

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

INTEGRATED DNA TECHNOLOGIES, INC.,
Petitioner,

v.

TECAN GENOMICS, INC.,
Patent Owner

Case No. IPR2024-01504
U.S. Patent No. 11,098,357

PATENT OWNER'S SUR-REPLY

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2002	Chiasson 2015	Mark J.P. Chiasson et al., <i>Genetic variation and the de novo assembly of human genomes</i> , 16 NAT. REV. (2015)
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2004	Goodwin 2016	Sara Goodwin et al., <i>Coming of age: ten years of next-generation sequencing technologies</i> , 17 NAT. REV. (2016)
2005	Kanagawa 2003	Takahiro Kanagawa, <i>Bias and Artifacts in Multitemplate Polymerase Chain Reactions (PCR)</i> , 96 J. BIOSCI. & BIOENG 4 (2003)
2006	Mamanova 2010	Lira Mamanova et al., <i>Target-enrichment strategies for next-generation sequencing</i> , 7 NAT. METHODS 2 (2010)
2007	Nakamura 2011	Kensuke Nakamura et al., <i>Sequence-specific error profile of Illumina sequencers</i> , 39 NUCLEIC ACIDS RES. 13 (2011)
2008	Sanger 1977	F. Sanger et al., <i>DNA sequencing with chain-terminating inhibitors</i> , 74 PROC. NATL. ACAD. SCI. USA 12 (1977)
2009	Satam 2023	Heena Satam et al., <i>Next-Generation Sequencing Technology: Current Trends and Advancements</i> , 997 BIOL. 12 (2023)
2010	Whiteford 2009	Nava Whiteford et al., <i>Swift: Primary Data Analysis for the Illumina Solexa Sequencing Platform</i> , 25 BIOINFORMATICS 16 (2009)
2011	Capurro 2015	Alberto Capurro et al., <i>Computational deconvolution of genome wide expression data from Parkinson's and Huntington's disease brain tissues using population-specific expression analysis</i> , 8 FRONTIERS IN SCI. (2015)

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2013	Wang 2015	Niya Wang et al., <i>UNDO: a Bioconductor R package for unsupervised deconvolution of mixed gene expressions in tumor samples</i> , 31 BIOINFORMATICS 1 (2015)
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2016	Sims Deposition	Transcript for the June 26, 2025 Deposition of Dr. Peter A. Sims
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2023	Aird 2011	Daniel Aird et al., <i>Analyzing and minimizing PCR amplifications bias in Illumina sequencing libraries</i> , 12 GENOME BIOL. (2011)
2024	Cock 2009	Peter J. A. Cock et al., <i>The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants</i> , 38 NUCLEIC ACIDS RES. 6 (2009)
2025	McKenna 2010	Aaron McKenna et al., <i>The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data</i> , 20 GENOME RES. 1297 (2010)
2026	Lam 2012	Hugo Y. K. Lam et al., <i>Detecting and annotating genetic variations using the HugeSeq pipeline</i> , 30 NAT. BIOTECH. 3 (2012)
2027	Li 2009	Heng Li et al., <i>The Sequence Alignment/Map format and SAMtools</i> , 25 BIOINFORMATICS 16 (2009)

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2029	IHGSC 2004	International Human Genome Sequencing Consortium, <i>Finishing the euchromatic sequence of the human genome</i> , 431 NAT. 21 (2004)
2030	Baker 2012	Monya Baker, <i>De novo genome assembly: what every biologist should know</i> , 9 NAT. METHODS 4 (2012)
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2034	N/A	<i>The Cost of Sequencing a Human Genome</i> , NAT'L INST. OF HEALTH NAT'L HUMAN GENOME RESEARCH INST., https://www.genome.gov/about-genomics/fact-sheets/Sequencing-Human-Genome-cost (last visited July 11, 2025)
2035	Bustamante Declaration	Declaration of Carlos D. Bustamante, Ph.D.
2036-2285		<i>Reserved</i>
2286	Beavers Declaration	Declaration of Timothy J. Beavers in Support of Notice of Intent to Designate Provisionally Recognized PTAB Attorney as Back-Up Counsel Under 37 C.F.R. § 42.10

IDT's Reply further highlights the deficiencies in its Petition. It has not and indeed cannot point to disclosures in the prior art where both a target sequence and an identifier are used in combination to identify duplicate sequencing reads. As explained in Tecan's Response, neither Kivioja nor Bielas disclose this limitation.

In an attempt to shoehorn the challenged claims to fit the prior art, IDT presents a construction of the claims that runs contrary to representations Applicants made during prosecution. With those representations, Applicants clarified that the target sequence and the identifier must be used *in combination*. When viewed in the context of the examiner's rejection, Applicants made clear that the claims were not directed to using the two pieces of information separately and indeed distinguished a reference disclosing a method similar to Bielas, on which IDT relies.

IDT does not argue that the cited references anticipate or render obvious the challenged claims under the proper construction of the identifying duplicates limitation. Thus, IDT's petition should be denied.

I. CLAIM CONSTRUCTION

The purpose of claim construction is to clarify the meaning of terms to assist with the Board's analysis. As explained in Tecan's POR, Tecan's proposed constructions articulate what is made clear through the intrinsic record. IDT, on the other hand, makes no effort to propose a construction that is helpful to the analysis

here. It is Tecan’s proposed construction that aligns with the plain meaning of the claim language and the intrinsic record.

A. “identifying sequence reads with identical identifier and target sequences as duplicates”

Term (Claims)	Tecan’s Proposed Construction	IDT’s Proposed Construction
“identifying sequence reads with identical identifier and target sequences as duplicates” (’357 patent, claim 1)	“identifying sequence reads as duplicates through a step that uses both the identifier and at least a portion of the target sequence”	“identifying sequence reads with identical identifier and target sequences as duplicates.” This limitation requires the entire “target sequence” and does not require a single “step.”

IDT raises two issues with Tecan’s proposed construction. First, IDT disagrees that the identifying step requires that the identifier and the target sequence must be used together. Paper 29, 7-12. Second, IDT attempts to expand the language of the claims to require that the step use the entirety of the target sequence. *Id.*, 12-13. Both of IDT’s positions should be rejected.

IDT seems to contend that proposing a claim construction that includes more words than the original claim language is somehow improper. This is not, and indeed cannot, be supported by any precedent. The goal of claim construction is to provide clarity to the term at issue, which often requires the concepts in dispute to be spelled out. Tecan’s proposal does precisely that—clarifies what Applicants

expressed during prosecution and sheds light on the point of dispute between the parties.

1. The “Identifying” Step of the Claimed Method Requires Use of Elements in Combination

The claims of the ’357 patent are all method claims that set forth the steps of the method. To meet the claims, each step must be “carried out or performed” as claimed. *See Kaneka Corp. v. Xiamen Kingdomway Grp. Co.*, 790 F.3d 1298, 1305-06 (Fed. Cir. 2015) (holding the method claims “affirmatively recite the step of ‘oxidizing,’ [and] ‘oxidizing’ cannot be interpreted as doing nothing, or to simply allow oxidation to occur on its own”). Thus, the ordinary meaning of the “identifying” step requires that both the identifier and at least a portion of the target sequence are used as part of the step that identifies duplicates.

The dispute here is whether the identifying step of the claims allows for (1) performing a series of steps that eventually lead to the identification of duplicates, without regard as to how the identifier and target sequences are used, as IDT contends, or instead requires (2) using the identifier and target sequences in combination in the step that identifies duplicates, as Tecan contends. This is not a question of the order of steps, but a question of what is required within the identification step. Here, the prosecution history, which IDT largely ignores,

confirms that Tecan's construction aligns with the inventors' and examiner's understanding of the claims.

There is no ambiguity in Applicants' representations that the identification of duplicates requires that both the target sequence and the identifier be used together. As explained in Tecan's Response (Paper 21, 13-15), Applicants repeatedly stressed the importance of the claimed identification step:

- “Samuels *et al.* do not teach (1) ***the active step of*** ‘identifying a duplicate sequencing read as the sequencing read comprising the same identifier site and nucleic acid fragment as another sequencing read in the population of sequencing reads.’” EX1018.0797-98 (emphasis added).
- “However, the instant invention relies on the indexing site for batch identification of samples, and the ***sequence of the identifier site and the sequence of the fragment that is amplified are used in combination to discern duplication.***” EX1018.0799 (emphasis added).
- “This is obviated in the claimed methods by using the identifier and fragment sequence to identify duplicate reads. Moreover, because ***the fragment sequence is used in conjunction with the identifier to find duplicates***, the identifier can be less complex than the ‘barcode’ in McCloskey.” EX1019.0453 (emphasis added).

The only reasonable reading of the prosecution history is that Applicants amended the claims to require that the identifying duplicates step require the use of these two pieces of information together. There is no ambiguity that would allow for using the target sequence and identifier in separate steps of the method. Applicants amended the related claim language to overcome a prior art rejection, which must be considered when construing the claims. Paper 21, 13-15; *Spectrum Int'l, Inc. v. Sterilite Corp.*, 164 F.3d 1372, 1378 (Fed. Cir. 1998) (“explicit statements made by a patent applicant during prosecution to distinguish a claimed invention over prior art may serve to narrow the scope of a claim”).

As the Federal Circuit has repeatedly emphasized, the “prosecution history ‘is often of critical significance in determining the meaning of the claims’ because it ‘contains ... any express representations made by the applicant regarding the scope of the claims.’” *Genentech, Inc. v. Iancu*, 809 F. App’x 781, 783 (Fed. Cir. 2020) (citations omitted). The prosecution history is of critical significance here because it unambiguously demonstrates how Applicants and the examiner viewed the identifying step. And neither *Phillips* nor *AquaTex* stands for the proposition that the prosecution history should be disregarded. *Phillips* emphasizes that even when ambiguous, prosecution history can still “often inform the meaning of the claim language by demonstrating how the inventor understood the invention and whether the inventor limited the invention in the course of prosecution, making the claim

scope narrower than it would otherwise be.” *Phillips v. AWH Corp.*, 415 F.3d 1303, 1317 (Fed. Cir. 2005); *see also AquaTex Indus., Inc. v. Techniche Sols.*, 419 F.3d 1374, 1381 (Fed. Cir. 2005) (finding the prosecution history unpersuasive because AquaTex’s arguments to traverse the rejection “neither support nor discredit any particular meaning of the term [at issue].”).

IDT seems to admit that Example 5 supports Tecan’s construction of the claim, arguing only that the specification does not support Tecan’s construction because it would not include Example 1. Paper 29, 9. There is no requirement, however, that the claims cover every embodiment discussed in the specification. *See Baran v. Med. Device Techs., Inc.*, 616 F.3d 1309, 1316 (Fed. Cir. 2010) (“It is not necessary that each claim read on every embodiment.”); *see also SIMO Holdings Inc. v. Hong Kong uCloudlink Network Tech. Ltd.*, 983 F.3d 1367, 1378-79 (Fed. Cir. 2021) (emphasizing its “repeated[] ... caution” that “we should not infer that any particular embodiment is included in a claim” when there exists “*probative evidence to the contrary*” (citations omitted)). Indeed, the Federal Circuit has consistently found that applicants have narrowed claims so as to cover only certain embodiments in light of prior art raised during prosecution. *See, e.g., Spectrum*, 164 F.3d at 1378.

Here, the specification describes different methods of identifying duplicates. EX1004.0019 (15:23-35), 18 (14:21-31). Examples 1 and 5 illustrate these different

methods. Example 1 describes using portions of the sequence reads to determine the genomic coordinates of the sequence (not to identify duplicates). EX1004.0020 (17:39-46). The starting coordinates, not the target sequence, are then used in the step of identifying duplicate reads. EX1004.0020 (17:42-43) (“***duplicate reads were identified by their genomic start positions.***” (emphasis added)), 11 (Fig. 5). Example 1, therefore, does not describe a duplicate identification step that uses the sequence and the identifier in conjunction. EX1124.0088:11-20 (“In order to practice claim 1, you need to be comparing the identifier sites and the target sequence sites and ensuring they are identical.”); *see also* EX1124.0086:24-87:13 (“I can’t point to a section [in Example 1] where they specifically discuss comparing the target sequence and ensuring that they are identical.”).

The prosecution history and the language of the claims, however, reflect the method described in Example 5. There, a sequence that includes both the identifier and a portion of the sequence is used to identify the duplicates. EX1004.0021 (20:58-62) (“The first 50 bases of the target sequence read are compared to each other. Any read that has identical sequence to any other read is identified as a duplicate”). There is no question that, in the method described in Example 5, both pieces of information are used “in conjunction” for the step of identifying duplicates.

The rest of the specification either does not contradict Tecan’s proposed construction or confirms it, including the method described in Example 5. Contrary

to IDT's representations, the *only* portion of the specification that explicitly describes a method that would not be covered by the claims as amended during prosecution is that in Example 1. *See* Paper 29, 9-10.

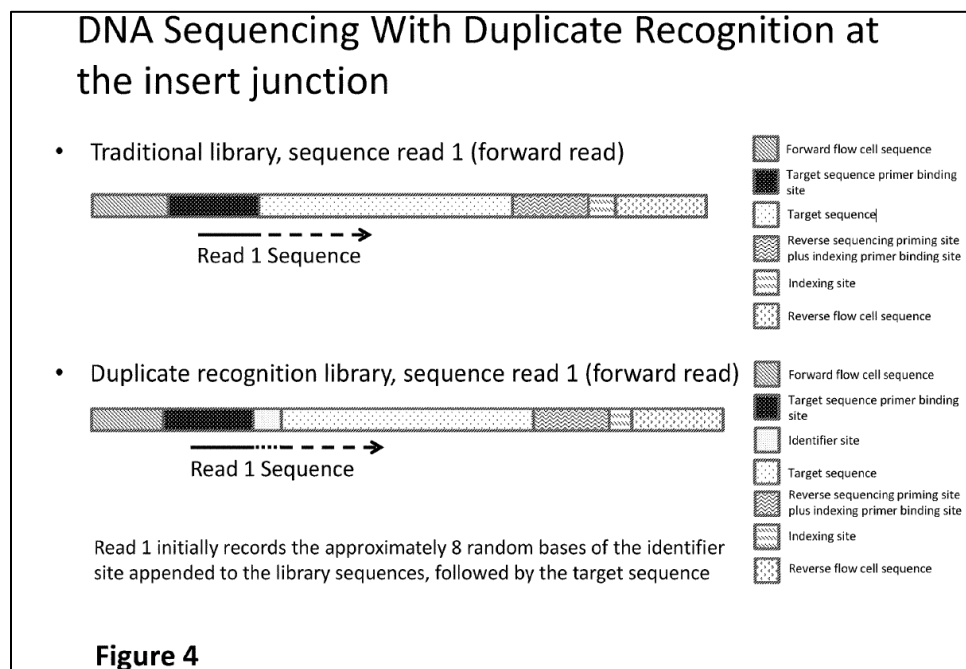
Further, Dr. Bustamante's testimony aligns with Tecan's proposed construction. IDT does not appear to dispute that the identifying step of the claims requires that the duplicates be identified. This is precisely what Dr. Bustamante confirmed. *See, e.g.*, EX1124.0051:15-52:4 (testifying that claim 1 requires target sequences to be compared against each other to identify duplicates). While sequencing can be conceptually described as operating nucleotide-by-nucleotide, such granularity is irrelevant. Dr. Bustamante confirmed that the claims require that both the target sequence and the identifier site be compared in the process of identifying duplicates. EX1124.0052:24-53:11.

IDT contends that the claims allow for the separate use of the target sequence and the identifier as part of a multi-step process. Paper 29, 7-10. This interpretation reads out the aspect of the invention that Applicants stressed during prosecution—that the target sequence and the identifier be used *in combination*. While, in theory, the identification step at issue can include multiple steps, the claims still require that the target sequence and the identifier be used together. There is no reference cited in the Petition that requires the Board to determine whether a multi-step process would meet the claims—as discussed further below, neither Kivioja nor Bielas

discloses the claimed duplicate identification method that uses the target sequence and identifier in combination.

2. The Claims Do Not Require Comparison of the Entire Target Sequence

IDT's construction oversimplifies the concepts described in the specification and the claims. The specification refers to the read sequence as something shorter than the target sequence, as shown in Figure 4.



EX1004.0010 (Fig. 4), 21 (20:52-60). As the specification illustrates, the length of any sequencing read may not extend to the entire target sequence length. Indeed, the read length will vary between fragments in the same sequencing reaction. No reasonable POSA would understand the claims to require comparison of the entire

target sequence, without regard to the read length in the reaction. *See, e.g.*, EX1124.0145:2-5.

Example 5 illustrates this difference. In Example 5, the fragments in the sample had an average length of 200 base pairs. EX1004.0021 (19:55-58) (“DNA was sheared with a Covaris S-series device (Covaris, Inc., Woburn, Mass.) using the **200 bp** [(base pair)] sonication protocol provided with the instrument (10% duty cycle, 200 cycles/burst, 5 intensity, 180 seconds).” (emphasis added)). These fragments were necessarily random due to the sonication protocol, meaning that many of the fragments would not include the entire target sequence. After sequencing, “[t]he first 50 bases of the target sequence read are compared to each other” to identify duplicates. EX1004.0021 (20:58-60). As noted in Figure 4, the *target sequence reads* were expected to be shorter than the entire *target sequence*. In addition, Example 5 notes that only the first 50 bases of the *target sequence read* were used for comparison. Example 5 illustrates that a portion of the target sequence can be used rather than the entirety of the target sequence.

Example 1 similarly uses only a portion of the read in the analysis. As discussed above, Example 1 does not illustrate the method of identifying duplicates in the claims. Example 1 does, however, further illustrate that a POSA would have understood that portions of a sequence are often used in data analysis. There, the samples included fragments that were approximately 500 base pairs long.

EX1004.0019 (16:51-54) (“Sample Description: 100 ng of DNA from a human HapMap sample (NA19238) was fragmented to approximately *500 base pair* in length by sonication with a Covaris system (Covaris, Inc., Woburn, Mass.)” (emphasis added)). Like Example 5, the sonication protocol would lead to random fragmentation. When these fragments were sequenced, the sequencing reads were of various lengths (36, 14, and 24 bases). EX1004.0020 (17:27-31). These shorter reads were used for further analysis, without reference to the length of the target sequence or the target sequence read. Example 1 confirms that a POSA would have understood that a portion of the target sequence can be used in the analysis of the data. Thus, there is no support in the record to require that the entire target sequence be used to identify duplicates.

B. A Method “Comprising” a Step that Identifies “Duplicates”

There appears to be no dispute that two sequences are duplicates when the reads being compared are identical. When read in combination with the “comprising” transitional phrase of the claims, the claims only require that duplicates are identified. The claims are agnostic as to whether the method also identifies non-duplicates, including those sequences that would be captured with a Hamming distance greater than zero and potential errors.

II. GROUNDS II AND III: BIELAS DOES NOT DISCLOSE KEY ELEMENTS OF THE CLAIMS

IDT does not present any argument that Bielas anticipates the challenged claims under Tecan's proposed claim construction of the identifying duplicates term. Therefore, under the proper construction of the claims, IDT's Grounds II and III must fail.

Bielas is a patent application directed at methods of identifying mutations, not duplicates. EX1013.0001. IDT attempts to discount Bielas's stated purpose, *see* Paper 29, 15, but this purpose underscores that Bielas does not disclose the identification of duplicates in the manner claimed. Bielas describes a method that purports to accomplish its stated goal and does not even mention identifying duplicate reads. EX1013.0001; EX2035.¶122. IDT relies on *Hewlett-Packard* to argue that a reference anticipates regardless of its stated goal so long as it performs the claimed method. *Hewlett-Packard Co. v. Mustek Sys., Inc.*, 340 F.3d 1314, 1324 n.6 (Fed. Cir. 2003). But *Hewlett-Packard* only held the stated purpose irrelevant because the prior art at issue *performed the claimed step*, and therefore, could not be distinguished based on its stated purpose. *Id.* at 1324. In contrast, Bielas does *not* perform the claimed method, and the stated purpose of the work described in Bielas illustrates the disparity. Bielas's stated goal of identifying mutations remains a

meaningful distinction, underscoring Bielas's failure to identify duplicates in the manner claimed.

IDT relies on Examples 1 and 3 of Bielas, but neither of these disclose all elements of the challenged claims. IDT's position that Example 1 anticipates claim 1 requires the Board to find that "computationally deconvolute" means not only deduplication (which there is no support for) but also that the target sequence is used in the alleged deconvolution to identify duplicates. There is no evidence in the record about what "deconvolute" means. Dr. Sims confirmed that he has used the term deconvolute broadly, including to mean data analysis steps other than duplicate identification. EX2016.0126:5-11. IDT has not presented any evidence to establish that Bielas's deconvolution process included duplicate identification. Neither Dr. Sims's testimony nor any other evidence on which IDT relies supports a conclusion that a POSA would have understood deconvolution to necessarily include analysis of duplicates. Any finding that deconvolute equates to identifying duplicates would be based on pure speculation.

Even if, however, deconvolution included deduplication, Bielas's Example 1 clearly states "***the unique cypher tags*** are used to computationally deconvolute the sequencing data." EX1013.0027 (emphasis added); Paper 29, 18. There is no mention of the target sequence being used in this process. *Id.* IDT's claims regarding Bielas's Example 1, therefore, are not supported in the record.

IDT's arguments based on Bielas's Example 3 are similarly misplaced. *See* Paper 29, 15-16. As an initial matter, the method of Example 3 is similar to the Samuels reference that was cited against the pending claims during prosecution. *See* EX1019.0451-452. Like Bielas, EX1013.0007, Samuels describes a method of distinguishing PCR-errors from nucleotide polymorphisms present in the original sample utilizing molecular barcoding. EX1033.0098-99, [338-341]. Samuels describes methods of applying adaptors containing molecule-specific barcodes prior to PCR, such that subsequently amplified PCR fragments will share the same barcode if originating from the same nucleic acid fragment. EX1033.0016 (Fig. 15), 62 (Fig. 62). Sequencing reads with the same molecular barcode are grouped and compared. EX1033.0044 (Fig. 43), 99, [340]. Samuels describes that the barcodes "can be used for highly accurate nucleic acid sequencing, particularly by enabling the discrimination between true SNPs and sequencing errors." EX1033.0098, [338].

As explained in Tecan's Response and highlighted above, Applicants overcame the examiner's rejection in light of Samuels by (1) amending the claims to include the identifying step that appears in the challenged claims, requiring the use of the target sequence and the identifier in combination, and (2) noting that Samuels, like Bielas, does not disclose a step where duplicates are identified. Paper 21, 13-15; *see supra* Section I.A.1.

Bielas's Example 3 uses the prior art steps that Applicants distinguished. *See* Paper 21, 35-37. First, Bielas groups the reads according to the cyphers alone. EX1013.0031 ("all sequencing reads with identical cypher pairs and their reverse complements were grouped into families"); EX1013.0043 (Fig. 3B). Then, the sequences are analyzed to identify differences. EX1013.0031 ("errors introduced during library preparation ... and during sequencing ... were computationally eliminated"). As Applicants explained, a process that identifies differences through comparing barcodes/identifiers is distinct from the method claimed. EX1019.0452; *see also* Paper 21, 16-17.

IDT again attempts to shoehorn the language of Bielas to match the challenged claims by claiming that Bielas's consensus sequence is necessarily a method of identifying duplicates. *See* Paper 29, 17-18. IDT's argument, however, is based on a fundamental misstatement of the record—there is no support for the conclusion that the formation of a consensus sequence is always equivalent to identification of duplicates. Contrary to IDT's representations, Dr. Bustamante testified that "the fact that you have derived a consensus sequence ... first is not the same thing as duplicate identification necessarily." EX1124.0065:6-10. Dr. Bustamante also clarified that there are many ways to generate a consensus sequence, EX1124.0171:22-172:2, but IDT cannot point to any information *in Bielas* that describes how the consensus sequence was generated in the method described. IDT cannot base its anticipation

arguments on mere speculation about the prior art or rely on a POSA's general knowledge to fill in critical elements of the challenged claims that do not appear in the prior art. *See PAR Pharm., Inc. v. TWI Pharms., Inc.*, 773 F.3d 1186, 1195 (Fed. Cir. 2014) (emphasizing that “inherency ... may not be established by probabilities or possibilities.”) (citations omitted). IDT has not presented testimony from Dr. Sims or pointed to anything in the record, other than misrepresentations of deposition testimony, to support its reliance on Bielas's consensus sequence as duplicate identification.

Since Bielas does not disclose the claimed step of identifying duplicates using both the target sequence and the identifier, it cannot anticipate the challenged claims. IDT has not presented any argument that a POSA would have been motivated to modify Bielas to cure this deficiency and arrive at the missing identifying duplicates step, and therefore, IDT has failed to show that any claim is obvious in light of Bielas.

III. GROUND I: THE COMBINATION OF KIVIOJA AND IAFRATE FAILS TO RENDER THE CHALLENGED CLAIMS OBVIOUS

A petitioner must explain where in the prior art each element is disclosed. 37 C.F.R. § 42.104(b)(4). IDT has not, and indeed cannot, identify where either Kivioja or Iafrate disclose the claimed step of identifying duplicates using the target

sequence and the identifier in combination. *See* Paper 29, 19-27. IDT's obviousness argument, therefore, cannot succeed.

IDT does not argue that Iafrate discloses the claimed step of identifying duplicates. As Dr. Sims admitted, Iafrate is not directed to methods of identifying duplicates and the adaptors used in Iafrate do not contain molecular tags or identifier sites. EX2016.96:13-97:2, 116:17-18. IDT also does not argue that Kivioja discloses the claimed identification of duplicates step under Tecan's proposed construction of this limitation. Ground I, instead, relies on an interpretation of the claims that would allow any use of the target sequence in the overall method to meet the claimed limitation. As explained above, such an interpretation is inconsistent with the prosecution history and the language of the claims. *See supra* Section I.A.1.

While IDT boldly claims that "Dr. Bustamante offered no obviousness opinion about Iafrate or Kivioja," Paper 29, 19, Dr. Bustamante provided ample testimony on the failure of these references to disclose the key elements of the claims. *See* EX1124.0147:2-7, 156:1-6; EX2035.¶¶125-132. IDT has not advanced an argument that a POSA would have been motivated to modify the duplicate identification step of Kivioja to arrive at the claimed method, relying only on the disclosure of Kivioja for that element. Dr. Bustamante's testimony that the prior art does not include the claimed identifying duplicates element is therefore directly relevant to the obviousness analysis, as explained in more detail below.

A. Kivioja Does Not Disclose the Claimed Identification of Duplicates

There is no dispute that Kivioja does not disclose a process where the target sequence and the identifier are used in the same step to identify duplicates. Instead, Kivioja uses the target sequence to identify the corresponding gene and position. EX1012.0005. Kivioja does not disclose using the target sequence for any other purpose. Kivioja then uses the gene and position data in its further analysis, not the sequence. *Id.* Kivioja explicitly defines the UMI used for grouping reads as “the sequence of the label and *the 5' mapped position of the fragment.*” EX1012.0003 (emphasis added); EX2016.0107:7-13 (Dr. Sims confirming that “Kivioja uses the name of the gene and the position ... within that gene to which the sequencing read aligned”). IDT has not presented any evidence of the target sequence and the identifier being used in combination, as required under the proper construction of the claims.

Kivioja’s use of the gene and position in place of the target sequence transforms one data set into a different data point. EX1012.0005. This transformation disregards the specific sequence of the read and adopts a simplified version that only refers to the position in the reference genome. As Dr. Sims admitted, these are different pieces of data. EX2016.0105:4-8, 107:1-13. There is nothing in the challenged claims that allows a substitute for the target sequence like the gene position in Kivioja to be used instead of portions of the actual target

sequence in combination with the identifier to identify duplicates. Thus, Kivioja's use of the gene and position in lieu of the sequence fails to disclose the identifying duplicates limitation of the challenged claims. *See* EX2035.¶¶126-132.

IDT's reliance on Figure 1(a) is similarly misplaced. *See* Paper 29, 21-22. Figure 1(a) does not describe a method of identifying duplicates using a target sequence and an identifier. Figure 1 presents a schematic explaining three methods of generating UMIs: "by adding oligonucleotide labels, fragmenting, taking a small enough aliquot or a combination thereof." EX1012.0001. Figure 1(a) illustrates a process of adding oligonucleotide labels that serve as UMIs. *Id.* As Kivioja explains, the green, blue, and black lines in Figure 1(a) represent three different DNA species in the sample being analyzed. *Id.* Figure 1(a) goes on to show how the UMI could be used to categorize the reads. *Id.* There is no other information regarding the process in Figure 1(a) that would lead to a conclusion that the target sequence and the identifier were used in combination to identify duplicates.

Dr. Bustamante's testimony is in line with this interpretation. *See* EX2035.¶¶107-110. IDT points to statements from Dr. Bustamante's deposition, in which he stated that Kivioja dealt "with duplicate reads one way or another." Paper 29, 22. But IDT cannot point to any testimony from Dr. Bustamante that Kivioja dealt with duplicates in the same way as the challenged claims. To the contrary, Dr. Bustamante testified that Kivioja uses the molecular barcode sequence and genomic

alignment to identify duplicates. EX1124.0151:3-18, 152:7-13; *see also* EX2035.¶129 (“Kivioja considers each sequencing read contained within a UMI group as a duplicate of the other reads within the same grouping” based on the molecular barcode sequence (“label[]”) and genomic alignment (“gene and position”).).

IDT, therefore, has not shown that Kivioja discloses the claimed step of identifying duplicates and cannot meet its burden of showing the challenged claims would have been obvious.

B. Neither Iafrate Nor Kivioja Disclose Removing Duplicate Reads (Claim 2)

Like in its analysis of claim 1, IDT does not contend that Iafrate discloses the additional limitation required in claim 2, the removal of duplicate reads. IDT’s argument is based on Kivioja’s alleged disclosure of this additional element, but even IDT’s expert can only assert that duplicate reads “*might* be removed in the collapsing process.” EX2016.0113:20-114:1 (emphasis added). Dr. Sims’s interpretation is nothing more than speculation—there is nothing in Kivioja that suggests that sequencing reads are removed from the data set. *See* EX2016.0030; EX1012.

That Kivioja’s Figures 3(b) and (c) reflect different values does not provide any information on whether duplicates were removed. *See* Paper 29, 26-27. These

figures are comparing different metrics: the number of total reads in 3(b) versus the number of UMI families (each counted once as representing a unique molecule) in 3(c). EX1012.0002. The fact that the reads within each of the UMI families are not plotted in this comparison does not mean this data has been removed. Moreover, the data reported in 3(b) shows the data is in fact kept because the total reads are reported. EX1012.0002-03. Kivioja also reports the copy number within each UMI, further confirming that reads are kept. EX1012.0005 (“The mapped reads with the same gene, position and label were collected to one UMI and the number of such reads was recorded as the copy number of that UMI. Average copy numbers were 10.7 and 17.0 for samples taken after 15 and 25 PCR cycles, respectively.”); EX2035.¶116; *see also* EX1012.0002 (Fig. 3(d)). Supplemental Figure 4 presents the same type of data as Figure 3 and similarly does not provide the disclosures that IDT alleges. EX1012.0010.

Because there is no disclosure of the removal of duplicates, the combination of Kivioja and Iafrate cannot render obvious claim 2.

C. Petitioner’s Motivation to Combine Kivioja and Iafrate is Deficient

There cannot be a motivation to combine references to arrive at the challenged invention if the prior art does not disclose critical elements of the challenged claims. *See PAR Pharm.*, 773 F.3d at 1194 (emphasizing that “prior art references[’]”

fail[ure] to mention” a critical claim element does not support an obviousness finding). Therefore, any arguments regarding a motivation to combine Kivioja and Iafrate are legally irrelevant to an assessment of the challenged claims. *See id.* (“We first must determine whether TWi carried its burden to prove that all claimed limitations are disclosed in the prior art” before considering any motivation to combine arguments.).

Even if, however, the Board considers IDT’s motivation to combine arguments, Dr. Sims’s and IDT’s analysis is too conclusory to succeed. IDT claims that Dr. Sims provides testimony about the differences between the adaptors in Iafrate and Kivioja, but Dr. Sims does not provide sufficient explanation regarding why a POSA would pick and choose certain elements of each adaptor to arrive at the specific adaptor claimed. *See Ecolochem, Inc. v. S. Cal. Edison Co.*, 227 F.3d 1361, 1371 (Fed. Cir. 2000) (“We cannot use hindsight reconstruction to pick and choose among isolated disclosures in the prior art to deprecate the claimed invention.” (citations omitted)).

IV. TECAN’S DISCLAIMER OF CLAIMS IN OTHER PATENTS IS IRRELEVANT

IDT improperly attempts to cast a shadow over the challenged patent by reference to Tecan’s decision to disclaim other patents in the same family. As IDT recognized, the Federal Circuit has affirmed that a disclaimer of patent claims is

irrelevant to a patent holder's ability to defend previously issued patent claims. *Softview LLC v. Apple Inc.*, 108 F.4th 1366, 1373-75 (Fed. Cir. 2024). There was no substantive assessment or ruling by the Board or another tribunal regarding the disclaimed claims that could possibly be persuasive to the Board on the merits of the current dispute. Further, there is no legal basis for the Board to make an adverse inference against the challenged claims based on Tecan's decision to streamline the dispute between the parties to a single patent in this family. IDT's arguments are merely an attempt to muddy the current dispute with irrelevant atmospherics.

V. CONCLUSION

For the reasons set forth in Tecan's Response and further explained above, IDT has failed to meet its burden of showing that any challenged claim is unpatentable.

Dated: December 12, 2025

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CERTIFICATE OF WORD COUNT

The undersigned hereby certifies that the foregoing **PATENT OWNER'S SUR-REPLY** complies with the type-volume limitation of 37 C.F.R. §§ 42.24(a)(1)(i) and 42.24(b)(1). The Sur-Reply contains 4,967 words, excluding the parts exempted by 37 C.F.R. § 42.24(a)(1), as measured by the word-processing system used to prepare the Sur-Reply.

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The undersigned hereby certifies that a copy of the foregoing **PATENT OWNER'S SUR-REPLY** was served on December 12, 2025, via email to Petitioner by serving the correspondence addresses of record as follows:

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