procedure, I just know that she was disciplined for not following policy, and that's the reason why she was terminated. So I really don't have all the details of what was involved.

MR. HOCHGLAUBE: I'll pass the witness, Judge.

THE COURT: Anything further from this witness?

MS. FULLER: Nothing further, your Honor.

THE COURT: All right. We're going to take a small break and take a plea.

(Break.)

THE COURT: All right. Ms. Fuller, would you like to call your next witness.

MS. FULLER: Yes, your Honor. The State would like to call Dr. Rick Staub.

THE COURT: You may proceed.

MS. FULLER: Thank you, your Honor.

DR. RICK STAUB,

having been duly sworn, testified as follows:

DIRECT EXAMINATION

BY MS. FULLER:

Q. Would you please introduce yourself to the Court.

A. Yes. My name is Dr. Rick Staub. I'm from Plano, Texas.

Q. All right. Let's start with your educational background, then we'll work forward to your work experience.

A. Sure.

Q. Tell us a little bit about your educational background.

A. I have a bachelor's degree in mathematics from the University of Wisconsin, and after that I proceeded to obtain a master's and a PhD in genetics from the University of Arizona.

Q. Okay. Were there any subspecialties that you focused your studies on during your master's and PhD work?

A. Well, at the time I did my masters and PhD work I was actually working on plant genetics that focussed on chromosomes and DNA, and after leaving there I became a standard professor at Carlton College in Northfield, Minnesota, where I was for eight years, teaching genetics and working on research in corn genetics, maze genetics.

After that, I left there to take a job in commercial identification industry, human identification industry, for paternity testing. I worked at a lab in North Carolina for three years doing that, and then I came to Houston, Texas in 1993 to start a laboratory with a woman called named Caroline Caskey, and that laboratory was called Identigene, and it became a very large paternity testing company, and then eventually branched off into forensic testing. We used to do testing for the Houston Police Department.

In 2000, though, I moved to Dallas to take a position as the laboratory director. I had been a laboratory director at Identigene, and I was named laboratory director and

compilations director at Orchid. At that time it was called Gene Screen and then it became Orchid Cellmark eventually, and I was there until 2012 when LabCorp purchased the company.

Q. All right. And where are you at now?

A. And now I am at my local police department, the Plano Police Department, where I manage the crime scene investigation unit and the property evidence room, and I'm also acting as a DNA liaison between the detectives and DNA labs.

Q. Okay. So you mentioned that in -- with Identigene all the way through to Cellmark that you were a lab director?

A. Yeah. Actually I was the lab director before that at the company in North Carolina which was called -- it was called -- gosh, I can't even remember -- anyways, it was a large paternity testing laboratory. Genetic Design. Sorry.

Q. Okay. So we've already heard from two DNA analysts in this case. Did you do DNA analysis work throughout your career?

A. Yes.

Q. And as a lab director, did you continue to do DNA analysis work?

A. Yes.

Q. Or did you then kind of shift more into a technical review?

A. Well, as a lab director I would basically be responsible for making sure that my analysts understood how the

process worked and how to carry out the tests, and then I would technically review their work and sign off cases with them.

Q. Okay. So back in 2011 you were the technical reviewer on -- let me back up first. Have you testified before as an expert in courts?

A. Yes, many times.

Q. Okay. And were you deemed an expert in the courts in Texas?

A. Yes, right here in Houston as well.

Q. Okay. And are you published?

A. Yes, I am.

Q. Okay. Back in 2011 you were given a case that you were the technical reviewer on. The case number was MF11-0007. Do you recall this case and have you had a chance to review it?

A. Yes.

Q. Okay. Now, Huma Nasir was the analyst in the case. However, you did some calculations in this case in addition to being the technical reviewer; is that correct?

A. That's correct.

Q. So at what point did Huma come to you, I don't mean point in time, but at some point in time Huma came to you to discuss this case; is that correct?

A. Yes.

Q. All right. What did you-all talk about in terms of the results in the first round of testing that came through

with this case?

A. Well, she showed me what had been done already, and asked me to look at it, and give her my opinion on it.

Q. Okay.

A. And at the time that I looked at it, my opinion was that the sample that was obtained, it was a sample from a penile swab from Dean Wood, and that penile swab, clearly the profile was obtained with MiniFiler, and it was -- it was a partial profile, so when you get a partial profile, typically that means it's a pretty low level sample. And I looked at the results, there were only two loci that gave results, but it was clear to me that there was a mixture of two people there.

Now, obviously, the prime candidate for one of those components would be Dean Wood because it was a swab from his own penis, and then there appeared to be another person as well. So my point to Huma was you could look at it two different ways. One would be that you could look at it as a -- you could do what's called an inclusion probability. So you look at the results that are there and then you calculate how many people out of various populations would be included in that mixture. But when you do that, you're looking at it just saying all the alleles that are there and anybody that has any kind of a profile that could be included in there would be included in your stats.

That's not taking into account all the information

you have, because you know that the penile swab is from a particular person, in this case Dean Wood, so it's important to look at his profile and then look at what else is there, and calculate what we call a likelihood ratio. And that likelihood ratio tells you the likelihood ratio that it's from Dean Wood and somebody else versus Dean Wood and the victim, which in this case was Flora Ryan I believe.

Q. Okay. So the likelihood ratio test would take into consideration all of the data that you had versus the random probability that leaves out some of the data that you have, is that --

A. Correct.

Q. -- correct?

A. Yeah. It's -- it's more all encompassing. You're taking into account more -- more of the genetics behind what you're -- what you're seeing. And granted, there's only two loci that came through in the data, so it's not very strong data, I'm just going to say that right off the bat. So because of that, the -- any statistics that you produce are going to be fairly -- not as probative as if you had eight loci, all the loci in the MiniFiler working.

Q. So the statistics are going to be lower because you have less loci to test versus having the whole nine available?

A. When you say lower, probably -- lower -- a lower statistic means a higher probability. So anyways, yeah, the

statistics would be worse, in other words, they're not as informative as if you had more loci.

Q. Okay. But did you feel that you had enough loci to actually do the likelihood testing?

A. Well, yeah. I mean, you still have results there and you can still look at them and say what they mean, even though it's a low level, yes.

Q. Okay. So you actually performed the statistics in the second report; is that correct?

A. Yes.

Q. How did you do that?

A. We have a -- you know, there's just standard protocol that you would use to calculate a likelihood ratio, and I just calculated it out mathematically using a spreadsheet, and then Huma checked my calculations using the known frequencies, or estimated frequencies that we have for alleles at the two loci that we had data for.

Q. Okay. So are you using a computer software program or are you just using the protocols and you're using, like an Excel spreadsheet to help you do those?

A. Yeah, I'm using an Excel spreadsheet and using the formulae that we know represent the likelihood ratio.

Q. Okay. And so what statistics did you come up with for the second report?

A. Well, on the second report, the statistic for the

likelihood ratio and -- you know, we calculated for three different races that we had allele data for, Blacks, Caucasians and Southwest Hispanics, and the likelihood ratio comparing Mr. -- and probably the best one to look at actually would be Caucasians because that's the race that the victim and the defendant are.

So when you look at Caucasian frequencies, the likelihood of getting those results from Mr. Dean and someone else is only 1 out of 102 times as likely as getting it from Mr. Dean and Flora Ryan. So that's the way a likelihood ratio works. In other words, it's 102 times more likely to get those results from the suspect and the victim as it would be from the suspect and someone else of the -- unrelated to that person, to the victim.

Q. Okay. Now, both of these types of testing, both types of testing are established tests that you can do, and when I say established tests, I mean the analysis, whether you do the random probability or the likelihood ratio, they're both standard means of analysis. Is that fair to say?

A. Yes.

Q. Okay. And you performed both in this case, or your lab did, and they reported both of those results. Is that fair to say?

A. Yeah. We issued a second supplementary report, supplemental report with this likelihood ratio statistics in

it.

Q. Okay.

A. And we also compared one other person in that report. It was a relative of Flora Ryan.

Q. Okay. And were you able to include or exclude that person?

A. Flora Ryan's daughter could not be excluded as a possible contributor, which is not un -- it's not unbelievable because she's, you know, shares many genes with Flora, but her granddaughter could be excluded as a component.

Q. So the bottom line, when you take the statistics and the numbers out, the bottom line is that you can't exclude Flora Ryan or her daughter as having DNA on that penile swab. Is that a fair statement?

A. Yes, we cannot exclude that possibility.

Q. Okay. And if you didn't have enough data or the data was inconclusive, you would have reported that?

A. Yes.

Q. Is that correct?

A. Yes.

Q. And if there wasn't enough data to -- or if there was enough data to exclude somebody, you would have and, in fact, you did exclude somebody in these tests?

A. Yes.

Q. Now, were you the lab director when -- when Elizabeth

Feller was let go from Orchid Cellmark?

A. No. I was no longer there.

Q. So you have no knowledge whatsoever about the circumstances that led to her leaving Orchid Cellmark?

A. No.

MS. FULLER: Pass the witness, your Honor.

THE COURT: Cross-examination?

MR. HOCHGLAUBE: Thanks, Judge.

CROSS-EXAMINATION

BY MR. HOCHGLAUBE:

Q. Dr. Staub, I just want to cover a couple of things with your background.

A. Sure.

Q. You said you were an assistant professor at Carlton College?

A. Yes.

Q. Which is a liberal arts college in Minnesota?

A. Yes, it is.

Q. And you were there for eight years and then you moved on, right?

A. Yes.

Q. So you did not receive tenure there?

A. I did not receive tenure and I appealed it and won the appeal but I still left.

Q. Then you went to Genetic Design in North Carolina?

A. Yes.
Q. And there you were the -- what was your title?
A. I started out as an assistant director, then was promoted to associate director. I was there for three years, and by the end of the three years I had been promoted to director of DNA operations.
Q. Okay. And from there you went to Identigene; is that right?
A. Yes.
Q. Now, when you went to Identigene, did you go there because of any problems at Genetic Design?
A. No.
Q. It was just a better job opportunity?
A. Yeah, it was a much better job opportunity.
Q. And you worked at Identigene for how long?
A. 'Til 2000, from '93 until 2000.
Q. So about seven years?
A. Yes.
Q. And when you left there you went to Orchid; is that right?
A. Yes.
Q. And when you left Identigene, was that under -- was that because you had a better job opportunity at Orchid?
A. Yes, very. It was a very good job opportunity.
Q. So you did not have any -- there were no problems at

Identigene that caused you to leave. Is that fair to say?
A. Well, I mean, there was some disagreement that I had with the president about the direction that I thought the company should go and we weren't agreeing, so I left to go to --
Q. So did you resign or were you terminated?
A. I was terminated.
Q. And then you were at Orchid Cellmark, right?
A. Yes.
Q. For how long?
A. 'Til 2012.
Q. So there you were there for about 12 years; is that right?
A. Yes.
Q. And ultimately they were bought out by LabCorp, right?
A. Yes, they were bought.
Q. And when they were bought out by LabCorp you lost your job, right?
A. I did.
Q. And that's when you went to the Plano Police Department, right?
A. That's correct.
Q. So now you work in law enforcement, correct?
A. I do.

Q. Are you a certified peace officer?
A. No. I'm a civilian employee.
Q. Okay. And you've been working there now for I guess a year?
A. No. Just since March 11th.
Q. Okay. So about six months?
A. Six months, yeah.
Q. Okay. All right. But you were the lab director at Orchid when these tests were performed?
A. I was, yes.
Q. Now, there's a whole bunch of different machines that get used in a DNA analysis, right?
A. Yes, there are.
Q. A part of the reason why there's so many different previous and current employees of Orchid here testifying in this case is because it can be more cost effective to do sort of an assembly line of tests, right?
A. Yes.
Q. You're aware that sometimes you can have one person go through each of the different steps, extraction, quantitation, amplification and analysis, sometimes one person can do it all, right?
A. That's -- that's possible, but it's not as efficient as separating it out.
Q. Right. It's more cost effective to have one person

do the extraction, then another person pick up where the first person left off and do the quantitation, right?

A. That's correct.

Q. And then have another person pick up and do the amplification, right?

A. Correct.

Q. And then another person pick up and do the analysis?

A. Yes.

Q. All right. But you agree with me that each and every person in that process is providing sort of pretty important work and analysis and information in coming up with the ultimate analysis in a DNA test, right?

A. Yes. All the steps are important.

Q. The -- and so is the credibility and sort of qualifications of each of the people that perform each of these tests is also important, right?

A. Yes.

Q. And you'd agree with me that one of the downsides to doing it this way is that one person may do hundreds and hundreds of extractions over the course of a couple of years, right? That's possible, right?

A. Yes.

Q. And that their memory of what they did in -- what they did in a certain case, it may be less solid than a person who actually takes the time to go through and do each and every

single part of the analysis and review every single step in the analysis themselves?

A. Well, not so much -- I'm not so sure I agree with that. I think either one you run the risk of the person not remembering a certain case they worked on. And that's exactly why we take detailed notes of every sample that we run through there, so that we can put together a case file at the end which explains precisely what happened with every sample in that case. Nobody could remember every case they worked on, even if they did it all themselves all the way through, you know, so whether -- whether you do it as an assembly line fashion or one person working the whole thing, I think you still run that risk of a person not remembering what they did.

Q. So you'd agree with me that the people who are actually performing these analyses, right, it just can't be expected of them that they would actually remember their actions on a particular analysis; is that right?

A. Well, you know, they might, but I wouldn't fault them if they didn't remember precisely. You know, like I said, that's why we'll take a note. For example, if something weird happens in a process that you carry out, like an extraction, say, oh, this tube fell out of the rack or something, and I had to put it back in, you would take a note of that just in case something down the line indicated that that was a problem.

Q. Right. But at this point now, because it's been more

than a couple of years since all of the analyses that Orchid Cellmark performed, right?

A. Yeah, I think so.

Q. Some of 'em I think the tests were performed in December of 2011, so let's say a year and a half?

A. Correct.

Q. But you'd agree with me that, I think we're saying the same thing, it would be too much to expect a perfect recollection by each of these analysts of the action they took in this case, right?

A. I think so. I think everybody, you know, relies pretty heavily on their case file to refresh their memory of what happened with the samples in the particular case they're testifying in.

Q. Do you have any personal recollection of your involvement in this case?

A. In this case, I do remember talking to Huma about it, because it was -- it was a -- an unusual case, you know, not one that we would get every day.

Q. Why was it unusual?

A. Hmm, I'd say, you know, it's -- uh -- first of all, it's from a penile swab, we don't do a lot of those, and then there's a certain thought process that you go through when you're looking at this sort of a sample, and I already explained that. If it's from a penile swab, that you would

fully expect to obtain some genetic data from the individual who was swabbed, unless they, you know, person that collected the swab was extremely careful not to -- not to touch them, but that's hard when you're doing a penile swab, so that's one thing. And it's a mixture and it was done with the MiniFiler.

Q. The MiniFiler is unusual?

A. Not unusual, but it's only used for samples that are degraded or low level. It really was designed for degraded samples.

Q. The -- it's my understanding it was initially performed on the victims of 911. Is that what you understood?

A. Well, it was used on victims of 911. That wasn't why it was developed, though, but it was used in those cases, yes.

Q. But because you would expect in sort of the mass carnage of those buildings that you would get a lot of degraded DNA?

A. Absolutely, and that's why it would be good for those. In fact, at that time our laboratory in Dallas was using this technology called Snips, on those sorts of samples, because Snips are all very good for degraded samples.

Q. Did you try to use Snips in this case?

A. No. By the time we did this case we no longer ran Snips in our lab.

Q. Are there any other types of testing that can be done on degraded or low level DNA?

A. Currently, I'd say STRs is pretty much the only thing you can do besides Snips.

Q. Okay.

A. And there's not that many labs that do Snips.

Q. Was there any testing done to determine what type of DNA cell you were analyzing, whether it was a blood cell or epithelial cell or sperm cell?

A. No. With a sample like this you just typically take the swab and test everything that's there. You just extract all the DNA you can from the swab. You don't look at it under a microscope or anything to see what kind of cells are there.

Q. The -- you're aware that after your test, after Cellmark's tests were completed there was still apparently some material left; is that right?

A. I'm not aware of that.

Q. Well, if Huma Nasir testified that there was, you wouldn't -- do you have information that contradicts that?

A. No. I just -- I'm just not aware of that.

Q. Okay. Now, the -- along the same lines of sort of going to memory and what people can remember of their own activities, all of these different machines that are involved in the process, there's a thermocycler, there's I think a 7000 does that --

A. Yeah. That's the quantification system.

Q. Right. There is a genetic analyzer, correct?

A. Yes.
Q. There is Qiagen?
A. Qiagen.
Q. Qiagen.
A. EZ-1.
Q. And the TKN Genesis?
A. Yes. That's a robot that transfers liquid from one tube to another.
Q. So again, along those same lines of memory, all these different machines and instruments require maintenance, right?
A. Yes.
Q. And I'm sure Orchid's policy was to provide proper maintenance, right?
A. Yes.
Q. But again, we can't have anybody who actually remembers performing all of the requisite maintenance on all these machines two years ago, right?
A. That's why we keep records of it.
Q. Sure. But if the record is meant to actually refresh the memory of what happened two years ago, that's not actually doing that, is it? Just because you see it on a record doesn't mean you necessarily remember doing the maintenance, right?
A. Not necessarily, right. I mean, but -- but if you have the record that indicates it was done.
Q. Right. The -- now -- now, you -- in this particular

case, you basically -- Huma came to you and said, you know, the numbers are pretty low, right? She said the numbers are only 6 to 1 for Caucasians in this case, and I want to see if there's any type of other statistical analysis we can do, right?

A. I don't think she actually said it that way. She just said is there some -- you know, is there another way we could you look at this and see, could we do the stats with a -- another technique.

Q. Now, and I guess part of the problem with the 1 in 6 number is that you really only had in Orchid Cellmark the mathematical numbers for one of the loci that was there?

A. That's correct, yes.

Q. And you didn't have the numbers for the other loci?

A. Correct.

Q. Am I saying that? Locus?

A. Locus.

Q. Locus is the individual?

A. Right.

Q. All right. By the time you left Orchid Cellmark, did you guys have the other, the numbers for both locus -- loci?

A. Yes. We -- in fact, this case probably was a case that stimulated us to change our statistics module in our laboratory information management system to include two new loci. D2 was one of them. D-19 was the other. But when I calculated our statistics, I used allele frequencies that were

published in the literature by the FBI, and I used those to compute our stats.

Q. The ultimate 102 number --

A. Yes, yes.

Q. -- that you used. Basically that's your analysis based on both of the loci that were detected?

A. Correct.

Q. Okay. Now, do you know what the RFU standard was for allele detection at Orchid back then?

A. Yes. We used a hundred RFU for allele detection.

Q. And did those, the machines that you're getting, this electropherogram -- did I say that right?

A. Yes.

Q. The seismograph looking thing?

A. Right.

Q. That machine is made by Applied Biosystems, right?

A. Correct.

Q. And Applied Biosystems has a recommended RFU for its machine, right?

A. No. Actually they -- hmm -- what's recommended is that you do your own validation in your lab, and figure out from your instrument where to set your allele calling threshold. And so that had been done and we decided on 100 RFU at that time.

Q. The -- if there was another expert that testified

that Applied Biosystems, that he recognized Applied Biosystems used a recommended RFU of a hundred fifty, would you dispute that?

A. I don't recall them ever recommending that, but --

Q. I guess I'm asking you whether you dispute that?

A. Yeah, I might. I mean, I think that the recommended way to do it is to do your own validation and determine where your threshold should be.

Q. And that's right too, that basically Applied Biosystems recognizes that different labs may come up with different numbers on their own.

A. Right.

Q. But that their recommended number was 150. I'm asking you whether you dispute that?

A. I'm not disputing it, but I don't remember it is what I'm saying.

Q. Now, and you'd agree with me that the numbers that you came back with, either the 6 to 1 or the 102 to 1, they'd be different if the RFU standard were raised higher than what Orchid Cellmark had, right?

A. Well, actually, in, hmm -- the second way I did it with the likelihood ratio, the reason that I looked at it that way was to essentially make the suspect cancel out, because there's nobody disputing whether he's there or not. It was from his penile swab. So when you're looking at the likelihood

ratio it's really, it's comparing the likelihood of getting those results from him and another person or him and Flora Ryan. So you see, if you set that up as a ratio, he cancels out of that, you know, he's on the numerator and denominator. So it's basically what's the likelihood of these results after you cancel him out, you know, of someone else versus Flora Ryan, 1 out of 102, that's really what it comes down to.

Q. Now, the number of 102 to 1, basically what you're saying is that it's much more likely that that DNA came from Flora Ryan than it came from a random citizen you see walking down the street, right?

A. Random Caucasian person.

Q. Random white person, right?

A. Yes.

Q. 102 times more likely, right?

A. Yeah, just based on the two loci that we have.

Q. But again, that number, if you just looked at that number, is in some ways misleading, right?

A. I don't think it's misleading. It's just -- you know, it's the answer to the question how likely is it these results came from someone else as opposed to Flora Ryan. Now, 102 isn't exactly astronomical, you know. I mean, it's like, many times if you get a full profile it's going to be in the quadrillions.

Q. But take this as an example, right, if the people in

Plano, right, have a .01 percent chance of getting lung cancer this year, right, but people in Dallas have 1.02 chance of getting lung cancer this year, right, the people in Dallas are 102 times more likely to get lung cancer, right?

A. I didn't --

Q. Point zero one --

A. Something like that.

Q. 1.02.

A. I didn't do the math on it yet, but, okay.

Q. But -- all right.

A. Something like that.

Q. So .01 to 1.02 percent, right?

A. Okay.

Q. That's 102 times, right?

A. 102 times more likely, right.

Q. Right? And yet it's still very unlikely that anybody, that if you take a random person in Dallas or a random person in Plano that they're going to have -- that they're going to get lung cancer this year, right? It's a small minority of people, right?

A. Right. I have to think about that one. I think --

Q. My point is --

A. Yeah.

Q. Just by saying, well, she's a lot more likely to be a contributor than if we took any other random person off the

street, right, that really doesn't tell us how likely it is to be her, right?

A. No. It can't tell you how likely it is to be her. It can only tell you how likely it is to get these results from her and the suspect versus someone else and the suspect.

Q. Right. But you understand, a lot of times with these DNA tests you come back with trillions to one or quintillions to one?

A. Correct, yes.

Q. In those cases you don't need to do this extra added analysis like you did in this case, right?

A. Well, if you already have a stat of, you know, four quadrillion to one then --

Q. Right. It's a strong stat, it stands by itself, right?

A. Right.

Q. And it makes it very clear that it's highly unlikely that this DNA could have come from any other source, right?

A. Correct.

Q. But in this case, you felt the need to do this additional mathematical testing, right?

A. Well, I didn't feel the need to do additional testing because of that. I felt the need to do it because I felt it much more accurately represented the data that we have, that it's a better way to look at it. And, you know, that's -- if

you look in the literature also, people say that, that likelihood ratios are a better way to look at mixtures if you can than inclusion probabilities because inclusion probabilities are fraught with all kinds of difficulties.

Q. So why do all these labs do that when they get a quintillion to one?

A. Well, those quintillion to one, those are typically from single source samples, so -- you know, in actuality, that is a likelihood ratio. It's a likelihood of getting those results from your guy versus someone else, for quadrillion to 1, that's what it really is. You're computing -- a match probability is essentially a likelihood ratio.

Q. Well, is 6 to 1 not a likelihood ratio?

A. Yeah, but that 6 to 1 did not include all the -- all the data. In other words, it -- it just was the match probability for one locus looking at it as being from one person so -- not the same.

Q. So this -- this loci, the -- the CSF?

A. Uh-huh.

Q. All right. That's the one where you-all didn't have the -- basically the statistics to compute into the analysis, correct?

A. No. Actually that is the one that we did. The D2 locus is the one that we did not. It's D2S1338.

Q. Okay. So the D2S1338 you didn't have the statistics?

A. Well, we didn't originally have the allele frequencies in our program that we use in our laboratory.

Q. Why not?

A. We just had never incorporated it yet, even though -- I mean, that was a kit that came on later. So the original 13 markers we had in our program -- and we got that program from the FBI. Okay. It was called Popstats. That Popstats did not include D2 and D19. They're two separate loci. So we typically did stats only using the 13 CODIS loci but not including D2 and D19.

Many other laboratories did the same thing for quite a while. We finally realized we -- you know, it would be a good idea to get D2 and D19 into our -- into our stats program.

Q. Okay. And lastly, the point, the idea is this DNA could have come from Flora Ryan or her daughter, right?

A. You can't exclude her daughter, but her daughter is related to her and shares --

Q. That makes sense.

A. -- a lot of genes.

Q. If you've got a pretty weak sample, that family members might both come up as consistent with the DNA sample, right?

A. Sure.

Q. But in this case then, basically, your 102 to 1 ratio, that's for -- that's including both Flora Ryan and her

daughter, correct?

A. Yeah, but the 102 to 1 is for Flora Ryan versus an unrelated person, not her daughter.

Q. Right.

A. Right.

Q. Right. In this case, we know specifically that this DNA that was supposedly recovered off of my client, right?

A. Right.

Q. Is consistent with Mary Ostlund, right?

A. Yes.

Q. And so specifically, we can say that this DNA, right, there's really a one in two chance, right, based on the two people that we know of as being tested in this case, that it could be DNA from either one, right?

A. Well, if you look at it like that, but, you know, you could do that with lots of relatives for lots of crime cases.

MR. HOCHGLAUBE: I pass the witness, Judge.

MS. FULLER: Nothing further, your Honor.

THE COURT: All right. Thank you so much for coming in.

Call your next.

MS. FULLER: The State has no further witnesses, your Honor.

MR. HOCHGLAUBE: We have nothing, Judge.

THE COURT: Okay. You-all want to argue?