

1 UNITED STATES PATENT AND TRADEMARK OFFICE
2 BEFORE THE PATENT TRIAL AND APPEAL BOARD
3
4

5 FORESIGHT DIAGNOSTICS, No. IPR2023-00224;
6 INC., IPR2023-00317
7 Petitioner,
8 VS.

9 PERSONALIS, INC, U.S. Patent Nos.
10 Patent Owner. 11,384,394; 11,408,033
11
12 _____/

13 CONFIDENTIAL VIDEOTAPED DEPOSITION OF
14 JOHN WEST
15 DECEMBER 8, 2023
16 Pages 1 - 176
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22 Reported by:
23 R. Chayo Ayon,
24 CSR No. 12372
25 Job No. 6319931

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17 Videotaped deposition of JOHN WEST, taken
18 before R. Chayo Ayon, a Certified Shorthand Reporter
19 for the State of California, commencing at 8:21 a.m.,
20 Friday, December 8, 2023, at Weil Gotshal & Manges,
21 LLP, 201 Redwood Shores Parkway, Redwood City,
22 California 94065 before R. Chayo Ayon, CSR No. 12372.
23
24
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PROCEEDINGS

REDWOOD CITY, CALIFORNIA

FRIDAY, DECEMBER 8, 2023

THE VIDEOGRAPHER: Good morning. We are 08:20:46
going on the record. The time is 8:21 a.m. on 08:20:49
December 8, 2023. 08:20:55

Please note that the microphones are 08:20:56
sensitive, and they pick up whispering and private 08:20:58
conversations. 08:21:02

Please mute your phones at this time. Audio 08:21:03
and video recording will continue to take place unless 08:21:06
all parties agree to go off the record. 08:21:09

This is Media Unit 1 for the video recorded 08:21:11
deposition of John West, taken by counsel for the 08:21:14
petitioner, in the matter of "Foresight Diagnostics, 08:21:17
Inc., versus Personalis, Inc.," filed in the 08:21:21
United States Patent and Trademark Office, Case Number 08:21:26
IPR 2023-00224. 08:21:31

The location of the deposition is 201 08:21:39
Redwood Shores Parkway, Redwood Shores, California 08:21:43
94065. 08:21:48

My name is Cameron Tuttle, representing 08:21:51
Veritext, and I'm the videographer. The court 08:21:55
reporter is Rosario Ayon also from Veritext. 08:21:56

1	I am not authorized to administer an oath.	08:22:00
2	I'm not related to any party in this action nor am I	08:22:05
3	financially interested in the outcome.	08:22:06
4	If there are any objections to the	08:22:08
5	proceeding, please state them at the time of your	08:22:10
6	appearance.	08:22:13
7	Counsel and all present will now state their	08:22:13
8	appearances and affiliations for the record beginning	08:22:15
9	with the noticing attorney.	08:22:19
10	MR. HEINRICH: Alan Heinrich of Irell and	08:22:19
11	Manella on behalf of Petitioner, Foresight	08:22:22
12	Diagnostics, and with me is cocounsel also for	08:22:25
13	Foresight, Amir Naini of Naini IP.	08:22:31
14	MR. LUMAN: My name is Nate Luman. I'm from	08:22:34
15	the law firm of Knobbe Martens. I represent	08:22:36
16	Personalis in this matter. I am joined by Steve Moore	08:22:39
17	who is from Personalis.	08:22:40
18	THE VIDEOGRAPHER: Will the court reporter	08:22:46
19	please swear in the witness.	08:22:48
20	THE REPORTER: Raise your right hand.	08:22:48
21	In the testimony you're about to give, do you	08:22:48
22	solemnly swear to tell the truth, the whole truth, and	08:22:48
23	nothing but the truth?	08:22:58
24	THE WITNESS: I do. Sorry. I do.	08:22:58
25	THE REPORTER: Thank you.	08:22:58

1	JOHN WEST,	08:22:58
2	was called as a witness on behalf of the Petitioner	08:22:58
3	and who, having been duly sworn, was thereupon	08:22:58
4	examined and testified as follows:	08:23:05
5	EXAMINATION	08:23:05
6	BY MR. HEINRICH:	08:23:05
7	Q. Good morning, Mr. West.	08:23:06
8	A. Good morning.	08:23:07
9	Q. We met just a moment ago, but again my name	08:23:08
10	is Alan Heinrich, and I represent folks at Foresight	08:23:11
11	Diagnostics.	08:23:11
12	Do you understand you've taken an oath to	08:23:17
13	answer my questions truthfully and completely today?	08:23:20
14	A. Yes.	08:23:22
15	Q. Do you understand it's the same oath you	08:23:23
16	would take if you were testifying in front of a judge	08:23:25
17	or a jury?	08:23:28
18	A. That's correct, yes.	08:23:29
19	Q. Well, do you understand it has all the	08:23:30
20	solemnity of an oath that you take if you were	08:23:32
21	testifying in court in front of a judge or jury?	08:23:36
22	A. Yes.	08:23:38
23	Q. Is there any reason why you can't give your	08:23:39
24	best and truthful testimony today?	08:23:41
25	A. No.	08:23:42

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1	Q. Have you been deposed before?	08:23:43
2	A. Yes, once quite a few years ago.	08:23:47
3	Q. What was the context of that?	08:23:50
4	A. I was the CEO of a company named "Celexa."	08:23:52
5	We had acquired a -- Celexa had been a British	08:23:56
6	company. We acquired an American company here in	08:24:01
7	Hayward, California, and we were sued by another	08:24:04
8	company about a patent that had been filed something,	08:24:08
9	like, ten years earlier that we knew nothing about	08:24:13
10	until it happened.	08:24:17
11	It was to do with somebody who had been an	08:24:18
12	employee years earlier, but the patent turned out to	08:24:21
13	be important for their technology, and so there was	08:24:25
14	litigation about that that was ultimately settled in	08:24:29
15	our favor.	08:24:33
16	Q. And you testified once in that matter?	08:24:35
17	A. I only recall being deposed once in that	08:24:39
18	matter.	08:24:43
19	Q. So you're familiar with the deposition	08:24:44
20	process in general?	08:24:46
21	A. I would say in general. It's -- and I have	08:24:48
22	had some preparation sessions with Personalis counsel.	08:24:52
23	So I think they have explained the process to me.	08:24:56
24	I would say my prior deposition was over ten	08:24:59
25	years ago, and it was only once. It was, actually,	08:25:02

1	held at my house. So this is a little different	08:25:06
2	circumstance. So if there is something that we need	08:25:08
3	to do differently, if you let me know, that would be	08:25:10
4	fine.	08:25:13
5	Q. Nothing different at all.	08:25:14
6	So what did you do in particular to prepare	08:25:17
7	for the deposition?	08:25:20
8	A. I had a number of meetings with Nate Luman	08:25:21
9	and Steve Moore, and I reviewed some documents.	08:25:26
10	Q. Approximately how long did those meetings	08:25:32
11	last for?	08:25:35
12	A. So we had a total of four meetings. There	08:25:37
13	were three meetings last week, which were by Zoom, and	08:25:40
14	each of those lasted approximately two hours, and then	08:25:46
15	we had a fourth meeting in person this week on	08:25:50
16	Tuesday, and that lasted up, maybe, approximately, 6	08:25:57
17	or 7 hours.	08:26:01
18	Q. Did you review any documents as part of those	08:26:02
19	meetings?	08:26:11
20	A. Yes, and I mentioned I had reviewed some	08:26:12
21	documents, yes.	08:26:14
22	Q. Did you review any documents that are not	08:26:15
23	exhibits in this proceeding?	08:26:18
24	A. If there is a document that -- I think we	08:26:22
25	will -- may want to raise later that is a publication	08:26:25

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1	from my group, a scientific publication from back in	08:26:28
2	2008, and we can talk about that whenever you'd like.	08:26:33
3	It was about the first time that my group sequenced a	08:26:41
4	human genome using the Celexa technology.	08:26:46
5	Q. All right. Did you review your declaration	08:26:53
6	in preparation for your deposition today?	08:26:55
7	A. Yes.	08:26:57
8	Q. So let's talk in general about your	08:26:57
9	declaration. It's Exhibit 2032 in your binder.	08:27:01
10	THE REPORTER: 2032?	08:27:08
11	MR. HEINRICH: Yes.	08:27:11
12	(Exhibit 2032 was marked for identification.)	08:27:13
13	THE WITNESS: I'm open to the first page of	08:27:13
14	it.	08:27:16
15	BY MR. HEINRICH:	08:27:16
16	Q. Okay. So did you write your declaration?	08:27:16
17	A. My declaration was drafted on a collaborative	08:27:20
18	basis with the two attorneys who are present here	08:27:23
19	today.	08:27:27
20	Q. Can you explain how that collaboration	08:27:28
21	worked?	08:27:32
22	MR. LUMAN: I'll just caution the witness not	08:27:32
23	to reveal any privileged communication that took place	08:27:34
24	between himself and his counsel.	08:27:38
25	THE WITNESS: I would say that -- I'll give	08:27:43

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1	you a brief summary of it, and then you can decide if	08:27:47
2	you need more information than that.	08:27:49
3	I would say I'm not an attorney, and so I	08:27:52
4	wouldn't know how to structure a declaration, and so	08:27:55
5	our counsel has helped with saying, "Here's how a	08:27:59
6	declaration, in general, would be organized for	08:28:03
7	something like this."	08:28:05
8	So they help with the framing of that.	08:28:07
9	In addition, there was some research that led	08:28:09
10	to identifying a number of documents, which are	08:28:13
11	exhibits to the declaration, and some of those were	08:28:17
12	obtained, I believe, by counsel working with	08:28:21
13	Personalis's IT staff to look up e-mails from more	08:28:24
14	than ten years ago. That kind of thing. They help	08:28:31
15	identify some of those documents.	08:28:33
16	I no longer have access to Personalis	08:28:35
17	e-mails. So I'm not able to do that searching, but	08:28:38
18	then they brought that together, and there are parts	08:28:41
19	of the declaration that I -- where I was the original	08:28:46
20	person writing them. There were other parts that were	08:28:48
21	drafted by counsel. I reviewed all of the parts, and	08:28:51
22	the parts that I wrote were also reviewed by counsel.	08:28:55
23	We had a number of meetings to discuss the	08:29:00
24	various parts of the declaration as it was being	08:29:04
25	developed and worked on it together.	08:29:07

1 At the end it is -- although it was developed 08:29:11
2 as a collaborative effort, which I think is normal, it 08:29:13
3 is my declaration, not anybody else's, and I have 08:29:17
4 signed it. 08:29:20

5 BY MR. HEINRICH: 08:29:21

6 Q. So Mr. Moore is the current general counsel 08:29:22
7 at Personalis; correct? 08:29:25

8 A. Yes, I believe so. 08:29:28

9 Q. And what was Mr. Moore's role in the 08:29:29
10 collaboration that resulted in your declaration? 08:29:34

11 MR. LUMAN: I'm going to instruct the witness 08:29:38
12 not to answer that question. That calls for 08:29:40
13 privileged communications. 08:29:41

14 BY MR. HEINRICH: 08:29:42

15 Q. Were you shown any exhibits during the course 08:29:43
16 of this collaboration that you didn't really 08:29:44
17 recollect? 08:29:47

18 A. I don't think so. These are mostly documents 08:29:50
19 that I was involved with. 08:29:54

20 The main documents that I might not have 08:29:56
21 recalled specifically were things like Google calendar 08:30:00
22 invitations. I don't remember every Google calendar 08:30:06
23 invitation from ten years ago. 08:30:11

24 But the documents that have more technical 08:30:13
25 substance were generally things that I was involved 08:30:15

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1 with at the time, either that I wrote them or that 08:30:18
2 people who reported to me, wrote them, and so I was 08:30:20
3 generally familiar with those documents. 08:30:23

4 Q. Which parts of the declaration did you write 08:30:25
5 in the first instance? 08:30:28

6 A. I don't remember the specific list. If there 08:30:30
7 was specific portions that it's important to know, 08:30:34
8 "Mr. West, did you write this portion," I guess we 08:30:38
9 could look at them part by part, but I don't know that 08:30:41
10 I could tell you. It was a process that took a series 08:30:44
11 of meetings over an extended period of time, and we 08:30:47
12 would have to look literally at section by section to 08:30:51
13 answer that. I don't know how important it is. 08:30:54

14 Q. Were there certain subject areas where you 08:30:56
15 took the lead in drafting and others where counsel 08:30:59
16 took the lead in drafting? 08:31:03

17 A. I would say that I have -- I don't have any 08:31:06
18 expertise in the legal field. So to the extent that 08:31:09
19 there are portions of the document that are -- that 08:31:12
20 relate to legal matters or -- or legal points, those 08:31:18
21 would obviously be things I would need help from 08:31:23
22 counsel on. 08:31:26

23 To the extent that there are things that are 08:31:27
24 more technological or that have to do with the 08:31:29
25 business matters of Personalis, I know more about 08:31:33

1 those, and I founded the company and was involved the 08:31:37
2 whole period of time. So I would have had more to say 08:31:40
3 about those. 08:31:42

4 Q. Do you recall which areas involving legal 08:31:44
5 issues? Some examples that counsel took the lead in? 08:31:50

6 MR. LUMAN: I'm going to instruct the witness 08:32:03
7 not to answer that question. It calls for privileged 08:32:05
8 communication. 08:32:06

9 MR. HEINRICH: It's following up on his 08:32:06
10 answer. He said that counsel wrote sections involving 08:32:06
11 legal issues, but what particular legal issues do you 08:32:07
12 have in mind? 08:32:11

13 MR. LUMAN: Same instructions. 08:32:12

14 MR. HEINRICH: I don't think that's proper. 08:32:15

15 MR. LUMAN: I mean, you're asking questions 08:32:16
16 that go deep into what occurred between Mr. West and 08:32:18
17 his counsel during his declaration. That's not a 08:32:22
18 proper line of questioning. 08:32:25

19 MR. HEINRICH: I don't agree with your 08:32:27
20 characterization. 08:32:29

21 BY MR. HEINRICH: 08:32:29

22 Q. How long, overall, did the process take to 08:32:30
23 draft the declaration? 08:32:32

24 A. I'm trying to remember. It seems to me that 08:32:34
25 it might have been spread over a period of 08:32:42

1	approximately a month.	08:32:45
2	To provide some explanation for that, during	08:32:46
3	the time that the declaration was being prepared, I	08:32:49
4	was living in England.	08:32:53
5	My wife and I bought a second home in	08:32:54
6	Cambridge, England. So that's very nice, but it's	08:32:57
7	also eight hours time difference from California.	08:33:01
8	So that limited the times that were available	08:33:03
9	for us to be able to have meetings. So I don't know	08:33:06
10	whether that's a long time or a short time to prepare	08:33:10
11	a declaration, but -- but it was probably a month or	08:33:12
12	two, something like that. I don't remember exactly.	08:33:16
13	Q. Many hours?	08:33:19
14	A. Yes.	08:33:20
15	Q. Over the course of those many hours -- well,	08:33:20
16	first of all, in reviewing your declaration for your	08:33:26
17	deposition, did you notice any errors or mistakes or	08:33:33
18	anything at all that you would like to change in your	08:33:40
19	declaration?	08:33:43
20	A. Yes. There is one paragraph that I think we	08:33:43
21	probably need to delete from the declaration. There	08:33:46
22	was an error that -- there are a number of sections in	08:33:52
23	the declaration which talk about board of directors	08:33:57
24	meetings of Personalis. Mostly -- I think maybe	08:34:02
25	entirely in the year 2012, and we had a schedule of	08:34:05

1	those.	08:34:09
2	There was a board meeting that had been	08:34:10
3	scheduled for August of 2012, and in looking back,	08:34:12
4	presumably with the help of the IT people, the	08:34:18
5	calendar invitation for that was identified, and a	08:34:21
6	paragraph was drafted saying that we had this board	08:34:25
7	meeting.	08:34:29
8	In fact, once we looked more carefully more	08:34:30
9	recently, we have realized that that board meeting was	08:34:32
10	actually canceled. If I recall, I think I was away on	08:34:33
11	vacation with my family. So the board meeting was	08:34:36
12	canceled.	08:34:39
13	So the paragraph that states -- it's a very	08:34:40
14	short paragraph -- that states that there was a board	08:34:43
15	meeting in August of 2012, there are actually -- there	08:34:46
16	was one scheduled, but we did not actually hold that	08:34:51
17	board meeting.	08:34:55
18	Q. Can you point me to that paragraph?	08:34:56
19	A. We could hunt it down. I don't know the	08:34:59
20	paragraph number, but we could -- I think it's in the	08:35:04
21	section where we talk -- actually, I don't know what	08:35:06
22	section it's in. There's a -- it might have been	08:35:08
23	where we had the -- talked about the diligence in	08:35:10
24	pursuing the invention.	08:35:14
25	THE REPORTER: In pursuing what?	08:35:14

1	THE WITNESS: There's a section of the	08:35:19
2	declaration which has to do with showing diligence,	08:35:20
3	showing that we, not only invented the invention at a	08:35:24
4	particular time, but we were diligent in pursuing its	08:35:28
5	reduction to practice. So that's it.	08:35:33
6	BY MR. HEINRICH:	08:35:46
7	Q. It's paragraph 372.	08:35:46
8	A. Hold on one second. Here we go. Diligence,	08:35:53
9	I guess, around page 212. I believe it is	08:36:07
10	paragraph 372, which is on page 213 of the declaration	08:36:39
11	and -- well, you can see it.	08:36:46
12	Q. And so that paragraph is incorrect?	08:36:49
13	A. Yes, that was a mistake and should be -- I	08:36:51
14	think probably would be best if it was just removed	08:36:56
15	because that board meeting didn't actually happen.	08:36:59
16	Q. So you did not, in fact, discuss updates on	08:37:02
17	the accuracy program with the board in August of 2012?	08:37:06
18	A. No. Generally, we discussed updates on that	08:37:09
19	at every board meeting. So that was -- given that we	08:37:12
20	had a board meeting, that was automatically populated	08:37:15
21	in this when this was written, but because we did not	08:37:18
22	have that board meeting, we obviously couldn't have	08:37:21
23	discussed anything with our board.	08:37:24
24	Q. Was there no update provided to the board	08:37:26
25	that month, August of 2012, on the accuracy program?	08:37:29

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1	A. Let's see. I think the next board meeting	08:37:32
2	was in September. I think that's described in Section	08:37:39
3	"E," beginning on page 214. Let me see if I can find	08:37:46
4	the date if you want that.	08:37:51
5	So I provided an update to the board in	08:37:56
6	paragraph 378. It says that I sent a presentation on	08:38:00
7	September 5th, and the following paragraph says that	08:38:08
8	we had a board meeting on Wednesday, September 5th	08:38:12
9	from 9:00 to 11:00 a.m.	08:38:17
10	Q. Now, in paragraph 372, you state:	08:38:21
11	"During the board of directors	08:38:28
12	meeting, we discussed updates on the	08:38:29
13	accuracy program"; correct?	08:38:31
14	A. That's what it said. I'm saying we should	08:38:33
15	remove that paragraph.	08:38:38
16	Q. I understand. I'm --	08:38:39
17	A. But you asked me before. You're repeating	08:38:40
18	the same question, I think. I'm just making sure.	08:38:43
19	Is there a different question you're asking?	08:38:43
20	I want to answer you correctly.	08:38:46
21	Q. Yes. Here's the question.	08:38:47
22	A. Okay.	08:38:50
23	Q. So that statement you made in paragraph 372	08:38:50
24	was not, in fact, based on your own independent	08:38:53
25	recollection of events in August, 2012; correct?	08:38:56

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1 A. We didn't have that board meeting. So 08:38:59
2 obviously it couldn't be, no. 08:39:02
3 Q. Okay. So are there any other statements in 08:39:03
4 your declaration that are not based on your own 08:39:06
5 independent recollection, but instead based on what 08:39:13
6 you gleaned from documents? 08:39:16
7 A. Oh, certainly. There -- there are many 08:39:20
8 statements in the declaration about, particularly, 08:39:22
9 Google calendar events, and I don't recall everything. 08:39:27
10 That's why I have a system with Google because it's 08:39:32
11 really good at keeping track of those things, but I 08:39:34
12 don't remember necessarily the dates and times of 08:39:37
13 everything, and I don't necessarily always remember 08:39:40
14 every detail of every document, which is why I review 08:39:42
15 the documents. 08:39:48
16 So we keep a system at the company where we 08:39:49
17 have maintained the -- the Google system at the 08:39:51
18 company since it was implemented in, I think, 08:39:54
19 September of 2011. 08:39:58
20 Those computer records still exist, and to 08:40:00
21 the extent that we had board meetings and there were 08:40:04
22 documents at those board meetings, we also have kept 08:40:07
23 records of all the documents at all of the board 08:40:11
24 meetings from the beginning. 08:40:14
25 And so I, naturally, would refer to all the 08:40:15

1	documents that we've kept over the years in preparing	08:40:20
2	material for the declaration. I think that's more	08:40:24
3	reliable than necessarily relying on memory.	08:40:27
4	Q. But in the case of the statements in	08:40:30
5	paragraph 372, that wasn't the case; right?	08:40:34
6	A. That paragraph, I expect was prepared based	08:40:37
7	on having looked for a list of the board meetings that	08:40:41
8	the company held by looking at Google calendar events.	08:40:46
9	I was not the one that did that Google search. I	08:40:51
10	don't have access to the Google system at the company	08:40:54
11	anymore. And so that would have been prepared by	08:40:57
12	someone else, and so that's how -- sort of that got	08:41:00
13	to.	08:41:06
14	Q. So let's take an example. Let's turn to	08:41:06
15	Exhibit 2038.	08:41:10
16	(Exhibit 2038 was marked for identification.)	08:41:10
17	THE WITNESS: 2038.	08:41:19
18	BY MR. HEINRICH:	08:41:20
19	Q. This is an exhibit that has a Google calendar	08:41:20
20	update for a "Dev Group Weekly Meeting" dated May 3rd	08:41:26
21	from 2:00 to 4:30 p.m.; correct?	08:41:32
22	A. Yes, that's right.	08:41:36
23	Q. Now, do you have an independent recollection	08:41:37
24	of this particular meeting?	08:41:39
25	A. I have a recollection of having attended many	08:41:41

1 of these types of meetings, and I recall a lot of the 08:41:46
2 substance that we discussed, and if we look at 08:41:51
3 documents that are dated from specific meetings, I 08:41:54
4 often have a good recollection of those. 08:41:58

5 Individual meetings just with a date with no 08:42:01
6 other documentation related to them, generally, I may 08:42:04
7 not recall the specific meeting. I, generally, have 08:42:07
8 better recollection of board meetings. As CEO, those 08:42:12
9 are pretty important. 08:42:15

10 Individual technical meetings, if there was a 08:42:18
11 key substance at them, I often have a good 08:42:21
12 recollection of the technical substance, but if there 08:42:25
13 were updates or people working on elements of things, 08:42:27
14 I don't necessarily recall every aspect of every 08:42:30
15 meeting from ten years ago. 08:42:34

16 Q. Sure, sure. Now, do you know that, if this 08:42:36
17 meeting took place, you -- can you tell me, sitting 08:42:42
18 here today, whether you have an independent 08:42:44
19 recollection of each of the listed attendees actually 08:42:46
20 did attend that meeting? 08:42:51

21 A. I don't have any proof of that. As I've 08:42:51
22 mentioned, I don't necessarily recall every detail of 08:42:55
23 every meeting. 08:42:58

24 I will say that the R and D team was very 08:42:59
25 motivated at that time. And so people -- this wasn't 08:43:03

1 a meeting -- the kind of meeting that people would 08:43:05
2 avoid. It was often something that people were 08:43:08
3 enthusiastic to be a part of. 08:43:11

4 So I don't know whether each person listed 08:43:14
5 was at each one of those meetings, but I will say that 08:43:17
6 they were often quite well attended, and that the 08:43:20
7 times that were listed here, the meetings often went 08:43:25
8 on longer than was indicated on the calendar because 08:43:28
9 people were so fired up about what they were doing 08:43:32
10 that the meetings might go quite a bit later. 08:43:35

11 Q. We've all been in meetings that go long like 08:43:38
12 that. 08:43:41

13 Now, other than paragraph 372, are there any 08:43:42
14 other changes that you need to make to your 08:43:47
15 declaration? 08:43:50

16 A. No, there are not. 08:43:50

17 Q. So we'll just cross out paragraph 372, and we 08:43:52
18 won't come back to that. So do you stand 100 percent 08:44:01
19 behind everything you state in your declaration with 08:44:05
20 that one excision? 08:44:09

21 A. Yes, and I have signed the declaration, and I 08:44:12
22 take the signature seriously as is indicated in the 08:44:14
23 text above my signature. 08:44:19

24 Q. Now, you cite a number of exhibits in your 08:44:23
25 declaration; correct? 08:44:25

1	A. Yes.	08:44:26
2	Q. Did you carefully review each of the exhibits	08:44:26
3	before signing your declaration?	08:44:31
4	A. Yes. As I mentioned, some of the exhibits	08:44:32
5	are things like calendar invitations, and I can't say	08:44:37
6	that I have looked at great detail at those. I wanted	08:44:42
7	to focus most of my attention on the more significant	08:44:46
8	substance of how the technology was developed and	08:44:50
9	where that came from.	08:44:54
10	Q. Sure. In fact, let's just put the calendar	08:44:54
11	invitations aside.	08:44:59
12	A. Okay.	08:45:01
13	Q. So just focusing on the other exhibits to	08:45:02
14	your declaration.	08:45:08
15	A. Okay.	08:45:08
16	Q. Did you carefully review those exhibits?	08:45:09
17	A. Yes.	08:45:12
18	Q. And during the course of your careful review	08:45:12
19	of those exhibits, did you notice any errors or	08:45:17
20	mistakes in any of those exhibits?	08:45:19
21	A. No.	08:45:22
22	Q. Now, in the course of preparing your	08:45:23
23	declaration, did you also review the '394 and '033	08:45:29
24	patents?	08:45:36
25	A. Yes, I did. I reviewed each of the claims of	08:45:37

Page 25

1 those patents. I can't say that I reviewed every 08:45:42
2 aspect of the specification because there are many 08:45:46
3 aspects of the specification that informed other 08:45:50
4 patents, which have come from that same patent family. 08:45:53

5 So to the extent that I reviewed the patents, 08:45:57
6 I tended to focus on the claims that were specific to 08:46:00
7 the '033 and '394 patents, and I believe my 08:46:03
8 declaration has sections that refer to each claim and 08:46:08
9 the background to each claim. 08:46:14

10 Q. But from what you did review of the patents, 08:46:16
11 did you see any mistakes or corrections that needed to 08:46:20
12 be made? 08:46:24

13 A. No. 08:46:24

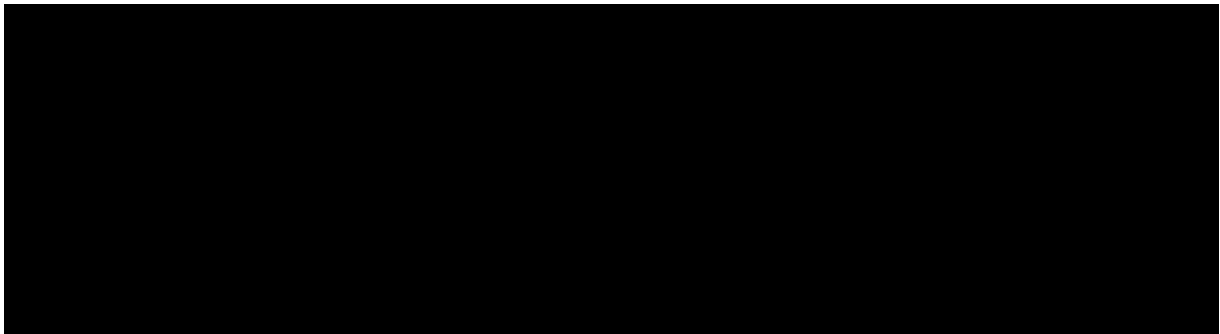
14 Q. So how long were you CEO at Personalis? 08:46:25

15 A. I cofounded the company with four Stanford 08:46:40
16 professors in February of 2011. The company existed 08:46:43
17 for a few months without any employees while we were 08:46:50
18 arranging financing for the company. I began to be 08:46:54
19 employed by the company in August of 2011, and I began 08:46:59
20 as the CEO of the company, and I stayed as CEO of the 08:47:04
21 company until I retired at the end of 2022, last year, 08:47:10
22 and that was my last day at the company. 08:47:16

23 My only -- the only position I ever held at 08:47:19
24 the company was CEO. 08:47:22

25 [REDACTED] [REDACTED] [REDACTED]

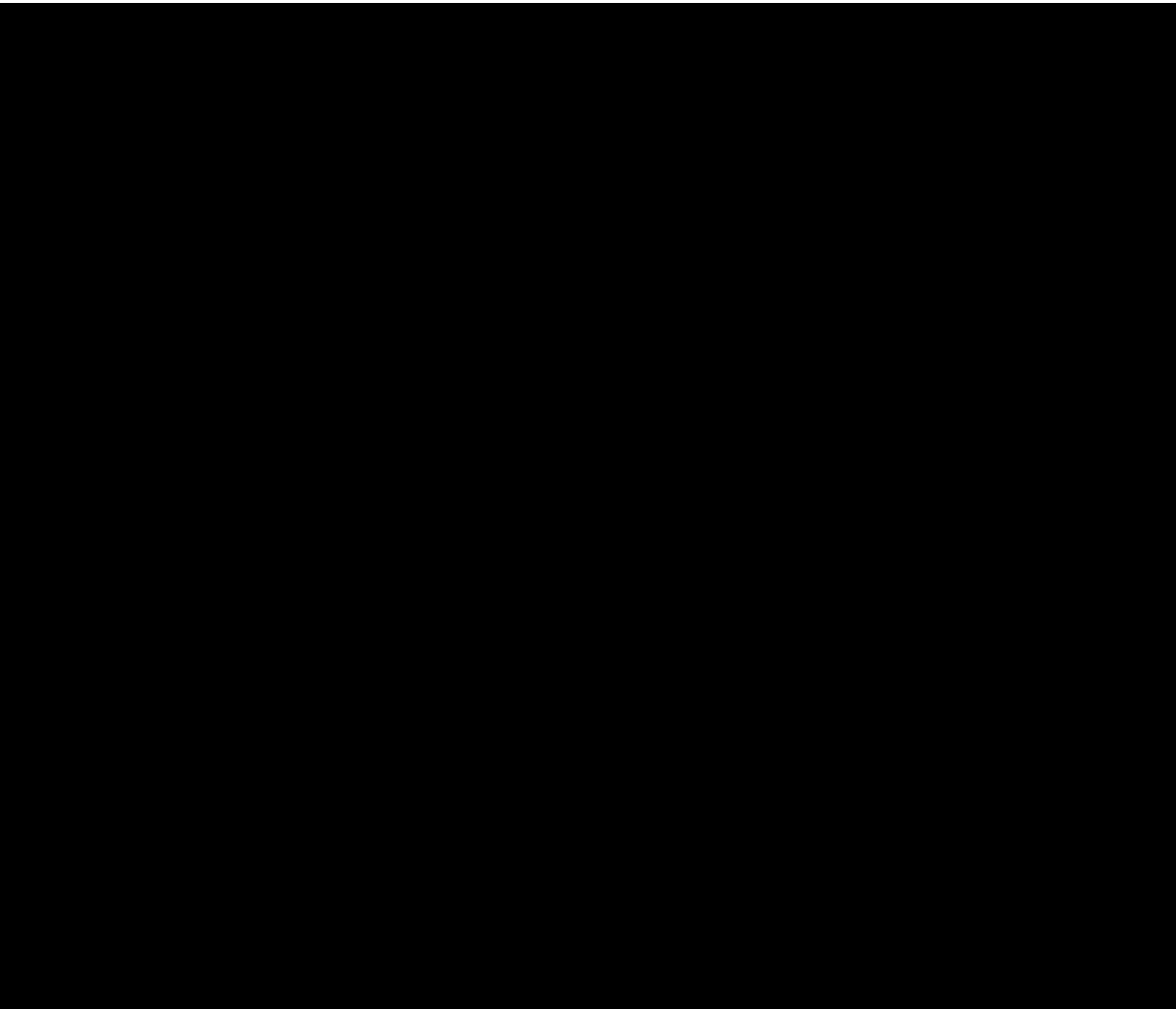
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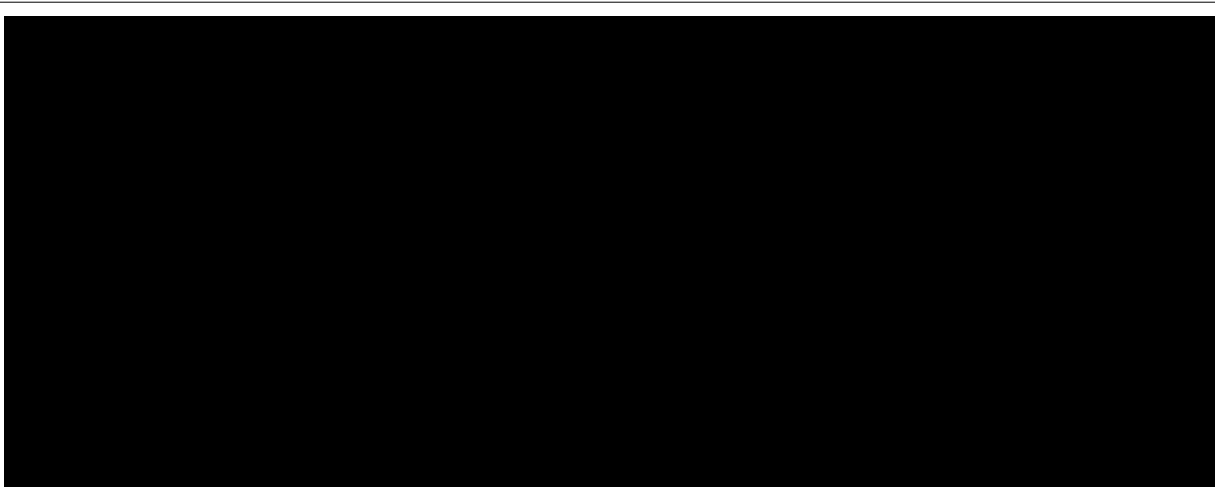
MR. LUMAN: And I'll just mention we may have 08:47:58
to mark this section of the transcript as 08:48:00
"Confidential." 08:48:03

MR. HEINRICH: Well, I think this is public. 08:48:03

MR. LUMAN: I'm not sure -- 08:48:05



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Q. What led to you stepping down in 2022? 08:48:58

A. I had turned 65 years old in December of 08:49:01
2021, and I had been the CEO of the company for over 08:49:07
ten years at that point, and I had thought about when 08:49:12
I should retire. 08:49:16

And part of my decision about retiring was 08:49:18
informed by the experience that I had seen of some of 08:49:22
my parents' friends a generation earlier. Some of 08:49:26
whom had not retired when they were 65 and continued 08:49:32
to work longer and assumed that then they would 08:49:35
eventually be able to retire and had plans for things 08:49:39
they hoped to happily do, travel and so forth, in 08:49:42
their retirement only to, then, have medical issues or 08:49:46
other problems that came up, which then prevented them 08:49:49
from ever being able to do the things they wanted to 08:49:54
do in retirement, and I took that -- I hope to be 08:49:57
happily doing some things in retirement for decades to 08:50:03
come, but you don't always get to choose those things. 08:50:05

1 And so I felt it had been ten years. I had 08:50:09
2 done a lot for the company. I felt that the company 08:50:11
3 was in really good hands with the management team. 08:50:14
4 And so I began to talk with the board of directors 08:50:16
5 about retiring. 08:50:18

6 Their initial response was, "John, you're way 08:50:22
7 too young to retire. I pointed out I was 65. We had 08:50:24
8 that back and forth for some time, and I began to look 08:50:29
9 at some of the specific things that I wanted to do in 08:50:32
10 retirement, which actually included living sometime in 08:50:36
11 another country in England, which actually we've now 08:50:39
12 done. My wife and I have purchased a second home in 08:50:44
13 Cambridge. 08:50:47

14 And during 2022, I made three trips to 08:50:49
15 England. Two of which were related to business 08:50:52
16 matters, but while I was there, I also was looking at 08:50:56
17 houses, and on some vacation time, I went there also 08:50:59
18 with my wife, and we looked at houses and became more 08:51:03
19 and more convinced that that was what we wanted to do. 08:51:06

20 And so I continued to discuss that with the 08:51:09
21 board, and we agreed that I would end my time at 08:51:12
22 Personalis at the end of December, 2022. 08:51:17

23 [REDACTED] [REDACTED]
24 [REDACTED] [REDACTED]
25 [REDACTED] [REDACTED]

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[REDACTED]

[REDACTED]

MR. LUMAN: And I'll state I do think this 08:51:37
part of the transcript is confidential. I think I've 08:51:39
made that statement. So I don't -- I won't have to 08:51:42
repeat it going forward. Okay. 08:51:45

BY MR. HEINRICH: 08:51:47

Q. Now, at the time you stepped down as CEO, 08:51:47
Personalis was going through a difficult stretch in 08:51:52
its history; is that fair? 08:51:56

A. No, I would say that Personalis has had 08:51:58
different challenges the entire time from when we 08:52:01
formed the company to when we overcame many of those 08:52:04
challenges. There were always challenges at the 08:52:07
company to get to the next level. I was proud of what 08:52:09
we accomplished, but any business I've ever run always 08:52:12
has challenges, which may vary in many different types 08:52:17
of challenges, but I would say that the company 08:52:21
actually was in pretty good shape from many 08:52:25
dimensions. 08:52:29

It did have challenges, but I didn't leave 08:52:29
because there were challenges. I left because, by the 08:52:32
time I actually left, I had turned 66, and I was 08:52:35
paying attention to wanting to move on with some of 08:52:39
the things I wanted to do in retirement. 08:52:43

Q. Is it fair to say that at the time you 08:52:45

1	retired Personalis's stock was trading substantially	08:52:48
2	below its cash assets; correct?	08:52:51
3	A. That's true of many companies in the field	08:52:54
4	because of changes in the stock market, driven,	08:52:57
5	perhaps, in part by changing interest rate policy from	08:53:02
6	the U.S. Federal Reserve.	08:53:08
7	Q. Do you still own Personalis stock?	08:53:09
8	A. Yes, I do.	08:53:12
9	Q. How many shares?	08:53:13
10	A. I don't know the number exactly. I can	08:53:16
11	answer you in three parts.	08:53:20
12	Q. Sure.	08:53:23
13	A. The first part is to say that the number of	08:53:23
14	shares that I own outright, [REDACTED]	[REDACTED]
15	[REDACTED]	[REDACTED]
16	[REDACTED]	[REDACTED]
17	[REDACTED]	[REDACTED]
18	[REDACTED]	[REDACTED]
19	And I can say that -- so the second part of	08:53:46
20	my answer is that I do also have a number of stock	08:53:48
21	options that are still outstanding. [REDACTED]	[REDACTED]
22	[REDACTED] [REDACTED]	[REDACTED]
23	[REDACTED]	[REDACTED]
24	[REDACTED]	[REDACTED]
25	[REDACTED]	[REDACTED]

1 [REDACTED] [REDACTED] [REDACTED]
2 [REDACTED] [REDACTED] [REDACTED]
3 [REDACTED] [REDACTED]
4 [REDACTED] [REDACTED]
5 The third part of my answer is, and I think, 08:54:21
6 the -- perhaps, the underlying part of your question 08:54:23
7 is whether my ownership of the stock would affect what 08:54:25
8 I'm testifying to today. And the answer is I have 08:54:28
9 sworn to tell the truth and the whole truth, and I 08:54:31
10 will, and that's not affected by my share holdings. 08:54:35
11 I do continue to be optimistic about the 08:54:38
12 future of Personalis. I think we have developed some 08:54:42
13 terrific technologies that I think will help cancer 08:54:46
14 patients, and I look forward to seeing that reflected 08:54:49
15 long term, but it may be very long term, and I can be 08:54:52
16 patient. 08:54:55
17 Q. You understand that this proceeding is taking 08:54:58
18 place in the context of a dispute between Personalis 08:55:01
19 and Foresight Diagnostics; correct? 08:55:06
20 A. Yes, I do. 08:55:09
21 Q. Personalis sued Foresight Diagnostics in 08:55:10
22 Colorado District Court? 08:55:15
23 A. Yes, I believe that's correct. 08:55:17
24 Q. And were you one of the proponents for that 08:55:18
25 lawsuit at Personalis? 08:55:22

1	A. Yes, I was. I was the CEO of the company.	08:55:23
2	Q. And you were one of the leading proponents of	08:55:26
3	the lawsuit?	08:55:29
4	A. I'm sorry?	08:55:29
5	Q. You were one of the leading proponents of the	08:55:30
6	lawsuit?	08:55:33
7	A. Yes, I would say I advocated the lawsuit. I	08:55:33
8	thought it was appropriate.	08:55:36
9	Q. You understand that in a recent quarterly	08:55:49
10	earnings call Personalis, sort of, promoted the	08:55:55
11	lawsuit as one of the key corporate undertakings for	08:56:00
12	that quarter?	08:56:11
13	MR. LUMAN: Objection; foundation.	08:56:12
14	THE WITNESS: No, I'm not aware of that. If	08:56:13
15	there is specific language that you would like to	08:56:15
16	point me to in a transcript of that, we can discuss	08:56:16
17	that, but that's not my characterization of that, and	08:56:19
18	I don't follow the quarterly results of Personalis or	08:56:22
19	the transcripts in -- in that kind of detail.	08:56:27
20	BY MR. HEINRICH:	08:56:36
21	Q. So you don't consider Personalis's lawsuit	08:56:37
22	against Foresight to be one of its key corporate	08:56:40
23	undertakings these days?	08:56:46
24	A. I think it's an important step for the	08:56:48
25	company. The company has many things that it's	08:56:50

1	pursuing that's important. I'm not going to	08:56:53
2	prioritize them. That's not my role anymore. But I	08:56:56
3	do think it is -- I think the lawsuit is important.	08:56:59
4	Ultimately, the decision about how the	08:57:02
5	lawsuit will be pursued by Personalis will be decided	08:57:06
6	by Personalis's new management, and I don't have any	08:57:10
7	input on that.	08:57:13
8	Q. All right. So let's talk about the personal	08:57:15
9	whole genome sequencing you had done on yourself and	08:57:24
10	your family back in the 2009 and 2010 time period.	08:57:29
11	A. Okay.	08:57:34
12	Q. So first you did, in fact, have whole genome	08:57:34
13	sequencing performed on you and your family in that	08:57:38
14	time period?	08:57:40
15	A. Yes, I did.	08:57:41
16	Q. And your personal experience with whole	08:57:42
17	genome sequencing played a role in you and your	08:57:46
18	coinventors ultimate conception of the claims that are	08:57:51
19	asserted in this case, claims between '394 and the	08:57:57
20	'033 patents?	08:58:03
21	MR. LUMAN: Objection; calls for a legal	08:58:04
22	conclusion.	08:58:08
23	BY MR. HEINRICH:	08:58:08
24	Q. Is that your position?	08:58:08
25	A. I'm not sure I can make a legal conclusion.	08:58:09

1 I can say that I had over 40 years of experience in 08:58:12
2 the DNA sequencing field starting in 1982. Having our 08:58:14
3 family's genome sequenced was a part of that. I do 08:58:19
4 think I learned things from that, and I do think that 08:58:22
5 helped to foster some of the ideas, which led to the 08:58:26
6 formation of the company and to the intellectual 08:58:33
7 property filings that the company made and that I was 08:58:39
8 a coinventor on. 08:58:41

9 Q. So in your declaration, one of the issues 08:58:43
10 that you address is that you claim that you and your 08:58:51
11 coinventors conceived of the claims of the '033 and 08:58:56
12 '394 patents no later than May 8, 2012; correct? 08:59:02

13 A. Yes, I believe that's correct. 08:59:07

14 Q. And you discussed your personal experience 08:59:08
15 with whole genome sequencing in your declaration 08:59:10
16 because you think it's relevant to that general 08:59:14
17 subject matter; right? 08:59:16

18 A. It is, but it wasn't the only experience. I 08:59:17
19 had been the CEO of the company that developed the 08:59:19
20 technology that was used for sequencing. So I had 08:59:22
21 wide experience in whole genome sequencing. My 08:59:24
22 family's genomes were part of that, and it was 08:59:28
23 helpful, but it wasn't the sole basis for what we did. 08:59:33

24 Q. I wasn't trying to suggest it was. 08:59:37

25 A. I'm just trying to be clear. 08:59:40

1	Q. So let's take a look at Exhibit 2114.	08:59:41
2	(Exhibit 2114 was marked for identification.)	08:59:41
3	THE WITNESS: 2114. Sorry.	09:00:00
4	BY MR. HEINRICH:	09:00:01
5	Q. I'm sorry -- yeah, 2114.	09:00:01
6	A. So this is the individual genome sequence	09:00:41
7	report that was generated for the sequencing of my	09:00:44
8	genome.	09:00:48
9	Q. Okay. So this is a report from Illumina on	09:00:53
10	the whole genome sequencing that was conducted for you	09:00:53
11	personally; correct?	09:00:57
12	A. Yes. The report was officially issued, not	09:00:57
13	to me, but it was ordered to a physician that I worked	09:00:59
14	with, and the physician ordered the test officially,	09:01:03
15	and then the data was, and results, were transferred	09:01:08
16	to me.	09:01:11
17	So that's why you see the report being	09:01:12
18	addressed to Dr. Naviaux because it was at -- at least	09:01:14
19	at that time was at the University of California	09:01:19
20	San Diego.	09:01:21
21	But, yes, this was -- this was -- went to	09:01:22
22	him, and then he conveyed it to me.	09:01:24
23	Q. Yeah, but this was the whole genome	09:01:26
24	sequencing performed on you?	09:01:31
25	A. Yes, that's right. This is from my blood	09:01:32

1	sample.	09:01:34
2	Q. Okay. If we go to page 2, this report -- let	09:01:34
3	me start over.	09:01:41
4	So on page 2, the summary statistics state	09:01:41
5	that the base pairs reported, paren, consensus are	09:01:46
6	just over 2.715 billion base pairs?	09:01:54
7	A. Yes, that's correct.	09:02:03
8	Q. That would be approximately 84 percent of the	09:02:04
9	entire genome consisting of 3.2 or so billion base	09:02:08
10	pairs?	09:02:14
11	A. The way that Illumina reported it was	09:02:14
12	relative to the known human reference sequence, which	09:02:19
13	they specifically list the NCBI, which is a U.S.	09:02:22
14	government group, the NCBI reference.	09:02:27
15	And so the consensus sequence they were able	09:02:31
16	to determine from my genome covered 95.1 percent of	09:02:35
17	the known human reference sequence. It was well known	09:02:40
18	at that time and is still mostly true that the --	09:02:43
19	there are portions of the human genome which are	09:02:47
20	difficult for current sequencing technologies and	09:02:52
21	sequencing technologies of that time to capture, for	09:02:56
22	example, the centromeres of some chromosomes. And --	09:02:59
23	and so those are not included in the reference	09:03:04
24	sequence.	09:03:09
25	So when people considered how complete a	09:03:09

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1 whole genome sequence was -- and certainly there was a 09:03:13
2 goal to try to sequence as much as possible. 09:03:16
3 Generally, the goal was to sequence as much as 09:03:19
4 possible of the known reference sequence because 09:03:24
5 the -- you could only form a consensus sequence by 09:03:27
6 aligning the sequence reads to the reference. 09:03:32

7 Any portion of the human genome, which was 09:03:34
8 not in the official reference, couldn't be included. 09:03:38
9 Even though sequence reads might be generated there, 09:03:41
10 you wouldn't know how to arrange them or where they 09:03:44
11 fit. 09:03:47

12 And so the standard that was typically used 09:03:48
13 at the time was what Illumina represented here, which 09:03:50
14 was that the consensus sequence that they established 09:03:53
15 covered 95.1 percent of the NCBI reference sequence. 09:03:59

16 Q. So in your view, in assessing the coverage of 09:04:07
17 this sequencing that was done on yourself, it wouldn't 09:04:12
18 be appropriate to use as your denominator the 09:04:16
19 3.2 billion bases of the human genome? 09:04:20

20 MR. LUMAN: Incomplete hypothetical. 09:04:24

21 THE WITNESS: No. That's exactly not what I 09:04:26
22 said. I said that the way that the calculation was 09:04:28
23 done by Illumina did not use the 3.2 billion. It used 09:04:32
24 the size of the human referenced sequence at that 09:04:37
25 time, which, if I recall, was approximately 2.85. 09:04:41

1	And so if you take the size of the consensus	09:04:45
2	sequence here that's shown as being approximately	09:04:48
3	2.71 billion bases, the -- that is 95 percent. So if	09:04:51
4	you added 5 percent onto that, it comes to probably	09:04:57
5	something like 2.85, and that would be the number.	09:05:01
6	So in general, we did not focus on the	09:05:04
7	3.2 billion because not all of the 3.2 billion was	09:05:09
8	considered accessible to the technologies of that	09:05:14
9	time.	09:05:19
10	BY MR. HEINRICH:	09:05:19
11	Q. But if you did compare it to the 3.2 billion	09:05:19
12	bases of the human genome, then this would have	09:05:23
13	covered about 84 percent of that; correct?	09:05:26
14	MR. LUMAN: Lacks foundation.	09:05:28
15	THE WITNESS: I haven't done that	09:05:30
16	calculation, and it really isn't relevant to what we	09:05:32
17	were trying to do at the time. So I think you're -- I	09:05:34
18	don't want to head down that direction because it	09:05:37
19	isn't -- you're, sort of, implying that that's how we	09:05:40
20	thought about it, and that isn't how we thought about	09:05:42
21	it.	09:05:45
22	BY MR. HEINRICH:	09:05:47
23	Q. Fair enough. Why don't you turn next to	09:05:47
24	Exhibit 2022 [sic], I believe.	09:06:08
25	(Exhibit 2122 was marked for identification.)	09:06:08

1	THE WITNESS: 2022?	09:06:14
2	BY MR. HEINRICH:	09:06:15
3	Q. I'm sorry. 2122.	09:06:15
4	A. 2122. Okay. So you're asking about the --	09:06:20
5	there's an article that was published in the journal	09:06:43
6	"PLOS Genetics"?	09:06:43
7	Q. Yes.	09:06:48
8	A. Okay. Thank you.	09:06:48
9	Q. And what is this article?	09:06:48
10	A. This is a publication by a group of --	09:06:52
11	primarily a group of academic researchers that I and	09:06:57
12	my family worked with on the interpretation of our	09:07:02
13	family's genomes. It includes researchers at Stanford	09:07:06
14	University, including all four of the Stanford	09:07:13
15	professors who were cofounders of Personalis, but it	09:07:16
16	also includes other researchers at Harvard University,	09:07:20
17	including, for example, George Church, Dr. Thakuria,	09:07:24
18	Heidi Rehm, and others from Harvard who were also	09:07:32
19	involved in the process of the initial interpretation	09:07:37
20	of our family's genomes.	09:07:39
21	Q. If you turn to page 2, I will direct your	09:07:55
22	attention to the first paragraph of the "Results"	09:07:59
23	section.	09:08:02
24	So I'm going to direct your attention in	09:08:24
25	particular to the last sentence.	09:08:26

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1	"We use the Illumina GAII sequencing	09:08:34
2	platform" --	09:08:39
3	A. Genome AnalyzerII.	09:08:40
4	Q. -- "to sequence genomic DNA from	09:08:43
5	peripheral blood monocytes from four	09:08:47
6	individuals in this nuclear family,	09:08:50
7	providing 39.3X average coverage of	09:08:53
8	92 percent of known chromosomal positions	09:08:58
9	in all four family members."	09:09:01
10	Do you see that?	09:09:03
11	A. Yes, I do.	09:09:03
12	Q. What is the article referring to when it	09:09:04
13	says, "known chromosomal positions"?	09:09:09
14	A. I don't recall exactly what it was referring	09:09:12
15	to. I assume that each of these would be positions	09:09:17
16	that are known on the human chromosomes.	09:09:20
17	Q. Would that also be a reference to the 2.8 or	09:09:27
18	so billion consensus sequence that you referred to in	09:09:30
19	your testimony a few minutes ago?	09:09:39
20	A. No -- it wasn't 3.8 [sic]. The number was	09:09:41
21	2.715.	09:09:45
22	The second thing is that this refers to the	09:09:47
23	four individuals.	09:09:50
24	The report that we looked at earlier was a	09:09:50
25	report just on my genome, and the coverage of the four	09:09:53

1	different genomes was not the same. There was some	09:09:57
2	variability from one individual to another.	09:10:00
3	The Illumina specification, at the time that	09:10:04
4	we purchased their service, was that they would	09:10:08
5	attempt to cover at least 90 percent of the reference	09:10:12
6	sequence. And as you saw in my genome, they achieved	09:10:18
7	that by achieving just over 95 percent.	09:10:21
8	The extent to which they covered the genomes	09:10:26
9	of the other family members, all of them were above	09:10:29
10	the 90 percent level. I don't recall exactly where	09:10:32
11	they were.	09:10:35
12	I would say that the results that were	09:10:36
13	published in this paper were based on a reanalysis of	09:10:41
14	the raw data. And so the exact coverage statistics	09:10:45
15	that would have been reported in this article may be	09:10:50
16	somewhat different from what Illumina had because	09:10:54
17	different software, using slightly different	09:10:57
18	algorithms, was used.	09:11:00
19	The group that did the -- I'll call it the	09:11:03
20	"technological, nonclinical level analysis" of our raw	09:11:08
21	data was the group at Stanford, not the group at	09:11:13
22	Harvard. And they used different software from what	09:11:19
23	was used by Illumina. So although the results were	09:11:22
24	similar, they were not necessarily exactly the same.	09:11:27
25	Q. But just to go back to this passage here --	09:11:30

1 well, actually, you said Illumina's goal was to report 09:11:40
2 at least 90 percent of the reference genome as part of 09:11:46
3 its whole genome sequencing service? 09:11:52

4 A. And in particular, that was defined by them 09:11:56
5 as identifying some sequence over that area. They 09:12:00
6 didn't necessarily specify what the coverage would be 09:12:05
7 at each of those positions, and they did not specify 09:12:09
8 that they would be able to identify genetic variants 09:12:12
9 over all of that. 09:12:18

10 The number that you saw in the report is a 09:12:18
11 consensus sequence number, which would be an estimate 09:12:20
12 of what they -- of what my genome sequence is, but not 09:12:22
13 necessarily taking into account all of the genetic 09:12:27
14 variants that would exist in the genome. 09:12:31

15 Q. So it was Illumina's goal to report at least 09:12:33
16 90 percent of the 2.8 billion base pairs in the 09:12:38
17 reference genome; correct? 09:12:46

18 MR. LUMAN: Objection; calls for speculation. 09:12:47

19 And please don't reveal any confidential 09:12:50
20 third-party information. 09:12:52

21 THE WITNESS: So the -- I have a copy of the 09:12:54
22 promotional material that Illumina showed us when we 09:12:58
23 were discussing spending the money to have our genomes 09:13:04
24 sequenced, and the specification that we -- that was 09:13:08
25 on the product was that they would sequence with a 09:13:12

1	goal of covering at least 90 percent of the human	09:13:16
2	reference sequence.	09:13:21
3	And sequencing human genomes was quite new at	09:13:22
4	that point. So we understood that that would be their	09:13:26
5	goal and that they would continue to add more raw	09:13:31
6	sequence data until they could achieve that level.	09:13:35
7	And it was my opinion that they did achieve	09:13:39
8	that level. The amount of sequencing actually	09:13:41
9	required for that was a little different from one	09:13:44
10	person in our family to another.	09:13:48
11	BY MR. HEINRICH:	09:13:50
12	Q. Have you ever heard of the term the "DEGAPed	09:13:51
13	genome"?	09:13:54
14	A. I have heard of that. I'm not sure I could	09:13:58
15	define it very carefully.	09:14:00
16	THE REPORTER: Degat, g-a-t?	09:14:00
17	MR. HEINRICH: DEGAPed.	09:14:14
18	BY MR. HEINRICH:	09:14:14
19	Q. Are you familiar with the fact that the DEGAP	09:14:16
20	genome is reported to have approximately 2.8 billion	09:14:19
21	base pairs?	09:14:23
22	MR. LUMAN: Outside the scope.	09:14:24
23	THE WITNESS: I think the idea is that in the	09:14:25
24	human reference sequence there are places along a	09:14:28
25	number of the chromosomes where we don't know what	09:14:33

1 the -- there is no reference sequence which has been 09:14:36
2 determined; and, therefore, there are gaps. 09:14:39
3 My recollection was that at approximately the 09:14:42
4 time that our family was sequenced, the version of the 09:14:44
5 human reference that was used had approximately 350 09:14:47
6 known gaps, and so that would not have been -- when we 09:14:54
7 say that the length of the human reference sequence at 09:15:00
8 that time was about 2.85 billion bases, I believe that 09:15:04
9 did not include any of -- gaps. 09:15:09
10 Some of the gaps were thought to be short, 09:15:11
11 and some of the gaps -- largest probably being the 09:15:14
12 centromere of Chromosome 1, almost 20 million bases 09:15:18
13 that were -- at that time the reference sequence could 09:15:24
14 not cover that. 09:15:26
15 BY MR. HEINRICH: 09:15:45
16 Q. And even today, there are known gaps in the 09:15:45
17 human genome; correct? 09:15:48
18 MR. LUMAN: Objection; foundation, incomplete 09:15:51
19 hypothetical. 09:15:55
20 THE WITNESS: So there are now newer 09:15:55
21 technologies which allow the sequencing of the human 09:16:05
22 genome, and it's my understanding that a team, using 09:16:08
23 the Pacific Biosciences technology, has now completed 09:16:11
24 what they refer to as the "Telomere to Telomere 09:16:16
25 Project," which I believe sequenced the genome of at 09:16:22

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1	least one individual with no gaps.	09:16:26
2	Obviously, there -- each chromosome is	09:16:31
3	separate, but within each chromosome, it's my	09:16:34
4	understanding that they were able to achieve a	09:16:36
5	complete sequence with no gaps, and that that data has	09:16:38
6	now been made public.	09:16:43
7	I don't know how many of those genomes there	09:16:45
8	are, and I wouldn't necessarily think of that as a	09:16:48
9	reference sequence, but it does show that it is, I	09:16:52
10	believe now, technologically possible today in a way	09:16:56
11	that was not possible at the time that my family's	09:17:00
12	genomes were sequenced to, in fact, sequence a genome	09:17:02
13	without any gaps.	09:17:06
14	BY MR. HEINRICH:	09:17:08
15	Q. When did it first become possible to sequence	09:17:13
16	a human genome consistent with approximately	09:17:18
17	3.2 billion base pairs without any gaps?	09:17:22
18	A. In the last few years, quite a long time	09:17:26
19	after we filed these patents or filed for the -- filed	09:17:31
20	the provisional filing. So -- but I don't know the	09:17:35
21	exact date. You could look it up.	09:17:39
22	If you look up the -- what was called the	09:17:41
23	"Telomere to Telomere Consortium," I think you'll find	09:17:44
24	their publications, and you could look up the dates.	09:17:50
25	Q. All right. I'm going to switch to a new	09:18:04

1 area. Why don't we take our first break. 09:18:15

2 MR. LUMAN: Sure. And I'll state that we'd 09:18:19

3 like to keep the breaks short today. Would five 09:18:20

4 minutes be okay? 09:18:24

5 MR. HEINRICH: Yeah. 09:18:26

6 THE WITNESS: Are you okay if I leave the 09:18:26

7 room to use the restroom? 09:18:28

8 MR. HEINRICH: Of course. That's the whole 09:18:31

9 point of the break. 09:18:32

10 THE VIDEOGRAPHER: Okay. We're going off the 09:18:34

11 record. The time is 9:18. 09:18:34

12 (Recess taken.) 09:24:28

13 THE VIDEOGRAPHER: We're back on the record. 09:24:28

14 The time is 9:24 a.m. 09:24:35

15 THE WITNESS: I just want to confirm, since I 09:24:37

16 put my microphone on, that you can hear me properly. 09:24:39

17 Thank you. 09:24:43

18 BY MR. HEINRICH: 09:24:43

19 Q. Did you have any discussions with counsel at 09:24:43

20 the break? 09:24:45

21 A. No. 09:24:46

22 Q. All right. So I want to ask you some 09:24:46

23 questions about the date of conception that you 09:24:56

24 provided in your declaration. 09:25:03

25 As we discussed earlier, you state in your 09:25:08

1	declaration that each of the claims of the '394 and	09:25:11
2	'003 [sic] -- '033 patents were conceived by no later	09:25:15
3	than May 8, 2012; correct?	09:25:23
4	A. Yes, that's correct.	09:25:26
5	Q. Now, what -- what do you think is the	09:25:27
6	earliest that it could have been conceived?	09:25:36
7	A. So the -- these patents are method patents.	09:25:41
8	So they include multiple elements, and we became	09:25:46
9	familiar with -- I became familiar with several of the	09:25:52
10	elements quite a bit before that.	09:25:57
11	So, for example, in -- by February of 2008, I	09:25:59
12	was aware of and thinking about the use of what's	09:26:06
13	called "Hybrid Capture Technology" in cancer.	09:26:10
14	And when our family's genomes were sequenced,	09:26:15
15	I became more aware of some of the inadequacies of the	09:26:21
16	sequencing technology, which I viewed as a business	09:26:28
17	opportunity to supplement the genome, and there are	09:26:31
18	other elements that are included.	09:26:38
19	I would say that the -- of all the pieces	09:26:41
20	that came together to form the basis for the '033 and	09:26:45
21	'394 patent, probably the last of those elements to	09:26:49
22	come together was from a paper that was -- I believe	09:26:54
23	it's an exhibit here -- that was published by Mike	09:26:59
24	Snyder's group at Stanford.	09:27:04
25	The publication came out in March of 2012,	09:27:07

1 and our group had seen a preview copy of it at least a 09:27:10
2 month earlier. We worked very closely with Mike since 09:27:15
3 he was a cofounder of the company. 09:27:19

4 And once the peer review was completed and it 09:27:21
5 was clear that the publication was going to come out, 09:27:24
6 just that it was being scheduled, we saw a preview 09:27:27
7 copy of that, and that had the elements there that 09:27:32
8 were helpful or understanding of looking at genetic 09:27:36
9 data over multiple time points. 09:27:43

10 In the case of that paper, they looked at, I 09:27:46
11 believe, 20 time points. 09:27:48

12 And that was probably the last of the 09:27:50
13 elements that, then, came together in the material 09:27:52
14 that we presented to our board on May 8th. 09:27:56

15 Q. So reading that paper was, sort of, your aha 09:28:00
16 moment for the claims of the '394 and '033 patents? 09:28:05

17 A. No. I would say that there are many elements 09:28:09
18 that we had -- many elements. These patents are not 09:28:12
19 only one concept. They are the confluence of a number 09:28:19
20 of concepts being used together. 09:28:25

21 And so our realization of the opportunity and 09:28:27
22 of, perhaps, nonobvious ways to go about solving those 09:28:32
23 problems, addressing those opportunities, those 09:28:36
24 accumulated over an extended period of time. 09:28:39

25 There was not what I would call a single aha 09:28:42

1	moment, but I would say the -- that was an important	09:28:46
2	input seeing that paper, and that the other elements	09:28:52
3	of the patent were things that we had thought of or	09:28:57
4	become aware of earlier than that, but I would say	09:29:02
5	that that would have been the last of the elements.	09:29:05
6	Q. Would you turn, please, to Exhibit 2041.	09:29:20
7	(Exhibit 2041 was marked for identification.)	09:29:20
8	THE WITNESS: So I think Exhibit 2041, just	09:30:03
9	to make sure we're talking about the same thing, is an	09:30:06
10	e-mail that I sent to Carol Tellis with the subject	09:30:08
11	"J. West Board Slides, with one slide revised, Number	09:30:12
12	8 of 14."	09:30:16
13	Does that sound correct?	09:30:17
14	BY MR. HEINRICH:	09:30:21
15	Q. Yes. So in this e-mail, you're attaching	09:30:21
16	your May 8, 2012, board presentation, which is also an	09:30:24
17	exhibit at 2112; correct?	09:30:31
18	A. So these are my board slides for the	09:30:36
19	May 8th -- what was the other one, 2112?	09:30:49
20	Q. Yes.	09:30:55
21	A. I just don't remember all the exhibit numbers	09:30:56
22	off the top of my head. So if you want me to check	09:30:59
23	that, I can look at that. I'm sorry.	09:31:02
24	Yes, it looks like Exhibit 2112 is also a	09:31:44
25	copy of my board of directors slides from the May 8,	09:31:47

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1	2012, meeting.	09:31:52
2	Q. And if we go back to Exhibit 2041 --	09:31:56
3	A. Do I need to, kind of, keep my hand here so	09:32:00
4	that I can flip back and forth between them? Or --	09:32:02
5	are we done with that one for now?	09:32:04
6	Q. Yeah, for now. Yeah, we're done.	09:32:06
7	A. Just so I don't have to flop through all	09:32:08
8	these pages again.	09:32:11
9	So I'm looking at the e-mail.	09:32:20
10	Q. In reference to having revised your deck for	09:32:21
11	the May 2012 board meeting; correct?	09:32:31
12	THE REPORTER: Your deck?	09:32:31
13	MR. HEINRICH: Deck.	09:32:31
14	THE WITNESS: Slide deck.	09:32:34
15	It looks like from the e-mail what was	09:32:35
16	revised was Slide Number 8 of 14.	09:32:38
17	BY MR. HEINRICH:	09:32:43
18	Q. So do you recall how far in advance of	09:32:43
19	May 8th you first drafted this deck?	09:32:46
20	A. No, I don't recall that.	09:32:48
21	Q. You drafted it in advance of May 8th, though;	09:32:51
22	correct?	09:33:02
23	A. Yes. I did not prepare board slides on the	09:33:02
24	morning of the meeting.	09:33:08
25	Q. Yes. Did you have a practice of circulating	09:33:09

1	a preread of slides for the board?	09:33:12
2	A. To the extent that we had slides ready ahead	09:33:14
3	of time, we did circulate them to the board earlier,	09:33:19
4	but I don't recall for this particular meeting.	09:33:24
5	I would say that at this time the company had	09:33:26
6	only been operating for less than one year. So it was	09:33:30
7	quite a small company. So I just don't remember what	09:33:36
8	we had in terms of when we circulated or even whether	09:33:39
9	these were circulated in advance to our board.	09:33:42
10	We certainly, for the board meetings at that	09:33:46
11	time, would have provided a printed board book. So	09:33:48
12	when the board meetings were all in person. So each	09:33:54
13	board member, when they came, would have received a	09:33:57
14	physical book. If we hadn't sent it out ahead of	09:34:00
15	time, they would have received it at the meeting, and	09:34:03
16	they would have had a binder that had presentations in	09:34:05
17	it.	09:34:08
18	Q. Did you have a practice of circulating draft	09:34:08
19	board slides to your team before board meetings?	09:34:14
20	A. I would say it was probably not a consistent	09:34:22
21	practice. The material that we presented to the board	09:34:28
22	was generally material that we had discussed in other	09:34:31
23	forms beforehand.	09:34:35
24	The board slides often were something of a	09:34:36
25	condensation or a summary of other things that might	09:34:40

1 have been described in more detail in scientific or 09:34:44
2 technical meetings. So I didn't expect anyone to be 09:34:49
3 surprised at the meeting. 09:34:53

4 We had our management team attend at least 09:34:54
5 the first part of each board meeting, and often other 09:34:59
6 members of the management team would have their own 09:35:03
7 presentations at the board meetings. 09:35:06

8 Q. And do you recall whether you circulated the 09:35:08
9 draft of your May 8th board presentation to anyone on 09:35:13
10 your management team? 09:35:18

11 A. Well, let's see. Certainly, I had sent 09:35:21
12 slides to Carol Tillis. Carol was our VP of finance 09:35:26
13 and handled other areas as well. I don't recall 09:35:33
14 whether this was circulated to other members of our 09:35:36
15 management team in advance of the board meeting or 09:35:40
16 not. 09:35:43

17 Q. Do you recall if you had any input on these 09:35:43
18 slides from anyone on the management team, including 09:35:49
19 also folks on the R and D and scientific teams? 09:35:51

20 A. Certainly. To the extent that we were 09:35:56
21 presenting scientific or technical matters or plans, 09:35:58
22 those were, generally, discussed extensively with the 09:36:02
23 R and D team and with the management team. So they 09:36:06
24 would have, certainly, been involved in that content. 09:36:10

25 Whether they saw a particular slide or 09:36:15

1 particular graphic that was made to show the idea to 09:36:19
2 the board, not everybody saw every slide ahead of 09:36:25
3 time, and I didn't see every slide of the R and D 09:36:28
4 presentation ahead of time either, but I was fine with 09:36:31
5 that because we shared the main elements of what we 09:36:37
6 were doing. 09:36:40

7 Q. So I realize this was a very long time ago 09:36:41
8 now. 09:36:43

9 A. Mm-hmm. 09:36:43

10 Q. But do you happen to have any specific 09:36:43
11 recollection of having any discussions or getting any 09:36:47
12 input from others on your May -- what became your 09:36:50
13 May 8th, 2012, board presentation in advance of that 09:36:56
14 board meeting? 09:37:00

15 A. I would say that we -- at that time, we had 09:37:01
16 board meetings fairly frequently, almost monthly, and 09:37:06
17 so we had had a board meeting, I believe, in March of 09:37:10
18 that year, in February of that year, in January of 09:37:15
19 that year, and so I certainly had a practice -- to the 09:37:18
20 extent that the slides, if they weren't shared before 09:37:24
21 the board meeting, then they would have been shared 09:37:27
22 after the board meeting. 09:37:29

23 And so if people had seen slides, they would 09:37:31
24 have seen slides from the prior meeting and the 09:37:34
25 meeting before that, and so forth, and there was -- 09:37:37

1	because it wasn't very long from one board meeting to	09:37:40
2	the next, people were certainly familiar with the	09:37:43
3	themes that we were discussing with the board.	09:37:49
4	Q. Just to go back to my question. I don't	09:37:52
5	think you answered.	09:37:56
6	Do you have any specific recollection of	09:37:59
7	discussing your -- any drafts of your May 8th	09:38:04
8	presentation with other Personalis employees,	09:38:11
9	scientists, R and D people in advance of that meeting	09:38:18
10	on May 8th?	09:38:21
11	MR. LUMAN: Asked and answered,	09:38:23
12	mischaracterizes the testimony.	09:38:25
13	THE WITNESS: The content of the slides, the	09:38:27
14	substance of them, certainly was discussed extensively	09:38:30
15	with other members of the scientific and technical	09:38:34
16	staff and management team.	09:38:38
17	I don't recall discussing the specific layout	09:38:41
18	of the slides with them. Generally, I prepared my own	09:38:46
19	slides, often borrowing from material that I had from	09:38:50
20	other meetings, and so I don't know that we discussed	09:38:52
21	the specific slides, but we certainly would have	09:38:56
22	discussed the scientific and technical content of them	09:38:59
23	and the -- and also the business implications of that	09:39:04
24	content.	09:39:07
25	BY MR. HEINRICH:	09:39:07

1	Q. So let's turn to 2112. Since you refer --	09:39:16
2	A. So that's the other one we looked at a minute	09:39:24
3	ago.	09:39:27
4	(Exhibit 2112 was marked for identification.)	09:39:27
5	BY MR. HEINRICH:	09:39:27
6	Q. And since that's the exhibit that you rely on	09:39:28
7	so frequently in your declaration, we'll focus on that	09:39:33
8	exhibit number for the questions on those issues.	09:39:37
9	A. Okay. I have turned to Exhibit 2112.	09:40:07
10	Q. And why don't we turn to Slide 5 of that	09:40:10
11	presentation.	09:40:17
12	A. One moment. Okay. I'm looking at Slide 5.	09:40:23
13	Q. And this is a slide that you refer to	09:40:35
14	frequently in your declaration; correct?	09:40:37
15	A. Yes, that's correct.	09:40:40
16	Q. The title of the slide is "Overview of	09:40:41
17	Personalis Accuracy Program"; correct?	09:40:44
18	A. Yes, that's correct.	09:40:47
19	Q. And you're providing this overview to the	09:40:48
20	board of directors on May 8th, 2012?	09:40:53
21	A. Yes, that's correct.	09:40:57
22	Q. And you were describing to the board a	09:40:58
23	proposed genome sequencing project; correct?	09:41:04
24	A. No. That's not what this is about.	09:41:07
25	Q. This is not about a genome sequencing	09:41:11

1	project?	09:41:16
2	A. Whole genome sequencing was one of the	09:41:17
3	technologies that we described using, but a genome	09:41:21
4	sequencing project would, generally, be a term used to	09:41:25
5	mean a project intending only to sequence the whole	09:41:29
6	genomes of a number of individuals, and that's not	09:41:32
7	what the focus of this slide was.	09:41:34
8	Q. So just to be clear, I didn't say "whole	09:41:36
9	genome." So let's go back. I'm going to make sure --	09:41:39
10	A. Okay.	09:41:39
11	Q. -- that you heard my question correctly.	09:41:43
12	A. Okay.	09:41:45
13	Q. So at this May 8, 2012, meeting with the	09:41:45
14	board of directors --	09:41:51
15	A. Yes.	09:41:52
16	Q. -- you were describing to the Personalis	09:41:52
17	board a genome sequencing project; correct?	09:41:55
18	MR. LUMAN: Mischaracterizes the document and	09:41:59
19	his testimony.	09:42:05
20	THE WITNESS: I was describing a plan we had	09:42:06
21	for using DNA sequencing technologies to derive	09:42:08
22	genetic information from human individuals, and that	09:42:16
23	included DNA sequencing, which in some cases was what	09:42:19
24	we described as "whole genome sequencing."	09:42:26
25	In other cases, you can see it refers to	09:42:28

1	exome sequencing. In other cases, it referred to	09:42:31
2	panels of various kinds that were provided.	09:42:36
3	So in general, it did include DNA sequencing	09:42:38
4	of human DNA, but not all of the sequencing would be	09:42:43
5	described as genome sequencing in the sense that, when	09:42:48
6	people use that term, they usually are implying	09:42:51
7	something that implies the whole genome or a large	09:42:55
8	portion of it, and we were also talking about	09:42:58
9	technologies that could cover only a targeted portion	09:43:00
10	of the genome.	09:43:06
11	BY MR. HEINRICH:	09:43:07
12	Q. So you were describing for the board a	09:43:07
13	sequencing project; correct?	09:43:10
14	A. We were describing our -- what was going to	09:43:12
15	be our product development plan. This was not a new	09:43:17
16	topic for our board. At prior board meetings, we had	09:43:23
17	laid out plans like this as well. And so this was	09:43:26
18	a -- perhaps, the most recent version of what our	09:43:30
19	planning was, and the goal was to develop a platform,	09:43:33
20	which had multiple capabilities, which could lead to	09:43:38
21	multiple products, which it did.	09:43:41
22	Q. But the project, the specific project and the	09:43:44
23	specific program you were presenting to the board at	09:43:51
24	this time in May of 2012 was a sequencing project;	09:43:53
25	correct?	09:43:59

1	MR. LUMAN: Asked and answered.	09:44:00
2	THE WITNESS: I would say that that's not	09:44:01
3	correct. I think it's just some confusion on	09:44:04
4	terminology. If somebody talked to me about a	09:44:06
5	sequencing project, I would usually interpret that to	09:44:08
6	mean a plan to sequence a specific set of samples to	09:44:12
7	derive a certain set of data.	09:44:16
8	And instead, we were here describing a	09:44:18
9	capability, which could be used for sequencing	09:44:22
10	projects, and later in the same board presentation --	09:44:25
11	I'm sorry. You're not paying attention. Do you want	09:44:30
12	me to answer?	09:44:33
13	BY MR. HEINRICH:	09:44:34
14	Q. I am.	09:44:34
15	A. Okay. So later in the same presentation to	09:44:34
16	the board of directors, we did propose a sequencing	09:44:37
17	project with a number of named specific DNA samples	09:44:41
18	and how they would be sequenced, and so there was a	09:44:46
19	proposal to do a -- to conduct a sequencing project	09:44:50
20	that's in the later slides of that presentation, but	09:44:55
21	the Slide Number 5 was not a closed end project to	09:44:58
22	sequence specific samples. It was a plan for a	09:45:06
23	platform capability.	09:45:11
24	Q. Where -- so what slide are you referring to	09:45:13
25	as describing a sequencing project?	09:45:16

1 A. So this begins on Slide Number 9 where we 09:45:18
2 talk about progression of genome datasets. The 09:45:36
3 founder genomes, these included my family's genomes. 09:45:41
4 We already had that data. 09:45:46

5 In the middle, you see "downloading." This 09:45:48
6 was DNA sequencing that had been performed at other 09:45:51
7 genome centers where we were able to download the 09:45:55
8 data. 09:45:58

9 And on the right-hand side of that slide, you 09:45:58
10 see a proposal, which we elaborate on on the 09:46:03
11 subsequent slides for us to contract the sequencing of 09:46:06
12 the genomes of 17 people from the -- what's referred 09:46:10
13 to as the "CEPH1463 family." This was a well known 09:46:15
14 set of samples and also to sequence the individual -- 09:46:21
15 the genome of a well known individual, Craig Venter, 09:46:25
16 as well. 09:46:30

17 And then on Slide 10, it shows the 09:46:31
18 organization of that family of 17 individuals, and 09:46:37
19 there was additional information about this on Slide 09:46:43
20 11 and a proposal for a -- what we would contract was 09:46:47
21 on Slide 12 with a budget for that project, and that 09:46:54
22 budget was approved by the board. 09:47:01

23 But that's -- I'm just clarifying, when you 09:47:03
24 talk about a sequencing project, that's what I would 09:47:08
25 think of as a sequencing project where you have a 09:47:13

1	specific set of samples, and you want to have them	09:47:16
2	sequenced to a certain specification to achieve	09:47:19
3	certain data.	09:47:21
4	Q. So the title of Slide 9 is "Progression in	09:47:22
5	Genome Datasets for Accuracy Studies"; correct?	09:47:30
6	A. Yes, that's correct.	09:47:34
7	Q. So the accuracy studies here, this is part of	09:47:35
8	how you propose to proceed with what you call the	09:47:43
9	Personalis Accuracy Program; correct?	09:47:48
10	A. It was one element of it, yes. It was to	09:47:51
11	provide data to reduce -- I think you would -- maybe	09:47:54
12	the right term is reduction to practice to generate	09:47:58
13	specific data that would help us reduce the invention	09:48:01
14	to practice.	09:48:04
15	Q. And so the datasets for accuracy studies that	09:48:05
16	are referred to in Slide 9, these were datasets that	09:48:19
17	you would use as part of your efforts to develop a --	09:48:23
18	what you thought would be a more accurate way to do	09:48:30
19	sequencing; correct?	09:48:36
20	A. Yes. It was intended in particular to	09:48:38
21	identify and to be able to document the errors that	09:48:42
22	existed in sequencing by studying a family, which we	09:48:48
23	began by studying my family's genomes. You can find	09:48:53
24	elements of the sequence, which aren't biologically	09:48:59
25	possible.	09:49:04

1	So, for example -- or it would be very	09:49:04
2	unlikely to be possible.	09:49:08
3	So simply, generally, the genome of a child	09:49:09
4	is composed of DNA that came from the father and the	09:49:12
5	mother. If you found significant differences, where	09:49:17
6	there were genetic variants in the genome of the child	09:49:20
7	that were not in either parent, a very small number of	09:49:27
8	those could be new mutations, but in general those	09:49:31
9	would be indicative of sequencing errors.	09:49:34
10	And so by looking at more elaborate families,	09:49:36
11	which is why we looked at a three-generation family of	09:49:39
12	17 people, it gave a -- we felt it would give us a	09:49:43
13	detailed dataset to identify errors that were being	09:49:47
14	caused by the sequencing technology.	09:49:52
15	And we saw a business opportunity in being	09:49:54
16	able to develop technologies that would let us improve	09:49:58
17	the accuracy of sequencing, not by changing the	09:50:04
18	sequencing instrument or sequencing reagents, but	09:50:08
19	alternative sample prep and data analysis techniques.	09:50:13
20	But we wanted to be able to have a clear	09:50:18
21	understanding of what the errors were that we were	09:50:22
22	trying to fix.	09:50:24
23	Q. Right. So the first step of your efforts to	09:50:27
24	come up with more accurate sequencing was to study and	09:50:32
25	characterize errors in existing sequencing techniques	09:50:37

1	and technologies; correct?	09:50:44
2	A. As it shows on Slide 9, we had already begun	09:50:45
3	that with my family's genomes, and the publication	09:50:50
4	that you pointed me to earlier in "PLOS Genetics"	09:50:53
5	showed some of the techniques that were used on my	09:50:58
6	family's data and helped to characterize some of the	09:51:00
7	errors in the sequencing of that time.	09:51:04
8	This was -- by this time, we were in 2012.	09:51:06
9	My family's genomes were sequenced starting in late	09:51:10
10	2009, and the technology had been improving.	09:51:14
11	So we wanted to have more up-to-date data on	09:51:17
12	more modern sequencing technologies, and we felt that	09:51:21
13	we could be more thorough by having data from a larger	09:51:26
14	family of 17 people over three generations than we	09:51:31
15	were able to with four people.	09:51:35
16	And lastly, there was a desire to move away	09:51:37
17	from use of the genomes of the CEO of the company and	09:51:40
18	his family because people felt that was a bit awkward,	09:51:47
19	and I was supportive of that. So we moved away from	09:51:51
20	my family's genomes and used sequencing data.	09:51:54
21	By the time of this meeting, we had already	09:51:57
22	began to download genomes that had been sequenced by	09:52:00
23	other people, including in particular the Broad	09:52:04
24	Institute, but also the Korean personal genome	09:52:07
25	project, and we were using those in the same way.	09:52:10

1 So this was a continuation of an effort that 09:52:13
2 had begun in 2010, once we received my family's 09:52:17
3 genomes, and this was progressing to come up with 09:52:21
4 better and better datasets that would allow us to do a 09:52:25
5 better and better job. 09:52:29

6 Q. So at the time of the May 8, 2012, board 09:52:30
7 meeting, you hadn't completed your work in 09:52:34
8 characterizing errors in the sequencing of current 09:52:39
9 technologies circa 2012; right? 09:52:45

10 A. I would say that, as of today in 2023, there 09:52:48
11 are still errors that we have not characterized. It's 09:52:51
12 not a process that you start and completely finish. 09:52:54
13 It's a question of having started it, improving on it, 09:52:57
14 and then continuing to improve on it. 09:53:02

15 So we were -- we had a sufficient 09:53:03
16 characterization from the work we had done in 2011 and 09:53:06
17 published in 2011 that we knew what some of the 09:53:11
18 problems were, which those led to the plans we laid 09:53:17
19 out for our board of directors at the beginning of 09:53:21
20 2012, and those underlined the plans that we described 09:53:25
21 on Slide 5 of the presentation. 09:53:29

22 So these were -- I would describe it as 09:53:31
23 progressively better and better reduction to practice, 09:53:35
24 not invention. 09:53:37

25 Q. So let's go back to Slide 5. Slide 5 has 09:53:40

1	three columns; correct?	09:53:47
2	A. Yes, that's correct.	09:53:48
3	Q. And the first column is to characterize	09:53:49
4	errors; right?	09:53:54
5	A. Yep.	09:53:55
6	Q. And it was important for your program to	09:53:56
7	improve accuracy of sequencing to characterize errors	09:54:01
8	in the sequencing technologies that existed as of	09:54:08
9	2012; right?	09:54:11
10	A. Yes, that's correct. And we had already been	09:54:12
11	working on that, and some of the -- many of the types	09:54:15
12	of errors that we were able to pin down even more	09:54:19
13	precisely as we got better datasets were things we	09:54:23
14	already knew about earlier and had identified, and so	09:54:27
15	that led to the approaches that we outlined on the --	09:54:31
16	on the slide for how we would go about it.	09:54:39
17	Q. And the datasets that are referenced in Slide	09:54:41
18	9 were to be used to help you characterize errors as	09:54:48
19	referenced in Slide 5; right?	09:54:54
20	A. It was to improve the characterization. It	09:54:57
21	isn't that we didn't have any characterization, but it	09:54:59
22	was to make a more comprehensive dataset than the one	09:55:02
23	we had so far, and it did make a better dataset.	09:55:08
24	Q. Now, as of May 8, 2012, you hadn't yet	09:55:12
25	downloaded all of the datasets that are listed in the	09:55:17

1	middle column of Slide 9; correct?	09:55:21
2	MR. LUMAN: Objection; foundation.	09:55:23
3	THE WITNESS: So as of the May 8th board	09:55:27
4	meeting, we had begun to download some of those	09:55:31
5	datasets, but we continued to download the data from	09:55:33
6	the Broad Institute for an extended period of time,	09:55:39
7	and that was partly because the Broad Institute	09:55:40
8	continued to generate additional data. But we had	09:55:45
9	downloaded those genomes, and we were looking at other	09:55:48
10	genomes, as I mentioned, from the Korean personal	09:55:52
11	genome project as well.	09:55:56
12	BY MR. HEINRICH:	09:55:58
13	Q. And that was all, sort of, underway, but in	09:55:59
14	process; correct?	09:56:01
15	A. Yes, and we also --	09:56:02
16	Q. I'm sorry. Did you --	09:56:04
17	MR. LUMAN: Let the witness complete his	09:56:05
18	answer.	09:56:07
19	BY MR. HEINRICH:	09:56:07
20	Q. Can you answer my question? That was	09:56:08
21	underway, but in process; right?	09:56:10
22	A. No. I would say we had analyzed some data,	09:56:11
23	and we had some understanding of the issues. We had	09:56:16
24	also collaboration with the group at Stanford	09:56:20
25	University. They had access to other genomes.	09:56:25

1 So, for example, Mike Snyder, who is the 09:56:28
2 chairman of the genetics department at Stanford and a 09:56:32
3 cofounder of the company, had -- had his sequence -- 09:56:36
4 his genome sequenced multiple times using both the 09:56:39
5 Illumina technology and also the technology of another 09:56:43
6 company named "Complete Genomics" and had compared 09:56:48
7 those, and we had also worked on understanding the 09:56:50
8 errors that came about from that. 09:56:52

9 I, also, had access to other more modern 09:56:56
10 genomes because I had friends at Illumina, and they 09:57:00
11 had sequenced other genomes, and so I received copies 09:57:03
12 of some of those genomes, and we used those as part of 09:57:07
13 our analysis. 09:57:13

14 So the analysis progressed, but we were -- I 09:57:14
15 think we had sufficient information for the conception 09:57:17
16 of the ideas that are presented on Slide 5, and as we 09:57:20
17 sought to reduce that to practice and generate our 09:57:26
18 first product, we generated additional datasets to be 09:57:30
19 more thorough. 09:57:34

20 Q. I'm just right now asking you factual 09:57:36
21 questions. I'm not -- 09:57:39

22 A. Yes, I understand that. I'm trying to 09:57:39
23 understand them. 09:57:41

24 Q. -- asking reduction to practice, which are 09:57:42
25 legal terms. I'm trying to get an idea of factually 09:57:44

1	what was going on at the company at the time.	09:57:47
2	A. Okay. That's fine.	09:57:49
3	Q. On Slide 9, there's also a reference to	09:57:50
4	"custom sequenced datasets"; correct?	09:57:55
5	A. They were custom sequence that -- meaning	09:58:01
6	that these were datasets that would be sequenced for	09:58:05
7	us as we would pay somebody to do sequencing. These	09:58:09
8	would be -- this -- these were not datasets that we	09:58:12
9	would necessarily share with someone else whereas	09:58:14
10	something we downloaded from the Broad Institute was	09:58:17
11	not -- that wasn't Personalis proprietary. It wasn't	09:58:20
12	custom to us. Anybody could have downloaded those	09:58:23
13	genome sets.	09:58:30
14	Q. Sure, sure. So for the datasets that would	09:58:31
15	be sequenced for Personalis specifically, those	09:58:33
16	datasets would also be used as part of your efforts to	09:58:36
17	characterize the errors that were found in current	09:58:40
18	sequencing technologies; correct?	09:58:43
19	MR. LUMAN: Objection; foundation.	09:58:45
20	THE WITNESS: Yes, that's correct.	09:58:46
21	BY MR. HEINRICH:	09:58:47
22	Q. And how many of the custom datasets listed in	09:58:47
23	Slide 9 had already been sequenced for Personalis at	09:58:52
24	this time?	09:58:57
25	A. The -- I refer to -- it's different for --	09:58:57

1 there are two different groups mentioned. One is 09:59:07
2 the -- that was called the "CEPH1463" -- that's the 09:59:10
3 C-E-P-H 1463 -- "family." And most of those 09:59:13
4 individuals had already been sequenced as part of 09:59:21
5 the -- what was called the "Thousand Genomes Project" 09:59:24
6 and others. 09:59:28

7 These were widely used samples. In fact, 09:59:28
8 the -- one person in the middle generation of that 09:59:31
9 group of three generations was the standard sample 09:59:36
10 that was used in the middle, in the downloading here. 09:59:40

11 In addition, I mentioned the Craig Venter 09:59:45
12 genome. Craig Venter was a well known figure in the 09:59:49
13 field at the time, and his genome, actually, had been 09:59:52
14 sequenced by his company, Celera Genomics, and that 09:59:55
15 data was also something we had access to. 10:00:00

16 So the -- we had access to these other 10:00:03
17 people's sequencing of those genomes, and we could use 10:00:06
18 that along with having the genomes sequenced in -- for 10:00:10
19 us specifically. 10:00:16

20 Q. As of May 8th, 2012, you didn't, yet, have 10:00:18
21 access to the custom sequence datasets listed in Slide 10:00:24
22 9; correct? 10:00:37

23 A. We were proposing to have those datasets 10:00:37
24 generated. I would say, though, that the -- a number 10:00:40
25 of the individuals whose genomes were going to be 10:00:43

1	sequenced had already been sequenced by others, and we	10:00:46
2	did have access to some of that data.	10:00:50
3	So to the extent that we wanted to have a	10:00:52
4	brand-new sequencing done for us with specific	10:00:54
5	parameters that we set and for which we had a budget	10:00:57
6	on Slide 12, none of that sequencing had started yet	10:01:00
7	because we didn't have board approval to spend	10:01:06
8	158,000 -- \$157,000 yet.	10:01:13
9	Q. That's where I was getting.	10:01:14
10	A. Yes. And so those new datasets have not,	10:01:16
11	yet, been generated.	10:01:18
12	Q. And you did receive board approval to obtain	10:01:20
13	those datasets; correct?	10:01:23
14	A. Yes, we did.	10:01:24
15	Q. And those datasets were used as part of your	10:01:25
16	efforts to characterize errors in current sequencing	10:01:28
17	technology as part of your accuracy program; right?	10:01:31
18	A. Yes, they were one element of that.	10:01:34
19	Q. Is the -- the product or service that you	10:01:51
20	were envisioning was what you referred to as the	10:01:54
21	accuracy program; right?	10:01:56
22	A. The accuracy program was to develop a set of	10:01:58
23	capabilities, which could lead to a number of	10:02:03
24	products.	10:02:06
25	At an earlier board meeting, we had described	10:02:07

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1 at least two of those possible products that could 10:02:10
2 come from the accuracy program. 10:02:13

3 The accuracy program was in general to 10:02:15
4 understand accuracy challenges, which we viewed as 10:02:17
5 opportunities in nexgen sequencing, and we had 10:02:21
6 discussed two plans for two products. One which we 10:02:26
7 called "Whole Genome Plus" and one which we called 10:02:30
8 "Exome Plus," and those products would be designed to 10:02:34
9 address some of the accuracy problems that we already 10:02:40
10 knew about. 10:02:44

11 Q. And those were two sequencing products that 10:02:44
12 you envisioned; correct? 10:02:47

13 A. Yes. Those would have been services, not 10:02:49
14 when you think of a product. "Product" sometimes is a 10:02:53
15 physical thing that you can buy, and I can ship to 10:02:58
16 you. 10:03:01

17 When we refer to a "product" in that sense, 10:03:01
18 it wasn't, you know, like, a box of something or, 10:03:04
19 like, an instrument. It was a service that we can 10:03:06
20 derive where people could send us those samples. We 10:03:10
21 would sequence them using these methods, and we would 10:03:12
22 return the data to the customer. 10:03:14

23 Q. Sure, but you often referred to them as 10:03:15
24 "products"; right? 10:03:18

25 A. Yes, we did. I'm just clarifying it because 10:03:18

1	sometimes people get -- the terminology can be a	10:03:21
2	little confusing between what's a product and what's a	10:03:23
3	service.	10:03:26
4	And to be honest, the company -- we tended to	10:03:26
5	refer to that as our product. And just clarifying	10:03:28
6	that, if you were being more precise about it, you	10:03:31
7	might refer to that more as a service.	10:03:34
8	Q. Understood, but -- and thank you for the	10:03:36
9	clarification.	10:03:38
10	Since you refer in your exhibits to it as a	10:03:40
11	"product," I'll probably --	10:03:43
12	A. That's fine.	10:03:43
13	Q. -- be referring to it as a product.	10:03:44
14	A. That's fine.	10:03:46
15	MR. LUMAN: If you guys can slow down the	10:03:48
16	questions and answers, that way the record will be	10:03:50
17	more clear.	10:03:52
18	BY MR. HEINRICH:	10:03:56
19	Q. So you considered your future potential	10:03:56
20	competitors to be other sequencing companies; right?	10:04:03
21	A. I think we felt there could be a lot of	10:04:06
22	different future competitors, and they certainly	10:04:11
23	included other people who provided sequencing as a	10:04:15
24	service, and it also would have included companies	10:04:18
25	that would have been described as diagnostic	10:04:22

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1	companies, providing medical diagnostic testing for	10:04:25
2	medical patients.	10:04:29
3	Q. Market developments on Slide 4, you list four	10:04:31
4	companies; right? Illuminous [sic] -- well, I guess	10:04:39
5	five. Illumina, slash, Roche; Complete Genomics;	10:04:43
6	Oxford Nanopore; and Lite Ion Proton (phonetic);	10:04:50
7	right?	10:04:55
8	A. I don't believe we characterized them as	10:04:55
9	competitors. I don't think that we were talking about	10:04:59
10	competitors here.	10:04:59
11	These are -- those four companies are	10:05:01
12	companies that were developing sequencing	10:05:02
13	technologies, and so we were -- this is describing the	10:05:05
14	market for sequencing technologies, which was an	10:05:08
15	important input to us because, if there were new	10:05:12
16	advances in the sequencing technologies, that would	10:05:15
17	impact what we could do about them.	10:05:18
18	So Illumina was a sequencing company. At	10:05:20
19	that time, Roche was trying to execute a hostile	10:05:23
20	takeover. That did not go through.	10:05:29
21	Complete Genomics was another sequencing	10:05:31
22	company. They provided sequencing as a service with	10:05:34
23	their own technology, which was quite different from	10:05:37
24	Illumina's.	10:05:40
25	Oxford Nanopore was, yet, another company	10:05:41

1 based in England. They had another very different 10:05:43
2 technology for DNA sequencing. 10:05:47
3 And Lise Ion Proton (phonetic) was another -- 10:05:50
4 a large company that had a fourth technology for DNA 10:05:53
5 sequencing. 10:05:56
6 So these were -- although in some cases, they 10:05:57
7 would provide sequencing as a service. For example, 10:06:01
8 Illumina did, and we were their customer in some 10:06:05
9 cases. 10:06:08
10 In general these companies were primarily 10:06:09
11 companies making the equipment and reagents that were 10:06:13
12 used for sequencing. These -- these were not 10:06:15
13 primarily diagnostic companies, and these companies' 10:06:16
14 businesses were not primarily sequencing services. 10:06:21
15 Q. The reason -- 10:06:23
16 A. So I'm just getting at -- that's why I'm 10:06:25
17 saying you characterize these as "competitors," and I 10:06:30
18 would say these were not our primary competitors. 10:06:34
19 Q. The reason that you listed these four 10:06:37
20 sequencing companies in your slide to the board titled 10:06:40
21 "Market Developments" is because you were presenting 10:06:44
22 the board with an update on the Personalis accuracy 10:06:50
23 program that was designed to result in products for 10:06:55
24 sequencing such as your Whole Genome Plus and Exome 10:07:01
25 Plus products you contemplated; correct? 10:07:08

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1 A. Yes. So understanding developments in the 10:07:10
2 market for sequencing technologies was important 10:07:13
3 because, if the sequencing technologies that we used 10:07:16
4 or that were available to us changed or improved in 10:07:18
5 some way, it was important for us to know about that. 10:07:21

6 Q. Right. Now, you didn't present the board 10:07:24
7 with an update on market developments and cancer 10:07:28
8 diagnostics, correct, in this presentation? 10:07:33

9 A. Not that I recall, no. 10:07:37

10 Q. And that's because, in part, Personalis's 10:07:41
11 expertise was in sequencing and not cancer biology; 10:07:49
12 correct? 10:07:54

13 A. No. I think we had people who were 10:07:54
14 knowledgeable about cancer. For example, Richard 10:07:58
15 Chen, who is our chief technology officer, was a 10:08:01
16 physician, and some of the patients that he sees are 10:08:05
17 people with forms of cancer or precancer related to 10:08:10
18 melanoma. So I think we knew things from a medical 10:08:14
19 standpoint. 10:08:18

20 Certainly, over my career, I had worked 10:08:19
21 extensively on cancer genomics. And so I think we 10:08:22
22 knew quite a bit about that. 10:08:28

23 And there were presentations that talked 10:08:29
24 about the market for diagnostic testing, and those 10:08:32
25 presentations were made -- I don't remember whether 10:08:36

1	they were at this board meeting or at some of the	10:08:39
2	earlier board meetings.	10:08:41
3	If I recall, Rich Chen gave a presentation	10:08:43
4	earlier in the year than this, which includes some	10:08:47
5	description of the different markets, including	10:08:50
6	research-related markets and clinical diagnostic	10:08:54
7	markets, and it included applications that included	10:08:59
8	Mendelian diseases, what were called "genetically	10:09:02
9	complex diseases," and cancer.	10:09:13
10	Q. It's fair that in this period of time cancer	10:09:16
11	genomics was not the forte of Personalis; correct?	10:09:18
12	A. No, I think that's a mischaracterization of	10:09:22
13	it. I think we had many people with substantial	10:09:24
14	knowledge of cancer genomics.	10:09:27
15	Q. So if you turn to Exhibit 2063.	10:10:01
16	THE REPORTER: -63?	10:10:01
17	MR. HEINRICH: Yes, please.	10:10:01
18	(Exhibit 2063 was marked for identification.)	10:10:01
19	BY MR. HEINRICH:	10:10:01
20	Q. This is an e-mail.	10:10:16
21	MR. LUMAN: Give us a minute to get there.	10:10:18
22	THE WITNESS: 2063. To confirm, this is an	10:10:37
23	e-mail that I sent to Richard Chen, Carol Tillis, and	10:10:42
24	Christian Haudenschild that says, "Draft board slides	10:10:46
25	for your comments."	10:10:49

1	This was on Monday, June 11, 2012.	10:10:50
2	BY MR. HEINRICH:	10:10:53
3	Q. Correct. And one of the issues you	10:10:53
4	explore -- you explored in these slides was potential	10:11:05
5	synergies with some kind of combination with Complete	10:11:14
6	Genomics sequencing company we just mentioned a few	10:11:19
7	minutes ago; right?	10:11:25
8	A. Do you want to point me to where specifically	10:11:26
9	you have in mind?	10:11:29
10	Q. Sure. So you can take a look at some slides	10:11:30
11	starting at Slide 11.	10:11:33
12	A. Okay. I'm looking at Slide 11.	10:12:12
13	Q. Does this refresh your recollection that in	10:12:16
14	this slide deck -- why don't you take a look at Slides	10:12:18
15	11, 12, and 13.	10:12:21
16	A. Okay. I have to understand your question	10:12:56
17	before I can go further.	10:12:58
18	Q. Yeah, I just wanted to point you to the	10:13:00
19	slides.	10:13:05
20	So does this refresh your recollection that	10:13:06
21	one of the things you did in your board deck for the	10:13:08
22	June 2012 board meeting was to throw out some ideas	10:13:11
23	about potential synergies doing some sort of	10:13:16
24	combination with Complete Genomics?	10:13:20
25	A. So that's the -- it shows that we were	10:13:22

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1	looking at different possibilities. It wasn't a	10:13:25
2	proposal that we should do that. But we were	10:13:31
3	considering whether there were ways we could	10:13:34
4	accelerate what we were doing by some kind of a	10:13:36
5	business combination.	10:13:39
6	Q. And let's turn to Slide 13.	10:13:40
7	A. I'm looking at Slide 13.	10:13:51
8	Q. In the second-to-last bullet, in this bullet	10:13:53
9	you're discussing the possibility of combining	10:13:58
10	Personalis's noncancer expertise with Complete's	10:14:03
11	cancer genome experience and deep genome dataset;	10:14:10
12	correct?	10:14:11
13	A. Yes, that's what it says.	10:14:13
14	Q. Okay.	10:14:13
15	MR. HEINRICH: Why don't we take our next	10:14:15
16	five-minute break?	10:14:17
17	THE VIDEOGRAPHER: Okay. We're going off the	10:14:18
18	record. The time is 10:14 a.m.	10:14:20
19	(Recess taken.)	10:21:14
20	THE VIDEOGRAPHER: We're back on the record.	10:21:14
21	The time is 10:22 a.m.	10:22:14
22	BY MR. HEINRICH:	10:22:16
23	Q. Mr. West, did you have any discussions with	10:22:17
24	counsel at the break?	10:22:19
25	A. No, I did not. And I would like to	10:22:20

1 supplement my answer to a couple of the last questions 10:22:22
2 if we can take a second with that. 10:22:26
3 Q. You can do that on redirect. 10:22:28
4 MR. LUMAN: The witness says his answers are 10:22:30
5 not complete -- 10:22:32
6 MR. HEINRICH: Well, that's not what he said. 10:22:33
7 MR. LUMAN: -- and he would like an 10:22:35
8 opportunity to do that. 10:22:38
9 MR. HEINRICH: -- don't coach the witness. 10:22:41
10 THE WITNESS: I can phrase it the way you 10:22:43
11 want it phrased. I think my answer was not complete, 10:22:45
12 and I think that your questions -- the last few 10:22:50
13 questions you asked, whether there was 10:22:52
14 cancer sequencing expertise at Personalis and implies 10:22:59
15 that there was not, I would say that's not correct, 10:23:00
16 and I wanted to illustrate that with a couple of 10:23:01
17 points. 10:23:03
18 I had been involved in DNA sequencing 10:23:04
19 starting in 1982 when the initial project to sequence 10:23:06
20 the human genome was started. It was actually under 10:23:10
21 the U.S. Department of Energy with the U.S. National 10:23:13
22 Laboratories. 10:23:18
23 And in 1986, when they laid out the 10:23:18
24 motivation for sequencing the human genome, they 10:23:21
25 listed seven different diseases. And the Number 1 10:23:24

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1 disease on the list that they focused on as the 10:23:32
2 benefit for sequencing the human genome the first time 10:23:32
3 was cancer, and I was involved in developing the 10:23:35
4 systems for that. 10:23:37

5 When I was at Applied Biosystems, which was 10:23:38
6 between 2001 and 2004, the -- I led the marketing of 10:23:43
7 the DNA sequencing business, and in particular 10:23:49
8 repositioned that business from the sequencing of 10:23:52
9 species, which had not been sequenced before, to the 10:23:57
10 resequencing of genomes that had already been 10:24:02
11 sequenced to identify variants. 10:24:06

12 And in particular, we developed and launched 10:24:08
13 products specifically for the sequencing of cancer, 10:24:10
14 and we introduced those as early as 2002. 10:24:12

15 So by the time that we're talking about here, 10:24:15
16 I had been involved in developing and commercializing 10:24:18
17 products for cancer sequencing for over a decade. 10:24:22

18 BY MR. HEINRICH: 10:24:28

19 Q. So going back to Slide 13 of Exhibit 2063. 10:24:29

20 A. Yes, I'm looking at that. 10:24:49

21 Q. This is from your own slide deck in June of 10:24:50
22 2012; correct? 10:24:57

23 A. Yes, that's correct. 10:24:58

24 Q. And in your slide deck in June 2012 -- 10:24:59

25 A. Yes. 10:25:03

1	Q. -- you were contemplating potential synergies	10:25:03
2	of a combination with Complete Genomics; correct?	10:25:09
3	A. Yes, that's correct.	10:25:13
4	Q. And you said in your slide deck:	10:25:14
5	"Combining Personalis noncancer	10:25:16
6	expertise with Complete's cancer genome	10:25:21
7	experience and deep genome dataset could	10:25:24
8	be a potential synergy"; correct?	10:25:27
9	A. Yes, that's correct. But that does not imply	10:25:30
10	that Personalis --	10:25:33
11	Q. That --	10:25:33
12	MR. LUMAN: You can't cut the witness off.	10:25:35
13	MR. HEINRICH: There's no pending question.	10:25:37
14	MR. LUMAN: Let him complete his answer.	10:25:39
15	THE WITNESS: At the beginning of this	10:25:41
16	session, we said that we would not talk over each	10:25:43
17	other. So if you would not talk over me while I'm	10:25:46
18	answering, I'd appreciate that.	10:25:50
19	If I can finish my answer, I'd like to do	10:25:50
20	that.	10:25:53
21	MR. LUMAN: Please.	10:25:53
22	THE WITNESS: So the -- at the time we were	10:25:54
23	considering combining with Complete Genomics, we, in	10:25:56
24	fact, did decide not to do that.	10:26:00
25	But Personalis had multiple staff that had	10:26:02

1	expertise in cancer sequencing. That doesn't mean	10:26:05
2	that it wouldn't be helpful to have even more.	10:26:08
3	Personalis had certain datasets, but it would	10:26:11
4	be helpful to have other datasets, and Personalis also	10:26:15
5	had expertise in other areas of cancer -- in other	10:26:19
6	areas of genomics, including areas outside of cancer	10:26:21
7	that we felt Complete Genomics did not have,	10:26:25
8	including, for example, in cardiology.	10:26:30
9	And so we felt that combining our areas of	10:26:31
10	expertise with theirs, it doesn't mean we had no	10:26:33
11	expertise in cancer, and it doesn't mean that they had	10:26:37
12	all the expertise in that, and it also doesn't mean	10:26:40
13	that they didn't have any expertise in areas outside	10:26:43
14	of cancer, but we did feel that there was the	10:26:48
15	possibility of adding both staff and datasets and	10:26:51
16	technology.	10:26:53
17	So I just want to be on the record that	10:26:54
18	this -- my slides -- these are my slides. So I'll	10:26:56
19	speak to them -- from the June 2012 board meeting were	10:27:00
20	an indication of a way to add to our capabilities, not	10:27:06
21	an indication of a lack of capabilities.	10:27:11
22	MR. HEINRICH: Move to strike as	10:27:15
23	nonresponsive to my question.	10:27:17
24	MR. LUMAN: That was very responsive. I	10:27:18
25	disagree with that.	10:27:21

1	MR. HEINRICH: I don't care.	10:27:23
2	BY MR. HEINRICH:	10:27:25
3	Q. You would never -- you -- you would never	10:27:25
4	have said that cancer genomics is not the forte of	10:27:27
5	Personalis's founders; right?	10:27:33
6	A. I do not agree with your statement.	10:27:35
7	Q. Let's turn back to Slide 5 of Exhibit 2112.	10:27:42
8	A. I'm looking at Slide 5 of Exhibit 2112.	10:28:52
9	Q. Okay. So let's just talk a little bit about	10:28:57
10	some terms you use here first.	10:29:07
11	So in the third column, the middle, there's a	10:29:10
12	reference to -- the third column is titled, "Lab	10:29:16
13	Content Solutions"; correct?	10:29:20
14	A. Yes, it is.	10:29:22
15	Q. And there's a reference in the middle of that	10:29:23
16	column to "pull out"; correct?	10:29:26
17	A. Yes, there is.	10:29:33
18	Q. What is a "pull out"?	10:29:34
19	A. Pull out -- a "pull out" refers to a method	10:29:59
20	of using hybrid capture to bind to a particular part	10:30:05
21	of the genome and to pull that out of the solution.	10:30:15
22	So if you have DNA molecules, which are	10:30:19
23	floating in solution mixed in with other molecules, if	10:30:23
24	you want to select just molecules from certain parts	10:30:27
25	of the genome, you can hybridize them with capture	10:30:30

1	probes, which have a chemical modification on them,	10:30:38
2	which allows them to be pulled.	10:30:42
3	Most commonly that's done by adding a	10:30:46
4	chemical element onto the capture probe with what is	10:30:49
5	called "biotin." And biotin binds to another chemical	10:30:54
6	called "streptavidin." And streptavidin, then, is	10:30:59
7	often on magnetic beads.	10:31:03
8	So if you hybridize those probes to the DNA,	10:31:05
9	which is in solution, and then apply a magnetic field	10:31:08
10	externally, you can pull those molecules and literally	10:31:12
11	pull them out of the solution so that you can	10:31:16
12	selectively capture those portions of the genome.	10:31:18
13	Q. Are you aware of any pullout probes that	10:31:22
14	don't employ any chemical modifications?	10:31:26
15	MR. LUMAN: Incomplete hypothetical.	10:31:33
16	THE WITNESS: I would say that the pullout	10:31:34
17	probes that we were considering using at the time and	10:31:37
18	which we, in fact, did use were from Agilent. They	10:31:40
19	were the SureSelect technology.	10:31:47
20	They had developed that technology actually	10:31:54
21	with my group's help when I was at Celexa, and I	10:31:54
22	believe that technology uses the biotin and	10:31:55
23	streptavidin magnetic bead approach.	10:32:01
24	BY MR. HEINRICH:	10:32:03
25	Q. So the biotin is part of the pullout probe;	10:32:03

1	correct?	10:32:08
2	A. It is part of the capture probe, and it makes	10:32:09
3	it essentially, like, a sticky piece that would stick	10:32:14
4	selectively to streptavidin, and streptavidin would be	10:32:18
5	used to coat the magnetic beads.	10:32:22
6	Q. Why -- so I asked you if biotin is part of	10:32:25
7	the pullout probe, and then you said it was part of	10:32:30
8	the "capture" probe. I'm wondering why you changed my	10:32:33
9	question that way.	10:32:36
10	A. Because the -- sorry. I wasn't trying to	10:32:37
11	intentionally change your question.	10:32:40
12	But I would say that we considered hybrid	10:32:41
13	capture to be done with a pullout probe because we	10:32:44
14	were describing the technology that we planned to use,	10:32:52
15	which was the Agilent SureSelect technology, and it	10:32:55
16	used capture probes, which were also referred to as	10:33:00
17	pullout probes because they use the -- the pull was	10:33:03
18	the magnetic field pulling on the beads.	10:33:06
19	Q. The pull was the combination of the biotin on	10:33:09
20	the probe and the bead; correct?	10:33:12
21	A. And the magnetic bead and the magnetic field,	10:33:14
22	yes.	10:33:19
23	Q. Now, an "array," does that refer to a	10:33:19
24	different type of capture probe?	10:33:23
25	A. I think you would have to tell me. The word	10:33:26

1	"array" is used in many different contexts.	10:33:30
2	Q. Well, well -- okay. Let's go back to Slide	10:33:34
3	5.	10:33:37
4	A. Okay.	10:33:37
5	Q. Right above "pull out," there's a reference	10:33:37
6	to "array"; correct?	10:33:40
7	A. Yes, there is.	10:33:41
8	Q. As you use it in Slide 5 of Exhibit 2112,	10:33:44
9	does "array" refer to a different type of capture	10:33:51
10	probe?	10:33:54
11	A. No. Where we refer to an "array" there, we	10:33:55
12	were referring to a technology that was used for	10:33:59
13	genotyping. These were made both by Illumina and	10:34:04
14	Affymetrix, for example.	10:34:10
15	And it specifically says here in parenthesis,	10:34:13
16	genotypes and SVs, which means "structural variants."	10:34:16
17	So these were variants at specific genetic	10:34:21
18	loci that would be targeted in the genotyping process,	10:34:24
19	and so there were genotyping arrays that were used,	10:34:27
20	and the data from those arrays could be used to	10:34:31
21	identify whether a particular genetic mutation existed	10:34:38
22	in that sample or not.	10:34:42
23	And the fluorescence data from those arrays	10:34:44
24	could also be used to identify certain structural	10:34:46
25	variants. So it's different from the pull out that we	10:34:51

1	were talking about in the line below that, which was	10:34:54
2	really intended more for a sequencing process.	10:34:56
3	Arrays are not -- do not use nexgen	10:34:59
4	sequencing. The arrays we were talking about were	10:35:02
5	ones where nexgen sequencing would not be involved.	10:35:06
6	Q. An array includes a set of capture probes on	10:35:18
7	a solid support; fair?	10:35:22
8	MR. LUMAN: Incomplete hypothetical.	10:35:25
9	THE WITNESS: The arrays that were used for	10:35:27
10	genotyping were not for the purposes of capturing	10:35:31
11	molecules for sequencing. They were -- we were --	10:35:35
12	when we were talking about pull out, the word "pull	10:35:38
13	out" implies that you're pulling the molecules out of	10:35:41
14	solution, which means that the molecules are in	10:35:45
15	solution, and that you would pull them out of the	10:35:47
16	solution by that.	10:35:51
17	Typically, when you talk about a genotyping	10:35:52
18	array, you are not trying to pull molecules out for	10:35:54
19	then subsequently sequencing them. You're --	10:35:59
20	actually, the molecules would stay stuck to the array,	10:36:00
21	and the fluorescence on them would be analyzed by	10:36:03
22	imaging them on the surface of the array itself, not	10:36:06
23	by sequencing them.	10:36:10
24	BY MR. HEINRICH:	10:36:12
25	Q. I'm not saying that arrays use what you refer	10:36:12

1	to as pullout probes. I'm asking you if you'd agree	10:36:15
2	that arrays use capture probes on a solid support?	10:36:20
3	MR. LUMAN: Incomplete hypothetical.	10:36:26
4	THE WITNESS: I think that it's a -- not a	10:36:27
5	helpful description of the technology because it's not	10:36:31
6	what we were talking about in this slide.	10:36:35
7	Some of these terms are used by different	10:36:38
8	people in the art in different context to mean	10:36:40
9	different things, but the -- when we referred to	10:36:44
10	"arrays" here, it wasn't just another method of doing	10:36:49
11	pull out. It was a different technology that was a	10:36:53
12	nonsequencing technology whereas, when we referred to	10:36:56
13	"pull out," that was the -- what we were really	10:36:59
14	talking about was the Agilent SureSelect capture	10:37:03
15	system, and that's what we designed in, and we had	10:37:07
16	discussed with our board as early as July of 2011.	10:37:10
17	BY MR. HEINRICH:	10:37:16
18	Q. Okay. Let's put aside -- well, first of all,	10:37:16
19	whether or not the purpose was for subsequent	10:37:21
20	sequencing steps, you are aware that arrays included	10:37:27
21	probes that were used to capture DNA molecules; right?	10:37:35
22	MR. LUMAN: Lacks foundation, incomplete	10:37:42
23	hypothetical.	10:37:45
24	THE WITNESS: I don't think that that's what	10:37:45
25	we were talking about when we referred to "pull out"	10:37:47

1 here, and so you can propose many different 10:37:50
2 circumstances that have nothing to do with what we 10:37:54
3 were doing. 10:37:57

4 What I can say is that the -- there had 10:37:58
5 been -- earlier in the development of these 10:38:01
6 technologies, there had been companies that used 10:38:05
7 surface arrays as a method of capturing molecules, 10:38:11
8 which were, then, released for sequencing, and that 10:38:15
9 didn't work very well. 10:38:18

10 It worked. People did publish things, but it 10:38:20
11 was not nearly as sufficient as the in solution 10:38:23
12 methods. And so what we were talking about with our 10:38:28
13 board of directors here was that the arrays would be 10:38:30
14 used, not for sequencing, but for genotyping and 10:38:32
15 structural variant determination, and that we would 10:38:35
16 use in solution hybrid capture, specifically using the 10:38:38
17 Agilent SureSelect system for -- to provide as part of 10:38:42
18 the sample prep for the DNA sequencing that we were 10:38:47
19 going to use. 10:38:51

20 BY MR. HEINRICH: 10:38:59

21 Q. I guess I wonder if we're talking past each 10:38:59
22 other. 10:39:04

23 You're familiar with the term "capture 10:39:05
24 probe"; correct? 10:39:07

25 A. Yes, I am. 10:39:08

1 Q. Now, when you -- at the time, when you were 10:39:09
2 developing this work, you were not using the term 10:39:14
3 "capture probe" to be synonymous with "pullout 10:39:20
4 probes"; correct? 10:39:25

5 A. What we planned to implement in our system 10:39:26
6 was to use pullout probes using the Agilent SureSelect 10:39:33
7 system. That was the type of capture probe we planned 10:39:39
8 to use, and we had described that to our board, and we 10:39:43
9 had discussed that in internal methods. 10:39:44

10 We had experience. One of our cofounders, 10:39:49
11 Euan Ashley, had developed an Agilent SureSelect panel 10:39:53
12 and talked about it in our board meeting in July 10:40:01
13 of 2011, for example. 10:40:04

14 I was quite familiar with both of the 10:40:04
15 technologies we were talking about because I had 10:40:06
16 worked -- when I was at Celexa as a CEO, we worked 10:40:09
17 closely with the people at Agilent and the Broad 10:40:14
18 Institute, who developed what became the SureSelect 10:40:18
19 technology. We probably did some of the first 10:40:20
20 sequencing using that technology. 10:40:23

21 But I was also familiar with arrays where DNA 10:40:25
22 is spotted or synthesized on a surface. When I ran 10:40:28
23 the DNA business at Applied Biosystems in years 2001 10:40:34
24 to 2004, we developed and commercialized products that 10:40:40
25 were DNA arrays. So I'm familiar with both 10:40:45

1	technologies and had been involved in commercializing	10:40:48
2	them.	10:40:51
3	And so when we were using the term, it	10:40:51
4	wasn't -- we weren't trying to be Webster's Dictionary	10:40:53
5	defining these terms. We were trying to explain to	10:40:57
6	the board what we were trying to do in terms of a	10:41:00
7	product development.	10:41:03
8	And so even though these terms do get used	10:41:04
9	for different things, that isn't what we were talking	10:41:06
10	about at that board meeting. We were talking about	10:41:09
11	what our product development was going to be.	10:41:11
12	Q. So you were not contemplating using	10:41:14
13	array-based capture probes with your solution that	10:41:18
14	you're referring to here in Slide 5; correct?	10:41:24
15	A. We were proposing to do hybrid capture using	10:41:27
16	the Agilent SureSelect system in which the capture	10:41:32
17	probes end up being captured by streptavidin coated	10:41:39
18	magnetic beads, and that that would be -- that's what	10:41:45
19	we would use -- excuse me -- to select portions of the	10:41:46
20	genome that we were interested in.	10:41:49
21	We were aware of the possibility of using	10:41:52
22	hybridization to arrays, and we were aware of the	10:41:57
23	technical problems with that. And so we were not	10:42:03
24	proposing to use arrays for that purpose.	10:42:06
25	The arrays do have performance. They are	10:42:09

1 still used today for genotyping and structural variant 10:42:14
2 analysis. And so we understood that they could be 10:42:19
3 useful for that, and that's what we were saying here 10:42:21
4 on the slide. 10:42:24

5 But in terms of our use of capture probes, 10:42:25
6 which is what's described by the word "pull out" here, 10:42:28
7 we were specifically referring to the Agilent 10:42:31
8 SureSelect system. 10:42:34

9 Q. So you weren't contemplating using arrays to 10:42:35
10 capture DNA for sequencing? 10:42:41

11 A. That is not what our product plan was, no. 10:42:43
12 We had a better method, which was using the Agilent 10:42:48
13 SureSelect capture probe technology. 10:42:51

14 Q. Did you ever make any effort to try to use an 10:42:56
15 array to capture DNA for a subsequent sequencing step? 10:42:59

16 A. There were groups that had done that, and we 10:43:04
17 were certainly familiar with the literature. I don't 10:43:08
18 remember whether anyone in our team previously had 10:43:10
19 experience with that. We had people on our team that 10:43:14
20 had pretty broad experience, and so I don't know 10:43:17
21 whether other members of our team were involved in 10:43:21
22 that. 10:43:24

23 But I do know that we were -- by that time, 10:43:28
24 we were confident with the approach we wanted to use 10:43:35
25 was to use the Agilent SureSelect system. 10:43:37

1	Q. I'm not asking about the prior experience of	10:43:40
2	anyone on your team.	10:43:42
3	A. Well, you asked what we contemplated, and if	10:43:42
4	we didn't have the experience to do it, we might not	10:43:46
5	have contemplated that. And I think the experience	10:43:49
6	that those people had helped us to make selections so	10:43:54
7	that we could move more directly to a product.	10:43:59
8	Q. Do you recall any efforts at Personalis to	10:44:03
9	use an array to capture DNA that was, then, sequenced?	10:44:07
10	A. The only arrays that were involved in the	10:44:13
11	capture process were that the DNA or the RNA probes	10:44:15
12	that are used in the Agilent SureSelect system come	10:44:22
13	from DNA which is originally synthesized on an array	10:44:25
14	and then cleaved off of the array, and then it's in	10:44:31
15	solution, and then you used it in solution.	10:44:33
16	So we were not -- we -- we're not planning to	10:44:40
17	make a product based on hybridizing DNA onto an array	10:44:41
18	and then alluding it off the array.	10:44:49
19	We were obviously aware that that was a	10:44:52
20	possible approach, but when DNA is close to a surface,	10:44:54
21	there can be problems if the DNA folds and then	10:44:58
22	doesn't behave properly. And so the -- it was, I	10:45:01
23	think, reasonably well established by that point that	10:45:04
24	the -- you could achieve better performance by doing	10:45:08
25	hybrid capture in solution.	10:45:12

1 And in particular, the three main companies 10:45:14
2 that offered hybrid capture technologies commercially 10:45:18
3 at that point all offered them on the basis of capture 10:45:25
4 in solution using biotin-labeled capture probes 10:45:29
5 captured by streptavidin coated magnetic beads. 10:45:35

6 That would have included Agilent. It would 10:45:40
7 have included Illumina's hybrid capture technology, 10:45:42
8 and it would have included the NimbleGen hybrid 10:45:46
9 capture technology. 10:45:49

10 Q. And those were all hybrid capture 10:45:50
11 technologies that were on the market as of 2012; 10:45:53
12 correct? 10:45:57

13 A. Certainly the Agilent technology had been on 10:45:57
14 the market since at least 2011, and I think maybe a 10:46:01
15 year or two before that. 10:46:05

16 Illumina had developed an exome that used 10:46:06
17 that technology at least by late in 2012. I don't 10:46:12
18 remember when they introduced that. 10:46:16

19 And I don't remember the dates on the 10:46:18
20 NimbleGen technology. We didn't use them. But the -- 10:46:21
21 certainly the Agilent SureSelect technology had been 10:46:26
22 on the market before 2011. 10:46:29

23 Q. Well, if you turn -- we're going to come back 10:46:37
24 to Slide 5, but since you raised this, if you turn 10:46:44
25 back to Slide 4, in one of the market developments, 10:46:47

1	you note that Illumina had already released its cancer	10:46:52
2	gene pullout panel; correct?	10:46:57
3	A. So that would have been using their in	10:46:59
4	solution hybrid capture technology.	10:47:03
5	Q. And the purpose of the Illumina cancer gene	10:47:06
6	pullout panel was to use these biotinylated probes to	10:47:14
7	pull out DNA for sequencing; correct?	10:47:21
8	MR. LUMAN: Calls for speculation.	10:47:23
9	THE WITNESS: Yes, I believe that is correct.	10:47:25
10	I don't know whether -- I don't remember whether they	10:47:28
11	had the ability for a customer to design their own	10:47:31
12	probes at that time, but Illumina had this cancer gene	10:47:35
13	pullout panel released at that point.	10:47:40
14	BY MR. HEINRICH:	10:47:45
15	Q. Did you ever try to use PCR primers to	10:47:45
16	capture DNA for sequencing?	10:47:54
17	A. So in my career, yes, I had certainly done	10:47:56
18	that, and when I worked at Applied Biosystems, we	10:48:00
19	commercialized thousands of PCR primers specifically	10:48:07
20	for that purpose using the old Sanger sequencing.	10:48:11
21	PCR primer methods are mostly used if you	10:48:13
22	have only one or a small number of genomic targets.	10:48:17
23	The more targets you try to combine in a single	10:48:22
24	reaction the more difficulties there can be of those	10:48:25
25	reactions interfering with each other.	10:48:29

1 So I would say it was quite well known at the 10:48:32
2 time that, if you wanted to target a large number of 10:48:34
3 locations, that hybrid capture was a better process 10:48:39
4 for that because you could easily have thousands of 10:48:42
5 probes, if you wanted to, whereas with multiplex PCR, 10:48:45
6 often it was difficult to go beyond relatively small 10:48:50
7 numbers. 10:48:55

8 And in addition, the PCR primers would need 10:48:56
9 to be synthesized, not -- and they were not 10:49:03
10 synthesized on an array. They had to be synthesized 10:49:08
11 individually. 10:49:12

12 And so the cost, if you wanted to have a lot 10:49:12
13 of PCR primers, would have been quite high because you 10:49:14
14 have the cost of synthesizing each one separately. 10:49:19

15 And for PCR, you need two primers. The 10:49:23
16 primers are also chemically different from hybrid 10:49:26
17 capture DNA. So there's quite a few differences. 10:49:28

18 We felt that there were places where you 10:49:32
19 could use PCR in validation. So, for example, if you 10:49:34
20 use next generation sequencing of a lot of content, 10:49:40
21 and you identified some -- a genetic variant, and you 10:49:46
22 wanted to, then, Sanger sequence it, you might make a 10:49:50
23 PCR reaction just for that one location, amplify that 10:49:54
24 up, and then sequence it on a Sanger sequencer. 10:49:59

25 And Personalis did buy an Applied Biosystems 10:50:02

1 Sanger sequencer for that type of validation, and we 10:50:05
2 did conduct that type of validation on samples for a 10:50:09
3 period of time. 10:50:12

4 Q. Let's say that you were only interested in a 10:50:13
5 small handful of genomic loci. Let's say two. As of 10:50:20
6 2012, it was known that PCR would be perfectly 10:50:28
7 adequate for capturing those two loci for subsequent 10:50:36
8 sequencing; correct? 10:50:36

9 THE REPORTER: Loci? 10:50:36

10 MR. LUMAN: Incomplete hypothetical. 10:50:49

11 MR. HEINRICH: Loci, l-o-c- -- c-i. 10:50:45

12 THE WITNESS: So I would say that the PCR 10:50:51
13 could be used for certain loci. There're also other 10:50:53
14 areas that -- where PCR does not work well. So the 10:50:57
15 answer is, no, that would not be true for all loci. 10:51:00

16 There are places where, if PCR did work, you 10:51:03
17 could conduct two reactions. You might conduct them 10:51:08
18 separately so they didn't interfere with each other. 10:51:13

19 But if you wanted to conduct two PCR 10:51:15
20 reactions for two different genomic loci, certainly 10:51:19
21 you could do that. 10:51:23

22 BY MR. HEINRICH: 10:51:39

23 Q. So continuing on Slide 5, underneath the 10:51:40
24 reference to "array" and "pull out," there's a 10:51:47
25 heading, "Custom Sample Preps," and under that, 10:51:50

1	there's a reference to "Problematic Motifs"; correct?	10:51:55
2	A. Yes.	10:52:08
3	Q. Is one example of a problematic -- so when	10:52:08
4	you say, "problematic," you mean problematic for	10:52:08
5	sequencing; correct?	10:52:12
6	A. They could be problematic in a variety of	10:52:13
7	ways, but certainly we were interested in regions that	10:52:17
8	were difficult to sequence.	10:52:20
9	Q. And one problematic region for sequencing	10:52:24
10	were repeats; correct?	10:52:28
11	A. Not all repeats are problematic for	10:52:34
12	sequencing. Certain repeats with certain structure	10:52:38
13	can be difficult for sequencing, but I wouldn't	10:52:41
14	generalize it to say that all repeats are problematic	10:52:43
15	for sequencing, and I'm referring specifically to the	10:52:47
16	sequencing technology of that time.	10:52:51
17	Q. Okay. Thank you for that clarification. Let	10:52:53
18	me just re-ask the question with your clarification in	10:52:55
19	mind.	10:52:58
20	For circa 2012, certain repeats were an	10:52:58
21	example of motifs that were problematic for sequencing	10:53:06
22	at the time; is that fair?	10:53:11
23	A. Yes, that's true.	10:53:13
24	Q. And so -- well, you know what, let's -- I	10:53:15
25	want to go back to the first column here.	10:53:23

1 So we talked about the first column, and the 10:53:25
2 step of characterizing errors in current sequencing 10:53:29
3 technology that you were studying. 10:53:35

4 At the bottom of Column 1, you identify 10:53:37
5 certain solutions that you would want to prioritize 10:53:43
6 for addressing those errors and other accuracy 10:53:48
7 problems in sequencing at the time; correct? 10:53:52

8 A. Yes, that's right. 10:53:55

9 Q. And under "Prioritize Solutions," the first 10:53:56
10 you list is "Bioinformatic Approaches"; correct? 10:54:03

11 A. Yes, that's what's there. 10:54:07

12 Q. So one solution to provide more accurate 10:54:08
13 sequencing would involve bioinformatics; correct? 10:54:16

14 A. Yes. 10:54:21

15 Q. And you list some of those bioinformatic 10:54:22
16 solutions that you were contemplating at the time in 10:54:31
17 the second column of your slide; right? 10:54:34

18 A. Yes, that's correct. 10:54:36

19 Q. And the next two solutions for the accuracy 10:54:37
20 problem in sequencing that you were trying to address 10:54:43
21 that you list here are laboratory approaches and 10:54:46
22 content approaches; correct? 10:54:49

23 A. Yes. 10:54:55

24 Q. And you list the laboratory and contact 10:54:56
25 solution that you were contemplating at the time for 10:54:59

1	addressing problems in sequencing accuracy in the	10:55:04
2	third column of your slide; correct?	10:55:07
3	A. Yes, although some of them are also	10:55:10
4	referenced in the second column.	10:55:15
5	Q. So the second column is not limited to	10:55:26
6	Bioinformatics Solutions?	10:55:30
7	A. The Bioinformatics Solutions would often	10:55:32
8	leverage specific content to implement those	10:55:37
9	bioinformatic approaches. So you could list them in	10:55:42
10	some cases in both places.	10:55:45
11	So as an example, on the right-hand column at	10:55:47
12	the bottom under "Content," it refers to gold standard	10:55:50
13	genomes. So these would have been genomes one could	10:55:54
14	refer to as known standard of a certain quality.	10:55:58
15	But in the second column, near the bottom, it	10:56:02
16	refers to "advances in reference." So this refers to	10:56:06
17	the reference sequence, and we knew there were	10:56:10
18	problems with the human reference sequence. So that's	10:56:14
19	a form of content as well.	10:56:17
20	And we had developed different reference	10:56:19
21	sequences for people who had different ethnic	10:56:22
22	background. So, for example, one for people whose	10:56:28
23	ethnic background was European, a different one for	10:56:30
24	people whose ethnic background was Asian, and the	10:56:33
25	third one for people whose ethnic background was	10:56:39

1	African.	10:56:40
2	And we found that by trying to align sequence	10:56:42
3	reads to an ethnically appropriate reference sequence,	10:56:45
4	we could -- we could solve some of the accuracy	10:56:52
5	problems. So that would require both an algorithm to	10:56:57
6	use that and the content, which was the specific	10:57:00
7	reference sequence.	10:57:02
8	Q. And you believe that that would result in	10:57:04
9	more accurate sequencing data?	10:57:08
10	A. Yes, and we had published on that approach in	10:57:10
11	the publication you pointed me to earlier this	10:57:14
12	morning, the September 15th article from 2011 in "PLOS	10:57:16
13	Genetics." It specifically described the ethnically	10:57:22
14	specific reference sequences.	10:57:29
15	Q. So we had our discussion about how you were	10:57:54
16	using the Agilent SureSelect pullout probes. How you	10:57:57
17	contemplated using them; right?	10:58:05
18	A. Yes, we had planned to use them.	10:58:07
19	Q. And that's an example of a laboratory-based	10:58:09
20	solution to the accuracy problem in sequencing; right?	10:58:15
21	A. They could be a component of that.	10:58:21
22	Q. And as you're listing here, the pullout	10:58:24
23	probes would be used as part of the overall work flow	10:58:34
24	that you were contemplating to make either whole	10:58:41
25	genome or whole exome sequencing more accurate; right?	10:58:44

1 A. Yes. It would be a component of the 10:58:49
2 solution. When we mentioned two possible products, we 10:58:53
3 had mentioned whole genome plus and exome plus, and in 10:58:57
4 both those cases, we would use a standard whole genome 10:59:03
5 or standard exome, and we would supplement those with 10:59:06
6 additional data. 10:59:12

7 And one of the types of additional data that 10:59:13
8 we planned was to use hybrid capture probes 10:59:15
9 implemented with the Agilent SureSelect technology to 10:59:18
10 capture portions of the genome or other sequences that 10:59:22
11 were not well-represented in the original data. 10:59:25

12 And as a result, we could fill in the gaps 10:59:28
13 and have -- provide our customers with more thorough 10:59:31
14 coverage of the genetic characterization of their 10:59:36
15 samples than they would get from just using a standard 10:59:39
16 whole genome or standard exome. 10:59:41

17 Q. So we talked about certain repeats that at 10:59:46
18 the time were problematic for sequencing; correct? 10:59:49

19 A. Yes. We talked about that earlier. 10:59:51

20 Q. And so one way you could use the Agilent 10:59:53
21 SureSelect probes would be to target those particular 10:59:56
22 problematic repeats, pull them out, and then sequence 11:00:01
23 that targeted region to supplement the rest of your 11:00:09
24 sequencing data; right? 11:00:13

25 A. Yes. So, for example, the repeats involved 11:00:15

1	in Huntington's disease are difficult to sequence, or	11:00:21
2	it had been difficult to sequence.	11:00:25
3	And when I received my family's genomes in	11:00:28
4	2010, I looked specifically for that because I was	11:00:33
5	already 46 years old. So many of the possible	11:00:35
6	diseases that you can find by looking at your genome	11:00:38
7	are diseases that happen when you're two years old or	11:00:43
8	younger. So most of those wouldn't be directly	11:00:45
9	relevant to any members of our family.	11:00:47
10	But Huntington's is a disease which can be	11:00:51
11	late onset, and so being able to -- and it was -- this	11:00:53
12	was a disease that part of our interest was to see if	11:00:55
13	we could see things in our genome that might give us a	11:00:59
14	future view. Is this something we need to worry about	11:01:03
15	for the future?	11:01:07
16	And when I examined my genome in -- I believe	11:01:08
17	it was April 2010 at the Huntington's locus, there	11:01:10
18	were no sequencing reads there.	11:01:16
19	And so this was an example that we knew about	11:01:20
20	where there's a known repeat structure. It's called a	11:01:22
21	"VNTR," and the -- we knew about Huntington's, and I	11:01:26
22	knew about the fragile X repeats because my group,	11:01:33
23	when I worked at Applied Biosystems between 2001 and	11:01:37
24	2004, already had dedicated products aimed at	11:01:41
25	characterizing those genetically on the sequencers	11:01:44

1	that we had at that time.	11:01:51
2	Q. Now, in Slide 5, you don't actually list	11:01:52
3	examples of regions that you would pull out; correct?	11:02:00
4	A. We had described some of those regions in	11:02:05
5	earlier presentations to the board and in earlier,	11:02:14
6	more detailed technical documents internally.	11:02:16
7	Q. I'm just talking about Slide 5. In this	11:02:18
8	slide you don't describe examples of specific regions	11:02:21
9	to pull out; right?	11:02:25
10	A. Well, we said that these might be custom	11:02:27
11	regions for each individual person, and certain	11:02:35
12	regions would be of interest if they were mutated.	11:02:40
13	And so in particular, we were interested in	11:02:43
14	using custom pull out -- this is why it was called	11:02:46
15	"custom" -- to pull out regions of the genome that had	11:02:50
16	genetic variants specific to that person.	11:02:55
17	So, for example, you might conduct whole	11:02:58
18	genome sequencing on the individual to start with,	11:03:02
19	perhaps, on their cancer or their tumor, identify	11:03:06
20	genetic variants in that tumor, and then you might	11:03:09
21	design capture probes specifically to target the	11:03:14
22	genetic variants of that person's tumor.	11:03:17
23	Q. Where is that stated in your slide here?	11:03:20
24	A. That's what we were talking about when we	11:03:23
25	talked about -- you can see that there are two	11:03:24

1 references in the right-hand column. One talks about 11:03:27
2 semi custom content, and one talks about custom sample 11:03:30
3 preps. 11:03:35

4 And so those could include -- semi custom 11:03:36
5 could include things where some of the content would 11:03:39
6 be specific to the individual person, and some of the 11:03:42
7 content would be something that, you know, would apply 11:03:44
8 to everybody. And the fully custom preps could be 11:03:47
9 ones where it would apply specifically to that person. 11:03:56

10 Q. Where -- where do you say that pullout probes 11:04:03
11 would be designed based on a whole genome sequencing 11:04:07
12 step? 11:04:12

13 A. We said that we would be interested in 11:04:12
14 specific content, and we had described that to 11:04:18
15 identify that content you would often sequence one or 11:04:24
16 more individuals to identify that content, and then 11:04:27
17 you would design capture probes to that. 11:04:31

18 Q. I'm asking very specifically where is that 11:04:34
19 here in this slide? 11:04:40

20 A. So I think we're describing here an overall 11:04:41
21 approach, and that would have been one of the 11:04:47
22 implementations of that that we were planning. 11:04:53

23 Q. There's nothing in the slide, for example, 11:04:57
24 that says, "We're going to identify a particular 11:04:59
25 individual's unique polymorphisms by comparing the 11:05:02

1	individual's tumor DNA sequence to a matched normal	11:05:11
2	sample"; correct?	11:05:17
3	A. I think that, for example, I had already	11:05:18
4	described a few minutes ago here and also to our board	11:05:21
5	that Huntington's disease is an area where in my	11:05:25
6	genome that was a problem because there were no	11:05:31
7	sequencing reads.	11:05:34
8	So that would have been an example of looking	11:05:35
9	at my genome, identifying a gap in the genomic data,	11:05:37
10	which would be relevant to me because I was of an age	11:05:44
11	where that disease could still affect me, and we could	11:05:47
12	have designed probes to supplement my genome to fill	11:05:52
13	in that gap.	11:05:56
14	Q. There's no reference to Huntington's disease	11:06:02
15	on Slide 5; right?	11:06:06
16	A. There's a reference to what are called	11:06:07
17	"VNTRs," which stands for "Variable Number Tandem	11:06:09
18	Repeats." That's a category of genetic variant, which	11:06:12
19	often leads to a class of diseases, and Huntington's	11:06:16
20	and fragile X are two of those diseases. And we had a	11:06:27
21	more thorough list of what all of those were.	11:06:30
22	Q. That's listed in your informatic solutions	11:06:32
23	column, VNTR?	11:06:36
24	A. Yes. You can see in the center column there,	11:06:38
25	it says, "VNTR specific," and we also had informatic	11:06:41

1	solutions. Where it says, "other algorithms," for	11:06:45
2	example, lobSTR, l-o-b-S-T-R -- l-o-b-S-T-R was an	11:06:50
3	algorithm that had been developed by a third-party	11:07:01
4	group that we were planning to use to analyze data	11:07:04
5	superficially from what are called "STRs," which are	11:07:04
6	the short tandem repeats that are the basis for VNTRs.	11:07:08
7	These elements were often used together. The	11:07:15
8	bioinformatics would be used to analyze data, but	11:07:17
9	you'd have to have an assay. The laboratory would	11:07:21
10	have to be able to actually generate sequencing data,	11:07:25
11	which, then, could be analyzed.	11:07:27
12	So these bioinformatic methods were often	11:07:29
13	paired with laboratory methods to make a complete	11:07:33
14	solution.	11:07:41
15	Q. Do you think a person in this field at the	11:07:41
16	time reading Slide 5 would have been able to develop	11:07:44
17	your NeXT Personal MRD test?	11:07:51
18	A. I don't think we were saying -- assuming that	11:07:54
19	from one single slide one could make that MRD test.	11:07:57
20	We had been describing to our board and amongst our	11:08:03
21	technical team what we were going to do for over a	11:08:08
22	year. There were many different documents that would	11:08:11
23	compose that.	11:08:16
24	And so I would say that by the time -- this	11:08:16
25	is a summary.	11:08:19

1 Typically, our board of directors was a 11:08:20
2 varying technical -- levels of technological 11:08:23
3 knowledge, often more business knowledge. And so this 11:08:27
4 was a summary of what we were doing. 11:08:29

5 But what it was summarizing was a more 11:08:31
6 detailed plan and description, which is included in 11:08:34
7 other documents. And one who was skilled would have 11:08:39
8 been able to do that. And, in fact, we had people who 11:08:43
9 were skilled, and we did it. 11:08:47

10 Q. So do you think that someone, who was 11:08:48
11 knowledgeable in this field, that poured over all of 11:09:04
12 the exhibits in your binder there, the exhibits from 11:09:07
13 your declaration, would have been able to take that 11:09:11
14 knowledge and come up with NeXT Personal MRD test? 11:09:15

15 A. I think that we had come up with the concepts 11:09:20
16 of NeXT Personal MRD, and I think that's described in 11:09:23
17 the material that's in the declaration and in the 11:09:27
18 exhibits. 11:09:29

19 And the proof is that we actually, then, did 11:09:30
20 take that. And we had people who had significant 11:09:33
21 experience in this area, but there were certainly 11:09:37
22 other people who were not at Personalis who had 11:09:40
23 similar levels of experience. 11:09:43

24 And I think with the guidance of the things 11:09:46
25 that we were planning that are described in these 11:09:51

1 documents, I think that somebody would have been able 11:09:53
2 to implement something like NeXT Personal, or at least 11:09:56
3 something that was as described in the '033 and '394 11:10:01
4 patents. Those two patents describe more than just 11:10:07
5 the current NeXT Personal product. 11:10:10

6 Q. Just focusing on the exhibits that you cite 11:10:11
7 for conception, okay, you think that someone, who is 11:10:16
8 in the field and poured over those exhibits that you 11:10:21
9 pointed to for conception, would have been able to 11:10:26
10 from that disclosure develop NeXT Personal MRD? 11:10:29

11 MR. LUMAN: Incomplete hypothetical. 11:10:35

12 THE WITNESS: I think that from that 11:10:37
13 description someone who was skilled in the art would 11:10:39
14 have been able to develop products that were covered 11:10:42
15 by the '033 and '394 patents. 11:10:47

16 NeXT Personal includes -- is a new product 11:10:52
17 developed more recently, and it also includes other 11:10:55
18 capabilities that were not described in the '394 11:10:59
19 patent and the '033 patent. 11:11:04

20 Not surprisingly the technology has advanced. 11:11:07
21 Our knowledge has advanced. We also filed other 11:11:10
22 patents in later years, and we incorporated all of 11:11:14
23 those things when we designed NeXT Personal. 11:11:17

24 BY MR. HEINRICH: 11:11:20

25 Q. One -- an example of a feature that's in the 11:11:21

1 NeXT Personal, but not in your conception documents or 11:11:24
2 the patents, is tracking 1800 different biomarkers; 11:11:31
3 correct? 11:11:35

4 A. You could have decided to track 1800 11:11:35
5 biomarkers based on what we have here. I wouldn't 11:11:39
6 consider that's something that the -- the number 1800 11:11:43
7 is something that one skilled in the art could have 11:11:46
8 performed normal analysis and decided on based on the 11:11:50
9 guidance we had in 2012 and normal product 11:11:54
10 development. 11:12:00

11 Q. Why did it take nine years from your 2012 11:12:03
12 presentation to come up with NeXT Personal? 11:12:08

13 A. So NeXT Personal was not the only product 11:12:14
14 that we developed based on the accuracy program. We 11:12:16
15 had a number of products over the years. I would say 11:12:20
16 that the -- it was not a question that it took nine 11:12:24
17 years to do it because we weren't working on it for 11:12:26
18 nine years. We were working on other products. 11:12:30

19 There were multiple products that were 11:12:33
20 enabled by the developments back in 2012, and I would 11:12:36
21 say that there was at that time a significant concern 11:12:40
22 on our board of directors and amongst our management 11:12:45
23 team of the commercial issues, not technical issues, 11:12:49
24 but the commercial issues to do with clinical 11:12:53
25 diagnostic products because of the lack of financial 11:12:57

1	reimbursement for those products by health insurance	11:13:00
2	companies.	11:13:04
3	So Personalis developed a variety of	11:13:05
4	potential products, and we decided to prioritize	11:13:10
5	commercializing the products that we could get paid	11:13:14
6	for first.	11:13:18
7	So in February of 2014, based on the work	11:13:18
8	that we had done in 2012, we released what was called	11:13:22
9	the "ACE exome." And we sold that both to research	11:13:26
10	customers, to clinical customers where we could be	11:13:34
11	sure that we would be paid and to pharmaceutical	11:13:36
12	customers.	11:13:38
13	And we followed that over the years by other	11:13:39
14	products, and many of which were used in other	11:13:41
15	applications in cancer.	11:13:44
16	Q. There is no disclosure in Slide 5 of	11:13:46
17	sequencing multiple samples taken at different time	11:13:52
18	points from the same individual, is there?	11:13:58
19	A. I think there's disclosure about that on	11:14:00
20	Slide 3. You can see that the -- the reference to the	11:14:03
21	Snyder paper, and we specifically talk about -- let me	11:14:07
22	turn to Slide 3 so I can quote it correctly.	11:14:11
23	On Slide 3, if you're looking at it, it says,	11:14:22
24	"Publications and Upcoming Presentations."	11:14:24
25	We refer to a seminal paper by Mike Snyder	11:14:26

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1	and team published in "Cell," which is a premiere	11:14:30
2	journal, "ongoing clinical use of genome scale	11:14:34
3	sequencing, not just a genome once in your life."	11:14:38
4	And so that specific paper, which I think we	11:14:41
5	also have included as an exhibit, is one where we talk	11:14:44
6	specifically about sequencing an individual person at	11:14:48
7	many time points in their life.	11:14:52
8	In that particular paper, the individual	11:14:55
9	was -- had sequencing data developed at, I believe, 20	11:14:58
10	time points over an extended period of time.	11:15:02
11	Q. That was not proprietary Personalis research;	11:15:05
12	correct?	11:15:09
13	A. But the --	11:15:10
14	Q. Can you answer my question?	11:15:11
15	A. I'm trying to.	11:15:14
16	Q. That was not proprietary Personalis research;	11:15:16
17	correct?	11:15:21
18	A. So Mike Snyder's publication was published in	11:15:21
19	a scientific journal. So that was not proprietary to	11:15:25
20	Personalis.	11:15:29
21	We realized that we could implement that	11:15:30
22	using the technologies described on Slide 5, and that	11:15:34
23	the combination of those things could be powerful, and	11:15:37
24	that is, for example, something that we have	11:15:40
25	implemented in the NeXT Personal product because NeXT	11:15:43

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1	Personal involves sequencing genetic material from an	11:15:47
2	individual at multiple time points.	11:15:51
3	Q. So the Snyder paper, that did not -- that was	11:15:53
4	not work that was done at Personalis; correct?	11:16:00
5	A. No.	11:16:02
6	Q. And you did not state in Slide 5, "Hey, you	11:16:03
7	know, there's this seminal paper from a different	11:16:07
8	group, and we could apply technologies listed here to	11:16:12
9	sequence multiple samples from an individual, the same	11:16:18
10	individual, taken at subsequent time points; correct?	11:16:24
11	A. We didn't feel an obligation to put every	11:16:31
12	idea all on one slide. We found it easier to describe	11:16:34
13	to our board of directors what we were doing by having	11:16:38
14	a slide presentation with multiple slides. Different	11:16:42
15	elements of what we were doing were on the different	11:16:45
16	slides.	11:16:47
17	You asked me about the sequencing of	11:16:48
18	individuals at multiple time points, and so the place	11:16:49
19	in this presentation where we discussed that was on	11:16:52
20	Slide 3.	11:16:55
21	Q. Right, and you discussed it as something the	11:16:56
22	different group was doing; correct?	11:16:59
23	A. I'm sorry?	11:17:00
24	Q. You discussed it as something a different	11:17:01
25	group was doing?	11:17:04

1 A. No. We discussed it as something where they 11:17:04
2 had done something, and we realized that this was 11:17:08
3 something that could be useful to us. 11:17:12

4 And in particular, it was a change in the 11:17:14
5 business model because, if you thought about whole 11:17:17
6 genome sequencing the way it had been done, for 11:17:20
7 example, with my family, normally you would have 11:17:23
8 sequenced our genomes once and then been done. 11:17:25

9 And so John West would not have been a repeat 11:17:29
10 customer for Illumina for sequencing my genome because 11:17:32
11 there was no point in sequencing my genome again and 11:17:35
12 again and again the way that they were doing that. 11:17:39

13 And so that's a business problem if your 11:17:41
14 customers are one-time customers rather than repeat 11:17:43
15 customers. 11:17:48

16 And so what we realized was that we could use 11:17:48
17 this idea of having valuable sequencing at multiple 11:17:51
18 time points, and that this would change the economics 11:17:57
19 of our business by having customers where, once you 11:17:59
20 started with a customer, it would be advantageous to 11:18:02
21 sequence them at multiple time points, and so there 11:18:10
22 would be a recurring revenue stream. 11:18:13

23 So that's -- that's a bit more of a business 11:18:16
24 point as opposed to a technological point. So, then, 11:18:16
25 we were describing that -- that concept here. 11:18:16

1	And then, when we were describing the	11:18:18
2	specific technologies we might use of the different	11:18:19
3	time points, that was more described in Slide 5.	11:18:21
4	Q. You're not describing any different time	11:18:31
5	points in Slide 5, are you?	11:18:34
6	A. What we're describing are technological	11:18:36
7	methods that we could use over multiple time points,	11:18:38
8	and we had, just two slides earlier, described to our	11:18:43
9	board that it would be useful, and from a business	11:18:45
10	standpoint, could be useful to sequence individuals at	11:18:47
11	multiple timelines.	11:18:52
12	Q. And you described that to the board in the	11:18:53
13	context of someone else's published research?	11:18:55
14	A. No. We discussed it as something that would	11:18:59
15	be useful for us.	11:19:01
16	Q. Well, that's not on Slide 3, is it?	11:19:02
17	A. We didn't -- we didn't, generally, in our	11:19:05
18	board, just discuss interesting scientific paper that	11:19:07
19	was irrelevant to us. We were clearly describing it	11:19:12
20	to our board because we thought it was relevant to	11:19:17
21	what we were doing and to what our plans were, not	11:19:20
22	just that we were making observations about	11:19:22
23	interesting scientific research done that was not	11:19:27
24	related to our -- our company.	11:19:27
25	So we clearly were highlighting it, and we	11:19:28

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1	called it a "seminal paper" because we thought it was	11:19:30
2	relevant to our business.	11:19:33
3	Q. The accuracy program that's described in	11:19:38
4	Slide 5, a program to come up with a product that	11:19:43
5	provided more accurate sequencing, not a product that	11:19:49
6	tracked the course of diseases over time; correct?	11:19:55
7	A. No, that's not correct.	11:19:58
8	Q. Okay.	11:20:01
9	A. We did not describe the accuracy program just	11:20:01
10	on Slide 5. We had been describing the accuracy	11:20:05
11	program in multiple presentations to our board. There	11:20:09
12	are numerous slides included in this presentation that	11:20:12
13	highlight different aspects of the accuracy program.	11:20:15
14	And it is important to understand that	11:20:18
15	certain genetic features only become visible over	11:20:23
16	time, and when they become visible, that's valuable.	11:20:27
17	So we were describing a program that could	11:20:31
18	include the technological methods that are listed on	11:20:33
19	Slide 5 and elsewhere, and that those could be done	11:20:39
20	over time.	11:20:42
21	Q. What were the cancer diagnostic companies	11:20:45
22	that you thought would be your competitors as of 2012?	11:20:49
23	A. So there were a fair number of companies that	11:20:52
24	had cancer diagnostic tests as of 2012, and we were	11:21:08
25	aware of many of them. They included Foundation	11:21:16

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1 Medicine. They included Genomic Health, for example. 11:21:23
2 They included cancer diagnostic tests that were 11:21:27
3 performed by Labcorp, and I could think of others. 11:21:32
4 But that would be an example of three of the companies 11:21:38
5 that we're aware of. 11:21:41
6 Q. Did you list in any of your exhibits 11:21:42
7 Foundation Medicine as a potential competitor to 11:21:50
8 Personalis? 11:21:52
9 A. I don't remember the second. We could look 11:21:53
10 through those documents if you want. 11:21:59
11 Foundation Medicine is certainly a company -- 11:22:01
12 I became aware of Foundation Medicine in April of 2010 11:22:04
13 when I attended a genome sequencing related conference 11:22:09
14 held at MIT, and Foundation Medicine had been spun out 11:22:12
15 of MIT in late 2009. And they were talking with 11:22:17
16 someone about -- that they had financed that, and this 11:22:23
17 became a company that we paid attention to. 11:22:27
18 So, yes, we were absolutely aware of 11:22:29
19 Foundation Medicine as a cancer diagnostic company 11:22:31
20 that we would need to compete with in that space. 11:22:36
21 Q. Sitting here now, you can't point me to any 11:22:44
22 documentation that you were actually contemplating 11:22:47
23 competing with Foundation Medicine circa 2012? 11:22:50
24 A. We could take time to walk through it. I 11:22:54
25 haven't thought about that in a long time. So it may 11:22:58

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1	well be in these documents here. The documents	11:23:01
2	weren't prepared to provide a competitive analysis at	11:23:05
3	that time. So I don't know whether we would find that	11:23:09
4	or not.	11:23:11
5	I know that we were certainly aware of	11:23:12
6	Foundation Medicine and other companies partly	11:23:14
7	because, if you recall, I had been running this --	11:23:18
8	companies that provided the DNA sequencing equipment	11:23:20
9	to almost everybody in the cancer diagnostic space.	11:23:26
10	So we knew these people because they were our	11:23:30
11	customers. So it's certainly something we had a lot	11:23:36
12	of awareness of.	11:23:39
13	Q. Let's turn to Exhibit 2046.	11:23:44
14	(Exhibit 2046 was marked for identification.)	11:23:44
15	THE WITNESS: 2046?	11:23:50
16	BY MR. HEINRICH:	11:23:52
17	Q. Yep.	11:23:52
18	A. So just to be clear, this looks like a	11:24:30
19	document, and starting with an e-mail that I sent to	11:24:33
20	Mark Pratt and others Friday, January 6, 2012.	11:24:36
21	Is that what you're asking to point to?	11:24:42
22	Q. Yes. Why don't you turn to Slide 11.	11:24:45
23	MR. LUMAN: Just for clarity, do you want us	11:24:56
24	to be at the page that has a dot 11?	11:24:59
25	MR. HEINRICH: Yes.	11:25:03

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1	THE WITNESS: So is this the slide that is	11:25:08
2	titled "Examples of Known Error Mechanisms"?	11:25:11
3	Is that the one you want me to point to?	11:25:25
4	BY MR. HEINRICH:	11:25:25
5	Q. Yes.	11:25:25
6	THE REPORTER: Known?	11:25:25
7	THE WITNESS: Known, k-n-o-w-n. "Examples of	11:25:12
8	Known Error Mechanisms."	11:25:13
9	BY MR. HEINRICH:	11:25:13
10	Q. So the error mechanisms that you're referring	11:25:26
11	to here were mechanisms that resulted in sequencing	11:25:29
12	errors; correct?	11:25:39
13	A. Yes.	11:25:40
14	Q. And some of those mechanisms that led to	11:25:40
15	sequencing errors in 2012 were, for example, low or no	11:25:48
16	coverage due to GC bias; right?	11:25:53
17	A. Yes. GC bias was considered to be an error	11:25:57
18	mechanism because in regions of the genome that had	11:26:02
19	high percentage of Gs and Cs, those reads might not be	11:26:10
20	very well represented in the data, and you might not	11:26:15
21	have enough data to detect genetic variants in those	11:26:16
22	regions.	11:26:21
23	Q. And one of your ideas was to use Agilent	11:26:22
24	probes to pull down regions of higher GC content and	11:26:30
25	separately sequence them?	11:26:40

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1 A. Yes. We knew that regions of the genome that 11:26:43
2 had different amounts of GC content could be 11:26:47
3 sequenced, but sometimes the conditions that would 11:26:51
4 allow you to sequence with a medium percentage GC 11:26:54
5 would be different from the conditions required for 11:26:58
6 the high GC. 11:27:01

7 So if they were captured separately, you 11:27:03
8 could -- you could use one set of sequencing 11:27:07
9 conditions to sequence the bulk of the genome or the 11:27:11
10 exome, and you could use specialized conditions such 11:27:12
11 as higher temperature or higher salt concentrations to 11:27:15
12 sequence the regions that had high GC content. 11:27:20

13 So, yes, we specifically described a set of 11:27:26
14 capture probes that would capture the high GC content 11:27:28
15 of -- that we were interested in. 11:27:33

16 Q. So GC bias was one of the errors that you and 11:27:35
17 others, many others, had identified in the sequencing 11:27:45
18 technologies of the time. 11:27:50

19 And then, you know, that was a laboratory -- 11:27:54
20 using the Agilent probes was a laboratory approach to 11:27:58
21 addressing that particular error; right? 11:28:06

22 MR. LUMAN: Objection; form. 11:28:06

23 THE WITNESS: Yes, that would be a method for 11:28:07
24 us to generate data in places that otherwise it would 11:28:09
25 be missing. 11:28:14

1	BY MR. HEINRICH:	11:28:14
2	Q. So in your Slide 5 of the May 8th, 2012,	11:28:14
3	presentation, again, first column, you had a step of	11:28:22
4	characterizing errors in sequencing; right?	11:28:28
5	A. Yes, that's correct.	11:28:31
6	Q. So if you turn to Slide 14 of Exhibit 2046,	11:28:32
7	so 2046.14, these are some additional categories of	11:28:39
8	errors in sequencing at the time that you	11:28:49
9	characterized; right?	11:28:54
10	A. I wouldn't phrase it quite that way. These	11:28:55
11	were methods to identify the errors. These weren't	11:29:01
12	mechanisms that caused the errors.	11:29:06
13	Q. Fair enough. Fair enough.	11:29:09
14	So in categorizing errors, these were some of	11:29:10
15	the experimental processes you undertook to identify	11:29:16
16	errors; correct?	11:29:20
17	A. Yes. These were experimental approaches to	11:29:22
18	identify which variants were real and which variants	11:29:26
19	were errors.	11:29:31
20	Q. So one method you used to try to identify --	11:29:36
21	ultimately address errors was to sequence the same	11:29:50
22	person twice and see if you get discordant results;	11:29:58
23	right?	11:30:02
24	A. Yes, because the results should be the same.	11:30:03
25	And if there are differences, one of them has to be	11:30:05

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1 wrong. At least one of them has to be wrong. And so 11:30:10
2 that would be a method of identifying certain 11:30:13
3 categories of errors. It wouldn't identify all 11:30:17
4 categories of errors, but it would -- there are 11:30:20
5 certain errors that would show up that way. 11:30:22
6 Q. Because with respect to the work you were 11:30:28
7 doing in 2012, if you -- let me start over. 11:30:31
8 You're referring to repeatability; right? 11:30:38
9 A. Yes, that's right. If you sequenced the same 11:30:41
10 sample twice and you found different results, then it 11:30:46
11 would seem that one of those results, at least, would 11:30:50
12 need to be wrong. 11:30:55
13 Q. And that's what you refer to here when you 11:30:56
14 say repeatability, same person twice or more, trying 11:30:59
15 to keep everything else constant; right? 11:31:02
16 A. Yes, that's correct. 11:31:04
17 Q. So if you're sequencing the same person twice 11:31:05
18 and you're getting different results, then that told 11:31:09
19 you in 2012, "Oh, there must be a problem with 11:31:12
20 sequencing, and let's see how we can address that as 11:31:15
21 part of our accuracy in sequencing program"; right? 11:31:19
22 A. Yes, that was one of the methods we used to 11:31:22
23 identify errors, and then to identify the underlying 11:31:26
24 mechanism was a separate step. 11:31:31
25 Q. Then the next bold, you have "controlled 11:31:36

1	process experiments."	11:31:41
2	Same person sequenced multiple times. Each	11:31:42
3	time varying just one parameter of the process.	11:31:46
4	What are you referring to there?	11:31:50
5	A. So DNA sequencing technology has many	11:31:51
6	chemical and also computational choices that are made.	11:32:01
7	Very simply, you could run a certain chemical	11:32:08
8	reaction at one temperature, or you could run it at a	11:32:12
9	different temperature.	11:32:16
10	And so you might want to say, "I'm going to	11:32:18
11	sequence the same person, but at Step 5,	11:32:20
12	hypothetically, maybe we'll try that at a couple	11:32:24
13	different temperatures and see if changing the	11:32:27
14	temperature consistently leads to changes in the error	11:32:30
15	rates.	11:32:34
16	And so, for example, in GC bias, regions of	11:32:34
17	the genome that have high GC content typically require	11:32:39
18	higher temperatures for the -- some of the elements of	11:32:46
19	the sequencing reaction compared to regions that have	11:32:49
20	lower GC content.	11:32:54
21	Q. So the -- the way you would do controlled	11:32:56
22	process experiments would be to just change one very	11:32:59
23	specific part of the process each time; right?	11:33:01
24	A. Yes, that would help to understand the	11:33:04
25	underlying mechanisms.	11:33:06

1 And some of the data that we were downloading 11:33:08
2 from the Broad Institute was exactly that kind of 11:33:12
3 thing. They had sequenced a very standard sample 11:33:17
4 multiple times with different parameters, and so we 11:33:21
5 were learning also from what they had done. 11:33:25

6 Q. So if you vary too much from one run to the 11:33:27
7 next, you wouldn't know which of the changes that you 11:33:33
8 made actually led to the discordant result; correct? 11:33:35

9 A. Yes. And as was mentioned above under 11:33:39
10 "Repeatability," you can have cases where you change 11:33:42
11 absolutely nothing, and you still get discordant 11:33:46
12 results. 11:33:51

13 Q. Which would tell you that there was an issue 11:33:58
14 with the sequencing, and if you wanted to make -- you 11:34:01
15 would address that to make the sequencing more 11:34:04
16 reliable so it could be repeatable? 11:34:07

17 A. Yes. And the problems could be either in the 11:34:10
18 sequencing, or they could be in the content like the 11:34:12
19 reference sequence, or they could be in the 11:34:15
20 bioinformatic algorithms that were used, and we found 11:34:17
21 mechanisms of error in all those categories. 11:34:24

22 Q. So what was your first product from the 11:35:07
23 accuracy program? 11:35:13

24 A. The first product that Personalis 11:35:15
25 commercialized that leveraged results from the 11:35:20

1 accuracy program -- let me make sure I get this 11:35:23
2 correct. I'll describe two products, and you'll 11:35:27
3 understand why I'm describing the two products. 11:35:33
4 The first product that we actually sold in 11:35:37
5 September of 2012 involved standard whole genome 11:35:42
6 sequencing, but with bioinformatic methods for 11:35:46
7 interpretation that leveraged some of what we had been 11:35:51
8 developing that would lead to better results just 11:35:55
9 because of better algorithms or because of different 11:35:58
10 content. 11:36:01
11 And we had a customer in the United States 11:36:01
12 government, U.S. Department of Veterans Affairs that 11:36:04
13 had a plan to sequence ultimately a million U.S. 11:36:08
14 veterans, and they were beginning that process. We 11:36:13
15 won a competitive bid, and we received an order for 11:36:15
16 the sequencing and data analysis of 1,370 human 11:36:19
17 genomes. 11:36:26
18 And at that time our laboratory did not have 11:36:26
19 that much capacity. So we outsourced the sequencing 11:36:29
20 part to Illumina that did have a lab that could do 11:36:32
21 that, and they sent us the data, and we analyzed the 11:36:35
22 data, and provided those analysis results to the VA. 11:36:39
23 So that was a product that leveraged some of 11:36:45
24 the bioinformatic advances that we had made in the 11:36:47
25 accuracy program. 11:36:49

1	Now let me answer the -- we had a second	11:36:50
2	product that also leveraged the assay methods, and we	11:36:52
3	called it our ACE exome. A-C-E. This stood for	11:36:59
4	"Accuracy and Content Enhanced." This was an	11:37:01
5	augmented exome.	11:37:06
6	We introduced that product at the AGBT	11:37:10
7	conference in February of 2013. "AGBT" stands for	11:37:13
8	"Advances in Genome Biology and Technology."	11:37:20
9	And the ACE exome used a standard exome that	11:37:24
10	we could purchase from Agilent and also included a --	11:37:33
11	an Agilent SureSelect capture panel to supplement	11:37:38
12	areas that were outside of the coding regions of the	11:37:44
13	genes and also regions of high GC content, which, as	11:37:47
14	we've discussed, often weren't well represented	11:37:53
15	because of the bias in the sequencing process.	11:37:56
16	And so because of that, that product was able	11:37:58
17	to fill in some of the gaps that would normally be in	11:38:02
18	the sequencing, even in the coding regions of the	11:38:05
19	genes, and it also included biologically or medically	11:38:10
20	important content that was known, but that was outside	11:38:16
21	of the coding regions of the -- of the genes, and so a	11:38:19
22	typical exome would not include content outside the	11:38:23
23	coding regions of the genes that we felt you could	11:38:27
24	supplement the exome by capturing that as well.	11:38:31
25	So that was -- that was a product which had	11:38:35

1 both the laboratory methods and the bioinformatic 11:38:36
2 methods and the content methods that were described on 11:38:41
3 the Slide 5 we were referring to. 11:38:44

4 Q. And when you say, "Augmented exome or whole 11:38:46
5 genome plus," what you're referring to is a more 11:38:52
6 accurate exome sequence or more accurate whole genome 11:39:00
7 sequence; correct? 11:39:06

8 MR. LUMAN: Objection; form. 11:39:07

9 THE WITNESS: I would say it was a more 11:39:08
10 complete dataset. It, actually, went beyond what you 11:39:10
11 would call an exome because an exome typically refers 11:39:16
12 only to the coding regions of the genes. So that was 11:39:27
13 something you -- wouldn't normally be on an exome, but 11:39:27
14 we used that term. 11:39:27

15 And so the exome was being augmented with 11:39:39
16 additional parts of the genome that were not normally 11:39:43
17 included in an exome, and we used that for sequencing 11:39:45
18 a wide variety of sample types, including both cancer 11:39:49
19 samples and noncancer samples. 11:39:52

20 BY MR. HEINRICH: 11:39:59

21 Q. And the deliverable that you provided was a 11:39:59
22 sequence of a sample -- provided a snapshot of time; 11:40:02
23 right? 11:40:06

24 A. The -- what we would provide was a 11:40:06
25 combination of the raw sequence data from that sample 11:40:10

1 and the -- and we would provide analysis of that where 11:40:13
2 we would identify variants. We would provide quality 11:40:20
3 information on the variants. How confident we were of 11:40:28
4 each variant. We would provide quite extensive 11:40:32
5 characterization of each variant, whether that variant 11:40:35
6 was known to have medical meaning or known to have 11:40:36
7 biological function. 11:40:39

8 And if we -- generally, customers would 11:40:41
9 provide us with multiple samples, and we would provide 11:40:44
10 data for each sample. 11:40:48

11 So if a customer provided us samples from, 11:40:50
12 let's say, 20 people, we would return those 20 11:40:54
13 datasets. 11:40:57

14 If a customer provided us with a -- with 20 11:40:58
15 samples from the same person spread out over time, 11:41:02
16 then we would provide them 20 datasets spread out over 11:41:05
17 time. 11:41:09

18 But in general the deliverables we had were, 11:41:09
19 one, both raw data and analysis and interpretation for 11:41:13
20 each sample that the customer provided to us. We 11:41:18
21 didn't limit where those samples came from or how many 11:41:21
22 time points there were. 11:41:25

23 Q. Did a customer ever provide 20 samples taken 11:41:26
24 at 20 different time points? 11:41:30

25 A. We certainly had customers who provided 11:41:32

1 multiple samples taken at multiple time points, 11:41:38
2 including specifically cancer samples like that. 11:41:41
3 But I don't recall when we had somebody who 11:41:46
4 did 20. I don't think the exact number matters, but 11:41:51
5 there were certainly people who looked at, for 11:41:54
6 example, four different time points, or that kind of 11:41:57
7 thing. 11:42:00
8 Q. And when -- when did -- did that happen? 11:42:00
9 A. I don't recall the specific time, but this 11:42:01
10 capability was something -- there was nothing built 11:42:06
11 into the product that limited the number of time 11:42:11
12 points or where the samples came from, and so it 11:42:13
13 wasn't unusual, for example, to -- a simple thing, 11:42:17
14 where you might have different samples from different 11:42:23
15 time points, would be in a cancer patient. You would 11:42:26
16 typically want to sequence both the tumor and the 11:42:29
17 person's, what's called their "normal," which is their 11:42:32
18 background genome from their blood sample, and those 11:42:38
19 are usually from different times. 11:42:39
20 Q. Is there any disclosure doing that in the 11:42:40
21 exhibits you submitted with your declaration? 11:42:43
22 A. I think we've -- for example, on Slide 3 of 11:42:48
23 my presentation from May of 2012, you see that we were 11:42:50
24 focused on it and considered it quite seminal the 11:42:56
25 ability to look at multiple time points, and so that's 11:43:00

1	an example of that.	11:43:04
2	I don't remember every single -- what we have	11:43:06
3	in every single exhibit in terms of that dimension.	11:43:08
4	But we certainly were -- there was nothing in	11:43:13
5	our product that would prohibit that, and it certainly	11:43:16
6	would make sense to be able to do that kind of thing.	11:43:21
7	Q. And just to be clear, the reference in Slide	11:43:24
8	3 of Exhibit 2112, you're referring to -- refers to	11:43:27
9	work that a different group did, not Personalis;	11:43:31
10	right?	11:43:35
11	A. The reference in Slide 3 was work that was	11:43:35
12	done at -- in Mike Snyder's group. Mike Snyder was	11:43:39
13	one of the cofounders of Personalis, and some of the	11:43:46
14	other people on the publication were also involved	11:43:48
15	with Personalis and became inventors.	11:43:51
16	But that specific project described in that	11:43:54
17	paper was done at -- by those people at Stanford was	11:43:58
18	not -- it was not a Personalis-initiated project.	11:44:01
19	Q. Let's turn to Exhibit 2084.	11:44:09
20	(Exhibit 2084 was marked for identification.)	11:44:38
21	MR. LUMAN: Alan, we're about 17 minutes from	11:44:38
22	noonish. Would that be about a good time for our	11:44:41
23	lunch break?	11:44:45
24	MR. HEINRICH: Sure.	11:44:46
25	THE WITNESS: That's fine for me.	11:44:47

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1	So Exhibit 2084, just to make sure we're	11:44:47
2	aligned here, is an e-mail that I sent to Carol Tillis	11:44:51
3	on September 4, 2012, and the subject is "Personalis	11:44:56
4	Board Meeting Tomorrow."	11:45:02
5	BY MR. HEINRICH:	11:45:04
6	Q. Correct. And in the portion of this thread	11:45:04
7	where you're e-mailing Jonathan, Roman, and Chris,	11:45:19
8	you -- identifies your biggest news that your R and D	11:45:27
9	team completed your prototype product; right?	11:45:34
10	A. I believe that's what it says at the top of	11:45:39
11	the second paragraph.	11:45:43
12	Q. Correct. And that prototype product that was	11:45:44
13	what you came to call your Exome Plus product?	11:45:50
14	A. I think that at the time the prototype we had	11:45:54
15	actually went beyond what ended up being the Exome	11:45:58
16	Plus product.	11:46:03
17	When we designed the first prototype, it also	11:46:04
18	included what we called a long read pull out, which	11:46:07
19	was specifically to separately pull out portions of	11:46:10
20	the genome where having a longer sequence read would	11:46:14
21	be beneficial, and we had identified quite a few of	11:46:18
22	those locations, and we pulled those out.	11:46:21
23	That capability to have a separate read	11:46:25
24	length was something that we ultimately did not	11:46:29
25	include in the product that was commercialized, but I	11:46:32

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1	believe we did include it in the initial prototype.	11:46:37
2	Q. And the way you describe the prototype here	11:46:43
3	is -- in the third sentence of that paragraph:	11:46:45
4	"We will sequence exomes from 130	11:46:48
5	clinical samples and analyze them using	11:46:51
6	our state of the art case-controlled	11:46:55
7	software"; correct?	11:46:59
8	A. It's been a while. I would like to read	11:46:59
9	this. It might take a minute.	11:47:02
10	Q. Mm-hmm.	11:47:03
11	A. Now that I read this and think about it more	11:48:06
12	carefully, this particular -- what was described in	11:48:11
13	this paragraph was a project we had with a customer at	11:48:13
14	a research group at Stanford University that was	11:48:22
15	working on a rare neurological disease that was called	11:48:25
16	"Moyamoya" disease. M-o-y-a-m-o-y-a.	11:48:30
17	It was a disease where, because of mutations	11:48:33
18	in the person's genome, their brain nerves don't get	11:48:38
19	wired the right way, and it leads to mental problems	11:48:44
20	for the patients, and they had specimens from 130	11:48:48
21	patients, and they asked us to sequence them and to	11:48:55
22	analyze that to try to identify what variants might	11:49:01
23	actually be causing the disease in those patients.	11:49:06
24	And so the sequencing that was performed for	11:49:09
25	that project was not our Exome Plus. The sequencing	11:49:13

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1 that was performed for that project was a standard 11:49:19
2 off-the-shelf exome because we had not yet released 11:49:22
3 our Exome Plus or ACE exome product. That wasn't 11:49:27
4 released until February of 2013. The work that was 11:49:30
5 done here was done using a standard commercial exome 11:49:34
6 kit. We did the sequencing in house in our 11:49:40
7 laboratory. 11:49:44

8 The elements that would have been labeled as 11:49:44
9 our prototype product would have been in what we 11:49:47
10 called our "disease variant discovery service" that's 11:49:51
11 described in some of Rich Chen's slides, and it was a 11:49:55
12 bioinformatic method to compare the data from healthy 11:49:58
13 people versus people who have a specific disease to 11:50:04
14 see if you can identify what's genetically different 11:50:07
15 that caused those people to have that disease. 11:50:12

16 And in that project, we were ultimately 11:50:14
17 successful at identifying both a variant that was 11:50:17
18 already known by the investigators, and we also 11:50:21
19 identified some new variants, and there were -- 11:50:25
20 sometime later, there were publications about these 11:50:29
21 results for this rare neurological disease. 11:50:32

22 It was a disease, as I recall, that primarily 11:50:36
23 affected people of Japanese ancestry. I don't know 11:50:40
24 why, but -- so this was -- this was not our Exome Plus 11:50:46
25 product, but it did leverage some of our bioinformatic 11:50:50

1	developments.	11:50:56
2	Q. Turn, if you will, to Exhibit 2099. I want	11:50:57
3	to ask you about Slide 3.	11:51:03
4	(Exhibit 2099 was marked for identification.)	11:51:03
5	THE WITNESS: To make sure I'm in the right	11:51:23
6	place, this is an e-mail that I sent to Carol Tillis	11:51:25
7	copied to some others. In the subject line, it says,	11:51:29
8	"Board slides from John West, ready to print." And	11:51:34
9	this was from November 1, 2012.	11:51:37
10	Q. Correct.	11:51:41
11	A. And you wanted me to turn to which slide,	11:51:42
12	please?	11:51:45
13	Q. Slide 3, please.	11:51:46
14	A. This is the slide titled, "Key Intellectual	11:51:54
15	Property and IP Potential Behind the Company."	11:51:58
16	Q. Correct. And on the left-hand side, you list	11:52:06
17	some IP license from Stanford; correct?	11:52:11
18	A. Yes, that's correct. It's not -- there were	11:52:14
19	other types of IP that we also licensed from Stanford,	11:52:16
20	but this is some of what we licensed.	11:52:21
21	Q. And that's not the IP at issue in this	11:52:24
22	proceeding; correct?	11:52:27
23	A. Actually, as I look at this, I believe that	11:52:28
24	this whole left-hand column includes elements that	11:52:32
25	were licensed from Stanford so that -- for example, we	11:52:36

1 licensed at least four different databases, PharmGKB, 11:52:40
2 Veramed, Mendel DB, and Regulon. So -- and those were 11:52:45
3 licenses. 11:52:50

4 We also had a license in August of 2011 that 11:52:50
5 included 17 different what Stanford called "dockets." 11:52:53
6 Each docket was a separate piece of intellectual 11:52:58
7 property, and we had licensed all of those. 11:53:02

8 So they also had patent applications that 11:53:05
9 were related to some key accuracy IP. And in 11:53:08
10 particular, they had a patent application related to 11:53:17
11 the idea of ethnically specific human reference 11:53:19
12 sequences. I think that's what was being referred to 11:53:22
13 there and then copyrights and trademarks that were 11:53:24
14 associated with that. 11:53:28

15 And then this other description here of IP 11:53:29
16 potential from the founders and team. So this was 11:53:32
17 describing some of the areas of expertise of the 11:53:36
18 founders. This does not describe the IP that we were 11:53:39
19 developing inside the company. It shows more, kind 11:53:43
20 of, the background expertise. 11:53:47

21 Q. What IP is -- so -- so on the right-hand 11:53:49
22 column, there is a bullet, "IP Potential from Founders 11:53:56
23 and Team"; correct? 11:54:01

24 A. Yes. 11:54:02

25 Q. And the very last bullet is "Sequencing 11:54:03

1	Accuracy"; correct?	11:54:12
2	A. Yes.	11:54:14
3	Q. And that is where the IP potential from the	11:54:14
4	team is referred to; correct?	11:54:21
5	A. Well, no, all of these people were on our	11:54:22
6	team, but I would say that the -- of the four Stanford	11:54:26
7	professors who were involved with us, three of them	11:54:33
8	had more medical or bioinformatic backgrounds.	11:54:38
9	Mike Snyder, who is also quite knowledgeable	11:54:43
10	about assays and issues of sequencing accuracy, so he	11:54:46
11	had quite a bit of expertise on that, and we,	11:54:49
12	certainly, worked with him on those items.	11:54:52
13	The sequencing accuracy, because I had worked	11:54:55
14	in the sequencing field for 30 years, I knew a lot	11:54:57
15	about the issues of sequencing accuracy. That's why I	11:55:02
16	was highlighted there. But this is not our whole	11:55:04
17	team. This is just the founding -- the -- the	11:55:08
18	founders.	11:55:09
19	Q. Now, the founders -- Altman, Butte, Ashley,	11:55:09
20	and Snyder -- they all had assignment obligations to	11:55:18
21	Stanford; correct?	11:55:23
22	A. All of them were professors at Stanford at	11:55:24
23	that time. All of them assigned their IP to Stanford,	11:55:28
24	and we had licensed some of it from Stanford in August	11:55:32
25	of 2011.	11:55:35

1 Q. Right. And some of that IP is also reflected 11:55:37
2 in the left-hand column under "License from Stanford"; 11:55:43
3 correct? 11:55:47

4 A. Yes. I think part of what we were trying to 11:55:47
5 show here was it doesn't just talk about IP. It talks 11:55:50
6 about IP potential. And so part of what we were 11:55:55
7 conveying was we have quite a brain trust here. This 11:55:58
8 is some of the world's leaders in this field. 11:56:01

9 And so the ability for us to bounce ideas off 11:56:06
10 of them or to understand what others are doing in the 11:56:08
11 field is supplemented by having people like experts 11:56:11
12 like that that we can work with. 11:56:15

13 Q. The sequencing accuracy reference here is a 11:56:17
14 reference to the IP, specifically the patent 11:56:25
15 applications, that you were contemplating filing for 11:56:32
16 the accuracy program; correct? 11:56:37

17 A. Let's see. The word "potential" is there. 11:56:39
18 So certainly at the time of this slide we had not yet 11:56:43
19 filed any -- a patent application. We did file about 11:56:47
20 two months after this, maybe 2 to 3 months after this. 11:56:50

21 So we were clearly thinking about that and 11:56:54
22 beginning to plan that, and that would have been the 11:56:57
23 IP that came out of the -- what we call the "Accuracy 11:56:59
24 Program," and that was developed entirely internally 11:57:04
25 to Personalis. 11:57:07

1	Q. Right. And -- and those applications,	11:57:09
2	through some continuations ultimately issued as '394	11:57:15
3	and the '033; correct?	11:57:23
4	A. Yes, that's correct.	11:57:23
5	MR. HEINRICH: Okay. Why don't we take our	11:57:24
6	lunch break now.	11:57:25
7	THE VIDEOGRAPHER: Okay. We are going off	11:57:27
8	the record. The time is 11:57 a.m.	11:57:28
9	(Lunch recess taken from 11:57 a.m. to 12:36 p.m.)	12:04:25
10	THE VIDEOGRAPHER: We're back on the record.	12:35:40
11	The time is 12:36 p.m.	12:36:14
12	BY MR. HEINRICH:	12:36:17
13	Q. Welcome back, Mr. West. Did you have any	12:36:17
14	discussions with counsel at our break?	12:36:20
15	A. Nothing to do with this deposition. We did	12:36:21
16	talk about the FDA approval of that drug and Steve's	12:36:24
17	son going out to Hawaii and all kinds of nice things.	12:36:28
18	Nothing to do with this deposition.	12:36:32
19	Q. Excellent. Let's see. So I'm going to go	12:36:33
20	back to 2112.	12:36:39
21	A. Okay. I'll return to that.	12:36:42
22	Q. And then I'll direct your attention to Slide	12:36:43
23	13.	12:36:48
24	A. Okay. Let me go back to -- so 2112 is the	12:37:25
25	CEO overview from 8th of May?	12:37:30

1	Q. Yep.	12:37:33
2	A. And I'm looking at Slide 13.	12:37:38
3	Q. Okay. So the third main bullet is titled	12:37:40
4	"Personalis Lab."	12:37:46
5	A. Yes.	12:37:49
6	Q. What's referred to there?	12:37:49
7	A. I'm sorry?	12:37:51
8	Q. What's being referred to there?	12:37:54
9	A. Let me just look and see.	12:37:56
10	So Personalis, at the time of this, did not	12:38:06
11	have a laboratory. We were in the process of planning	12:38:10
12	for a laboratory. I think we had just signed a lease	12:38:13
13	on a property that had a -- there was a room that had	12:38:17
14	previously been the lunch room for the company that	12:38:23
15	was there before, and we were looking at -- at the	12:38:26
16	possibility of turning that into a small laboratory.	12:38:28
17	And so we would have been talking about plans	12:38:31
18	for what our laboratory would do. We did not have a	12:38:33
19	laboratory at that -- we might have done a few things	12:38:38
20	with borrowed space or something at that time, but we	12:38:42
21	did not have a fully operating laboratory at that	12:38:44
22	point.	12:38:47
23	Q. But you were contemplating having one; right?	12:38:47
24	A. Yes.	12:38:50
25	Q. And you had in mind what would be the	12:38:50

1	internal processes for the Personalis lab; right?	12:38:54
2	A. Yes, and some of them are listed here.	12:38:59
3	Q. What's the first step listed here under	12:39:05
4	"Personalis Lab"?	12:39:09
5	MR. LUMAN: Mischaracterizes the document.	12:39:11
6	THE WITNESS: Let's see, the first bullet	12:39:14
7	point underneath where it says, "Personalis Lab,"	12:39:15
8	says, "Received, de-identify samples."	12:39:18
9	BY MR. HEINRICH:	12:39:18
10	Q. Just to address the objection that I was	12:39:27
11	mischaracterizing the document, when I said first	12:39:29
12	step, would there be a step prior to receiving the	12:39:34
13	sample? You can't do anything with a sample until you	12:39:37
14	receive it; right?	12:39:40
15	A. There are steps before you receive a sample.	12:39:46
16	Typically, you have to send certain kits to the	12:39:49
17	customer so that they have the right things in which	12:39:53
18	to send the sample to you that may involve certain	12:39:58
19	containers for sealing the sample or preservatives or	12:40:02
20	things like that.	12:40:05
21	So you obviously, you don't -- there's	12:40:07
22	nothing you can physically do with the sample until	12:40:07
23	you have it, but the -- but you would typically	12:40:10
24	receive -- you'd coordinate with the customer. There	12:40:12
25	might be a shipping list to say a list of the samples	12:40:15

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1	that are coming, what their characteristics are,	12:40:19
2	coordinate what the plans -- so there would be	12:40:22
3	planning and so forth before receiving the sample.	12:40:24

4	Q. In terms of what's happening in the lab,	12:40:26
5	first the lab has to receive the sample; right?	12:40:28

6	A. Generally, the lab has to receive a sample	12:40:30
7	before they can process it, yes.	12:40:33

8	Q. Right. So that bullet is "Receive,	12:40:35
9	De-identify Samples."	12:40:40

10	What does that refer to, "de-identify	12:40:41
11	samples"?	12:40:43

12	A. So the -- the issues of genetic ethics, which	12:40:44
13	have to do with the fact that the information derived	12:40:52
14	from a sample may be of medical consequence to the	12:40:55
15	person if it's a clinical sample.	12:40:58

16	And so you often want to be careful about who	12:41:02
17	can actually have access to knowing, for example, who	12:41:08
18	the patient is.	12:41:12

19	So an example of de-identifying a sample	12:41:13
20	would be, if the sample came in and it was a group of	12:41:17
21	them and said, "This is from John West, and this one	12:41:21
22	is from somebody else," it had people's names on it,	12:41:24
23	you would -- you would separate that off, put a --	12:41:29
24	maybe put a number on the sample, like a random	12:41:30
25	number, so Sample 7204, so the person in the lab	12:41:33

1	processing it couldn't accidentally say, "Oh,	12:41:38
2	that's -- John West has such and such a result." They	12:41:43
3	just say, "Oh, Sample 7204 has a certain result."	12:41:47
4	And so you are separating the identification	12:41:53
5	of who the person was from the sample. You can still	12:41:54
6	refer to the sample and keep track of it, but you	12:41:57
7	wouldn't be -- but the people handling it in the lab	12:41:59
8	or handling the data wouldn't have to know the	12:42:01
9	identity of the person.	12:42:04
10	Q. And you would be keeping track of the sample	12:42:06
11	by the number?	12:42:09
12	A. Yes, that's right.	12:42:09
13	Q. So let's turn to paragraph 162 of your	12:42:12
14	declaration.	12:42:18
15	A. Do you know what page that's on?	12:42:40
16	Q. 101.	12:42:42
17	A. Okay. I'm looking at paragraph 162.	12:42:51
18	Q. Okay. So you said that, "I attended the	12:42:55
19	July 2011 meeting with the following additional	12:43:03
20	persons, all of whom are appropriately not named as	12:43:07
21	inventors of the '033 patent."	12:43:12
22	And the first name you mentioned here was	12:43:15
23	Michael Snyder; correct?	12:43:18
24	A. Yes.	12:43:20
25	Q. So you testified repeatedly in our morning	12:43:20

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1	session about the importance of Dr. Snyder's paper	12:43:31
2	from March of 2012. It's referenced in Slide 3 of	12:43:43
3	your May 8, 2012, board presentation; correct?	12:43:46
4	A. Yes.	12:43:50
5	Q. So why was Dr. Snyder appropriately not named	12:43:51
6	as an inventor given the importance that you ascribe	12:44:00
7	to his work?	12:44:05
8	MR. LUMAN: Objection; calls for a legal	12:44:07
9	conclusion.	12:44:10
10	THE WITNESS: So I would say that the work	12:44:10
11	that Mike Snyder had done did not contribute to the	12:44:13
12	elements of the patent. It did not contribute to	12:44:19
13	the -- or conception of it.	12:44:23
14	Mike was knowledgeable about many things, and	12:44:26
15	you can be -- if you see something from somebody else,	12:44:29
16	it can spark an idea that you have. It doesn't mean	12:44:38
17	that who came up with that something else came up with	12:44:41
18	the idea. And I would say that's, kind of, the case	12:44:43
19	here.	12:44:46
20	So Mike had done some things. He didn't do	12:44:48
21	what we described in the patent, and so he's not an	12:44:51
22	inventor on that, but some of the things he did, when	12:44:58
23	we thought about it with the context of other things	12:45:02
24	we were thinking about, which he had not participated	12:45:05
25	in, we were able to see that we could take something	12:45:08

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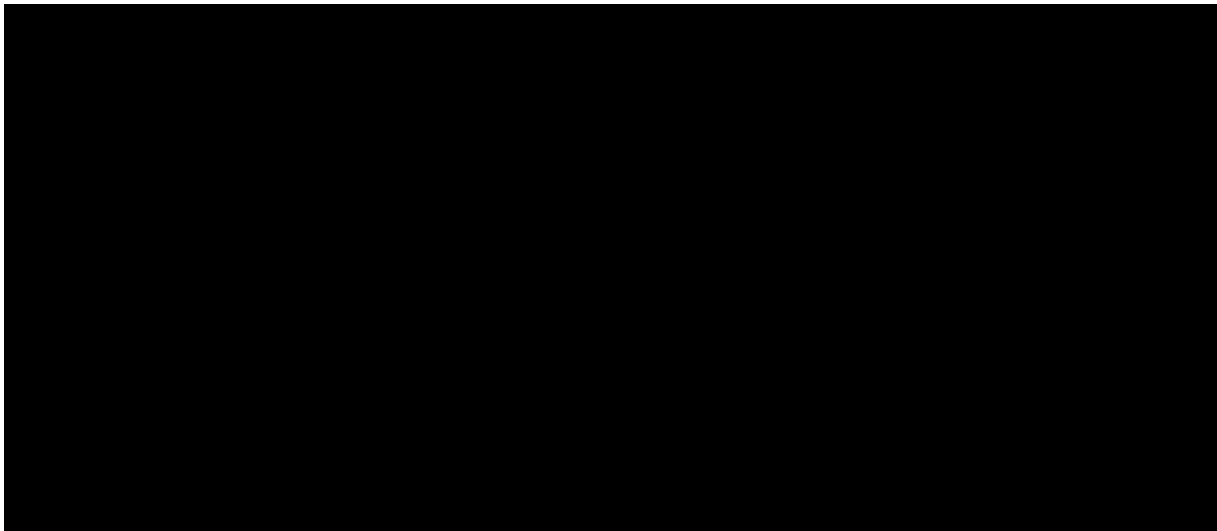
1	further that was not what he described.	12:45:12
2	BY MR. HEINRICH:	12:45:14
3	Q. Isn't it the case that you didn't want to	12:45:15
4	name him as an inventor because, then, Stanford would	12:45:17
5	co-own your -- your patent applications?	12:45:21
6	MR. LUMAN: Objection; foundation,	12:45:26
7	argumentative.	12:45:27
8	THE WITNESS: No.	12:45:30
9	BY MR. HEINRICH:	12:45:30
10	Q. So is it your testimony that Personalis did a	12:45:31
11	careful inventorship analysis and named the correct	12:45:36
12	inventors and appropriately excluded Dr. Snyder as an	12:45:43
13	inventor?	12:45:50
14	A. I would say that when we submitted the patent	12:45:51
15	application we included the people that we felt	12:45:54
16	contributed to that invention, and we didn't think	12:45:58
17	that Mike had contributed to that invention.	12:46:01
18	It didn't mean that Mike hadn't contributed	12:46:05
19	to the company. He contributed actually in many ways	12:46:07
20	to the company, but we didn't feel he contributed to	12:46:09
21	that invention.	12:46:12
22	Q. Now, you testified earlier that you -- you,	12:46:13
23	sort of, focussed your review of the patents, the '394	12:46:20
24	and '033 patents, on the claims, correct, in preparing	12:46:26
25	your declaration?	12:46:30

1 A. Yes. I spent more time on the claims than on 12:46:32
2 other parts. I've, certainly, seen the rest at 12:46:35
3 various times in the past. 12:46:38
4 Q. So do you have the claims of the patent 12:46:40
5 handy? 12:46:45
6 A. I don't. But actually, is it -- is the 12:46:46
7 patent one of the exhibits? I don't remember. 12:46:48
8 Q. It's one of the exhibits in the IPR 12:46:51
9 proceedings. I have copies of the patents. 12:46:56
10 A. If I recall, we didn't make it an exhibit 12:47:04
11 here because it was already something everybody knew. 12:47:06
12 MR. HEINRICH: These are for you 12:47:21
13 (indicating). 12:47:22
14 BY MR. HEINRICH: 12:47:22
15 Q. Why don't we start with the '394? 12:47:23
16 A. One second. Can I close this for the time 12:47:26
17 being -- 12:47:29
18 Q. You certainly can. 12:47:29
19 A. -- and move it out of the way here. So I'm 12:47:30
20 looking at the '394 patent. 12:47:42
21 Q. If you go to Claim 1. 12:47:47
22 A. Yes. I'm looking at the beginning of Claim 12:48:10
23 1. 12:48:13
24 Q. And your declaration has an 12:48:13
25 element-by-element discussion -- I should say a 12:48:16

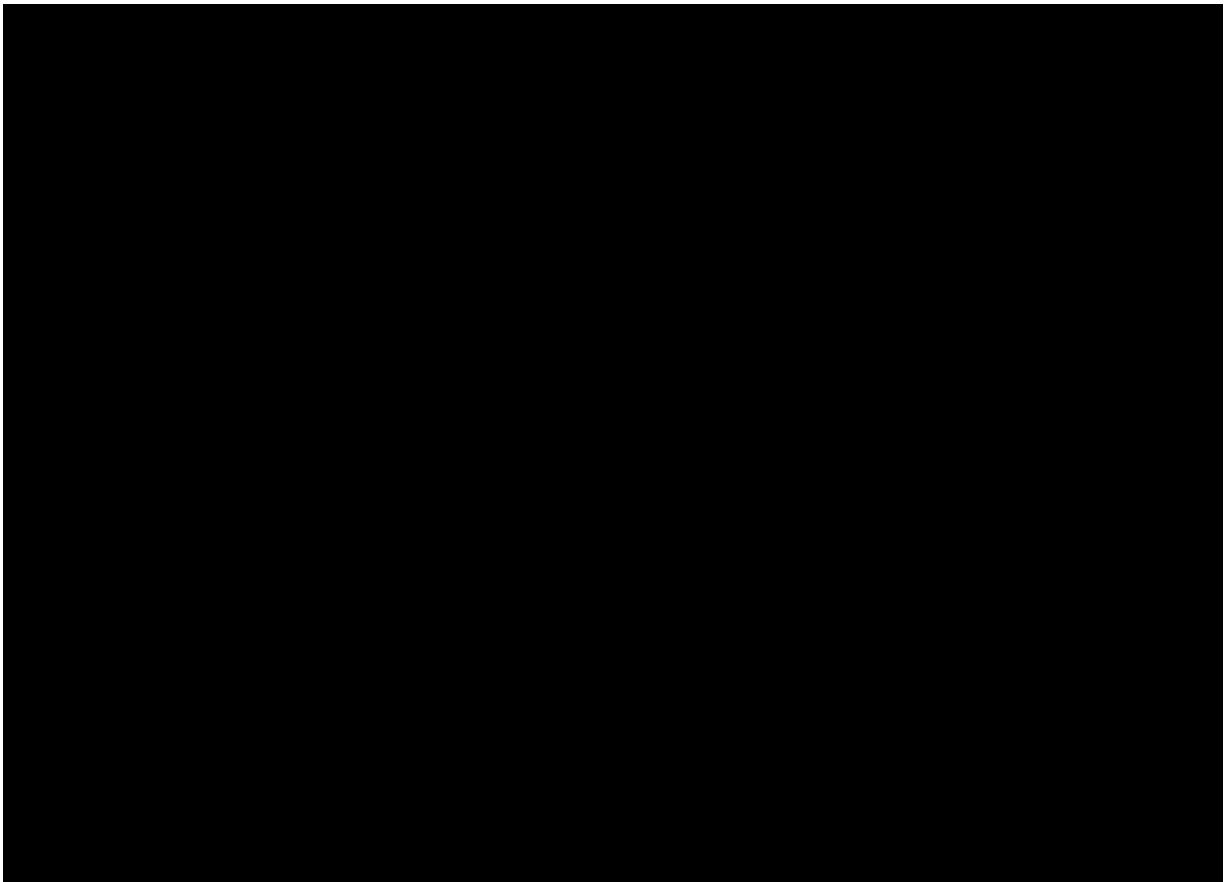
1	step-by-step discussion of Claim 1 and your purported	12:48:19
2	conception of it; correct?	12:48:26
3	A. As I recall, when we wrote the declaration,	12:48:28
4	we went claim by claim and talked about the background	12:48:34
5	of it. And where there -- certain of the claims are	12:48:39
6	relatively simple, and some of the claims have many	12:48:42
7	elements, and Claim 1 is -- has more elements.	12:48:46
8	And so I think we had broke that into several	12:48:49
9	parts when we described it.	12:48:52
10	Q. Claim 1 includes a series of steps?	12:48:53
11	A. Yes, it does.	12:48:57
12	Q. And even though you went through it in detail	12:48:59
13	in your declaration, feel free to review it again now	12:49:06
14	if you would like. I have a few questions about it.	12:49:10
15	A. Okay. And I'm happy to review it, but if you	12:49:13
16	can tell me what you think the questions are, then	12:49:18
17	I'll know when I'm reviewing --	12:49:19
18	Q. Why don't you just --	12:49:21
19	A. Scan that claim?	12:49:23
20	Q. Yes.	12:49:27
21	A. Okay. I've read the first claim.	12:51:27

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MR. LUMAN: I'll object to that question to 12:52:25
the extent it's calling for a legal conclusion and 12:52:29
outside the scope of his declaration. 12:52:31
BY MR. HEINRICH: 12:52:33



1	BY MR. HEINRICH:	12:53:16
2	Q. Okay. So what about the whole Exome Plus or	12:53:16
3	ACE Exome Plus product that you did commercialize?	12:53:25
4	Are there any steps recited in Claim 1 that	12:53:30
5	were not included in the work flow for the	12:53:32
6	commercialized whole exome product?	12:53:35
7	MR. LUMAN: Same objections.	12:53:38
8	THE WITNESS: So the ACE exome product that	12:53:39
9	we released, which was, essentially, the commercial	12:53:45
10	version, the first commercial version of exome would	12:53:49
11	have been originally the Exome Plus, was generally	12:53:52
12	based on a single initial sample and analysis of that	12:53:58
13	sample.	12:54:02
14	It could be used, and we did use our	12:54:04
15	augmented exome at multiple time points on some -- in	12:54:09
16	some cases of some patients, and we did use it in a	12:54:15
17	number of cases because it's a real product. So we	12:54:17
18	actually had experience with that.	12:54:21
19	And so we did use it in some cases, for	12:54:22
20	example, to look at both a tumor and separately the	12:54:27
21	blood of the patient. So you could do -- look at what	12:54:30
22	was called "tumor" versus "normal" and end up	12:54:32
23	identifying a somatic variance in the sample.	12:54:35
24	So those were places where there could be	12:54:40
25	multiple samples, and they could do multiple time	12:54:44

1	points, but you could also use the ACE exome just on a	12:54:48
2	single germ line, you know, a blood sample of an	12:54:53
3	individual, particularly in the cases that had to do	12:54:57
4	with Mendelian disease where you didn't need to	12:54:59
5	separate out somatic variance.	12:55:05
6	BY MR. HEINRICH:	12:55:08
7	Q. Had you provided in any of your exhibits	12:55:08
8	evidence of when you first or when Personalis first	12:55:13
9	did a match tumor normal analysis?	12:55:17
10	MR. LUMAN: Outside the scope.	12:55:22
11	THE WITNESS: So Personalis' team had been	12:55:24
12	involved in tumor normal work, certainly some of them	12:55:32
13	before joining Personalis. So it was something that	12:55:40
14	they were experienced with both from a laboratory	12:55:44
15	standpoint and from a bioinformatic standpoint.	12:55:47
16	So I don't know if that answers your	12:55:57
17	question, but -- maybe otherwise -- if you could ask	12:55:59
18	the question again, maybe I can.	12:56:00
19	BY MR. HEINRICH:	12:56:02
20	Q. Yeah, no, it didn't.	12:56:02
21	A. Okay.	12:56:02
22	Q. So I'm wondering if there is a documentary	12:56:03
23	evidence that was submitted in this proceeding to help	12:56:06
24	us understand with proof when Personalis may have	12:56:08
25	first done a match tumor normal analysis as part of	12:56:15

1	its whole exome product?	12:56:20
2	MR. LUMAN: Outside the scope, asked and	12:56:23
3	answered.	12:56:25
4	THE WITNESS: I don't recall if there's ever	12:56:25
5	been any request to document that. So I don't think	12:56:28
6	we documented that in the declaration. I don't think	12:56:30
7	it was considered relevant.	12:56:35
8	BY MR. HEINRICH:	12:56:37
9	Q. Okay. Was the whole exome product as	12:56:37
10	marketed at launch, did it follow the steps of Claim 1	12:56:45
11	of the '394 patent?	12:56:54
12	MR. LUMAN: Calls for a legal conclusion,	12:56:56
13	outside the scope.	12:56:58
14	THE WITNESS: We have derived several	12:56:59
15	different patents from the original patent filing, and	12:57:05
16	the exome -- the ACE exome certainly followed the	12:57:09
17	steps that are in some of those other patents.	12:57:17
18	In particular, separately pulling out regions	12:57:20
19	of high GC content and using that to fill in the gaps	12:57:25
20	and the sequencing, that was one of the areas that was	12:57:29
21	covered in -- in one of the other patents.	12:57:32
22	In terms of all of the steps of this Claim 1,	12:57:39
23	the product could have been used as the front end for	12:57:42
24	that. Again, the Exome Plus was not a personalized	12:57:46
25	product the way we implemented it commercially. It	12:57:52

1	was the same hybrid capture set for each sample.	12:57:57
2	So the genetic variants that were covered by	12:58:03
3	the ACE exome were not different from one person to	12:58:09
4	another. And so the idea of identifying variants from	12:58:15
5	a first sample and then using that to design a second	12:58:18
6	capture set, that was not part of what we commercially	12:58:23
7	implemented in the ACE exome.	12:58:26
8	BY MR. HEINRICH:	12:58:36
9	Q. As marketed at launch, the ACE exome	12:58:37
10	similarly focused on analysis of a single sample;	12:58:43
11	correct?	12:58:48
12	A. It could be used for analysis of multiple	12:58:48
13	samples, and I believe it was used with some customers	12:58:49
14	for analysis of both tumor and normal samples and also	12:58:50
15	in some cases for samples from tumors and biopsies at	12:58:54
16	multiple time points.	12:59:05
17	I would say that -- when I'm saying that,	12:59:07
18	the -- the first product that we released in February	12:59:10
19	of 2013, we referred to as the "ACE Exome," but I	12:59:17
20	think it was called "Version 1."	12:59:17
21	Over the years, we had new versions of that	12:59:23
22	product. They became better and better	12:59:26
23	implementations of that product and added new	12:59:29
24	capabilities that were covered in other IP.	12:59:32
25	But when I say we worked with tumor versus	12:59:35

1 normal samples, multiple samples that way or multiple 12:59:39
2 time points, it would have been from either the 12:59:43
3 original product or the Version 2, Version 3, Version 12:59:46
4 4 of the product over the years. 12:59:51

5 Q. Was it marketed at launch as a product that 12:59:53
6 involved the analysis of multiple samples from single 12:59:56
7 individuals? 01:00:01

8 A. It was certainly marketed as a -- something 01:00:04
9 where you would analyze multiple samples that were 01:00:09
10 genetically related. 01:00:13

11 So, for example, it is common in genetic 01:00:16
12 medicine, where you have typically a child that's 01:00:20
13 afflicted with seizures or some terrible disease, to 01:00:25
14 then also sequence the parents because you're trying 01:00:29
15 to understand where the variants, genetic variants 01:00:31
16 came in from which parent and so forth. 01:00:34

17 And so that would be what's called a "family 01:00:37
18 trio," and those would be three related samples, and 01:00:39
19 so we certainly would have described that kind of 01:00:42
20 thing. 01:00:45

21 I don't remember specifically the brochures 01:00:45
22 we had and the presentations that we made. They were 01:00:49
23 pretty extensive presentations. 01:00:53

24 So we might have gone through a lot of 01:00:56
25 different applications of the product, but I don't 01:00:58

1	recall whether the commercial material -- what it	01:01:03
2	included. We hadn't been asked to review that or	01:01:04
3	present that. So it's not -- I haven't been over it	01:01:08
4	recently.	01:01:10
5	Q. Okay. So you don't know the answer?	01:01:10
6	A. I'm sorry?	01:01:12
7	Q. But you don't know the answer?	01:01:13
8	A. I don't -- I don't -- I can't answer that	01:01:15
9	question because I haven't reviewed the relevant	01:01:18
10	material recently.	01:01:22
11	Q. That would have been shorter, but you know,	01:01:22
12	it's where we're at.	01:01:25
13	When did Personalis start working on NeXT	01:01:27
14	Personal?	01:01:33
15	A. I would say Personalis progressively	01:01:33
16	developed the ideas that went into NeXT Personal over	01:01:48
17	the years. Obviously, many of the ideas are covered	01:01:51
18	in the patents that are in front of us here.	01:01:54
19	We filed additional patents in August of	01:01:56
20	2013, also in 2014, also in 2016, I believe. And --	01:01:59
21	and so all of those were elements that contributed to	01:02:06
22	the base of technologies we could draw on, and so	01:02:11
23	those are the things that, then, led to what became	01:02:17
24	NeXT Personal.	01:02:22
25	We did not work continuously from 2012 until	01:02:23

1 the product was released. We did not have a focused 01:02:29
2 product development effort during that whole time 01:02:33
3 trying to make just NeXT Personal. We had quite a few 01:02:36
4 other products. We had a lot of other priorities in 01:02:41
5 cancer, particularly to do with personal cancer 01:02:41
6 vaccines and what were called "neoantigens." 01:02:44

7 So those were other cancer areas that we 01:02:49
8 worked on. 01:02:51

9 And as we built expertise, different aspects 01:02:52
10 of our expertise were things that we, then, drew on 01:02:56
11 for the ultimate development of what became the NeXT 01:03:02
12 Personal product. 01:03:05

13 Q. When did Personalis begin its focused product 01:03:05
14 development efforts on NeXT Personal? 01:03:09

15 A. I don't recall exactly. Certainly, it was 01:03:13
16 after the January 2013 initial patent filing here. 01:03:16

17 Q. Turn please to Exhibit 2098. 01:03:55
18 (Exhibit 2098 was marked for identification.) 01:03:55

19 THE WITNESS: Can I set the patents aside for 01:04:00
20 the time being? 01:04:02

21 BY MR. HEINRICH: 01:04:04

22 Q. We're done with them. 01:04:04

23 A. So 2098? 01:04:40

24 Q. 2098. 01:04:42

25 A. Just to confirm, this is an e-mail that I 01:04:43

1	sent to Rich Chen and Carol Tillis Friday, October 19,	01:04:46
2	2012.	01:04:58
3	Q. Yes.	01:04:58
4	THE REPORTER: What was the date?	01:04:58
5	MR. HEINRICH: October 19, 2012.	01:04:58
6	BY MR. HEINRICH:	01:04:58
7	Q. And you state in your e-mail:	01:05:00
8	"I think we should consider ASAP	01:05:02
9	applying for a patent on our ideas related	01:05:05
10	to panels reflection to the exome, slash,	01:05:12
11	genome level as well as other directions	01:05:15
12	related to our exome plus and whole genome	01:05:19
13	plus."	01:05:21
14	Do you see that?	01:05:23
15	A. Yes, I do see that sentence.	01:05:24
16	Q. And that -- your idea here about applying for	01:05:25
17	a patent, that's what led to the filing of the	01:05:33
18	provisional application in January of 2013 that	01:05:39
19	ultimately led to the issuance of patents that include	01:05:46
20	the '394 and '033; correct?	01:05:51
21	MR. LUMAN: Objection; foundation,	01:05:55
22	mischaracterizes his testimony.	01:05:58
23	THE WITNESS: I -- I don't know that I can	01:05:59
24	say it led one for one to that because we might have	01:06:01
25	been thinking about other ideas that we, then, didn't	01:06:04

1 file on. We might have been thinking about those 01:06:07
2 ideas. 01:06:10
3 But certainly this is a few months 01:06:10
4 beforehand, and in general, we were thinking that it 01:06:12
5 was time to start formalizing our IP in terms of 01:06:16
6 filings. 01:06:21
7 You can see in the -- one of the last 01:06:21
8 paragraphs here -- it's very short -- it says: 01:06:25
9 "I think the trade secret approach 01:06:27
10 would be too restrictive in terms of what 01:06:29
11 we would eventually tell customers." 01:06:32
12 And so this meant that was -- that was an 01:06:35
13 alternative, possible approach to us for IP, was to 01:06:36
14 handle things as trade secrets. 01:06:40
15 And people debated the merits of trade 01:06:43
16 secrets versus disclosure in patents, and in this 01:06:46
17 e-mail, I was weighing in, saying, I think, given that 01:06:49
18 we were going to want to describe our product to the 01:06:51
19 customers and we're now -- we were only a few months 01:06:55
20 away from launching what was going to be our first 01:06:58
21 product, I felt it was important not to rely on the 01:07:00
22 trade secret approach and to make filings. 01:07:03
23 And then prior to our -- the launch of our 01:07:07
24 first product in February of 2013, the first assay 01:07:11
25 product, the month before that in January of 2013, we 01:07:17

1	did file our first provisional, and that provisional	01:07:22
2	ultimately led to the two patents being discussed here	01:07:25
3	today.	01:07:29
4	BY MR. HEINRICH:	01:07:29
5	Q. Was any work done on drafting that first	01:07:29
6	provisional in January of 2013 you just referenced	01:07:36
7	prior to your e-mail on October 19, 2012?	01:07:40
8	MR. LUMAN: That calls for privileged	01:07:48
9	information. I'll instruct him not to answer.	01:07:50
10	MR. HEINRICH: You're -- you're relying on a	01:07:54
11	constructive reduction to practice, and you're going	01:07:56
12	to block me from inquiring on when work started on the	01:07:59
13	patent application that you're relying on for	01:08:06
14	constructive reduction of practice?	01:08:15
15	MR. LUMAN: I'm just looking at the question.	01:08:16
16	THE WITNESS: I'm sorry. I didn't really	01:08:21
17	follow what you just said, or if you need a minute.	01:08:23
18	MR. LUMAN: But you're asking about was any	01:08:26
19	work -- drafting done on the patent application. And	01:08:28
20	work done on drafting a patent application, that's	01:08:34
21	privileged.	01:08:38
22	MR. HEINRICH: Well, you've put at issue the	01:08:38
23	filing -- work and filing of the provisional	01:08:43
24	application. So I'm entitled to know when that work	01:08:46
25	started.	01:08:49

1	MR. LUMAN: The work on the provisional	01:08:52
2	application?	01:08:54
3	MR. HEINRICH: Yes, yes.	01:08:54
4	MR. LUMAN: The question you asked is calling	01:09:01
5	for privileged information. Maybe you can do a	01:09:03
6	different question that doesn't call for privileged	01:09:06
7	information.	01:09:11
8	MR. HEINRICH: I'm not asking for the	01:09:11
9	contents of any attorney-client communication. I'm	01:09:12
10	asking for information on when an act started. The	01:09:16
11	act of drafting. That's not privileged in any	01:09:18
12	conceivable legal sense.	01:09:26
13	MR. LUMAN: Can you re-ask your question	01:09:28
14	specifically?	01:09:30
15	BY MR. HEINRICH:	01:09:31
16	Q. Was any work done in actually drafting the	01:09:31
17	provisional application that you're relying on for	01:09:35
18	your constructive reduction to practice prior to	01:09:40
19	October 19, 2012?	01:09:45
20	A. I'm sorry. I don't know what "constructive	01:09:48
21	reduction to practice" means.	01:09:53
22	I think I do know what you mean by did we	01:09:54
23	start drafting the patent.	01:09:57
24	Q. That's what I'm asking.	01:09:57
25	A. But I don't know what all the other words you	01:10:00

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1	just used mean.	01:10:02
2	Q. Let me ask it again.	01:10:02
3	A. And if you can do it -- more lay terms would	01:10:02
4	be fine.	01:10:06
5	Q. Fine. Was there any work done on drafting	01:10:06
6	the January 2013 provisional application prior to your	01:10:08
7	e-mail on October 19, 2012?	01:10:13
8	A. So I don't know what we have in terms of	01:10:26
9	documentation of that or whether there's any of that	01:10:29
10	in the disclosures here, but let me finish answering.	01:10:31
11	I know that the -- the process of being	01:10:35
12	prepared to file with the U.S. Patent Office would	01:10:40
13	have started with writing an invention disclosure and	01:10:44
14	having, like, an internal invention disclosure form,	01:10:49
15	and then you would begin building the pieces that	01:10:53
16	would go into writing a patent.	01:10:55
17	And the -- I recall that earlier than this we	01:10:58
18	had begun the process of having a patent disclosure	01:11:04
19	form at least set up. If I recall correctly, it was	01:11:09
20	Mark Pratt who is one of the coinventors here.	01:11:14
21	Mark had a lot of IP. He wasn't an attorney	01:11:18
22	by any means, but he had just invented a lot of stuff	01:11:21
23	over the years that was patented, and so I think he --	01:11:24
24	he was an advocate for beginning to have the process	01:11:29
25	and so forth.	01:11:29

1 So probably in the summer of 2012, we would 01:11:33
2 have started some of that kind of thing, and some of 01:11:37
3 the content that would have gone into the provisional 01:11:41
4 application. There are extensive tables, for example, 01:11:44
5 there. 01:11:44

6 Those tables would have been being prepared, 01:11:47
7 not just for the purposes of drafting a patent, but 01:11:50
8 for the process of designing the product. 01:11:53

9 And so the -- I'm not sure I can answer 01:11:55
10 exactly when what -- what you would actually call a 01:12:01
11 patent application draft, but certainly materials that 01:12:03
12 then -- you know, people weren't starting from scratch 01:12:07
13 when they sat down to actually write whatever the 01:12:10
14 patent was. 01:12:13

15 There was a lot of material to draw on, and 01:12:14
16 that material was material that came from the product 01:12:16
17 development, which was going on through most of 2012. 01:12:19

18 So I would expect that -- you know, if you 01:12:23
19 see these -- patents are 50 or 60 pages, and they have 01:12:26
20 a lot of technical detail and examples and tables and 01:12:30
21 so forth, that would have come from the kind of work 01:12:34
22 that we were doing throughout 2012. 01:12:38

23 So that's a -- it doesn't really separate out 01:12:40
24 the patent drafting process as a -- like a word 01:12:44
25 document from the process of coming up with the 01:12:48

1	content for it, but I'd say those were kind of --	01:12:51
2	tended to be the same people working on them both. So	01:12:55
3	I'm not sure we really separated it out.	01:12:59
4	At some point it became more formalized as	01:13:02
5	the patent application, but the content was being	01:13:05
6	developed all through 2012 as we explored all the	01:13:09
7	different aspects of what we wanted to do in the	01:13:13
8	patent and all of the specifics that are called out.	01:13:16
9	So I feel like it was -- the development of	01:13:19
10	the first filing happened over the course of 2012.	01:13:23
11	Whether that officially got called a "draft" document	01:13:28
12	for the patent, I don't remember what date that would	01:13:33
13	have been more formalized.	01:13:36
14	Q. Do you recall receiving a response to your	01:13:38
15	e-mail to the effect of, "Gosh, John, the process of	01:13:41
16	putting together a patent application is already well	01:13:45
17	underway"?	01:13:48
18	A. I don't recall what responses there were to	01:13:49
19	this e-mail.	01:13:55
20	Q. Was any of the development work that you	01:13:58
21	referenced performed for the specific intention of	01:14:04
22	including it in a patent application prior to your	01:14:07
23	e-mail here in October of 2012?	01:14:11
24	A. We, generally, did not do work specifically	01:14:17
25	for the purposes only of including it in a patent	01:14:20

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1	application.	01:14:23
2	I would say the company was primarily focused	01:14:23
3	on developing a product, and then the patent	01:14:26
4	application was to protect that product, and the --	01:14:29
5	and the -- the technological base that underlay it.	01:14:32
6	But the efforts of the company were almost	01:14:36
7	entirely focused on developing a product, and then the	01:14:39
8	patent was -- the patent application was a bit of a	01:14:42
9	side product from the core focus, which was on the	01:14:44
10	product only.	01:14:47
11	Q. Now, this October 19, 2012, e-mail is the	01:14:48
12	first instance that we've seen in the documentation	01:14:55
13	that is provided to us in connection with your	01:14:59
14	declaration of a reference to, "Hey, let's, you know,	01:15:03
15	write up a patent application."	01:15:07
16	Are you aware of any earlier decision point	01:15:09
17	where Personalis decided to pursue a patent	01:15:14
18	application that ultimately resulted in the	01:15:25
19	January 2013 provisional one?	01:15:27
20	MR. LUMAN: That's privileged. I'll instruct	01:15:28
21	him not to answer that.	01:15:36
22	MR. HEINRICH: Okay. We'll hold that against	01:15:36
23	you, constructive reduction to practice.	01:15:40
24	MR. LUMAN: Constructive reduction to	01:15:40
25	practice is his -- his filing the patent application.	01:15:40

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1	MR. HEINRICH: And I'm going to tell you	01:15:41
2	we're going to hold your privilege instruction against	01:15:41
3	you in connection with your arguments on diligence.	01:15:43
4	I just want to make that clear we're going to	01:15:46
5	take that position.	01:15:49
6	MR. LUMAN: How are you going to do that?	01:15:50
7	MR. HEINRICH: Well, I'm not going to get	01:15:52
8	into a discussion on that. I just want you to know	01:15:53
9	our position. So I'm -- so I want to give you the	01:15:55
10	opportunity to withdraw your instruction if you'd	01:16:00
11	like. You don't have to. I just want to give you	01:16:03
12	notice.	01:16:07
13	MR. LUMAN: Yeah, that's asking for	01:16:12
14	privileged information.	01:16:14
15	MR. HEINRICH: Okay. Excellent.	01:16:15
16	BY MR. HEINRICH:	01:16:26
17	Q. Do you know as a matter of fact that there	01:16:27
18	was an invention disclosure form submitted on which	01:16:29
19	the January 2013 provisional was ultimately based?	01:16:34
20	A. I don't know. I know that the -- like, a	01:16:40
21	blank form was created at some earlier point. Like,	01:16:45
22	if somebody has an invention, they should fill out	01:16:49
23	this form. I don't recall whether anybody actually	01:16:51
24	filled it out for this before that. They may have,	01:16:54
25	but I don't know.	01:16:57

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1	Q. I want to turn to page 103 of your	01:17:05
2	declaration.	01:17:08
3	A. I'm sorry. I'm happy to go wherever. I just	01:17:10
4	didn't quite hear where you want me to go.	01:17:16
5	Q. Page 103.	01:17:20
6	A. Page 103 of my declaration, not an exhibit.	01:17:22
7	Okay. I'm looking at page 103 of the -- my	01:17:49
8	declaration. Somewhere in there it has paragraph 166.	01:17:53
9	Is that what you're looking at?	01:18:03
10	Q. So it's directing you to the first line of	01:18:05
11	the page here. It says:	01:18:10
12	"At least Mark Pratt and I were aware	01:18:14
13	that it was possible to multiplex multiple	01:18:17
14	samples into each lane -- lane of a	01:18:22
15	sequencing instrument flow cell by adding	01:18:25
16	a DNA barcode to the end of each molecule	01:18:27
17	of DNA" --	01:18:31
18	A. I'm sorry. I thought we were starting with	01:18:32
19	paragraph 166, but that's not --	01:18:35
20	Q. No, I said --	01:18:36
21	A. Are you above that?	01:18:38
22	Q. The first line of the page.	01:18:39
23	A. First line of the page. Okay. I'm sorry.	01:18:40
24	Okay. I see, yeah, "At least Mark Pratt and I."	01:18:42
25	Sorry.	01:18:47

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1 Q. Why don't you just go ahead and read that to 01:18:48
2 yourself so I don't have to repeat it. 01:18:51
3 A. So I've read that -- everything down to where 01:19:55
4 it says, "166." 01:19:58
5 Q. So I want to just make sure we have a common 01:19:59
6 understanding of where in the work flow this step 01:20:12
7 would happen. Okay? 01:20:19
8 So let's take a work flow that -- like yours 01:20:20
9 uses the Agilent biotinylated SureSelect probes. 01:20:27
10 A. Okay. 01:20:35
11 Q. So prior to the step we're talking about here 01:20:35
12 at the top of page 103, the DNA of interest would be 01:20:39
13 pulled down from your sample using the Agilent 01:20:47
14 biotinylated probes; correct? 01:20:54
15 A. No. 01:20:59
16 Q. The DNA of interest would have to be pulled 01:20:59
17 down from the sample before it's sequenced; right? 01:21:04
18 A. Yes. 01:21:08
19 Q. Okay. So you're talking here about -- what 01:21:09
20 you're talking about here at the top of 103 is a step 01:21:17
21 where the DNA has been pulled down and is now about to 01:21:21
22 be sequenced on the instrument; right? 01:21:27
23 A. No. 01:21:29
24 Q. You're talking about multiplexing multiple 01:21:30
25 samples into each lane of a sequencing instrument flow 01:21:40

1	cell; correct?	01:21:46
2	A. Yes.	01:21:47
3	Q. The DNA has already been captured before it	01:21:47
4	goes onto a flow cell; isn't that fair?	01:21:52
5	A. The DNA is captured before it goes onto the	01:21:54
6	flow cell, yes.	01:21:58
7	Q. So after the DNA is captured, the Agilent	01:21:59
8	probes are alluded or washed away; correct?	01:22:04
9	A. So after the DNA has been captured. That's	01:22:09
10	not what this paragraph is talking about. This	01:22:17
11	paragraph is not talking about capture. This	01:22:20
12	paragraph is talking about barcodes.	01:22:24
13	Q. So we'll come back to the paragraph. Just	01:22:27
14	focus on my questions. Okay?	01:22:34
15	So after DNA is captured, the capture	01:22:36
16	probes -- in this example the Agilent SureSelect	01:22:42
17	probes -- are washed away, and the DNA that's been	01:22:46
18	captured, sequenced; correct?	01:22:50
19	A. There are other steps, but yes, those two --	01:22:52
20	those steps do happen.	01:22:58
21	Q. First there's capture, and then the capture	01:22:59
22	probes are alluded, and then the DNA is sequenced;	01:23:03
23	correct?	01:23:11
24	A. I'm not sure you'd quite use the term that	01:23:12
25	the capture probes are alluded because the capture	01:23:15

1	probes are typically attached to the molecule.	01:23:20
2	It might be that the correct terminology	01:23:24
3	might be that the DNA, which has been captured after	01:23:25
4	it's been separated by being pulled out, that DNA is	01:23:28
5	alluded off of the beads.	01:23:31
6	Q. Fair enough.	01:23:33
7	A. It's a question of which is alluded off of --	01:23:34
8	Q. Yeah, yeah, yeah. Okay.	01:23:35
9	A. -- which. But the word "alluding" --	01:23:35
10	Q. Yeah, yeah, yeah.	01:23:35
11	A. -- usually refers to the thing that ends up	01:23:35
12	in solution, whereas the beads and the probes might	01:23:38
13	not be in solution. It's the DNA that we're trying to	01:23:41
14	capture that ends up in solution and goes on into the	01:23:44
15	sequencing process.	01:23:49
16	Q. Thank you. My question was fuzzy. So I	01:23:50
17	appreciate that.	01:23:52
18	A. But so far what you said, it doesn't have	01:23:52
19	anything to do with the paragraph you pointed me to.	01:23:55
20	Q. So the -- we talked about this earlier. The	01:23:57
21	probes that you used or the biotinylated Agilent	01:24:04
22	probes that would pull down the DNA so we would have	01:24:10
23	the bead with the probe magnetized to it with the	01:24:14
24	captured DNA; correct?	01:24:23
25	A. The probe is not magnetized. The bead is	01:24:25

1	magnetized.	01:24:29
2	Q. The probe is attached to the bead, to the	01:24:31
3	biotin streptavidin relationship?	01:24:35
4	A. It is attached through the -- the probe has	01:24:35
5	the biotin on it. That binds to streptavidin, which	01:24:38
6	is covalently bound to the bead, and the bead has --	01:24:43
7	in the interior of the bead has paramagnetic material	01:24:47
8	which can then be pulled out.	01:24:53
9	Q. So at that point, the DNA that's been	01:24:54
10	captured is alluded for subsequent sequencing;	01:24:57
11	correct?	01:25:03
12	A. Yes.	01:25:04
13	Q. And as part of that next series of steps that	01:25:04
14	results in sequencing of the captured DNA, barcodes	01:25:12
15	can be ligated to the DNA molecules to be sequenced;	01:25:19
16	correct?	01:25:25
17	A. No.	01:25:25
18	Q. That's incorrect?	01:25:26
19	A. That's incorrect.	01:25:27
20	Q. So how's that incorrect?	01:25:32
21	A. The barcodes are generally added to the --	01:25:35
22	during the library prep process prior to the hybrid	01:25:39
23	capture.	01:25:43
24	Q. And so the -- what's the point of using the	01:25:45
25	barcodes?	01:25:52

1	A. It is to be able to process samples together	01:25:53
2	and have the data at the end be demultiplexed so that	01:25:58
3	even though all the sequence reads end up coming out	01:26:04
4	together from the sequencing instrument, by looking at	01:26:07
5	a portion of a sequence read, which is the portion	01:26:11
6	that has the barcode, you can identify which sample	01:26:15
7	that sequence read came from even though they were all	01:26:18
8	processed together on the same sequencer.	01:26:22
9	And if you didn't have a barcode, all of the	01:26:24
10	data would be mixed together, and you wouldn't know	01:26:26
11	which came from which sample.	01:26:28
12	Q. So the barcodes are sequenced along with the	01:26:30
13	DNA catch; correct?	01:26:35
14	A. They are part of the molecule which is	01:26:37
15	sequenced.	01:26:40
16	Q. Correct. The capture probes themselves --	01:26:41
17	and we're talking about these Agilent pull down	01:26:49
18	probes. The capture probes themselves are not	01:26:53
19	sequenced; correct?	01:26:55
20	A. No. The capture probes are not sequenced.	01:26:56
21	It's the DNA that you have captured which is	01:26:59
22	sequenced.	01:27:02
23	Q. Right. But the barcodes are sequenced?	01:27:02
24	A. Yes, they are part of the molecule. They're	01:27:06
25	not part of the capture probe.	01:27:10

1	Q. Right. So the barcodes are not part of the	01:27:12
2	capture probes. They're part of the molecule that's	01:27:14
3	being sequenced; correct?	01:27:17
4	A. Yes, that's correct.	01:27:19
5	MR. HEINRICH: So I think that's all I have	01:27:25
6	obviously subject to redirect.	01:27:27
7	MR. LUMAN: Okay. Let's go off the record.	01:27:29
8	THE VIDEOGRAPHER: We're going off the	01:27:41
9	record. The time is 1:27.	01:45:45
10	(Recess taken.)	02:28:16
11	THE VIDEOGRAPHER: We're back on the record.	02:28:16
12	The time is 2:28 p.m.	02:28:38
13	EXAMINATION	02:28:42
14	BY MR. LUMAN:	02:28:42
15	Q. Mr. West, do you remember being asked	02:28:43
16	questions about PCR primers earlier today?	02:28:46
17	A. Yes, I do.	02:28:49
18	Q. Do you remember being asked whether you ever	02:28:50
19	tried to use PCR primers to capture DNA for	02:28:52
20	sequencing?	02:28:57
21	A. That's not what I remember thinking the	02:28:57
22	question was at the time. I've seen a preliminary	02:29:00
23	draft transcript of the session and now understand	02:29:04
24	that the question did include that term, "capture."	02:29:07
25	And so I guess I would clarify that PCR is	02:29:11

1 not a capture process. It makes copies of the DNA, 02:29:15
2 and that in PCR, it wouldn't be unusual that the 02:29:20
3 original molecule that created all the copies doesn't 02:29:24
4 even end up in the result at all. All you end up with 02:29:27
5 is the copies. 02:29:31

6 And so I don't consider PCR to be a capture 02:29:32
7 process, and I wouldn't use that term. 02:29:35

8 We have used PCR, not to capture, but just to 02:29:39
9 amplify DNA so that it can be selectively sequenced, 02:29:43
10 but I wouldn't use the term "capture." 02:29:48

11 MR. LUMAN: No further questions. 02:29:50

12 EXAMINATION 02:29:52

13 BY MR. HEINRICH: 02:29:52

14 Q. Okay. So after my questioning ended at 02:29:53
15 1:27 p.m., you and counsel took over an hour break; is 02:29:57
16 that right? 02:30:02

17 A. I don't know. I didn't keep track of the 02:30:02
18 time. I'm sorry. 02:30:04

19 Q. We started here at 2:28. So an hour and one 02:30:05
20 minute; correct? 02:30:10

21 A. I don't know what the time was. As I said, I 02:30:10
22 didn't keep time. You sound like you kept track. So 02:30:13
23 if you want to make a statement, you can make a 02:30:15
24 statement. 02:30:15

25 You can't ask me, "correct," because I can't 02:30:20

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1 verify that. I didn't -- somebody else could verify 02:30:21
2 it, but I -- I just didn't keep any records of that. 02:30:23
3 Q. So during this long break, you and your 02:30:24
4 counsel discussed the fact that you agreed that PCR 02:30:29
5 primers captured DNA; correct? That was your 02:30:38
6 testimony earlier today? 02:30:41
7 MR. LUMAN: Objection; mischaracterizes his 02:30:43
8 testimony. 02:30:45
9 THE WITNESS: So I discussed a number of 02:30:45
10 things with my -- with our counsel. I don't know if 02:30:47
11 it's appropriate for me to be discussing materials 02:30:49
12 that I discussed with our counsel. 02:30:52
13 BY MR. HEINRICH: 02:30:55
14 Q. You've seen references to PCR primers 02:31:00
15 capturing DNA in the literature, haven't you? 02:31:10
16 A. I -- I don't recall any. It's -- there 02:31:13
17 are -- lots of things can be in the literature. It 02:31:16
18 doesn't make them technically correct. 02:31:19
19 And so what actually happens in PCR -- this 02:31:21
20 was developed by Kary Mullis back in the '80s -- was 02:31:25
21 that you make a copy going in one strand and then a 02:31:29
22 copy going in the other strand. 02:31:32
23 You can end up with hundreds of thousands of 02:31:34
24 copies, and generally, all of those copies are the 02:31:37
25 same length, and they are generally all shorter than 02:31:39

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1	the original molecule.	02:31:43
2	And as a result, if you have any kind of a	02:31:45
3	size selection process later on in your sample prep,	02:31:47
4	the original molecule typically would get left out,	02:31:51
5	and all you'd end up with being left for the	02:31:54
6	sequencing would be the -- the copies, not anything	02:31:57
7	that's been captured.	02:32:01
8	I tend to think of a capture as being	02:32:02
9	something -- where there's something out there, and I	02:32:05
10	go get it as opposed to that I go make Xerox copies of	02:32:07
11	it and keep the Xerox copies.	02:32:12
12	Q. That's how you think of capture?	02:32:14
13	A. I think of capture as being something where I	02:32:16
14	go get something. I'm going to capture something	02:32:18
15	that's out there whereas opposed to I'm going to go	02:32:20
16	synthesize something new and make many copies of a --	02:32:23
17	an original.	02:32:26
18	Q. Do the claims of the '394 and '033 patents	02:32:27
19	require sequencing the original DNA molecules in the	02:32:34
20	sample?	02:32:40
21	MR. LUMAN: Calls for a legal conclusion.	02:32:41
22	THE WITNESS: The claims do not require	02:32:42
23	sequencing the original molecule. However, that	02:32:47
24	doesn't make capture and targeted PCR the same.	02:32:52
25	BY MR. HEINRICH:	02:32:56

1	Q. In fact, just using an Illumina sequencer	02:32:57
2	involves making CAD copies of the DNA that you want to	02:33:03
3	sequence; correct?	02:33:07
4	MR. LUMAN: Objection; foundation.	02:33:08
5	THE WITNESS: I think the question is not	02:33:10
6	quite right because there are two different kinds of	02:33:12
7	PCR amplification involved. One is PCR amplification	02:33:15
8	of a specific genomically specific target, and that's	02:33:20
9	one thing.	02:33:24
10	And then, as a separate thing, where you put	02:33:25
11	a -- an adaptor on the molecule so that every molecule	02:33:27
12	has the same tail, and then the PCR primer just target	02:33:31
13	the tail. And that's different from using PCR to	02:33:37
14	selectively amplify just one part of the genome.	02:33:40
15	So those are different things, and I think	02:33:46
16	it's important to separate them out and not conflate	02:33:47
17	them when it really isn't the same thing.	02:33:52
18	Q. The claims of the '394 and '033 patents don't	02:33:55
19	require sequencing the original DNA in this sample;	02:34:02
20	correct?	02:34:04
21	MR. LUMAN: Asked and answered, foundation.	02:34:04
22	THE WITNESS: So the claims of the '033	02:34:05
23	patent and the '394 patent do not call for sequencing	02:34:07
24	the original molecules from the sample, but there is a	02:34:14
25	difference between site specific amplification, PCR	02:34:19

1 amplification of a particular type of the genome and 02:34:26
2 just broadly amplifying everything in a sequencing 02:34:31
3 library. Those should not be treated as being the 02:34:34
4 same thing. 02:34:37

5 MR. HEINRICH: I'm done. No more questions. 02:34:44

6 MR. LUMAN: I would like to mark the 02:34:52
7 transcript "Confidential" now, and I want everybody to 02:34:54
8 make sure we can get as much unredacted as possible. 02:35:00

9 MR. HEINRICH: -- 02:35:02

10 THE VIDEOGRAPHER: We're going off the 02:35:03
11 record. The time is 2:35 p.m., and this concludes the 02:35:05
12 testimony given by John West. 02:35:09

13 (Whereupon, the December 8, 2023, deposition of
14 JOHN WEST ended at 2:35 p.m.)

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1 R E P O R T E R' S C E R T I F I C A T E

2 I, R. CHAYO AYON, duly authorized to
3 administer oaths pursuant to Section 2093(b) of the
4 California Code of Civil Procedure, do hereby certify
5 that the witness in the foregoing deposition was by me
6 duly sworn to testify the truth in the within-entitled
7 cause; that said deposition was taken at the time and
8 place therein cited; that testimony of said witness
9 was reported by me and thereafter transcribed under my
10 direction into typewriting; that the foregoing is a
11 complete and accurate record of said testimony; and
12 that the witness was given an opportunity to read and
13 correct said deposition and to subscribe the same.

14 Should the signature of the witness not be
15 affixed to the deposition, the witness shall not have
16 availed himself/herself of the opportunity to sign or
17 the signature has been waived.

18 I further certify that I am not of counsel nor
19 attorney for any of the parties in the foregoing
20 deposition and caption named nor in any way interested
21 in the outcome of the cause named in said caption.

22 DATED: DECEMBER 13, 2023

23

24 R. CHAYO AYON
 Certified Shorthand Reporter
25 Certificate No. 12372

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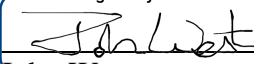
ERRATA SHEETCase Name: *Foresight Diagnostics Inc. v. Personalis, Inc.*

Date: December 8, 2023

Deponent: John West

Page(s)	Line(s)	Change	Reason
44	12	“DEGAPed” to “degapped”	Misspelling
44	17	“DEGAPed” to “degapped”	Misspelling
49	8	“helpful or understanding” to “helpful for understanding”	Incorrect transcription
71	5	“nexgen” to “nextgen”	Misspelling
73	6	“Lite Ion Proton” to “Life Ion Proton”	Misspelling
74	3	“Lise Ion Proton” to “Life Ion Proton”	Misspelling
84	21	“Celexa” to “Solexa”	Misspelling
87	3	“nexgen” to “nextgen”	Misspelling
87	5	“nexgen” to “nextgen”	Misspelling
90	16	“Celexa” to “Solexa”	Misspelling

Dated: 12/20/2023

DocuSigned by:

 John West