

UNITED STATES PATENT AND TRADEMARK OFFICE

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ILLUMINA INC.,

Petitioner,

IPR2024-01419

vs.

U.S. Patent
No.
11,840,730

MOLECULAR LOOP
BIOSCIENCES, INC.,

Patent Owner.

-----X

787 7th Avenue
New York, New York
July 9, 2025
9:07 a.m.

VIDEOTAPED DEPOSITION of STACEY GABRIEL,
PH.D., held at the law offices of Sidley Austin
LLP, on July 9th, 2025, before Teneja Soltau, a
Notary Public of the State of New York.

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IPR2024-01419

Illumina Inc., v. Molecular Loop Biosciences, Inc.

Molecular Loop's Exhibit 2024

EX2024, Page 1

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23 THOMAS DEL VECCHIO, VIDEOGRAPHER

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25 MARIEYA JAGROOP, SIDLEY AUSTIN

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 MARCUS BURCH, ILLUMINA

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I N D E X

WITNESS

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EXHIBITS

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1 - P R O C E E D I N G S -

2 THE VIDEOGRAPHER: Good morning.

3 This is Media Number 1 of the videotaped
4 deposition of Dr. Stacey Gabriel in the
5 matter of Illumina, Inc., petitioner,
6 versus Molecular Loop Biosciences, Inc.,
7 patent owner, in the United States Patent
8 and Trademark Office, Case Number 1PR
9 2024-01419.

10 This deposition is being held at
11 the office of Sidley Austin LLP, 787 7th
12 Avenue, New York, New York 10019.

13 Today is Wednesday, July 9th, 2025.
14 The time is 9:08 a.m. My name is Thomas
15 Del Vecchio from the firm of Henderson
16 Legal Services, Inc. and I'm the legal
17 video specialist. The court reporter today
18 is Teneja Soltau, also in association with
19 Henderson Legal Services, Inc.

20 Would counsel please identify
21 yourselves for the record.

22 MR. BROUGHAN: Thomas Broughan from
23 Sidley Austin on behalf of petitioner
24 Illumina. With me is Marcus Burch and
25 Marieya Jagroop.

1 MR. WUESTE: Michael Wueste,
2 Desmarais LLP on behalf of patent owner
3 Molecular Loop. With me is Kevin Goon and
4 Brendan Genaw.

5 THE VIDEOGRAPHER: Thank you.
6 Will the court reporter please
7 swear in or affirm the witness.

8 S T A C E Y G A B R I E L, the witness herein,
9 having been first duly sworn by a Notary Public of
10 the State of New York, was examined and testified
11 as follows:

12 BY THE COURT REPORTER:

13 Q. Can I have your full name and address?

14 A. **Stacey Lynn Gabriel. 15 Manhattan Drive,**
15 **Burlington, Massachusetts 01803.**

16 (Whereupon, a discussion was held
17 off the record.)

18 **EXAMINATION**

19 BY MR. WUESTE:

20 Q. Good morning, Dr. Gabriel.

21 A. **Good morning.**

22 Q. Dr. Gabriel, you've testified under oath
23 and under the penalty of perjury before, correct?

24 A. **That's correct.**

25 Q. Okay. And you understand the oath you just

1 took requires you to tell the truth?

2 **A. Yes.**

3 Q. Is there any reason you cannot provide your
4 best truthful testimony today?

5 **A. No.**

6 Q. Okay. And in general, if I ask you a
7 question and you answer it, I will assume you
8 understood the question; is that fair?

9 **A. That's fair.**

10 Q. Have you ever served as an expert for
11 Illumina's law firm, Sidley Austin, before this
12 case?

13 **A. No.**

14 Q. Have you ever served as an expert for
15 Illumina before this case?

16 **A. No.**

17 Q. Have you ever consulted for Illumina before
18 this case?

19 **A. No.**

20 Q. Okay. Your --

21 **A. I've given a lecture where I was provided**
22 **an honorarium years ago, but I -- I -- it wasn't**
23 **under a consulting contract.**

24 Q. Right. And you weren't paid for your
25 services in the course of giving a lecture or

1 anything like that, correct?

2 **A. No.**

3 Q. Okay. Dr. Gabriel, you're familiar with
4 Sanger sequencing technology, right?

5 **A. I am.**

6 Q. And Sanger sequencing was first developed
7 sometime in the 1970s; is -- is that right?

8 **A. I don't know the exact date, but it was a**
9 **while ago.**

10 Q. Okay. Have you ever, yourself, used Sanger
11 sequencing in your work?

12 **A. In graduate school.**

13 Q. Okay. And if you don't mind me asking,
14 when was that?

15 **A. That was between the years of 1993 and**
16 **1998.**

17 Q. Okay. How many sequence reads were typical
18 in -- in a standard Sanger sequencing run?

19 MR. BROUGHAN: Object to form.

20 **A. That's really hard to answer because it**
21 **really depends on the device or the means by which**
22 **you were performing Sanger sequencing.**

23 Q. Okay. You know, just as a reference
24 number, are we talking the magnitude of -- let's
25 say hundreds? Or?

1 **A. Again, it really -- it really depends on**
2 **the method and the device that you're using to**
3 **perform a Sanger sequencing reaction.**

4 Q. Okay.

5 **A. It's hard to generalize --**

6 Q. Okay.

7 **A. -- in that way.**

8 Q. I'm going to hand you a document that's
9 previously been marked EX-1005. I see you have a
10 copy of it in front of you, as well.

11 (Whereupon, previously marked,
12 Exhibit EX-1005, was introduced.)

13 MR. WUESTE: Here's one for you,
14 Counsel.

15 MR. BROUGHAN: Thank you.

16 Q. Dr. Gabriel, can you confirm that EX-1005
17 is the declaration you submitted in this matter?

18 **A. It is.**

19 Q. Okay. And -- and I see you have a copy of
20 it in front of you, as well. I'm fine with you
21 using the copy you brought in.

22 Can you confirm for me, first, two things:
23 One, the version you brought in, is that clean of
24 annotations or notes or anything like that?

25 **A. This -- Tom gave me this one, so yes.**

1 MR. BROUGHAN: Should be.

2 A. Yes.

3 Q. Yes. And just crossing my Ts and dotting
4 my Is, can you confirm that the version you brought
5 in, that your counsel gave to you, is the same as
6 the version that is going back with the court
7 reporter today?

8 A. Yes, this is the same.

9 Q. Okay. Would you call Sanger sequencing a
10 first-generation approach for sequencing?

11 A. I think that's fair.

12 Q. Okay. I'd like you to turn to paragraph 55
13 of your declaration, EX-1005, which I believe is on
14 Page 19.

15 And there's a -- the third sentence in
16 paragraph 55: Next, again, technologies, also
17 called massively perilous sequencing, made it
18 possible to produce millions of sequencing reads in
19 a single instrument run compared to hundreds for
20 first-generation approaches. Do you see that?

21 A. I do.

22 Q. Is it fair to say that a typical run for a
23 Sanger sequencing first-generation approach would
24 be in the realm of hundreds of reads?

25 A. Well, again, it depends on the instrument

1 **and the way that you're performing Sanger**
2 **sequencing. But, certainly, there were instruments**
3 **that would permit you to perform hundreds of reads**
4 **in a given run of a machine.**

5 Q. Okay. And would those hundreds of reads be
6 at the top end of the range for a typical run? Or
7 somewhere in the middle? Or at the bottom?

8 MR. BROUGHAN: Object to form.

9 **A. Again, it depends on the time period, the**
10 **device, the context of performing the Sanger**
11 **sequencing run.**

12 Q. Okay. But you stand by the sentence you
13 wrote in paragraph 55 of your declaration, right,
14 that next-gen technologies made it possible to
15 produce millions of sequencing reads as compared to
16 hundreds for first-generation technologies for
17 Sanger sequencing?

18 **A. I do.**

19 Q. Okay. And, obviously, you're familiar with
20 next-gen sequencing, right?

21 **A. Definitely.**

22 Q. Okay. I've seen it referred to as
23 next-generation sequencing, next-gen sequencing,
24 NGS. If we use any of those three, can we have an
25 understanding that we're talking about the same

1 kinds of technology as the ones you've described
2 here in paragraph 55?

3 **A. Definitely, yes.**

4 Q. Okay. And I've also seen it, you know --
5 you note that's called massively parallel
6 sequencing at times?

7 (Reporter clarification.)

8 Q. Is that right?

9 **A. That's right.**

10 Q. When and why did the terminology change?

11 **A. I think next-gen and massively parallel**
12 **sequencing were used, I'd say, interchangeably**
13 **through the years. So I don't see much of a**
14 **distinction.**

15 Q. Okay.

16 **A. We can use either.**

17 Q. Fair to say that next-generation sequencing
18 technologies produced many, many more reads than
19 first-generation technologies like Sanger
20 sequencing, right?

21 **A. Definitely.**

22 Q. Okay. With -- and that would be on the
23 scale for millions of reads for a typical
24 instrument run for a next-generation sequencing
25 approach compared to, as you've put it, you know,

1 hundreds of reads in the first-generation approach,
2 right?

3 A. Depends on time frame, but here, we're
4 talking about the mid 2000s, correct?

5 Q. Uh-huh.

6 A. So then I think it's fair. But what I've
7 written here is millions of sequencing reads in
8 parallel on a single instrument run.

9 Q. Okay. So for the record, in the mid-2000
10 time frame, next-generation sequencing technologies
11 were capable of millions of sequence reads on a
12 single instrument run, compared to hundreds of
13 reads for a first-generation technology like Sanger
14 sequencing?

15 MR. BROUGHAN: Object to form.

16 A. Correct.

17 Q. Okay. What's a consensus base call?

18 A. I'm going to refer back to my declaration
19 to make sure that the testimony stays consistent
20 with what I've provided here.

21 So I've used the ordinary meaning in the
22 art of a consensus base call, which refers to using
23 multiple reads of the same molecule, which are
24 aligned to determine the nucleotide base call that
25 is most likely right or the consensus at a given

1 **position of sequence.**

2 Q. Okay. And for my clarification, are you
3 referring to paragraph 103 of your declaration?

4 A. **Yes, that's where it's discussed.**

5 Q. And again, for the record, I'm just going
6 to read that out, so it's clear.

7 In paragraph 103 of your declaration,
8 EX-1005, the ordinary meaning in the art of
9 consensus base call referred to using multiple
10 sequencing reads of the same molecule to determine
11 the nucleotide base at each position of the
12 sequence, right?

13 MR. BROUGHAN: Object to form.

14 A. **Yes, that's what I provided here.**

15 Q. Okay. And I think I heard you refer to
16 this before. Put another way, when determining the
17 consensus base call, you would perform multiple
18 sequence reads of the same molecule and then you
19 would count up which nucleotide occurs most
20 frequently at a given position in the sequence,
21 right?

22 MR. BROUGHAN: Object to form.

23 A. **That sounds like an approach to generate a**
24 **consensus call.**

25 Q. Okay. And not trying to hide the ball

1 here. If you turn to paragraph 72 of your
2 declaration, you know, that's where that language
3 came from.

4 **A. I see that.**

5 Q. And then, again, for clarity of the record,
6 multiple sequence reads -- strike that.

7 In paragraph 72, you state, "Multiple
8 sequence reads may also be used to generate a
9 consensus sequence for each particular sample of
10 DNA. The consensus sequence is derived by
11 determining which nucleotide occurs most frequently
12 at each position in the sequence and at each
13 position there can be a consensus base call,"
14 right?

15 **A. That's what it says.**

16 Q. Okay. I skipped over the second "by"
17 there. So I appreciate the lack of an objection to
18 form.

19 So the consensus base call is for a given
20 nucleotide at a given location or position within a
21 sequence, correct?

22 MR. BROUGHAN: Object to form.

23 **A. Well, the call is derived for a base at a**
24 **position within the sequence.**

25 Q. Is there an appreciable difference to you

1 between, you know, the base or, the, you know -- or
2 the nucleotide, that's my question asked?

3 **A. The base call represents the nucleotide.**

4 Q. Okay. All right. So let me rephrase,
5 then.

6 A consensus base call is -- determines the
7 given base or nucleotide at a given location or
8 position within a sequence, correct?

9 MR. BROUGHAN: Object to form.

10 **A. Say that again, please?**

11 Q. Sure. A consensus base call determines a
12 given base or nucleotide at the given location or
13 position within a sequence?

14 MR. BROUGHAN: Object to form.

15 **A. I think that's fine.**

16 Q. Okay. And the way you make that base call
17 is after performing multiple sequence reads, you
18 basically count up how many Cs or Gs or Ts or As
19 are at that location and whichever one appears most
20 frequently is the consensus base call for that
21 location, correct?

22 MR. BROUGHAN: Object to form.

23 **A. I don't think it's, necessarily, that**
24 **straightforward. I mean, I think that's a loose**
25 **description. But I think that there's also, as**

1 I point to, for example, in the Bentley reference,
2 you know, there's information about the base calls
3 that also gets used, depending on your approach.
4 So, I mean, I think a consensus call can be derived
5 in different ways, in different approaches. So
6 I think we would have to be, sort of, more specific
7 for me to just say something is as simple as what
8 you've just described.

9 Q. Okay. Terminology-wise, right, the
10 consensus sequence is the entire sequence and it's
11 made of base calls for each location within the
12 sequence, right?

13 MR. BROUGHAN: Object to form.

14 A. I think, in the art, we can refer to a
15 consensus in a different way. I mean, there's a
16 reference genome we compare to which is a genome of
17 sequence many time [sic] and then there's -- there
18 can be consensus data derived within your
19 experiment, within a -- for any given position in a
20 genome.

21 Really, there's, like, a lot of, I would
22 say -- we should -- rather than be more general, if
23 there's a specific to point to, it would be more
24 helpful to make sure that we're on the same track
25 and talking about the same thing.

1 Q. Completely agreed. And to clarify. I'm
2 trying to get the difference between what the
3 consensus sequence is versus a consensus base call,
4 right?

5 And my understanding is that the consensus
6 base call is for a given base or nucleotide within
7 the sequence. And then if you have multiple
8 consensus base calls across the sequence, that
9 would be the consensus sequence; is that fair?

10 MR. BROUGHAN: Object to form.

11 A. You're going from a base call to a
12 sequence, a consensus base call, to saying does
13 that make a consensus sequence? I suppose that's
14 okay with me.

15 Q. Okay.

16 A. Yeah.

17 Q. The reason I ask is if you look back at
18 paragraph 72 of your declaration, right, you say,
19 "Multiple sequence reads may also be used to
20 generate a consensus sequence for a particular
21 sample of DNA," in Sentence 1.

22 Do you see that?

23 A. I do.

24 Q. And then two sentences down, "At each
25 position there can be a consensus base call."

1 Do you see that?

2 A. Yes.

3 Q. So just the distinction between those two,
4 could you explain that to me?

5 A. Yes. I think it's just like the question
6 you asked me. Base calls make up a sequence --
7 overall sequence, right? So as I've said here, we
8 generate a consensus sequence for a sample and the
9 consensus sequence is derived by determining a
10 consensus base call at each position.

11 Q. Okay.

12 A. That gives you a consensus sequence.

13 Q. I see. So a consensus base call is the
14 given nucleotide at each position within the
15 sequence, right?

16 MR. BROUGHAN: Object to form.

17 A. Yeah.

18 Q. Okay. And if you turn the page in your
19 declaration, you reference that Bentley figure,
20 right?

21 A. Yes.

22 Q. And that's Bentley EX-1017. And we're
23 looking at Figure 2 of Bentley, I believe. It's
24 not labeled here, but that was my memory.

25 And so at the bottom of the figure in

1 Bentley, there's the consensus. And that entire
2 line beginning at "A" and ending at "T," that would
3 be the consensus sequence, right?

4 **A. That's how -- as it is labeled here in the**
5 **figure.**

6 Q. Okay. And then if -- you know, we've got a
7 box around one position within that sequence and
8 the consensus base call for that position within
9 the sequence is "G," correct?

10 **A. That's how it's reported here. But as you**
11 **read in the -- in the figure legend here, the**
12 **consensus quality of that -- that represents --**
13 **well, the gray shading represents low quality**
14 **because there's actually two base calls that are**
15 **high quality indicating that that site is a**
16 **heterozygous position. So there's a -- it's a "G"**
17 **and a "C" at that position, so one from your mom,**
18 **one from your dad and that is true.**

19 **And so the consensus is reported as -- as**
20 **G, but it -- it's a heterozygous position.**

21 Q. Right. And heterozygous means that there's
22 two -- you know, two nucleotides right at that --
23 at that position, correct?

24 And strike that. Let me rephrase that.

25 A heterozygous, you know, base call would

1 im- -- would imply that there are two different
2 nucleotides at that position, right?

3 MR. BROUGHAN: Object to form.

4 **A. Correct. A heterozygous position has**
5 **alternate alleles, one herit- -- one inherited from**
6 **mom, one inherited from dad to represent the two**
7 **copies of the -- the chromosomes that are in the**
8 **cell.**

9 Q. And you would contrast a heterozygous base
10 call from a homozygous base call?

11 **A. A homozygous base call means those two**
12 **copies are -- the two nucleotides are the same. So**
13 **it would be G and G. G from mom, G from dad, that**
14 **would be homozygous for G.**

15 Q. And so in this figure in Bentley, the
16 consensus base call for the boxed position within
17 the sequence is a heterozygous G because -- at
18 least as -- you know, put in this box, there are
19 six Gs across the multiple reads in that position
20 and only five Cs, right?

21 MR. BROUGHAN: Object to form.

22 **A. That's how he's labeling it in this figure**
23 **as the algorithm he was using made the call a G.**
24 **But, again, made it the quality -- made it a low**
25 **quality call signalling a region where you would**

1 look and see that there was also a high
2 representation of Cs, as well. And so that
3 indicates that there's, you know, about the 50/50
4 Cs and Gs. So it's a heterozygous C and G.

5 Q. And if the ratio had been different, if you
6 had, say, seven Gs and four Cs, in your expert
7 opinion, what would the consensus base call for
8 that position be? How would it change?

9 MR. BROUGHAN: Object to form.

10 A. That's entirely dependent on the algorithm
11 you're using. The way you've set the parameters of
12 your algorithm, of which there were many that had
13 been developed over the years. So I don't know
14 that it's a matter of opinion. I think it's a
15 matter of the algorithm for variant calling that
16 you're using, based on your application.

17 Q. Okay. Your declaration in this case,
18 Exhibit EX-1005, contains all your opinions
19 regarding the invalidity of the '730 patent, right?

20 A. Yes.

21 Q. And this declaration includes all of your
22 opinions to date regarding the validity of the '730
23 patent, correct?

24 A. Yes.

25 Q. As of the date you signed your declaration,

1 you had no additional opinions that were not
2 included here, right?

3 **A. No.**

4 Q. Okay. Do you still stand by all the
5 opinions in your declaration?

6 **A. I do.**

7 Q. Are there any opinions in your declaration
8 that you no longer agree with?

9 **A. No.**

10 Q. Are you aware of any mistakes in your
11 declaration?

12 **A. No.**

13 Q. Okay. How confident are you in the
14 opinions as expressed in EX-1005?

15 MR. BROUGHAN: Object to form.

16 (Reporter clarification.)

17 **A. Very confident.**

18 Q. Are there any opinions in EX-1005 that you
19 are more confident in than others?

20 MR. BROUGHAN: Object to form.

21 **A. None that I can think of right now.**

22 Q. All right. And you describe a number of
23 different grounds in this declaration, right?

24 **A. Yes.**

25 Q. A couple of grounds based on Chee?

1 **A. Yes.**

2 Q. And a couple of grounds based primarily on
3 a combination of McCloskey and Bignell?

4 **A. Yes.**

5 MR. WUESTE: For the court
6 reporter's benefit, McCloskey is
7 M-C-C-L-O-S-K-E-Y. Bignell, B-I-G-N-E-L-L.
8 (Reporter clarification.)

9 Q. Which claims to the '730 patent are you
10 most confident are disclosed by Chee?

11 MR. BROUGHAN: Object to form.

12 **A. The claims that I point to here in the**
13 **declaration, all of them.**

14 Q. Are there -- are there any of the claims
15 that you are less confident are disclosed by Chee?

16 MR. BROUGHAN: Object to form.

17 **A. No.**

18 Q. What claims are you most confident are
19 disclosed by McCloskey in view of Bignell?

20 MR. BROUGHAN: Object to form.

21 **A. I stand behind all my opinions here on the**
22 **claims.**

23 Q. There are no claims that you are less
24 confident are disclosed by McCloskey and Bignell,
25 correct?

1 **A. No.**

2 Q. In your opinion, what is Illumina's most
3 difficult invalidity argument?

4 MR. BROUGHAN: Object to form.

5 **A. I don't have an opinion on that.**

6 Q. When were you retained to work on this
7 case?

8 **A. I don't remember exactly. I would say**
9 **about a year ago. I would -- let me say, within**
10 **the past year. I don't remember exactly, though.**

11 Q. So sometime in 2024?

12 **A. Yes.**

13 Q. Okay. When you were retained, what was
14 your assignment on this matter?

15 MR. BROUGHAN: I'll caution the
16 witness not to reveal the substance of any
17 communications with counsel. Subject to
18 that, you may answer.

19 **A. The attorneys reached out, said there was a**
20 **patent dispute and asked if I would like to talk**
21 **about it and find out if I could help or not.**

22 Q. Okay. And then after you were hired by
23 Illumina, what did you set out to do in connection
24 with this -- this patent matter, as you put it?

25 MR. BROUGHAN: I'll object to the

1 extent it calls for privileged information.

2 But I'll caution the witness not to
3 reveal the substance of any communications
4 with counsel. Subject to that, you may
5 answer.

6 **A. I agreed to have a few phone calls with the**
7 **attorneys to talk about the issues at hand, the**
8 **patent, prior art. That.**

9 Q. And I don't want to get into conversations
10 you may have had with counsel, right?

11 What did you understand your assignment to
12 be with regards to the patent at hand, the '730
13 patent and prior art?

14 MR. BROUGHAN: Similar objection.
15 I'll caution the witness not to reveal the
16 substance of communications with counsel.
17 If you can answer, you may.

18 **A. My assignment was to be an expert witness.**

19 Q. And what did that entail?

20 MR. BROUGHAN: Same objections, I'd
21 caution.

22 **A. Reviewing intellectual property and prior**
23 **art.**

24 Q. And why, specifically, were you
25 reviewing -- well, let me take a step back.

1 By "intellectual property," you mean
2 Molecular Loop's '730 patent, right?

3 **A. In this case, yes.**

4 Q. And did you go out and look for prior art
5 yourself? Or was it provided to you by counsel?

6 MR. BROUGHAN: Objection to the
7 extent it calls for privileged information.
8 Do not reveal the substance of what was
9 communicate -- sorry, the substance of
10 communications with counsel. Subject to
11 that, you may answer.

12 **A. The answer is both.**

13 Q. When you received prior art from counsel in
14 connection with this matter regarding the '730
15 patent, did you understand your assignment to be
16 determining the invalidity of the '730 patent?

17 MR. BROUGHAN: Objection to form.
18 Also to the extent it calls for privileged
19 information -- if you have an independent
20 understanding that's not from counsel, you
21 may answer. But do not reveal the
22 substance of communications with counsel.

23 **A. My understanding was there was an**
24 **intellectual property dispute and I was being asked**
25 **to consider the patent and the claims of the patent**

1 **and prior art.**

2 Q. Okay. And in view of that, when you were
3 hired, did you believe that Illumina's expectation
4 was that you would determine that the '730 patent
5 was invalid over the prior art?

6 MR. BROUGHAN: Object to form and
7 to the extent it calls for privileged
8 information.

9 If you have an independent
10 understanding, in your own view, you may
11 answer, but do not reveal the substance of
12 what counsel communicated to you.

13 **A. Yeah. I don't think I have an answer for**
14 **that.**

15 Q. When you were hired by Illumina and
16 provided with a copy of the '730 patent and prior
17 art, you have no idea, whether or not, you would be
18 asked to determine that the '730 patent was invalid
19 in view of the prior art you were given?

20 MR. BROUGHAN: Objection to form
21 and to the extent it calls for privileged
22 information.

23 The same caution as before.

24 **A. Well, any time in -- in performing this**
25 **type of work, one considers the claims, the prior**

1 art, the specification, my own knowledge as a
2 person skilled in the art. So all of that together
3 is -- is what I was considering when I was
4 determining if this was expert witness work that
5 I would take on.

6 Q. And I fully understand the scope of
7 information or materials you were considering. But
8 when you were considering them, did you believe
9 that Illumina's expectation was that you would
10 determine that the '730 patent is invalid in light
11 of those materials?

12 MR. BROUGHAN: Object to form.
13 Foundation. How is she supposed to know
14 what her expectation is?

15 MR. WUESTE: I'm asking her what
16 her sense was, what her belief was.

17 A. I understood that there was a dispute and
18 I was being asked if I was willing to be an expert
19 witness on behalf of Illumina in the dispute.

20 And after reviewing the evidence and
21 discussing my opinions, I arrived at the decision
22 that I could represent Illumina in this matter that
23 calls for the invalidity of this patent.

24 Q. Okay. Prior to this case and your contact
25 with Illumina, were you aware of Molecular Loop?

1 **A. I was.**

2 Q. In what respect?

3 **A. I would say -- I would describe a vague**
4 **knowledge that the -- Greg Porreca had -- who had**
5 **once been at one company called Good Start**
6 **Genetics, had left that to form a new company that**
7 **he called Molecular Loop.**

8 **I had an understanding that they generally**
9 **worked on a technology called molecular inversion**
10 **probes, or MIPs, and that's basically what**
11 **I understand.**

12 Q. You knew Greg Porreca before this case,
13 right?

14 MR. BROUGHAN: Object to form.

15 **A. I knew who he was, yes.**

16 Q. Had you ever worked with Mr. Porreca?

17 **A. No.**

18 Q. Had you ever used any of Mr. Porreca's or
19 Molecular Loop's products?

20 **A. No.**

21 Q. Had you ever heard of George Church before
22 this case?

23 **A. Definitely, yes.**

24 Q. Yeah. In what sense had you heard of
25 Mr. Church -- Dr. Church, I should say.

1 **A. Dr. Church is a very famous genome**
2 **technologist, Harvard professor. So obviously,**
3 **being in the Harvard/MIT community, I knew who**
4 **George was.**

5 Q. How many total hours have you spent working
6 on this case since you were retained sometime in
7 2024?

8 **A. I don't know exactly.**

9 Q. Rough ballpark. Are we on the order of
10 tens, hundreds?

11 **A. Somewhere between ten and a hundred.**

12 Q. Okay. Closer to the hundred side or the
13 ten side?

14 **A. I don't know exactly. I don't think it's**
15 **closer to a hundred -- so tens.**

16 Q. More than 50?

17 **A. I don't know. I actually don't know.**
18 **I don't want to be wrong.**

19 Q. How much has Illumina paid you for your
20 work so far on this case?

21 **A. My rate is \$900 an hour.**

22 Q. So 900 times somewhere between 10 and,
23 let's say, 75 hours would be the amount, right?

24 **A. Well, you know, I haven't been paid yet for**
25 **the work that I've done in the past couple of weeks**

1 on the -- you know, to prepare for this. But --
2 but I bill at a rate of \$900 an hour.

3 Q. Okay. How many of those hours have you
4 spent talking to and meeting with Illumina's
5 lawyers?

6 A. I don't know. Part of it is meeting with
7 the lawyers, part of it is independent work.

8 Q. At what point in your analysis did you
9 reach your opinion that the '730 patent is invalid?

10 MR. BROUGHAN: Object to form.

11 A. Early on, after reviewing the claims of the
12 patent and the materials that I cite here.

13 Q. Roughly, how many hours would you estimate
14 you spent working on the case before you reached
15 that opinion early on?

16 A. A couple, couple hours reviewing the
17 materials.

18 Q. So within a couple hours of receiving the
19 '730 patent and the prior art -- or at least a
20 portion of the prior art that were provided to you
21 by Illumina's counsel, you reached your conclusion
22 that the '730 patent was invalid; is that correct?

23 MR. BROUGHAN: Objection to form
24 and foundation.

25 A. Again, reviewing the claims, specification,

1 prior art, and my own knowledge, yeah. A couple
2 hours of reviewing all that.

3 Q. Okay. Who wrote your declaration?

4 MR. BROUGHAN: Object to form.

5 A. The declaration is my work. I worked with
6 the attorneys. We met, we discussed the claims,
7 the evidence, my conclusions, my opinions. The
8 attorneys take -- create drafts from there and then
9 we worked through a series of drafts where we
10 iterated back and forth to make sure the opinions
11 are my own.

12 Q. You did not personally write every single
13 word of your declaration, but you stand by all the
14 opinions in there; is that fair?

15 A. That's fair.

16 Q. And you reviewed every single word of your
17 declaration before you signed it, correct?

18 A. I did.

19 Q. Okay. Your declaration includes all
20 documents or materials you're relying on for your
21 opinions in this matter to date, right?

22 A. Yes.

23 Q. And just to put it another way, when you
24 were forming or informing your opinions as set
25 forth in your declaration, you didn't review any

1 additional documents or materials that are not
2 cited in the declaration itself, correct?

3 **A. Not that I recall right now.**

4 Q. Okay. What did you do to prepare for your
5 deposition today?

6 MR. BROUGHAN: I'll caution this
7 witness not to reveal the substance of
8 communications with counsel; but subject to
9 that, you may answer.

10 **A. I reviewed my declaration, I reviewed prior**
11 **art, I reviewed the patent and the specification,**
12 **I booked my flight to come here, and I met with the**
13 **attorneys.**

14 Q. And, specifically, who did you meet with?

15 **A. Yesterday, I met with Tom. I met with**
16 **Ching-Lee, who's not here. And I met with Marcus.**

17 Q. And how long did you meet?

18 **A. Yesterday, I was here about seven hours.**

19 Q. Did you speak with anyone other than
20 attorneys to prepare for your deposition today?

21 **A. No.**

22 Q. And aside from Mr. Burch -- correct -- have
23 you spoken with anyone from Illumina over the
24 course of your work in this matter?

25 **A. Not about this matter, but I speak to**

1 people at Illumina because I'm a customer of
2 Illumina. So to be accurate, I have, but not about
3 this matter.

4 Q. Okay. As it pertains to issues in this
5 matter, you did not speak to anybody else at
6 Illumina apart from Mr. Burch, correct?

7 MR. BROUGHAN: I'm going to object
8 to that one, to the extent it calls for
9 privileged information. If you want to ask
10 if she spoke to another attorney, I think
11 that's fine.

12 Q. Well, I'm just looking for a yes-or-no
13 question here -- yes-or-no answer here. As it
14 pertains to issues within this matter, you did not
15 speak to anybody else at Illumina apart from
16 Mr. Burch?

17 MR. BROUGHAN: "Yes" or "no" is
18 fine.

19 A. No.

20 Q. Okay. And you mentioned you had reviewed a
21 number of documents in preparing for your
22 deposition today, including your declaration,
23 correct?

24 A. Yes.

25 Q. The prior art?

1 **A. Yes.**

2 Q. That would be Chee, McCloskey, Bignell, and
3 the other secondary references?

4 **A. Yes.**

5 Q. Okay. In preparing for your deposition
6 today, did you review any documents that you had
7 not previously reviewed before submitting your
8 declaration?

9 MR. BROUGHAN: Object to form.

10 **A. I did review the institution decision that,**
11 **I believe, came after my declaration. So that**
12 **was -- I reviewed, as well.**

13 Q. Okay. Have you reviewed the petition that
14 Illumina submitted in this matter?

15 **A. I don't think so.**

16 Q. Okay. Have you reviewed the preliminary
17 response that Molecular Loop filed in this matter?

18 **A. Yes, I did have that document. Yes.**

19 Q. Okay. So in addition to the materials
20 already mentioned, you also reviewed the board's
21 institution decision and Molecular Loop's
22 preliminary response in preparing for today's
23 deposition, correct?

24 **A. Yes.**

25 Q. Okay. Any others?

1 **A. No.**

2 Q. Okay. And just to close that out, aside
3 from the -- strike that.

4 Aside from the institution decision and
5 Molecular Loop's preliminary response, in your work
6 on this matter, have you reviewed any additional
7 documents other than the exhibits listed as
8 materials considered in your declaration?

9 **A. Not that I can recall, no.**

10 Q. Okay. Could you please turn to paragraph 4
11 of your declaration? It begins on Page 2 and
12 continues onto Page 3.

13 **A. Yes.**

14 Q. Do you see that?

15 **A. Yes.**

16 Q. And paragraph 4 describes some of the work
17 that your lab has done, correct?

18 **A. Yes.**

19 Q. Okay. In the last sentence of paragraph 4,
20 it states, "As of 2023, my lab has produced genomic
21 profiles for over 10,000 cell-free tumor DNA
22 samples," right?

23 **A. That's what it says, correct.**

24 Q. Okay. What's a "genomic profile"?

25 **A. It is a profile of the DNA or RNA of a**

1 tumor sample. So it tells you all the various DNA
2 or RNA changes that are in a cell-free tumor DNA
3 sample.

4 Q. Is the process of determining a genomic
5 profile sometimes called genotyping?

6 A. That's a subset of a way to perform a
7 genomic profile, genotyping or sequencing. You can
8 use either.

9 Q. My background is in English literature. So
10 when you say a subset, what do you mean -- you
11 know, what would you define genotyping as?

12 A. Genotyping (pronouncing).

13 Q. Genotyping (pronouncing). Apologies.

14 A. That's okay.

15 Genotyping is simply determining a sample
16 genotype which is the report-out of that identity
17 of the base on one chromosome and the identity of
18 the base of the other chromosome. That's
19 genotyping, reporting out the base identity at the
20 position. And you can determine a genotype by
21 genotyping. Typically that would be like -- on a
22 microarray, you would say I'm genotyping. Or you
23 can sequence and you would say I'm sequencing to
24 determine the genotype.

25 Q. Are genotyping and sequencing, you know,

1 two words for the same thing? Or would you
2 consider those different processes?

3 **A. Typically, genotyping, again, is done in a**
4 **very directed manner. I'm going to look at the**
5 **genotype using, for example, a microarray or a PCR**
6 **reaction to get the genotype of a particular locus,**
7 **or a seat of loci. Whereas, sequencing is more**
8 **expansive, you will determine the nucleotide of --**
9 **identity of many bases; but you still determine a**
10 **genotype from sequencing.**

11 **Q. I see. So that's why you said genotyping**
12 **is a subset, in a way, of sequencing because -- is**
13 **it fair to say that genotyping would be determining**
14 **the base for, as you said, a particular locus**
15 **within the sequence?**

16 **MR. BROUGHAN: Objection to form.**

17 **A. Genotyping is determining the genotype at a**
18 **locus or a set of loci.**

19 **Q. Okay. Whereas, sequencing would be across**
20 **a -- you know, a broader set of loci than you would**
21 **use for -- to determine the genotype.**

22 **MR. BROUGHAN: Object to form.**

23 **A. Well, you can sequence to determine -- to**
24 **determine a single genotype at a single locus. So**
25 **again, they're, kind of, words that can be a bit**

1 **interchangeable.**

2 Q. Right.

3 **A. Ultimately, both resulting in determining a**
4 **genotype.**

5 Q. Okay. Okay. And were you using both
6 genotyping and sequencing in the course of
7 producing the genomic profiles for over 10,000
8 cell-free tumor DNA -- tumor -- cell-free tumor DNA
9 samples?

10 **A. The technology we used was sequencing. And**
11 **via that sequencing, we would arrive at tumor**
12 **genotypes.**

13 Q. I see. So --

14 **A. Or tumor mutation calls. You can --**
15 **there's lots of different terms you can use, but --**
16 **yeah.**

17 Q. So genotyping would be, kind of, the result
18 of the analysis performed after going through a
19 sequencing process?

20 **A. You can call it that.**

21 Q. And those 10,000 cell-free tumor DNA
22 samples, these were naturally occurring? They came
23 from, like, biological samples?

24 **A. Blood samples, yes.**

25 Q. It's also possible to construct, you know,

1 artificial genomes as opposed to, say, like the
2 naturally-occurring sequences that you were
3 profiling in your work here, right?

4 MR. BROUGHAN: Object to form.

5 **A. You can construct synthetic DNA, yes.**

6 Q. Okay. Is the process for constructing
7 synthetic DNA sometimes called synthetic biology?

8 **A. Yes, synthetic biology includes**
9 **constructing synthetic DNA molecules.**

10 Q. All right. Have you ever, you know,
11 constructed synthetic DNA molecules as opposed to,
12 you know, sequencing or genotyping and -- you know,
13 the kind of work you're doing in creating the
14 genomic profiles?

15 **A. With my own hands, I haven't done that.**
16 **But I have certainly ordered synthetic oligos --**
17 **synthetic pieces of DNA from companies many times,**
18 **yes.**

19 Q. But your lab itself hasn't done that in
20 your work?

21 **A. My lab orders such synthetic DNA from**
22 **companies.**

23 Q. All right. Okay. I'm going to be moving
24 into a different area. So I'm happy to continue
25 on, if you're willing to continue on, Dr. Gabriel?

1 It's been close to an hour. So if you prefer to
2 take a break, I'm fine with that, too. If you'd
3 like to power on through, we can power on through.

4 MR. BROUGHAN: You want to go,
5 like, ten more minutes? Or do you want to
6 break now?

7 **A. I'm fine now.**

8 Q. Okay.

9 **A. We can power on through.**

10 Q. What is --

11 (Reporter clarification.)

12 Q. You know what? If everyone is saying --
13 maybe ten, at the most. Let's take a break now and
14 get that out of the way.

15 THE VIDEOGRAPHER: This is the end
16 of Media Number 1. The time is 10:00 a.m.
17 We're off the record.

18 (Whereupon, a recess was taken at
19 this time.)

20 THE VIDEOGRAPHER: This is Media
21 Number 2. The time is 10:17 a.m. We are
22 back on the record.

23 BY MR. WUESTE

24 Q. Welcome back, Dr. Gabriel.

25 **A. Thanks.**

1 Q. What is PCR amplification?

2 A. **PCR stands for Polymerase Chain Reaction**
3 **and it is a method to amplify or make many copies**
4 **of DNA.**

5 Q. Amplification, generally, is a process for
6 making copies of the original nucleic acid
7 molecules in the sample, right?

8 MR. BROUGHAN: Objection to form.

9 A. **Making copies can be done with**
10 **amplification, yes.**

11 Q. Again, I'm not trying to hide the ball. If
12 you turn to paragraph 62 of your declaration.

13 A. **Yes.**

14 Q. Second sentence in that paragraph.

15 A. **Yes.**

16 Q. Amplification is a process for making
17 copies of the original nucleic acid molecules in a
18 sample, right?

19 A. **That's correct.**

20 Q. And PCR is one form of amplification that
21 you could use?

22 A. **That is correct.**

23 Q. Okay. If you were to perform multiple
24 cycles of PCR amplification, you can create copies
25 of DNA fragments exponentially, correct?

1 **A. That's correct.**

2 Q. Okay. If you performed enough cycles of
3 PCR amplification, you could rapidly produce
4 millions to billions of copies of a specific
5 segment of DNA, correct?

6 **A. That's right.**

7 Q. Okay. But PCR amplification has been
8 available before NGS technologies, correct?

9 **A. That's right.**

10 Q. It could have been used in -- it was used
11 in first-generation approaches, like Sanger
12 sequencing, right?

13 **A. Yes. It's been around since the '70s.**

14 Q. And I think, as we established earlier,
15 Sanger sequencing -- strike that.

16 As we established earlier, Sanger
17 sequencing in a single run could produce, you know,
18 somewhere along the realm of several hundreds of
19 reads as opposed to the millions of reads that you
20 would do for NGS sequencing, right?

21 **A. Yes.**

22 Q. Okay. So you wouldn't need nearly as many
23 cycles of PCR amplification to generate amplified
24 sequences for a run of hundreds of reads in Sanger
25 sequencing as you would to produce millions of

1 reads for NGS, correct?

2 **A. No, those are two different concepts.**

3 **Q. Okay. In what way?**

4 **A. Well, again, depending on how you're**
5 **performing a Sanger sequencing reaction, you may**
6 **still need a lot of copies of a DNA sample. And so**
7 **there's a lot of input parameters I would put into**
8 **this, sort of -- into that question to tell you, do**
9 **I need more cycles for Sanger or less cycles for --**
10 **or more for NGS. Some NGS approaches actually**
11 **don't require PCR at all. It just -- it really**
12 **depends on what you're trying to do or what your**
13 **starting material is. So I can't characterize it**
14 **as simply as you did in your question.**

15 **Q. Okay. That's fair. Amplification occurs**
16 **at random, correct?**

17 **A. I'm not sure what you mean by "random."**

18 **Q. Amplification occurs at random. So not**
19 **every nucleic acid molecule is amplified the same**
20 **number of times, correct?**

21 **A. It's true there can be variation in a PCR**
22 **reaction of how many times a given region is**
23 **amplified. There can be variation, yes.**

24 **Q. Okay. Again, if you look at paragraph 77**
25 **of your declaration, the paragraph beginning "The**

1 amplification stuff can also introduce bias."

2 **A. Yes.**

3 Q. And then the second sentence reads,
4 "Amplification occurs at random. So not every
5 nucleic acid molecule is amplified the same number
6 of times." Right?

7 **A. That's right.**

8 Q. Okay. Some molecules may be over or under
9 amplified, right?

10 **A. That's right.**

11 Q. And so when you are overamplifying or
12 underamplifying some of these molecules, if you
13 counted the copies -- or the number of the copies
14 after amplification, that may not necessarily
15 accurately capture the nucleic acid molecules that
16 were originally in the sample, right?

17 **A. Yes.**

18 Q. Okay. And as you say, that's called
19 amplification bias, right?

20 **A. Yes.**

21 Q. Is that, kind of, like a quantitative
22 error, because it's, you know, a difference in the
23 number of count?

24 MR. BROUGHAN: Object to form.

25 **A. I would say it would obscure quantification**

1 **if you didn't correct for it.**

2 Q. Okay. Absent a correct in supp later on,
3 amplification bias would obscure quantification?

4 **A. It could.**

5 Q. Okay. And that would be a difference from,
6 let's call it, like a sequencing error, by which
7 I mean an error in the sequence read itself, right?

8 MR. BROUGHAN: Object to form.

9 **A. A sequence error is another type of error.**

10 Q. Right. So in a sequence error, if you
11 were -- you're familiar with sequencing by
12 synthesis?

13 **A. Yeah.**

14 Q. If you incorrectly incorporated the wrong
15 nucleotide for a given position in the
16 complementary strand during sequencing by
17 synthesis, the sequence itself would have an error,
18 right?

19 **A. Yes.**

20 Q. And that's a different kind of error than
21 the kind of quantitative error that, you know,
22 would arise when amplification bias obscures the
23 count?

24 MR. BROUGHAN: Object to form.

25 **A. It's a different type of error.**

1 Q. Okay. In an NGS process flow, at a high
2 level, would you agree there's three major steps?

3 MR. BROUGHAN: Objection to form.

4 A. No. I mean, it really depends on what you
5 want to do. We can talk about a specific context
6 and we talk about the steps, but...

7 Q. Okay. The typical workflow for a next-gen
8 sequencing platform, generally, is preparing a
9 library of nucleic acids for sequencing, sequencing
10 nucleic acids, and analyzing the sequence reads.
11 Would you agree with that?

12 MR. BROUGHAN: Object to form.

13 A. That's a general workflow.

14 Q. Okay. Again, your declaration at paragraph
15 57. You see the --

16 A. Yes, I do. Generally, yes.

17 Q. Okay. Just to make sure we're on the same
18 page. Since the mid 2000s, next-gen sequencing
19 platforms have employed diverse sequencing
20 biochemistry, but they generally follow a similar
21 workflow of preparing a library of nucleic acids
22 for sequencing, sequencing the nucleic acids, and
23 analyzing the sequence reads, right?

24 A. That's right.

25 Q. Okay. And the way you describe it, if we

1 talk about the first step of library preparation,
2 at a high level, that would include
3 fragmenting DNA -- strike that.

4 The first step of next-gen sequencing
5 library preparation would include fragmenting DNA,
6 ligation of adapter sequences to the ends of the
7 DNA fragments, and amplification of the fragments
8 to generate copies, right?

9 **A. Yes.**

10 Q. And as we -- you know, that's Step 1. So
11 you have to prepare the library before beginning
12 the sequencing step, correct?

13 **A. Yes.**

14 Q. You can't sequence the molecules without
15 having prepared the library to sequence first?

16 **A. Typically, no. The way most sequences work**
17 **is that you would prepare a library before you put**
18 **it on the sequencer.**

19 Q. Okay. And, generally, the sequencing step
20 involves clonal amplification and then a readout?

21 MR. BROUGHAN: Object to form.

22 **A. Typically, yes.**

23 Q. Clonal amplification generates additional
24 copies of each template DNA molecule?

25 **A. Yes.**

1 Q. Can I ask what's the difference in purpose
2 for the clonal amplification step after the
3 amplification step during the library preparation?

4 A. Yes. The clonal amplification is done to
5 generate enough copies of the template, so that
6 they can be detected on an instrument in the
7 sequencing readout. It's just about generating
8 more material.

9 Q. And what's the distinction between that and
10 the amplification, you know, step of -- for
11 generating copies?

12 A. Well, there can be two amplification steps.

13 Q. Got it.

14 A. One that's part of library prep that
15 prepares the DNA sometimes by adding adaptors to
16 it, making copies to it, amplifying it. And then
17 on Illumina sequences, for example, after that step
18 happens and the prepared molecules bind to a flow
19 cell -- so they find a spot where they're going to
20 be sequenced -- the next step is making clonal
21 copies of each of those molecules, so that there's
22 enough material at that spot on the flow cell that
23 it can be detected.

24 Q. I see. So the clonal amplification step,
25 where necessary for a given platform, right, is

1 meant to generate the material sufficiently, you
2 can have a reasonably competent read of the
3 sequence, right?

4 **A. Yeah.**

5 Q. Okay. And that read is --

6 (Reporter clarification.)

7 Q. Let me rephrase.

8 After clonal amplification, the nucleotides
9 are read out using a variety of techniques?

10 **A. Yeah.**

11 Q. Okay. And if you were reading multiple
12 clonal copies of the same original template
13 sequence, all of those reads of the multiple clonal
14 copies would be performed during the sequencing
15 step, but obviously after clonal amplification,
16 right?

17 **A. The readout of the -- sorry. The readout**
18 **occurs after the clonal amplification.**

19 Q. Okay. Is there a distinction between
20 "readout" and "read" that you're making there?

21 **A. Well, you read out the bases one at a time**
22 **and that makes the read.**

23 Q. Got it. Okay. So is this, kind of,
24 similar to the consensus sequence versus consensus
25 base call distinction, we were talking about

1 earlier, where the readout is for a given
2 nucleotide at a given location within the sequence
3 and then the read is of the entire sequence?

4 MR. BROUGHAN: Object to form.

5 A. Yeah, that's close enough, yeah.

6 Q. Again, English literature background. If
7 I'm getting the terminology wrong, you know, I'd
8 appreciate your expert opinion on correcting me.

9 A. Appreciate that. Thank you.

10 Q. Okay. And then after sequencing, according
11 to the description of the NGS flow -- or workflow
12 that you've got here, you've got analysis of
13 sequence reads right?

14 A. That's correct.

15 Q. And, again, this is basic, right? Again,
16 English major.

17 That makes sense because, obviously, you
18 can't actually analyze the sequence reads until
19 you've read out the nucleotides and read every
20 sequence, right?

21 A. That's right.

22 Q. Okay. That analysis could involve a number
23 of different things, correct?

24 A. Yes.

25 Q. You might compare the sequence reads to a

1 reference sequence to identify mutations?

2 **A. Yes.**

3 Q. If you've done multiple sequence reads of
4 copies of sequences derived from the same original
5 molecule, you could perform a consensus base call
6 for a given nucleotide at a given location within
7 that sequence, right?

8 **A. Yes.**

9 Q. You could do some other things. You could
10 detect copy number or compare the number of
11 occurrences of a sequence to a reference sample,
12 right?

13 **A. Yes.**

14 Q. Okay. But each of those forms of analysis
15 are only possible after you've completed
16 sequencing, including sequence reading, correct?

17 **A. I would say you're -- those steps you've**
18 **described are analyses that you perform with data**
19 **that comes off of the sequencing machine.**

20 Q. Okay. The data that comes off of the
21 sequencing machine is data generated by software,
22 correct?

23 **A. There's software on the machine, yes, that**
24 **is turning signals into reads.**

25 Q. Okay. And then you rely upon that

1 software-generated data and stay the course of your
2 work to make determinations, right? Or, you know,
3 analyze something from the perspective of an
4 expert, right?

5 **A. You depend on that software on the machine,**
6 **right, to do that converting fluorescent signals to**
7 **reads. And then there's all types of downstream**
8 **analysis you might perform.**

9 Q. Right. They are downstream analyses after,
10 you know, the reading process.

11 **A. Yes.**

12 Q. Okay. I'm handing you a copy of
13 Exhibit 1001.

14 MR. WUESTE: A copy for you, sir.

15 Sorry for the reach.

16 Would you like one?

17 Q. EX-1001 is the '730 patent, right?

18 **A. Yes.**

19 Q. And do you recognize EX-1001 as the patent
20 you opined upon for this case?

21 **A. Yes.**

22 Q. You reviewed the '730 patent, I should
23 hope.

24 **A. I did.**

25 Q. And I'd like to talk about some of the

1 problems the '730 patent was trying to solve.

2 You agree that one of the fields the '730
3 patent is directed to is determining genotypes in
4 patient samples, right?

5 **A. Yes.**

6 Q. Okay. And my apologies. I didn't write
7 down exactly what you wrote. So this is a little
8 bit of a paraphrase.

9 Genotyping, you're trying to determine what
10 the combination of alleles at a given locus is,
11 right?

12 **A. Yes.**

13 Q. Okay. So you're -- to put it another way,
14 you're determining what alleles -- or would you use
15 the word -- versions of a locus an individual
16 inherited from their parents, for example?

17 MR. BROUGHAN: Object to form.

18 **A. Yes.**

19 Q. Okay. And a locus is a fixed location on a
20 chromosome which contained a gene or other genetic
21 marker, correct?

22 **A. Yes.**

23 Q. Okay. And I think we already established a
24 sequence can be heterozygous or homozygous, right?

25 MR. BROUGHAN: Object to form.

1 **A. Well, a position in your genome can be**
2 **homozygous or heterozygous.**

3 Q. Thank you for the clarification.

4 A position in a genome can be heterozygous
5 or homozygous, correct?

6 **A. In a diploid organism, yes, in humans, yes.**

7 Q. Okay. You would agree that amplification
8 bias in next-generation sequencing was one of the
9 problems that the inventors of the '730 patent were
10 trying to solve, correct?

11 **A. Yes.**

12 Q. Okay. Amplification bias can arise if a
13 large fraction of the reads are derived from a
14 single originating molecule, correct?

15 MR. BROUGHAN: Object to form.

16 **A. I'm sorry. Could you say -- I missed that**
17 **last part?**

18 Q. Sure. Yeah, yeah. No worries.

19 Amplification bias can arise if a large
20 fraction of the reads are derived from a single
21 originating molecule, correct?

22 MR. BROUGHAN: Object to form.

23 **A. In a way that is not representative of the**
24 **original population.**

25 Q. I see. Good point. So just for the

1 record's sake, amplification bias can arise if a
2 large fraction of the reads are derived from a
3 single originating molecule in a way that is not
4 representative of the original population, correct?

5 **A. Yeah.**

6 **Q.** Okay. And amplification bias can result in
7 a skew of the population of target sequences
8 observed, correct.

9 **A. Yes.**

10 **Q.** And skewing could result in attributing the
11 incorrect genotype to the sample, right?

12 **A. Yes.**

13 **Q.** For example, skewing could result in
14 incorrectly genotyping the sample as homozygous
15 instead of heterozygous because you've overcounted
16 a given allele?

17 **A. Yes.**

18 **(Reporter clarification.)**

19 **Q.** Okay. To solve this problem, the '730
20 patent tags each target molecule sequence with a
21 different differentiator tag, so that each target
22 molecule sequence can be considered independently.
23 You would agree with that?

24 **MR. BROUGHAN:** Objection to form.

25 **A. So with a unique -- one approach the '730**

1 **uses is to tag molecules with unique differentiator**
2 **tags.**

3 Q. Sure. So I'll rephrase.

4 To solve that problem, the '730 patent tags
5 each target molecule sequence with a unique
6 differentiator tag, so that each target molecule
7 sequence can be considered independently, right?

8 MR. BROUGHAN: Object. Objection
9 to form.

10 A. Yes.

11 Q. Okay. And if you could turn to Claim 1 of
12 the '730 patent, the very, very last page.

13 The '730 patent claims, (As read.)
14 "Correcting for error or bias introduced during
15 said workflow by collapsing target:differentiator
16 tag combinations observed more than once into a
17 single count," right?

18 A. Yes, I see that.

19 Q. Okay. You agree that that's one step of
20 Claim 1, claimed by the -- apologies.

21 You agree that that's one step of Claim 1
22 claimed by the '730 patent, right?

23 MR. BROUGHAN: Object to form.

24 A. That is written here in Claim 1.

25 Q. Yeah. And then if you look at Claim 2, the

1 method of Claim 1, wherein said, "Correcting step
2 further comprises collapsing all sequence reads
3 comprising the same differentiator tag into a
4 single read before determining a consensus base
5 call for the target nucleic acid molecule
6 sequences."

7 Do you see that?

8 **A. I do.**

9 Q. Collapsing all sequence reads comprising
10 the same differentiator tag into a single read is a
11 separate step from determining a consensus base
12 call, correct?

13 MR. BROUGHAN: Object to form.

14 **A. That's what the inventors wrote here
15 because they say they do the collapsing before
16 determining. So they're considering this two
17 steps.**

18 Q. Okay. And they claim two different
19 processes, right? Because they're considering two
20 steps, but they use different language for each of
21 those steps.

22 **A. Yes.**

23 Q. Okay. I'm handing you a copy of previously
24 marked EX-1006 [sic].

25 (Whereupon, previously marked

1 Exhibit EX-1010 was introduced.)

2 Q. EX-1006 is the Chee prior art reference you
3 relied on, correct?

4 A. **Yes.**

5 Q. Did you find Chee yourself? Or did
6 Illumina provide Chee to you?

7 MR. BROUGHAN: Objection to --
8 sorry. One second.

9 If you can recall, you can answer.

10 A. **I believe this was provided as prior art.**

11 Q. If you turn to column 1 around lines 20
12 to 23.

13 MR. WUESTE: And apologies. For
14 the record, Chee is EX-1010. I think
15 I misspoke.

16 Q. Column 1, beginning at line 23, that first
17 paragraph. Chee states, "Synthetic biology is a
18 promising new field at the interface of engineering
19 and biology," correct?

20 A. **That's what it says.**

21 Q. "Synthetic biology," as Chee describes it,
22 means constructing the genome as opposed to
23 decoding or -- decoding a genome, correct?

24 MR. BROUGHAN: Object to form.

25 A. **I think it refers to -- to synthesizing**

1 **nucleic acid fragments.**

2 Q. And referencing our discussion earlier, you
3 know, that would be an artificial nucleic acid
4 sequence as opposed to a naturally occurring one,
5 like the ones you're developing in your genomic
6 profiles, for example, correct?

7 A. **That's fair.**

8 Q. Okay. And actually Chee cites to an
9 article in Science by an Endy, D., for this
10 discussion of synthetic biology; is that correct?

11 A. **I see that.**

12 Q. I'm going to hand you a document that we
13 are going to mark EX-2005.

14 (Exhibit EX-2005, an article, was
15 marked for identification.)

16 Q. EX-2005 is an article titled Reconstruction
17 of the Genomes by Drew Endy, correct?

18 A. **Yes.**

19 Q. You see at the bottom, it says Science,
20 Volume 319, 29 February 2008?

21 A. **I see that.**

22 Q. This is the February 28th, 2008, Volume 319
23 article by Drew Endy cited by Chee, correct?

24 A. **Yes.**

25 Q. Had you seen this article before?

1 **A. No.**

2 Q. Did you review the EX-2005, the Endy
3 article, in forming your opinions in this case?

4 **A. No, I didn't review it.**

5 Q. I believe that Drew Endy is in the
6 biological engineering department at MIT?

7 **A. That's what it says here.**

8 Q. Yeah. Given your work in the Boston area,
9 do you know Drew Endy?

10 **A. I don't.**

11 Q. Okay. Thought it might be another
12 small-world situation.

13 If you turn to 1196, which is the first
14 face of the Endy article, EX-2005, there's a
15 comment under that -- that first figure titled
16 Genome Construction. Do you see that?

17 **A. Yes.**

18 Q. Okay. That comment, in this Endy article
19 cited by Chee, contrasts DNA sequencing technology
20 from DNA synthesis and genome construction
21 technologies, correct?

22 MR. BROUGHAN: Object to form.

23 **A. I've never read this article before, so --**
24 **so in order to have the context, I need a little**
25 **bit of time. If you want to give me time to review**

1 **it?**

2 Q. Sure. But I think this is one area in
3 which the English background might be helpful.

4 So if we look at that first sentence, "DNA
5 sequencing technology decodes the genome of an
6 organism."

7 That's what the Endy article says, right?

8 **A. That's what it says.**

9 Q. Then the second sentence, "DNA synthesis in
10 genome construction technologies enable the
11 opposite process."

12 That's what the Endy article cited by Chee
13 says, right?

14 **A. That's what it says.**

15 Q. Okay. And then, you know, it goes on to
16 say, "Bacterial genomes can be built from DNA
17 sequence information and raw chemicals," right?

18 **A. That's what it says.**

19 Q. So if synthetic -- strike that.

20 If DNA sequence and genome construction
21 technologies, as described by Endy and cited by
22 Chee, is the opposite process of DNA sequencing
23 technology, you would agree that -- that Endy
24 contrasts those two, right?

25 MR. BROUGHAN: Object to form.

1 A. I mean, you know, you're asking me for an
2 opinion on a sentence here without -- without the
3 context of really what he's trying to get at
4 because I've never read this article before. So
5 I'm happy to read it and give you an opinion. But,
6 otherwise, we can agree on what the -- you know, on
7 what these sentences say --

8 Q. Right.

9 A. -- which is what you've read.

10 Q. Right. And -- and you would agree that
11 Endy describes DNA synthesis and genome
12 construction technologies as the opposite process
13 from decoding the genome of an organism using DNA
14 sequencing technology, correct?

15 MR. BROUGHAN: Objection to form.

16 A. No, I -- I don't agree with that without a
17 full time to review and get context of what we're
18 talking about here. I mean, for example, I think
19 it's odd to refer to it as the "opposite process"
20 because it very well may be -- they may be
21 complementary processes.

22 Because often -- and as Chee talks about
23 and as other people talk about, you do want to
24 perform genome seq- -- sequencing of a synthetic
25 DNA construct. So I, kind of, think he's

1 getting -- they may be getting at two different
2 broad concepts here. So that's why I don't want to
3 just automatically agree without, you know, really
4 being specific about context.

5 Q. Okay.

6 A. And in fact, I mean, you can -- if you read
7 the -- the green, "DNA sequencing and synthesis
8 technologies are making it possible to read and
9 write genomes."

10 So these are complementary processes being
11 used together to do different things, but can --
12 that can still have some, kind of, complementarity
13 to them.

14 Q. Sure. That's fair.

15 So DNA synthesis and DNA sequencing
16 technology are complementary processes. That's
17 part of what you said, correct?

18 A. Complementary in the sense that you may use
19 DNA sequencing in your synthetic DNA work.

20 Q. But they are directed to different goals.
21 Is that fair to say?

22 MR. BROUGHAN: Object to form.

23 A. No. I mean, they're different -- they --
24 they're activities. I mean, synthetic biology is
25 creating the DNA strand -- writing genomes. DNA

1 sequencing is reading genomes.

2 And so you -- you -- it's totally fair, as
3 it says here, to use DNA sequencing to read out
4 your synthetic biology experiment.

5 Q. Okay. I -- I don't want to get any of this
6 twisted up, so let me -- let me use your words.

7 "DNA synthesis and DNA sequencing are
8 different activities. DNA synthesis, or synthetic
9 biology is writing genomes where DNA sequencing is
10 reading genomes," correct?

11 MR. BROUGHAN: Object to form.

12 A. Yeah, that's what I said.

13 Q. Okay. You can put that one away. Thank
14 you.

15 If you can pull Chee back in front of you
16 and look at the front page of Chee.

17 Chee was first filed as a PCT application
18 on April 29th, 2010, correct?

19 A. Yes.

20 Q. And then if you would humor me and pull up
21 the '730 patent, EX-1001?

22 A. Yes.

23 Q. The April 29th, 2010 PCT filing date of
24 Chee is after the dates of any of the provisional
25 applications cited on the face of the '730 patent,

1 right?

2 **A. Yes.**

3 Q. Chee also cites a provisional application
4 number, 61/174,442 that was filed on April 30th,
5 2009, correct?

6 That's at --

7 **A. Where's that -- where's the line there?**

8 **I wanted to --**

9 Q. So, yeah. If you look at the -- the face
10 of Chee and go down the --

11 (Simultaneous speakers.)

12 **A. I'm sorry, I see it. It's on line 60.**

13 Q. Yeah.

14 **A. Yes, I see that.**

15 Q. Yeah.

16 **A. Correct.**

17 Q. Okay. So just for the -- the record's
18 sake, Chee recites a provisional application number
19 61/174,442 filed on April 30th, 2009, right?

20 **A. Yes.**

21 Q. And I think you called it the '442
22 provisional. It's okay if we use that?

23 **A. Yes.**

24 Q. Okay. It's your understanding that for
25 Chee to be entitled to the April 30th, 2009 filing

1 date of the '442 provisional at least one claim of
2 Chee must have written description support in the
3 '442 provisional, correct?

4 **A. Yes.**

5 Q. And -- and you're not an attorney, right.

6 **A. Excuse me?**

7 Q. You're not an attorney?

8 **A. No, definitely not.**

9 Q. Okay. So again, don't want to -- don't
10 want to get things twisted. I think you cite to
11 that at paragraph 121 of your declaration?

12 **A. Correct. I just -- I have that right here,**
13 **yes.**

14 Q. Okay. And the first sentence of that
15 reads, "I understand that for Chee to be entitled
16 to the priority of its provisional application" --
17 (Reporter clarification.)

18 Q. Sorry. When I read, I get a little quick.
19 Starting over.

20 In paragraph 121 of your declaration, you
21 say, "I understand that for Chee to be entitled to
22 the priority of its provisional application,
23 EX-1011, at least one claim of the patent must have
24 written description support in the provisional,"
25 correct?

1 **A. Yes.**

2 Q. Where did you get that understanding?

3 **A. I believe that's -- it is a legal**
4 **requirement and it was described to me by the**
5 **attorneys.**

6 Q. Right. Because you're not an attorney
7 yourself?

8 **A. I am not.**

9 Q. And so you relied upon Illumina's lawyers
10 to tell you the legal requirements of the law
11 for -- for this kind of priority date analysis,
12 right?

13 **A. That's right.**

14 Q. Okay. And then the rest of the section --
15 well, actually, let me do it another way. Sorry
16 about that.

17 You -- you then go on to state, in
18 paragraph 121, "I have reviewed the '442
19 provisional and found that at least Claims 1 and 2,
20 in the issued Chee patent, were sufficiently
21 described by the '442 provisional," correct?

22 **A. Yes.**

23 Q. And that's the entirety of your analysis
24 regarding whether Chee was sufficiently described
25 in the '442 provisional, correct?

1 MR. BROUGHAN: Object to form.

2 A. Yes.

3 Q. You don't analyze any other claims, just 1
4 and 2 of -- of Chee, right?

5 A. I'm not providing any other analysis beyond
6 Claims 1 and 2.

7 Q. All right. Now, if you can turn to page 54
8 of your declaration.

9 Beginning at page 54, on paragraph 137 and
10 continuing on to -- sorry. Paragraph 143 on the
11 next page. So 137 through 143 comprise your
12 analysis of whether or not Chee discloses the
13 obtaining of a biological sample limitation of
14 the '730 patent, correct?

15 A. Yes.

16 Q. If you could quickly review paragraphs 137
17 to 143 and let me know when -- when -- when you've
18 finished that and just have that in mind for my --
19 for my next question, if you don't mind?

20 A. Okay. Okay. I read it.

21 Q. In the portion of your analysis of whether
22 or not Chee discloses the obtaining of a biological
23 sample limitation of the '730 patent, you do not
24 opine that the '442 provisional also describes the
25 subject matter, correct?

1 MR. BROUGHAN: Object to form.

2 A. Right. My opinion given here is that a
3 person skilled in the art would understand that the
4 method can be used for several purposes which
5 normally involves obtaining and analyzing target
6 nucleic acid molecules for many loci.

7 Q. And I appreciate the recitation of your
8 opinion here. But just for confirmation, in the
9 portion of your analysis of whether or not Chee
10 discloses the obtaining of a biological sample
11 limitation in the '730 patent, you do not opine
12 that the '442 provisional also describes that
13 subject matter, yes or no?

14 MR. BROUGHAN: Objection to form.

15 A. I don't offer that opinion in this section,
16 right here.

17 Q. Okay. I'm handing you a copy of
18 previously-marked Exhibit 1012.

19 (Whereupon, previously marked
20 Exhibit EX-1012 was introduced.)

21 Q. EX-1012 is the McCloskey reference you rely
22 on, correct?

23 A. Yes.

24 Q. Okay. Did you find McCloskey on your own?
25 Or was it provided to you?

1 MR. BROUGHAN: You can answer.

2 A. I believe this was provided to me.

3 Q. And, actually, apologies. But before we
4 turn to McCloskey, if you could pull back up
5 EX-1001, the '730 patent?

6 A. Yes.

7 Q. And if you look at the face of the '730
8 patent, at line 56, the References Cited column.

9 A. Yes.

10 Q. Do you have any patents of your own?

11 A. Not issued, no.

12 Q. Okay. You're in the process of applying
13 for some patents?

14 A. No, I -- at one point there was a
15 provisional filed, but it was a very long time ago.

16 Q. I see.

17 A. So let's disregard it.

18 Q. Okay. But you would agree that the
19 References Cited column on the face of a patent,
20 like the '730 patent, identifies patents and other
21 publications that the Patent and Trademark Office
22 had before it during prosecution, correct?

23 A. Yes.

24 Q. And the '730 patent was allowed, right?

25 A. Yes.

1 Q. And the '730 patent was allowed over all of
2 these patents and patent applications identified on
3 the face of the '730 patent, correct?

4 MR. BROUGHAN: Objection to form.

5 A. **That's my understanding.**

6 Q. Okay. Turn to Page 2 of the '730 patent.
7 And if you'll look at column 2, the right-hand
8 column, on the References Cited page. If you look
9 about ten lines up from the bottom of the
10 right-hand column.

11 A. **I see.**

12 Q. You should see a 2007/0020640 application
13 to McCloskey, et al, correct?

14 A. **Yes.**

15 Q. And just for confirmation, that's the same
16 McCloskey that is EX-1012 that you opine on,
17 correct?

18 A. **It appears to be, yes.**

19 Q. And that means that the Patent and
20 Trademark Office was notified of McCloskey during
21 prosecution of the '730 patent, correct?

22 A. **Yes.**

23 Q. And that means the '730 patent was allowed
24 over McCloskey?

25 MR. BROUGHAN: Object to form.

1 **A. Yes.**

2 Q. Okay. And, now, if you could pull up your
3 declaration, again, and turn to paragraph 108.

4 **A. Yes.**

5 Q. In paragraph 108 of your declaration,
6 that's where you identify McCloskey as prior art,
7 correct?

8 **A. Yes.**

9 Q. Okay. And then if you look, again, in your
10 declaration at paragraph 239. Apologies for having
11 you flip around through this.

12 **A. Yes.**

13 Q. Okay. In paragraph 239, you provide an
14 overview of McCloskey, correct?

15 **A. Yes.**

16 Q. Okay. And that overview continues on
17 through paragraph 246?

18 **A. Correct.**

19 Q. You don't address in your declaration the
20 fact that the PTO was aware of McCloskey during
21 prosecution of the '730 patent, right?

22 **A. I didn't -- I didn't discuss that, but, as**
23 **you know, my analysis is based on McCloskey in**
24 **combination with other prior art.**

25 Q. When you submitted your declaration, were

1 you aware that McCloskey was identified to the PTO
2 during prosecution of the '730 patent?

3 **A. Well, it's on the -- it's listed there in**
4 **the patent.**

5 Q. So the answer to the question is "yes"?

6 **A. Yes.**

7 Q. Okay. And then I think, as you said, you
8 analyzed it in combination with Bignell, correct?

9 **A. That's right.**

10 Q. Okay. I'm handing you what has previously
11 been marked as EX-1013.

12 (Whereupon, previously marked
13 Exhibit EX-1013 was introduced.)

14 Q. EX-1013 is the Bignell prior art that you
15 rely on, correct?

16 **A. Correct.**

17 Q. Did you find Bignell on your own? Or was
18 it provided to you?

19 **A. I believe this was provided.**

20 Q. Okay. You would agree that Bignell is
21 useful for techniques for next-gen sequencing such
22 as on an Illumina genome analyzer, right?

23 **A. Yes.**

24 Q. Okay. And Bignell is directed to methods
25 for identifying the source of a polynucleotide,

1 correct?

2 MR. BROUGHAN: Objection to form.

3 A. Yes, Bignell uses -- it tags the sample
4 identifiers to get to the source of the sequence
5 data.

6 Q. Got it. The sample identifier tags are for
7 identifying the source of the sequence data,
8 correct?

9 A. Yes.

10 Q. Okay. The sample identifier tags are
11 sometimes described by Bignell as sample specific
12 tag sequence, right?

13 A. Do you want to point me to that?

14 Q. Yeah, yeah. Happy to.

15 If you look, for example, at Bignell at
16 column 4, beginning around line 10, step C, that
17 begins "Amplifying adapter target, adapters."

18 Do you see that?

19 A. Yes.

20 Q. And then there's a "wherein" clause after
21 that, "Wherein, one, as said amplification primers
22 comprises a sample specific tag sequence," correct?

23 A. Yes.

24 Q. The tag sequence is specific to a sample,
25 right?

1 **A. In what is described here, that's right.**

2 Q. Yeah. And the sample specific tag sequence
3 or the sample identifying tag would be applied to
4 all molecules from a given sample, right?

5 **A. That would be the purpose -- the intent of**
6 **what you were doing, yeah.**

7 Q. It wouldn't make sense to apply different
8 tags to every molecule in the sample if your
9 goal -- if Bignell's goal was identifying the
10 source of the sample, right?

11 MR. BROUGHAN: Objection to form.

12 **A. If the goal is being able to tell one**
13 **sample from another sample, you wouldn't want to**
14 **have different tags applied within a sample.**

15 Q. Right. So in order to differentiate
16 molecules originating from a Sample A from
17 molecules originating from a different Sample B,
18 using Bignell's method, you would have to apply the
19 same tag to all molecules originating from
20 Sample A, right?

21 MR. BROUGHAN: Objection to form.

22 **A. That's a type of tag you can use. If you**
23 **want to do sample specific tagging, you would use**
24 **sample specific tags for A and sample specific tags**
25 **for B, if the purpose was simply to tell the**

1 **samples apart.**

2 Q. Right. And that's one of the purposes of
3 Bignell, right, is to tell samples apart?

4 A. **Yes.**

5 Q. Okay. Now -- therefore, in order to
6 accomplish its goal of identifying the source or
7 sample of the molecule, Bignell describes, for
8 example, attaching the same tag to every molecule
9 from a given sample, right?

10 MR. BROUGHAN: Objection to form.

11 A. **I think your last part -- I think you**
12 **said -- could you say that again? I think you said**
13 **it incorrectly.**

14 Q. Sure, sure. I might have misspoken.

15 Therefore, in order to accomplish its goal
16 of identifying the source of a sample of a
17 molecule, Bignell describes attaching the same tag
18 to every molecule from a given sample, correct?

19 MR. BROUGHAN: Objection to form.

20 A. **Right. The goal is to assign sequence data**
21 **to samples.**

22 Q. If you can, now, turn to Bignell at column
23 3, Bignell on line 33. Feel free to -- actually,
24 start with the sentence beginning at line 28, "The
25 problem with enabling" and then down to the end of

1 that paragraph at line 35. And keep that in mind
2 for my next question.

3 **A. Yes.**

4 Q. Okay. And this section is in the
5 "Background of the Invention," right?

6 **A. Yes.**

7 Q. So this section is describing, say, you
8 know, the state of the industry and the prior art,
9 correct?

10 **A. Seems to be.**

11 Q. Okay. At line 33, Bignell states, "Whilst
12 this is ideal for treating one sample such that
13 each individual molecule in the sample carries a
14 different tag, it does not permit attachment of the
15 same tag to every molecule in the sample," correct?

16 **A. That's what it says referring to other
17 piece of prior art that they point to.**

18 Q. Right. So Bignell would contrast its
19 approach of attaching the same tag to every
20 molecule in a given sample for identifying the
21 source of that sample with approaches that attach
22 different tags to each individual molecule in the
23 sample, correct?

24 MR. BROUGHAN: Objection to form.

25 **A. Well, they're just saying that in that**

1 **approach, you're not tagging each individual**
2 **molecule because they find problems with it but --**
3 **yeah.**

4 Q. Right, right.

5 A. They're just distinguishing one set of
6 conditions to go about and accomplish sample
7 specific tagging that weren't used previously.

8 Q. Right. They're distinguishing approaches
9 that tag each individual molecule because they find
10 problems with it, correct?

11 MR. BROUGHAN: Objection to form.

12 A. They find problems with a particular older
13 example of doing some type of tagging.

14 Q. Right. And that particular older example
15 involves treating one sample such that each
16 individual molecule in the sample carries a
17 different tag, correct?

18 A. In that particular example, which is,
19 again, a distinct method, they are distinguishing
20 their method from it.

21 MR. WUESTE: Let's take a break.

22 THE VIDEOGRAPHER: This is the end
23 of Media Number 2. The time is 11:19 a.m.
24 We are off the record.

25 (Whereupon, a recess was taken at

1 this time.)

2 THE VIDEOGRAPHER: This is Media
3 Number 3. The time is 11:33 a.m. We're
4 back on the record.

5 BY MR. WUESTE:

6 Q. Welcome back, Dr. Gabriel.

7 A. **Thanks.**

8 Q. Do you have any changes to your testimony
9 today?

10 A. **Nope.**

11 Q. I'd like to return briefly to the Sanger
12 sequencing.

13 A. **Sanger, yes.**

14 Q. Yes.

15 You would agree that Sanger sequencing is
16 much slower compared to next-gen sequencing?

17 A. **Yes.**

18 Q. And you would agree that Sanger sequencing
19 is much more expensive compared to next-gen
20 sequencing, correct?

21 A. **On a per-data basis, yes.**

22 Q. Okay. You would agree that next-gen
23 sequencing reduces the cost of sequencing by over
24 two orders of magnitude compared to first-gen
25 approaches like Sanger sequencing, correct?

1 MR. BROUGHAN: Objection to form.

2 A. On a per-data basis, yes.

3 Q. And just to make sure we're all on the same
4 page, if you look at your declaration on page --
5 paragraph 55, the sentence I'm reading starts at
6 the very bottom of that page, but it continues on
7 to the next.

8 A. Yes.

9 Q. They had already reduced the --
10 (Reporter clarification.)

11 Q. Sorry. I'll repeat.

12 In paragraph 55 of your declaration, you
13 state, "Next-gen technologies had already reduced
14 the cost of sequencing by over two orders of
15 magnitude and had greatly improved efficiency,"
16 correct?

17 A. Yes.

18 Q. As part of your analysis in this case, you
19 rely on an article by Shendure, correct?

20 A. That's right.

21 Q. Okay. I'm going to hand you what's
22 previously been marked as EX-1014.

23 (Whereupon, previously marked
24 Exhibit EX-1014 was introduced.)

25 MR. WUESTE: Ms. Lee, if you'd like

1 a copy, I have one for you, too.

2 Q. EX-1014 is an article by Jay Shendure and
3 Hanlee Ji titled Next-gen DNA Sequencing, correct?

4 A. Yes.

5 Q. And this is the article that -- that you
6 cite to and rely on in your declaration, right?

7 A. Correct.

8 Q. Okay. I'd like you to turn to page 1,141
9 of Shendure. And then there -- we've got the
10 Advantages and disadvantages of different
11 approaches column?

12 A. I see that.

13 Q. All right. And then if you look down the
14 middle of that first full paragraph, it
15 describes -- I'm going to direct your attention to
16 the sentence, "In this context, the
17 requirements..."

18 A. Okay.

19 Q. Okay. So now we're situated.

20 "In this context, the requirements of a
21 Sanger sequencing approach include major costs
22 beyond just reagents."

23 Do you see that?

24 A. Yes.

25 Q. And then it goes on to describe some of

1 those requirements and major costs.

2 And I want to direct your attention to the
3 next sentence reading "In a recent informal
4 survey..."

5 Do you see that?

6 **A. Yes.**

7 Q. And that states, in Shendure, "In a recent
8 informal survey we conducted of the overall cost to
9 conventionally sequence one hundred genes from one
10 hundred samples, assuming each gene has an average
11 of 10 exons, quoted estimates for noncommercial
12 genome centers and commercial sequence service
13 provides range from \$300,000 to over \$1 million."

14 Do you see that?

15 **A. I do.**

16 Q. Do you have any reason to doubt that in
17 2008, when Shendure was published, the cost to
18 sequence one hundred genes from one hundred samples
19 using conventional Sanger sequencing range from
20 \$300,000 to over \$1 million?

21 MR. BROUGHAN: Objection to form.

22 **A. No, I believe he's accurate.**

23 Q. Okay.

24 **A. I mean, he's -- I believe he conducted this**
25 **survey and is giving what he found from that**

1 **survey, yes.**

2 Q. Okay. So next-gen sequencing would have
3 represented cost savings of over two orders of
4 magnitude from that estimate, right?

5 MR. BROUGHAN: Objection to form.

6 **A. Theoretically, for any given, you know,**
7 **experiment or in any given lab, I guess you could**
8 **say, you would have to really be wanting to**
9 **compare, I think, some specifics about what you're**
10 **trying to accomplish with that kind of sequencing.**

11 **But, yeah, in theory, the, you know,**
12 **next-gen sequencing would be faster and cheaper.**

13 Q. Okay. And, again, right, as you put it,
14 next-gen sequencing technologies had already
15 reduced the cost of sequencing by over two orders
16 of magnitude and had -- and had greatly improved
17 efficiency, right?

18 **A. Yes.**

19 Q. If you turn to page 1,143 of Shendure and
20 on the right-hand column, there's an acknowledgment
21 section.

22 Do you see that?

23 **A. Yes.**

24 Q. And it states: "We thank G. Church and G.
25 Porreca for helpful comments on the manuscript?"

1 **A. Yes.**

2 Q. Porreca is one of the inventors on the '730
3 patent, right?

4 **A. That's right.**

5 Q. And we -- we've already established you're
6 very familiar with Dr. Church, right?

7 **A. I am. That's right.**

8 Q. Okay. Dr. Gabriel, did you discuss the
9 substance of your testimony today with counsel
10 during breaks?

11 **A. No.**

12 MR. WUESTE: Okay. I will pass the
13 witness.

14 MR. BROUGHAN: Can we take a very
15 quick break?

16 THE VIDEOGRAPHER: This is the end
17 of Media Number 3. The time is 11:41 a.m.
18 We're off the record.

19 (Whereupon, a recess was taken at
20 this time.)

21 THE VIDEOGRAPHER: This is Media
22 Number 4. The time is 11:51 a.m. We're
23 back on the record.

24 EXAMINATION

25

1 BY MR. BROUGHAN:

2 Q. We have a few redirect questions.

3 Dr. Gabriel, do you recall earlier when
4 counsel asked you questions about the biological
5 sample elements of Chee?

6 A. Yes.

7 Q. And counsel directed you to -- I think it
8 was paragraphs 137 to 143 of your declaration?

9 A. Yes.

10 Q. And you considered the Chee provisional
11 publication, correct?

12 A. Yes.

13 Q. If you turn to paragraph 129 in your
14 declaration.

15 A. Yes.

16 Q. Have you offered an opinion about whether
17 the Chee provisional discloses a biological sample?

18 A. For Claim 2?

19 Q. Sorry.

20 Have you offered an opinion about whether
21 the Chee provisional discloses a biological sample?

22 A. Yes.

23 Q. And --

24 A. The provis- -- I'm sorry.

25 The provisional states that the constructs

1 **can be --**

2 **(Reporter clarification.)**

3 **A. Sorry.**

4 **-- used in quantitative analysis of nucleic**
5 **acids derived from a biological sample.**

6 **Q. Okay. Thank you.**

7 And could you turn to paragraph 194 of your
8 declaration, please.

9 **A. Yes.**

10 **Q. The Genetic Variation Manual, is that the**
11 **one that you are an editor of?**

12 **A. Yes.**

13 **Q. And does the Chee provisional application**
14 **incorporate by reference The Genetic Variation**
15 **Manual?**

16 **A. It does.**

17 **Q. And you've offered that opinion in your**
18 **declaration?**

19 **A. I have.**

20 **Q. Do you have an opinion as to whether**
21 **Chee -- the Chee provisional discloses sequencing**
22 **nucleic acids for a biological sample?**

23 **A. It does.**

24 **MR. BROUGHAN: We have no further**
25 **questions.**

1 FURTHER EXAMINATION

2 BY MR. WUESTE:

3 Q. Just one or two follow-ups.

4 Dr. Gabriel, could you please turn back to
5 paragraph 129?

6 A. Yes.

7 Q. Paragraph 129 is for Claim 2 of Chee,
8 correct?

9 A. Yes.

10 Q. And Claim 2 of Chee further cites, "Wherein
11 the nucleic acid targets are isolated from a
12 biological sample," correct?

13 A. Yes.

14 Q. That is not the biological sample
15 limitation of the '730 patent, correct?

16 MR. BROUGHAN: Object to form.

17 A. I don't know what you mean.

18 Q. Well, sure.

19 Let's turn to page 54 of your declaration.

20 A. Yes.

21 Q. The limitation from the '730 patent recites
22 "Obtaining a biological sample comprising a
23 plurality of target nucleic acid molecule from more
24 than one locus of origin," correct?

25 A. That's what it says.

1 Q. That is a different limitation than the
2 '730 patent than Chee's Claim 2, correct?

3 A. Well, I think the point is the provisional
4 provides for the use of nucleic acids from a
5 biological sample, just like in the '730 they're
6 claiming that they can use biological samples in
7 their invention.

8 Q. Apologies, Dr. Gabriel. That wasn't my
9 question.

10 My question was that the '730 patent claim
11 limitation recites different words and different
12 limitations than Chee's Claim 2, correct?

13 A. The words are different, but the way I --
14 I read it, is that the claim limitations are
15 obtaining a plurality of target nucleic acids --
16 sorry. Let me back up.

17 They're obtaining a biological sample
18 comprising a plurality of target nucleic acid
19 molecules. And I also understand that the Chee
20 provisional wants to do quantitative analysis of
21 nucleic acids derived from a biological sample, so
22 there must be a plurality of molecules if you want
23 to quantitate them.

24 And -- in what Chee is providing for in
25 the '442.

1 Q. The words in '730 patent claim limitation
2 are different from the words of Chee's Claim 2,
3 correct?

4 A. **Different words are used, but I think the**
5 **intent overlaps.**

6 **(Reporter clarification.)**

7 THE WITNESS: Overlaps.

8 Q. And your analysis in paragraph 129 is
9 devoted to Chee's Claim 2 and not the '730 patent,
10 correct?

11 A. **Paragraph 129 is about Chee Claim 2.**

12 MR. WUESTE: All right. No further
13 questions.

14 THE REPORTER: Sorry, before we go
15 off the record, if both attorneys can just
16 state if they're ordering the transcript or
17 a rough draft and video?

18 MR. BROUGHAN: We'll take a rough,
19 I guess.

20 MR. WUESTE: I believe our usual
21 order. So an expedited rough and final, if
22 at all possible.

23 THE VIDEOGRAPHER: Counsel, video?

24 MR. WUESTE: Whatever the order
25 says.

1 THE VIDEOGRAPHER: Off the record.

2 One moment, please.

3 This is the end of Media Number 4
4 and completes the videotaped deposition of
5 Dr. Stacey Gabriel on Wednesday, July 9th,
6 2025. The time is 11:59 a.m.

7 We are off the record.

8 (Time noted: 11:59 a.m.)

9

10

11

STACEY GABRIEL

12

13 Subscribed and sworn to before me
14 this _____ day of _____ 20__.

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Notary Public

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C E R T I F I C A T E

I, TENEJA SOLTAU, hereby certify that the
Deposition of STACEY GABRIEL was held before me on
the 9th day of June, 2025; that said witness was
duly sworn before the commencement of her
testimony; that the testimony was taken
stenographically by myself and then transcribed by
myself; that the party was represented by counsel
as appears herein; That the within transcript is a
true record of the Deposition of said witness;

That I am not connected by blood or
marriage with any of the parties; that I am not
interested directly or indirectly in the outcome of
this matter; that I am not in the employ of any of
the counsel.

IN WITNESS WHEREOF, I have hereunto set my
hand this _____ day of _____ , 20__.

TENEJA SOLTAU

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