@IN THE CIRCUIT COURT OF THE
SIXTH JUDICIAL CIRCUIT OF THE
STATE OF FLORIDA IN AND FOR PINELLAS COUNTY

STATE OF FLORIDA,

Plaintiff,

vs. CASE NO. 23-02935-CF

TOMASZ KOSOWSKI,

Defendant.
_____/

DEPOSITION OF CHAD SUMMERFIELD

DATE: July 17, 2024

TIME: 9:33 a.m. - 4:13 p.m.

PLACE: Zoom Video Conference

APPEARANCES:
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Stenographic Court Reporter

I-N-D-E-X

7-17-2024

DEPOSITION IN DISCOVERY

CHAD SUMMERFIELD

Pursuant to notice duly given, the deposition of CHAD SUMMERFIELD, called by the Defendant in the above-styled cause, was taken by me, a Notary Public in and for the State of Florida at Large, at the time and place and in the presence of counsel enumerated on Page 1 hereof.

Thereupon, it was stipulated and agreed by and between the attorneys for the respective parties, by and with the consent of the said CHAD SUMMERFIELD, that signature to the said deposition be waived.

THE COURT REPORTER: Do you swear or affirm the testimony you'll give will be the truth and nothing but the truth?

THE WITNESS: I do.

CHAD SUMMERFIELD, having been first duly sworn, upon interrogation in discovery, testified as follows:

DIRECT EXAMINATION

BY MS. TUOMEY:

Q. All right. Good morning, sir.

Can you please state your full name for the record?

A. Yes. My name is Chad Summerfield. The last name is spelled S-U-M-M-E-R-F-I-E-L-D.

Q. And we are here on the State of Florida versus

Tomasz Roman Kosowski, Case Number 2023-CF-2935.

You have been listed as an expert witness for the state, so this is my opportunity to ask you some questions about your reports, your opinions, and your testimony.

So I'm assuming you have had your deposition taken before, probably hundreds of times?

A. I'm not sure of the number, but it's been numerous, yes.

Q. Okay. So then I'm sure you're familiar with the rules.

We can't speak over each other.

If I ask you a question that you don't understand, which I'm sure that I will do, you can ask me to rephrase it.

And pretty much those are the simple rules.

A. No problem. I'm here for you.

Q. Okay. Fantastic.

All right. So it's my understanding that you work for the Pinellas County forensic lab?

A. That's correct.

Q. And in what capacity?

A. My official title is the DNA technical leader.

Q. And how long have you worked at PCFL?

A. Can I refer to my notes? Because I can never

remember when I started.

Q. I think it's 2003 or 2007.

A. Yeah. 2003, I started here.

Q. 2003.

A. Yeah.

Q. And prior to working for the Pinellas County crime or forensic laboratory, how were you employed?

A. I was employed at the Philadelphia Police Department forensic laboratory.

Q. All right. And how long did you work there?

A. I worked there -- sorry. I think I told you incorrectly.

I started in Pinellas in 2007.

Q. Okay.

A. I worked in -- 2003 to 2007 in the Philadelphia Police Department, as a DNA technical leader.

And from 2000 to 2003, I was a scientist there.

Q. I'm sorry. I didn't get that first year. From?

A. Well, I worked totally at the Philadelphia Police Department from 2000 to 2007, so about seven years.

Q. Okay. Seven years.

And it appears that you were -- when you left

there, you were a DNA technical leader; correct?

A. Yeah. I was an analyst for three years, and then I took over for the technical leader at the time.

Q. And then from 1998 to 1999, you were a lab technician?

A. Yes. I was at a place called PerkinElmer Animal Genetics, which PerkinElmer was the prior company of Applied Biosystems before they changed their names.

Q. So this company was -- turned out to be Applied Biosystems?

A. Well, there was --

Q. Or --

A. Yeah. Prior to, yeah.

Q. Okay.

A. It was PerkinElmer originally. Then they -- they -- because a lot of science companies constantly are changing names. That was the original.

So I was just a technician there.

Q. All right. And then when you were a technical leader at the Philadelphia Police Department, you were responsible for developing laboratory procedures and policies and creating the quality assurance manual for FBI --

A. That is correct. Yes.

Q. And then you successfully prepared that lab to

be able to participate in CODIS?

A. I -- I prepared the lab for the first audit they ever undertook, yes.

Q. All right. And -- I'm sorry. Go ahead.

A. That was -- under my initial tenure, that technically was the first audit that the laboratory had had. So that was the first FBI quality assurance audit the laboratory had.

Q. And how long had that lab been qualified to enter profiles into -- into CODIS? Would it have been just a year or something else?

A. It was probably -- let's see. Starting in 2000 and probably '3, because that was after our first audit. So around -- after 2003, is the first time they put samples into CODIS.

Q. Right.

And would you have considered yourself, like, a CODIS administrator for that police department at the time?

A. We had a separate person that was the CODIS administrator there.

Q. And did you train that person at the --

A. Originally, that person trained me.

Q. Okay. That person trained you?

A. Yeah. When I was a technical leader, I was

probably about five to seven years younger than everybody else there. So everybody was there prior to me.

Q. All right. And then during your time at the Philadelphia Police Department, you also had acquired funding to outsource over 1,600 forensics casings (sic). It's my understanding that during that time frame, even as we sit here right now, that Philadelphia Police Department has a backlog of forensic DNA cases, I guess, if you will, that need to be processed.

So you were part of, at least through 2003 to 2007, to outsourcing those cases in order to get those analyses accomplished?

A. That's correct.

I'm not sure about their current status of backlog. I would probably assume they still have a tremendous backlog, because there's a tremendous amount of crime in Philadelphia.

But when I was there, yeah, I was part of the outsourcing to Bode Technology of quite a few cases.

Q. You've answered my next question.

You said Bode Technology. Is that a lab?

A. Yes. Bode Technology is a laboratory.

Q. Can you spell that?

A. It's just B-O-D-E.

Q. Okay.

A. It was named after the founder, which was a guy by the name of Thomas Bode.

Q. And is that lab still in existence?

A. Yes. Absolutely.

Q. All right. And your current position at the Pinellas County forensic laboratory, I think, as you said, you are a DNA technical leader; right?

A. Yeah. I hold the same position that I held when I left Philadelphia.

Q. All right. And how long have you held that position with the Pinellas County forensic lab?

A. Since I started here. I was actually the first employee hired for the Pinellas County DNA section. I was originally hired as a consultant to see about the feasibility of starting a DNA section. Prior to myself, they did not have a DNA section.

So that's been since 2000 and -- like, 2000 --

Q. '7, since you left --

A. Yeah. Yeah. 2007.

Q. Okay. And as part of -- so first, originally, you were consulting with the lab to see whether or not it was something that was feasible for the laboratory?

A. Yeah. Exactly what they would need equipment-wise so they could get the necessary

budgetary -- so they could see what -- if they could obtain the money to start a laboratory.

So I worked with them for a while.

Q. When you say a while? A year?

A. Maybe six months.

Q. Six months.

And during that six months, you were able to determine and/or assist them in starting up a DNA, forensic DNA, section within that lab?

A. Yes. That's correct.

Q. All right. So is it fair to say that within six months, the DNA or the serology section of that lab had been started?

A. No.

Q. No?

A. No. It was quite a -- it was a little bit of time later before, you know, the funding came through. So I can't remember exactly the time, but it wasn't right away. It was probably several months, at least, several months later. And once the funding was approved, then I officially started here.

Q. All right. When you say funding, are these grants that you were applying for or something else?

A. It was funding through the county, because the money is allocated towards the -- to the medical

examiner.

Q. Okay.

A. And the county commissioners had to allocate money in order to have the necessary funding so that they could buy the necessary equipment and pay employees.

Q. And do you recall how much funding initially was approved by the -- by the county?

A. I -- I do not know that. I know that's public information, but I don't know the number.

Q. Do you think that the Pinellas County forensic lab is properly funded now?

A. Yes. We're one of the few labs in the country that do not have, really, a backlog. We have a working backlog, which is -- which is quite unusual for forensic laboratories.

Q. When you say backlog versus working backlog, what's the difference?

A. It means the cases that we have in our backlog that has not yet been completed is expected to be completed within a 30-day turnaround time. So it's just as cases come in, cases are typically going out within 30 days.

So we don't have, like -- a lot of laboratories have backlogs of hundreds, if not thousands, of cases

that they just cannot get to.

Q. Are you ever sent a case where it's an expedited analysis that you have to do?

A. Yes.

Q. And --

A. Yeah. We do -- we have cases that are sent that need to be expedited, yes.

Q. Okay. And was this determined to be something that was expedited at your lab, this case?

A. Expedited in the fact that it was done within 30 days. I don't know if it was necessarily put in as an official request that we, you know, drop everything. But it was -- I want to say it was typically -- it was put in my next batch of cases.

So I don't think it was like I dropped everything and only working on this case. So in that sense, I don't think it was expedited in the sense we dropped everything.

Q. So was it kind of bumped in the line of cases?

A. It was bumped up in -- like, when I was done, this is the case that was called right up first.

Q. Okay.

A. Not necessarily like -- because when you say -- sometimes when you say expedited, it means I drop all the cases I'm working on, and I'm just -- I'll just

go work on that one. I was still working on other cases, but when I was done with my analysis, this was the one I called right up first.

Q. How many forensic DNA analysts do you have currently at the Pinellas County forensic lab?

A. Give me a second to count through my head in the room.

We're right now at 12 -- sorry, 13, and one technician. I believe that's the case.

We recently just had a couple hires. A couple people still in training, but we have ten people that's actually performing casework.

Q. All right. And Desiree Beecher no long -- if I'm pronouncing that last name correctly, B-E-E-C-H-E-R -- no longer works at your lab?

A. That is correct. Yes.

Q. Do you know what was the reason for her either retiring, leaving, or seeking employment --

A. Only through -- this is just me, talking to her.

Q. Okay.

A. I mean, maybe she has other reasons. You would have to ask her directly. But I know she was wanting to prepare to go to medical school.

Q. Okay.

A. So she was wanting to take time off to go prepare for medical school.

Q. That's a good reason.

All right. So what is your formal education?

A. I got an undergrad degree in microbiology, a bachelor of science in microbiology, from Alderson Broaddus College in West Virginia.

Also, I have a master's of science in forensic science from the University of New Haven.

Q. And do you belong to any organizations presently?

A. No. But I am -- I do hold a certification in forensic -- forensic molecular biology from the American Board of Criminalistics.

Q. And that, you received, I believe, in 2011?

A. I'm not sure of the date. But I've had it a while now, yeah.

Q. Is that certification done through ANAB or ANSI?

A. No. It's actually through the American Board of Criminalistics. It's --

Q. Okay. Then maybe -- is it sponsored through them?

A. I know some of the standards recommended that laboratory stuff become certified. But I know through

-- I'm trying to think.

I know through ANSI, they kind of promote them, but I don't know if they're necessarily sponsored through them. I think they're a separate organization.

Q. Yes, they are a separate organization, but it's my understanding that they sponsored. And I could be incorrect.

A. No, I'm not sure of the affiliation.

I know they -- if you go on, like, ANAB's website, there will be links to the American -- the ABC website, but I'm not sure the relationship they have with each other.

Q. Sure.

And what accreditations does the Pinellas County forensic laboratory have, to your knowledge?

A. We have the -- it's actually the ANAB accreditation.

Q. All right. And what else, if anything?

A. Well, the ANAB accreditation includes us following the FBI quality assurance standards.

Q. Okay. And does it require the lab to follow any other standards?

A. Well, with ANAB, we're also following ISO 17025 international requirements, so.

Q. Anything --

A. That's pretty much the extent. I mean --

Q. If you need to look at any of your documentation, just let me know what you're looking at. I probably have the same documentation, hopefully, that you're looking at, but --

A. I mean, under ANAB, there's, you know, that accreditation encompasses in it other things to follow, if that's what you're meaning. Like following ISO 17025 FBI quality assurance standards.

We are not necessarily audited to any of the ASB standards, but we strive to follow the ASB standards.

Q. All right. Does -- I think maybe I had, like, kind of touched on this, but maybe not.

Does the Pinellas County lab, forensic lab, outsource any of its DNA analysis?

A. No. We have never outsourced anything.

Q. Is there any forensic DNA methodologies that your lab is not validated to perform? I.e., related individuals, comparing related individuals, or things of that nature?

A. Yes, there is.

In essence, it's not outsourcing as it's defined within, like, to say the FBI assurance standards defines outsourcing as we are taking ownership of the data. In that case, if a detective wanted, like, a genetic

genealogy done, we don't do that type of testing.

We don't do single nucleotide polymorphism testing. We don't do mitochondrial DNA testing. So that would not be under the outsourcing, because we could not take ownership of that data.

Q. I see. So you wouldn't even consider conducting analysis in the first place. You wouldn't take it and outsource it.

A. It -- that would go not from us, not from us sending it to someone else. That would go from the detectives.

Q. Right.

A. Or whoever was sending the evidence, they would send it to another laboratory.

So -- but we do not outsourcing, but there is, you know, testing that we do not do.

Q. Okay. That makes sense.

If that kind of testing is needed for whatever reason your lab is not validated for, is there a specific lab that is normally used to do those testings -- those tests?

A. If the -- if the detectives will call us, we'll suggest some laboratories.

But I know Bode Technology is one laboratory, of course.

I know -- I know they've used a laboratory like Intermountain Forensics.

I'm trying to think of some of the others.

Parabon, which is another lab.

But, yeah. So it's really what the agencies, who they want to send them to. We will try to sway them into using an accredited laboratory, of course.

Q. Okay. So it depends on the detective and what perhaps they're looking -- looking for?

A. Yeah. We'll try to tell them that, you know, they need to look and make sure the laboratory is accredited. Because there's -- there's a lot of private labs out there that just fly by the seat of their pants and do what they want, and it's not really, really that scientific.

So we'll try to send them to a laboratory that's actually had an independent audit of their policies and procedures, so they can ensure that the results they're getting are scientifically sound.

Q. When you say independent, now, are you saying like a third-party audit or not?

A. Yeah, a third-party audit. Typically, an FBI quality assurance audit.

Q. Understood.

All right. And the three labs that you gave me,

are those labs in the State of Florida or somewhere else?

A. No. Bode is in --

Q. Pennsylvania?

A. -- right outside of Virginia.

And the Intermountain, I think they're in Vermont.

Q. Okay.

A. And I'm -- and I'm not sure where Parabon is at.

Q. Okay. All right. So as part of being a DNA technical leader, you perform DNA forensic analysis; correct?

A. That is correct.

Q. And you also are trained and qualified to conduct body fluid identification as well?

A. That's correct.

Q. All right. So with regards to the body fluid identification, what are the validated methods at your lab for body fluid identification?

A. In respect to what body fluid?

Q. Blood.

A. Blood. Okay. Blood, there's HemaTrace and also phenolphthalein. So two methods.

Q. Say that last one, because I think I pronounce that differently than you do.

A. Phenolphthalein.

Q. Oh, phenol -- okay. The same. Yeah.

And with the phenolphthalein, were you involved in the validation of using -- I guess, they're -- they're kits; right?

A. Phenolphthalein is not a kit.

Q. It's not a kit?

A. It's -- no. It's -- it's chemicals that you add up in succession. And with the addition of the chemicals that -- there is a color change that indicates an oxidative reaction that is indicative of -- presumptively for blood.

Q. Okay. And then the other validated method that you mentioned, remind me of the name. Hemo?

A. It's Hema, like -- like H-E-M-A -- Trace. And that's just a -- it's just a spot test. Think of, like, a -- what a pregnancy test looks like.

Q. Sure.

A. You know, where you see the line. And we see the -- if you see the two lines, you know you're pregnant. It -- it looks just like that.

Q. Okay. And how -- if you could explain to me the procedure on how that -- that is performed.

A. Which one, the HemaTrace or the phenolphthalein?

Q. The HemaTrace.

A. Well, the HemaTrace is typically not utilized unless we have some indication it may -- we're unsure if it's human blood or animal blood.

Q. And how would --

A. So --

Q. Go ahead.

A. A lot of times -- a lot of times when you -- you get a really good phenolphthalein result, you run the result, and you get no profile. Where you should expect, if you have a decent phenolphthalein result, you should have a profile.

So a lot of times, you'll go back and use the HemaTrace test to say -- to indicate that this was, you know -- so tested positive for possible human blood, or if it's negative, that could indicate that it wasn't necessarily human blood. So you kind of see if the results confirm -- confirm.

Sometimes, if we have, like, some really weak results, we'll also do a HemaTrace test to confirm.

Q. All right. And what about stain extraction? What's the method that you guys use for extracting stains?

A. In an instance for blood, typically, we use a kit that's called PrepFiler. It's a magnetic-based

extraction method.

We have other methods in the laboratory besides PrepFiler. We have an organic method. We have Chelex.

It just depends on -- a lot of times, we use the organic on really old samples. But PrepFiler does really pretty good for the vast majority of samples. So it's typically the one we go to first.

Q. And explain to me the procedures in using that kit, PrepFiler.

A. You would take a sample. Let's say -- let's say the sample tested presumptively positive for blood. You would then take a sample of that. You add it into a little -- it's like a spin basket type of thing. You put the sample in that.

Then you add necessarily -- a necessary fluid, which is some chemicals to help lyse the material. That's done with an incubation after a period of time.

Then you will actually take that out, and we put it into a robotic system that's called the AutoMate Express. And it uses DNA's ability to be negatively charged, and the ability of magnetic beads to help capture and clean up the DNA.

And then we have a process on the robotic system. We get a final solution of the DNA into a tube.

Q. All right. And what about quantitating DNA?

What method does your lab use to do that?

A. We use a kit that's through Applied Biosystems. It's called Quantifiler Trio. And --

(Court reporter asks for clarification.)

A. And that's the name of the kit. It's Quantifiler Trio.

Q. And explain to me how that kit is used.

A. Okay. That kit has several different probes. And one of the probes is called a small autosomal probe. It also has a large autosomal probe.

Q. Well, let me just stop you there. Can you explain to us the difference between small and large, and why would you one versus the other?

A. Well, they're all within the same -- within the kit. Every one of them -- what I'm getting ready to say, every one of these are ran within it.

Q. Okay.

A. And so the small autosomal and the large autosomal probes is looking at the lower end of the DNA range and the higher end of the DNA range.

And what that gives us the ability to do is, you can compare the small autosomal with the large autosomal, and you can see if the sample quantification, if it has a degradation.

So you can kind of look at that small versus the

large to measure -- or look if the sample is somewhat degraded. And it allows us to determine what we're going to do for the next steps.

It also has another probe in there. It's called a Y autosomal probe, which tells us how much -- how much male DNA we have in the sample.

You can take the small autosomal and the Y autosomal, and you can make a comparison. And you can actually see within the quantification, the male to female ratio of the DNA.

So not necessarily in this case, but a lot of times in sexual assaults, that allows us to determine if we need to take a sample forward or go straight to Y-STR.

With quantitation, this gives us a value that we know within our validation of when we go forward, we know ideally of how much DNA we need to make copies of. So this allows us to know how much of that DNA we need to take forward, so.

Q. Right. And what is the amount of -- amount of DNA required to be extracted in order to carry that forward?

A. Well, there is no amount required. But the ideal range where we expect to have full -- a full DNA profile would be between .5 and 1.0 amps of DNA.

Q. So is that what you shoot for, .5 and 1.0

nanogram?

A. Yeah, somewhere in there.

Q. And what --

A. That's when -- that's -- when we go to the next step, that's the amount of DNA we would target, based upon the quantification amount.

Q. Less than --

A. I'm sorry. Go ahead.

Q. What if you had less than that amount? How would you proceed?

A. You would proceed by adding the maximum volume that you -- that you could for your amplification.

So for our kit that we're using, that's 15 microliters. So it doesn't necessarily mean the results are invalid when it's less than .5 nanograms. It just means you're not expected to obtain a full DNA profile.

And you can have what we call stochastic issues where -- where you get one copy of your DNA from your mother and one copy from your father. Looking at an individual location, they may not be balanced when you get to lower levels.

So you start seeing some stochastic issues. But that doesn't necessarily mean results are not valid below .5. It's just that .5 is where we expect to

obtain optimal results, where we expect to obtain a full profile.

Q. All right. And then PCR amplification, what -- what kit do you -- does your lab use to amplify the DNA?

A. We actually use two kits.

Q. Okay.

A. In this case, only one of the kits was used. But we usually -- the two kits we use are both from Applied Biosystems.

And the first kit is a kit, it's called GlobalFiler. And it's G-L-O-B-A-L filer.

And the other kit is YFiler.

The kit that wasn't used in this case, YFiler, that's just looking at just the male portion of the DNA.

The kit GlobalFiler is looking at several locations of the DNA.

Q. Okay. And the kit that you used in this case, is it the five-dye kit? I know they have a six-dye kit as well.

A. Yeah.

Q. Is it the five?

A. Yeah. It's a -- blue, green, yellow, red -- yeah, five -- five-dye.

Q. All right.

A. And it's on the 3500 instrument.
Q. The 3500 Genetic Analyzer?
A. That's correct. Yes.
Q. All right. Tell me what separation typing is.
A. Separation is just -- because DNA is different sizes, the ability to run a current allows for the separation of DNA based upon sizes.
That allows us to make a comparison. And we make a comparison based upon sizes. So it's just a means to allow the DNA to flow through a medium that then will separate based on size.
We have known -- what we call allelic ladders that are known sizes that are run. And from that, we can make a comparison.
Q. The bins and ladders that you receive with the kits?
A. Well, they're not received with the kits, but they're -- the bins are within the software based upon our validation.
So those are step, a point of validation. And then that allows us to, in combination with allelic ladders, to -- they will then give an allelic destination.
Q. And the allelic ladders are -- aren't they part of, like --
A. The -- I'm sorry. You go ahead.

Q. Like, GlobalFiler, they have their own allelic kit. And that also -- and, by the way, that kit also has to be validated to be used within your lab as well; correct?

A. Oh, yeah. It was extensively validated, yes.

And the ladders are included as part of the kit, yes.

And every time we obtain a new lot, they are quality controlled to make sure that they are still acting appropriately.

Q. Okay. Back to the separation typing.

Which of the -- of the primary methods are -- does your lab use for DNA separation?

A. Capillary electrophoresis is the type of separation we use. And it's just running the samples through a capillary that contains a medium, which then allows for separation. And that's what the 3500 instrument does.

Q. Right.

Okay. Is there any policy, procedure, methodology that's used at your lab to determine whether or not you have overlapping of alleles?

A. When you're -- what are you meaning by overlapping? I'm sorry.

Q. Overlapping of alleles.

(Overlapping speakers.)

A. If something is a mixture, is what you're talking about or --

Q. Yes.

A. Oh, okay. Yeah. Yeah. Yeah.

One of the things that we determine if something is a single source or a mixture is also trained in what, you know, a single-source profile looks like.

And within that, if you're looking at a profile, you know, you expect to see, say, two peaks at a locus, and you see a third peak that's not in a position that would be expected, then that would indicate that there's a mixture of DNA.

Is that what you're meaning?

Q. No.

A. Okay.

Q. If someone has two of the same alleles potentially, or there's a mixture, and if some -- within that mixture, that individual happens to have the same allele, then those two alleles would overlap; right?

A. Yeah. That's -- that's exactly when you're -- we have what we call binary threshold, which is around 400-some RFUs. And what that would mean when you're looking at, say, a single-source sample and you see one allele, is there are two copies there versus one.

That's a point where the data indicates that there's two copies there. Yeah. Below that, you can have facts where you're not so sure if there's one copy or two.

The software that we use -- or to help us aid in mixture interpretation, STRmix, uses a dynamic threshold which is based upon the overall of the profile, and it also does the same thing.

Q. Okay. So it seems -- and you correct me if I'm wrong. But it seems to me that you indicated that if the RFUs are higher, that that may indicate that there's overlapping of alleles? Did I hear you correctly, or am I misinterpreting what you said?

A. Well, that's correct and not correct, depending on the context you're using it.

Yeah. Let's say -- because you have to look at the entire mixture as a whole --

Q. Sure.

A. -- you know, to make that determination, not just one individual location. So it can, yes.

Q. And could that also be indicative -- either overlapping, or could that 400 RFUs -- I'm just going to use what you used -- also indicate a larger amount of DNA for that specific loci? Does that make sense?

A. Can you repeat that, please? I want to make

sure I tell you correctly.

Q. Sure.

Would that peak, would that 400 RFU peak just simply indicate maybe more DNA at that specific loci?

A. Yes. That could indicate. The RFUs -- the higher the RFUs can be an indication of what you're saying, overlap of the single allele.

But that's also -- has to be taken in conjunction with looking at the rest of the profile, not just by itself.

Q. Yes, of course. I understand.

All right. Either at your training -- or in your training in the Philadelphia crime lab or the Pinellas County crime lab, were you trained on the specifics of touch or transfer DNA?

A. I don't -- I'm sure there was training. I don't know, because we've actually, like, gave our individual -- our personnel training on touch, making sure everybody has read all the various articles out there with touch.

And right now in the community, the people is trying to get away from the word touch because that indicates that someone may have touched the item, and that's not necessarily the case.

But, yeah, we're all very trained on -- on the

literature that's out there regarding touch.

Q. All right. So when you -- can you expand on what you were indicating in your last statement about we're trying to get away from touch DNA because it doesn't necessarily mean that the person touched. Are you talking about transfer and secondary transfer?

A. Well, we can never say, as scientists, how -- how -- how the DNA got there. Was it through a primary? Was it through a secondary, tertiary? That's really outside of our realm.

So the word touch would indicate that someone actually physically touched that item, which would be, I guess, because of a primary transfer. But you -- we can't state that as that's a fact. So, I mean, could the DNA have gotten there from a secondary transfer? That's -- that's not our job to decide.

Q. And you can't really decide that. No one can really decide that, and no one can reliably --

A. There is -- there is some work that's being done --

Q. Okay.

A. -- that we're not doing right now. And I think it might be the Armed Forces DNA lab, some labs overseas, where they will actually give a probability or, I should say, a likelihood ratio, to the event being

a primary versus secondary transfer.

To do that, I've researched into it, and it is so much work that you would spend all of your time on one case just to try to get -- to get a statistic for that.

Q. Get a probability on something that's probably not --

A. It would be -- and your statistic would be really low with all the work you did. Because what you have to do is you have to take into account the extraction method you used, what -- the quantification value. So you're taking all of this data into account, and then you're applying a statistical weight to being a primary versus secondary.

So there is labs out there that's doing that. But it's quite a bit of work for one case. And it wouldn't be appropriate for us to do it in our laboratory, because we would not have the resources to do that.

Q. And is part -- and if you know, is that part and parcel based upon determining who is the major donor or the minor donor, things of that nature?

A. That's part of it. But that's not always -- you can't necessarily rely on someone being a major. You know, that that's the per -- you know, that's the -- because everybody transfers DNA slightly different.

Someone can be what's called a shedder, which

means, for some reason -- we're not really sure why -- they shed more cells than other people. And they're called a shedder.

But one of the things with a shedder is, they're not necessarily a shedder throughout their life. They might be a shedder for one period of time, and another period of time, they're not.

So if someone was a high shedder, that doesn't necessarily mean -- they could have been not the last one. You know, they could have touched it a long -- or transferred it a long time ago. It doesn't mean they're necessarily the last one. They just transferred, somehow, a lot more DNA.

So you can't always go by major versus minor when you're looking at that -- at that.

Q. Okay. And am I correct in saying that -- you, as a forensic scientist, can't determine who is a shedder and who is not; right?

A. There was at least one article that I read that -- I don't think it gained any traction -- where you could determine someone's shedder status. And -- but I've never seen -- I read it, but I've never -- I've never seen it go anywhere after that.

So -- but, no, there's no way, currently, that people are doing it, the shedder status.

Q. All right. And you had indicated earlier about reading various articles and keeping up with the literature.

What's the main journal or forensic journal or what have you that you and your colleagues use to keep up with forensic DNA analysis?

A. It varies, but typically, the Journal of Forensic Science.

Q. I'm sorry. Journal of Forensic Science, is that what you --

A. That's just one -- one of the main ones. There are some other journals out there, but that's the main one.

Q. All right.

A. And I should mention, a lot of these journal articles that's out there, it's not accurate to what we do. You know, like, for example, they'll have someone hold an item for 15 to 20 seconds.

Q. Uh-huh.

A. You know, they're not really simulating, you know, like, a real quick contact or something like that. So they're always on the extreme -- extreme ends of what they're looking at for transfer DNA.

Q. So it seems like you're talking about the various studies that they're performing. Is that --

A. Yeah. Yeah. They're -- and there still continues to be a lot of work being done in this area.

One we're calling things for our staff is -- this is why I say we're so well versed on transfer DNA, is because when we go to trial, a lot of times, it's not necessarily about the disputing of our DNA results. It's about disputing how the DNA results got there.

So that's commonly the type of questions. So we want to make sure that we're relaying the information to the jury, you know, accurately. So we're constantly trying to keep up with what the literature says.

Q. So I want to skip to a different subject.

As a DNA technical leader, part of your position is to review both internal and external DNA audit documents; correct?

A. That is correct. Yes.

Q. I believe you, along with some other people at your lab, review those kind of documents?

A. Yeah. I am required to review and approve according to the FBI quality assurance standards, yes.

Q. Okay. And I know it's called different things within different labs, but you correct me if I'm wrong. But if -- if there's a deviation, if there's a policy, a deviation from the policy, or there's an issue at the lab, it seems like you guys call them corrective action

requests?

A. Yeah. I think that's -- I know it varies for labs. But I think a lot of labs are kind of a little bit more standard, and call it corrective action requests or short for CAR.

Q. Right.

Okay. And how -- how is this process initiated? I know it probably depends on the issue but, in general, how is this process initiated?

A. The process is initiated by anybody within the laboratory can issue a, like, something -- you know, something we have is against policy or against the standard. And then that will be evaluated.

We have a group within our laboratory that is people outside our DNA section, too, and some people within our DNA section. There's a quality assurance committee that will take a look at that and determine if it is a true nonconformance. They'll look at it and see if it was just a once-off, meaning, you know, someone didn't check a -- it was a one-off incident, or is it something that is more systemic. And --

Q. If I could just -- if I could just stop you there.

So if I heard you correctly, if it's kind of, like, a one-time thing and this hasn't happened before, isn't

gonna -- I guess doesn't happen --

A. And it's not impacting anything with casework. That's the main thing.

Q. Okay. Not be documented through the corrective --

A. It would still be documented --

Q. Okay.

A. -- within the file as a correction, but it wouldn't necessarily go to the point of a corrective action request. But it would -- it's investigated to see is it -- is it, you know, just one time. Just like anybody. You know, a lawyer -- anybody who says they -- that's why we have policies and procedures in place, why you have quality assurance standards in place, is to mitigate any -- any -- anything. That's why we document everything, is to avoid -- and making sure that we're following the policies and procedures.

Q. And you mentioned --

A. I'm sorry. Go ahead.

Q. I'm sorry. I keep interrupting you.

A. You're fine.

Q. Interrupting your thought.

There's -- are there certain levels of nonconformance? I think, Level 1, Level 2? Could you explain?

A. Yeah. I cannot remember how our levels are here.

But, yes, there is levels of compliance, where 1 is just kind of, like -- you know, it's minor.

But then there's ones that can affect all of the cases. And those are really ones that are really severe. And those are required to be reported to our accreditation organization, where they have to make an independent assessment of our corrective action for that.

Q. And I believe you're involved in approving those corrective actions?

A. That's correct.

Q. All right. So I have the corrective action requests from March of 2012 through, I think it's September of 2022.

And my question for you is: If you were employed -- became employed working at this lab in 2007 --

A. Only -- only if -- only approve the effects of DNA analysis. So they should have all came to me if it affected the DNA analysis. If it was something outside of that, then they don't necessarily come to me.

Q. Okay. But my question is --

A. Yes.

Q. -- from '07, until March of 2012, are you

aware of any corrective action requests during that time frame? I mean, that's a pretty large time frame.

A. I'm sure I'm aware of some. I can't think of any offhand but, yeah. I know there's been -- been some.

Q. Is that something that you can provide us? Because it wasn't provided to us.

A. I looked over --

Q. Okay.

A. I looked over what was sent to you guys. And at least according to the documentation I have within our file, those were sent, because I looked over them this morning before I got here.

Yeah. I'm looking at -- if you don't mind, I'm looking at our attachments. And --

(Court reporter asks for clarification.)

A. Attachments for our case file, which has -- I don't know if they will open. Let's see.

Yeah, you should have got those.

Q. Okay. I got, like I said, from March of 2012, through, I think, September, maybe October of 2022.

So is there another -- another set of documents, perhaps?

A. Let me make sure what I listed the first time because I'm not involved with the -- the subpoena for,

like, records.

Q. Uh-huh.

A. So -- but when I was looking over the file for today, I looked and seen what was sent over.

And I -- there should have been two files. It looks like there's a CAR Part 1 and a CAR Part 2. Did you get that?

Q. Yes.

A. And what was your question about? Those go --

Q. 2012 to, like, '22.

And my question is: From 2007 to 2012, approximately, I'm missing those corrective action requests.

Who would I -- who would -- do you have a contact for me? I mean, I can get it or I can ask --

A. Yeah. It may have been just -- yeah. If you didn't get those, I can make sure you get those.

Q. Okay.

A. But, yeah. Pam Foster, head of our laboratories, one of our secretaries that puts this together. So she would be the contact.

Q. All right. And that would also include, I guess, the tail end of 2022, until the present time?

A. I guess so. I didn't look at the dates of what you got. I just seen that there was two -- two

different files for CARs.

Q. Okay. Very well. But you said that you had reviewed these documents prior to --

A. I -- yeah, prior to my deposition. When I say reviewed, I really just opened them and seen that they were there. I never really, like, looked look at them. So, yeah, I just seen the two files sent to you guys.

Q. Sure.

Do you recall having -- well, have there been any corrective action requests made due to contamination?

A. Yes.

Q. And to your recollection, what types of contamination are we talking about?

A. I know we at least had one analyst that had -- had recurring instances of contamination.

Q. What?

A. Had recurring instances of contamination.

Q. Is that Watson?

A. Yeah. And so it was just a period of time where we were trying to figure out exactly what was happening and what she could change procedural-wise to minimize, and direct observation.

And -- and -- and the important thing with that is -- and, see, like, people get all, like, upset about contamination. But the more important thing is, you

would be more worried about the labs that had contamination and didn't even figure out they had contamination.

So, at least, we had mechanisms in place to detect that. With that, we went through and monitored what she was doing procedural-wise, and -- and gave suggestions. And I don't think she's had hardly any instances of contamination since then. So --

Q. So you had determined what was -- what was the issue. What was the issue with how she was contaminating the DNA that she's working on with her own DNA; right?

A. Yeah. It's so hard to pinpoint exactly what the issue was. But it was just -- you know, like, changing -- you know, wiping down the tubes, changing gloves more frequently. You know, just various things.

Q. So, essentially, she had -- was she retrained in quality assurance?

A. It wasn't retraining. It was just observation of -- of a work practice to see what we could do to minimize her having contamination in the future.

Because any analyst out there that says they've never had contamination is, one, not -- doesn't have a system that's able to detect it or they're fibbing.

So -- so we just monitored her procedures and made

suggestions. And over time, monitored -- monitored her, and showing that we have minimized the amount of contamination they're seeing.

Q. What is the mechanism that you guys have in place to --

A. Work --

Q. Go ahead.

A. Go ahead. I'm sorry.

Q. No. What's the mechanism that you have in place to discover potential contamination or contamination?

A. Sure. We have several methods.

One, with every extraction, we'll run what's called a reagent blank. A reagent blank with extractions is all the chemicals that are used in the extraction process, minus, of course, a DNA sample. And that's carried through the entire process.

At the point of amplification, we issue what we call a native control. That's all the reagents that's used in the amplification. And that's carried throughout the process.

So at the point of detection, we have reagent blank and native control, which is evaluated to see if there's any peaks or any type of contamination in the samples.

In addition to that, within GeneMapper ID-X,

there's an insertion mechanism. Every sample within a run is searched against itself to see if there's any potential hits from a sample within -- within the run. So Sample A to Sample B, et cetera.

In addition to that, we have an internal database that has all of our DNA staff, all the administrative staff. It pretty -- it pretty much has everybody within our building.

We also try to collect samples from any maintenance, if they'll volunteer. Any reported sources of contamination or contaminated profiles that I observe from any of the message boards or -- is also entered into the database.

We also have, within the database, samples from law enforcement. And all those are searched. Every sample is searched against that. And -- to see if there's any instances of contamination.

So that search is all done through GeneMapper ID-X.

In addition to that, to the samples that are carried forward to STRmix, we also have an additional search which is done within STRmix that's a database search which it searches. It's a little bit more expanded database, a little bit more samples. And we'll see if there's any potential matches within samples from that.

So we're looking at samples from law enforcement, for the ones that have provided, and within -- within our own staff.

Q. All right. So law enforcement, is that every -- how many different agencies are we talking about?

A. You're talking all the agencies we serve in Pinellas County. But not everybody has submitted.

The way -- the way it works is -- because I don't understand this. But law enforcement is more scared of DNA than anybody else, and they don't want to give their sample.

So the only way we could get the police unions to agree to allow their staff was, they would maintain a list of people that have submitted a sample. And we will anonymously put the sample in the database, but there will never be a name tied to the database.

So we know that sample has been taken from a person, say, from the Pinellas County Sheriff's Office, but that person is now only recognized as EL-1. So we would know we had a hit to a Pinellas County Sheriff's Office personnel, but we would never be able to tell you who that person's name was.

Q. Gotcha.

And how often is that list updated, do you know? Or is it updated?

A. It's updated -- we get samples probably monthly. Some samples -- some agencies are much more compliant than others with, like, giving samples, because it's a -- totally a voluntary thing.

Q. Yes.

A. We try to tell them that this actually benefits you, as an agency, because if we have a profile, we want to be assured that if we're putting a profile into CODIS, that it's not coming from somebody at the scene, you know.

So we're trying -- it's actually helping them to keep them out of the national database. So some agencies -- the Pinellas County Sheriff's Office is much better than other agencies. Some agencies, we don't get a whole lot, and some we do.

Q. All right. And who is the current CODIS administrator at your lab?

A. The current CODIS administrator is Beth Ordeman.

Q. Was it, at some point, Ryan Satcher? Am I --

A. Ryan Satcher was the CODIS administrator. And he's still employed. It's a switching of positions.

Q. And when did that occur?

A. That's probably been a little over a year ago now, give or take. I'm not sure of exact dates, but it

feels like it's been a little over a year.

Q. And are you aware of any corrective actions that needed to be taken regarding the security of the software programs at your lab?

A. I would have to go back and look at some of their corrective actions. But I think there was some -- it might have been something in relation to the CODIS software. Yeah. But I can't remember the exact specifics, but I think there might have been something with regards to that.

Q. Security. So, like, antivirus or -- you know, so that --

A. Yeah. I think -- oh, yeah, that's right. I remember that now.

Like, the antivirus software wasn't run on a weekly schedule, which I think NDIS recommended that it was run on a weekly schedule or something. Yeah. Yeah. I think it was updated, you know, to ensure that it was being run.

Q. All right. And then are you familiar with the corrective action that was required because of the lack of maintenance on the quantitative instruments at your lab, the 7500?

A. Can you remind me what -- I -- what the maintenance that wasn't being done was, and I can

probably tell you?

Q. It required semi-annual maintenance. And it hadn't been maintained for probably two years or so.

A. Okay. Yeah. I'm aware of that.

Q. Okay. Can you tell me a little bit about -- about that?

A. I would have to go back and look at that corrective action, because that's been -- mind you, it's not the only one I've -- I can't remember where it was at in the --

Q. I think it was in 2012. But -- so you're saying there's more than one of those instances where --

A. Excuse me. You're asking me -- you're asking me for many years of --

Q. Sure.

A. Yeah. And I honestly can't remember.

Q. Well, was there one incident, if you recall, or more than one incident?

A. There's probably -- there's probably been instances with other equipment, but it's not anything that was major that would affect the results.

But do you remember what the CAR number was? It was -- it should have it at the top of the form.

Q. 12-04?

A. 12-04.

I see 12-03, and then it goes to -- oh, there it is. Okay.

Q. Okay. And it looks like the quantitation instruments had not been maintained for, it looks about --

(Loss of video signal.)

(Court reporter asks for clarification.)

Q. -- about two years.

A. Yeah. I mean -- yeah, that's correct.

It was -- it was corrected. And I think this was something we were anticipating that the people that were coming in and servicing our instruments were doing. Which, mind you, they come in and service our instrument, and they sign off on your instrument that it's working within specifications. So we assumed that they were doing this.

And so it was actually added back in.

Also, it was not done -- I wouldn't be too concerned, because every -- every run that was performed, we run what's called standards. It's a solution of DNA. And they have to have a certain value for it to be accepted.

Every single run had acceptable values to be accepted. So it was still -- it was still running efficiently. It's just like -- for example, you get a

car, and you go in for an oil change. And you're supposed to be getting an oil change. And you don't get an oil change for a while, your car still runs. You know that's the suggested time. It still runs.

This is just a means to check to see if everything was still working. And, actually, when it was checked, it was still -- everything was still working appropriately. It didn't really affect anything, but it was definitely outside of our policy, because it was not being followed.

Q. Okay. If I don't change my -- the oil in my car, then it's -- according to my maintenance manual, then my car is not going to be running at optimal performance. If I'm supposed to be changing it every 5,000 miles and I don't change it for 15, 20 thousand miles, right, then my vehicle is not running at optimal performance; right? I mean, that's the purpose. That's the point.

A. Well, that would be one point. But you're also -- you're also looking at your gauges, et cetera, to tell you your car is still working appropriately.

And we have standards in place that are showing that actually everything was still working appropriately. So it was nothing -- nothing that I would be concerned about, but it was not being followed.

But it still didn't have any impact on anything.

Q. But it was a Level 2 nonconformance; correct?

A. I don't know what that got put to. Let me see.

Yes.

And -- and part of this, now, is, like -- and one of the things is, this is good, because you now add this to your procedure so it doesn't happen in the future.

Every year, we have equipment audits, where we actually are checked, the maintenance, you know, procedures and everything. This is in addition to being audited by the outside. But we actually audit -- just -- an example, just for equipment. You know, we have audits just for reagents, you know. So --

Q. Okay. And then there's -- it's CAR Number 14-7, which apparently it looks like there were over 40 instances of refrigerators/freezers being out of acceptable temperature range. I believe that was also a Level 2?

A. Which one is that? 14-7, you said?

Q. 14-7, yes, sir.

And I guess my -- my question is, what's the policy and procedure on ensuring that the refrigerators are kept within that certain temperature?

A. Every one of our refrigerators that's critical

has temperature monitors on them. And when they go outside of the range, they are -- notifications sent that go directly to our supervisor and to our lab director.

Q. Okay. So if there were 40 instances of the refrigerators/freezers being out of acceptable temperature range --

A. I'm telling you what the policy is now.

Q. Oh, okay.

A. I would have to see what --

Q. Okay. So back in 2014, it did not directly go to your supervisor if something was going on with the refrigerators or freezers?

A. I don't know that for sure, but I know it does now.

Q. Okay.

A. I'm trying to find -- find this for you so I make sure I tell you correctly.

Q. It's CAR Number 14-7.

A. I know. I wish this document was searchable.

Q. Yeah. It always makes it easier.

A. Oh, there it is. 14-7.

I'm sorry. I'm not finding that. Do you know if -- do you know if it's in the Part 1 of the PDF or Part 2 or --

Q. I would assume Part 1 but, honestly, I don't know, because I had to upgrade.

A. Okay. No problem.

Q. It's okay. We can move on. It is 14-7. And I'm reading directly from the -- from the document, so.

A. I'm also there, I think.

Q. You think?

A. Maybe not.

Yeah, there it is.

Yeah. The -- if you read in the CAR -- yeah. It was outside the range. So it's in our procedures. But the range was still outside what was recommended by our kit storage.

Q. Okay. And then I'm going to move on to Corrective Action Request or CAR 15-04.

It looks like Level 2 nonconformance in September of 2015, where there were nine instances in which the required equipment maintenance, and in parentheses, DNA autoclaves, DNA drying cabinet, tox centrifuges were not correctly documented in the instrument and maintenance logs.

Are you familiar with that, as well? If that's --

A. No. Some of these -- like the DNA drying cabinets, that one is funny. We never use that. That has never been used. So we actually just recently gave

that away.

Originally, when we purchased that for the laboratory, we thought we was going to need it for, like, drying swabs or bloody evidence. And we never used that.

But, either way, there was some maintenance that we said we would follow, you know, but it wasn't followed.

Q. And why would it be part of this corrective --

A. Yeah, it would have been part of this corrective.

The centrifuges, the tox centrifuges, and I don't even know what PCMS pump is. But that's outside of our lab.

Q. Okay.

A. I'll find it. Yes, outside the DNA section.

Now, the autoclave, yeah, that was just -- yeah, that was not documented.

Q. Okay. On that -- I'm sorry.

On that complaint, corrective action request --

A. Yeah.

Q. -- there's a bunch of documents that are attached regarding instrument equipment, maintenance, and things of that nature. And it appears to be almost as if there was maybe a PowerPoint that was created. Was there a training involved for the technicians --

A. Yeah.
Q. -- on that?
A. It was training for everybody, actually, on that one, if that's the case.
Yeah, it was just a reminder to everybody that when you do the maintenance, you actually sign off in the book or the maintenance didn't happen. It's not necessarily that the maintenance wasn't done --
Q. Right.
A. -- but like anything -- like anything, if you didn't document it, it didn't happen.
So it was pretty much a training to remind everybody to sign the book when they complete the maintenance.
Q. All right. So I'm going to skip to 2017, July of 2017.
It appears that -- I wish we had Bates stamps, but I don't.
Several profiles, DNA profiles, were uploaded to CODIS based on -- it looks like a K9 search. And that those profiles --
A. Don't get me started about this. I think they're probably wrong on this.
One of the things that --
Q. Give me one second.

And it appears that those profiles were determined to be ineligible for entry into CODIS without -- it says without additional information. It looks like DOJ got involved in this complaint --

A. Well, it was --

Q. -- corrective --

A. Well, it was the result of an Office of the Attorney General visit. And their people, their auditors, decided that -- so, for example -- okay. Your house is robbed; right? And so the guy takes off running. And then they see a piece of clothing. They get a K9 out, right, to go track down the suspect.

As they're going down -- the suspect -- where the K9 is leading, the K9 leads them to a piece of clothing where they believe their guy may have struck off.

So with that, we would take that piece of clothing and put that into CODIS. They would determine that the K9 was not a reliable source to make that determination that that piece of -- that -- that item was associated with the crime. So we couldn't put it into CODIS.

That was their determination.

Q. Okay. So I'm looking at the audit of compliance of standards attached to that where it appears to indicate that the -- they just indicate that there was a lack -- there was a lack of sufficient

information in the forensic case file to support eligibility.

So are you saying that it was because the K9 was involved or because --

A. That's what they originally -- they said -- they said that that was not a means. There has to be other adequate information besides just a K9.

Q. But that's not in -- in their report.

Was it because there wasn't enough information or data or loci in the DNA profile that were uploaded or attempted to be put in CODIS or NDIS, and it wasn't -- it wasn't eligible because of that?

A. Yeah. We might not be talking -- because we had results where, like, the K9 was not -- I'm looking at these and this is -- may not be the one I'm thinking of.

Q. I mean, it does reference K9, but the K9 issue doesn't seem to be what the issue is for DOJ.

A. Oh, yeah. It was just an issue of -- and they believed that we didn't have enough adequate information for some of the samples.

Q. I'm sorry. Say that --

A. Which one are you referring to? And I can probably explain it a little bit.

Q. Well, could you say that last statement again?

A. Which one are you referring to? And I can discuss it.

Q. Prior to that, about the samples, inadequate information in the samples that were uploaded.

A. Yeah. You're talking in reference to the -- oh, the profile sample we found in the profiles?

Q. I'm talking about in 2017. 17-7 would be, I guess, the CAR or the case, the corrective action request.

A. Yeah. It was just their determination that we needed additional information.

Q. And how was --

A. Because one of the things that -- I'll try and explain. The -- in order for a sample to be put into CODIS or the national database, one, the sample has to be associated with a crime.

Q. Okay.

A. So it can't be just from an innocent.

Also, it can't be something that's removed from a person. We'll constantly get, like, can't you put this gun we took off of this suspect into CODIS? No, because it was physically removed from the person, so it can't be.

So we have to be able to show there's documentation that a crime has occurred, there's evidence it's

believed to be associated with the crime, and it was not physically removed from a person.

So, like, we obtain information from the detectives and make a determination.

And this was -- in our belief, we had enough information. But when the auditors from the outside, they thought we did not have enough information, and they wanted more information. So that's all this was. They didn't believe that we had some information that the sample was either associated with the crime scene or --

Q. And based on -- based on -- upon that, what corrective actions did your lab take?

A. We removed the sample that they -- that they -- the detective from the -- from the national database.

Q. And then what about any policies and procedure -- procedures that were changed, or were they?

A. Yeah. Let's see.

Well, one of the things that -- we get training every year on CODIS eligibility. So all the staff was trained on -- again, on CODIS eligibility. And we also receive training once a year from the database on CODIS eligibility.

Q. Okay. So there was a retraining of the staff at your lab?

A. Yeah.

And -- yes, that's why I remember this, because the big -- the big issue with this is -- for us, is the K9 tracking, I'm still not convinced that they're right on that, because I think you can use the K9 to show that that's -- but -- so we've now not -- we don't put samples in when it's a K9.

Q. Because in your mind, it wasn't taken from the suspect. It was -- it was found by the K9; is that --

A. Right. It's still associated with the crime. The guy, you know, it's not -- it's something left behind by -- left behind by the suspect. It was just a secondary means to get there with the dog.

But the FBI actually agreed with us, but the OAG made the determination that we couldn't put it in.

Q. Understood.

All right. And then I think we briefly discussed the antivirus software issue. And it appears to be on the main CODIS server computer that wasn't maintained for three weeks. It looks like it appeared -- or this occurred in 2018. And we already addressed --

A. Yeah.

Q. -- that. We don't need to go through that again.

A. Okay.

Q. I'm assuming there was -- it looks like there was some additional training that was done.

A. I'm sure -- I'm sure there was.

Q. Yeah.

All right. And then there was another -- this is going to be 18-12. Actually, 18 -- yeah, 18-12. The date initiated --

A. Okay.

Q. -- would be August 15, 2018.

I'm sorry?

A. Yes.

Q. It's regarding the report writing, where you guys were using the word conclusions, instead of opinions?

A. Yeah. And the funny -- the funny thing is, now they've changed it back.

So now they're -- one of the PSP standards changed it back. But, yeah.

So it's just -- at the end of our report, you'll see --

Q. Interpretations and opinions. And now --

A. Yeah.

Q. Is it changed back to conclusions or something -- or now?

A. Yeah. It's actually -- well, let me see.

Yeah, it's actually -- oh, it says interpretations and opinions right now.

Q. Inter --

A. Interpretations and opinions.

And so, yeah, they actually -- I think it was they said you had to have a separate section with that, is what happened.

To me, it's semantics as long as you're accurately portraying that information. But, yeah, it's just wording of conclusions versus interpretation and opinions.

Q. All right. And then there's another complaint and observation in September of 2019, regarding reagents that had not been quality checked by the analyst prior to use.

A. Which one was that one?

Q. 19-10, it looks like?

A. It's probably on the CAR, too.

Q. The date initiated is 9-12-2019.

A. Okay. Let me read it real quick.

Q. Sure.

A. Yeah. This is -- this is semantics, because they were against policy, one, because our policy stated that it had to be signed off by an analyst. So we had our technician. So the technician could do the work,

but the analyst had to sign off on it. And that's what was not being done.

Q. Because a nonanalyst was performing the quality checks?

A. Even though the technician -- the technician is qualified to do it. But our policy said that it had to be signed off by an analyst. So that was the issue.

So it was being done. It just was not being documented by an analyst that --

Q. The initial testing shall be completed by an analyst if a nonanalyst does the initial preparation.

A. Right.

Q. And that, apparently, affected both the DNA section and the chemistry and toxicology section of the Pinellas County forensic lab.

A. Yes.

Q. And then I think we've also touched on this as well, about contamination control. This is a corrective action request, 20-01, May of 2020, analyst being retrained in contamination control.

Was this the same analyst? I think it was Rachel Watson or Watson, Ms. Watson?

A. I don't know if this was -- yeah. I don't know if this was Watson or not. I'm trying -- we probably wouldn't have said a name in here.

Which one is this? 20-01, you said?

Q. It's 20-01. Date completed, May 26th of 2020.

A. Okay.

Q. It looks like there was a policy/method change as well.

A. Yeah. No, this was a -- let me make sure I've got it right.

No, this wasn't Jennifer Watson.

Q. Okay.

A. I remember this. This was Ryan Satcher.

Q. Ryan Satcher, the prior CODIS administrator?

A. Yes. I remember -- I remember this.

Yeah. He had -- in his work, he had a transcriptional error, which caused a few samples to be mixed up. And that was it. That was what happened in this case.

And so when we reviewed this, the only way you could have prevented this is when you suspect it -- you can see discussion with him. He believes there was a transcriptional error, and proceeded.

The only way is -- if you think there's a transcriptional error, in fact, you just need to go back and suspend that analysis, and start over. That's the only way to be really sure. So I think that's what that policy change was for.

Q. And then Corrective Action Request 20-02, date initiated August 5 of 2020. Perhaps this is Watson. I don't know. Where an analyst contaminated their own samples during extraction. They had previously explained that.

Yes. This is Jennifer Watson, so I'll, I think --

A. Yeah.

Q. -- skip that.

And that included quite a bit of documentation.

And then I'm going to ask you about 20-08, date initiated 9-10 of 2020. It looks like there was an external quality assurance audit provided by -- or conducted -- in 2018, by ANAB regarding whether or not --

A. What's the number for that? 20-09?

Q. 20-08.

A. Oh, 20-08.

Q. It says the YSTR.

A. Oh, yeah. Okay.

Q. Got that?

A. I haven't found it yet, but --

Q. Okay.

A. -- if this is the one you're talking about? This is in relation to YSTR?

Q. Yes.

A. Okay. They provide -- actually, the audit -- the auditor screwed up on this. Because they are -- we send them a list of what we're qualified to do in our laboratory, qualified STRs, YSTRs. Okay? So when they provide auditors, they are supposed to provide us auditors that's qualified in --

Q. If I could just interrupt you for one second?

When you say they, just for the record, who are you referring to?

A. I'm not sure who we reached out -- usually, it's, like -- I'm not sure who it would go through.

Q. So --

A. It would be through ANAB, I would assume.

But the auditors they provided us, they gave us an auditor, which is our lead auditor, that stated she was qualified in Y, but never was qualified.

Q. The auditor was not, you said?

A. Yes. That is correct.

And we didn't find out until -- we found out later on, when we -- because I had to review her documentation. And after I was reviewing her documentation and I was looking at the audit, I can't see where she's qualified in Ys.

So that's what this was about. They sent us an auditor that was not qualified.

So, now, we require documentation -- and this went all the way through the --

Q. Uh-huh.

A. -- through the FBI. They were really, like, upset about this because --

Q. Well, like --

A. -- they never sent us somebody that wasn't qualified.

Q. Right. So I guess my question is: ANAB is one of the accreditations, right, for your lab? So their --

A. They had to write a corrective action. They had to issue a corrective action, theirselves, so this would not happen again.

And, now we require -- now we require -- I have to review documentation of any auditor prior to them coming.

Q. Okay.

A. So --

Q. So it's your position that the very body that accredits your lab sent you someone that was not qualified to do an external audit?

A. Only in part of the process. He was qualified to do it in the STRs but not Ys. Yeah.

And I know even had they -- they also, like us,

will have to do corrective actions. If something is outside their policies and procedures, they ended up having to do a corrective action for this, too.

Q. All right. Then I want to draw your attention to 20-6.

A. What one is it? 20- --

Q. 6.

A. I'm sorry. Okay.

Q. Okay. And I'm just going to read -- perhaps this will jog your memory, because I'm kind of unsure what this really means.

PCFL submits very few UHR profiles into CODIS, so staff forgot the policy to remove partial loci for UHR profiles when submitting into CODIS.

A. Yes.

Q. What does that mean?

A. Okay. We are probably one of -- everybody stopped processing across --

Q. Across --

A. -- Florida, okay? So UHR is unidentified human remains.

Q. Okay.

A. So when you enter an unidentified human remain into the CODIS portion, there is actually a partial indicator. And so when people are entering and they

were not clicking the box that this was a -- at a particular location, this was a partial result.

Q. Okay. So, really, if I --

A. This was not forensic samples. This was from -- they find a body in the ocean, in a skeletal, in the process of bone, we will run that through CODIS to see if we can find a relative of the missing person.

They -- when they entered that in, they forgot to check the indicators when there was a partial result at a particular location.

They were not for forensic cases, but they're for missing persons or unidentified human remains.

Q. Right. Right. Right. Right.

Okay. All right.

All right. And then another one, 20-4, date initiated August 19th -- and I know some of these are not in order. I printed them out.

A. I don't think they're in order here, either.

Q. Yeah. It seems -- it appears that way.

Date initiated, August 19th of 2020, where it looks like your lab did not -- or the Pinellas County forensical lab did not retain CODIS database backup data from 2-15-2020 to 4-9 of 2020.

A. Yeah.

Q. Lab did not meet the minimum CODIS encryption

requirements for the dig -- digital signature and hash.

How was that rectified?

A. I know it was, but I can't remember offhand.

I'm trying to find that one.

And you know how you're trying to remember some of this stuff, and it's like --

Q. Sure.

A. The -- I know it was a big deal with the encryption, because hardly anybody could meet that requirement because of the way they set it. And then I think it was rectified.

Let's see. Let me see.

Q. Yeah.

A. Okay. And this is more on the CODIS people than me -- CODIS administrator than me.

But it just says that they switched from digital signature and hash -- I'm not quite sure what that is -- to switch to an SHA512 encryption.

Q. Okay.

A. Which I think that was part of the problem, was, like, they were -- the FBI was telling everybody they needed to do there. And everybody was, like -- no one knew how to do this.

But I think that's been rectified. And -- and had been just rectified by backing up the logs.

Q. All right. You had indicate -- indicated that Beecher no longer works for the Pinellas County forensic lab. But Beecher was responsible, it looks like, for one, two, three -- four separate reports for body fluid identification. And I'm talking about -- for the record, it would be --

A. Yeah. Yeah. I think you're right.

Q. -- laboratory report date March 29th of 2023, and then lab report date -- and this is for Beecher -- April 4th of 2023. That will be Request Number 3. And then Request Number 5, which is dated -- report date of 4-25 of 2023. And then request 6, which has a report date of 5-10 of 2023.

And the other reports would have been --

A. Mine.

Q. -- yours.

A. Yes. That's correct.

Yeah. And that's a Level 2 request.

Q. Okay. So --

A. Mine. Mine.

And there's additional two requests that I just completed, like, yesterday or so.

Q. Oh, so there's two more reports that were done?

A. Yes. Correct. They just -- just -- just got

done.

Q. All right.

A. So a serology report and a DNA report.

Q. All right. Let's just talk briefly about phenolphthalein, because that appears to be what was used -- and I'm looking at Beecher's first report.

What's the brand of the kit that's used, and was used in all of these fluid -- fluid identification reports?

A. Would you repeat that? What was --

Q. What kit? What's the name of the kit? Is there a specific brand name, the kit that's used?

A. For the serology?

Q. Yes.

A. It's just phenolphthalein. It's just -- it's just chemicals. Yeah. It's actually chemicals we make up in-house.

Q. All right.

A. Yes. That's known, that's been used for 40 years or more.

Q. Is that the Kastle -- Kastle-Meyer? Kastle --

A. Yeah. The same exact test, just a different name. Yeah.

Q. All right. And are you familiar with the false-positive reactions for phenolphthalein?

A. Yeah. Quite a few.

Q. Tell me about that. Tell me about that.

A. Anything that causes an oxidative reaction can cause a -- a positive reaction. A lot of times, sometimes bleach. Anything that has a peroxidative activity.

Yeah. It's a presumptive test. It means it's presumptively blood, when we say blood is indicated, which is another term for presumptive. It's a confirmatory test for blood. It's used in our laboratory. It's really a --

(Court reporter asks for clarification.)

Q. Confirmatory?

A. Yes.

Meaning that this is absolutely blood. It's used in our laboratory more as a means to determine what samples to take forward to DNA. It's an indication that there was blood there, but it's not an absolute that that was blood.

I mean, it's red, reddish-brown staining, indicating it -- it presumptively tested positive for blood, like an assay, but we cannot say it's positively blood, no.

Q. All right. And there's numerous other things that can cause false-positive reactions. You had

indicated --

A. Yeah.

Q. -- bleach, iron --

A. Yes. Anything that causes it to oxidize is going to give a false-positive. Yeah, bleach, iron.

Q. Can urine also create a false-positive?

A. It's been a while since I researched. Maybe. But at the same time, you may have a little bit of blood in your urine, so maybe it's not.

Like, I would have to -- I would have to go back and look at the literature. It's been a while since I --

Q. A false-positive. If it's just urine and there's no blood, then -- right?

A. Then I would -- yeah. I have to go back and look at the literature and see if that's something. But possibly.

Q. And what about blood from an animal? Can that also cause a false-positive as well?

A. Well, that's not necessarily a false-positive --

Q. Okay.

A. -- because it's blood. It's just not -- it's just not positive for -- it's not -- it can still be a correct positive result. It's just not human.

Q. Understood.

A. Yeah.

Q. All right. And in your mind, what does a weak phenolphthalein result mean to you? Is it --

A. It's a very weak color, a very weak color change.

Q. And when you say weak and I say weak, that's kind of a subjective observation.

A. Not immediate change. Not a dark -- not a dark color change. It's just lighter. You know, because a lot of times, the amount of blood that's present could be indicative of how quickly something turns or -- or the amount of material that's there.

So when it's weak, it's just -- and it can also be indicative when you see a weak result, you get the result and it's not the best result that coincides with the results you got. Serology says unexpected. If you got a pretty positive result, kind of, you should expect to get somewhat of a decent result downstream.

Q. All right. And what is TNB?

A. TNB is something we're no longer using. It -- it's just another alternative method for blood determination. A lot of times it's used when the color change cannot be detected because the material that the color is changing from, you can't detect because it's

the same color. So you could use TNB, which is a greenish color change, so you can actually be able to see that.

Q. Is that --

A. We brought that back online because this was one time that -- I mean, it's a valid procedure. We just -- it was not typically used because it was not needed to be used.

So this is one of the few times that it actually was needed to be used because of the material.

Q. And in using that, that was a deviation from the policies and procedures at your lab; correct?

A. Yeah. Just to bring it back online. It was already, you know, essentially validated. It's been used for many years. It's just that we took it out of procedure because we're not using it much.

Q. When you say essentially validated, what do you mean by that? I mean --

A. Well, essentially -- it was validated. If you go back and look at the validations, you'll see that the TNB was validated originally with the phenolphthalein.

Q. All right. And what about the training of your analysts?

A. They were all trained. They were all trained in that, the use of TNB.

Q. Okay. Training when it was being used, but --

A. Now, the analysts that are hired now would not be trained in that. But she was trained in use of TNB.

Q. When you say she, you mean Beecher --

A. Yes. That's correct. Yes.

Q. -- was trained?

What about her competency in the use of TNB? Do you know whether or not -- well, do you know the time frame of when her competency was tested in relation to this policy deviation, April of 2023, where TNB was --

A. I don't know the time frame, but it would have been right before -- you know, in part of her training, she would have had competency within TNB. But I'm not sure. It was right before she became a serologist. So I'm not sure what time that is.

Q. And do you know why this deviation from policy was done?

A. Because we took that -- we took TNB -- because we were reviewing our policies and procedures. We were like, we never use this policy and procedure. So we saw -- and we never used it. We're still having to retain the reagents.

So in doing so, we decided to take it out of the policy because it had a limited use. It's limited when you're looking at something and you cannot tell the

results of the change because the color you're looking at is masked by the color. So you can't tell if it's positive or negative.

Q. Let me ask you now. My question was: Why was this policy deviated from?

A. Because -- because of that fact. Because it was something that, after review, she, I believe -- in this case, was letting me know that she couldn't determine if this was positive or not because of the material that it was on.

And so it was my recommendation that we bring back TNB so you could actually use it as a method to determine, because you could then see the green color change to see if it was presumptively blood or not.

Q. Okay. You mentioned reagents being -- I can't recall the -- the word that you used, but you -- the reagents for TNB being kind of kept up or -- or --

A. Right. We had to remake those reagents and QC them before using them in this case, yes.

Q. All right. Specifically for this case, you made the reagents for TNB?

A. Yes. That's correct.

Q. All right. Has that been done after in any other case that you're familiar with, this policy deviation?

A. No. No. Because like I said, it's just unusual. It has a limited purpose that we just -- it just happened to be -- had a purpose in this case.

Q. All right. All right. So let's go through -- okay. Okay. So I'm going to ask you some questions about --

A. Sure.

Q. -- your lab report dated April 3rd of 2023, wherein you analyze some buccal swabs that were received from Michael Montgomery, which would be Item Number 2; Item Number 3, which was a toothbrush represented to be from S. Cozzi; Item Number 4-A, rim of mug, represented to be from S. Cozzi; Item Number 5, which is a swab from the Toyota tailgate, and then Item Number 8, which was a swab from the middle garage, Number 2.

And it appears as if, according to your report, the results -- all of those items resulted in a -- well, strike that.

The first four items, 2 through 5 -- 2, 3, 4, and 5 -- resulted in a DNA profile. And Item 8 resulted in a DNA mixture.

A. That's correct.

Q. All right. The toothbrush, Item 3, that was represented to be from S. Cozzi, am I correct in indicating that his DNA profile -- well, why don't you

tell me. When was his DNA profile developed? What date?

A. Well, I can't say it was his profile. It was a toothbrush that was represented to be taken from him.

Q. Yes.

A. Is that what you mean?

Q. Yes.

A. Do you want the date that I got his profile? Is that what you want?

Q. What's the date that you developed the profile that would belong to this toothbrush?

A. One second, please. Hold on.

I just need to open the data up, so I can give you --

That would have been -- I would have made the interpretation on that on March the 31st of 2023.

Q. March 31st of 20 --

A. '23.

Q. -- '23.

All right. And then the DNA profile that was obtained, developed from the buccal swabs that Item Number 2 from Michael Montgomery, can you give me the date when that profile was developed?

A. Michael Montgomery?

Q. I have March 30th of 2023. If --

A. Well, you asked -- you asked when I was able to develop a profile. But my interpretation is that date. The actual dates on the electropherograms, when I did it, was all on March the 30th, '23.

Q. Okay. So then it would have been the next -- understood.

A. Because what you're looking at is the allele call table where I actually made an interpretation based upon that data. That's the date I gave you first.

Q. The electropherograms; you're correct.

A. But for the electropherograms, it would be March the 30th, for all the samples.

Q. March 30th for the buccal swab. So Item 2, Item 3, and Item 4? And then Item 5 as well?

A. Yes. Item 5 and also Item 8.

Q. Okay. So let's -- let me direct you to the electropherograms on the swabs from the Toyota tailgate. It looks like it's 5-A-1?

A. Uh-huh.

Q. How is that -- why is that labeled 5-A-1, as opposed to Item?

A. Instead of 5?

Q. Yes.

A. Okay. It's just -- the individual item that comes in is listed as a cloth from the tailgate. It was

Item 5. It was an actual swab.

So when I'm trying to process, 5-A would be my actual substrate. Okay? So that's the piece of cotton that I used, that I'm saving. And the extract would be 5-A-1. So that's what's taken from the substrate.

So when you're looking at the chain of custody, you'll see 5-A, 5-A-1, which is the substrate. And the extract is coming from that item.

So our numbers get carried through. 5-A-1, that's the extract carried through all the way. But when you report it out, you're reporting it back to the original item, which is the swabs.

Q. All right. Maybe I should back up for a second.

And I'm going to ask this for all of the reports that you authored: How much of the forensic DNA analysis did you perform? Did you -- from the extraction, amplification, to uploading the information into STRmix, did you perform all those steps, or were other individuals involved?

A. Everywhere where you see my name on the report, I was fully involved.

Q. Okay. So extraction --

A. That's correct.

Q. -- amplification --

A. Yeah. All the way through detection and separation, it was interpreted, yeah.
Q. So you performed everything?
A. That's correct.
Q. Okay.
A. What -- the ones where my name is on the report. Minus Desiree; that's right.
Q. I'm sorry. What was last statement?
A. Minus the reports where Desiree was the serologist. You know, of course, she's the one that performed that work. But anywhere you see my name, I performed all of the work involved.
THE COURT REPORTER: What was the name of the serologist, please?
THE WITNESS: Desiree Belcher.
THE COURT REPORTER: What was it?
THE WITNESS: Desiree Belcher.
(Discussion off the record.)
THE WITNESS: Belcher.
THE COURT REPORTER: Belcher. Okay. Thank you.
MS. TUOMEY: Isn't it Beecher?
THE WITNESS: I am so bad with names. Everybody always picks on me. We'll get an intern, and they'll be like, you'll never remember her

name. So I'm horrible with names.

Q. (By Ms. Tuomey) All right. So I want to bring you to, I think, prior to this tangent here we went off on.

The electropherograms for the swabs on the tailgate, 5-A-1, which is a substrate from the swabs themselves --

A. It's actually the extract from the swabs. That's what you're -- there's what your data is taken from, is what the 5-A-1 represents.

Q. Now, it's my understanding that your lab uses across the board for all of the different five dye colors in GlobalFiler, you use 50 RFUs as your analytical threshold.

A. With the exception of the internal link standard. It's 100.

Q. I'm sorry. Say that again.

A. Except for the internal link standard, the orange dye.

Q. Oh.

A. That's 100. But for the actual --

Q. Okay.

A. -- alleles, you're looking at 50 across, yeah.

Q. And my question for you: Are you familiar with the effects of how these different color dyes

refract and are picked up by the genetic analyzer differently because -- just simply because of the different color?

A. Yes.

Q. Like there's other -- okay.

Because there are other -- there are other labs -- and, also, whether it's a large autosomal STR, versus a small one. That's kind of a side note.

There are other labs that use different RFUs for the different colors. Higher, lower. And yours -- your lab's seems to be quite low.

A. Yes. And the reason for that is because when I -- when you're looking at determining what they call the analytical threshold, you have to take, like, a series of native samples. And you put them through multiple times. And I have to analyze the data at one RFU.

So I have to go through every one of those points and determine where the -- you know, each of these points is at, outside of the bench, which is just because -- or known artifacts.

And based upon that, I may end up giving an average of the RFUs observed. And then I'm taking it out to 10 standard deviations of the average. And that's where the numbers come from.

And then the numbers are rounded up to 50. It actually could be a slightly little bit more -- lower than the 50, but it's rounded up for ease's sake, up to about 50.

Other labs that are having slightly higher are typically using the analytical to avoid going through artifacts, which is actually against what SWGDAM recommends as you should set your analytical threshold high to avoid artifacts.

So that's maybe one of the reasons that you see it a little bit higher, because they just try to make their lives a little easier.

Q. Higher, but they're different for the different colors, is my question.

A. Sometimes.

(Overlapping speakers.)

A. Sometimes. But in all the times I've been here and analyzed the data from various kits -- because we used to have what we call an IdentiFiler kit, IdentiFiler-Plus kit. We had a MiniFiler kit. We had a YFiler kit, YFiler-Plus, and then GlobalFiler. And all of those kits have been pretty close to the same.

Q. And what about the validation for GlobalFiler, which is the five-dye kit? What does it recommend in determining what the correct or appropriate or, you

know, appropriate RFU for each of the different colors?

A. I would have to go back and look back and see what they recommend. But it's not really about what they recommend, because they're not the ones that actually are governing us. It's actually the scientific community which tells us how we need to define what an analytical threshold is.

So laboratory -- and I'm sure what they're probably saying in the manual is, laboratories need to do their own studies to decide. So there's studies out there that shows a laboratory should define what an analytical threshold is.

Q. Well, what is your stochastic threshold?

A. Well, it depends.

Are you talking binary or are you talking STRmix?

Q. Well, STRmix is a whole different thing.

Binary.

A. 400. And it's 400 based upon -- I think it's based upon TPOX locus. It ends up being around 400.

Q. And TPOX is one of those larger -- larger --

A. Yeah. It's just a crap locus, yes.

Q. Yeah.

A. And that's the -- it's there mostly for historical purposes. You know, it was always in the original kits, the CTT kit and then in the CCTV. It was

always there, so it was just kept over. But --

Q. You had indicated that, you know, a lot of labs don't want to use that lower threshold because they don't want to have to deal with all the stochastic effects, the noise, the artifacts, whether they're biological or technical.

So my question for you is specifically regarding the swabs on the tailgate, Toyota tailgate, 5-A-1.

A. Right.

Q. What, if any, data was removed from this electropherogram?

A. Removed?

Q. Yes.

A. Nothing.

Q. No data was removed whatsoever?

A. Nope. You're talking about the -- the swabs from the Toyota tailgate; right?

Q. Yes.

A. Yeah. You're -- because -- yeah. I'm looking at E-grams. What is represented in the E-grams is represented there.

And I would have to -- let's see.

Yeah. There was absolutely nothing removed.

Yeah. There was no edits whatsoever on this.

Q. All right. So if you look -- let me find one

for you to kind of --

So if you look at -- and this look -- it looks like it was done -- this is an electropherogram done on May 4th of 2023. It was Item 23-A-1, men's bathroom floor --

A. You're asking about the spot on the tailgate 5-A; right?

Q. I understand.

I want you to look at the electropherogram, a different electropherogram.

A. Okay. Which one?

Q. It's 23-A-1, the swab from the men's bathroom floor PMH.

A. Okay.

Q. Do you see that? Are you looking at it?

A. Give me just a second. I have to figure out what request it's on. You're looking at 27?

Q. 23-A-1.

A. The no result?

Q. I'm sorry?

A. 23-A-1?

Q. Yes.

A. The no result?

Q. Yes.

A. Yes.

Q. So my -- I guess my question for you is: And you're indicating that no data was removed from Item 5-A-1. But if you look at the electropherograms associated with 23-A-1, there appears to be a lot of noise, things of that nature, on these -- on this electropherogram, as opposed to the 5-A-1.

What -- what do you -- how do you account for the difference in that? Was the threshold lowered in the 23-A-1, or --

A. You're looking at two different scales.

Q. Okay. Explain that to me, please.

A. Okay. You're looking at the scale from the 5-A-1. You're looking at a scale of about 4 to 8 hundred on the left-hand side. You'll see those numbers.

Q. Yes.

A. So if I erase it, you're going to see the same threshold below it. But everything is the analytical of 50. It's only going to call above 50 RFUs.

So if you go back to the -- the 23-A-1, you'll see that scale is set to about 100. So what you'll see is you'll see more of the baseline. You'll see more of that -- that. I set that up for clarity so you can just -- so, visually, you can see if there's any data below, peaks, whatever.

But when you go to the 5 -- 5-A-1, the scale is set so you can actually see the top and the bottom of the peaks that were observed. So it's just a different scale.

Q. So the scaling is different. You didn't just --

A. It's the -- the scaling is different by the software.

Q. Okay. You've got to wait for --

A. When I print it --

Q. If you could just wait for me to finish so that I can finish my thought. And I apologize.

A. I know. No problem.

Q. So -- so am I correct in indicating that the 23-A-1, the scale is different? Not necessarily that the RFUs were changed or was -- there was -- or there was a deviation from any policy or things of that nature. You just scaled it differently to show the baseline noise on that specimen?

A. That's correct. Like, one of the things with the software -- the software, when you're printing the electropherogram for the case file, you have the option to -- everything gets processed. If it's a peak above 50 RFUs, it goes there, no matter what. That's not changed. That's set in stone.

The only person that can change that is myself. And it has to be authorized even beyond farther to changing our policies, to do that.

Now, so everything is set at 50. The only way to physically change this is -- it's always set at 50.

When you're printing this on the left-hand side where it's like -- you have the option to -- just like you're making a document larger or bigger --

Q. Sure.

A. -- that's all you're doing, is just -- and it's just for printing purposes. If you go back and look at the raw data, you can -- you could -- you could take this one that's 400, the 5-A-1, you could actually scale that so it's the same as the other one, but you wouldn't be able to see the tops of the peaks. That's why they're like that.

It's just for visual purposes. It has nothing to do with the analytical threshold being changed.

Q. Okay. And you told me the stochastic threshold, I think you said, is 400. Am I --

A. The stochastic threshold, it's also -- I also like to use that term, homozygous threshold. It's the point where you can truly determine that the two peaks are present, like we talked about earlier. So, yeah, but it's 400.

Q. Okay. So back to the 5-A-1.

How -- how do you measure -- or what do you do with any peak height imbalances that you see? How do you handle that?

A. Well, you're looking at the level of data, too. If you're seeing big time imbalances, that's -- you try to use that to determine if it's a result in a mixture or if it's single-source profile, so.

Q. Did you notice any peak height imbalances in the 5-A-1 --

A. Well, you can see by your difference of color. When something is highlighted a little bit different, you'll see a green that's a different color. That's usually -- that's an indication that there's a little something going on in there.

So 5-A-1, there's a high imbalance there. And that's really the only peak height imbalance that I would say.

And that peak height imbalance there did not give me cause to think that this is more than one contributor on the sample. More than one contributor, it was probably not influencing the one contributor I'm seeing.

Q. All right. Okay. Hence my question: How do you make that determination when you see a peak height imbalance? Is there a certain formula, a certain thing

that you do with these two peaks?

A. Well, your -- one of the things, I'm looking at this. I'm looking -- am I seeing more than two peaks in any locus?

If I'm seeing more than two peaks in a locus, is that -- what I'm seeing, could that be an indication in the stutter positions as something that's a little bit elevated stutter? Am I seeing imbalances in more than one places? Is the RFU level at a point where I expect to see imbalance? Or if it's not -- yeah. So -- and you make a determination on that. And you make a determination, I believe it's this. A number of contributors is more than one on this.

Then we'll actually use STRmix as an aid to determine, based upon our number-of-contributors assessment. You know, it will actually come back with some diagnostics that actually can aid us in seeing if our determination was correct or favors our -- our interpretation.

Q. So is it -- is it your -- you really haven't answered my question.

But is it your testimony that when there -- when you see a peak height imbalance at one location or one loci or two loci or what have you, that that is an indicator to you that there's a potential of more than

one contributor?

A. I didn't say that. I said it could be.

Q. Could be. Could be.

A. Yeah. That's one of the things that you -- one of the things you look for in a mixture, is imbalance. But imbalance at one locus, that's not necessarily significant. You have to look at the profile, the individual locus and the profile, the results you're seeing as a whole.

Looking at this sample, I really did not see any indications that I believe that there was a mixture. Or if there was a mixture, it was so low level, it was not influencing the results I have -- had above my analytical.

Q. Okay. So when you say low level, did you have a low level amount of DNA that was extracted?

A. I have to -- you mean, like, what was the quantifiable sample?

Q. Yes. Yes. Because you used the word low level, so.

A. Yeah.

Give me a second to open this, please.

Q. Sure.

(Discussion off the record.)

Q. (By Ms. Tuomey) And then, Mr. Summerfield,

while you're -- while you're looking for that, can I ask you whether or not the two new reports that you completed yesterday, have you turned those over to state as of yet?

A. I have completed my report. It went through technical review.

Q. Okay.

A. I am not positive that the administrative review has been done yet, which then it gets released. And it might have been done yesterday or it might be done today.

So -- and the next thing they do is they turn it over to, you know, notifying the state that it can be looked at. So I'm not sure if it's been released yet or not.

MS. TUOMEY: Okay. And I believe Madam Court Reporter wants to break, so then I guess this is probably a good time.

A. It's .01.

Q. .01?

A. Nanograms of DNA. So you're looking at about 10 picograms in the sample.

Q. So this was low-level?

A. Yeah. It was the lower level. Yeah. But that's about the results you would expect. That's about

the results I would expect for that quantification value for that sample. Not low-low level, but it's -- it's -- yeah, these are the results I would expect.

(Discussion off the record.)

(The proceedings recessed for lunch from 11:59 a.m to 1:04 p.m., then reconvened with the same appearances.)

MS. TUOMEY: Okay. So, Mr. Summerfield, I hope you had a good lunch.

THE WITNESS: Thank you.

You, too.

MS. TUOMEY: Thank you.

MR. BRUNVAND: Debra, make sure you start the recording?

MS. TUOMEY: I did. Thank you for the reminder.

Q. (By Ms. Tuomey) I kind of wanted to go back to the -- the scaling we talked about in relation to the 23-A-1, where you said you adjusted the scale, and the scale that was used in the 5-A-1 swabs of the tailgate.

And then my question for you is: If you adjusted the scale on the 5-A-1, would there be more data in the form of either potential stochastic -- just -- either whether it's, you know, analytical or biological, artifacts? Would there be more data if you adjusted the

scale?

A. If you adjusted the scale, there would be no differences with what was called --

Q. Right.

A. -- because the peaks would -- would show anything above 50 RFUs. Without -- without looking at the raw data, I can't tell you if there was any, like, peaks below the analytical threshold.

So I -- I can't say that without looking at the --

Q. The raw data?

A. -- the raw data, yeah.

Q. So that kind of goes back to my question I think I asked you earlier, whether or not there was either -- I guess maybe not the removal of data or data that's not reflected because of the different scales.

A. Well, no. The data would be reflected in the same because -- because the only data that is looked at is -- is data that's above our analytical threshold of 50 RFUs.

Q. Okay. Understood.

All right. So let's kind of move on to -- I think you also testified this is low quality DNA, 01 nanograms on the 5-A-1 swabs of the Toyota.

A. I wouldn't say low quality. It's a low quantity of DNA.

Q. Yes.

A. It's just a lower -- it's below the optimal target. And that's probably, you know, potentially why you see some imbalance. It's not unexpected with the lower amount of DNA.

Q. Would you characterize these electropherograms -- and when I say these, I'm talking about 5-A-1 specifically -- as degraded, potentially degraded, DNA, or how would you characterize it?

A. It was not degraded.

Q. Not degraded. Okay. Because --

A. If you -- if you look at the electropherogram, you look on, say, the blue channel, and you look at D3 versus TPOX, you're seeing maybe a little slight degradation, but not -- the RFUs, when you add them up, are not too much of a difference.

Yeah. There's minimal to no, like, degradation, in the sample.

Q. There's no, like, ski slope effect, which --

A. No. No, no. You would -- yeah, you're not seeing that in any of these channels for this sample.

Q. All right. Let's move on to the swabs from the middle garage, which would be 8-A-1, which I believe corresponds to your report, Request Number 4, which --

A. 2 -- Number 2 and 4.

Q. Number 2 would be the --

A. Initial interpretation.

And 4 would be a supplement comparison to that sample.

Q. All right. So Request Number 4 would be the body -- bodily fluid identification. And Request Number 4 would be your analysis. Am I correct?

A. Make sure -- we're talking about Sample Number -- Item Number 8 in the report; right? The swabs from the middle garage, Number 2?

Q. Yes.

A. Yeah. That -- the original interpretation of that was on my Request Number 2, which was a report dated April the 3rd, 2023. And there was a subsequent --

Q. Yes.

A. -- interpretation on Request 4, which was April the 6th, 2023.

Q. Okay. Thank you for that clarification.

So then we'll start with your report dated 4-3-2023 report or Request Number 2, and then we'll kind of work our way to Number 4.

Let me see. I had it tabbed.

Okay. So, yes. And that would be 8-1-A, the electropherograms that I'm looking at.

A. 8-A-1. 8-A-1.

Q. Thank you, yes. The swabs from the middle of the garage.

So going back to kind of the bodily fluid identification, were you given any information regarding the type of surface of this garage floor?

A. No, I was not.

Q. Were you given any information regarding whether or not there were any, perhaps, rust stains or otherwise that potentially could have been from the undercarriage of a vehicle that may have been stored in that garage?

A. I was not given any -- any indication other than that it was the swab from the middle garage, Number 2.

Q. Do you know whether or not there were any cleaning agents that could have potentially resulted in a positive -- like we discussed before -- a positive phenolphthalein test specifically for this swab?

A. I -- I cannot -- I was not at the scene to collect the samples. I -- that's probably maybe a better question for the crime scene personnel that collected this sample, than myself.

I -- I know no other information about the sample other than it was a swab that was collected from the

middle garage, Number 3. I can't tell you anything about the area, what the garage looked like or surrounding areas or things.

Q. Or (inaudible) that this garage floor was, either?

A. I -- I cannot tell you.

Q. Does Luminol or Bluestar and phenolphthalein cross-react? That is, can one agent cause a positive result in the other?

A. It could cause a potential false-positive, but it usually causes -- the Bluestar, especially, which is a horrible thing to use -- causes downstream effects on amplification and causes a loss of -- yeah, it causes a lot of inhibition.

Luminol usually -- because you think when you're using Luminol, that any stain that was there potentially diluting the sample causes a less amount of material. So that would be reflective of the downstream application.

So there is a possibility of some cross-reactivity, false-positives. More so that those -- those things can affect the downstream analysis.

Q. All right. So loss --

A. Loss of data.

Q. Okay. So loss of data.

Could that loss of data also include potential alleles dropping out when it comes down to the amplification and your analysis? Does that make sense?

A. I know what you're saying.

If -- if that was a situation, then that is a possibility. It could also be just a possibility that it's just the nature of the quality of the sample minus that, too.

So you really couldn't tell if the loss of data was coming from some agent that was picked up with the swab, or if it was actually just because that was the inherent nature of the sample that was collected. You really can't tell.

Q. Is there anything within either the extraction amplification process that would assist you in determining whether or not the Luminol is affecting the phenolphthalein result?

A. If it was affecting and it was causing some sort of inhibition, there is a quantification that actually is -- looks at what's called the cycle threshold value. And if the Ct value is elevated, that can be a sign that a sample has inhibition.

So it indicates that the sample cycle threshold is high enough, then that indicates that we have a potential inhibitor in the sample that can affect

downstream amplification.

In that case we would take the sample and other process, try to clean up the sample and try to remove the inhibitor prior to processing.

So, yes, there is something that's in our quantification method that can help us detect that.

Q. Okay. Do you know whether or not that was done in this specific sample, i.e. the item, 8-A-1?

A. It's done on all of our samples. It's -- you know how I mentioned earlier about we have the small autosomal value, the large autosomal value, the Y autosomal, and the fourth point is the Ct -- Ct. That's for every single sample.

So that is a measure for Ct internal positive control which allows us to see if there's potential inhibition.

Q. Okay. So --

A. It's done for every sample.

Q. Okay. So specific for this sample, did you see anything indicating that there would have been anything affecting the amplification and ultimately the loss of data or your ultimate DNA analysis?

A. Again, you're talking about our sample 8-A-1; correct?

Q. Yeah.

A. Make sure.

No. I'm looking at the quantification results right now for the IPC, the -- and -- the internal positive control. And it's well within range.

Q. Okay. What is the range? What range?

A. Typically, when you start to see stuff getting about 31 to 33, that's where it can show inhibition. And this is at 27.9. So it's well within range that you would not expect the sample to be inhibited.

Q. So that sounds below that -- those numbers that you gave me, I'm assuming -- you tell me -- probably a terrible word -- but is there some kind of margin of error within that threshold?

A. Yeah. Yeah, there is.

Q. So that is?

A. It all depends on your quantitation value.

As you have a higher amount of DNA, that number becomes higher. As you have a lower amount, the number is a little bit lower.

So if you had a sample that was 50 nanograms, then your IPC may naturally be slightly higher, maybe 29, maybe 30. So that's not a real concern. But when it's lower amounts of DNA and you see a value that's in this range, I would not expect it to be an inhibition.

Q. Okay. So the margin of error in relation to

this specific, do you know what -- do you know what this -- that is?

A. I had determined that in one of our validations. I would have to go back. It's -- it's all based upon the variation and the IPC. It doesn't vary a whole lot. It's -- it's --

Q. Like --

A. It could vary, but it's not -- it's not going to vary -- it's not -- on this sample alone, it's not going to vary to the point where it goes from, like, 27.9 to 31, 33. It's not going to vary that much.

Q. But you don't know what that variation is, as you sit here?

A. I do.

Q. You do?

A. It just would take me a little bit to find it in one of our validations.

Q. Okay. And when you say validation, which validation are you talking -- are you talking about?

A. You're talking about the validation of the Quantifiler Trio.

Q. Okay. Is that something that you are able to provide us?

A. You have -- you have it.

Q. I don't think I do. But, okay, I'll look for

it?

A. It's in -- the validation document I sent, it's in there, because I've actually seen it.

Q. Okay. I'll take your word.

A. Yeah. There's -- I think the validation documents we sent you is, like, 22 or 25 hundred pages of documentation, so. And that's not including the data. That's just the raw notes.

Q. Understood.

If a technician obtains -- let's say out in the field obtains a positive phenol -- phenolphthalein -- I'm not pronouncing that correctly -- in the field, and a negative result is obtained in your lab, what is the significance to you of that?

A. No significance because I don't -- I don't really know -- I can't speak for how they test it, their use of phenolphthalein. I can't speak to how they maintained the reagents. How they tested the positive control. Did they test the negative control? Did they test it prior to testing on the samples? I can't speak to their policies and procedures.

Q. Okay.

A. I can only speak to ours.

There also could be an indication if they had a negative result. If they had a positive result, maybe

they took the sample that was the most and didn't leave us with much of a sample left.

So it's hard to say. I have never reviewed any of their policies and procedures on how they conduct phenolphthalein, to make a -- a statement on that.

Q. All right. And would you believe or would you kind of take or would you rely upon a -- I see that the answer to your -- to my question is no. But would you believe or rely upon a positive result obtained in the field, over a result obtained in your lab?

A. I would never -- I never would rely on a result obtained in the field.

Q. Okay. And does rust cause a false-positive for phenolphthalein in the phenolphthalein test?

A. Yes, it can.

Q. All right. So if I could take you back to the electropherograms, the 8-A-1 swabs in the middle of the garage.

Did you notice any -- and this might be a silly question. But did you notice any peak high imbalances in the electropherograms?

A. Yeah. There were some. There were peak high imbalances that can be explained by being a two-person mixture.

Q. Okay. And that leads me to my next question.

Like a two-person -- so the contributors -- would you agree with me that determining the number of contributors to a sample is not an exact science; right? That's something that is done by an analyst subjectively; right?

A. Yeah. I would agree with that, with the exception, of course, it's really straightforward in determining if a contributor is one -- one person. That's simple.

As you go up in NOC, or number of contributors, it becomes much more difficult. As the data is lower for those, it becomes more difficult.

So, yes, there is some -- some variability with NOC.

Q. So it's not an exact science. You would agree with that; right?

A. Well, you never can know the exact number of contributors, like I say, with the exception of one. If you have pretty high-level data, you can feel a lot more confident in your assumption of number of contributors.

Q. Hence the word assumption; right?

A. It's exactly the word assumption. Your -- your statement is only true based upon your assumption of your number of contributors.

But your assumption or your number of contributors

needs to be supported by the data, too. You can't just -- like, for this sample here, I assumed two contributors. I would never assume three contributors on this sample. I have no indications of three contributors in this sample.

So your assumption has to be based upon the data, too.

Q. All right. So you -- you indicated that this, you assumed to be a two-contributor mixture?

A. That's correct.

Q. And no reason to believe that it wasn't a two-person mixture; right?

A. The data supports it being a two-person mixture, yes.

Q. And these are kind of yes or no -- the next series of questions.

A. Sure.

Q. If you look at an electropherogram, if you look at -- let's just take D-8. Would you agree with me that you called four, four alleles, four peaks?

A. Yes. The software called four peaks, yes.

Q. And then on -- at D-21, four peaks as well?

A. That's correct.

Q. And then D-18, four peaks as well?

A. Yes.

Q. As well as FTA, which I know is a large -- larger, more weightier STR autosomal. But four peaks as well for FTA.

A. That's correct.

Q. And SE as well, four peaks?

A. That's correct.

Q. Just give me a moment.

If you could pull up the contributor contribution that was associated with this electropherogram by some --

A. For -- for 8; right?

Q. For Number 8, yes. 8-A-1.

A. Okay. I have it up.

Q. Okay. Fantastic.

Let me just -- okay. So in the component interpretation for that first locus, D-3, it gives you at least one, two, three, four different combinations, four different genotypes of alleles; correct?

A. That's correct.

Q. All right. And I'm not going to go through each one of these.

But what about CFS, it gives you six different genotypes for that STR loci?

A. Let me find CFS.

That's correct.

Q. And then D-8-S as well, it gives you six different genotypes or combinations of alleles as well?

A. Yes.

Q. And I'm sorry for going back and -- kind of going back and forth. I'm not trying to trick you. So if I confuse you, just let me know.

A. No. You're fine.

Q. So at the D-3 loci, the genotypes it gives are four. And that first genotype, 16-18, it gives a 4 -- a weight of 46.

A. Yeah. It gives the highest weight to that -- that combination, yes.

Q. Okay. And the other combinations, in all of these different loci, STRmix gives you a weight -- a percentage of potential -- the percentage it attributes to that contributor if that genotype -- does that make -- kind of make sense? That wasn't good.

A. No. Yeah. It's giving a -- yeah, it's giving a --

Q. A weight to each --

A. When it goes through its iterations and it comes back, it's actually coming back with -- mind you, the way STRmix is working, it's running eight independent assessments of the data.

Q. Yes.

A. And it's coming back to all those eight independent assessments. And when it's going through the data, it comes back to, hey, this is the combinations we've seen, the software has seen. And we've seen this combination of 16-18, you know, X -- you know, X number of times. We've seen this combination 16-18, and it's giving the weight of how many times it's seeing this combination when it's going through the iterations.

Q. Okay.

A. So it's giving -- it gives a higher weight. There's someone that -- they're giving a sample to us, and it's on D-3, they'll go get a higher weight with the statistical result if they're a 16-18 versus being a 16-17.

Q. Okay. Let's go back to FTA. Would you agree with me there are seven genotypes, seven potential combinations of alleles that STRmix called?

I counted seven. I could be wrong.

A. Yeah. I count six.

Q. Oh, you count six?

A. Yeah. We're looking at -- might be looking at -- you're talking about Contributor 1?

Q. Contribute --

A. 1. Yeah, six.

Q. And then if we could go to Contributor 2 for that same 8-1-A, Contributor 2 --

A. Yeah.

Q. -- two contributors in there, it contributes -- it's got to add up to 100 percent; right?

So that's 46 percent for that second contributor. And within those different genotypes for all of those different loci --

A. Yeah. And to help you out a little bit.

Q. Yeah.

A. If I was analyzing this sample binary in the past, prior to the aid of the software, I would go through this mixture and say, here's my possible combinations for my contributors; right? And I would have the exact, really, same contributors as the software.

The only difference is, this is now applying a weight based upon the ratios and what's going on in the sample, where I just mathematically would not have that ability to do that.

So that's -- the big difference is, I would still -- at, say, D-8, I would still give those six possible combinations. And there used to be a statistic that we would call CPI, combined probability of inclusion --

Q. So that's no longer used; correct?

A. That's no longer used. And one of the reasons it was no longer used is, when you did that calculation, and let's say you don't have D-8, if you was a 20 -- if he was a 20 -- that doesn't work here.

You would have -- you have to have, like -- you have 20, 22, 23, 24. If you had any of those combinations, in any combination, you were included with CPI.

So what happens is, that doesn't allow the possibility of an exclusion based upon someone being a 20, 24, 20, 21, you know, so this allows better ability to use the data for exclusions, also.

Q. Well, am I correct in saying that those old methodologies, CPI, random match probability, those were more reliable and used for single source?

A. They could be used better for single source. Because any time -- for random match probability, for single source samples, that was pretty easy. You just assign frequency to each of them and multiply them across.

With mixtures, the only time you could actually do a random match probability when you have a mixture sample is if you had a major that was extreme enough that you could call with 100-percent certainty and a minor.

In a case where you had, like, a 50-50 mixture where you could not call a major-minor, you would then have to rely on a combined probability of inclusion statistic, which also falsely includes a lot of people with allele combinations.

So it -- you know, RNP was still reliable. It just has limitations. And now, like -- with the ability to use likelihood ratios, that allows us to analyze data we could not analyze under limitations of random match probability.

In its simplest form, a LR is just one over the random match probability for a single-source sample.

Q. Right. It's the inversion of.

A. Yeah. It gets more difficult when you have mixtures. But in its simplest form, it's -- yeah.

Q. I mean, the reason for STRmix and the reason for these software programs is because the technology of DNA has become so sensitive --

A. That --

Q. -- that you don't need, you know, a quarter size sample in order to do an analysis. You can do -- you can do an analysis on something that you can't even see; right? That's --

A. Yeah, absolutely.

And in the past, when we were looking at samples,

could we have done what we do with STRmix manually? Yes. You can actually manually do everything that STRmix does, but it would be the next six months doing it.

Q. Right. Okay.

A. So there's a part of our training we have to go through and manually do one locus. And it would take us -- you know, like one locus for one iteration, it would take hours, you know.

So you could do what STRmix is doing. It just now allows us the ability to have a computer to do that interpretation, where it would take us forever to do by hand.

Q. Well, let me ask you this: How long did it take to run this specific 8-A-1 through STRmix?

A. Hold on. I can answer you. It should be at the end of the first report.

17 seconds.

Q. 17 seconds.

A. And that's 17 seconds starting with a -- it does a million -- it does a burn-in of 1 million iterations before it ever starts. So it goes through the data and comes to a point where this is where we both started, and it has eight independent chains.

Q. Right.

A. And with different pathways to come back to the same answer. So it took 17 seconds, which it would take us six months.

Q. Okay. We'll get to STRmix in a little bit.

But -- all right. So let's move on from the middle garage.

So I think that accounts for -- with the exception of the buccal swab from Michael Montgomery we didn't discuss, and the toothbrush. But those are just --

A. Yeah. And I should mention the -- just --

Q. Sure.

A. The -- it's within the documentation. You can see it in the case file.

The rim of the mug and the toothbrush -- the rim of the mug --

Q. Okay.

A. The rim of the mug and the toothbrush, they both obtained the same profile. So I just used the toothbrush for comparison throughout. So you'll see that documented inside the -- in the case file.

Q. I saw that. Thank you.

A. Yeah. I wanted to make sure you -- so you're, like, why wasn't there a comparison? Well, they were --

Q. The same.

A. You could interchange, A, my conclusion says

toothbrush with rim of the mug, it would be the exact same conclusion.

Q. All right. So let's move on.

I'm looking at Request Number 3. I know that's Beecher's report.

And then your report would be --

A. Number 4.

Q. -- Number 4.

My first question for you is: When did you develop the profile for Tomasz Kosowski, which would be Item 17, Agency Item 30?

I have April 5th of 2023. I don't know if that helps you.

A. I opened up the -- that's why. I opened up Request 3. Sometimes our system is slow.

Make sure I tell you --

For Number 17, yeah, April the 5th, 2023.

Q. And I apologize for going back.

We had talked about -- or you had mentioned positive and negative control for the -- I think you said the phenolphthalein test.

A. Yes.

Q. Can you tell me a little bit about the procedures for -- involved in the positive and negative controls?

A. Yeah. We have known blood. I think it's -- a lot of times, with known blood, we have one of the staff members, and it's dried on a cloth. And prior to testing on any sample, for -- for the data that you're using phenolphthalein, a sample will be taken from the known blood and tested.

Also, something to where that does not contain any blood will be tested. So it could be a piece of filter paper or a swab, a blank swab. And then the necessary reagents are tested with the positive and negative.

And in order for the results to move forward so you can actually test the item, the sample that was blood, we used to indicate that it was blood, and the sample that was not blood needs to show a negative result.

Q. Okay. Are those -- do you label them as -- or not you -- Beecher label them in this report as control swabs?

A. I would have to look at her report to see. They probably -- they might either be in -- in her notes or they might be stored inside of our DNA LIMS system, our LIMS system, which records the controls.

And you may or may not have given a copy of -- I think you probably did.

Q. Okay. Well, let me ask you this: You talked about the positive and negative controls being -- you

use your lab techs to do that, I think you said?

A. Yeah. Yeah. Our -- not -- not our lab techs, but someone who's a trained serologist will do that, yes.

Q. A serologist will do that.

All right. And are those done at the same time? Like --

A. No. Our policy requires these to be tested prior to testing on any questioned samples. So the testing is done prior to the testing.

Q. And what reagents -- you mentioned the word reagents. What reagents are used in the positive quality control in the phenolphthalein?

A. Just the reagents that comes with the kit, the phenolphthalein, hydrogen peroxide, and ethanol. That's -- that's the reagents that are used in the phenolphthalein test.

Q. And are those -- those the same reagents that are used in the negative quality control test?

A. They have to be, yes. So both the positive and negative. And the same ones need to be used on the case file. And that -- the lot number of those are recorded within the case file.

Q. Of the reagents?

A. Of the reagents. And -- and -- yeah.

Q. All right. So --

Okay. So I think we were on Request Number 3, which would be -- that's the serology of the bodily fluid identification.

And then the interpretations of those would be your request for -- right -- Number 4 --

A. Yes.

Q. -- your report dated April 6th of 2023?

A. That's correct.

Q. No. Wait. It would be --

A. Yeah. The Request 4 is -- I'm sorry -- the report date, April the 6th, 2023. My Request 4.

Q. Yes. Okay.

All right. Because we just went through your Request 4, we went through the --

A. Yeah. We haven't really went -- the only thing we've went over on Request 4 so far would have been, you asked me a question about when I processed the buccal swab from. Two months.

Q. Thank you.

All right. Now, I'm on track.

Going back to Number 3, which would be Beecher's report --

A. Okay.

Q. -- and I'm looking at Item 13, where there was

a manila envelope containing one swab sleeve containing two swabs from the interior trunk lid, driver's side.

A. Okay. Yeah. I'm reading from my report, yeah.

Q. Okay. Which appears -- trunk lid.

Okay. So on the trunk lid, there was -- blood was not indicated.

And then Item 14 -- I'm looking at Beecher's -- blood was not indicated. That would have been the interior trunk back wall.

Do you know --

A. According to the report, that's what it says, yes.

Q. And then the interior N -- which I'm assuming would be north -- wall of maybe left lobby door -- I don't know -- blood was not indicated; right?

A. According to the report, yes.

Q. Okay. And then you have Item Number 16, which would have been swabs, men's bathroom floor drain.

A. Yeah. Yes. According to the report, that's what's on there.

Q. So in your report, it appears -- so those items --

A. This was -- this was Desiree's report, not mine.

Q. I understand. I understand.

A. Yeah. I just want to make sure so there's not any confusion for my responsibility in this.

Q. I understand. I understand.

So -- but you still processed or analyzed Items 13, 14, and 15. And each of those resulted in a DNA mixture; right? 13, 14, and 15, your request number?

A. That's correct. Well, actually, 16 did not result in a mixture.

Q. Right. 16 resulted in a DNA profile?

A. 13, 14, and 15 resulted -- and 16 resulted in a no profile.

Q. And according to your interpretations and opinion with regards to Item 5, the swab of the Toyota tailgate, that resulted in a male profile, but comparisons can be made to the profile upon the submission of suitable reference standards.

And Doctor -- or Tomasz Kosowski was excluded as a possible contributor to that DNA mixture.

A. Well, that wasn't -- are you talking about Item 5? Make sure.

Q. Yeah. Where's your 13 at?

Oh, you did the -- okay.

A. Yeah, because 5 was a single source profile that he was excluded from.

Yeah, it's on the next page.

Q. All right. I'm sorry.

A. The previous report, which was Report -- Request Number 2 --

Q. Yeah.

A. -- because additional samples came in, those are repeated on this report so a comparison can be made.

Q. Okay.

A. So you'll see, like, on Request Number 2, you'll see 5 and 8 again. It says exactly the same thing again for the first statement, but then an additional new comparison is made.

Q. All right. So I'm going to look at Item 13, which is the interior trunk lid which resulted in a DNA mixture. It looks like you interpreted or assumed two contributors, with the mixture proportion of 67 percent and 33 percent.

A. Yeah. Correct. Yes.

Q. All right. So I'm going to ask if you could go to the electropherograms that are associated with that. And that --

A. I am there.

Q. Okay. So 13-A-1; right?

A. Yes.

Q. Looking at those electropherograms, would you

agree with me -- and correct me if I'm wrong for my counting -- but it appears that there -- three, four, five -- 11 different loci that -- there's dropout, right, at 11?

A. Oh, yeah. This is a very low level DNA mixture, yes, with dropout.

Q. With -- and so how many different -- how many different loci -- how many different dropouts did you note it? Am I correct in my counting?

A. Yeah. I mean, where we're seeing a complete dropout at several loci, D3, VWA, 16-CSF. You have potential dropout at almost every other loci because of the low RFUs.

So you have potential dropout at every locus and complete dropout at the loci where you don't see a peak indicated. So pretty much every locus has possible dropout.

Q. Okay. So, potentially, every loci in this electropherogram for this interior trunk lid, there is either complete dropout or the potential for dropout on the other loci that's not a complete dropout.

A. That's correct.

Q. My question for you is: You reported that the mixture of DNA is approximately 11 times more likely if originated from Item 3, the toothbrush, represented as

Cozzi's toothbrush, an unknown, unrelated contributor?

A. That's correct.

Q. And in the -- I think you used verbal equivalent -- equivalents in your --

A. Yes.

Q. Where does that -- where does that 11 fall?

A. That falls --

Q. I think it says inconclusive, but I just want to make sure.

A. Yeah. It's inconclusive, yeah. You're correct.

Yeah, we put out the likelihood ratio. In our validations, we've seen false inclusions in this range. That's what I'm letting you know.

Q. Okay. So am I correct in stating that Item 13, the swabs from the interior trunk lid, the likelihood ratio overall is inconclusive?

A. That's correct. Yeah.

Q. All right. So Item 14, which would be Agency Item 32, the trunk back wall, which would be the DNA mixture, if you could look at those electropherograms as well. That's 14-A-1.

A. I have. And 14 up.

Q. All right.

A. This one is not that low level, not like the

other one.

Q. Okay. What -- what were the quantitated DNA that was extracted? Or how much DNA was extracted from these sam -- from these swabs -- this swab?

A. .0112.

Q. .0112. So not very different than from that other -- I think it was the middle garage -- of .01?

A. Yeah. It was very similar.

Q. Okay. So low level.

A. Not -- yeah. Lower. A little bit lower level.

Q. A little bit lower level than the garage?

A. And you're looking at -- what was it that I said? .01.

Q. 1?

A. 1.

Q. Uh-huh.

A. .11; right?

Q. .01. I have .01.

A. Okay.

Q. .01 nanograms. So for this -- this --

A. So it amplified it. The point amplification, I took 15 -- you're looking at about 15, 18 grams of DNA, the .15 that was amplified.

Q. And this -- this applies to any of your

reports. Did you amplify or overamplify any specific loci? Does that make sense?

A. Well, you really -- I know what you're saying. But, no, to try to get results from -- no. No. No, you're looking at just single amps for these samples. You're not looking at combining amplifications or anything like that. Is that what you're getting at?

Q. Yes. Yes.

A. Yeah. You're not looking at that. And, actually, that's really frowned upon to do.

Q. Some labs do it?

A. Yeah, some labs do it. And it's actually considered a low copy number technique when you do it. And, actually, those type of samples, when you do that, are not eligible for CODIS. So the labs that's doing that should not be putting those samples into CODIS. They lose that ability, so.

Q. Does your lab have its own database that you input profiles?

A. Yeah. We have the CODIS database. And, you know, as a CODIS database, you have your local database and your state and your national. So, you know, we enter everything through the local database. And then once it's eligible to be uploaded to the state database, you're uploading to the state. And once it's eligible

to be uploaded to the national, it's uploaded to the national.

Q. But does the Pinellas County forensic lab have its own database?

A. Only -- only as part of the local CODIS database. And we have -- like I mentioned earlier, we have a database for contamination purposes.

Q. Under -- yes. Understood.

A. But, no. We don't have our own -- outside of the eldest portion of CODIS, no.

Q. All right. So I think you had indicated this is low level.

And let's just get this on the record. We can do it for this -- these swabs 14-A-1.

You've got 16 -- I'm just going to look at D-3. 16, that will be the specific allele, right, the first number there?

A. You're talking of which number? Which E-gram? 14 or 16 now?

Q. 14-1. I'm sorry.

A. Okay. And you're looking at D-3?

Q. Yes.

A. Okay. Yes.

Q. So the 16 is the allele?

A. 16 is the first allele indicated, yes.

Q. And the 346, is that the RFUs?
A. That is the RFU; correct.
Q. That third number, that's the length?
A. Yeah. The base curve size.
Q. All right. With regards to this specific item, Number 14, could you have inadvertently switched Mr. Cozzi's alleged putative DNA profile and Mr. Kosowski's samples, or mislabeled them, so that the results would be revealed that it's 94 percent Kosowski and --
A. No.
Q. -- and 6 -- no?
A. No. No. The questioned samples and the known samples are processed at different times and spaces. So -- and the questioned samples are always processed prior to, so -- and the known samples are always processed last. So they would have been processed in different areas. Yeah, it's not -- I don't believe it's possible. Especially if they was transferred, I would expect that his buccal swabs would be so much higher RFU values than this.
Q. Well, then let's -- while you're talking about that -- well, can you go to the DNA profile that was developed from Dr. Kosowski's buccal swabs and the electropherograms?

A. Yes.

Q. And then we'll go back to your report. I'm sorry I'm kind of jumping around here.

A. You're fine.

Q. So can you look at D-13? You have -- it appears to be an off-ladder allele; am I correct? Not a true allele? There was one peak that was removed, it appears, from this.

A. Oh, yeah. Those are -- you can see real quickly, like, at D-13.

Q. Yeah.

A. Go -- if you look right below it and you look at D-12, you see the 232.46 and you see the 244.54, you look directly below at the 18-21, those are known bola that is done from the previous stock. So it's spectral pull-up.

And you can see the same thing for SE-33 at 309 for the pair. It would be 33.59. If you look down at D-2, you can see why those are clicked off is because they're spectral pull-up.

Q. Okay. So it looks to me -- let's see. I'm counting. One, two, three, four, five, six. It seems like I'm more accurate if I count out loud. Six peaks that were pulled up that were removed from this electropherogram regarding --

A. Yeah.
Q. -- 17-A; would that be correct?
A. That's correct.
Q. All right.
A. Not unexpected for this type of RFU that you're seeing. This is typical of where you see pull-up.
Q. With the 50 RFU?
A. No. With having -- because you're looking at about 6 to 7 thousand RFUs, give or take a cross. So it's easily a point where you're seeing pull-up.
Q. Gotcha.
Okay. And then you have OMR associated with -- I can't really tell if it's D-1 or D-12.
What is OMR? Is that an obligate or what is that?
A. It's outside marker of range.
Q. Okay.
A. That's the way the software labeled it.
But if you look -- let's just look directly above D-13. You'll see the 210. If you actually look at the raw data and you line them up, they'll line up through the spectral pull-up.
Q. So --
A. D-13.
Q. Are you saying that the OMR, that 76 that you

have marked, it's like in between D-1 and --

A. Yeah.

Q. It's really kind of more associated or should be associated with the D-13?

A. No, no. It's just -- it's pull-up from the one dye. It's just -- it's just color that's coming over into the other dye.

And one other thing I should mention is, like, a lot of labs when you'll see data, they just actually clean them up. And you can actually, like, see where it says NTA, like, showing that we --

Q. Yes.

A. They will just give you the data with that removed.

We want to be very transparent and show you, yes, we removed data. So that's why you'll see this.

So, yeah, this is normal.

Q. And you had indicated because of the RFUs, it was -- the RFUs were so high, this is -- this is common?

A. Yeah. It's expected. You -- you would expect to have some pull-up with these RFU values.

Q. So let's go back to your Request Number 4.

Item 15, the interior north -- presumably north -- wall to L lobby door. I don't know what L means, but it could be left, what have you?

A. I think -- I think -- the designation, that does mean left but I have to go see in the original report what that meant.

Yeah. When you see like an N or an L, it's a limitation of our report writing system. Because if you -- it goes too long, it gets cut off. So -- so usually, we'll have to, like, shorten N for north and L for left.

Q. Okay.

A. Because if you spelled it all out, the only thing you would see would be interior north wall to, and the rest would get cut off.

Q. Understood.

All right. So in this analysis, Michael Montgomery was excluded as a possible contributor. Cozzi was excluded.

Once again, this was a mixture, I believe, a DNA profile mixture?

A. Yeah. This was a mixture of -- yeah, that was -- as being two contributors. And, yeah, 63 percent, 37. Michael Montgomery was excluded, and the toothbrush represented to be from Steven Cozzi was excluded, and also Tomasz Kosowski was excluded.

Q. All right. Let's go to the Item 16, the swabs from the men's bathroom drain.

A. Yeah. And if you could also maybe just pull up the E-grams on that one as well. Item 16-A-1.

Q. All right. Were you provided any information as to -- once again, kind of the same questions as the garage floor. Do you know what kind of surface these swabs were taken from?

A. The only information I know is there was what was represented, that the swab was from men's bathroom floor drain. I can't tell you what that floor drain looked like or -- that's the only thing I know, is just that description.

Q. It's composed of or whether there was (inaudible) --

A. Yeah. I can't tell you.

Q. All right. And the amount of DNA that was extracted from these swabs, can you tell me how many nanograms?

A. It was -- the amount extracted was .165. So that would have been about approximately .25 nanograms of DNA in the Sample 5.

Q. I'm sorry?

A. It was .0165, so using the maximum volume, it would be about 15 microliters, it would be about .25 nanograms of DNA sample.

Q. And when you input this into STRmix, I think

you indicate two contributors, or how many contributors did you -- did you --

A. This was 16? No, this was a single con -- a single source contributor.

Q. Single source.

All right. And then Item 17, you went through, which was the buccal swabs from Tomasz Kosowski.

And I think that's it for Number 4.

A. Yeah. I think that's -- I believe that's it.

Q. And then real -- real quick on Request Number 5, it looks like it's Beecher's report of April 25th of 2023. Some swabs were taken from a dumpster, the phenolphthalein test was negative. There was -- was there anything else done with that?

A. Not according to her report on that, no.

Q. Okay.

A. I think -- let's see. One second, please.

I did take swabs forward from this, to DNA. I took the swab from the dumpster, forward.

Q. Okay.

A. A report.

Q. A report?

A. Yes, I did. It was on Request Number 7. It just did not result in a DNA profile.

Q. Yes. All right. Thank you.

A. Yeah.

Q. All right. Then let's move to your report, Request Number 6, dated May 10th of 2023, Items 21, 22, 23, 24, 25, 26, 27, 28, and 29, and 30. And this would have been Beecher's report?

A. That's correct. Yeah.

Q. If you could look at Item 28, Agency Item 45, which appears to be -- it's notated as a paper bag sealed with evidence tape, containing three napkins from bathroom trash can. It's got Napkin 1, Napkin 2, Napkin 3.

I noticed in her handwritten report, or handwritten notes, I should say, that all of those three napkins were combined together in one paper bag. Am I --

A. Let me look at that and make sure.

That's Request Number 6.

Yes. Correct. All three napkins were in the same containers, according to her notes.

Q. So they weren't separately packaged? The three napkins weren't separately packaged; they were all together in a paper bag?

A. According to her notes --

Q. Okay.

A. -- that's what I'm reading.

Q. All right. And then I think we -- we

addressed the deviation from the policy -- from policy regarding the TNB for the paper towel?

A. Yes. Was it paper towel?

Q. Yeah. It's Item 27. I'm looking at --

A. Yeah, 27. There were two items.

Q. And then, also, a deviation from policy for Item 29, TNB was used for the driver side front floorboard, as well as Item 30 as well?

A. That's correct.

Q. And it looks like the swabs -- and I know this is not in your report, but perhaps you can give me your thoughts regarding 21, 22, and 23, why those -- why there was no analysis performed on those -- on those three swabs.

A. I can tell you typically, yeah. Okay.

Q. Okay.

A. Typically, if we look at a stain, right, and is the stain is very, very limited amount of a material, we'll make a decision, am I going to waste some of this sample on a blood test, or is it better to preserve that as much as I can, as possible, to take forward for DNA.

So the sample was -- you know, in my instances, when a sample is so limited there's not a whole lot of material there, you don't want to take some of that material and you now don't get that back because you

consumed it for that test, when it would be better to just take that forward and save that material for DNA testing.

So in looking at her notes, she has too limited for sero for those.

So that's typically within our policy. If samples are very limited amount of material -- of staining, then we will just go ahead and go straight to DNA, if that's preferable.

Q. Is that -- and I know --

A. And I'm seeing it -- I'm seeing it in her notes, that it says too limited for sero for those samples.

Q. Okay.

A. So that's what I would have done. I would have looked at the sample. And you'll see that on samples I just gave you, you'll see that I did the same thing. If you look at it, it's not a whole lot of material. So I just decided it's better to go forward with DNA.

Q. Because then you're going to use the entire --

A. You're going -- yeah. And -- and so why call it presumptively for blood, if you don't have -- maybe that's important in the case sometimes. But without having some type of comparison of that sample, which you

need to weigh what's more important. So a decision is made to do the DNA.

Q. All right. And I neglected to include the swabs from the men's bathroom exterior door, Item Number 26, Napkin 1, Napkin 2, as well. No analysis was performed.

A. Yeah. She has the same -- the same note there.

Q. All right. I think we can move on to your Request Number 7.

A. I should mention, just make sure so I don't sound like I'm speaking for her. But that's just -- based upon our policies and procedures, that's what we would have done. You would still have to ask her if that's what her thought process was. But that's the thought process for a laboratory. If it's too limited, go for it.

Q. Because you don't -- you don't want to consume the entire sample. And I know you're not speaking for her.

A. Yeah.

Q. I just kind of wanted to know what your thoughts were on that.

A. Yeah.

Q. So I appreciate that.

Okay. Request Number 7, report date of 5-10 of 2023. Looks like Item Number 19, which was a stain from the interior dumpster, which is associated with the serology report Request Number 5, you did not get a DNA profile?

A. No.

Q. And then Item Number 21, swab of the top of the toilet tank resulted in limited DNA?

A. That's correct.

Q. And then Item 22, swab bottom left, I'm assuming, right, as per your testimony previously, of the toilet seat resulted in a DNA profile?

A. Yes. Resulted in a male DNA profile.

Q. And then 23, men's bathroom floor, PM Number 8. Do you know the difference between the PM Number 8 and the PM Number 10?

A. No. And I'm only guessing what PM stands for. I would guess it stands for photo marker, but that was just indicated to us as PM Number 8. I don't know what that's associated with. It would be an educated guess that it stands for Photo Marker Number 8.

Q. All right. So 23 did not result in a DNA profile.

24, swabs of the men's bathroom floor, PM Number 10, resulted in a DNA mixture.

25, swabs, men's bathroom exterior stall, resulted in a DNA profile; right?

A. That's correct.

Q. And then it looks like 26, 27, 27-B resulted in a DNA mixture?

A. That's correct.

Q. And then 28-C-1, 28-C-2 resulted in a DNA profile?

A. Correct.

Q. And then Item 29-C-3, area avoiding stains on Napkin 3 resulted in a DNA mixture?

A. That's correct.

Q. And then the swabs that were taken from a latent area in -- it looks like Photo Area 2, did not result in a DNA profile?

A. That's correct.

Q. All right. So if we could look at the electropherograms associated with the Item 21, the top of the toilet tank, resulted in limited DNA. So that would be 21-A-1. I'm looking at either total allelic dropout --

A. Which one? You're at 21-A-1?

Q. The swabs.

A. Yeah. You're looking at this. This is -- either you're having dropout, complete dropout, of the

loci and possible dropout at numerous other loci.

And that's why -- that's why -- and you're looking at only one -- not counting this section identification marker, it's like Y, you're looking at -- one, two, three, four, five -- only five locations.

And with our STRmix software, we need, at least -- to validate, we need to have at least 10 locations. So it's too limited for us to do anything.

Q. And which leads me to another -- an additional question now, talking about STRmix for just a second.

Am I correct in indicating that your lab is validated -- maybe I asked you this already. I don't recall.

A. Yes.

Q. Your lab is validated for doing analyses through STRmix, through the software program, for four or less contributors.

A. Correct. Yeah. We have not validated STRmix for past four contributors, so --

Q. When you say -- yes.

A. -- anywhere from a NOC one to a NOC four.

Q. So when you say resulted in a -- resulted in limited DNA for the top of the toilet -- I don't see where you have maybe limited DNA. I mean, I guess you have the two which is, right, male?

A. Yeah. The most you could say on this is, if you had some L-DNA because of the end L. But us analyzing this would not be in support of our validation of the software because we have a limitation within the software. You have to have ten location -- ten alleles, minimal, to use the software. So it's just too limited to utilize the data.

Q. Okay. We'll move on to Item 22, which is swabs, bottom left of toilet seat, resulted in a DNA profile.

A. Yes.

Q. Which would be 21-A-1.

It appears that there is at least one allele that has dropped out, or there is one -- not one allele. One loci, one location, looks like D-16 that there was complete dropout?

A. Yeah. That's correct.

Q. Would you consider this a degraded sample?

A. It does show -- and, initially, you see some degradation from left to right. So you'll probably see some degradation, maybe some slight -- maybe inhibition, maybe not. But you see, like, when you compare the peak heights, combined D-3 RFUs together, compared to what you see TPOX, you're looking at two or three hundred RFUs, 50, draw a line. You see a nice degradation

curve. Yeah, it's slightly degraded.

Q. Okay. So I think that was -- the point I was trying to ask you about before, you just -- you just indicated that you add -- added the height.

A. Yes.

Q. If there's a peak height imbalance, you add those to get --

A. Yes.

Q. Is there some kind of formula that you do? You add them together, and then --

A. No. I mean, that's -- I mean, binary, that's what we would always do to determine. But STRmix -- STRmix does the exact same thing I just did right there. And it applies the database and curve to the sample so it actually will model looking at D-3, looking at all the alleles, and apply a curve. This is the degradation that we're seeing, and applied that throughout the process, so --

Q. Well, I want to go back --

A. -- it does -- it does what I just did simply, a little bit more complex.

Q. Okay. So -- but there is some type of -- let's take STRmix out of the mix, if you will.

A. Okay.

Q. 150 and the 201, what would you normally do

with that, those -- that imbalance of those peaks? What would you do with those two numbers?

Would you take a ratio of the imbalance?

A. No. I mean, it's just there's nothing else you could -- let me look at something real quick. Make sure.

And the sample we're looking at is 22-A; right?

Q. Yes.

A. Okay. Okay. I just wanted to make sure I told you correctly.

For this sample, there's really nothing else you could do because the sample is degraded. It's just what it is.

The maximum amount was amplified for that sample. So there's no really going back and amplifying more to get one -- you know, to get it to come up a little bit better on one side. Because if you have a higher amount DNA and it's still degraded, you could amplify more and maybe get the TPOX to come up a little bit better. But in this sample, this is the best you're going to get.

So there's nothing, really, you could do. You know that D-3, you know, there was 16-18, VWA, 18-19. 16, profile. What do you have? You have 12 and 12. Anything else in the world. TPOX, you have an 11 and any other adult in the world.

So there's really nothing else you would do with the sample.

Q. Well, maybe the better -- the better -- the better question would be: That -- that middle peak that you see between -- it's a very, very -- honestly, it doesn't even register. It looks like it could be potentially --

A. It's not at the point where we say it's reliable, but it does look like a peak, yes.

Q. With a peak. Like, it could be an allele. It doesn't look like it's stochastic?

A. Right.

Q. An artifact --

A. It's at the point where it's below our analytical threshold, so you can't reliably.

And what that analytical threshold means for us is, it's a point above which you could say with 99 -- I think it's 99.97 percent certainty that it's a -- you know, graded as a true peak.

So with this here, you're not certain. You have, like, a .3 percent uncertainty that it's a true peak. So could it be a peak? Yes. But based upon our validation, it also could not be a peak.

Q. What's -- you know, taking STRmix out of the equation.

A. This is binary, that part.
Q. I understand.
A. Yeah.
Q. For this specific peak, what -- what are your policies and procedures as to either consider this specific peak being either -- it could be a forward stutter or a backward stutter because it's in between those two peaks. What --
A. You're talking about the 16? I'm sorry. Where are you talking?
Q. D-3.
A. D-3?
Q. Yes.
A. Okay.
Q. What's -- what's kind of your standard policy and procedure for determining whether something is backward or forward stutter. Like, is it two base pairs? I mean, what's your --
A. It's four, four base pairs.
Q. Four?
A. Plus four -- plus four, minus four. Forward, plus four. Minus, minus 4.
Q. Okay.
A. And I said -- when this data gets imported into STRmix --

Q. Yes.

A. -- the software automatically takes out the stutter peaks. So when you print, they don't show up.

But when we export the data into STRmix, it's exported with the stutter peaks that's above being analytical. So they'll be in the import files.

Q. All right.

A. So I can't see -- it's probably too low. But, like, the peak is in the 17 position. If that was above 50 RFUs, that would be imported into our STRmix for interpretation.

Q. Because if I'm correct -- and maybe you can correct me if I'm wrong -- but STRmix doesn't consider noise or things of that --

A. Yeah. That's correct. It doesn't consider anything below your analytical threshold. It only interprets what you give it.

Q. What the parameters have been set by the --

A. By our validation, yes.

Q. And then 23, which would be 23-A-1, men's bathroom floor, PM 8, that's really inconclusive. There's --

A. Yeah.

Q. Right?

A. No result in that one.

Q. No result?
A. 23 -- yeah, 23-A-1.
Q. Yes, sir.
A. Yeah. No DNA was detected.
Q. All right. And then men's bathroom floor, PM Number 2, Item Number 24, would be 24-A-1?
A. Yes.
Q. It appears like there -- is it -- well, let me ask you this: How many nanograms of DNA was extracted from this?
A. The 24-A-1?
That was pretty -- pretty low. It was .0053. That's how much per nanogram.
Q. And according -- according to my review of these electropherograms, TPOX, there's dropout at -- it looks like that specific loci?
A. Well, there's dropout at several loci because you're seeing two contributors potentially here. So, yeah, we have dropout there.
Q. And when I -- I say that because if you look at TPOX on 24-A-1, you've got that -- you call that 8, which is at 52, just right above that 50 RFU.
A. Yeah, there's -- there's another peak that's at RFU.
Q. There's another peak. That seems to be --

A. That's below the analytical.
Q. Below, but it appears to be a true allele.
A. It's below the point where we can reliably say it's true, but you can't rule out that the possibility is true.
And it would be the same thing at -- you know, at VWA, there's also, you know, a peak.
Q. Yes, before the 18?
A. And -- yeah. And that's, I think -- and that's one reason looking at this as a mixture. It's going to not -- well, the purpose of the mixture that peaks up. Everything that's above analytical is not dropping in and out. So I run this as a two-person mixture, to account for that possibility.
Q. Okay. Explain that to me. Why did you -- why did you run this as a two-person? I understand the various peak -- the number --
A. See, if you look at VWA as an example, okay -- I can explain this where -- I want -- without getting a little closer --
(Indiscernible. (Discussion off the record.)
A. In a VWA, say that peak that's below analytical -- let's just say it's a 15 -- that is fairly close in RFU value to the peaks that are above 100 or 84 RFUs.

So when you're seeing the 18, I can't say that peak could be a 15-18. I did not feel comfortable calling this a one -- one contributor, because I'm not comfortable, looking at this and saying that's an 18-19. There's a possibility that could be a 15-18, 15-19, or it could be an 18-19 -- you know, 18-19.

So when I'm running this, I'm looking at it for two contributors so it will take all those considerations into the possibility. Does that make sense?

Q. Yes.

A. Okay. So that's why, as your peaks below your analytical approach your peaks towards your analytical, you need to err on the side of caution and increase your NOC. So that's what was done.

Q. So just out of curiosity, why wasn't it run as three contributors? Why didn't you attempt to run it as one or three contributors?

A. Well, you're not seeing three. And I'm not seeing two. I'm seeing potentially -- I think there's potential to call this incorrectly if you said two, absolutely two.

The best thing is to account for the possibility of dropout, because you know you're seeing dropout from VWA, because that's approaching the RFUs of where you're seeing. So when you run this as a NOC two, it accounts

for that.

Like, it would have been incorrect to put it as NOC one, and you're not seeing enough data here to bump it up to a NOC three.

Q. Okay. All right. Then let's go to 25-A, which are the swabs, men's bathroom exterior stall, where you developed or were able to develop a DNA profile.

A. Yeah. That one is pretty -- pretty good.

Q. How much DNA was extracted from this?

A. That was .163 nanograms.

Q. But -- I'm sorry. 163?

A. Yeah. So you're looking at -- you know, so that was actually amplified within the target range, so.

Q. Okay. And then as we discussed earlier with those buccal swabs on Item 17, it looks like you have an off marker?

A. Yeah. It's -- because, again, you're seeing a little higher RFU, it's not unexpected.

Those -- if you look at the D-13 marker above, you'll see the base pair sizes. That's pull-up from the channel. The guy could be a 13. You see the 210 under the 8, and you see the 223 under the 11. That's what that's corresponding to.

Q. And just so the record reflects what colors

we're talking about, what are the two dye channels? What --

A. The -- the dye channel that the pull-up is seen in is purple, and the dye channel that the pull-up is originating from is the red channel.

Q. All right. And then 26 would be swabs, men's bathroom exterior door results in a DNA mixture?

A. Yes.

Q. Which would be 26-A-1.

How many contributors did you assume in this?

A. I assumed two.

Q. Two?

A. Yes.

Q. Okay. And what did you base that on?

A. The number of peaks. The number of peaks at each individual locus, and the overall pattern of DNA. The pattern to the major to the minor, and the number of peaks.

Q. All right. Let me just -- I apologize. Let me go back to Item 24 for just one second.

A. No problem.

Q. Involving your inclusion -- excuse me -- interpretations and opinions, where you indicate that the mixture of the DNA is approximately 270 times more likely it resulted from two unknown, unrelated

contributors, and it -- it originated from Item 2, the buccal swabs from Michael Montgomery and unrelated contributor.

So are you including --

A. Oh, no. It's in favor of exclusion.

Q. Gotcha.

A. It's not -- he's not excluded, but it's favoring him being excluded.

Q. He's not excluded, but it's favoring him being excluded?

A. Correct.

Q. He's not excluded.

A. He's not excluded, but it's favoring. Given the evidence, it's 270 times more likely that it originated from Michael Montgomery and an unrelated contributor. So we are taking those two probabilities. It's actually favoring exclusion. It doesn't reach to the point where he's excluded.

Q. Is he excluded, or is he favoring exclusion?

A. He's favoring exclusion.

Q. Okay. And then the same for the -- Tomasz Kosowski. The mixture of the DNA is approximately 250 times more likely that it originated from two unknown, un -- is that favoring exclusion, or is Dr. Kosowski --

A. That's favoring exclusion. And it's also

favoring exclusion for the -- for Tomasz Kosowski.

Yeah, it's the same statement as the one above. They're both favoring exclusion. They're not fully -- I can't say they're excluded, but there -- the data is favoring them being excluded.

Q. All right. And then with regards to this Item 24, the men's bathroom floor, Number 10, would you expect there to be DNA on the floor from someone that was in that bathroom on a daily basis?

A. I can't really speak to -- it's a very open-ended question because I don't want to state it right or wrong. But it all depended upon their habits, you know, like -- you know, some people when they go in the bathroom, doesn't touch anything. You know -- you know, they touch the door with the -- the hands with the door. And they walk up and, you know, they barely touch the water faucet. Maybe not. Other people may be different.

So, yes, in this instance, maybe so. It also depends how long they were in the bathroom, you know.

So I don't think you can say, one way or another, you expect or not expect. So it's not really something I could answer.

Q. All right. And then with regards to Item Number 4, as you had indicated, that resulted in a DNA

mixture of 91 percent. I think if you're looking at the STRmix output, 91 percent Steven Cozzi or the purported toothbrush to be from Mr. Cozzi, and 9 percent, Michael Montgomery, Steven's husband; is that right?

A. No. That's -- that's not -- well, because you're talking about -- the 91-9 percent is just the proportions, are statistical -- are assigned to the mixture as a whole, not necessarily to an individual proportion.

So what we're saying is, with this, that given the DNA results, the mixture is approximately 36 sextillion times more likely to originate from the toothbrush represented to be from Steve Cozzi, an unknown, unrelated contributor, that originated from two unknown contributors.

So -- and then you said -- who was the other person? Michael Montgomery?

Q. Yes, sir.

A. That is actually stating -- 924 -- that he is favoring exclusion from that sample.

Q. Right. We just -- yes.

A. But the Tomasz Kosowski was included. That's the contributors you said were together. One is included, and one is favoring exclusion.

Q. Okay. So which one is included? Because it's

270 times more likely for Michael Montgomery and 250 times more likely for Tomasz Kosowski. So I thought -- you had indicated that both --

A. Yes. I'm sorry.

I thought you -- I thought you had told me Michael Montgomery and Tomasz -- it's getting late -- and Steve Cozzi. Sorry.

Steve Cozzi's is included. Both the other -- the other individuals, Michael Montgomery and Tomasz Kosowski are both favoring exclusion.

Q. All right.

A. If I said it otherwise, I apologize.

Q. Oh, no worries. I figured you got confused.

All right. So I think we were on Item 25.

No, we went through that. Did we go through that?

A. Hold on.

Q. 25 is --

A. Yeah, I don't -- I don't think we did.

We might have went over initially, like, the DNA profile, but we never went over the individual comparisons, though.

Q. Okay. Because you gave me .163 nanograms that were am --

A. .163. Let me make sure. I'll tell you. That -- that -- we haven't went over that sample, 25-A, .163.

Q. 25 -- yes.
A. Okay. Yeah. That's where we left off, that means.
Q. Okay. And 25-A-1, you said it was .163 nanograms?
A. That's correct. Yes.
Q. Okay. And then we talked about the off marker, the off ladder, and the purple and red dye, too.
A. Yes.
Q. Okay. Then if we could move on to -- and just for -- for record purposes, Item 25, what we were just talking about, Tomasz Kosowski is excluded as a possible contributor to that DNA profile on Item 25.
A. Yes. That is correct. He is excluded.
Q. So Item 26, the swab -- swabs, the men's bathroom exterior door, this would be 26-A-1. How many contributors did you assume?
A. I assumed two contributors.
Q. And looking at these electropherograms, did you determine whether or not there was any -- any dropout, any allelic dropout?
A. Well, I mean, there's always -- there's a possibility of dropout, yeah. And you're seeing a very clear major contributor, with a very small minor contributor. If there's any dropout, it's going to be

in the minor contributor.

And there's some locations where there could be a possible, you know, dropout. For example, D-21, maybe. There is some indications because it's lower level RFU, that it would not be unexpected to have a dropout.

Q. All right. And can you -- can you tell me, for example -- not for example -- but you indicated that you assume two contributors for the sample.

Did you take into consideration homozygous versus heterozygous alleles?

A. Yes. Yes, I do.

Q. And how do you do that? We -- for you, yourself. For you, how do you do that?

A. Well, this one is pretty easy. When you're looking at a major contributor, it's -- if you go across the first channel, D-3, it's obvious your major is going to be 16-18, and VWA 18-19, D16 11-12, CFS 12-14, TPOX 11.

You go -- you see what your -- VWA, you've got a 14. You're not seeing an indication of anything but two.

Go down to the next channel, you'll see a D8, major 13-14, minor 10-12.

D2 -- D-21 29-30, you're seeing a minor of 31.

So you're seeing an indication that there's two

contributors throughout, and it's staying pretty consistent. So two contributors would be a very good assumption with this sample.

Q. So am I correct in stating that your decision is based upon --

A. Looking at the mixture as a whole and looking at the major, looking at the minor, looking at the ratios and across, yeah.

Q. When you say major contributor, it appears that you're just looking at that D3S and --

A. You're looking -- you're looking all the way across.

Q. In the --

A. Every locus.

Q. Every locus.

Okay. But it looks like -- and I'm looking at this electropherogram. And it looks like there's a substantial amount of DNA at that D-3. But then at TPOX, I wouldn't necessarily say that there is.

A. Right. You are seeing -- you know, you're seeing degradation. You're probably potentially losing some of the minor as you go down. You can see that the minor is probably dropping out. But you see the major contributor is holding steady all the way across, but the minor is potentially dropping somewhat.

But, yeah. You're not seeing an indication of anything but two contributors here.

Q. All right. So if you could go to the component interpretation by STRmix for the 26-A-1.

A. Okay.

Q. And once again, the contributors have to add up, right, to 100 percent. So if there's two contributors, like in this assumed number of contributors, you have 83 percent for Contributor Number 1 and then 17 percent for Contributor Number 2.

A. Yeah.

Q. Okay.

A. And what I was briefly, you know, just spelling out quickly, you notice that, like I said, oh, 16-18 --

Q. Uh-huh.

A. -- I am -- what I've seen is, the software we use is much more conservative than we are as humans. Like, I would look at that and said 16-18, 100 percent, you know.

The software is taking into account variabilities and saying, no, there is a remote possibility it could be an 18-18. So it actually does a much better job of being much more conservative than we can as humans.

Q. Well, because it's a mixture; right?

A. Yeah. It's a mixture. And mathematically, we just cannot comprehend, you know, everything that's going on. And so it does a good job of helping us.

Q. So if I were to look at Contributor Number 1 associated with 26-A-1 and the component interpretation by STRmix, it looks like there's -- one, two, three, four -- five different genotypes or five different possible combinations at SE?

A. Let me see.

For Contributor 1; right?

Q. Yes.

A. Why do I keep scrolling past SE?

Q. It's --

A. Yeah. There's one, two, three -- there are five possibilities.

Well, yeah, with the higher probability -- the highest weight being the highest two peaks.

Q. And then D2, we've got one, two, three, four, five -- another five possible genotypes for that specific loci as well.

A. Yeah. You've got five possibilities. But, of course, the top possibility being 99.83, and the rest being .0-X percent. So very low weights to those, but there are still a possibility.

Q. And then with regards to this swab, Item 26,

Michael Montgomery is excluded as a possible contributor?

A. That's correct. Yes. He is excluded.

Q. And then what about Tomasz Kosowski?

A. Tomasz Kosowski was included within the mixture.

Q. And then what about the toothbrush that's represented to be from Steven Cozzi?

A. The toothbrush represented to be from Steven Cozzi was also included in the mixture.

Q. Let's talk about Item 27-A, stained paper towel which resulted in a DNA mixture.

A. Yes.

Q. What were the number of contributors assumed in this mixture?

A. The number of contributors was two.

Q. And the amount of DNA that was extracted?

A. There's a .0905.

Q. .0905?

A. Yes, ma'am.

Q. And in your interpretations and opinions, the mixture of the DNA is approximately 200 times more likely that it originated from two unknown, unrelated contributors than it originated from Michael Montgomery.

So is Michael Montgomery --

A. Is favoring exclusion; right. He's not excluded, but he's favoring exclusion.

Q. And then you indicate that there's moderate support for the proposition that the buccal swabs from Michael Montgomery not being a contributor to this DNA mixture?

A. That's correct.

Q. When we talked about -- strike that.

A. Okay.

Q. And then with regards to the toothbrush represented to be from Steven Cozzi --

A. Yes.

Q. -- what was --

A. He was included in the mixture.

Q. All right. And then --

A. The toothbrush sample -- yeah, the toothbrush -- the DNA on the toothbrush was included.

Q. Yes, sir.

And then what about the buccal swabs for Tomasz Kosowski?

A. He was also included, but that fell within our inconclusive likelihood ratio. So those results would be inconclusive.

Q. So when it says -- when you report out 2.4 times --

A. Yes.
Q. -- so, like, when -- within a range of 0 to 10, that's what we're talking about, 2.4?
A. Yes. 2.4.
Q. And then 27-B, area avoiding stain on the paper towel, it looks like you assumed three contributors for that?
A. That's correct.
Q. 52 percent, 37 percent, and 11 percent as broken down by STRmix.
A. Yes.
Q. Michael Montgomery is excluded. And then no determination could be made with regards to a comparison to the toothbrush or the profile developed from the toothbrush; right?
A. That's correct.
Q. And as regarding Item Number 17, the buccal swabs from Tomasz Kosowski, he's excluded from 27-B?
A. Yes. He is excluded.
Q. All right. Moving on to Item 28-C-1, Stain 1, Napkin 3.
A. Yeah. Results in a male profile.
Q. Male pro -- yes.
Let's see. What -- how much DNA was extracted?
A. On 28-C?

Q. Yes, sir.
A. 1.8 nanograms.
Q. Stain 1. Okay. Stain 2.
A. It was 1.8.
Q. 8.
Okay. I'm sorry. Could you repeat that? 1?
A. 1.8 nanograms.
Q. So within that threshold, your target threshold?
A. Yeah. Yes. Well, a lot of these samples, when you add -- because you take the value they report to you, and add the maximum amount. So, yeah. It's well within our optimal range.
Q. How do you know, since these napkins were submitted to you in -- and not separated in one paper bag, whether there was transfer from one napkin to another? I mean, you can't tell that; right?
A. I can absolutely not tell that, yeah. Yeah. I can't tell you if there was transfer from one to another.
Q. Would you say that the way that those items of evidence were packaged, that's really not the proper procedure to package items of evidence from a crime scene?
A. It depends. I -- I wouldn't say it's not

necessarily correct, because it depends. Did they find the napkins, all three together? I don't know the answer to that, so I'm just speculating.

If they found all the napkins bunched together and were sorting them out, 1, 2, 3, that's probably appropriate. You know, they say found all three, they're all intertwined together.

But if they found a napkin in one area, and a napkin in another area, and a napkin -- three areas, and put them together, that's probably not appropriate.

I don't know information about the scene --

Q. Sure.

A. -- to make a comment whether that would be appropriate or not. So it would depend. It still could be, depending on the circumstances.

Q. All right. And with regards to that Stain 1 on Napkin 3, we have --

With regards to the toothbrush represented by Mr. Cozzi, what was your opinion?

A. He was included in that opinion -- in the mixture.

Q. And it looks like Michael Montgomery was excluded?

A. That is correct. He was excluded.

Q. And then Item 17, buccal swabs from Tomasz

Kosowski. He was excluded as well?

A. He was also excluded, yes. Correct.

Q. Okay. Item 28-C-02, which would be Stain 2 on Napkin 3.

A. Yes.

Q. How many contributors did you assume?

A. This was a single contributor, so one contributor.

Q. And how much DNA was extracted?

A. From 28-C-2?

Q. Yes, sir.

A. It was a .0139.

Q. I'm sorry? Could you repeat that?

A. Sure. No problem.

It was .0139 nanograms.

Q. All right. In a single -- single source?

A. Yes, ma'am.

Q. And you had determined that single source originated from?

A. Well, I included the sample represented to be from the toothbrush of Steven Cozzi.

Q. Yes. And Michael Montgomery was excluded?

A. Correct.

Q. And Tomasz Kosowski was excluded?

A. That's correct.

Q. All right. Then 28-C-03, which would be an area avoiding stains, Napkin 3.

A. Yes.

Q. How many contributors did you assume?

A. Two contributors on the sample.

Q. And that would be the area avoiding stains -- stain. Excuse me. Two contributors. And how many -- how much DNA was extracted?

A. On this sample, it was .0075.

Q. .0075?

A. Yes, ma'am.

Q. Would you -- would you consider that to be a --

A. You're also -- I got some small autosomal, which is .0075. The -- and the Y target, you're having a higher value, which is .0125.

Q. .0 --

A. 125.

So it can be some indication. There's a little bit of discrepancy between the values between Target Y and small. They're both a different base pair size, so that could be some indication.

So for a total DNA, you are seeing .0075, but you're seeing a little bit higher in the male target. So just -- for some reason, it amplified a little bit

better with that --

Q. And so -- so when you say the male target, are you talking about just Y or are you talking about the NEMO gene as well?

A. No. It's for quant -- for when you quant, you have -- we're looking at three different targets. Every one of the values stem from the small autosomal target, because that's the one we use.

Q. Yes.

A. But I just look at the sample, and it has -- the small autosomal was .0075. The largest, pretty much equivalent, .0087. But the target for the Y is .0125.

So it's -- you're not -- it could be just something that's weird and simple.

Q. But still no copy, low level?

A. It's probably -- I still consider this lower.

Let me see.

We have -- yeah, the results are matching up with the quant values, you know, of being a little bit lower level.

(There was a recess from 3:07 to 3:17 p.m., and the proceedings reconvened with the same appearances.)

Q. (By Ms. Tuomey) All right, Mr. Summerfield. I think we left off at Item 28-C, area avoiding the stains

on Napkin 3.

A. Yes. That's correct.

Q. Okay. And with regards to Michael Montgomery being a possible contributor to this DNA mixture, what was your opinion?

A. He favors exclusion on that sample.

Q. And would that be the same, would you say favor exclusion for the buccal swabs with regards to Tomasz Kosowski, Item 17?

A. That's correct. If -- Tomasz Kosowski also favors exclusion for that sample.

Q. All right. I noticed in -- with regards to this specific -- your -- your opinion regarding Item 28, you indicate that there's limited support favoring exclusion for Michael Montgomery, and then moderate support with regards to Tomasz Kosowski being -- favoring exclusion as well?

A. Yeah. Yeah. That's just the difference in the number, being 3.2 and 10. That's where the verbal qualifier lies between those two.

Q. Who creates that verbal equivalency -- equivalency? Is it your --

A. No. The portion here for the exclusion, that's following the FBI quality assurance. Well, it's actually SWGDAM recommendations for reporting the

likelihood ratio. That's a verbal scale that they use.

Q. Okay. That was -- that was my question.

A. 4-point. That's where this comes from.

Q. So you use the verbal equivalency scale by SWGDAM, not the verbal equivalency that's used by STRmix?

A. That is correct. Yeah.

Q. And the reason for that?

A. Is to convey to the reader of the report if you have different RL values, the weight associated from one to another. So anything over --

Q. Now --

A. I'm sorry. Go ahead.

Q. No. I understand why you -- why you -- why you use. But why -- why not use the software program's verbal scale?

A. We did. We stated that it was 3.2 times more likely.

Q. No, no, no. My question is: You said you used SWGDAM's recommended verbal scale, as opposed to STRmix.

A. STRmix doesn't have a verbal scale. It's just a -- the -- the score is all -- there's no verbal scale.

Q. So your testimony is, STRmix does not have a verbal equivalency scale?

A. No, they do not.
Q. All right. Let's move on to Item 29, swabs from the driver's side front floorboard. No analysis was performed on that?
A. That's correct. That's correct.
Q. All right. And is that -- is that because of the deviation from policy, or something different?
A. No. It tested negative for blood.
Q. Oh.
A. So there was no reason taken for it.
Q. So let me ask you this: If something tests negative for blood and there could be some other DNA from some other type of biological source that's not blood -- right --
A. Yes.
Q. -- conceivably there could be a DNA profile or mixture that's developed, even though it doesn't test positive for blood; right?
A. Yeah. That's correct. Yes.
Q. But is it your policy and procedure at your lab that if it doesn't test positive -- test presumptively positive for blood, that you don't take that forward?
A. If it does not test positive?
Q. Right.

A. We do not -- that's -- typically, the way -- when you're -- we have quite a few samples, and you're trying to streamline your process, yes. It also depends on what you're looking for, too.

So you can't always say that's absolutely we do that all the time, because -- take an example. A sexual assault case. You know, tested negative for semen, but we know there may have been contact between the individuals. And you'll still want to try to take a sample forward.

So a sample from the floorboard tested negative, we really didn't see any indication to take it forward.

But, you know, you still -- there could have been results there, but we just didn't see an indication of a reason why to.

Q. Okay. So with the exception of the two new reports that were just provided by the state today, those are all of your reports thus far; right?

A. No. There's still two more reports.

Q. Right. There's two more reports that we haven't discussed, because I just got them today; right?

A. No. There's still two more -- two reports, minus the two you got today.

Q. Okay. So there's a potential four? Two that were provided, and another two that are coming down the

pike?

A. No. You should have already received the report dated 9-20 of '23, and a report dated 10-10 of '23. And these both are in regards to the black ballistic vest.

Q. Okay. And that's Request Number?

A. 8 for the serology, and Request 9 for the DNA.

Q. Okay. For some reason, I don't -- I don't have those.

The serology would have been done by Beecher?

A. I -- I did the serology on this one.

Q. Oh, you did the serology?

A. Because she's no longer here at this point in time, I think.

Q. Okay.

A. I did the serology.

Q. Okay. I might save those so that when you're deposed on the other two reports that I was provided. But let me --

A. That will give you a chance to look over them.

Q. Okay.

A. It's no problem.

Q. I appreciate that. But just kind of -- so I kind of wanted to determine the time that's necessary.

You did the serology. Did it test positive for

blood?

A. Yeah. It was just a -- there was -- I'll tell you what was submitted. There was two samples from two ballistic vests, samples from ballistic vests. One was an EMS ballistic vest, and one was a black ballistic vest.

The EMS ballistic vest, blood was not indicated.

The black ballistic vest, blood was indicated. So that vest extended the serology on that.

Q. And what's the date of your report? September --

A. September 20th of 2023.

Q. All right. And then 9?

A. I'm sorry?

Q. Number 9 or Request Number 9 --

A. Yeah.

Q. -- which would have been the DNA analysis.

A. The one that tested positive for blood was taken forward. That was the black ballistic vest. And that resulted in a DNA profile. And it resulted in a male profile.

And Michael Montgomery was excluded. Tomasz Kosowski was excluded. And the sample from the toothbrush represented to be from Steven Cozzi was included. And it was -- the DNA profile was 100

septillion times more likely that it originated from the sample from the toothbrush, that it originated from an unknown, unrelated contributor.

Q. Did you said 170?

A. 100 septillion.

Q. Oh, I'm sorry. Okay.

A. 100 septillion times more likely.

So that was the extent of the two reports, in a brief synopsis for you.

Q. I appreciate that.

And the number of single contributors?

A. That was a one-contributor.

Q. And --

A. You're looking for the amount and quantity, aren't you?

Q. Yes, please. Thank you.

A. Let's see. You're looking at .0129 nanograms.

Q. .021 --

A. I'm sorry. .0129. .0129.

Q. All right. So if you had to add up the amount of DNA that was extracted from all of the samples, do you have a number for me of how much that would be?

A. I don't. I could calculate that for you, but I would have to take the time to go through. And it would be -- I could get that value for you, but I don't

have it right now.

But I would have to go through each -- each -- and you're not talking about the reference samples. You're talking about just the questioned evidence?

Q. Yes.

A. Yeah. I would have to go through each one of them to see. That could be done. I just don't have the value.

Q. Sure. But we would just essentially add up all of the DNA?

A. Yeah. You go through the quant report. And typically, what we use for amplification, and what you'll see in the quant report is the T small autosomal when you open it up. And you just take that value and add each one of the samples one by one, to get a value. That's what you see, the total value.

It would be very easy to do. I just don't want to do it incorrectly.

Q. Understood.

All right. So how long do you think DNA could survive -- or how long could DNA survive on a door, from, let's say, a handprint and still be picked up, if you will?

A. It depends. It all depends upon, one, how much DNA was there to start with. Of course, if you

have a larger amount of DNA on the door to start, then it's going to last longer. If you had a small amount of DNA, that could easily, over time, dissipate with each person's handling.

It all depends on how much people have access to the room. Like, as someone, you know, approaches a door, one by one, they're, you know, potentially -- or someone is cleaning, potentially. But the big factor -- all -- the big factor depends on how much was left there in the beginning, more than anything.

So those are all unknown variables that we just really never know.

Q. All right. And you could never testify when a -- when DNA is deposited on --

A. I could testify -- this is the most I can testify to when DNA was deposited: Prior to me ever receiving it in the laboratory. That's the best I can say. The DNA was there prior to me receiving it. That's it.

Q. And -- I'm sorry.

You can't -- you wouldn't be able to testify how long that DNA was on that object; right?

A. I -- I would have no way of testifying to that.

Q. And you would have no way of testifying

whether or not the DNA that was -- was picked up and extracted was transferred from some other person and/or object?

A. Yeah. I would have no way. The only thing I could testify to would be, you know, a lot of telling you how DNA is transferred, and giving general information. But I could not still -- I could not tell you how long something was there, you know.

Generally, if someone leaves DNA behind generally by -- if someone is touching an object. By length of time someone touches an object, of course, they'll leave more. How much pressure they put on the object, of course, they're going to leave more.

Some types of materials adhere DNA better than others. Like a rough surface versus a smooth surface.

But those are all, you know, just -- the bottom line is, I really can't tell you, you know, how long something was there or if something potentially got transferred.

Q. And you can't also equally testify how many different types of transfers, whether it's secondary or tertiary transfer?

A. You can't -- I can't testify to that.

I mean, as -- and, again, that depends on the amount of material that you had to start with, was how

many times it could transfer out. I think possibly you could probably say that the probability of a secondary versus tertiary decreases each time less of obtaining material. But you still can't testify that that could not be a possibility.

Q. All right. So just to kind of summarize your findings, would you agree that Tomasz Kosowski's DNA was not found inside the bathroom? It was only found --

A. I would have to look through your reports to see if that was the case. I don't want to say correctly, without making -- you know, which samp -- do you know which reports those samples were on, the bathroom? It was just the first couple reports; right?

And then later on there's more articles.

Q. Right. So we have the -- so Number 7.

A. I just don't want to say that without putting my eyes on it. I don't want to say.

Number 7.

Q. You've got the napkins that were found inside the bathroom. The napkin. The bathroom floor. And the interior swabs that were taken inside the bathroom, as well.

A. Sorry for the delay. I just want to make sure.

Q. No, you're fine.

A. I believe that's correct. Yes. I'm looking. You are correct in your statement.

Q. Okay. And then would you agree with me that Dr. Kosowski's or Tomasz Kosowski's DNA was not found on any evidence like the napkins or the paper towels recovered?

A. Yes. That's -- that's -- that's what I reported, yes.

Q. Okay. It was only Steven Cozzi's, which was from -- allegedly represented from the toothbrush that was found, and the napkins, and the paper towel?

A. That's correct.

Q. And I have some notes here that you tested some ammunition -- ammunition that was seized from Dr. Kosowski's?

A. Did I? What report is that in?

I think there was some.

Q. I believe it's referenced in the police reports.

Were you provided -- were you provided --

A. Oh, no, no.

Q. No?

A. No. I was not provided those samples.

Q. Okay. So you weren't provided any ammunition?

A. That's correct. Yes. Yes.

Q. So --
A. As of the time I came down for this deposition, I was not provided any.
Q. Okay. All right. And were you the ultimate recipient of Tomasz Kosowski's buccal swabs from his warrant, from his body warrant?
A. I'm assuming that. I mean, I don't know how they obtained those samples. But, yes, I'm the one -- I'm the recipient of the samples.
I don't know how they -- if they came about from a warrant. Yes. I don't know.
But, yes. I'm the one that received -- when the laboratory received, and it was transferred to my chain of custody.
Q. And was Dr. Kosowski's DNA profile uploaded to any databases? Was --
A. Yes. Yes, it was.
Q. What database or databases was it uploaded to?
A. It was uploaded to the CODIS database.
Q. Were there any other DNA profiles that were eligible for CODIS?
I'm assuming probably the toothbrush. No?
A. No -- yeah. The toothbrush, because that would be a secondary standard for -- under missing persons for CODIS. Yes, the toothbrush and --

Q. Michael Montgomery?

A. No, because he was not listed as a suspect. So he was just listed as an elimination. So we cannot enter elimination samples into the database. So, no, his was not.

Of course, Tomasz.

And none of -- none of the questioned samples met the requirements.

Q. Now, I know we talked about the -- the exclusionary standards that you have a -- create a database that's a voluntary database that law enforcement can provide anonymously their samples.

But were you provided any exclusionary samples from law enforcement involved -- not necessarily involved, but were at any of the crime scenes?

A. In direct comparison to this case, no. I mean, there's a pos -- like I said, the way samples are, the agencies maintain lists of -- there's something, if you need this, to see this, you could probably find it. The agencies maintain lists of samples they submitted to the laboratory for our database, so they would have a list.

And so you could cross that and see. If a sample was submitted to us, it would be in the database. So some of the people could have been compared against our

database, but we wouldn't know necessarily, without having additional research done.

Q. Other than Michael Montgomery --

A. He's the only one that was submitted as an elimination; that's correct.

Q. There were no other civilian elimination standards or profiles, samples, swabs, what have you that --

A. Yeah. That was compared -- that was sent to be compared directly to this case; that's correct.

Q. Did you share Dr. Kosowski's DNA profile with any other agencies or entities other than your lab?

A. Well, it's in the national database, so.

Q. Sure.

A. Yeah. If it -- if it -- the sample is to a forensic unknown, then his profile will become available to the laboratory where the forensic sample hit to.

But, no. We never shared it with anybody else. You know, it's -- all our data is confidential, you know, unless under, like, a subpoena for a court order for you guys.

The data only can be maintained in our laboratory, with the exception, his profile was uploaded to CODIS. And no other laboratory would see what his profile was unless somebody's forensic unknown, forensic sample, hit

the sample. Then they, you know, would be let know that there was a match.

Q. But there could be a potential hit from CODIS saying he's a potential contributor, based upon the upload?

A. The buccal, yes. Yeah.

Q. All right. And if you had to retrieve Dr. Kosowski's DNA from all of the entities you shared it with, and from all of the computers you've upload it to, would you be able to?

A. I think in order for a sample to be removed from the database, upon a nolle-pros or some sort of expungement of the case or -- then a request could be made to, I think it's to the state laboratory, that his sample could be removed.

But I think that's only under -- there's some -- there's some laws about it, too. I would have to look it up, the legal. But I think you have to write a written request after expungement, to have a sample removed.

Q. But specifically --

A. There's no legal requirement if there's a conviction or anything like that.

Q. Okay. What about specifically your computer is ever used to upload his DNA profile or the DNA

profile onto your computer, are those --

A. We cannot remove -- his profile is evidence in a homicide investigation, so we cannot remove that. That's part of our permanent record. And that would be altering our case file. So, no, we cannot.

Q. I think we're mis -- I think you misheard me. I didn't say remove. I said retrieve.

A. Oh, you mean -- what do you mean by retrieve? I'm sorry.

Q. So if you input Dr. Kosowski's DNA profile into your commuter at your lab to compute the STRmix calculations, is that still on your lab's computer?

A. Yes.

Q. And how long is it kept there for?

A. Well, it's a -- because this is a homicide investigation, we're required to keep these pretty much indefinitely. That's part of the case file. And, you know, it's part of the input file. So it's still a part of the data.

Q. It's my understanding that you testified at the grand jury on or about April 27th of 2023, regarding this case; is that correct?

A. I testified in the grand jury --

Q. Maybe I'm wrong with the date. I don't know.

A. Yeah. That's what I was just trying to see.

Yeah. Around the end of April, around April 26th.

No, it was a little bit after that. That was when I was sent this.

Q. And if you can recall, how long did you testify for?

A. Oh, my gosh. I honestly can't -- I can't remember. We have records in our laboratory that talks about how long I would have testified, but I don't have that with me right now.

Q. And at the time that you testified in April of 2023, before the grand jury, what reports had you authored at that point? What analysis had you performed at that point?

A. I'm trying to think of the date of the grand jury. It would be any reports prior to the date of the grand jury would have been authored -- would have been authored.

So, yeah. It was 4-27-23, is the date.

Q. Okay.

A. So -- so it looks like Request 6, Request 6 would have not been on there. It probably would have been at the request -- hang on a second.

I've only copied that. It would have been Requests 1 through 4. I'm not so confident that I would -- because it's, like, so close in the date for

Request 5, on. Like, 5 is dated, like, 4-25, most likely the day before. So -- but Requests 1 through -- 1 through 4.

Q. 1 through 4?

A. Yeah.

Q. Would that have included testimony regarding the --

MR. VONDERHEIDE: Ms. Tuomey, I'll have to object. The testimony before the grand jury is, you know, sworn. He can't disclose it or divulge it without a court order.

So whether we get there, maybe we get there, but we're not there yet. So I can't -- I'm going to have to object to testifying to what he said before the grand jury, because it's specifically in the oath that they take, that they can't divulge it unless ordered to do so by a court of competent jurisdiction, so.

MS. TUOMEY: So it's my understanding that the privilege belongs to the witness. So if the witness wants to testify --

MR. VONDERHEIDE: It says -- the oath that he would have taken would have been, unless you are ordered to do so by a court of competent jurisdiction, so --

THE WITNESS: That is the -- that is the oath I took. That's the oath I took. You are correct.

Q. (By Ms. Tuomey) Okay. So are you, Mr. Summerfield, also asserting that privilege as well?

A. I -- if I took that oath, then, yes, I should take that privilege, yes.

Q. All right. So if I were to ask you what your testimony would be, then you would decline to answer; correct? What your test --

A. I would have to decline to answer what I testified on this in the grand jury.

Q. All right. And I think I asked you before, give me an amount of the total blood, in volume, that was extracted, quantified at the -- in the bathroom at 1501 Belcher Road.

And you indicated or told me that the total amount could be added up by the amounts that were extracted from the small autosomal.

A. Yeah. If you look at the quantitation reports for each of -- each of the samples, you can look at the small autosomal target, and just, one by one of those samples, add them up.

And I could do that if you need me to do it. I just did something on the fly. I would want to make sure I gave you the right answer.

Q. Okay. So maybe perhaps -- because we're going to continue your deposition. If you could perhaps have maybe an estimation or -- you could do that?

A. It's something I would not put into a report, but I could give you -- you know, because it's not something we report out. But I could give you -- I could do that calculation so I have an answer to put on record for the next deposition.

Q. Great. I would appreciate that.

A. And you're looking at just for the bathroom; correct?

Q. For the bathroom.

And if you could do just an overall -- overall amount of DNA that was extracted.

A. Okay. And you want -- you want just the extraction? I want to make sure I give you correctly. The amount of DNA just from the extraction in nanograms, not necessarily the amount amplified, or just say 15 microliters?

Q. The amount extracted.

A. Okay. Okay. I can do that.

Q. Okay. All right. So let's kind of move on.

I'm going to move on to STRmix.

What's the current version that your lab is using for that specific software program?

A. It's 2.6 -- 2.6.3.

Q. All right. And do you know what the most current version of STRmix is?

A. 2. -- 2.11.

Q. And do you know how many miscodes have been reported since STRmix went online?

A. I don't know exact number.

Q. Do you know -- okay. Do you know whether or not any of the miscodes that have been reported would affect or make a difference because you're not using the most up-to-date version of the software program?

A. To my knowledge, there is nothing that would have affected my results with the newer versions.

Q. Do you know how these miscodes are reported to STRmix?

A. I -- I do not know that.

Q. I think you already -- I think I already asked you this, but STRmix is not able to filter out noise; right?

A. No. It's only able to utilize the data that you -- that you -- you give it. So if it's data that's below the analytical, that data is not interpreted within STRmix.

Q. And then it's my understanding that the data that's obtained from the genetic analyzer is uploaded to

STRmix. Meaning it's not raw data. It's data from the genetic analyzer that's uploaded by yourself; right? And in this case, to the STRmix program and input into that program; right?

A. That's correct. So of the guide we looked at, the only edits that would have been made on my part was the ones that were marked as NTA (phonetic), which I determined was pull-up.

The actual data imported to STRmix would include the stutter that was above -- the minus stutter and plus stutter that was above 50 analytical. So that would have been included in there. It's just not included on the printout. But in the -- in the data to STRmix, that's also included.

And when you look through our files, you can see at the end of the STRmix interpretation report --

Q. Yes.

A. -- you'll see, like, a little -- a little section as for the input file. And it has exactly what was inputted.

Q. Right.

A. So you can see within exactly, which includes the stutter and the RFUs, the base page for everything. So you can -- you can see exactly what was inputted.

Q. And the parameters that are set by your lab

are the parameters that were determined to be, I guess, reliable on your instruments, based upon the validation that your -- your lab conducted?

A. Yes. It's not just based on our lab. We actually -- actually, we analyze all of our data, and then we send all of our data to ESR, which is the company that really invented the software. And they're the ones that actually took a look and analyzed our data.

And after we got the results back from them, we redid another subsequent study to confirm the results that they had in, and make decisions of how we're using STRmix.

So we actually sent it out to ESR out of New Zealand. And they're the ones that looked at the initial data.

Q. What -- now, it's my understanding that STRmix has a variety of different populations to use. But what are the populations for the allele frequencies that are routinely used by your lab?

A. We use the Caucasian, Hispanic, and African-American. They're typically the three most common, so.

Q. And do you know how those population databases were created?

A. Yes. They're actually through NIST, and they're published. So you can actually find the information on them. I think I included -- we put it in in our report, I think.

Yeah. They're published in Forensic Science International. And it's using the NIST 36 revised population database.

So in our appendix report, you can find out exactly where they were published. And it talks about how the database was created.

Samples are collected from individuals based upon, usually typically self-reporting their own ethnicity or direct observation of, you know, this person is Caucasian. And a sampling is taken. And then a forensic station will look over the data.

In this case, the database that we use is published in Forensic Science International.

Q. Do you have a date for that?

A. It is actually July, 2017.

Q. I was going to -- okay. 2017.

A. And you can see the exact -- the exact citation in the appendix if you need to find it exactly.

And a lot of times, articles, you can find it without having to pay for it. It's pretty popular. I think it's probably free off their website.

Q. When you run or upload date through STRmix, isn't true that every time you run, if you were to run the same data a second time, you will never get the same likelihood ratio?

A. True and not true. You may get the same likelihood ratio, and you might get some spike variation, but it's always going to be within -- like, within a range.

If -- if I ran -- if I ran the same sample, any of these samples, and I set the software to start at Position A, which they call it within the software, C. I say I want to start at C 24,589, which means this is going to start at the exact -- it's going to start in that place.

If I rerun the software and start it at the exact same place, it's going to get exactly the same result.

So I can get the same result if I start at the exact same spot. But there is some small minor variations within the likelihood ratios.

Q. Are you talking about the burn-in, if you start at the same spot, but the software program --

A. Right.

The software program -- if you look at the STRmix reports, you'll see a thing that says C. That's a random place that the software starts. Okay?

I could set the software -- I could rerun these samples and start at the exact same spot, and we'll get the exact same answer, the exact same LR. But if I start at a random C, it's going to be a different -- it's going to be a slightly different LR within a small variation.

Q. Okay. Are you familiar with a NIST publication regarding experts to cau -- to use caution in their presentation of likelihood ratios in court?

A. It's probably an older article, if there was one. What's the year on it?

Q. It's 2017.

A. Yeah. Now it's the preferred method of reporting. All of the SB standards everywhere state that likelihood ratios should be reported.

So if that was the original -- and, of course, you -- that statement, you should say about any statistical statement, you should use caution. Meaning you want to make sure you convey the information properly to the jury so they can make an educated decision. You don't want to say the likelihood ratio incorrectly so you're not swaying the evidence.

So the word caution should be applied to anything that you're doing in a legal matter.

Q. But the manner in which STRmix conducts these

statistical calculations --

A. Is -- is scientific.

Q. -- they're just random guesses; right? I mean MCMC, you're familiar with that; right? Those are just educated guesses?

A. Educated guesses based upon previous data that's been submitted within bounds. So it's not like -- it's -- it's using our existing validation data to then make informed decisions of interpretation.

So it's not -- it's -- yes, it is using the MCMC process, which is using the hot-cold game of this -- this data looks -- this is the best fit. I -- this is not. I accept this one. I don't accept this one.

But it's not like -- it's random, but it's actually random in eight different directions that all have to come back to the same spot to have an acceptable answer.

So you have eight random independent samplings of data. So it's a single profile. We look at one of the cases. It's independently looking at one profile, Position 1. It started at another position, the second, third, fourth, fifth, sixth, seventh, eighth. All of those. When it gets to the end, it has to converge for the results to be accepted.

So it's -- yes. Even though it's independent guesses, it's having to converge on the same result at

the end.

So it's the same thing that -- MCMC is used for code breaking. It's used for, you know, weather reporting. It's used pretty much everywhere.

Q. Did you say weather reporting?

A. Yes. Tracking it for hurricanes. You know, they use an MCMC process for hurricane tracking. Of course, the data is only as good as the data you feed it. So, they -- you know, it's -- as for hurricane tracking, you'll notice that as the data is -- as a hurricane approaches and they have much more information about the hurricane, the wind speed, et cetera, the path of trajectory becomes a lot more probable. Well, that's all based upon the data that you feed it.

So our -- our STRmix is based upon our validation. And so it's -- it's very scientific. I don't know.

Q. Would you agree with me that if an evidence profile is determined to be a single source, which I think you did in -- on multiple samples in your various reports, that the likelihood ratio is reduced to one, which is essentially the random match probability?

A. Yes. Correct. Under -- yes. For the full profile where you don't have any dropout, yes, it would be 1 over the random math probability. So that would be simple.

When you have dropout, you have to take the dropout into calculation. But in the simplest terms, yes, it would just be 1 RNP for the likelihood ratio. One giving to the prosecution that you have instances supported by an inclusive person versus the second over the random act probability.

So, yeah. So you're correct on that.

Q. Are you familiar with the -- with transposed conditions regarding like --

A. Yes. And it's like -- it's very easy. It's conditional.

So when I am testifying to STRmix, you will see me read this word for word, because a lot of times, what happens is, you're not speaking to the evidence, you're speaking to a person, and that's transposing the condition.

So for one of the samples, like, I'll state the DNA profile is approximately X times more likely if it originated from. Then I will not state that, you know, it's more likely that it originated from this person. That's transposing conditions.

Q. Would you agree with me that the statistical calculations that you include Dr. Kosowski as being a contributor to, he's -- his DNA profile is always included in that statistical probability when performing

that statistical calculation? Does that make sense?

A. I would have to look through all the samples to make sure. But there was quite a few samples.

Yeah. I would have to make sure that's a correct statement. There's quite a few samples where he was included. He showed -- he showed strong support for the possibility that he was a contributor.

Q. Why did your laboratory decide to go with STRmix, as opposed to any other probabilistic genotype software program?

A. Well, there's only two -- two software programs out there for probabilistic genotyping. There are some other -- this is semi-continuous, meaning there's not different thresholds to be used.

So there is some other programs out there that uses a somewhat continuous model, but there's, like -- it doesn't allow for peak heights, you know.

So the only semi-continuous models for probabilistic genotyping would be STRmix and TrueAllele.

One, STRmix is much more used throughout the community.

And meeting Dr. Perlin in person, I don't think I want to deal with him.

Q. And STRmix --

A. Because, actually, I had an extensive

conversation when I was in Philadelphia, way back, as TT, I was bringing him in and -- to use TrueAllele within our case work. And he pretty much told us that we were all too stupid to use his software. So, yeah.

Q. Okay. So STRmix, you would agree with me, that the source code, the algorithm -- the algorithms that were created by STRmix are not open; right? You don't -- you don't know what that -- that's not --

A. Not necessarily true. As a defense counsel, you can actually set and request STRmix, actually. And they will give -- they will work with you, that you can actually look at it, at the software. You just have to work with them.

Unlike TrueAllele, which has refused, to date, to encompass any of their source code whatsoever.

STRmix will work with you. You just have to put in a request. You can actually go through the STRmix website and put in a request to do that, if you need to.

Q. Yeah. And then you have to go to Australia and then go sit there and not make -- take any notes.

A. I don't know what you have to do. But it's possible.

But True -- the TrueAllele software, they have yet to actually disclose any of their source code.

Q. Okay. It's my understanding that TrueAllele

provides a source -- it's an open source code.

A. No way.

Q. Okay. And you said those are the only two software programs? I thought there were -- the names escape me, because they're not --

A. There might be -- there may be some other names out there, but they're not really popular or I really don't know much about them.

Q. And STRmix --

(Overlapping speakers.)

A. What's that?

Q. STRmix was created by the -- a government in Australia; right?

A. Yeah. It was a joint collaboration. And, yeah, it was not in Australia. Out of New Zealand.

Q. New Zealand.

A. New Zealand.

Q. And when I say government, law enforcement, really, ultimately?

A. Yeah. There's -- yes. Correct.

MS. TUOMEY: Okay. I think we can go ahead and suspend this deposition, if that's okay with everyone. We're going to go off the record.

(Discussion off the record.)

(Deposition recessed at 4:13 p.m.)

STATE OF FLORIDA
COUNTY OF POLK

I, CHAD SUMMERFIELD, under penalties of perjury, declare that I have read the foregoing transcript of my testimony which was taken in the case of State of Florida v. Tomasz Kosowski, on July 17, 2024, and the corrections I desire to make are as indicated on the attached Errata Sheet.

Done and signed this ____ day of _____, 2024.

_____

CHAD SUMMERFIELD

State of Florida v. Tomasz Kosowski July 17, 2024

ERRATA SHEET

PAGE	LINE	CORRECTION	REASON

Under penalties of perjury, I declare that I have read the foregoing document and that the facts stated in it are true.

_____ _____

DATE CHAD SUMMERFIELD

CERTIFICATE OF OATH

STATE OF FLORIDA
COUNTY OF POLK

I, the undersigned authority, certify that CHAD SUMMERFIELD remotely appeared before me and was duly sworn on July 17, 2024.

Witness my hand and official seal this 19th day of December, 2024.

LINDA A. McGILL, RPR Qualified
Notary Public, State of Florida
Commission #HH598038
Expires November 17, 2028

Known Personally _____ OR Produced Identification __x___

Type of Identification Produced: Florida DL

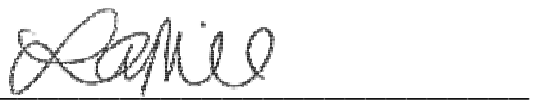
REPORTER'S DEPOSITION CERTIFICATE

STATE OF FLORIDA
COUNTY OF POLK

I, LINDA A. McGILL, certify that I was authorized to and did stenographically report the deposition of CHAD SUMMERFIELD; that a review of the transcript was requested; and that the transcript is a true and complete record of my stenographic notes.

I further certify that I am not a relative, employee, attorney, or counsel of any of the parties, nor am I a relative or employee of any of the parties' attorney or counsel connected with this action, nor am I financially interested in the action.

Dated this 19th day of December, 2024.



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