, or alleles, those alleles will stack and give  
8 you a more -- a taller peak or more intense result.

9 Q. Does the FBI's SOP account for allele stacking?

10 A. Yes. Yes, it does.

11 Q. What is stutter?

12 A. Stutter is a -- a byproduct of the amplification  
13 process. And this is something -- was one of the first things  
14 characterized when we started amplifying DNA. It's a  
15 phenomenon that happens -- there's a physical explanation for  
16 it. But what it is is that when you amplify a DNA fragment,  
17 an STR fragment, ideally it should make nothing but that  
18 fragment.

19 So, again, I'm going to use my 11 as an example. When  
20 I amplify my DNA and I have an 11, I really just want the 11  
21 to amplify. However, because of the nature of PCR, the -- the  
22 product chemical process, there is a phenomenon that occurs  
23 where I will get a small peak one STR unit less than the 11,

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1 so it will be a 10. And that's called stutter.

2 Now, it is a minor -- it's a minor component. So  
3 stutter is something that always -- pretty much always occurs  
4 with STR loci, and it's a reproducible, actually quantifiable  
5 byproduct. And that's part of how -- you know, so we account  
6 for that when we do our analysis. And that actually was  
7 something that we validated.

8 So for a given STR locus, when I amplify it, how much  
9 stutter do I get? So if I'm supposed to have an 11, 14, I'm  
10 going to have a 10, 13 much shorter that represents stutter.  
11 So that's something -- you know, it's -- it's an unavoidable  
12 byproduct, but we account for it when we do our analysis.

13 Q. Once a forensic scientist's work is done, does his  
14 work product undergo any type of internal review process at  
15 the FBI?

16 A. Yes, indeed. After I've done my analysis, if I'm  
17 doing a comparison, I'll -- you know, or not. Sometimes I do  
18 just unknown subject DNA profiles.

19 But regardless, once my -- I issue -- when I write up  
20 my report with my conclusions based upon my interpretation and  
21 analysis of the DNA profiles, that entire data packet will be  
22 given to another qualified examiner and he or she will do the  
23 exact same thing I just did. They will look at all the data.

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1 They will draw their own conclusions. They will do their own  
2 interpretations. And at the end of the process, they come  
3 back to me and say, I agree with your conclusions, or did you  
4 think about this or have you considered this?

5 It's a way to really catch any errors that I might  
6 have made in my interpretation. So it's a review step that is  
7 designed to ensure the quality of the original analyst's  
8 interpretation and conclusions.

9 Q. Does the FBI Lab have chain of custody protocols?

10 A. Yes, we do.

11 Q. Generally speaking, what are those protocols?

12 A. Essentially, they -- they indicate that as -- once  
13 evidence is received by the FBI Laboratory, it will be tracked  
14 throughout the laboratory. So the evidence may go to one unit  
15 and then will go to another unit. It will move, say, from  
16 discipline to discipline. So it may go to hairs and fibers or  
17 trace evidence first and then come to DNA, then go to latent  
18 fingerprints.

19 So any movement of evidence through the laboratory is  
20 tracked so that we know who has control of the evidence at any  
21 given time.

22 Q. I'd like to switch gears again and ask you questions  
23 specific to your work on this case. Can you tell the judge

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1 how you became involved and what you were asked to do.

2 A. Yes. As I mentioned yesterday, I returned to the DNA  
3 Casework Unit in 2010, and went through a requalification  
4 process. And a request came in, I believe it was 2013 --  
5 probably 2013 because the report was 2014 -- to analyze some  
6 evidence -- items of evidence that had not been previously  
7 analyzed for this case.

8 Well, unfortunately, the original examiner had retired  
9 and passed away. He was a friend of mine, you know, very --  
10 unfortunately.

11 Q. What was his name?

12 A. That was Dr. F. Sam Baechtel, F. Samuel Baechtel.

13 Q. Okay.

14 A. So he had retired and unfortunately passed away. So  
15 given that I had worked with this type of DNA testing with the  
16 Profiler Plus and Cofiler kits, I was assigned the case to do  
17 additional testing and -- and then do any comparisons, if  
18 necessary.

19 So at the time, not only -- excuse me -- not only did  
20 I do the additional items that were requested, but I did a  
21 complete review of all of the previous work that had been  
22 done, looked at the results, came to my own conclusions.

23 And as I was going through the previous reports, I

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1 noticed there were some typographical errors, some comparisons  
2 that had not been done. So in addition to my conclusions, I  
3 cleaned up everything that had been omitted the first time  
4 around. And that report, I believe, was issued in February of  
5 2014.

6 Q. Did you compare the piece of evidence K470 with the  
7 known standard, K19?

8 A. I did.

9 Q. And did you come to your own independent conclusions  
10 on that?

11 A. Yes, I did.

12 Q. And did those conclusions deviate from what had  
13 previously been found?

14 A. No, they did not.

15 Q. What happened next on this case?

16 A. Well, I believe there were -- I believe there were  
17 some other analyses that were requested, but for the most  
18 part, when I finished those, my -- you know, my reports were  
19 done and issued.

20 However, in 2015, during another validation process by  
21 our DNA Support Unit, they began to reanalyze every sample in  
22 our population databases, so the African American, Caucasian,  
23 Southeast, Southwestern Hispanic. They were -- analyzed

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1 them -- analyzing them using a new kit, one that had 21 STR  
2 loci and three sex-typing loci, a very, very powerful kit. So  
3 they had to generate new population tables that accounted for  
4 all 21 STR loci.

5           When they compared those results to those that had  
6 been generated from the databases back in 1999, they  
7 discovered some errors. So there were actually, I believe,  
8 about 11 -- 1,175 population database samples. They  
9 discovered errors in -- I believe it was 27 of them. So those  
10 errors in the DNA types had to be incorporated into these new  
11 population tables.

12           So they did that. There was actually a -- a letter  
13 published in the Journal of Forensic Sciences in 2015 just  
14 entitled Erratum, and it described what had happened and what  
15 the new population databases were. The effect was -- was  
16 minimal, and the letter even states that, that ----

17           MJ [COL ACOSTA]: I'm sorry. I need you to slow down a  
18 little bit.

19           WIT: Oh, I'm sorry. I'm sorry.

20           A. The effect was, based upon their analyses, was  
21 minimal. Generally, there was no worse than a twofold change  
22 in a random-match probability with these errors. So if you  
23 had a random-match probability of one in a billion, it may

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1 have gone to one in 2 billion or one in, you know, 500  
2 million. So still didn't impact the rarity of the profile.

3 But because that -- those errors had been discovered  
4 and -- and updated, during a meeting that I had regarding this  
5 case, I offered would you like -- you know, do you want me to  
6 recalculate using the correct databases? The answer was yes.  
7 So I did that.

8 So anything involving statistical analysis that had  
9 been done in this case, I recalculated the random-match  
10 probabilities and issued a new report, which I believe came  
11 out in 2017.

12 Q. Now, the original report had random-match probability  
13 defined in terms of four ethnic groups; is that correct?

14 A. Yes, it did.

15 Q. Did any of those figures change in this case?

16 A. Actually, only one of the random-match probabilities  
17 changed based on the recalculation.

18 Q. And how did that random-match probability change?

19 A. It went -- I believe it was in the Caucasian  
20 population. The original random-match probability was one in  
21 6.2 trillion. The recalculated was one in 5.9 trillion. So  
22 it changed -- I'm not -- you know, I mean, less than a factor  
23 of two. I'm not sure of the math, but it did not change

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1 dramatically.

2           And all of the other -- the African American,  
3 Southeastern Hispanic, Southwestern Hispanic, stayed the same  
4 because the database changes did not impact those  
5 calculations.

6           Q. Did you subsequently generate a written report to  
7 document those findings?

8           A. Yes, I did.

9           Q. I'm going to show you some of the documents that were  
10 prepared in this case.

11          ATC [MAJ ROSS]: And permission to use the ELM0, sir?

12          MJ [COL ACOSTA]: You may.

13          Q. What I'm showing you is Attachment B, Tab 7 of  
14 AE 460C. Can you tell me what we're looking at here, sir?

15          A. Yes. This is a worksheet that is -- was generated in  
16 our laboratory during the analysis of evidence in this case.  
17 And it's a slot -- it's called a slot blot quantitation. And  
18 it's a representation of the values for the amount of DNA that  
19 were estimated from the slot blot. So what you're seeing are  
20 the numerical values that were derived from that slot blot for  
21 these samples.

22          Q. I'd like to point your attention to the block column 3  
23 down to letter D that's highlighted there.

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1 A. Yes.

2 Q. Are those the results for the sample K470?

3 A. Yes, they are.

4 Q. And what is -- what do those results tell you?

5 A. All right. Well, this -- this sheet actually has  
6 several different functions, but it's not only -- helps me  
7 interpret the data, but it also performs some automatic  
8 calculations that also assist the biologist processing the  
9 evidence.

10 So what I'm looking at is there's -- the log number is  
11 an abbreviation for the lab number for that sample where you  
12 see the K470 at the end. The quant value -- and it says in  
13 nanograms -- is the conclusion drawn from that piece of x-ray  
14 film that I mentioned for the slot blot.

15 So when that -- sorry -- that result for that sample  
16 was examined, it was determined to be less than .1 nanogram,  
17 which was the lowest standard. Actually, I can -- I guess I  
18 should clarify.

19 If you look at the box that says column 1, you see  
20 the -- the standard. That's -- those are the DNA rulers that  
21 I mentioned before. So you see it goes from 20 nanograms,  
22 mostly doubling dilutions, sort of, down to .1. So the lowest  
23 standard is 0.1 nanograms, or 100 picograms.

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1           This sample for K470, the result -- the DNA result was  
2 fainter than 0.1, so it has the -- it's entered in as less  
3 than .1.

4           Q. Now, from this document, where you go down and you see  
5 the quant value and it says less than .1, is that telling you  
6 that you had less than .1 nanograms in the evidentiary sample  
7 K470?

8           A. No. What that's telling me is that there was less  
9 than .1 nanograms in that one-tenth of the sample, that two  
10 microliters, that was put on the slot blot. And that's  
11 actually in the second column. The second column tells you  
12 how much DNA was put on the slot blot. So it wasn't the  
13 entire sample. It was only two microliters or one-tenth of  
14 the total sample.

15          Q. Now, if you scroll to the right of the same  
16 highlighted row, underneath where it says "targeted DNA  
17 nanogram to amp," what is target DNA again?

18          A. That's the amount of DNA that we prefer to amp -- or  
19 to -- I'm sorry, I keep talking in shorthand here -- prefer to  
20 amplify. So, again, going back to our validation, we found  
21 that to get the best possible profile, it's ideal to have one  
22 nanogram of DNA. So that is -- that's a constant. You can  
23 actually see that column in pretty much every box.

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1           And the reason it's there is because this actually  
2 comes from an Excel spreadsheet. It's going to use that to  
3 calculate how much of a DNA extract to use to get one  
4 nanogram.

5           Q. And again, is there any minimal amount of DNA that --  
6 in an evidentiary sample that you've got to have before you  
7 submit it to testing?

8           A. No. No. When we -- I don't think I said this before.  
9 When we go for a target amount and we say one nanogram is our  
10 target, that really is kind of an upper limit. Because,  
11 again, validation -- and even the developers found this. If  
12 you put too much DNA into your amplification, it can actually  
13 make your DNA profile look horrible. It becomes very  
14 difficult to interpret.

15           So you really don't want to go -- for our process, we  
16 don't want to go over one nanogram because that actually can  
17 make things worse. But there is no lower limit for the amount  
18 of DNA we can attempt to amplify.

19           Q. I'm going to scroll down to the bottom of this page.  
20 And I'd like to note this particular section right here where  
21 there ----

22           MJ [COL ACOSTA]: Make sure you're next to the microphone.  
23 Nobody can hear you.

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1 Q. This particular section here where it says asterisk,  
2 asterisk, less than target DNA, ng amount for amp. What does  
3 that mean?

4 A. Yes. That -- that refers back to -- if you look at  
5 the highlighted row that has the results for K470, you'll see  
6 that under the DNA extract volume in microliters, it says 20  
7 with the two asterisks, which means the entire extracted DNA  
8 sample is going to be used for amplification.

9 Because it's less than -- because it's less than  
10 the .1 nanograms, or 100 picograms, we can't hit one nanogram.  
11 That sample, I know it, the biologist knows it, anybody who  
12 looks at that from our lab will know we're not hitting one  
13 nanogram. So that's an alert to say less than target DNA  
14 amount for amp. Doesn't mean we're not going to amplify it,  
15 but it's a flag to say you do not have one nanogram,  
16 basically.

17 Q. Why do you have that flag?

18 A. It's a -- it's in a way to both alert the biologist  
19 that he or she is going to have to use the entire sample.  
20 It's also a way for the examiner to know that we don't have  
21 the optimal amount; that there may be some -- if -- you know,  
22 there may be some limitations on the DNA profile that we get.  
23 We may not get all the information we need because we have

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1 less than the ideal target amount.

2 Q. Does that suggest whoever is doing this test is  
3 violating any protocol?

4 A. No. No. It's -- it's an -- it's an aid. It's an  
5 interpretation aid, and it's a processing aid for our  
6 biologists.

7 Q. Does that suggest that any result would be unreliable?

8 A. No. No.

9 Q. I'm now going to show you a second document,  
10 Attachment B, Tab 8 of AE 460C. And again, I'd like to point  
11 your attention to -- or first, tell me what is this document,  
12 sir.

13 A. Yep. As it says, it's the PCR amplification record.  
14 It is, again, a spreadsheet that documents what samples are  
15 going to be amplified, and in this case, it's using the kit  
16 Profiler Plus. So this tells me that the samples listed, 1  
17 through 14, which include positive and negative controls as  
18 well, are going to be amplified using the Profiler Plus kit.

19 It also says the total sample volume -- and you'll see  
20 it's always 20 microliters because, according to the protocol,  
21 you have to add 20 microliters to the reaction mix for it to  
22 work properly.

23 It's going to list the amplified mass in nanograms,

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1 and you see most of them actually say one, which means with  
2 the exception of three samples and the blanks, there was  
3 enough DNA to hit that one nanogram target.

4           Then it says the volume of the sample, and that is a  
5 calculation that's done that says, okay, so if I want to  
6 get -- we'll use -- look at the first one, that 385.1. It  
7 says if I want to get one nanogram of DNA, I need five  
8 microliters. Well, I still need a total of 20, so I'm going  
9 to add 15 of water. So those last two columns, volume sample,  
10 volume water, are always going to add up to 20.

11           The difference is when you see those samples that say  
12 less than one nanogram, those are where the entire sample, the  
13 entire 20 microliters, is going to be used and no water will  
14 be added. And it has the double asterisk -- asterisk on it  
15 which actually refers back to the previous page that says less  
16 than one nanogram is going into the reaction or whatever the  
17 wording is.

18           Q. So this tells you how much was actually amplified?

19           A. Yes.

20           Q. Okay.

21           A. How much of the sample is actually amplified, yes.

22           The amount of DNA is indicated for those samples where it says  
23 one. If it says less than one, I don't actually know the

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1 exact amount of DNA.

2 Q. I'm going to show you Attachment B, Tab 10 of AE 460C.  
3 I'm going to scroll out a bit. What are we looking at here?

4 A. Just to make sure -- actually, could you zoom in a  
5 little bit just to make sure I can read. Old eyes. Oh, too  
6 far. Okay. I'm sorry.

7 This is the -- the electropherogram for item K470. So  
8 that is the -- I'm sorry. That's the end product  
9 post-electrophoresis that contains the DNA profile for item  
10 K470.

11 Q. If you could, please, walk us through what these  
12 results mean. Help us interpret what we're looking at.

13 A. Sure. This is -- this is for the Profiler Plus  
14 amplification kit. So there's nine loci, plus a sex-typing  
15 region. The way -- one of the ways to mix the nine together  
16 is to give them different colored dyes that I mentioned before  
17 that get excited by a laser.

18 So the fragments have three different colored dyes  
19 attached. There's blue, green, and yellow. So what these  
20 individual lines are indicating, the first one is showing  
21 those -- those STRs that were tagged with a blue dye. And  
22 you're actually seeing three different STR regions, and you  
23 can see spaces in between them. So the first one ----

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1 Q. Let me interrupt you.

2 A. Sure.

3 Q. On this first line you see three STR regions?

4 A. Yes.

5 Q. So three loci?

6 A. Yes, three loci.

7 Q. How do you tell where one starts and one ends?

8 A. Well, there's space built in between them, so you can  
9 look at the space in between. But there's also another  
10 control sample that's included that's not shown here that we  
11 can compare it to, and it's called an allelic ladder. And I'm  
12 just trying to think of a good way to describe that.

13 If you think of the alleles in an STR locus as cars,  
14 and if you've got two different numbers, you've got two  
15 different cars. And let's say they're both Fords. An allelic  
16 ladder would be the equivalent of lining up all the cars in  
17 the showroom that Ford makes, and you could say, oh, yeah --  
18 and I'm showing my age. This is a Taurus and this is an  
19 Explorer. So that's how you determine the nature of the  
20 allele. That allelic ladder will span a size range that says  
21 everything between here and here are the possibilities for  
22 this single STR locus.

23 So what you don't see here, but what we can do a --

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1 what we do comparisons to is looking at these individual  
2 results, we compare them to that allelic ladder and say, oh,  
3 yeah, this one lines up with 15, and this one lines up with  
4 16, and that's how we assign those numbers. If you look at  
5 that allelic ladder, you'll see gaps in between them, and  
6 that's how we know where one begins and ends and the next one  
7 begins and ends.

8           On here, you can see some flat lines in between. And  
9 that's a pretty good indication of where they -- you know,  
10 that there is -- you know, one has ended and the other one  
11 begins.

12           Q. Now, I see in looking at this first row, the height of  
13 the peaks descend as you go from left to right.

14           A. Yes.

15           Q. Does that concern you at all?

16           A. No. No. In fact, with forensic evidence -- well,  
17 I'll back up a bit.

18           When you get DNA from an item of evidence, it may not  
19 be of the highest quality. It may have been affected by  
20 environmental factors, and it may start to break down. And a  
21 good way to understand why this is not a concern is that if  
22 you look at the first region, you see two pretty tall peaks  
23 standing up there. And they're roughly, you know, like 100 --

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1 what does it say? About 130 or 140 or so. Those are  
2 considered smaller STR peaks. And smaller peaks tend to  
3 survive harsh conditions better.

4 As you move out, the next peak you look at 17 -- I'll  
5 use that as an example because it's pretty tall -- is at 180.  
6 That's a little bit longer, which means the environment might  
7 start to break it down a little bit more.

8 And then finally, when you get out to the other -- the  
9 last one, where you're looking, say, in the 240 range, those  
10 peaks are considered -- you know, they're almost twice as long  
11 as the original ones. Those are longer pieces of DNA. The  
12 environment will tend to break them down faster. As DNA  
13 breaks down, there's less of it. It doesn't amplify as well.

14 So looking at these results, I see a perfectly normal  
15 forensic profile, that the smaller fragments have amplified  
16 reasonably well, and these larger fragments, not so well. So  
17 that is something we -- we call that a ski slope effect,  
18 actually, and we see it routinely in forensic samples.

19 Technology has gotten better. We don't see it --  
20 well, no, we still see it. I was going to say it has gotten  
21 better, but we still see longer fragments break down faster  
22 and don't amplify as well in forensic samples.

23 Q. If I could point your attention to this first group of

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1 peaks here.

2 A. Yes.

3 Q. Can you explain what all these boxes mean down  
4 beneath.

5 A. Sure.

6 Q. Boxes and numbers.

7 A. The first box that you see is the allele assignment.  
8 So that's the 15, the 16, the 17, and the 18. That just  
9 represents the number of repeats for that particular DNA  
10 fragment that's present.

11 The sort of greenish box is the length of the  
12 fragment, and it says -- so for 15, it says 123.49. Now,  
13 ideally these things should be multiples of four, but it's  
14 very hard to measure something this small to, like,  
15 zero percent accuracy. The important thing is that it can be  
16 compared to other fragments.

17 And then the third value -- excuse me. In the red box  
18 is the height of the peak, so that's -- represents the height  
19 of that particular peak. So each one of these represents the  
20 allele designation, the size or length of that fragment, and  
21 the height of that peak.

22 And I -- I'd like to point out sort of what I was  
23 talking about the -- the four base pair or four-unit

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1 difference. If you compare the 15 to the 16, you see the 15  
2 has 123.49. The 16 has 127.58. That's pretty good, four  
3 bases apart. So that shows you as those -- as you add  
4 boxcars, they pretty much go nicely in units of four. And I  
5 think even the next one goes from 127.58 to 131.6. That's  
6 almost a perfect four.

7 I mean, so as I say, it's not dead-on accurate, but  
8 it's -- it's pretty close and it's a pretty good assessment of  
9 the space between these peaks.

10 Q. The 15, which peak does it go to? Does it go to this  
11 one? And let me mark it here.

12 A. Yes, the 15, the 15 is a very -- a very short peak  
13 compared to the others.

14 Q. And what does the 16 go to?

15 A. The 16 is one of the alleles in the DNA profile, one  
16 of the results in the profile.

17 Q. And is that represented by the long -- the tallest  
18 peak in that first group?

19 A. Yes.

20 Q. What about the 17?

21 A. The 17 -- actually, I'm going to jump back. The 17 is  
22 a short peak. It's associated with the 18. That actually  
23 represents the stutter. So I mentioned before that stutter is

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1 a byproduct of amplification.

2 In this particular profile, the 15 and the 17, you can  
3 see they're both four units shorter, and they're -- it's a  
4 very small percentage. Those represent the stutter peaks for  
5 the 16 and the 18.

6 Q. So at this particular locus, what is the finding that  
7 you can report?

8 A. Based on this result, there is a DNA profile that  
9 would be -- a DNA profile that would be a 16, 18. I would not  
10 count the 15 or 17 because they're a stutter.

11 And one thing I didn't mention is that, again, during  
12 validation we determine the percentage of stutter that we  
13 expect to see. Generally, it's about 10 percent. So when I  
14 see a peak that is four units less and less than 10 percent of  
15 the larger peak, that's stutter.

16 So the 15 -- I'll go to the red box -- is 147, is the  
17 height. The 16 is 1702. Well, 10 percent of 1702 would be  
18 about 170. So that 15 falls below that threshold, so the 15  
19 is considered stutter.

20 And you can do the same math for the 17 and the 18.  
21 You can see the 17 is less than 126, which would be 10 percent  
22 of the 18, so the 17 is stutter.

23 Q. Now, you're saying four units less. Let me just make

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1 sure we're all on the same sheet of music here. 17 is stutter  
2 from the 18, right?

3 A. Yes. If you look at the 17 and 18, if you go to the  
4 green box, you see 131.6 and 135.67. That 17 is four units  
5 less; therefore, it is in the stutter position for 18.  
6 Because it's below 10 percent, it fits the criteria --  
7 criteria for stutter. So that is considered stutter. It is  
8 not part of the DNA profile.

9 Q. If the allele is at 18, where would the stutter  
10 position be?

11 A. If the allele is at 18?

12 Q. If we're using 18 as a numeric value, where is the  
13 stutter position, 17?

14 A. It would be 17, yes.

15 Q. Okay. Tell me about this next group of peaks here.  
16 What do you see?

17 A. Okay. This one is the next blue STR region. There is  
18 a single peak at 17, which is pretty dominant. It has a peak  
19 height of 1191, so it's a pretty tall peak. And I see three  
20 other peaks. I see a 14, a 16, and an 18. Now, those are all  
21 pretty small peaks. You can see they really just barely blip  
22 above the background.

23 Now, what's interesting is that the stutter for 17

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1 would be in the 16 position. And again, you can look at the  
2 green boxes or -- you know, that 16 is four units less than  
3 the 17, so that's the stutter. It's less than 10 percent.  
4 And again, I'm -- that's a ballpark figure, but it's -- it's  
5 pretty accurate. The protocol has -- never mind. The  
6 protocols have our actual numbers, but -- so the 16 is stutter  
7 from the 17. But the 14 and the 18 are not in stutter  
8 position. They're small peaks. The 14 is only 82, and the 18  
9 is only 64, but they're not in any byproduct position like  
10 stutter.

11 So even though they're short, I interpret those as  
12 actual DNA peaks. Those are DNA profile results of what I  
13 would call a minor contributor. So if the 17 is the dominant  
14 DNA type, that 14, 18 is the minor contributor.

15 It represents -- it indicates there's a mixture of DNA  
16 and that I have a strong contributor and a weak contributor,  
17 so it's at least a two-person mixture.

18 Q. How do you go about distinguishing between the major  
19 and the minor contributor?

20 A. It's actually established in our protocol. It's --  
21 it's based upon the peak heights. And without getting too --  
22 you know, too into the mathematics, we expect when we get an  
23 STR result that if it has two peaks, we expect it to have --

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1 those two peaks are -- should be within a certain percentage  
2 of -- of each other. Hopefully -- you know, ideally they'd be  
3 100 percent the same size. There's always a little bit of  
4 variation.

5           So depending on the STR locus, we expect generally for  
6 a tall peak, that it's going -- that the two peaks are going  
7 to be within 70 percent of each other. So, for example, if I  
8 had a peak at 1,000 units, I would expect a matching peak to  
9 be about, you know, no less than 700 or no more than -- I'm  
10 not going to do the math, but I'll just stick with that. So  
11 that ratio between the two peaks would be our measure.

12           Whenever you have peaks that fall outside those  
13 ranges, that indicates another contributor. So in this case,  
14 there is no way you could match the 14 or the 18 peak with the  
15 17 and have it get anywhere near 70 percent. It's more like  
16 probably 5 percent. I mean, I'm not doing the math properly,  
17 but it's maybe 4 percent. So those peaks, you cannot match up  
18 a 14 with a 17 or a -- the 17 with the 18.

19           And so when we have peaks that can be associated  
20 within the proper ranges, we consider that a -- as a potential  
21 contributor and a potential either major contributor or minor  
22 contributor. So that's how we distinguish major from minor,  
23 is based on the relative peak heights of everything we see in

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1 the profile.

2 Q. I'd like to move down to the last row here. Can you  
3 explain your findings for the -- or your interpretation of the  
4 first group, the first locus on that last row?

5 A. Yes. This is a -- an STR locus. It's called D5S818.  
6 And I'm seeing five different -- I'm seeing five peaks. So  
7 I'm seeing an 11, a 12, a 13, a 14, and a 15. The 13 and the  
8 15 are the tallest peaks. And if you look at them and you  
9 look at the red box, I think it's 614 and 641 are the heights.

10 Well, if I were to do a ratio, if I would divide one  
11 by the other, it's -- it's going to be over 70 percent. I'm  
12 not going to try to do the math, but I guarantee it will be  
13 over 70 percent.

14 So to me, that indicates those two peaks -- and  
15 they're much taller than everything else. So that tells me  
16 those two peaks can be associated and that they represent a  
17 potential major contributor at that region, at that D5 region.

18 The 14 peak is less than 10 percent. It's at 51. So  
19 that's less than 10 percent, so the 14 is stutter off of the  
20 15. So that's not a -- a contributor. That's byproduct.

21 What's interesting is that -- first, I'll start with  
22 the 11. The 11 is not in a byproduct position. So to me that  
23 is contributor. Now, it's a low-level contributor. There's

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1 95. It's a short -- relatively short peak, but it's there.

2           What's interesting is if you look at the 12 peak, it's  
3 at 137. Now, again, can't do the math accurately, but I do  
4 know that 137 is more than 10 percent of 614. Stutter would  
5 be like 61 or less. So that tells me stutter could be present  
6 but there's also something else there. And to me, that  
7 indicates there is another DNA contributor that is a mixture  
8 of stutter and another DNA source.

9           So at this profile, I would say I have a major  
10 contributor at 13 and 15, and a minor contributor of 11, 12.  
11 So there's a little bit more going on at that profile, but  
12 when you break it down piece by piece, it -- it be -- it comes  
13 clear, at least to me.

14         Q. You mentioned that 11 is not in the stutter position  
15 for 12, but it -- it looks ----

16         A. Well ----

17         Q. Can you ----

18         A. I'm sorry.

19         Q. ---- explain that a little more?

20         A. Well, 11 is in the stutter position for 12, but it is  
21 way above 10 percent. I mean, 11 is at 95. 12 is at 137.  
22 That's closer to, like, probably 80 -- 70, 85, 70, 80 percent.  
23 That 11 is way above the stutter position for 12, so it's not

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1 stutter. It's another DNA source, another contributor.

2 Q. So you have two contributors here?

3 A. Yes. Based on this profile, I'd say so.

4 Q. Is there anything to suggest three contributors?

5 A. I'm not seeing three, but when you get into low-level  
6 amounts of DNA, you really never know how many -- truly how  
7 many contributors you have. You have to look at the results  
8 you've got.

9 There could be -- theoretically, there could be a  
10 third contributor who never developed, who didn't result --  
11 doesn't have any -- any results that are visible. There's  
12 other interruptions, but, you know, based on the results I'm  
13 seeing here, I'm only seeing two contributors.

14 Q. Even if there's more than two contributors at that  
15 locus, would it affect your determination of who the major  
16 contributor is?

17 A. No. Based on these results, the major contributor, in  
18 fact, at every locus clearly stands out. So there -- there's  
19 no confusion about the major contributor in this case ----

20 Q. All right.

21 A. ---- or in this sample.

22 Q. Moving on to the peak in the middle there, the 11, is  
23 there any indication there of any allele dropout?

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1 A. It's possible. Again, I'm seeing the 11 is a strong  
2 peak. That's 774 is above our stochastic threshold, so that's  
3 a reliable peak. The 12, on the other hand -- again, it's not  
4 in the stutter position. It's not byproduct. It's a  
5 contributor. But it's only at 60.

6 Now, our stochastic threshold is 200, so anything  
7 below 200, you have to consider allele dropout. So I can see  
8 a 12, but there could be -- from that contributor, whoever  
9 that other contributor is, there could be another result that  
10 did not amplify enough or adequately to -- to give a result.  
11 I mean, if ----

12 MJ [COL ACOSTA]: Hold on. Defense counsel is standing.

13 LDC [MR. NATALE]: Excuse me, Your Honor.

14 MJ [COL ACOSTA]: Yes.

15 LDC [MR. NATALE]: I have been informed that we have a  
16 need for a comfort break.

17 MJ [COL ACOSTA]: Oh, yeah. I was planning on taking it  
18 in ten minutes, but if ----

19 LDC [MR. NATALE]: I've been told ----

20 MJ [COL ACOSTA]: ---- if you need it now, we could take  
21 it.

22 LDC [MR. NATALE]: ---- that it's more emergent now.

23 MJ [COL ACOSTA]: Yes. Understood.

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1 LDC [MR. NATALE]: Thank you, sir.

2 MJ [COL ACOSTA]: All right. What we're going to do is  
3 we'll take a 20-minute recess.

4 Sir, while you're on the -- when your -- when I ask  
5 you to step down, I want you to remember that you are still on  
6 the stand, so you're not to discuss your testimony with  
7 anyone, including counsel for the government. Do you  
8 understand that?

9 WIT: Yes, of course, Your Honor.

10 MJ [COL ACOSTA]: Can you comply with that instruction?

11 WIT: Yes, I certainly can.

12 MJ [COL ACOSTA]: Okay. You can go ahead and step down.

13 WIT: Thank you.

14 **[The witness was warned, temporarily excused, and withdrew  
15 from the courtroom.]**

16 MJ [COL ACOSTA]: We'll come back at ten after the hour.  
17 The commission is in recess.

18 **[The R.M.C. 803 session recessed at 1051, 08 December 2021.]**

19 **[The R.M.C. 803 session was called to order at 1111,  
20 08 December 2021.]**

21 MJ [COL ACOSTA]: The commission is called to order. All  
22 parties present as before, Government?

23 TC [MR. MILLER]: Yes, Your Honor.

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1 MJ [COL ACOSTA]: Defense? Defense, are all parties  
2 present as before?

3 LDC [MR. NATALE]: Yes, Your Honor. I apologize.

4 MJ [COL ACOSTA]: All right. Thank you.

5 Witness, re-call the witness.

6 **[The witness, Alan M. Giusti, resumed the witness stand.]**

7 MJ [COL ACOSTA]: Sir, I remind you that you remain under  
8 oath.

9 WIT: Yes, Your Honor.

10 MJ [COL ACOSTA]: All right. Government.

11 ATC [MAJ ROSS]: Yes, Your Honor. Again, permission to  
12 use the ELMO? I believe we were discussing AE 460, page 48,  
13 which would be Attachment B, Tab 10.

14 MJ [COL ACOSTA]: You may proceed.

15 ATC [MAJ ROSS]: I'll zoom out a little bit.

16 **DIRECT EXAMINATION CONTINUED**

17 **Questions by the Assistant Trial Counsel [MAJ ROSS]:**

18 Q. Mr. Giusti, I believe we were talking about this  
19 middle peak, the -- if you could, please, pick up where you  
20 left off, sir.

21 A. Yes. The 11 peak in that middle STR locus in the  
22 bottom row.

23 Q. Tell me what you see with the middle locus.

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1 A. Again, there's an 11 peak, an 11 peak that is 774  
2 units tall, so it is over our stochastic threshold, meaning  
3 it's a reliable representation of the STR result at that  
4 region.

5 There's also a 12 peak that is next to it -- excuse  
6 me -- that is only 60 units in height. So it is not in a  
7 byproduct or stutter position, but it -- and it is -- is  
8 detected. So to me that indicates that there is a minor  
9 contributor that has at least a 12 allele associated with it.

10 Q. Would any allele dropout affect your determination of  
11 the major contributor here?

12 A. No. The major contributor peak is clear and it's  
13 above our interpretation threshold, so allele dropout would  
14 not be a factor.

15 Q. So in this middle one it's an 11, 11 value?

16 A. Yes, that's correct.

17 Q. Okay. And finally the last group of peaks here, is  
18 this the result that was inconclusive?

19 A. Yes. This is the result that was listed as  
20 inconclusive in the report. You can see that there is a 9, 12  
21 designation for the two peaks, but they are both below 200  
22 units. So when you look at the red box, I think it's, it  
23 looks like 151 or 161, and then 133 or 132. Regardless,

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1 they're both below 200. So that tells me that there is the  
2 potential for allele dropout.

3 Q. Now, if you have inconclusive results, you can use  
4 those results to exclude somebody as a possible source, right?

5 A. Yes. According to our protocol, we can use those  
6 results for exclusionary purposes only. We can't use them to  
7 include, we can't use them in statistics, but we can exclude  
8 if -- if possible.

9 Q. Would you exclude the accused in this case?

10 A. No. I would have to -- I'd want to refresh my memory  
11 with his profile, but I don't -- I believe he was also a 9,  
12 12. So based on that, it would not exclude.

13 Q. Okay.

14 ATC [MAJ ROSS]: Beg the court's indulgence.

15 [Pause.]

16 Q. If the results of the accused were 9, 12, would you be  
17 able to use ----

18 MJ [COL ACOSTA]: I need you to speak up. You're kind of  
19 fading out there on me.

20 Q. If the results of the accused's K19 were 9, 12, would  
21 you be able to use that to exclude Mr. Nashiri?

22 A. If his -- if his result at that locus was 9, 12, I  
23 would not be able to exclude him based on these results. If

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1 the results here were, say, 9, 13, then I would be able to.  
2 But if they're the same, there's not enough information there  
3 for me to exclude him.

4 Q. And you performed that analysis in this case, correct?

5 A. Yes, I did.

6 Q. Okay. Low-copy testing, can you tell the commission  
7 what low-copy testing is.

8 A. Low-copy testing -- well, there's two terms that are  
9 routinely used. There's low-copy testing, sometimes called  
10 low-copy number testing and then there's the term just  
11 low-copy number. Low-copy number testing refers to  
12 modifications to the PCR -- generally to the PCR process or  
13 some aspect of the analysis. According to SWGDAM, it's also  
14 called enhanced STR analysis.

15 And what it refers to is making modifications to the  
16 PCR process, such as increasing the number of cycles or doing  
17 a process called nested PCR, or injecting more of the sample  
18 during electrophoresis. These are all modifications to the  
19 standard DNA testing process designed to enhance or increase  
20 the information that you get from a PCR -- from a sample that  
21 has a limited -- a very limited amount of DNA.

22 Low-copy number is a term that describes the amount of  
23 DNA in a sample. So a good example of -- and by low-copy

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1 number, I'm going to go back and say when we talk about --  
2 again, talk about DNA, you have one copy per cell, one  
3 complete copy of your DNA per cell. If you have three, five,  
4 seven cells, that's a low number of copies of DNA or low-copy  
5 number.

6 So low-copy number can be used to describe the amount  
7 of DNA in a sample, but low-copy number testing refers to a  
8 modification to established protocols. So they -- they really  
9 are two separate concepts to -- to consider.

10 Q. Are you familiar with the Scientific Working Group on  
11 DNA Analysis and Methods?

12 A. Yes, SWGDAM.

13 Q. What are they?

14 A. Well, SWGDAM -- SWGDAM is a -- an organization that is  
15 administered by the FBI Laboratory. It has a set of bylaws,  
16 but it essentially has members of -- that consist of forensic  
17 scientists from all over the country and I believe there are  
18 some even from Canada, so between the U.S. and Canada. They  
19 also, I believe, will invite academicians sometimes.

20 Their purpose is to review the state of forensic  
21 science and to offer opinions or guidelines on the new  
22 technologies as they develop or on existing technologies as  
23 they're modified.

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1           In fact, a while ago when I was talking about the  
2 FBI's quality assurance standards, originally they were  
3 determined by a group of scientists called the DNA Advisory  
4 Board. However, their commission ended, I believe, in 2000 or  
5 somewhere in the early -- or early aughts, and now SWGDAM is  
6 the group that is responsible for -- for providing  
7 recommendations when changes to the quality assurance  
8 standards are required or are requested.

9           So SWGDAM is a very -- it's a very knowledgeable body  
10 of some of the, you know, most prominent forensic scientists  
11 and laboratories in this country that weigh in on technology  
12 issues.

13          Q. Do they have guidelines on testing small amounts of  
14 DNA?

15          A. Well, they do have guidelines on what they call the  
16 enhanced PCR analysis method, and that is a -- it's a document  
17 that first kind of summarizes the history of low-copy number  
18 testing -- low-copy number testing, which, again, refers to  
19 changes in the protocols. But it also recommends that -- or  
20 it prepares guidelines for how labs should implement these --  
21 and validate these -- these methods if they're going to use  
22 them.

23          So if a lab wants to use the enhanced PCR method or

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1 the low-copy number testing method, they recommend that the  
2 lab do certain validation steps to -- so that the lab  
3 understands what kind of results they can get and how to  
4 reliably and accurately interpret them.

5 Q. Does the FBI do low-copy number testing?

6 A. No, we do not.

7 Q. Has it ever done low-copy number testing?

8 A. We have -- no. Our approach has always been what we  
9 call the standard STR or standard PCR approach. We don't have  
10 any modified procedures designed to enhance the -- the  
11 results.

12 Q. Now, even if -- you were talking earlier about the  
13 ideal amount of DNA. Even if you don't have the ideal amount,  
14 can -- even if you do have the ideal amount, can you still run  
15 into issues where you only get a partial profile?

16 A. It's possible. I mean, it -- again, it depends on the  
17 quality of the DNA. So, for example, you could have -- and  
18 I've -- I've seen this happen. You could have like a huge  
19 blood stain where you would think you would get a ton of DNA,  
20 and -- but the person bleached the surface. You know,  
21 apparently everybody watches TV and they know bleach destroys  
22 DNA.

23 So there -- what looks like a blood stain, it gets

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1 bleached. The DNA gets destroyed. The quantitation result  
2 will still show because quantitation is very good even with  
3 broken up -- excuse me, broken-up DNA. It will still give a  
4 quantity. But when you go to amplify it, the STR regions have  
5 been destroyed where -- to the point where they won't amplify.

6 So you can have what looks like a large amount of DNA  
7 and still not get a full or even a -- you know, you may not  
8 get any DNA profile from it depending on the quality of the  
9 DNA, not just the quantity.

10 Q. Was low-copy number testing done on K470?

11 A. No. The standard procedure, PCR/STR procedure that we  
12 were using at the time, was used on sample K470.

13 Q. And those standard procedures were validated, correct?

14 A. Yes, they were.

15 Q. In your validation process?

16 A. That's correct.

17 Q. And under that validation process, is there any type  
18 of minimal amount or threshold of DNA you need to conduct  
19 testing?

20 A. No. The validation process was designed and carried  
21 out to allow us to assess the results from low-copy number DNA  
22 amounts.

23 Q. Are the results here reliable?

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1 A. Yes.

2 Q. How do you know that?

3 A. Because the samples were processed according to our  
4 standard protocol. All the controls that were examined during  
5 the analysis behaved as they should. The interpretation was  
6 reviewed prior to a report being issued. It went through our  
7 standard protocol from start to finish.

8 Q. Does the fact that this was a mixed sample affect your  
9 analysis whatsoever?

10 A. No, it does not.

11 ATC [MAJ ROSS]: Beg the Court's indulgence for one brief  
12 moment.

13 [Pause.]

14 ATC [MAJ ROSS]: That's all the questions I have for you,  
15 Mr. Giusti. If you would, please answer anything the defense  
16 has.

17 MJ [COL ACOSTA]: Defense, are you prepared to begin your  
18 cross now or do you need time to consult with your consultant,  
19 or your expert?

20 DC [MS. CARMON]: I can go forward now, Your Honor. Just  
21 give me a few moments to set up at the podium, please. Thank  
22 you.

23 [Pause.]

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1 DC [MS. CARMON]: May I, Your Honor?

2 MJ [COL ACOSTA]: You may proceed.

3 DC [MS. CARMON]: Thank you.

4 CROSS-EXAMINATION

5 Questions by the Defense Counsel [MS. CARMON]:

6 Q. Good morning, Mr. Giusti.

7 A. Good morning.

8 Q. You have been in the field of forensic DNA analysis  
9 over 35 years. Is that about right?

10 A. Actually, it will be 40 years next year, yes.

11 Q. Okay. And so I am -- safe to assume that you are  
12 familiar with the noted researchers and experts in your field;  
13 is that right?

14 A. Yes.

15 Q. And some of those researchers and noted experts would  
16 be your former colleague, Dr. Budowle; is that correct?

17 A. Yes, that's correct.

18 Q. And are you familiar with Dr. Peter Gill and John  
19 Buckleton?

20 A. Yes. As a -- yes, I am.

21 Q. And what about John Butler?

22 A. Yes. I actually -- I was working at the research unit  
23 at Quantico when John Butler was doing his Ph.D. project, so I

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1 was well acquainted with him then.

2 Q. And so these folks that I've mentioned, Dr. Budowle,  
3 Dr. Gill, Dr. Buckleton, and Dr. Butler, these are all people  
4 that you would agree are noted forensic experts and  
5 researchers in your field; is that right?

6 A. I would agree with Drs. Gill, Budowle, and Buckleton.

7 Dr. Butler has published books that summarize forensic  
8 science, but his number of actual forensic science research  
9 articles I believe have been limited. I think he's a very  
10 knowledgeable curator for forensic science, but he's -- his  
11 research is not something that I think we routinely rely on.

12 Q. I want to ask you about the definition of low-copy  
13 number, and I mean particularly here, the amount of DNA in the  
14 sample according to some of your colleagues that I just  
15 mentioned.

16 A. Yes.

17 Q. You are aware that Dr. Budowle routinely characterizes  
18 low-copy number as testing done with less than 100 picograms  
19 of DNA?

20 A. I believe I've seen that in several of his  
21 publications, yes.

22 Q. And, in fact, he published pretty extensively on the  
23 caution with which someone should approach low-copy number

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1 testing involving less than 100 picograms; is that right?

2 A. Yes. Is that the -- the 2009 publication?

3 Q. 2009, 2006.

4 A. Okay.

5 Q. 2010. Yes, sir. Same with Dr. Gill. Now, Dr. Gill  
6 has also published on that definition, and specifically on the  
7 amount of DNA that we characterize as low-copy number. And  
8 you've read his publications?

9 A. Yes, I have.

10 Q. And again, he quantifies that as less than 100  
11 picograms of DNA prior to amplification; is that correct?

12 A. I believe one of his earlier publications did. I  
13 think he may have upped it to 200 picograms in later  
14 publications.

15 Q. You saw where I was going.

16 Other -- other researchers in the field, other noted  
17 experts in the field, I think the consensus, and please  
18 correct me if I'm incorrect, but the consensus is that  
19 low-copy number, that measurement is between 100 and 200  
20 picograms. Would that be accurate?

21 A. I would say that's the consensus of the field, yes.

22 Q. And so when we're discussing low-copy number DNA, that  
23 is the DNA that you begin with before amplification; is that

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1 correct?

2 A. Yes. That is -- that is one way to characterize it.

3 Q. And again, just so we're all clear, the consensus  
4 among scientists in your field is that number is between 1 to  
5 200 picograms?

6 A. Yes, I would agree.

7 DC [MS. CARMON]: Your Honor, may I make use of the ELMO,  
8 please?

9 MJ [COL ACOSTA]: You may.

10 DC [MS. CARMON]: And for court and counsel, this is  
11 AE 460C Attachment B, and this is going to be Tab 6. If I  
12 could make this available to the witness and not public.

13 MJ [COL ACOSTA]: You may.

14 DC [MS. CARMON]: Thank you.

15 Q. Mr. Giusti, let me know when it pops up on your  
16 screen.

17 A. I can see it.

18 Q. Got it, okay. Do you recognize this?

19 A. Yes, I do. That is a copy of the x-ray film for the  
20 slot blot associated with the evidence that we've been  
21 discussing.

22 Q. And particularly, this is the slot blot for the  
23 evidentiary sample that we've discussed, which is K470?

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1 A. Yes, that's correct.

2 Q. Okay. I want to take you through what we observe  
3 here. And if you need to, for column and row purposes, to  
4 refer to the slot blot worksheet, please let me know and we  
5 can interchange them.

6 A. Okay.

7 Q. Okay. I want to start here at the very left. This  
8 first column, this is the standards column; is that correct?

9 A. That's correct. That's one of the two standard  
10 columns on the slot blot.

11 Q. And so this goes from the greater amount of DNA up at  
12 the top with the darker and larger circle, down to the lower  
13 amount of DNA at the bottom; is that correct?

14 A. Yes, that's correct.

15 Q. And it flips on the furthest column to the right; is  
16 that correct?

17 A. Yes, that's correct.

18 Q. And so, again, we're looking at a standard, but it  
19 starts with, at the bottom this time, the most amount of DNA  
20 up to the least amount; is that correct?

21 A. Yes, that's correct.

22 Q. Now, in your standard, when this testing was done in  
23 2002, this lowest amount of your standard is 0.1 nanogram; is

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1 that correct?

2 A. Yes, that's correct.

3 Q. And could you do public math and transfer that to  
4 picograms for us.

5 A. 0.1 nanograms would be 100 picograms.

6 Q. Okay. And so this is, again, the lowest standard on  
7 the -- is this the QuantiBlot that we're using now?

8 A. Actually, can you move that up so I can see the date?

9 Q. I can.

10 A. All right. I know we used both. It could be the  
11 QuantiBlot. It may have been the predecessor to the  
12 QuantiBlot, but it is definitely one of the chemiluminescent  
13 slot blot results.

14 Q. Okay. I'm going to zoom in just a bit so we can get a  
15 little bit closer of a picture. And again, just for  
16 reference, furthest to the left we're looking at the standard,  
17 and particularly this 0.1 nanograms; is that right?

18 A. Yes, that's correct.

19 Q. Let me go ahead and show you ----

20 DC [MS. CARMON]: And for court and counsel, AE 460C  
21 Attachment B. This is going to be Tab 7.

22 Q. I'll show you the worksheet so that we're all looking  
23 at the same thing. And so this is, again, the slot blot

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1 quantitation worksheet here.

2 A. Yes.

3 Q. I want to on the actual slot blot film find K470,  
4 which appears to be in the third column in the -- what would  
5 be the fourth row, row D; is that correct?

6 A. Yes, that's correct.

7 Q. Okay. So can we switch back to the film and -- and go  
8 from there?

9 A. Sure.

10 Q. And again, this is now Tab 6. So I start with your  
11 standard here. This would be first column, second column,  
12 third column; is that correct?

13 A. Yes.

14 Q. And am I correct as well that when we're talking about  
15 rows, we count from the top, meaning this would be the A  
16 position, this would be the B position, and this would be the  
17 C position ----

18 A. Yes.

19 Q. ---- is that correct?

20 A. That is correct.

21 Q. And for the record, I've moved my pen from the very  
22 top in the third row, to the second from the top, to the third  
23 from the top.

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1 A. Yes.

2 Q. I am pointing my pen here where I don't really see  
3 anything. Is this where the K470 quantitation would have  
4 occurred?

5 A. Well, yes, actually, it did occur. There is a  
6 admittedly very faint result, as ----

7 Q. And is that what I'm -- I'm just under it right here.

8 A. That's correct.

9 Q. Is that ----

10 A. Yes, that's the -- that's the result. It doesn't  
11 photocopy well, but that is the result.

12 Q. Okay. And so from this result for K470, the only  
13 thing you have to compare it to that is even close is the  
14 standard of .1 nanograms of DNA; is that right?

15 A. That's correct.

16 Q. And so do you make a determination how much less this  
17 could be, or is it enough to say less than .1 per --  
18 or .1 nanogram?

19 A. Since we don't have any lower control standards than  
20 the .1 standard, the way it's noted is less than .1. We have  
21 no way to assign any more specific value when the results look  
22 like that compared to the standard.

23 Q. Okay. And so from this slot blot information, we then

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1 switch to our worksheet where you transfer the numerical  
2 information; is that correct?

3 A. Yes, that's correct.

4 Q. And I'm going to switch back to Tab 7 and the slot  
5 blot quantitation worksheet. Let me zoom out for you.

6 Mr. Giusti, the worksheet that we are looking at, this  
7 is an FBI-created worksheet, correct?

8 A. Yes. Yes, it is.

9 Q. Okay. And just to make it clear, the -- I understand  
10 that amplification comes in a kit, a commercial kit. In this  
11 case, Profiler Plus, right?

12 A. Yes. The -- you know, most of the components for the  
13 amplification come in a kit, yes.

14 Q. And so the corresponding amplification worksheet,  
15 again, that is an FBI-created worksheet. That didn't come  
16 with the kit?

17 A. That's correct.

18 Q. Okay. And again, each analyst is charged with filling  
19 out this sheet -- is that correct? -- during the DNA process?

20 A. Yes, that's correct.

21 Q. So if we can zero again in on column 3, row D, which  
22 is sample K470, you've noted here, just like we spoke about,  
23 that less than .1 nanogram is as best you could estimate?

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1 A. That's correct.

2 Q. And so at that -- and again, public math, this would  
3 be less than 100 picograms; is that correct?

4 A. Based upon the result on the slot blot, yes. That  
5 very faint band you saw would be considered less than  
6 100 picograms.

7 Q. Okay. The target amount of DNA that you have  
8 referenced here, and again, it corresponds to the double  
9 asterisks at the bottom of the -- the slot blot quantitation  
10 worksheet, that comes from your internal studies? That is  
11 your internal target; is that correct?

12 A. Yes. The target amount was derived from our  
13 validation studies as being the optimal amount to give a  
14 reliable, full DNA profile.

15 Q. And just to be clear, because this is your worksheet,  
16 that is your lab's target; is that correct?

17 A. Yes. That target was based on our validation work.

18 Q. And that target is .1; is that correct? At least .1  
19 nanograms of DNA, is that your target?

20 A. No. The target amount that we performed ----

21 Q. Oh, I'm sorry. I'm looking at the wrong column.

22 A. Yeah.

23 Q. One nanogram of DNA?

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1 A. Yes. If possible, we prefer to amplify one nanogram  
2 of DNA.

3 Q. And that is what you are left with after amplification  
4 is one nanogram. That's your target; is that correct?

5 A. I'm sorry, I'm not ----

6 [Alarm in courtroom went off.]

7 MJ [COL ACOSTA]: Hold on. Do you need to check? All  
8 right.

9 It was just our cell phone detection device, which  
10 apparently has gone off a couple of times I know in my  
11 practice here as well when it -- when there has been nothing  
12 there. If it goes off again, we'll -- we'll take a break and  
13 have everybody inspect their material, but I don't believe  
14 it's 100 percent accurate all the time. So go ahead and  
15 proceed.

16 DC [MS. CARMON]: Okay. Thank you, sir.

17 Q. Mr. Giusti, let me direct -- sorry -- your attention  
18 to the column target DNA nanograms to amplify. The target  
19 here would be one nanogram; is that correct?

20 A. Yes. Ideally, yes.

21 Q. Okay. And what this -- and I think you testified to  
22 this on direct, but what these two asterisks -- asterisks are  
23 is a warning that you're not going to get one nanogram; is

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1 that right?

2 A. That's correct. It's -- it's an indication that there  
3 is not one nanogram of DNA.

4 Q. And so at this point, the DNA that you have quantified  
5 from the slot blot is less than 100 picograms, to put it in  
6 picograms?

7 A. That's the amount on the slot blot. It does not  
8 represent -- necessarily represent the DNA in the entire  
9 sample.

10 Q. And so where would that measurement be?

11 A. That is actually something I can't determine because  
12 the -- because there is no standard that goes below the 0.1 or  
13 100 picograms.

14 There -- I can tell you that one-tenth of that sample  
15 was put onto the slot blot. And so however much is there -- I  
16 mean, I can't give you a number unfortunately, but whatever is  
17 there, there is ten times that amount of DNA left in the tube.

18 So, for example, if I had .05 nanograms or  
19 50 picograms, there would be 500 picograms still in the tube.  
20 So -- but since I don't have any numbers below .1, I cannot  
21 give you that -- that value.

22 Q. And just to continue with that example, if what we  
23 were seeing on the slot blot were one-tenth of .1 nanograms,

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1 we would have 100 picograms; is that correct, .01 nanograms?

2 A. That's correct. If you could measure that -- that --  
3 that band, that -- that result, and if it came up as .01 or --  
4 nanograms or ten picograms, the total amount would be 100  
5 picograms. But again, it's all speculation. I can't -- I  
6 can't determine that amount.

7 Q. And, in fact, we could not even determine the  
8 concentration of the sample; is that correct? I'm looking at  
9 the third column over, concentration per nanogram, and it  
10 looks to be a hyphen or a dash in that column.

11 A. For the K470 sample?

12 Q. Yes, sir.

13 A. That's correct. Since there was no fixed  
14 quantification value, such as, you know, two or 20, there's no  
15 way to calculate the overall concentration. The less than .1  
16 precludes calculating a concentration.

17 Q. And so we are essentially left with an unknown as to  
18 the measure of DNA, the amount of DNA; is that correct?

19 A. That is correct.

20 Q. And that unknown, it could be 500 picograms or it  
21 could be 100. We don't know?

22 A. That's true.

23 Q. Now, I believe you also noted on direct that the

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1 entire sample was used during this DNA forensic analysis  
2 process, and the sample being K470; is that correct?

3 A. Yes, that's correct. When the amount of DNA is  
4 limited, then our standard practice is to use the entire DNA  
5 extract for amplification.

6 Q. And so in an instance such as that, where the entire  
7 sample is consumed during the process, this testing itself  
8 cannot be repeated; is that correct?

9 A. That's correct.

10 Q. And there is not enough DNA to repeat the testing that  
11 has been done on K470; am I understanding that correctly?

12 A. I -- I don't believe so. I'm not sure what the status  
13 of the item of evidence is, if there's any material remaining  
14 that could be tested. But based on the -- the extraction we  
15 did, there is no more DNA.

16 Q. I understand that you have in the years preceding this  
17 hearing gone back and reviewed the casework done on sample  
18 K470; is that right?

19 A. Yes, that's correct.

20 Q. Did you do -- did you go back and look at the  
21 electronic data or did you simply look at the  
22 electropherogram?

23 A. No, I -- I looked -- no, I looked at the

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1 electropherogram because that was the official record in our  
2 case notes to refer to.

3           The other issue was that the computer and software  
4 used in 2000 or 2002 was not really available anymore. It had  
5 been phased out. But it didn't matter because the printed  
6 electropherogram is the official record.

7           Q. Now, one of the ----

8           DC [MS. CARMON]: I'm sorry, Your Honor. I don't know how  
9 to clear that. Is that coming up on the screen, the red dots?

10          MJ [COL ACOSTA]: You mean your red lines?

11          DC [MS. CARMON]: Yes, sorry.

12          MJ [COL ACOSTA]: It is -- it is not a thing. Don't worry  
13 about it.

14          DC [MS. CARMON]: Okay.

15          MJ [COL ACOSTA]: Move on.

16          DC [MS. CARMON]: Got it. Thank you.

17          Q. Now, one of the benefits of being able to use the  
18 electronic data, had it been available to you, is that you  
19 could go in and manipulate the size of what you were looking  
20 at in order to zoom in or out; is that correct?

21          A. Yes, that would have been possible.

22          Q. And you would have been able to see more fully peaks  
23 that were perhaps under 50 RFU, which is, I believe, your

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1 analytic threshold; is that correct?

2 A. At the time, yes, that was our analytical threshold.

3 And, yes, I could have zoomed in to see if there was anything  
4 that was not marked but may have been present.

5 DC [MS. CARMON]: Your Honor, if I may use the ELMO again.  
6 This is, again, AE 460C Attachment B, and this is going to be  
7 Tab 10.

8 Q. Mr. Giusti, I'm going to attempt to zoom in a bit on  
9 the locus that was not called, that was called inconclusive,  
10 and that would be where we are seeing to the far right the 9  
11 and the 12 in black boxes.

12 A. Yes.

13 Q. Okay. And I am correct that this is the locus that  
14 because the RFU fell below 200, you determined this to be  
15 inconclusive, meaning it could not be used for identity  
16 purposes?

17 A. Not to make associations, correct, and not for  
18 statistical purposes. It could be used for exclusions.

19 Q. Now, I am seeing -- and please correct me if I am  
20 wrong, but I am seeing some peak between the 9 and the 12,  
21 actually two very small bumps here. Do you see the same?

22 A. I -- I see what you're pointing to, yes.

23 Q. And again, because you did not go back and look at the

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1 electronic data, this image is what we have. We're not able  
2 to zoom into those two peaks to determine what might be there;  
3 is that correct?

4 A. That's correct.

5 Q. I believe you talked on direct that allelic dropout is  
6 possible at this locus because of the low amount of  
7 amplification that -- the low RFU at hand; is that correct?

8 A. Yes, that's correct.

9 Q. And because, again, these two peaks fall below 200,  
10 they're not used in your statistical analysis; is that  
11 correct?

12 A. That is correct.

13 Q. Zoom in just a bit more. Now, because allelic dropout  
14 is possible here, I know that opposing counsel discussed  
15 Mr. al Nashiri's reference profile with you, and I think you  
16 were reminded that at this locus, he is a 9 and a 12.

17 A. Yes, that's correct.

18 Q. If a 10 had dropped out or if an 11 had dropped out  
19 here, what would that do to your ultimate opinion regarding  
20 the comparison between K19 and K470?

21 A. I'm not sure I can speculate -- well, no.

22 ATC [MAJ ROSS]: Objection. Speculation, Your Honor.

23 DC [MS. CARMON]: Your Honor, I believe this is within the

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1 ambit of his expertise.

2 MJ [COL ACOSTA]: Ask the question again.

3 Q. We have here a 9 and a 12 that are below your  
4 stochastic threshold of 200. You had previously testified  
5 that allelic dropout is possible ----

6 A. Yes.

7 Q. ---- at this locus.

8 I've previously pointed you to the two bumps here  
9 between the 9 and the 12. I'm asking whether if a 10 had  
10 dropped out, as you said that there is danger that could have  
11 happened, if a 10 dropped out here, how would that impact your  
12 opinion regarding the comparison between the evidentiary  
13 sample and the reference sample?

14 A. Okay. No, I've got it now.

15 MJ [COL ACOSTA]: Overruled. I'll allow -- I'll allow him  
16 to answer the question. Go ahead.

17 A. It still wouldn't change the conclusion, because even  
18 if there was a 10 or 11, regardless of whether they dropped  
19 out or not, there is still a 9 and a 12, which is consistent  
20 with Mr. al Nashiri; and, therefore, even with a 10 or 11 in  
21 there, I still could not exclude him because he potentially  
22 could be the source of that 9 and 12. As -- so I -- even if  
23 there were other peaks present, I still could not exclude him.

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1 I think, as I said before, had there been a 9 and a  
2 13, then I would have been more inclined to exclude because  
3 there was not complete concordance.

4 Q. Now, staying with this sort of example, if the 10 or  
5 11 or the 13 that you've mentioned were paired as a sister  
6 peak with the 12, and that was the major contributor, you  
7 determined that that would be the major contributor, how would  
8 that have impacted your opinion?

9 A. If this result indicated the presence of a reliable  
10 major contributor, then -- and we say like a 10, 12 was the  
11 major contributor?

12 Q. Yes, sir.

13 A. Based on the entirety of the other profile, I'm not  
14 sure I could still exclude him, but it would indicate a  
15 potential different major contributor.

16 The problem is, since everything here is below that  
17 stochastic threshold, there's a lot of different things that  
18 can happen. So I can't make a more definitive statement about  
19 necessarily excluding somebody when you get into that, that  
20 zone, if you will.

21 Q. And what I think I hear you saying is that when we're  
22 talking about a locus with this low RFU, we don't really know  
23 what could happen. It would really be speculation to try to

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1 call one allele over the other, given that we've had a lot of  
2 data loss here; is that fair?

3 A. I wouldn't say speculation. I would say that there is  
4 an awareness and an understanding that with low-level DNA  
5 profiles such as this, there are phenomenon that can occur,  
6 such as allele dropout predominantly. Sometimes you can see  
7 stutter imbalance. So knowing that the profile is this weak,  
8 for lack of a better word, I have to be extremely cautious  
9 with how I interpret it.

10 Q. Back in 2002, the full -- a full profile for the FBI  
11 involved 13 core STR loci; is that right?

12 A. That was what we were shooting for, yes.

13 Q. And again, back in 2002, that would have involved  
14 testing with two different kits; is that correct?

15 A. Yes, that's correct.

16 Q. And so one would have been the Profiler Plus, which  
17 gives us nine locations and a sex type; is that right?

18 A. Yes. Yes.

19 Q. And then the second kit would have been COfiler, which  
20 I believe gives us six with two overlap and a sex type as  
21 well?

22 A. That's correct.

23 Q. With K470, you mentioned -- we're talking about a low

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1 amount here, and the fact that it was, we believe, consumed in  
2 the Profiler Plus process; is that correct?

3 A. No. It -- it was -- the DNA was consumed in the  
4 Profiler Plus, yes.

5 Q. And so we were not able -- or your lab was not able to  
6 run it through COfiler for those additional loci for a full  
7 profile; is that right?

8 A. That's correct.

9 Q. And so the reason that we only have Profiler Plus and  
10 the nine loci here is because there was not enough of the DNA  
11 to run it through the second testing system?

12 A. That is correct.

13 Q. You mentioned enhanced detection measures when you  
14 were differentiating between low-copy number, meaning the  
15 measurement of DNA, and low-copy testing, which is the  
16 methodology that you described. Am I getting those distinct?

17 A. You are. Yes, that's correct.

18 Q. Okay. The -- some of these enhanced detection  
19 measures include testing in triplicate; is that correct?

20 A. Yes. That has been suggested as an -- as an option.

21 Q. And one of the reasons that testing in triplicate has  
22 been suggested as an option and is used is because that gives  
23 us a reproduced result; is that correct?

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1           A. I'm relying on the -- on the publications I've read,  
2 since I've never done low-copy number testing. But that was,  
3 if I remember correctly, that was proposed as an option, and I  
4 believe Dr. Gill was one of the proponents of that, was that  
5 not so much for reliability, but if you were to see the same  
6 DNA result across three different amplifications from a small  
7 amount of DNA, it was considered a more reliable determination  
8 of the presence of that STR result.

9           So, yes, it was not so much getting the entire  
10 profile, because they did -- they did indicate that you could  
11 see differences if you were to split your sample three ways,  
12 but they thought that anything you saw in common among those  
13 three could be considered reliable.

14           But I also believe the -- it also said if you didn't  
15 see it in two or three, if you only saw it once, you had a  
16 result only in one of those three amplifications, your  
17 interpretation rules had to be more conservative or cautious.

18           Q. I know that you have read multiple research articles  
19 and multiple notes on low-copy number and low-copy number  
20 testing, specifically by some of the authors that we've  
21 discussed today.

22           One of the cautions about this, or one of the problems  
23 with low-copy number and low-copy number testing, is the lack

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1 of reproducibility because we consume the entire sample in the  
2 one run. Do you recall reading those cautions and that  
3 concern in the article?

4 ATC [MAJ ROSS]: Judge, I would just object. Is she  
5 talking about low-copy testing or testing a low-template DNA?

6 DC [MS. CARMON]: I believe these articles are discussing  
7 low-template DNA, because it's talking about the ----

8 MJ [COL ACOSTA]: What I'm asking about, is it the low --  
9 the -- the small amount of DNA ----

10 DC [MS. CARMON]: Correct.

11 MJ [COL ACOSTA]: ---- or the enhanced techniques that he  
12 talked about that are used for the other ----

13 DC [MS. CARMON]: The low amount.

14 MJ [COL ACOSTA]: The low amount?

15 DC [MS. CARMON]: Yes.

16 MJ [COL ACOSTA]: Yeah.

17 A. Yes. I mean, so in terms of low-copy number or small  
18 amount of DNA, yes, pretty much ever since we started doing  
19 STR -- PCR/STR testing, we knew that a limited amount of DNA  
20 or low-copy number amount of DNA could present interpretation  
21 issues, or they would require more attention when interpreting  
22 them.

23 So, yes, I realize that a number of those publications

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1 address that. But they also -- well, I'll leave it at that,  
2 yeah.

3 Q. And when you say address that, the "that" is the  
4 concern that you cannot reproduce the result; is that correct?

5 A. Yes. In the term -- in terms of a limited amount of  
6 DNA, if you only have enough for one -- or if you only do one  
7 amplification, you have to -- you have to live with that  
8 single result. You only have that result to interpret, so  
9 yes.

10 Q. I would like to ask you briefly about the technical  
11 note published by Dr. Moretti and Dr. Budowle in 2001, which I  
12 think you referred to as your validation study.

13 A. Yes. The -- yes, the technical paper. Yes.

14 Q. Yes. And just so we're on the same page, this is the  
15 technical study -- or, excuse me, the validation study that  
16 you referenced that was published in the Journal of Forensic  
17 Science in 2001.

18 A. Yes. Actually, I believe there were two publications,  
19 one having to do with the validation of the kits, the other  
20 with using CE, or capillary electrophoresis, for the analysis.  
21 So there were kind of two partner papers that were published.

22 Q. I want to concentrate on the paper having to do with  
23 the validation of the kits ----

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1 A. Yes.

2 Q. ---- and specifically Profiler Plus, since that's the  
3 kit at issue today.

4 A. Uh-huh.

5 Q. The -- you mentioned that some testing was run with  
6 78 picograms of DNA.

7 A. Yes.

8 Q. Do you have any details regarding how many test cycles  
9 were run and exactly what -- I'm assuming it was the  
10 Profiler Plus amplification kit, but how many testing cycles  
11 were run? Do you know?

12 ATC [MAJ ROSS]: Judge, again I would object. Is she  
13 talking about testing cycles or how many cycles of  
14 amplification? It's ----

15 MJ [COL ACOSTA]: Hold on one second. I believe the  
16 question is whether or not -- your objection is whether or not  
17 your question is clear or not on ----

18 DC [MS. CARMON]: Let me ----

19 MJ [COL ACOSTA]: Are you talking about how many  
20 testing -- how many tests were run with 78 picograms or how  
21 many testing cycles were done in the process of validating the  
22 Profiler Plus kits? Can you be clearer? Can you clear that  
23 up?

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1 DC [MS. CARMON]: Yes, I can. I can.

2 Q. And, Mr. Giusti, correct me if I'm wrong, but I don't  
3 believe any enhanced cycles were used in this validation  
4 study; is that correct?

5 A. No, I -- well, I think in the early part of that  
6 paper, they do -- I may be wrong, but I think they do  
7 reference different numbers of cycles as part of the  
8 developmental validation. But when they ultimately settled on  
9 an approach, it was 28 cycles for the standard process.

10 Q. And so I won't use the word "cycles" again, but what I  
11 am asking is how many tests were run with the 78 picograms.  
12 Do you have any more details about that?

13 A. No, I -- no, I don't. I wasn't involved in that  
14 research, but the paper does clearly state that, so I know the  
15 data exists somewhere.

16 Q. Do you have any details about the types of profiles  
17 that were able to be seen after the running of 78 picograms  
18 through the process?

19 A. The only information in the publication says a  
20 complete profile was observed. So my assumption is that both  
21 Profiler Plus and COfiler gave full results at nine and six  
22 STRs between the two kits.

23 Q. But we don't have any details as to how many times a

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1 full profile was observed; is that right?

2 A. No, we do not.

3 Q. Now, the technical note also references post-PCR  
4 purification that was done. Are you familiar with that  
5 technique?

6 A. A little bit. I haven't -- I've never used it. And I  
7 remember it was discussed during developmental validation, but  
8 I -- I know of it, but I don't have any experience with it.

9 Q. And you don't have any experience with it because the  
10 FBI does not do it; is that correct?

11 A. That's correct. I believe the finding in that paper  
12 was that it was not necessary.

13 Q. And the post-PCR purification that is discussed,  
14 that's enhanced detection measure; is that correct?

15 A. I do believe that is one of the changes that can be  
16 made during the development of an enhanced STR detection  
17 system, yes.

18 Q. And so when we were discussing the difference between  
19 low-copy number, the measurement, and low-copy number testing,  
20 the methods, you are familiar, obviously, with the Office of  
21 the Chief Medical Examiner in New York; is that correct?

22 A. Yes, I am.

23 Q. And the low-copy number testing, meaning the methods,

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1 the enhanced detection methods that they perform?

2 A. I'm aware that they did perform them. I -- I don't  
3 know their protocols, but I -- I was aware that they were  
4 pretty much the only lab in the country, the U.S., the  
5 United States, doing it.

6 Q. And when you say doing it, you mean employing these  
7 enhanced detection methods; is that correct?

8 A. As I understand it, yes.

9 Q. And just to be clear, the FBI does not employ those  
10 methods, nor have they validated them internally?

11 A. That's correct.

12 DC [MS. CARMON]: The Court's brief indulgence, please?

13 MJ [COL ACOSTA]: Yes.

14 [Pause.]

15 DC [MS. CARMON]: Thank you, Mr. Giusti. And thank you,  
16 Your Honor. I have nothing further.

17 MJ [COL ACOSTA]: All right. Government, before we do  
18 redirect, I'm going to recess for lunch at this time. We'll  
19 do an hour and 15 minutes.

20 ATC [MAJ ROSS]: Yes, sir.

21 MJ [COL ACOSTA]: Defense, any issue with that?

22 LDC [MR. NATALE]: No, Your Honor.

23 MJ [COL ACOSTA]: All right. Mr. Giusti, I remind you the

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1 same warning I gave you before. You're still on the stand, so  
2 please don't discuss your testimony even with the government  
3 counsel before you come back. Okay?

4 WIT: Yes, sir.

5 MJ [COL ACOSTA]: If they try to talk to you, tell them I  
6 told you you can't talk to them. Okay?

7 WIT: Yes, Your Honor.

8 MJ [COL ACOSTA]: The commission is in recess.

9 [The R.M.C. 803 session recessed at 1202, 08 December 2021.]

10 [The R.M.C. 803 session was called to order at 1318,  
11 08 December 2021.]

12 MJ [COL ACOSTA]: The commission is called to order.  
13 Government, all parties present as before?

14 TC [MR. MILLER]: Yes, Your Honor.

15 MJ [COL ACOSTA]: Defense?

16 LDC [MR. NATALE]: Good afternoon, Your Honor. We are not  
17 all here because Ms. Morgan had to go and take a COVID test,  
18 so she's having a COVID test this afternoon. And obviously,  
19 we will let you know as soon as she knows what the results  
20 were of that.

21 But other than that, we are all here. I notice a  
22 sense of disappointment in your ----

23 MJ [COL ACOSTA]: No, no, no. I'm always disappointed

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1 when I don't have the full defense team here.

2 LDC [MR. NATALE]: So am I.

3 MJ [COL ACOSTA]: I don't know that we have -- oh, now we  
4 have Commander Piette back, that's at least one more.

5 Does Mr. Nashiri consent to Ms. Morgan not being  
6 present for this time period?

7 LDC [MR. NATALE]: Yes, Your Honor.

8 MJ [COL ACOSTA]: Mr. Nashiri, Ms. Morgan is not present  
9 for this portion now. Commander Piette has returned.  
10 Ms. Morgan is apparently at a medical appointment. Do you  
11 consent to proceeding without Ms. Morgan being present this  
12 afternoon?

13 ACC [MR. AL NASHIRI]: **[Gave a thumbs up.]**

14 MJ [COL ACOSTA]: Okay. All right. Re-call the witness,  
15 sir.

16 You're good. You're good, Government. Come on up.

17 Sir, have a seat. Take off your mask. I remind you  
18 you remain under oath.

19 WIT: Yes, Your Honor.

20 **[The witness, Alan M. Giusti, resumed the witness stand.]**

21 MJ [COL ACOSTA]: Government, I assume you have redirect.

22 **[END OF PAGE]**

23

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1 REDIRECT EXAMINATION

2 Questions by the Assistant Trial Counsel [MAJ ROSS]:

3 Q. Mr. Giusti, even if you have less than 100 picograms  
4 in a DNA evidentiary sample, you can still test it and get  
5 reliable results at the FBI Laboratory, correct?

6 A. Yes, that's correct.

7 Q. And that's because y'all have validated that process,  
8 right?

9 A. Yes, that's correct.

10 Q. And during the validation process, y'all established  
11 that you can test evidence without regard to any minimum  
12 threshold, right?

13 A. That's correct.

14 Q. And was there any deviation from the standard  
15 procedures in this case?

16 A. No, there were not.

17 Q. You were shown the QuantiBlot by opposing counsel.

18 A. Yes.

19 Q. And you had a chance to review the copy on the screen,  
20 right?

21 A. Yes.

22 Q. That was a -- that was a copy of the actual x-ray  
23 document, right?

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1 A. Yes, that's correct.

2 Q. In reviewing this case, in analyzing this case, did  
3 you look at the actual x-ray?

4 A. Yes, I did.

5 Q. And in preparing for court, did you look at the actual  
6 x-ray?

7 A. Yes.

8 Q. And that's a better look than the copy on paper?

9 A. It -- it is definitely more clear. There's better  
10 contrast on the film, yes.

11 ATC [MAJ ROSS]: Your Honor, that's all the questions I  
12 have for him.

13 MJ [COL ACOSTA]: All right.

14 EXAMINATION BY THE MILITARY COMMISSION

15 Questions by the Military Judge [COL ACOSTA]:

16 Q. Sir, is there any standard that requires a minimum  
17 amount that you're aware -- does any agency or any laboratory  
18 in the United States require an amount of DNA before it can  
19 say that a test is valid?

20 A. I can't speak to the protocols or requirements for  
21 other laboratories, but I will say that the quality -- the FBI  
22 quality assurance standards for forensic DNA testing do not  
23 specify the need for a minimum amount. They acknowledge that

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1 any amount can be subjected to the standard PCR/STR  
2 procedures.

3 Q. And the reason that there were only -- in this case,  
4 that there's only the nine areas that were tested is because  
5 that was the only -- that's all that was permitted by the  
6 amount of DNA that you had?

7 A. That -- that's correct. To do the test back in 2002  
8 with the two kits, the Profiler Plus and COfiler, they were  
9 two separate reactions, so you would have to have DNA for both  
10 tubes. But there was not only enough -- well, there's only  
11 enough DNA for one reaction because it was limited, yes.

12 Q. Is that common, that there -- at the time that this  
13 was conducted ----

14 A. Uh-huh.

15 Q. ---- was it common for there to be a test done where  
16 you were only able to do the Profiler test as opposed to the  
17 Profiler and the COfiler test?

18 A. Yes. Because we never know how much DNA we're going  
19 to get from an item of evidence, so things like licked stamps  
20 or -- well, cigarette butts are pretty good, but things where  
21 there was a -- where you wouldn't expect to get a lot of DNA,  
22 a licked envelope, samples like that generally only give  
23 enough DNA for the one reaction. So it was something we ran

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1 into pretty routinely.

2 Q. I believe I know the answer to this, but is there a  
3 reason that you -- that the testing was done with the Profiler  
4 as opposed to the COfiler?

5 A. Yes. Strictly a numbers game, Your Honor, that you  
6 have -- if you have nine STR regions, you've got more  
7 information than from six, so it's a more discriminating test.

8 Q. Just because you had more areas that you were looking  
9 at ----

10 A. Exactly.

11 Q. ---- to compare to whatever controls -- whatever known  
12 sample you had?

13 A. Exactly. So it would be like comparing nine physical  
14 characteristics versus six. You've got more information with  
15 nine.

16 Q. Okay.

17 MJ [COL ACOSTA]: Any questions based upon mine,  
18 Government?

19 ATC [MAJ ROSS]: No, sir.

20 MJ [COL ACOSTA]: Defense?

21 DC [MS. CARMON]: No, Your Honor. Thank you.

22 MJ [COL ACOSTA]: Permanent for the purposes of this  
23 hearing or temporary?

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1 ATC [MAJ ROSS]: Permanent, sir.

2 MJ [COL ACOSTA]: All right, sir. You're permanently  
3 excused for the purposes of this hearing. Do not discuss your  
4 testimony with anyone other than counsel for either side. You  
5 can step down and return to your duties or you may return --  
6 return to the table with counsel.

7 WIT: All right. Thank you very much, Your Honor.

8 **[The witness was warned and permanently excused.]**

9 MJ [COL ACOSTA]: Government?

10 ATC [MAJ ROSS]: Your Honor, that's our only witness for  
11 this hearing.

12 MJ [COL ACOSTA]: Any other evidence to present?

13 ATC [MAJ ROSS]: No, sir.

14 MJ [COL ACOSTA]: Thank you. Defense?

15 DC [MS. CARMON]: Yes, Your Honor. We would call  
16 Dr. Reich to the stand.

17 MJ [COL ACOSTA]: Sir, take a seat.

18 WIT: Thank you, Your Honor.

19 MJ [COL ACOSTA]: Counsel, did you want to swear the  
20 witness?

21 ATC [MAJ ROSS]: Raise your right hand.

22 **[END OF PAGE]**

23

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1 **KARL A. REICH, civilian, was called as a witness for the**  
2 **defense, was sworn, and testified as follows:**

3 ATC [MAJ ROSS]: Please have a seat.

4 WIT: Thank you.

5 DC [MS. CARMON]: May I, Your Honor?

6 MJ [COL ACOSTA]: You may.

7 DC [MS. CARMON]: Thank you. And, Your Honor, I would ask  
8 that Dr. Reich can be recognized as an expert based on his  
9 qualifications listed yesterday and the areas that Your Honor  
10 allowed his expertise yesterday.

11 ATC [MAJ ROSS]: No objection, sir.

12 MJ [COL ACOSTA]: He's so recognized.

13 DC [MS. CARMON]: Thank you.

14 **DIRECT EXAMINATION**

15 **Questions by the Defense Counsel [MS. CARMON]:**

16 Q. Good afternoon, Dr. Reich.

17 A. Excuse me. Good afternoon.

18 Q. I want to start by looking at the slot blot and the  
19 actual -- the copy of the film that we have.

20 DC [MS. CARMON]: And for court and counsel, that is  
21 AE 460C Attachment B, Tab 6. And if I could use the ELMO,  
22 Your Honor?

23 MJ [COL ACOSTA]: You may.

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1 Q. Dr. Reich, has that appeared on your screen yet?

2 A. It has now.

3 Q. Great. Great. Dr. Reich, do you recognize what this  
4 is?

5 A. I do, and it was explained earlier by Mr. Giusti.

6 Q. And you certainly have worked with this measure; is  
7 that correct?

8 A. Unfortunately, I can say I have.

9 Q. In 2002, was this the -- was this the way that  
10 laboratories measured the amount of DNA to be amplified?

11 A. This was the way. There was no other approved method  
12 for quantifying human -- or performing a quantification of  
13 human DNA for forensic DNA. There were other methods of doing  
14 DNA quantification, but for forensics, this was our only  
15 choice at the time.

16 Q. And so in 2002, safe to say that you were also using  
17 this instrument or this assay?

18 A. Sad to say, yes.

19 Q. Okay. I want to draw your attention to what we  
20 discussed earlier as being K470 on this particular film, and  
21 I'm going to draw your attention to where the fourth row would  
22 be in the third column from the left. Do you see where my pen  
23 is?

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1 A. I do.

2 Q. Okay. And I understand that this is a copy, but we  
3 are comparing what we see here in this third column, fourth  
4 row, to the standard here; is that right?

5 A. That's correct. You're actually comparing it to all  
6 the standards, if you want to be precise, and you are -- I can  
7 say, having looked at autoradiograms for quite some time, that  
8 I can actually see a band at that position. I know roughly  
9 what to look for and so was -- so able was Mr. Giusti.

10 It is faint, but it is in the right location. It's  
11 the right size. And so I believe that's the band of the  
12 evidentiary sample that was -- a percentage of which was added  
13 to this slot blot.

14 Q. Okay. And let me -- I'm going to zoom in just a bit  
15 here. The faint band that we see, is my pen in the right  
16 place, which would be the fourth row down?

17 A. Actually, you're over a bit, but it's a little harder  
18 to see as you've zoomed in because the image has become more  
19 pixilated. That, to me, is the best image of the Xerox of the  
20 film you're going to get.

21 Q. And so in looking at this, what standard is closest to  
22 what we are seeing for K470?

23 A. Well, you're obviously going to use the standard which

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1 has the least amount of signal, and so there are two sets of  
2 standards on this slot blot. One is largest amount of DNA to  
3 smallest on the left. One is smallest amount of DNA to  
4 largest on the right.

5 So you can compare it to either the bottom slot on the  
6 first column or -- one, two, three, four, five, six -- or the  
7 top one on the most leftmost column. So take your pick.

8 Q. Is there a more precise way to measure? And let me  
9 actually back up one sentence and show you AE 460C  
10 Attachment B. I'm going to Tab 7 now.

11 And let me verify that you -- excuse me. Let me  
12 verify that you have reviewed this document in preparation for  
13 your testimony; is that right?

14 A. I've seen this before.

15 Q. Okay. I'm going to zoom in to show K470, which is in  
16 column 3, in row D. Do you see that here?

17 A. I do, and it was shown earlier today as well.

18 Q. Okay. The quant value in nanograms is reflected as  
19 less than .1 nanogram. Do I have that right?

20 A. You do.

21 Q. Okay. Now, is that because, going back to Tab 6, all  
22 we have here, we know that the standard that I'm pointing to,  
23 bottom left, first column, is .1, and we know that this must

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1 be less. And this being K470. Is that right?

2 A. That's correct. The FBI chose the simplest notation,  
3 which is its -- the signal strength. The intensity of that  
4 band, the darkness of the band, the shade of that band is less  
5 than the smallest DNA standard on this autoradiogram, and so  
6 it has to be at a minimum less than that standard, which is  
7 the last slot on the left and the first slot on the right.

8 Q. Let me switch back to Tab 7, which is the slot blot --  
9 excuse me, quantitation worksheet. Is there a more precise  
10 number that can be quantified? Is there a more precise way to  
11 measure rather than just having to say it must be less than .1  
12 nanogram?

13 A. Well, there certainly is a -- there are other methods  
14 of deriving quantification from this technique. So some  
15 laboratories would take that film and use a scanner and scan  
16 those standards and try to develop a -- a linear comparison  
17 and then use the same scanner to scan the evidentiary or  
18 unknown item and try to compare the intensity of those bands  
19 against the standard curve that they would develop from the  
20 standards, so ----

21 Q. And when you say intensity, do you literally mean --  
22 and then just going back to Tab 6, the -- the darkness?

23 A. I do. So there's two factors going on here. There is

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1 how black is the band or the slot. There's also, as everyone  
2 can observe, the size of that band. And you can see that  
3 they're all very dark, so the film has been saturated. The  
4 maximum blackness of the film has been reached, and so the  
5 only number you have here is the size of the band you see, how  
6 wide or big it gets.

7           But the -- I won't say the correct way, if you would  
8 like to get a quantifiable number, a number rather than  
9 almost, then you would have to be within the linear range of  
10 the film, and you generally have to take several films so that  
11 the blackness isn't saturated and you have variable amounts of  
12 gray in those bands.

13           And then that scanner can tell you how gray it is,  
14 what the intensity of that band is. That gives you a number.  
15 You can plot that on a graph and get a curve. And then you  
16 would compare your unknown samples or your reference samples,  
17 because you have to do this with both, and then you would  
18 compare that darkness from the unknown or the reference to  
19 your standard curve which you developed.

20           It's slow. It's painful. You use more film. But  
21 there were certainly laboratories that did that. It doesn't  
22 fix this unfortunate method, but that's what we had at the  
23 time.

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1 Q. And in 2002, was the method available which you've  
2 described in order to get more of an accurate measurement and  
3 not a less-than measurement?

4 A. Absolutely. There were labs that would go through  
5 that process that I described to do that. An argument could  
6 be made about whether that's a terrific advantage or not.  
7 That's a different argument. But there were certainly labs  
8 that were doing that.

9 And using x-ray film for quantification, it's been  
10 used for many other fields besides forensics, and so it isn't  
11 a revolutionary technique by any stretch.

12 Q. Let me refer you back to the slot blot quantitation  
13 worksheet, which is, again, Tab 7. I'm going to ask you to do  
14 some math, so ----

15 A. Okay.

16 Q. -- prepare yourself.

17 A. I'll try.

18 Q. I'm going to zoom in to K470 again. Let's, for now,  
19 hypothesize that there is not a less-than symbol in front  
20 of .1 as the quant value. So that would be .1 nanograms. And  
21 let's take away the less-than symbol for now.

22 A. Certainly.

23 Q. Can you tell us with .1 nanograms that were

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1 quantified, what the actual amount of DNA is that would go  
2 into the polymerase chain reaction?

3 A. So as was described, I believe, earlier, that only  
4 approximately 10 percent, one-tenth of the recovered DNA was  
5 put into the slot blot. So if there's 22 microliters  
6 recovered from the extraction purification and then recovered,  
7 and two microliters of that are used in the slot blot, what  
8 remains is 20.

9 So you've tested one-tenth. If that is .1 nanogram,  
10 that would be a tenth of the whole. You would  
11 multiply .1 times 10 to come to one nanogram, which would be  
12 the target that the FBI would like to have, and that's listed,  
13 as was described by Mr. Giusti, in the column that says target  
14 DNA, how much do you want? And that would have reached the  
15 target that the FBI prefers.

16 Q. If -- because we don't have a specific measurement  
17 here, if for K470 the quant value was .01 nanograms, meaning a  
18 tenth of .1 nanograms, how many picograms would we be putting  
19 into the polymerase chain reaction?

20 A. So we can arrive at that number at least two ways. We  
21 can go back and do the same calculation we just did and say  
22 one-tenth of the recovered DNA is put into the slot blot and  
23 we're now at 0.1 nanograms, is what you would measure. And

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1 that's only a tenth of the material. So we would multiply .01  
2 times 10 and reach .1 nanograms or 100 picograms.

3 We could also arrive at that same number by just  
4 recalling what we just calculated for the .1, and now you  
5 asked me to do a tenth of that. And a tenth of one nanogram,  
6 which was our final a minute ago, would be .1 nanograms or  
7 100 picograms.

8 So either way, you're going to arrive at 100 picograms  
9 or 0.1 nanograms, depending on which unit you prefer.

10 Q. What information can we glean from the slot blot  
11 quantitation as far as how many picograms may have gone into  
12 the PCR reaction ----

13 A. Well, we ----

14 Q. ---- based on what data you see on the worksheet.

15 A. From the worksheet, that's as much information as we  
16 can get. If you'd like to examine the autoradiogram, we might  
17 be able to do better or do different. But from the worksheet,  
18 the FBI chose to simply put less than .1, less than their  
19 standard. So we have no additional information on this  
20 worksheet to the amount of DNA, and that's what Mr. Giusti  
21 correctly described.

22 Q. I'd like to show you again the actual slot blot, and  
23 again, that is Tab 6. Is this an appropriate zoom for you to

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1 be able to see the K470 band?

2 A. I can see it. It is faint for all concerned, but it's  
3 there.

4 Q. And what more information can you gather from looking  
5 at the actual slot blot here?

6 A. Well, we would have to perform an estimate. We would  
7 have to examine the band strength and use, perhaps, our  
8 imagination and compare the barely visible band in the third  
9 column, fourth row, to either of the lowest standards and  
10 imagine how much darker the standards are to that faint band  
11 we can see.

12 And it's not terribly fair for this audience because I  
13 doubt if there's another person besides Mr. Giusti who has  
14 worked with x-ray film, but you can still imagine that there's  
15 ten times more darkness in the lowest standard. Is it 15? Is  
16 it 12? There's no way to determine that. But you can round  
17 it out to the best of your estimate, and then that would be  
18 your guess as to the quantity of DNA that the slot blot  
19 measured on that day on this film.

20 Q. But the best we can do with the information that we  
21 have is that it is less than .1 nanograms that were  
22 quantified using the slot blot?

23 A. I think you can do better. It's clearly not just

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1 less; it's considerably less. How much is that considerable?  
2 Perhaps a matter of debate. But certainly ten times less. I  
3 don't think that's much of an argument from just looking at  
4 it.

5 We will leave aside the narrow range of linearity in  
6 x-ray film and just assume that this was developed equally  
7 across. It looks like that.

8 We'll also ignore that the lowest standards are not  
9 really uniform across the slot. If you look at that carefully  
10 at all, you'll see that there's speckles and it's not  
11 completely uniform through the entire length of the slot.  
12 That's more illustrated on the right-hand set of standards,  
13 normal for slot blot, one of the difficulties with it.

14 Also, notice that some of the slots are leaking  
15 material. So that's particularly evident on the right-hand  
16 set of standards, the one that goes from the smallest band to  
17 the largest. You can see there's some arms coming off.  
18 That's leakage from the slot onto the membrane. Also a  
19 standard issue with this particular approach. It's one of the  
20 reasons nobody liked this, and the minute a better approach  
21 came, this was abandoned in haste.

22 But it does work. You can get some information. It's  
23 tougher when you're below the standard. It's less,

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1 considerably less. How much? You pick.

2 Q. And so if it were one-tenth less than the standard,  
3 again, how many picograms does that put into the PCR?

4 A. We would go back to your second calculation that you  
5 just asked to do, and that would be a total of 100 picograms  
6 or .1 nanograms, assuming the band strength is a tenth of the  
7 lowest standard shown here.

8 Q. I'd like to discuss with you briefly low-template DNA,  
9 and specifically the amount of DNA that goes into the  
10 polymerase chain reaction.

11 Why is it important to quantify and get a number for  
12 the amount of DNA when you are going to go through the  
13 amplification process?

14 A. It's been mentioned a couple times, but I'll sort of  
15 do it again. There are two reasons. One is you have to,  
16 according to the accreditation standards. And if you wish  
17 your laboratory to have to continue its accreditation, you  
18 need to do that.

19 You also would like to know that number in order to  
20 put the proper amount of DNA into the amplification kit so it  
21 operates at its best. And so in that way, the hope is that  
22 your electropherogram, your profile you're going to try and  
23 deduce, is also at its best.

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1           So those are two perfectly good reasons why in  
2 forensic DNA you would want to develop a quantification number  
3 that is as accurate as you can get.

4           Q. When we are talking about low-copy number, meaning the  
5 measurement of DNA, quite literally, what are we defining?

6           A. Literally, you're defining how many copies of the  
7 target DNA, how many copies of those genetic elements you are  
8 putting into the tube for the amplification to work.

9           As has been mentioned, we are using a genetic element  
10 called a short tandem repeat, and those are on human  
11 chromosomes. And the nucleus in the cell contains those  
12 chromosomes, and when you isolate the DNA, you get those  
13 chromosomes and you get a certain number of them. And the  
14 number of copies of those chromosomes depends on how much DNA  
15 you put in the amplification reaction.

16           So that's the template. That's how many copies you  
17 have to start with in the amplification.

18           Q. And so when we speak of or read about template DNA, we  
19 are referring to the amount of DNA prior to amplification; is  
20 that correct?

21           A. Correct. We do not -- we don't measure how much DNA  
22 is made in the amplification. We do analyze that DNA, but we  
23 don't go and measure it. We could if we wanted to. There's

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1 no real reason to do that. To some extent the strength of the  
2 electropherogram provides an estimate of how much was made in  
3 the amplification, but we don't actually measure it.

4 So the measurement comes before it goes in the  
5 amplification for the reasons discussed. We have to, and it's  
6 helpful to know how to put together the recipe for  
7 amplification. And the amount of DNA is directly correlated  
8 to how many copies of those genetic markers go into the tube,  
9 which is then amplified.

10 Q. How -- approximately how many copies are in  
11 100 picograms of DNA?

12 A. That would be about 30 copies of each of the markers.  
13 This assumes that the DNA is homogeneous, that you have  
14 successfully recovered an equal amount of all the chromosomes.

15 We can make this calculation quite sophisticated if we  
16 have to take into account the fact that the chromosomes are of  
17 different size and so forth, but we're just going to make a  
18 simple number and say it's approximately 30 copies at  
19 100 picograms.

20 Q. Are you familiar with enhanced detection measures?

21 A. Yes. That's not a term of art. Nobody in a  
22 laboratory is going to use that term, but there are certainly  
23 methods for either improving the profile or trying to get more

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1 data from a weak profile.

2 Q. And why would you need to improve a profile? What  
3 characteristics of the profile would cause that -- the need  
4 for improvement?

5 A. The need? How about the want?

6 Q. Got it.

7 A. So you have -- this is -- the sample under discussion  
8 is not a bad example. You have clearly data that is at low  
9 level. You have data that is on the electropherogram that you  
10 haven't fully identified. And the concept is to get more data  
11 because more data is better.

12 And to some extent Mr. Giusti described that quite  
13 nicely when asked why did you use -- why was Profiler Plus  
14 used since you had a minimal amount of DNA? And the answer is  
15 because Profiler Plus has nine markers versus COfiler which is  
16 six, and nine is better than six. You get more data. You can  
17 do more with it. It's more informative.

18 So in profiles that have data that are at or below the  
19 limit of the software detection, you would like more -- you'd  
20 like those data. What do they show? Are they exculpatory,  
21 inculpatory? Do they show more mixtures? You want that data.  
22 And so that's when you would use or would like to use methods  
23 that would improve that profile so that those data become

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1 visible.

2 Q. And the profile needs this sort of assistance because  
3 there is a small amount of DNA to begin with; is that correct?

4 A. Yes. So it's a little more complicated than that, but  
5 essentially, there isn't enough DNA for the kit to work at its  
6 best, and the process of analyzing the amplification is very  
7 limited. So the manufacturer has made that part of its  
8 process, and so one of the methods is to go back to the  
9 amplification. But there are others you can do on the machine  
10 itself, that's CE, to improve that profile or to -- improve is  
11 a tough one -- to make more data visible.

12 Q. And what are some of the methods laboratories use to  
13 improve the data, to make more data visible?

14 A. So one method that was talked about was increase the  
15 number of cycles. I cannot recommend that as an option.  
16 There is a lot of work demonstrating that that's a poor  
17 choice. And it was thought for a while that that would be  
18 good; it's bad. So we're not going to do more cycles.

19 You can try and assay, take more of the amplification  
20 reaction, and to clean it up, to improve it, and then put it  
21 on the CE machine. That's very effective.

22 Q. Is that post-PCR purification? Is that ----

23 A. That is post-PCR processing, and you can purify those

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1 amplified fragments and put those on the capillary  
2 electrophoresis machine, and you will get an enhanced profile.  
3 You're just taking more of the data that you made. It's in  
4 your tube. You paid for it. And now you get to use it all.

5           The analogy I use there is of an apple, and you're  
6 only taking one tiny slice of that apple. And the rest of the  
7 apple you've bought, but you're not eating it. And using  
8 post-PCR, you get to actually eat the rest of that apple which  
9 you spent all this time and effort making and buying. So  
10 that's a good method.

11           Another method is -- and again, Mr. Giusti referred to  
12 it in passing, is the length of time for the electrokinetic  
13 injection. Would like not to go into how that works, but  
14 there's a way that the fragments of amplified DNA go into the  
15 CE, and you can manipulate that a little bit, and that's a  
16 very standard approach.

17           Typically, at the time, the injection time was  
18 five seconds. Very standard laboratories would go back to the  
19 same amplification tube prepped and do 10-second injections,  
20 and that increases the peak heights of all the peaks in the  
21 electropherogram, and that can be helpful.

22           You can also slightly manipulate one of the samples  
23 called the size standards. They're an obligatory part of the

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1 process. I didn't mention it, but in one of the maps you  
2 showed earlier there in the bottom -- we don't have to go into  
3 it. But you can manipulate how much of those go into your  
4 final prep, and that will also enhance the peaks.

5 So those are all methods that laboratories have used  
6 to improve or get more data from the same amplification  
7 reaction they started with.

8 Q. And what about consensus sequencing? When you  
9 are ----

10 A. I'm going to interrupt you. We're not doing any  
11 sequencing here.

12 Q. Okay. When we're doing triplicate testing ----

13 A. Ah.

14 Q. ---- can you describe that for us?

15 A. So the idea of consensus, so all scientific  
16 measurement is consensus. There's no exceptions to that. The  
17 common expression, "measure twice, cut once" is the example  
18 that we all use every day, but in science, measurement is  
19 consensus. How close do you get to the real number? You do  
20 that by doing multiple measurements, defining your variance or  
21 your error, and that tells you how close you are to the real  
22 number.

23 And so in order to try and overcome the stochastic or

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1 random events that can happen when you have low amounts of  
2 DNA, which Mr. Giusti described quite nicely, you have one  
3 very good method, which is to run that sample -- and run can  
4 mean several things -- more than once.

5           Do you get the same result when you do it multiple  
6 times? That is the reliability. That's accurate measurement.  
7 That's consensus work. And that's all measurement in science.  
8 And so typically, if you do it twice, you can get an average.  
9 If you do it three times, you can get a standard deviation,  
10 which tells you more about your data.

11           So when low amounts of DNA are present and there's a  
12 concern about the random events that might give you a peak or  
13 not, the best solution is to amplify it multiple times and  
14 assay it on the CE multiple times and then see which results  
15 are reproducible and to report the reproducible results.

16           Q. Given the nature of the evidentiary sample K470 and  
17 the low amount of DNA that we are working with, Mr. Giusti  
18 testified that the DNA sample was consumed during this  
19 process, so triplicate testing would have been impossible.

20           Is there something that could have been done to allow  
21 for reproducible results with K470, given the amount of DNA  
22 that we are working with?

23           A. I'm actually going to dispute your comment about it

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1 wasn't possible. There was no obligatory reason to use all  
2 20 microliters in the one reaction. Now, the FBI would argue  
3 that they didn't have enough because they didn't know how much  
4 was there and they weren't going to risk it. The answer is  
5 they didn't really know how much they had, so it's certainly  
6 possible they could have duplicated it.

7           You can also, although the FBI doesn't like this, you  
8 can run your PCR reactions at reduced volumes, and so you need  
9 less DNA per amplification. This is a widely used method, not  
10 in the United States, but there's a whole world out there that  
11 does this successfully. And so those are two choices.  
12 Probably not ones they would have liked or done, but they are  
13 available.

14           And the other thing that could have been done, which  
15 is easily accomplished, is they have their amplification  
16 reaction, and that was put into a tube and prepped. There's a  
17 little change that goes into the CE. That you could do  
18 another, what was it, 60 times, if you wanted to, and put it  
19 back on the CE and see if that alone gave you the same profile  
20 that we see here. Is there any variation at that last step?

21           So at the very least, they could have either  
22 reprepped -- excuse the slang -- from the amplification, or  
23 they could have gone back into the same prep and just put it

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1 back on the CE a second time. And that happens very often  
2 because sometimes that instrument has a hiccup and you are  
3 forced to do it a second time. No harm, no foul.

4 And so, yes, there are some things they could have  
5 done even within their own decision to restrict how they do  
6 their work, and so that was possible for them, without  
7 question.

8 Q. In your review of the materials provided, which  
9 include the case files for both the reference and evidentiary  
10 sample, in your review of those materials, did you find that  
11 any of these methods to counteract the concerns with small  
12 amounts of DNA, do you find that the FBI employed any of those  
13 methods?

14 A. Well, the answer is there isn't, they didn't, and  
15 Mr. Giusti confirmed that more than once. So there's a reason  
16 there's nothing in that case file, is that they didn't do  
17 that.

18 The only thing I would change in that is you don't do  
19 it necessarily because you're worried. You do it because you  
20 see the result and there's data you want more of. That's why  
21 you're going to do that. You're not going to do it beforehand  
22 because you don't know what you're going to get.

23 But once you have it, or you think you will, that's

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1 the time when you would consider implementing one of the  
2 methods we talked about.

3 Q. And in your review of both case files, particularly  
4 K470, the evidentiary sample, did you find that the FBI tested  
5 a low-template DNA sample?

6 A. I think there's no argument that they did. They  
7 didn't know what that was because in their world, if you will,  
8 they just have less than .1. And for them, it could be  
9 anything less than .1. It could have been .9 of a nanogram  
10 for all they know from their nomenclature.

11 We have good reason to think it's considerably less  
12 than that by examining the autoradiogram ourselves. But in  
13 their approach, less than just means less, and they go  
14 forward.

15 Q. And so understanding what amount we were working with,  
16 the FBI took no steps to either account for, in your review of  
17 the documents, account for the possible stochastic -- the  
18 stochastic occurrences with a small low-template DNA sample?

19 A. Actually, I don't think that's accurate. So they  
20 didn't do anything at the bench or experimentally, that is  
21 correct. But Mr. Giusti was clear in that he, by examining  
22 the electropherogram, tried to take those concepts in mind.

23 So I think in the analysis part, the examiner is doing

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1 his best. But from the experimental part, the answer is no.  
2 They didn't. They haven't. For whatever reason, they chose  
3 not to, and there's plenty they could have done and chose not  
4 to.

5 Q. You mentioned in your testimony that these methods are  
6 often employed so that you get more data, so that you can see  
7 more data. I'd like to show you AE 460C Attachment B, Tab 10,  
8 which is the electropherogram.

9 You have reviewed this electropherogram in preparation  
10 for your testimony; is that right?

11 A. I've seen this before and it's been shown on the  
12 display a number of times.

13 Q. I'm going to zero in here on the last locus, where we  
14 see 9 and 12. When you noted that these methods are used so  
15 that we can see more data, is this a location where more data  
16 would have been helpful?

17 A. Well, there are actually two locations in this dye set  
18 where there's clear -- well, that's not fair -- where there's  
19 a bump in the electropherogram that is a good indication that  
20 there's additional alleles that have not been noted by the  
21 software settings that the FBI has used.

22 So in the very last marker, the one that has 9 and 12  
23 on the outsides, you can see there are two bumps. They are

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1 the thickness of the line, and they are clearly in a -- what's  
2 the word I'm going to use here? -- they're in a pattern. So  
3 there's a spacing between 9 and the bump to the right, and  
4 there's a spacing from the bump to the next bump, which is one  
5 spacing below 12.

6 So Mr. Giusti was very good at describing stutter.  
7 And those are not stutter because the peak heights here are so  
8 small that stutter would be lost in the noise. So those are  
9 very likely two alleles that have not been noted and, given  
10 the other data, form part of the profile of the minor  
11 contributor.

12 If you scan over to the left, to the marker with the  
13 substantial 11 peak, and the minor 12 to the right of it, you  
14 will see that the electropherogram has another bump well  
15 within the organized spacing between 11 and 12. And I would  
16 hypothesize -- I'm going to guess that that would be an allele  
17 13 ----

18 ATC [MAJ ROSS]: Objection, Your Honor. He's going to  
19 guess? He's not allowed to guess.

20 WIT: We've discussed guessing yesterday ----

21 MJ [COL ACOSTA]: Hold on, sir. Sir. Sir.

22 WIT: Excuse me, Your Honor.

23 MJ [COL ACOSTA]: Defense.

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1 DC [MS. CARMON]: Yes, Your Honor. I think within the  
2 ambit of his expertise, he is allowed to hypothesize, as  
3 Mr. Giusti did, as to what these bumps are that are not making  
4 it through and being called on the allele call sheet.

5 MJ [COL ACOSTA]: So this is his interpretation of what  
6 he's saying?

7 DC [MS. CARMON]: Yes, sir.

8 MJ [COL ACOSTA]: Okay. I'll allow him to discuss what  
9 his interpretation is.

10 A. So you can see the two bumps to the right of allele  
11 call 11. One of those is above the peak detection threshold  
12 of 50 that the FBI used. The other is going to be below that  
13 peak detection threshold, and will be an allele call 13.

14 There are other examples of that in this  
15 electropherogram. And from that we could hypothesize, we  
16 could deduce, that a minor profile could be derived from this  
17 data. Those kinds of data could have been enhanced using one  
18 or other of the techniques described earlier.

19 Q. I would like to, once again, zero in on the locus with  
20 the 9 and 12 that is below the 200 RFU for analysis or  
21 inclusion purposes per the FBI.

22 Do you agree with Mr. Giusti that at this locus, there  
23 is certainly the opportunity for allelic dropout?

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1           A. By the FBI's validation or the FBI's work, for them,  
2 they would allow for allele dropout because of the peak  
3 heights at 9 and 12.

4           Q. And do you see the opportunity or the danger of  
5 allelic dropout in other places on the electropherogram?

6           A. Well, there's always a danger because you don't really  
7 know how reproducible these data are. It's done once. It is  
8 true that the -- the taller the peak, the stronger the  
9 profile, that risk decreases. No question.

10           And so as this profile gets weaker from left to  
11 right -- and by weaker, I mean the peak heights are decreasing  
12 as you examine the peaks from left, where they're tallest, to  
13 the very right-hand side, where they are the smallest peaks,  
14 the lowest values. I should note that the scale we are  
15 referring to in terms of peak height is the scale all the way  
16 to the right, 200, 400, 600, or 500,000, 1,500 or 2,000  
17 depending on the dye system you look at. That's the scale for  
18 the peak height value. So it's not just pulled out of the  
19 software. There is actually a scale that is used.

20           So Mr. Giusti was perfectly accurate in describing the  
21 ski slope that you can see here. And that's a lab slang term,  
22 absolutely. Imagine you take a ruler and place it across the  
23 tips of those peaks, and that ruler is going to be slanted.

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1 And if you go skiing, that's the kind of slope you would like.

2 And so that illustrates one of two possibilities for  
3 this sample. And Mr. Giusti described one of them quite well,  
4 which is maybe the DNA is damaged, and the type of damage what  
5 he was referring to is a size degradation.

6 The average size of the DNA piece that you recover is  
7 small. And so if the average size is small, the larger  
8 fragments are harder to amplify. They're going to amplify  
9 less well. And that's why the markers that are of longer  
10 length -- and the scale for the length is the top scale that  
11 is just not visible in my screen -- that's why those are --  
12 peaks are lower.

13 Now, another reason for a ski slope electropherogram  
14 is PCR inhibition. So the enzyme that makes the DNA fragments  
15 in the amplification reaction has to work at some rate. And  
16 if you have inhibitors or bad things -- we'll just use that  
17 expression -- in the amplification reaction, the enzyme will  
18 go slower. It can't work as fast. And again, the larger  
19 fragments take longer for the enzyme to make. The enzyme is  
20 slowed down, you don't make as many of them, and you get this  
21 same pattern.

22 So from the pattern, we don't know which is the  
23 problem. It could be both, too, or a little bit of both. But

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1 one of those two is definitely involved in this sample.

2 Q. I'd like to direct your attention to a couple of  
3 factors that could weigh on the low-template DNA and the  
4 reliability of the profile that we see here. I'd like first  
5 your observation as to whether this is a partial profile.

6 A. It is by several definitions, so as has been  
7 described, a full profile at this time was 13. The maximum  
8 number of genetic markers that can be obtained from running  
9 the Profiler Plus reaction is nine. If COfiler is not run,  
10 you will by definition have a partial profile, one definition.

11 The FBI chose to analyze but eight of the nine.  
12 Again, a partial. We don't say partial partial, although that  
13 would be a silly thing, but it's partial in both sense, that  
14 13 wasn't attempted and only eight are noted. I won't say  
15 recorded. But eight were assumed to be -- eight were the  
16 deduced profile. Pardon me.

17 Q. And we will go into a little bit further detail on the  
18 partial profile and we will also -- for the next  
19 characteristic, which I'd like you just to confirm that you do  
20 observe, that this is, in fact, a mixture.

21 A. Oh, it's undeniably a mixture. So how is that  
22 determined? If you could focus on the middle dye, the green  
23 dye, that might be an easier way to explain it.

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1 Q. Would it be helpful if we went to the slide deck that  
2 you've reviewed and to zoom in on one of the ----

3 A. Sure.

4 Q. ---- locus?

5 DC [MS. CARMON]: Your Honor, if we could switch the input  
6 to the HDMI cord?

7 MJ [COL ACOSTA]: You may.

8 DC [MS. CARMON]: Thank you.

9 Q. Dr. Reich, are you seeing it on your screen?

10 A. I can see -- I can see a blank slide.

11 Q. Great. Let me take you back one sentence and let's  
12 start with the partial profile and what that might mean for  
13 the reliability of the testing here.

14 Now, the profile that you observed in the  
15 electropherogram consisted of eight loci out of 13. Could you  
16 give us the analogy for identity and why that is important  
17 using the telephone? I know that you've given this analogy  
18 before.

19 A. I have. I've often sought an analogy for a DNA  
20 profile that would be effective. And I've used the analogy of  
21 a phone number, and I think it incorporates many but not all  
22 of the issues in a DNA profile.

23 So the concept is that if you have a full phone

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1 number, country code, area code, city code, block code,  
2 extension, however many numbers your country or your phone  
3 number can obtain, if you dial that number accurately, one  
4 phone on the planet will ring.

5           Now, the nice thing about the analogy is that if you  
6 misdial one of those numbers, just one of them out of the  
7 whole string of either 10 or 13, you get someone else's phone.  
8 And if you've ever been at the end of the phone that was just  
9 one number off a popular phone, your phone is going to ring  
10 and they're not going to get who they're trying to reach. So  
11 that level of precision, profile to phone number, is a good  
12 analogy.

13           Now, what happens if you have a partial profile? So  
14 now we're going to eliminate some of the numbers in that phone  
15 number. And you can take your pick which one you're going to  
16 take out. If we just have the country code, let's say, and  
17 the area code, our phone is going to work a little different  
18 from a real phone, but only those numbers that have the  
19 country code and the area code will ring. So there will be a  
20 lot of phones ringing, and you don't really know whose phone,  
21 and you certainly haven't gotten to one person with that  
22 partial phone number.

23           And so the other thing that's nice about the phone

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1 number analogy is you can make each section like an allele.  
2 So let's call the country code D3, one of the alleles that  
3 we're working with, and let's call the digit at the country  
4 code the allele.

5           So now we have a pretty good analogy between the  
6 profile, the locus, and the allele that everyone can gather.  
7 And the choice in the alleles in the phone number are 0, 1, 2,  
8 3, et cetera, to 9, in the same way that the allele for the  
9 genetic marker is the number of repeats, right?

10           So that's a nice part of the analogy, and most people  
11 have a phone, most people have experience with misdialing.  
12 It's a good analogy. It's not perfect, but it gets us a long  
13 way to explain what a profile is, why you need a whole  
14 profile, and what happens if you have a missed number in that  
15 profile.

16           Q. And how is the partial profile related to the amount  
17 of DNA that we have in K470?

18           A. All right. Well, that is now not part of the phone  
19 number analogy. That's part of the amplification reaction.  
20 That's part of how the process works in the tube using the  
21 commercial kit.

22           The commercial kit is a recipe. They -- the  
23 manufacturer gives you everything you need except the DNA that

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1 you're going to put in in the tube which you're going to have  
2 in the laboratory anyway. And that's a pretty strict recipe.  
3 Just like when you bake, you don't have a lot of leeway with  
4 how much flour or egg or oil you put into that recipe. Your  
5 cake might fall. It might not be a good recipe when you're  
6 done. So you have to follow the manufacturer's recipe at  
7 least at some level because otherwise, it's not going to work  
8 for you.

9           So the amount of DNA you put in does affect the  
10 profile you get out. Mr. Giusti was correct in describing  
11 that it's a rough link. It's not a perfect link, because  
12 there's the quality of the DNA that's been mentioned.

13           There's also the DNA itself. As it turns out, DNA is  
14 really not just DNA. So people's DNA does vary in how well it  
15 amplifies. Turns out we don't know why that is, but it's  
16 clearly true. And so to some extent, you can get the quant,  
17 and then you have to see what you get in the profile.

18           Q. Let me move on to the mixture, again, another  
19 characteristic of this K470 sample. And if I could have you  
20 look at the screen here, I have zoomed in on locus D5.

21           Can you tell us how many contributors are possible at  
22 this locus?

23           A. Right. So this is a much sharper picture than the

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1 overall view we looked at a minute ago. So let me go -- let  
2 me try and set the stage a little bit.

3 So there are a whole set of numbers on here, and,  
4 unfortunately, this version of the software presented the  
5 results like this. There wasn't any choice. It's not  
6 anybody's fault except Applied Biosystems which isn't so good  
7 at software.

8 But there are three numbers associated with each of  
9 the software-identified peaks, and there's a number in a black  
10 box, there's a number in a greenish box, and then there's a  
11 number in a red box. And each identified peak has those three  
12 boxes, a black, a green, and a red.

13 And it's a bit of a jumble the way the software does  
14 it, so we're going to have to try and figure out which peak  
15 has which set of three boxes, okay? So the 11 peak, the very  
16 first one on the left-hand side, that's pretty clear, because  
17 the software has put that to one side. So that's an allele  
18 call 11, as Mr. Giusti would mention. That means 11 repeats  
19 at the D5 locus.

20 You may recall that I said that there was a vertical  
21 scale. That's the red box, so it's 95 units tall. And there  
22 is a scale at the very top electropherogram, which we haven't  
23 focused on, which tells us the length of the amplified

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1 fragment. Here it's 148-1/2 base pairs in length. So that's  
2 11. Let's call that allele 1.

3 The next one over is allele 12, and under the black  
4 box is the green box at 152. Mr. Giusti helped me a lot by  
5 going -- should be four base pairs different. 148 plus four  
6 is 152, so we're pretty confident that that box refers to 12.  
7 And we know that the peak height, the red box, is 137.

8 Let's move over again to the 13, black box 13. We  
9 know that that peak is taller. We can just look at it and  
10 see, and, sure enough, the red box says 600-odd units tall,  
11 and that is approximately, a little more, a little less, four  
12 base pairs bigger than 152. We're at -- we're almost at 153,  
13 152.88. I'm going to round that up to 153. I add four to  
14 153, I come to 157. So I'm happy with that.

15 And so I now have three alleles, and the only way I  
16 can have three alleles is to have a minimum of two people. We  
17 discussed earlier about how people are made and how you have  
18 two complete copies of locus D5. And so if you have three  
19 alleles, you can account for two of them from one person; they  
20 have two copies of D5. Where did that extra allele come from?  
21 It has to come from an additional chromosome, somebody else.

22 We can continue our analysis from left to right to  
23 allele call 14, black box. And here we have to kind of follow

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1 our way down. It's not so obvious. The software has put  
2 things a little out of order, but we know we were at 157.  
3 That was allele call 13. That's one more repeat. Should be  
4 about 161. And sure enough, there's a green box with 161 ----

5 Q. Dr. Reich, I'm going to actually give you an even  
6 closer look. How about this?

7 A. Okay. So now we've -- we've taken away all those  
8 numbers, and we just have the number of peaks we can see.  
9 Thank you.

10 So we have allele call 11, 12, 13, a peak at 14, and  
11 then another peak at 15. And the question is -- that would  
12 call us -- let's count them. One, two, three, four, five  
13 peaks. If we believe all three of them are genuine alleles,  
14 we have to have an additional contributors -- contributor to  
15 this.

16 So the question is do we believe that allele call 14  
17 is a real peak, or is this the stutter artifact that we know  
18 is made in this system? So that's a decision that you have to  
19 make.

20 And the peak height at 15 is 640. Mr. Giusti  
21 mentioned that he takes a 10 percent value to look at it.  
22 That's very reasonable. So 10 percent, a tenth of 640 is 64.  
23 Peak 14 is only 50 or so RFU, so it's at or below the

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1 10 percent. And we would arguably, correctly probably, label  
2 14 a stutter and not add an additional contributor. That's  
3 most likely correct.

4 Q. You mentioned calling, and I think what you were  
5 talking about is that there are human choices made when  
6 analyzing an electropherogram. Can you talk about where these  
7 choices are made and specifically what choices an analyst has  
8 to make with the data that he or she is given.

9 A. Absolutely. Mr. Giusti described it -- he didn't say  
10 those terms, but he described that he was involved in making  
11 those decisions and making the deduced profile. That's a  
12 human intervention, and so these kinds of choices and  
13 decisions about is it stutter, is it real, is it elevated  
14 stutter, is it another contributor, are made all the time.  
15 That's how you deduce your profile from the data.

16 Sometimes it's straightforward. You have a single  
17 contributor, one person's profile, and you zip through it.  
18 Other times, the mixture is more complicated. There's more  
19 stuff to look at, and it takes far longer.

20 Q. Now, the choices that have to be made, are those  
21 choices made more difficult when you are looking at a sample  
22 that started with a very small amount of DNA?

23 A. I don't actually think the choices are more difficult.

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1 The difficulty is, are you as accurate? So you're still going  
2 to make the same choices. You don't have as -- you don't have  
3 as much information as might be available, and it's just  
4 harder to know whether you're right or wrong on some of them.

5 It's not harder to do because you still have the data,  
6 but is it really correct? It's -- it's harder to know if  
7 you've done the right -- if you've made the right decision, I  
8 think is a better explanation.

9 Q. And why is it harder to know that you've made the  
10 right decision?

11 A. You have less signal, less data, less surety of the  
12 peaks that you're observing.

13 Q. And what about the fact that there was no replicate  
14 testing here and this cannot be reproduced?

15 A. Yeah. I don't really know how to answer that.  
16 I've been a scientist for 40 years, and in every other science  
17 I've ever done, you never report anything unless it's  
18 reproducible. Forensics doesn't do that.

19 Q. And in your laboratory, when you were faced with  
20 low-template DNA, how does your laboratory handle the  
21 analysis?

22 A. We make a consensus profile from multiple  
23 amplifications for what we call touch DNA or DNA which does

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1 not have body fluids in the sample.

2 Q. And let me show you one more slide here. As someone  
3 with that amount of time in your field, I am assuming and I  
4 know that you are familiar with Dr. Budowle and his  
5 publications on low-copy number testing; is that right?

6 A. Dr. Budowle is a well-known person in the field.

7 Q. If you will, take a look at the screen. This is from  
8 a publication in 2010, and he describes some problems with  
9 low-copy number typing.

10 Can you describe for us the issue in discerning  
11 whether a peak on the electropherogram is truly from a  
12 homozygous individual, meaning 11, 11 or 17, 17, or if there  
13 is -- has there -- excuse me, or a dropout has occurred and  
14 it's actually a pair of alleles from a heterozygous person?

15 A. Right. This is the problem of loss of data on the  
16 electropherogram, very simply, and that risk or that chance of  
17 that happening increases as the amount of DNA decreases.

18 You can say it in the reverse way in that the chance  
19 of dropout decreases as you add more DNA. And laboratories  
20 attempt to account for that by developing what they call a  
21 stochastic threshold, that is a peak height at which the  
22 laboratory feels more comfortable that maybe they haven't lost  
23 that allele. That's what they do to try and overcome this

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1 problem. It's a band-aid on a problem, and it is an issue.

2 And Dr. Budowle mentions it.

3 I note that this doesn't really have a solution in  
4 this paragraph, but we do know what the solutions are. But  
5 they have to be implemented to solve it.

6 Q. And what are those solutions that you mention?

7 A. You have to go back and improve the quality of the  
8 profile that you have using one or other or all of the  
9 techniques that were mentioned earlier about improving or  
10 recovering, getting more data from the amplification you have.

11 Q. And let me show you, Dr. Reich, one final slide here.  
12 I've pointed you to allelic imbalance and, again, allelic  
13 dropout. In your opinion, are these well-known stochastic  
14 effects that occur with low-copy DNA -- template DNA testing?

15 A. Right. This is usually called actually peak imbalance  
16 rather than -- it is allele imbalance, but it's really known  
17 as peak imbalance. And it's another event that happens when  
18 the amount of DNA that goes into the amplification reaction is  
19 less than optimal or the DNA is damaged or there's PCR  
20 inhibition. So this particular -- I won't say artifact. This  
21 particular observation can occur based on a number of  
22 different factors that might be in your sample.

23 And so as Dr. -- as Mr. Giusti really nicely

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1 described, if you have enough DNA and you have two copies,  
2 recall of each of the markers we're testing, you expect that  
3 both of those peaks would be the same, right? If you have  
4 1,000 RFU units for one of the peaks, you would like the other  
5 one to be 992. Very close to 1,000.

6 Turns out that doesn't -- that can happen, but we know  
7 there's variation. And Mr. Giusti was very good at saying we  
8 would like to have 70 percent between the two, which means  
9 you'd like them close, okay?

10 It turns out that even in the best samples from the  
11 purist DNA, from the freshest kit, you have between --  
12 depending on the locus, up to 50 percent peak imbalance just  
13 out of the tube. It's more complicated what's going on in  
14 that multiplex reaction than we can completely describe. And  
15 so that issue becomes larger as you have less and less DNA.  
16 And there is some peak imbalance in the electropherogram  
17 profile at issue in this case. It isn't a destructive amount,  
18 but it's clearly present.

19 So this is another effect that gets larger as you have  
20 less DNA, and if you want to call it based on the random  
21 event -- it's really based on having less DNA template in the  
22 sample than you would like. This is another example. So  
23 there's allele dropout, there's peak imbalance, and then

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1 there's the combination of low-level data that you don't  
2 actually measure or observe in the electropherogram because of  
3 your settings.

4           So all of those impact the data that you obtain which  
5 impacts the profile you deduce which impacts the conclusions  
6 you can reach.

7           Q. And if I may, Dr. Reich, ask for your -- one final  
8 observation from you.

9           DC [MS. CARMON]: And, Your Honor, if I can switch to the  
10 ELMO now?

11           MJ [COL ACOSTA]: You may.

12           DC [MS. CARMON]: This is AE 460C Attachment B. This is  
13 Tab 10.

14           Q. Dr. Reich, you're looking again at the  
15 electropherogram, which is the visual expression of the data  
16 of the DNA profile from K470.

17           Given what we know about the sample, that it began  
18 with low-copy template DNA, perhaps less than 100 picograms,  
19 it is a mixture, and it is a partial profile. Given those  
20 characteristics of this sample, can you be confident that  
21 allelic dropout or other stochastic effects have not occurred  
22 that would impact the reliability?

23           A. The reliability? The FBI would claim that all of the

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1 peaks above 200 meet the criteria for reliability, and that  
2 would be sufficient for them. They would argue that they took  
3 that into account by only noting eight out of the nine loci  
4 and, according to Mr. Giusti, who re-reviewed the material, it  
5 was done properly the first time.

6 My comment is a little different, perhaps, is that  
7 there's at least two contributors to this sample, and the only  
8 contributor that's really been examined is the major  
9 contributor. There's no information about whether the minor  
10 contributor could be just as important or more to the case,  
11 and those data are ignored completely.

12 In terms of the overall DNA profile, the FBI's going  
13 to just mention they did it. There's more data here. Some of  
14 the data is better than others, and that could probably be  
15 taken to the bank. Others, not as much. And it's hard to  
16 know where to draw the line. The FBI has an arbitrary line.  
17 I can't really speak to that.

18 Q. And so given the characteristics of K470 here, do you  
19 agree that data has been lost in this profile?

20 A. Absolutely.

21 Q. And that there is the danger of allelic dropout  
22 present?

23 A. That risk is certainly always present, and it's

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1 present here.

2 Q. And is that risk amplified by the fact that this is  
3 low-template DNA?

4 A. I don't think -- I wouldn't use "amplify." That  
5 implies a different comment, but it's increased ----

6 Q. Okay.

7 A. ---- by the minimal amount of DNA in this sample.

8 Q. And there were no measures taken -- there were no --  
9 there was no methodology taken, measured steps taken by the  
10 FBI to counteract the potential problems brought on by a  
11 low-copy template sample; is that correct?

12 A. I think that's very correct. Mr. Giusti couldn't have  
13 been more clear. They ran a standard protocol. That's all  
14 they ever do, period.

15 Q. And so in this particular case with sample K470, the  
16 FBI performed just regular old PCR/STR testing on a low-copy  
17 template sample; is that right?

18 A. I would change that slightly. I would say that the  
19 FBI ran their standard protocol from which they do not deviate  
20 no matter what the sample is.

21 Q. And they did that here?

22 A. They did that here.

23 DC [MS. CARMON]: Court's brief indulgence, please.

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1 MJ [COL ACOSTA]: You may.

2 DC [MS. CARMON]: Thank you, Dr. Reich. Thank you, Judge.  
3 I have nothing further.

4 MJ [COL ACOSTA]: Okay. Before we allow -- I'm going to  
5 allow you a recess in case you need to consult with your --  
6 even though you appear like you're ready to get up,  
7 Government, I'm still going to take a recess for everybody's  
8 benefit, but you can use that time to consult with your  
9 consultant if you need it.

10 We're going to take a 20-minute recess, which will put  
11 us back at five to the hour.

12 Sir, I just remind -- everybody sit back down. I'm  
13 not quite there yet. Let me warn the witness before you get  
14 up.

15 The -- you remain on the stand -- like even during the  
16 recess, you remain as if you were on the stand. Don't discuss  
17 your testimony even with your -- with the defense counsel. Do  
18 you understand that?

19 WIT: Understood, Your Honor.

20 MJ [COL ACOSTA]: Okay. Thank you. You may step down.

21 WIT: Thank you.

22 **[The witness was warned and temporarily excused.]**

23 MJ [COL ACOSTA]: The commission is in recess.

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1 [The R.M.C. 803 session recessed at 1435, 08 December 2021.]

2 [The R.M.C. 803 session was called to order at

3 1456, 08 December 2021.]

4 MJ [COL ACOSTA]: The commission is called to order.

5 Government, all parties present as before?

6 TC [MR. MILLER]: Yes, Your Honor.

7 MJ [COL ACOSTA]: Defense?

8 LDC [MR. NATALE]: Yes, Your Honor.

9 MJ [COL ACOSTA]: Recall the witness. Sir, if you could  
10 please take your seat back on the bench -- pardon me, at the  
11 witness stand.

12 [The witness, KARL A. REICH, resumed the witness stand.]

13 MJ [COL ACOSTA]: You can remove your mask.

14 WIT: Thank you.

15 MJ [COL ACOSTA]: I remind you that you remain under oath.

16 Government, cross-examination.

17 **CROSS-EXAMINATION**

18 **Questions by the Assistant Trial Counsel [MAJ ROSS]:**

19 Q. Dr. Reich, we talked yesterday about your  
20 participation in the case of Anderson v. City of Chicago.

21 A. I did.

22 Q. Do you recall testifying in that case?

23 A. I do.

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1 Q. Do you recall testifying on December 5th of 2019, in  
2 the Northern District of Illinois in front of Judge Kendall in  
3 that case?

4 A. My recollection is that I testified twice in that  
5 case, once at a hearing, and I think I was the last witness at  
6 trial. And I don't know which date you're referring to.

7 Q. Well, let me ask you if you recall giving a statement  
8 on -- do you -- let me ask you. Do you recall being asked  
9 about testing, when -- when you test a sample if the ----

10 A. I'm sorry?

11 Q. I'll repeat my question.

12 Do you recall being asked about testing low amounts of  
13 DNA and responding, quote -- and listen to the quote: If the  
14 amount of DNA that -- that's put into the recipe for the PCR  
15 is too low, then the electropherogram that is generated from  
16 that amplification is too incomplete or too low to interpret  
17 it, then you can't interpret it. But you aren't going to get  
18 inaccurate data. You're not going to get allele calls that go  
19 from 11 to 13. That doesn't happen.

20 A. I do remember that.

21 Q. The amplification is not going to be incorrect.

22 Do you recall giving that statement?

23 A. I do.

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1 Q. Was that true then?

2 A. I think it was true then, and I think that's true now.  
3 There's no evidence or observations that allele calls become a  
4 different call.

5 Q. Okay. Do you recall being asked about the ski slope  
6 phenomenon in that case?

7 A. I don't, but it's not an unusual finding, as has been  
8 discussed today.

9 Q. Do you recall testifying on that date that ski slope  
10 does not impact the ability to use the data that was present?

11 A. That's correct. Just the actual slope is not the  
12 relevance. The relevance is the peak heights and the rest of  
13 the information that's in front of you.

14 Q. And with regard to partial profiles, do you recall  
15 testifying that there is no inherent issue with partial  
16 profiles?

17 A. That's correct. The interpretation of what that  
18 partial profile might mean is under discussion, but the fact  
19 that it's partial is not the issue.

20 Q. But you do it all the time, in fact, right?

21 A. Well, all laboratories have partial profiles because  
22 that's the nature of the analysis.

23 Q. Now, in this case, you have a \$250 an hour billing

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1 rate; is that correct?

2 A. I believe that's correct.

3 Q. And in 2015, you were authorized to spend 30 hours of  
4 work on the case?

5 A. I have -- I'm sure you have the numbers. I do not  
6 recollect the numbers of hours I was -- that was in the  
7 contract ----

8 Q. But that sounds ----

9 A. ---- no concept.

10 Q. ---- right to you, right?

11 A. Could be, certainly.

12 Q. And in 2021, you were authorized an additional 30  
13 hours in the case?

14 A. It's possible.

15 Q. And this week, you've been authorized to work 40 hours  
16 on the case?

17 A. I'm sure your numbers are perfect. I have frankly  
18 paid no attention to those at all.

19 Q. So 30 plus 30 plus ----

20 A. Is 60.

21 Q. ---- 40 is 100?

22 A. That is correct.

23 Q. And if your rate is 25 -- \$250 an hour, that's \$25,000

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1 in fees?

2 A. If all of those hours are submitted on an invoice,  
3 that would be the multiplication.

4 Q. Have you paid attention to that figure?

5 A. I do recall -- I've submitted invoices, I do know  
6 that. I certainly have not submitted an invoice for the work  
7 up until today, but I will.

8 ATC [MAJ ROSS]: Nothing further, Your Honor.

9 MJ [COL ACOSTA]: Defense Counsel, redirect?

10 DC [MS. CARMON]: No, Your Honor. No questions. Thank  
11 you.

12 **EXAMINATION BY THE MILITARY COMMISSION**

13 **Questions by the Military Judge [COL ACOSTA]:**

14 Q. Sir, I have a couple questions for you.

15 A. Yes, Your Honor.

16 Q. You said there was a couple things that the -- the FBI  
17 could have tested this sample in several different ways but  
18 they didn't. But was the method they used an accepted method  
19 at the time that they did the testing?

20 A. Absolutely.

21 Q. Was it a reliable method that they used?

22 A. Yes.

23 Q. The slot blot, there's a lot of discussion about the

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1 intensity of the dark mark on that slot blot. Isn't that  
2 test, and I'm basically basing it on what I've learned about  
3 it today, that's just telling you that there's DNA in the  
4 sample that you have; is that correct?

5 A. That's correct. Let's be precise. The slot blot is  
6 an attempt to measure or, if you wish, estimate how much DNA  
7 you recovered from the first several steps of the process.  
8 That's all it's doing. It's not telling you anything about  
9 the quality of the DNA. It's not telling you anything about  
10 the profile which you don't have yet. It's simply trying to  
11 figure out how much DNA did you get from the sample you were  
12 provided.

13 Q. Right. So that slot blot is just telling you in that  
14 slot there's DNA. There's some. Because if it was empty, you  
15 would say there was no DNA there?

16 A. If it's empty, you should see no band at all or a  
17 background band that you should have in there as well. Should  
18 be the same as a blank ----

19 Q. Right.

20 A. ---- as a negative control, no DNA.

21 Q. So is the slot blot run to determine whether or not  
22 you were able to recover some DNA from the sample that you  
23 have?

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1 A. Certainly. We can -- that's an acceptable approach.  
2 You don't know what you have until you look, and this is one  
3 way of looking what's in the tube.

4 Q. If it had shown up blank, they would have never  
5 test -- they would have never tried to run any test on that  
6 slot, correct, or on that -- that sample?

7 A. I hesitate to speak for the FBI. You have an examiner  
8 here who can answer that question. But in general -- that's  
9 not fair.

10 So you can run it -- you can -- you can amplify  
11 whatever you get, even if there's nothing there. You can put  
12 it in the tube, you can run the test, you can see what you  
13 get.

14 Q. Okay.

15 A. If there's no DNA in your recovery and you try and put  
16 it into the amplification, if you've done it right, knock  
17 wood, you should get no profile. Correct.

18 But because the quantification is not exact, and  
19 certainly the slot blot is not the best option to try and  
20 figure that out -- it's all that was available at the time --  
21 you may not trust that result sufficiently to say I won't  
22 attempt it. Because you want those data at the end, and so  
23 you might run it anyway.

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1 Q. Understood.

2 MJ [COL ACOSTA]: Any questions based upon mine, Defense?

3 DC [MS. CARMON]: No, Your Honor.

4 MJ [COL ACOSTA]: Government?

5 ATC [MAJ ROSS]: No, sir.

6 MJ [COL ACOSTA]: Permanent or temporary, Defense?

7 DC [MS. CARMON]: Permanent.

8 MJ [COL ACOSTA]: Sir, you're permanently excused from  
9 this hearing. While the hearing is in session, don't discuss  
10 your testimony or your knowledge of this case with anyone  
11 other than counsel for either side. You can step down and  
12 return to counsel table.

13 WIT: Thank you, Your Honor.

14 **[The witness was warned and permanently excused.]**

15 MJ [COL ACOSTA]: Defense?

16 DC [MS. CARMON]: Yes, Your Honor. Would the commission  
17 permit the evening to digest the testimony that we've heard  
18 today and consult with our experts and provide a summation at  
19 0900 in the morning?

20 MJ [COL ACOSTA]: I prefer to move into argument now. Are  
21 you finished presenting evidence is what you're telling me?

22 DC [MS. CARMON]: Yes, sir.

23 MJ [COL ACOSTA]: Let's see if the government has any

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1 rebuttal evidence. Government, do you have anything you would  
2 like to present in rebuttal?

3 ATC [MAJ ROSS]: No, sir.

4 MJ [COL ACOSTA]: Are you prepared to argue?

5 ATC [MAJ ROSS]: Yes, sir.

6 MJ [COL ACOSTA]: Defense, are you saying that you're --  
7 that you're unable to argue now?

8 DC [MS. CARMON]: Not that I'm unable, but I certainly  
9 would be able to deliver a more coherent and cogent argument  
10 with just a bit of time to consult with Dr. Reich and digest  
11 the day full of testimony. But if Your Honor is ready to  
12 move, we can certainly do that.

13 MJ [COL ACOSTA]: I think I'm ready to hear your argument  
14 today.

15 Government, you may present argument.

16 ATC [MAJ ROSS]: Your Honor, although we have the burden  
17 of proof as a proponent of this evidence, it's not a high  
18 burden. Relevant and reliable, under Daubert.

19 And as Your Honor is aware, your function is to act as  
20 the gatekeeper, not the armed guard. If you have competing  
21 opinions in any case, then the issue to -- the people that  
22 resolve that is going to be the jury, not the judge.

23 As a gatekeeper, you prevent junk science from coming

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1 in. This isn't junk science. Dr. Reich just said they were  
2 using -- the FBI was using accepted and reliable methods. And  
3 when he said that, it just reinforced why are we here.

4 There is a universal agreement in the legal and  
5 scientific community that this methodology is reliable, and  
6 the FBI did not deviate from any accepted and validated  
7 methodology.

8 Now, the defense argument is based on semantics, not  
9 science. In their filings they've said this is a low-copy  
10 testing, a low-copy test. And they cite the McCluskey case  
11 for the proposition that if you do low-copy DNA testing, then  
12 it's unreliable.

13 We would agree that McCluskey is on point. And the  
14 key takeaway from McCluskey is that it's not for the court to  
15 decide what the definition of low-copy testing is because, as  
16 you heard during the course of this proceeding, it's used in  
17 two ways. You have low-template DNA, which is a low amount of  
18 DNA, and then you have low-copy number testing, which is a  
19 deviation in the methods that are used. The FBI didn't  
20 deviate its methods from any SOP, any validated process, that  
21 had been already found reliable.

22 In McCluskey, again, the key to that case was not the  
23 amount of DNA that was used, it was that the New Mexico

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1 Department of Public Safety tested an amount that that  
2 laboratory had not validated as reliable. So the case really  
3 doesn't have anything to do about low-copy number testing.  
4 What it has to do with is a lab testing -- or conducting tests  
5 that it has not validated as reliable. It's as simple as  
6 that.

7 The SWGDAM guidelines are quite clear. You can test  
8 any amount of DNA. You may get a partial profile, but you can  
9 test it, and the results are reliable.

10 In their filings, they've -- they've argued that the  
11 amount of DNA in this case -- they've based their calculation  
12 on the results of the QuantiBlot. That's a separate figure.  
13 That's 10 percent of the sample. That's not the amount that  
14 was used for amplification. So they're simply wrong on the  
15 facts and they're wrong on the law.

16 This is a situation where any issue -- any issues with  
17 the FBI's testing, the results go to the weight of the  
18 evidence and that's for the jury to decide. This is reliable,  
19 it's relevant to the case, and it satisfies the Daubert  
20 standard.

21 MJ [COL ACOSTA]: Defense?

22 DC [MS. CARMON]: Your Honor, the fundamental requirements  
23 for forensic evidence and evidence of a scientific nature is

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1 that such evidence has to be relevant and reliable. And I  
2 would submit to Your Honor that in this capital prosecution,  
3 the state of heightened reliability is at play here.

4 And understanding you are not an armed guard, but you  
5 are a gatekeeper, the gatekeeper has to mean something. There  
6 certainly would not be Daubert or Kumho Tire or even Military  
7 Commission Rule of Evidence 702 if there were not some pieces  
8 of evidence that should not be allowed in. It has to mean  
9 something. And I do think the McCluskey case gives Your Honor  
10 a road map for excluding this evidence.

11 In McCluskey there was a partial profile; 11 of 15  
12 loci were identified. In this case, in K470, there were eight  
13 of 13 loci identified. In McCluskey the determination that  
14 low-copy number testing, meaning the amount of DNA that was  
15 tested, had occurred is because the New Mexico laboratory did  
16 have, in fact, a definition of their own, which was less than  
17 250 picograms, and in McCluskey 215 picograms were used in the  
18 testing.

19 In our case we, unfortunately, do not have a firm and  
20 reliable amount. And that is because the QuantiBlot that was  
21 used in order to estimate the amount of DNA quantified in  
22 the -- in the slot blot, we don't have a firm amount. It is  
23 an estimate, but that estimate is less than .1 nanograms.

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1           We are not wrong on our calculation. I had Dr. Reich  
2 perform that calculation with the amount of microliters that  
3 were added to it to come to that final number that would have  
4 gone into the PCR amplification, which is the number at issue.  
5 It is the amount of template DNA that goes into the PCR  
6 reaction that is defined as low-copy template or low-copy  
7 number DNA.

8           And what Dr. Reich observed from the QuantiBlot assay  
9 is that it was probably more like one-tenth of less  
10 than .1 nanogram of DNA. That gets us, after the microliters  
11 are added, to 100 picograms of DNA going into the PCR  
12 amplification. And I think that you heard Mr. Giusti agree  
13 that the consensus amongst those who are noted in the field  
14 and researchers who are noted in the field, that the  
15 scientific consensus for that low-copy template number is  
16 between 1 to 200 picograms. And that number is the number  
17 that goes into the PCR reaction.

18           And so if we are to take Dr. Reich's testimony and his  
19 observations, given his expertise, we are certainly below the  
20 threshold or the -- excuse me, not the threshold, but we are  
21 certainly below the target amount of DNA that the FBI wished,  
22 and we are probably somewhere around 100 picograms. And so  
23 given the scientific consensus that exists for the definition

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1 of low-copy number DNA, we are there. And so I think that's,  
2 again, another similarity to McCluskey.

3 And I think the big issue here is there were not  
4 enhanced detection methods or extra steps taken in order to  
5 counteract the known stochastic problems with low-template  
6 DNA. The FBI does not do that. In McCluskey, the same thing;  
7 no special procedures or methods were used.

8 And so the McCluskey court found that low-copy number  
9 testing had occurred because the lab had tested a low-copy  
10 amount of DNA. They did not rely on the other methods or the  
11 extended methodology or the enhanced methodology to make that  
12 determination.

13 And, in fact, in our -- in my brief, and I can't  
14 recall at this point if it was the AE 460 or its -- or the  
15 reply. Most courts who have had these dueling definitions  
16 agree that, at a minimum, the definition of low-copy number  
17 testing, meaning the amount of DNA that was tested, is between  
18 1 to 200 picograms. And it's at that low amount that the  
19 dangers of stochastic features and unexpected results and  
20 allelic dropout exists.

21 And it's because of that danger that the McCluskey  
22 court said I can't trust this result. And again, McCluskey,  
23 partial profile, mixture, less than their own definition of

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1 low-copy number DNA, which is more than the definition than  
2 I'm using. I think we're on all fours with McCluskey. And I  
3 think the same concerns that the McCluskey court had are  
4 present here.

5           The fact that this is a mixture and the fact that it  
6 is a partial profile that is -- we don't believe sufficient  
7 for identity, I think are compounding features of the -- the  
8 problems that are here.

9           Mr. Giusti agreed that the last locus that is  
10 identified as inconclusive -- we had the 9 and the 12 that are  
11 below the 200 RFU which would be needed for a match or an  
12 identification, that at that locus there is certainly danger  
13 of allelic dropout having happened because of the low amount  
14 of DNA that was present, that was amplified onto the  
15 electropherogram.

16           The danger in missing data is that we are missing  
17 pieces that could exclude Mr. al Nashiri, and that danger is  
18 very real. If one of those small peaks between the 9 and the  
19 12 were attributed to the major profile but have dropped out,  
20 Mr. al Nashiri is excluded. If it's -- if the major profile  
21 to K470 is consistent with Mr. al Nashiri everywhere but we  
22 have an allele that is dropped out at the very locus that  
23 Mr. Giusti identified there was danger of, then he should be

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1 excluded.

2           And so when you are missing data, what you are missing  
3 is potentially exculpatory data, which is, I think, very  
4 dangerous given the fact that the government intends to offer  
5 this not only in its case in chief as independent evidence but  
6 also in its corroboration of AE 166 and the hearsay statements  
7 that it wishes to offer.

8           I understand that the Profiler Plus amplification kit  
9 was validated. I recognize that PCR/STR testing in and of  
10 itself is a valid science and has been accepted by courts the  
11 country over. That is not our argument.

12           The issue here is that the amount of DNA was so small  
13 that even though they use an accepted method, that's not an  
14 accepted method when you have an amount of DNA that small.  
15 And that is evidenced by other laboratories across the country  
16 employing these enhanced detection methods, understanding that  
17 they need to see more data and that these methods are  
18 necessary in order to counteract the potential stochastic  
19 effects that we're going to see, to counter allelic dropout,  
20 and to get more data and able to see more data so that a more  
21 robust analysis can occur.

22           The sample here suffers from a myriad of problems.  
23 And even though the government -- or the FBI says, well, we

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1 validated Profiler Plus and ran it at 78 picograms and it  
2 seemed to do okay, we don't have any underlying data for that  
3 conclusion. We don't know how many times 78 picograms was  
4 run. We don't know how many times a full profile was  
5 exemplified or a full profile was gained from how many runs of  
6 78 picograms.

7           And I'll remind the commission that we don't know that  
8 we don't have less than 78 picograms here. That is a large  
9 unknown, and we just don't have a firm answer. And the  
10 firm -- if the firm answer is 72 picograms, then the FBI's not  
11 validated to run. If the firm answer is 100 picograms, I  
12 don't think we have the data to say that the FBI ran an  
13 appropriate test, its principles and methods that it used, in  
14 this case.

15           Now, yes, PCR/STR testing is a principle and method  
16 that is accepted, again, the country over, but was it reliably  
17 applied in this case to this low-copy number sample? And we  
18 would submit to the commission that it was not; that this  
19 falls on all fours with McCluskey, and we'd ask the commission  
20 to exercise its gatekeeping function, which does mean  
21 something in this state of heightened reliability of evidence  
22 that capital cases demand and that the commission exercise its  
23 gatekeeping function in excluding the DNA and any subsequent

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1 analysis that was done. Thank you.

2 MJ [COL ACOSTA]: Government, rebuttal?

3 ATC [MAJ ROSS]: Briefly, Your Honor.

4 Judge, the defense argument has become somewhat of a  
5 moving target. It's remarkable that now the defense finds  
6 fault in the FBI for not conducting enhanced detection  
7 methods. Those methods are not validated, they're not  
8 reliable, and the FBI did the right thing in not doing that.

9 The defense is also saying that the amount of DNA in  
10 this evidentiary sample was too small to conduct any testing  
11 on. I think we've beaten a dead horse at this point. The  
12 guidelines of the Scientific Working Group on DNA Analysis and  
13 Methods are in plain English. You can conduct the -- you can  
14 conduct tests on small amounts of DNA using the standard  
15 methods, and you can get a partial profile. That's what  
16 happened in this case. It's -- it's reliable and it should be  
17 admitted under the Daubert standard, Judge.

18 MJ [COL ACOSTA]: All right. Counsel, I'll take all of  
19 that under consideration before issuing a ruling. I think are  
20 we prepared to move into 442 or do we want to ----

21 TC [MR. MILLER]: The Government is ready, Your Honor.

22 MJ [COL ACOSTA]: Government's ready. Defense, ready?

23 DDC [CAPT MIZER]: We can do 442, Judge.

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1 MJ [COL ACOSTA]: Okay. Again, my standard question is do  
2 the parties consent to my taking your motions and the  
3 attachments thereto, argument and any evidence presented in --  
4 in resolving that motion?

5 DDC [CAPT MIZER]: Please, Judge.

6 MJ [COL ACOSTA]: Government?

7 TC [MR. MILLER]: Yes, Your Honor.

8 MJ [COL ACOSTA]: Defense, do you have any evidence to  
9 present?

10 DDC [CAPT MIZER]: We don't, Judge ----

11 MJ [COL ACOSTA]: Okay. You can ----

12 DDC [CAPT MIZER]: ---- other than the pleadings. Just  
13 argument.

14 MJ [COL ACOSTA]: Okay. Government, no evidence to  
15 present?

16 TC [MR. MILLER]: No evidence, Your Honor. Thank you.

17 MJ [COL ACOSTA]: All right. Go ahead, Defense.

18 DDC [CAPT MIZER]: Judge, we're seeking videotapes of the  
19 interrogation of Mr. al Nashiri that took place at Echo II  
20 between 31 January and 2 February 2007. I'm not going to  
21 stray into classified information here, obviously, even though  
22 all of the pleadings with respect to this series are  
23 classified, and we largely rest on those -- those pleadings.

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1 I would note, Judge, I think that we have clarified  
2 that the fact that Echo II is a former black site is not  
3 classified, obviously, and that's one of the facts that we  
4 would invite the Court's attention to.

5 On 29 March 2017, the government replied to our  
6 discovery request and informed the defense that it believed no  
7 videotapes of that -- those interrogation sessions existed.  
8 It notes in footnote 1 of its response that it could have been  
9 more precise with that language.

10 And I think that that's part of the problem with some  
11 of these issues, Judge, is this sort of gauzy language that we  
12 get back that we don't believe when we ask for specific pieces  
13 of evidence and we get a response that they don't believe that  
14 the evidence exists, and I think that that's what has -- has  
15 provoked this litigation.

16 But it's also really the history of this case, the  
17 history of the RDI program, and the Central Intelligence  
18 Agency's interactions with courts that also differentiate this  
19 from a court-martial that you may have perhaps at Fort McNair  
20 or over at the Navy Yard in Southeast, I think if I had a  
21 response from the government in that court-martial at Fort  
22 McNair that said they don't believe a piece of evidence exists  
23 that that would probably end the matter. But this is a pretty

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1 important piece of -- of evidence and we need that commitment  
2 on the record from the government.

3 Judge, we're going to get into 354, I believe,  
4 tomorrow on -- per the commission's direction. But the court  
5 is well aware -- and this isn't speculation. This is from  
6 United States v. Moussaoui, Fourth Circuit decision, 591 F.3d  
7 at 305, that on 9 May 2003 the CIA submitted a sworn  
8 declaration to Judge Leone Brinkema in the Eastern District of  
9 Virginia that, quote, there were no such recordings of  
10 interrogations of what the Fourth Circuit refers to as ECWs.  
11 It's a 2010 decision, so we're going back to the -- at that  
12 point, the old language of enemy combatants, and ECW is enemy  
13 combatant witnesses, for Your Honor's edification.

14 We know that that wasn't true, Judge, as we're going  
15 to talk about in 354. At that point, at the very least, there  
16 were 92 videotapes, 90 -- and this is, again, unclassified, 90  
17 of a man that goes by Abu Zubaydah, and then two of  
18 Mr. al Nashiri.

19 A lot of things were happening in 2004 and 2005:  
20 Abu Ghraib. And then in 2005, there was legislation before  
21 Congress. There was also a leaked story, I believe it's  
22 November 4th, dealing with the existence of these tapes.  
23 Judge Brinkema inquires again on November 5th saying, you

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1 know, essentially, I've read about this. Are you sure that  
2 there aren't any tapes? The tapes were destroyed a number of  
3 days later.

4 And then there's a second declaration, which is  
5 arguably accurate, that was filed 14 November 2005, again  
6 citing from the Moussaoui opinion that, quote, a second CIA  
7 declaration representing that there were no such recordings.

8 And again, Judge, I mean, that comes out of the Fourth  
9 Circuit's opinion recounting. I mean, those are facts that  
10 shouldn't be in dispute, that U.S. Attorneys -- I believe the  
11 ultimate conclusion was they weren't aware of the tapes. I  
12 think the Moussaoui opinion makes clear that -- that it comes  
13 out later.

14 But, Judge, in the event that we are in the Moussaoui  
15 position seven, eight, nine years after trial and those tapes  
16 do appear, we're going to have to have those commitments on  
17 the record, just as my colleagues -- my former colleagues in  
18 the federal public defender's office in EDVA had, and then  
19 they could litigate that motion. And that's really what this  
20 motion is about.

21 Judge, we have heard, again getting back to the tapes,  
22 through the years that there were these 92 tapes, they were  
23 destroyed in 2005, and there were no -- no new tapes. And I

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1 don't know if you -- if you paid any attention to the  
2 proceedings in United States v. Majid Khan who, in an unsworn  
3 statement, talked about some of the abuse that was meted out  
4 by the CIA in his case.

5           And there was a passing reference that he made during  
6 that unsworn statement, again in open session of the  
7 commission that I watched from the -- from the Pentagon,  
8 dealing with some of his interrogations. He noticed, or  
9 discussed in open session, the presence of video cameras  
10 during his interrogations.

11           And so this -- what was taped, when it was taped, and  
12 what happened to it seems to be, again, a moving target. And  
13 we're seeking to have, again, the government not merely reply  
14 with discovery requests, but come in and make that affirmation  
15 to Your Honor.

16           Judge, I think we're also going to talk about [REDACTED]  
17 [REDACTED] at some point with respect to 354. And, Judge, on  
18 [REDACTED] testimony before the Senate Committee on  
19 Intelligence, Senator Joe Manchin [REDACTED] ----

20           TC [MR. MILLER]: Judge, we're straying way, way far on --  
21 and we've talked about this particular issue.

22           MJ [COL ACOSTA]: Objecting to the relevance of his  
23 argument, Counsel?

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1 TC [MR. MILLER]: Yes, I am.

2 MJ [COL ACOSTA]: Then -- okay.

3 DDC [CAPT MIZER]: Judge ----

4 MJ [COL ACOSTA]: Is this relevant to the -- this is about  
5 the existence of whether or not there were tapes of his FBI  
6 interviews, correct?

7 DDC [CAPT MIZER]: That's right, Judge.

8 MJ [COL ACOSTA]: And we're talking -- since you've been  
9 talking about destruction, an existence of destruction  
10 of Central Intelligence Agency tapes, correct?

11 DDC [CAPT MIZER]: That's right, Judge, and how the  
12 narrative tends to wobble as to the existence of tapes. And  
13 the government's position is here, and I think it's going to  
14 be brief, is that there are no tapes. And I intend to offer  
15 examples of why we don't think that we're being unreasonable  
16 when the government says there are no tapes.

17 They told, again, a federal district court judge that  
18 there were no tapes in that instance. And I can make this  
19 immediately relevant if you'll just let me read what is about  
20 four or five sentences ----

21 MJ [COL ACOSTA]: Go ahead.

22 DDC [CAPT MIZER]: ---- from -- from the Senate.

23 TC [MR. MILLER]: Judge, I would object. If they have

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1 evidence that there were tapes, then I'd ask them to put it on  
2 the record. If they're just going to try to smear people,  
3 then I don't think it's relevant.

4 DDC [CAPT MIZER]: Judge, I'm not trying to smear anyone.

5 TC [MR. MILLER]: That's exactly what he's doing.

6 MJ [COL ACOSTA]: Counsel, objection overruled. I'll let  
7 him read the four sentences that he wants to read. Go ahead.

8 DDC [CAPT MIZER]: Let me go this direction, Senator  
9 Manchin says. [REDACTED]

10 [REDACTED]  
11 [REDACTED]  
12 [REDACTED]  
13 [REDACTED]  
14 [REDACTED]  
15 [REDACTED]  
16 [REDACTED]  
17 [REDACTED]  
18 [REDACTED]

19 And so, Judge, that's not a smear. It's uncertainty  
20 and an affirmative ----

21 MJ [COL ACOSTA]: But that's uncertainty about [REDACTED]  
22 agency's tapes, right?

23 DDC [CAPT MIZER]: Yeah. Yes, Judge. And so I think ----

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1 MJ [COL ACOSTA]: [REDACTED] was being asked about [REDACTED]  
2 those agency tapes and not in the tapes -- whether or not they  
3 existed or not, of the Federal Bureau of Investigation,  
4 correct?

5 DDC [CAPT MIZER]: Yes, Judge. And so I think the thing  
6 that is going to become clear -- what has become clear in the  
7 9/11 case is that -- and when we get to the suppression motion  
8 in this case, is that there's a pretty blurry line between, at  
9 least during this time frame, between what is an FBI  
10 questioning and where the line is between the CIA and the FBI.

11 And, Judge, if you -- if you look at page 3 of the  
12 reply brief, which there are two unclassified paragraphs  
13 there. The letterhead memorandum that is ultimately going to  
14 be at issue in this case is not drafted on an FBI Form 302  
15 like many of the other statements that are going to come  
16 before the -- before the commission. It's on a letterhead  
17 memorandum because, as I understand it from the 9/11 case, the  
18 [REDACTED] -- or the FBI not use the  
19 Form 302.

20 We mentioned that the [REDACTED] computers, they  
21 directed the Miranda warnings weren't going to be given. And  
22 so the fact that -- that we're talking about CIA tapings and  
23 given that the statement was taken in Echo II, which is a

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1 former CIA facility, I think that these things are actually  
2 relevant as to why the CIA may be interested in what was said  
3 there.

4           And again, we're trying to here get -- we have a  
5 reasonable basis to believe ----

6           MJ [COL ACOSTA]: Let me see if I can cut to the -- to  
7 crystallize your argument. Your statement is that you believe  
8 that because of the CIA's close involvement with the FBI  
9 interview, that because of what you present as CIA  
10 misrepresentations about the existence of tapes previously in  
11 other forums, means that it's hard to trust whether or not  
12 there were any tapes of these interviews that you're referring  
13 to.

14           DDC [CAPT MIZER]: I think that's exactly right. And in a  
15 nutshell, the CIA has always been very interested in the  
16 high-value detainees, and, from their view, protecting the  
17 information. Indeed, one of the other things that [REDACTED]  
18 [REDACTED] in this case was to segregate  
19 allegations of abuse into a separate document from what the  
20 government calls a clean team statement.

21           So there's [REDACTED] in the so-called  
22 clean team statements. We believe that there's obviously  
23 [REDACTED] interest. It was taken in Echo II. And I won't go

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1 any further than that, Judge.

2           It was reasonable for us, we think, based upon the  
3 history of the RDI program dating back to the Moussaoui case,  
4 where Moussaoui's attorneys are seeking to interview witnesses  
5 that the government had, and representations were made as to  
6 the existence of videotaped statements of witnesses that the  
7 defense was seeking in that case.

8           And so look, Judge, if the government comes in the  
9 well and says that there are no tapes, that's -- that's the  
10 record. We preserve the record and can litigate that on  
11 appeal in the event we are on appeal and seek to raise that  
12 issue. That's it, Judge.

13           MJ [COL ACOSTA]: Okay.

14           DDC [CAPT MIZER]: We're -- we are following the Moussaoui  
15 opinion and seek to have the same record. That's it.

16           MJ [COL ACOSTA]: All right. Thank you, Counsel.  
17           Government?

18           TC [MR. MILLER]: Good afternoon, Your Honor.

19           I agree with the defense that if we had -- if there  
20 was a recording or videotape, they would be entitled to it.  
21 And if I had one, Your Honor, I'd be the happiest guy in GTMO  
22 because it's certainly one that I would want to use, but the  
23 fact of the matter is that there was no taping of the

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1 interviews.

2 Now, to have listened to Captain Mizer, you would have  
3 thought that the CIA conducted this particular interview, and  
4 nothing could be farther from the truth. The interview was  
5 conducted in January of 2007 by the FBI while the defendant  
6 was in DoD custody. And as the attachments to the  
7 government's filing reflect, the defendant was treated  
8 incredibly fairly by those particular FBI agents.

9 And, in fact, Your Honor, I believe it was on 3  
10 November of 2017, the investigating agents who conducted the  
11 interview of the defendant testified in this courtroom before  
12 Judge Spath regarding what occurred, and at no time was there  
13 any indication given that there was any CIA involvement.

14 Counsel talked in terms of there being CIA involvement  
15 in this, but like so many of their allegations, so many of the  
16 pleadings that they file, there's a lot of -- there's a lot of  
17 allegations, there's a lot of finger pointing, but they're  
18 always really short on evidence. And in this particular case,  
19 they're really short on evidence.

20 I made the inquiries of the parties that I thought  
21 might know whether or not there was a recording. I received a  
22 resounding no by all persons who were involved in the  
23 investigation, as well as ones, like the CIA, who weren't.

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1 There was nothing that I came across, Your Honor, that during  
2 my inquiry and the inquiry of persons involved with the case  
3 or through my review of the discovery that would indicate to  
4 me that those representations were incorrect.

5 And for those reasons, Your Honor, I feel confident  
6 making the representation to you and to the defense team that  
7 there is no videotape or audio recording of those interviews  
8 that were conducted in January of 2007 here at GTMO.

9 MJ [COL ACOSTA]: All right.

10 TC [MR. MILLER]: Pending any questions that you might  
11 have, Your Honor, I have nothing further.

12 MJ [COL ACOSTA]: You asked the FBI if they had any tapes?

13 TC [MR. MILLER]: I did, Your Honor.

14 MJ [COL ACOSTA]: You asked the entire Department of --  
15 you sent this inquiry through the Department of Justice?

16 TC [MR. MILLER]: Well, the FBI.

17 MJ [COL ACOSTA]: Through the FBI.

18 TC [MR. MILLER]: Yes. That would be the department,  
19 although sometimes I don't think they think they're part of  
20 it, but the FBI is. And I did talk to some of the AUSA --  
21 some of the lawyers that were involved at the time just  
22 because I happened to know that they were down here.

23 So no, there is no indication that any recordings were

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1 ever made and, in fact, that is consistent with FBI policy.  
2 Having been a federal prosecutor for over 35 years, I can tell  
3 you that I never received a recording or videotape of a  
4 confession. It just wasn't FBI policy. And it was  
5 particularly strong policy in 2007. Now, it may have changed  
6 since I've been here at the commissions, but at that time,  
7 they never -- it was just simply not their policy to do so.

8 So what actions were taken are consistent, or the lack  
9 of actions, was consistent with how they operated.

10 MJ [COL ACOSTA]: You also inquired with the Central  
11 Intelligence Agency?

12 TC [MR. MILLER]: I did, Your Honor.

13 MJ [COL ACOSTA]: And they responded negatively?

14 TC [MR. MILLER]: And they assured me that they did not.

15 MJ [COL ACOSTA]: All right. Thank you, Counsel.

16 Defense, any rebuttal?

17 DDC [CAPT MIZER]: No, Judge. Thank you.

18 MJ [COL ACOSTA]: All right. All right, Counsel, for  
19 tomorrow, Defense, I assume you want your client here in the  
20 morning or do you want to roll directly into the -- I don't  
21 know how long the closed session -- the parties anticipate how  
22 long the closed session will go tomorrow. Defense?

23 DDC [CAPT MIZER]: Judge, I don't know. Between both

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1 sides, an hour.

2 MJ [COL ACOSTA]: An hour for each or the total of an  
3 hour?

4 DDC [CAPT MIZER]: I think a total of an hour, Judge. As  
5 I understand it, we're talking about one witness.

6 MJ [COL ACOSTA]: Government, any anticipation? And it  
7 doesn't have to be -- obviously, I'm ----

8 TC [MR. MILLER]: I think Captain Mizer -- that's a fair  
9 estimate, Your Honor.

10 MJ [COL ACOSTA]: For the closed session.

11 TC [MR. MILLER]: Yes.

12 MJ [COL ACOSTA]: All right. Then let's plan on taking up  
13 the other issues that I've got on the docket in the morning,  
14 doing closed session in the afternoon. Start at -- and just  
15 for planning purposes for public knowledge, we'll do the  
16 closed session at 1300.

17 We'll start with the 0-9 here to take up -- and  
18 forgive me, I don't have the -- I left my schedule in the back  
19 as far as which numbers I'm going to take up tomorrow. I'll  
20 have that communicated to you which ones we're going to take  
21 up. We're going to take up at least 444 tomorrow -- hold  
22 on -- at least 444 and any others that I look at this evening  
23 when I -- when I look at the schedule that I think that we can

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1 resolve tomorrow that we might otherwise have taken up next  
2 week when we were not in the -- in the time for those  
3 designated times. I'll send you whichever ones I've got left.

4 So with that, I plan on recessing for the day until we  
5 start with -- at 0-9 tomorrow to take up 444, and we'll take  
6 up the closed session at 1300 tomorrow.

7 Government, any issue with that? You don't have to  
8 run. You don't have to run. We're not running late on  
9 anything.

10 TC [MR. MILLER]: No, Your Honor. But the only other  
11 issue is I know that we have 437, I believe, the motion -- I  
12 may be wrong on the number, the Fourth Amendment to the  
13 seizure of the buckle swab, and we anticipate the evidence  
14 being taken on Monday.

15 However, the government has raised the issue of  
16 whether or not the defendant even has standing to raise that.  
17 So if the court wants -- because I think we're going to have a  
18 fair amount of time, we might be able to make a -- have the  
19 court make a determination of that prior to Monday, if you  
20 will and if you want to ----

21 MJ [COL ACOSTA]: I think we'll have time between now and  
22 the close of business Friday to take that up.

23 TC [MR. MILLER]: I'm just bringing it to the court's

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1 attention.

2 MJ [COL ACOSTA]: Yes. No, understood.

3 TC [MR. MILLER]: Thank you, sir.

4 MJ [COL ACOSTA]: Okay. Defense?

5 LDC [MR. NATALE]: Your Honor, so long as we have some  
6 insight tonight.

7 MJ [COL ACOSTA]: You'll have it. You'll have it. And  
8 it's nothing that's not fully briefed that isn't -- that is an  
9 argument that -- I'm not going to have you try to present  
10 anything that you're not prepared to argue for that hasn't  
11 been fully briefed.

12 LDC [MR. NATALE]: Right. The only thing that I think I  
13 can say, Judge, is that in light of the -- Mr. Nashiri's  
14 condition, he might not be wanting to come tomorrow because of  
15 the transportation and travel issues that he has. And so I  
16 just want to alert that we won't know that until tomorrow  
17 morning, but from what I gather, that seems to be what is  
18 going to be the case.

19 MJ [COL ACOSTA]: I understand. I was just leaving you  
20 the time to -- I was putting it in the morning because  
21 normally that is when you have an extra meeting with your  
22 client in the morning. Trying to accommodate that, as we  
23 always do.

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