

UNITED STATES PATENT AND TRADEMARK OFFICE

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BEFORE THE PATENT TRIAL AND APPEAL BOARD

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ILLUMINA INC.,  
Petitioner,

v.

MOLECULAR LOOP BIOSCIENCES, INC.,  
Patent Owner.

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IPR2024-00964  
Patent 11,041,852 B2

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Before ERICA A. FRANKLIN, ZHENYU YANG, and  
ROBERT A. POLLOCK, *Administrative Patent Judges*.

YANG, *Administrative Patent Judge*.

DECISION  
Granting Institution of *Inter Partes* Review  
35 U.S.C. § 314

## I. INTRODUCTION

Illumina, Inc. (“Petitioner”) filed a Petition (Paper 1, “Pet.”) seeking *inter partes* review of claims 1–8 of U.S. Patent No. 11,041,852 B2 (Ex. 1001, “the ’852 patent”). Molecular Loop Biosciences, Inc. (“Patent Owner”) filed a Preliminary Response. Paper 6 (“Prelim. Resp.”).

We have authority under 35 U.S.C. § 314, which provides that an *inter partes* review may not be instituted “unless . . . there is a reasonable likelihood that the petitioner would prevail with respect to at least 1 of the claims challenged in the petition.” 35 U.S.C. § 314(a).

For the reasons provided below, we determine Petitioner has satisfied the threshold requirement set forth in 35 U.S.C. § 314(a). Accordingly, we institute *inter partes* review of all challenged claims based on the ground raised in the Petition.

### A. *Related Matters*

According to the parties, the ’852 patent is involved in the following litigations: *Molecular Loop Biosciences, Inc. v. Illumina, Inc. et al.*, No. 1:24-cv-00680 (D. Del.) and *Illumina, Inc. et al. v. Molecular Loop Biosciences, Inc.*, No. 1:24-cv-11501 (D. Mass.). Pet. 64–65; Paper 3, 1.

Petitioner filed IPR2024-00965, challenging the claims of U.S. Patent No. 11,768,200, a patent in the same family as the ’852 patent. Pet. 65.

### B. *The ’852 patent*

The ’852 patent relates generally to “methods for maintaining the integrity and identification of a nucleic acid template in a multiplex sequencing reaction.” Ex. 1001, Abstract. The methods include the steps of “obtaining a template nucleic acid, incorporating a pair of sequence identifiers into the template, and sequencing the template.” *Id.*

According to the '852 patent, maintaining accurate sample identification during a multiplex sequencing reaction is problematic because “the sample preparation phase frequently introduces errors into the subsequent sequencing reaction.” *Id.* at 1:37–39. “For example, template molecules may physically overlap on a substrate; and in some cases result in a detectable erroneous signal.” *Id.* at 1:39–41; *see also id.* at 1:52–54 (stating that errors can be introduced from “improper pairing of template strands from different samples,” which can “form during the amplification of the multiplexed samples”). Because these errors have a significant effect on the results, the '852 patent states that “methods for reducing or eliminating errors in such procedures are needed.” *Id.* at 1:60–62.

The '852 patent explains the undesired introduction of sequencing errors when using a single barcode identifier. *See id.* at 4:17–63, Fig. 1 (showing “one example of how molecular overlap can lead to apparent high quality, but incorrect sequence data”). The '852 patent states that its method uses “two or more identifiers that are uniquely associated with an analyte of interest, such that the identifiers will only be present when the analyte of interest is detected.” *Id.* at 2:5–8. According to the '852 patent, “[i]n this way, false positive and/or false negative results are avoided by requiring concomitant detection of two or more independent markers associated with the analyte to be detected.” *Id.* at 2:8–11.

The '852 patent states that, using two or more nucleic acid barcodes as identifiers, its method is especially useful in multiplex next-generation sequencing. *Id.* at 2:12–18. The '852 patent explains that:

in sequencing applications, a pair of barcodes are placed such that they flank the sequence of interest. The identifiers are unique to the sample, so that valid sequence data are confirmed

by the presence of the pair of flanking identifiers. In contrast, template containing only one identifier or an incorrect pair (i.e., a pair or more of identifiers not associated with the same template) will be excluded from analysis. Thus, methods of the invention make it possible to determine whether the integrity of a sample was maintained during a multiplex sequencing reaction, and prevent the assigning of sequence data to the wrong sample.

*Id.* at 2:18–29; *see also id.* at 4:64–6:6 (describing Figure 2 show “how methods of the invention allow one to detect, during analysis, whether the integrity of a patient's sample was maintained during a multiplex sequencing reaction”), Fig. 2.

### *C. Illustrative Claim*

Of the challenged claims, only claim 1 is independent. Claim 1 is illustrative of the claimed subject matter and is reproduced below.

1. A method for reducing template cross-over error introduced during sequencing workflow, the method comprising the steps of

incorporating at least two members of a plurality of identifier sequences into template nucleic acids obtained from at least two different samples, wherein said two members constitute a distinct pair associated with said template;

combining said nucleic acid templates into a single sample;

amplifying said nucleic acid templates on a surface of a flow cell thereby to form clusters, at least one of which comprises a chimeric sequence comprising a combination of identifier sequences that are different than any of said distinct pairs;

sequencing amplicons obtained in said amplifying step; and

discarding sequence reads obtained in said sequencing step that contain said combination of identifier sequences that are different than any of said distinct pairs, thereby to reduce cross-over error.

Ex. 1001, 20:65–21:19.

*D. Asserted Challenges to Patentability*

Petitioner asserts the following challenges to patentability:

| Claims Challenged | 35 U.S.C. § <sup>1</sup> | References                                    |
|-------------------|--------------------------|-----------------------------------------------|
| 1–6               | 103                      | Parameswaran, <sup>2</sup> Gloor <sup>3</sup> |
| 1–6               | 103                      | Parameswaran, Bentley <sup>4</sup>            |

As support for its patentability challenge, Petitioner relies on the Declarations of Gregory B. Gloor, Ph.D. (Ex. 1002) and Paul T. Spellman, Ph.D. (Ex. 1003).

**II. ANALYSIS**

*A. Claim Construction*

In an *inter partes* review, we construe a claim term “using the same claim construction standard that would be used to construe the claim in a civil action under 35 U.S.C. [§] 282(b).” 37 C.F.R. § 42.100(b) (2020). Under that standard, the words of a claim “are generally given their ordinary and customary meaning,” which is “the meaning that the term would have to a person of ordinary skill in the art in question at the time of the invention,

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<sup>1</sup> The Leahy-Smith America Invents Act (“AIA”), Pub. L. No. 112-29, 125 Stat. 284, 287–88 (2011), amended 35 U.S.C. § 103, effective March 16, 2013. On its face, the ’852 patent claims priority to several applications filed before the effective date of AIA. Ex. 1001, code (60). Accordingly, we apply the pre-AIA version of §§ 102 and 103.

<sup>2</sup> P. Parameswaran, et al., *A pyrosequencing-tailored nucleotide barcode design unveils opportunities for large-scale sample multiplexing*, 35 NUCLEIC ACIDS RSCH, 19(e130) (2007) (Ex. 1004, “Parameswaran”).

<sup>3</sup> G.B. Gloor, et al., *Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products*, Cornell University Library, arXiv:1007.5075v1 (2010) (Ex. 1005, “Gloor”).

<sup>4</sup> D.R. Bentley, et al., *Accurate whole human genome sequencing using reversible terminator chemistry*, 456 NATURE 6, 53–59 (2008) (Ex. 1006, “Bentley”).

i.e., as of the effective filing date of the patent application.” *Phillips v. AWH Corp.*, 415 F.3d 1303, 1312–13 (Fed. Cir. 2005) (en banc).

Petitioner proposes that we construe the term “template cross-over error” to mean “sequences of chimeric molecules made from template nucleic acids derived from different samples.” Pet. 22–23 (citing Ex. 1001, 5:41–6:6, 6:53–7:38; Ex. 1003 ¶ 122). For purposes of its Preliminary Response, Patent Owner “does not set forth an alternative claim construction.” Prelim. Resp. 16. On the current record, we adopt Petitioner’s proposed construction because it appears consistent with the claim language and specification of the ’852 patent.

On this record and for purposes of this Decision, we see no need to expressly construe any claim term. *See Vivid Techs., Inc. v. Am. Sci. & Eng’g, Inc.*, 200 F.3d 795, 803 (Fed. Cir. 1999) (stating that only claim terms that are in controversy need construed and only to the extent necessary to resolve the controversy).

*B. Alleged Obviousness over Parameswaran and Gloor*

Petitioner asserts that claims 1–8 would have been obvious over the combination of Parameswaran and Gloor. Pet. 23–51. Based on this record, and for at least the following reasons, we determine Petitioner has established a reasonable likelihood that it would prevail in this assertion.

1. Parameswaran

Parameswaran is titled “A pyrosequencing-tailored nucleotide barcode design unveils opportunities for large-scale sample multiplexing.” Ex. 1004, 1. Parameswaran uses 454/Roche Genome Sequencers for sequencing. *Id.* The technology of these pyrosequencers is based on the detection of pyrophosphates released during DNA synthesis. *Id.*

Parameswaran describes “a high-information-content barcoding approach in which each sample is associated with two uniquely designed, 10-nucleotide barcodes.” *Id.* at 2. According to Parameswaran, “[t]he presence of these assigned barcodes allow for independent samples to be pooled together for sequencing, with subsequent bioinformatic segregation of the pyrosequencer output.” *Id.* In addition to barcodes, Parameswaran incorporated forward and reverse cloning linkers into nucleic acids. *Id.* at 2–3.

Figure 1 of Parameswaran, reproduced below, depicts the design of forward and reverse primers. *Id.* at 3.

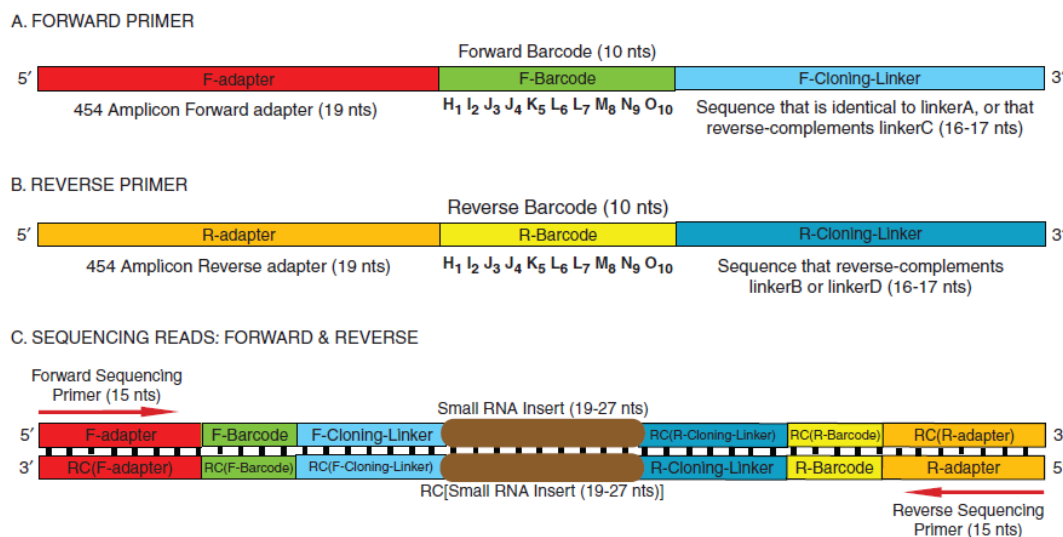


Figure 1. Design of forward and reverse primers. The synthesized primers are 45–46 nt long. (A and B) The template for the primers is: 454-Adapter:: Barcode:: Linker-Primer. Individual specifications for forward and reverse barcodes are also indicated. (C) Diagrammatic representation of the GS20 forward and reverse sequencing reads. ‘RC’ stands for Reverse Complement. Teeth denote base pairing.

*Id.* at 3. Parameswaran’s Figure 1, above, shows that a forward primer comprises the Roche-specific forward adapter (“F-adapter”), the forward barcode (“F-Barcode”), and the forward cloning linker (“F-Cloning-Linker”). *Id.* It also shows that a reverse primer comprises the Roche-specific reverse adapter (“R-adapter”), the reverse barcode (“R-Barcode”), and the reverse cloning linker (“R-Cloning-Linker”). *Id.*

Parameswaran describes expanding the 10-nucleotide barcodes to “barcode motifs,” which included three additional nucleotides from linkers adjoining the barcodes, to maximize the uniqueness of dual-indexing and facilitate definitive sample assignments. *Id.* at 7. Parameswaran’s study aimed to determine “how much of the (fixed) linker sequence will be required in addition to the (variable) barcode for definitive sample assignment.” *Id.* at 7–8. Ultimately, “a search motif of 13 nt was determined to be ideal for our studies in minimizing false-discovery rate.” *Id.*

Parameswaran states that using 13-nt barcode motifs, approximately 94% of sequences were identified to have “perfect forward and reverse barcode motifs.” *Id.* at 7. Parameswaran subdivided the sequences having a perfect match to only one of the expected barcode motifs into three classes. *Id.* One of the three classes includes those having “perfect identity to an unexpected motif, resulting in an unassigned 5’–3’ motif combination (perfect, unexpected occurrence).” *Id.* According to Parameswaran, “[p]erfect, ‘unexpected’ occurrences may be attributed to motifs with rare coincidental sequence matches (due to multiple fortuitous errors during barcode synthesis or sequencing), to contamination in PCR primer stocks, or to cross-contamination of template DNAs in the second round of PCR.” *Id.* at 7. Parameswaran reports that “[t]he false-discovery rate, defined by the percentage of ‘perfect and unexpected’ occurrences, was observed to decrease to <0.005%.” *Id.* at 8.

## 2. Gloor (Ex. 1005)

Gloor is titled “Microbiome profiling by Illumina sequencing of combinatorial sequence-tagged PCR products.” Ex. 1005, 1. Gloor describes “a low-cost, high-throughput microbiome profiling method that uses

combinatorial sequence tags attached to PCR primers that amplify the rRNA V6 region.” *Id.*; *see also id* at 2 (reporting “the methods used to perform microbiome analysis of the V6 region of 272 clinical samples using the Illumina sequencing technology”). Gloor describes sequencing amplified PCR products “using an Illumina paired-end protocol to generate millions of overlapping reads.” *Id.* at 1. According to Gloor, “[c]ombinatorial sequence tagging can be used to examine hundreds of samples with far fewer primers than is required when sequence tags are incorporated at only a single end.” *Id.*

Gloor added primers and sequence tags to nucleic acids prior to sequencing. *Id.* at 3–6. Gloor “var[ied] the length of the sequence tags between 3 and 6 nucleotides long” and “chose sequence tags to ensure all 4 nucleotides were represented in each of the first four positions of the primers using parameters similar to those in the barcrawl program.” *Id.* at 5. Gloor describes developing custom programs “to identify the overlapping segments of the forward and reverse reads” and to extract “overlapping reads with proper primer sequences and correct sequence tags.” *Id.* at 7. Gloor inspected sequences with “incorrect sequence tags” to determine the sources of the errors. *Id.* at 7–8.

### 3. Analysis

We focus our analysis on independent claim 1. Petitioner provides detailed analysis to support its argument that the combination of Parameswaran and Gloor teaches or suggests each limitation of claim 1. Pet. 23–36. Petitioner also contends that an ordinarily skilled artisan would have been motivated combine the teachings of the two references and would have had a reasonable expectation of success in doing so. *Id.* at 36–45.

Patent Owner counters that the combination does not teach or suggest two limitations, namely the amplifying and discarding steps of the method. Prelim. Resp. 18–24. Patent Owner also challenges Gloor’s prior art status. *Id.* at 24–28.

Based on the current record, we find Petitioner’s argument with respect to the amplifying and discarding steps more persuasive. With respect to the remaining limitations, we find persuasive Petitioner’s analysis on the prior art’s teachings. We also find persuasive Petitioner’s analysis on the motivation to combine and reasonable expectation of success. For the purposes of institution, we adopt those analyses as our own. We address Patent Owner’s counterarguments below.

*a. Gloor’s Prior Art Status*

Relying on the Declaration of Dr. Gloor, the first named author, Petitioner contends that Gloor was published on July 29, 2010, and thus, “is prior art under at least pre-AIA 35 U.S.C. §102(a).” Pet. 12 (citing Ex. 1002). Dr. Gloor testifies that he submitted Gloor to arXiv.org on July 28, 2010, and received an email from arXiv.org confirming the public availability of Gloor as of July 29, 2010. Ex. 1002 ¶¶ 16, 17 (citing Ex. 1002, Exhibit E). According to Dr. Gloor, “[r]ecently, arXiv Technical Support confirmed in an email to [him] that *Gloor*’s release ‘would have been announced on Thursday, July 29, 2010.’” *Id.* ¶ 17 (citing Ex. 1002, Exhibit F). Dr. Gloor also testifies that he presented a poster at a conference held between August 31 and September 2, 2010, and the poster “provides a complete citation to” the Gloor reference. *Id.* ¶ 18 (citing Ex. 1002, Exhibit H).

Patent Owner counters that Petitioner has failed to show a reasonable likelihood that Gloor was publicly accessible as of December 23, 2010, the alleged priority date of the '852 patent. Prelim. Resp. 24–28. Patent Owner contends that the exhibits Dr. Gloor relies on in support of his declaration “at best indicate[] his article was *submitted*, but do[] not show if and when it was actually *published*, much less published in July 2010.” *Id.* at 26. Based on the current record, we find Petitioner has shown a reasonable likelihood that Gloor qualifies as prior art.

Indeed, Exhibit E to the Gloor declaration shows that the Gloor reference was assigned an arXiv identifier as of July 29, 2010. Ex. 1002, Exhibit E. It provides a hyperlink to the abstract and states that the abstract would appear in that day’s mailing. *Id.* In Exhibit F to the Gloor declaration, the arXiv Technical Support states that the submission with the same hyperlink “would have been announced on Thursday, July 29, 2010.” Ex. 1002, Exhibit F.

Patent Owner argues that Exhibit H to the Gloor declaration also does not support Dr. Gloor’s testimony of the public availability of the Gloor reference. Prelim. Resp. 27. According to Patent Owner, neither Petitioner nor Dr. Gloor even contend that Exhibit H “actually include[s] any of the details of Dr. Gloor’s article that are relevant to Petitioner’s challenge here.” *Id.* As we understand it, however, Petitioner does not rely on the substantive teachings of Exhibit H to support its unpatentability argument. Instead, Petitioner relies on Exhibit H to support the public availability of the Gloor reference before the priority date. *See* Pet. 12; *see also* Ex. 1002 ¶ 18 (Dr. Gloor testifying that “the References section” of Exhibit H provides a complete citation to the Gloor reference).

Patent Owner asserts that Petitioner's evidence to show the public availability of Gloor is inadequate "particularly when compared to at least one prior case where the Board accepted an arXiv publication, relying on testimony from a Cornell University Library employee who was actually responsible for arXiv.org and knowledgeable regarding its practices."

Prelim. Resp. 27 (citing *Great West Casualty Company v. Intellectual Ventures II LLC*, IPR2015-01706, Paper 10 at 11 (PTAB Feb. 9, 2016)).

We agree with Patent Owner that testimony from a "custodian with any personal knowledge of arXiv.org or its regular practices" would have strengthened Petitioner's argument that Gloor is prior art. *See* Prelim. Resp. 27; *see also, e.g., Murray & Poole Enters. LTD v. Institut De Cardiologie De Montreal*, IPR2023-01064, Paper 49 (PTAB Jan. 14, 2025) (considering testimony regarding the internet archive service known as the Wayback Machine (<https://web.archive.org/>) in determining public accessibility). At the institution stage, however, Petitioner needs to show that Gloor qualifies as prior art by "a reasonable likelihood" standard. *See Hulu, LLC, v. Sound View Innovations, LLC*, IPR2018-01039, Paper 29, 13 (PTAB Dec. 20, 2019) (precedential) ("[A]t the institution stage, the petition must identify, with particularity, evidence sufficient to establish a reasonable likelihood that the reference was publicly accessible before the critical date of the challenged patent and therefore that there is a reasonable likelihood that it qualifies as a printed publication."). We find that, for the purposes of institution, with Dr. Gloor's declaration and the supporting exhibits attached therein, Petitioner has met this burden.

To prevail in this *inter partes* review, Petitioner must meet the preponderance of the evidence standard. *See* 35 U.S.C. § 316(e). Thus, we

encourage the parties to fully develop the record during trial to facilitate the ultimate resolution of this issue.

*b. The Amplifying Step*

Claim 1 recites “amplifying said nucleic acid templates on a surface of a flow cell thereby to form clusters, at least one of which comprises a chimeric sequence comprising a combination of identifier sequences that are different than any of said distinct pairs.”

Petitioner argues that Gloor used Illumina paired-end sequencing, and thus, necessarily teach “amplifying said nucleic acid templates on a surface of a flow cell thereby to form clusters.” Pet. 31–32. Petitioner points to Parameswaran’s teaching of mismatched barcode motifs, where “the forward identifier was incorrectly paired with the wrong reverse identifier.” *Id.* at 32 (citing Ex. 1004, 8, Abstract; Ex. 1003 ¶ 147). According to Petitioner, Parameswaran’s “sequences with mismatched barcode motifs include chimeric sequences resulting from cross-over events.” *Id.* (citing Ex. 1003 ¶ 148). As a result, Petitioner concludes that Parameswaran teaches at least one nucleic acid template comprising “a chimeric sequence comprising a combination of identifier sequences that are different than any of said distinct pairs.” *Id.* at 32–33.

Patent Owner argues that “by dividing the claimed step in this manner, Petitioner fails to show that the combination discloses or renders obvious *clusters* formed on a surface of a flow cell, with at least one *cluster* comprising a chimeric sequence, as the claim requires.” Prelim. Resp. 18. According to Patent Owner, Petitioner fails to show that (1) Parameswaran discloses a cluster comprising a chimeric sequence (*id.* at 21), and (2) Parameswaran’s mismatched barcode motifs resulted from the

cross-over events (*id.* at 18–21). Based on the current record, we find Petitioner’s argument more persuasive.

Petitioner relies on the combination of Parameswaran and Gloor as teaching the amplifying step. *See* Pet. 31–33. As such, Patent Owner cannot show non-obviousness “by attacking references individually.” *In re Keller*, 642 F.2d 413, 426 (CCPA 1981). Patent Owner argues that “because Parameswaran used pyrosequencing on the surface of beads in a Roche 454 sequencer, it does not disclose the formation of **clusters**.” Prelim. Resp. 21 (citing Pet. 31). Petitioner, however, relies on Gloor for teaching “amplifying said nucleic acid templates on a surface of a flow cell thereby to form clusters.” Pet. 31–32. Patent Owner does not challenge this reliance. *See generally* Prelim. Resp.

Patent Owner contends that Petitioner “equat[es] the claimed chimeric sequences with ‘mismatched’ or ‘misassigned’ sequences containing an ‘unexpected’ pair of forward and reverse barcode motifs identified in Parameswaran.” Prelim. Resp. 18–19. But, according to Patent Owner, “Petitioner does not point to any disclosure in Parameswaran identifying these “mismatched” motifs as **chimeric** sequences—as opposed to mere sequencing or sample handling error—nor does Petitioner cite any disclosure in Parameswaran regarding such sequences resulting from cross-over events.” *Id.* at 19.

We find Patent Owner’s characterization of Petitioner’s argument inaccurate. As we understand it, Petitioner does not “equat[e]” the claimed chimeric sequences with “mismatched” sequences in Parameswaran. Instead, as Patent Owner acknowledges, “Petitioner argues that ‘sequences with

mismatched barcode motifs’ in Parameswaran ‘*include* chimeric sequences resulting from cross-over events.’” *Id.* (quoting Pet. 32) (emphasis added).

Moreover, claim 1 requires “a chimeric sequence comprising a combination of identifier sequences that are different than any of said distinct pairs.” It does not specify the origin of the chimeric sequence. On this record, Patent Owner has not pointed to persuasive evidence to show that claim 1 limits the claimed “chimeric sequence” resulted solely from cross-over error.

In sum, on this record and for purposes of institution, we find Petitioner has shown sufficiently that the combination of Parameswaran and Gloor teaches the amplifying step of claim 1.

*c. The Discarding Step*

Claim 1 recites “discarding sequence reads obtained in said sequencing step that contain said combination of identifier sequences that are different than any of said distinct pairs, thereby to reduce cross-over error.”

Petitioner argues that Parameswaran teaches this step. Pet. 34–35. Petitioner contends that Parameswaran distinguished the sequences with a pair of perfectly matched barcode motifs (“perfect and expected”) from those with only one perfect barcode motif (“perfect but unexpected”). *Id.* at 34 (citing Ex. 1003 ¶¶ 152, 153; Ex. 1004, 7). According to Petitioner, an ordinarily skilled artisan “would have understood that Parameswaran disclosed a method in which these chimeric sequences could be discarded, and thus, reduce cross-over error.” *Id.* at 35 (citing Ex. 1003 ¶ 154).

Patent Owner disagrees. Prelim. Resp. 22–24. Patent Owner points out that Petitioner does not “argue that Parameswaran discloses *discarding*

those sequences that were allegedly ‘distinguished.’” *Id.* at 22. Patent Owner emphasizes that, in fact, Parameswaran discloses the opposite, explicitly stating that sequences with perfect but unexpected barcode motifs were “***kept and included in the analysis.***” *Id.* (citing Ex. 1004, 8). Based on the current record, we find Petitioner’s argument more persuasive.

Patent Owner is correct that, in Parameswaran, “all sequences with a match to one of the two expected sequence motifs were considered as true members of the corresponding dataset.” Ex. 1004, 8. Parameswaran, however, calls sequences with “mismatched 5’ and 3’ motifs (i.e. sequences that do not have corresponding 5’ and 3’ motifs)” “false-discover[ies]” with “misassignment[s].” *Id.* at 7–8.

Patent Owner emphasizes that Parameswaran included the sequences with perfect but unexpected barcode motifs because it achieved “reasonable accuracy” due to its “low false-discovery rate.” Prelim. Resp. 23–24 (citing Ex. 1004, 8). We do not disagree with Patent Owner on this observation. Nonetheless, we understand Petitioner as arguing that lowering false-discovery rate would increase accuracy. *See* Pet. 35 (citing Ex. 1003 ¶ 154); *see also* Ex. 1003 ¶ 131 (“*Parameswaran* teaches that lowering the false discovery (misassignment) rate allows sequences to be assigned to correct samples more accurately.”).

In sum, on this record and for purposes of institution, we find Petitioner has shown sufficiently that Parameswaran suggests excluding the false discoveries to increase accuracy, i.e., the discarding step of claim 1.

*d. Summary*

In sum, based on this record, we determine Petitioner has established a reasonable likelihood that it would prevail in its assertion that claim 1 would have been obvious over the combination of Parameswaran and Gloor.

Petitioner also asserts that the combination of Parameswaran and Gloor renders claims 2–8 obvious. Pet. 45–51. Patent Owner does not argue these claims separately. *See generally* Prelim. Resp. In any event, we institute an *inter partes* review as to all challenges raised in the Petition. *See SAS Institute, Inc. v. Iancu*, 138 S. Ct. 1348, 1356 (2018); *see also* 37 C.F.R. § 42.108(a) (“When instituting *inter partes* review, the Board will authorize the review to proceed on all of the challenged claims and on all grounds of unpatentability asserted for each claim.”).

*C. Alleged Obviousness over Parameswaran and Bentley*

Petitioner asserts that claims 1–8 would have been obvious over the combination of Parameswaran and Bentley. Pet. 51–61. Based on this record, and for at least the following reasons, we determine Petitioner has established a reasonable likelihood that it would prevail in this assertion.

1. Bentley

Bentley provides a detailed description of Illumina paired-end sequencing. Ex. 1006. It describes a “massively parallel synthetic sequencing approach” that involved shearing DNA strands into double-stranded DNA fragments for sequencing and ligating (joining) Illumina-specific adapters to both ends. *Id.* at 1–2, 13–14. Bentley “generated high-density single-molecule arrays of genomic DNA fragments attached to the surface of the reaction chamber (the flow cell) and used isothermal ‘bridging’ amplification to form DNA ‘clusters’ from each

fragment.” *Id.* at 1. It describes that these DNA fragments were then denatured into single strands so that Illumina-specific adapters on the ends of the templates annealed to complementary oligonucleotides on the surface of the flow cell. *Id.* at 3.

## 2. Analysis

We, again, focus our analysis on independent claim 1. In this challenge, Petitioner makes similar arguments as those in the challenge based on the combination of Parameswaran and Gloor, except it relies on Bentley instead of Gloor for teaching “amplifying said nucleic acid templates on a surface of a flow cell thereby to form clusters.” Pet. 52–55.

In response, Patent Owner makes similar counterarguments as those in addressing the obviousness challenge based on the combination of Parameswaran and Gloor, namely, the combination does not teach or suggest the amplifying and discarding steps of the method. Prelim. Resp. 28–29.

For the same reasons explained above (*see supra* Section II.B.3), we find Petitioner’s arguments more persuasive. Moreover, because Petitioner has met the threshold requirement of § 314(a), we institute an *inter partes* review as to all challenges raised in the Petition. *See SAS*, 138 S. Ct. at 1356. We encourage the parties to further address all relevant issues of all challenges to fully develop the record during trial.

## III. CONCLUSION

Based on the current record, and for the reasons explained above, we find Petitioner has demonstrated a reasonable likelihood that it would prevail with respect to at least one claim challenged in the Petition. We therefore institute an *inter partes* review of all challenged claims on all asserted grounds.

#### IV. ORDER

In consideration of the foregoing, it is hereby:

ORDERED that, pursuant to 35 U.S.C. § 314(a), *inter partes* review is hereby instituted on all challenged claims of the '852 patent based on the assert ground set forth in the Petition; and

FURTHER ORDERED, pursuant to 35 U.S.C. § 314(c) and 37 C.F.R. § 42.4(b), notice is hereby given of the institution of a trial commencing on the entry date of this decision.

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