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Datasheet for the decision of 9 March 2023

Case Number: T 1360/21 - 3.3.08

Application Number: 16170857.3

Publication Number: 3115468

IPC: C12Q1/68

Language of the proceedings: EN

Title of invention:
Increasing confidence of allele calls with molecular counting

Patent Proprietor:
Agilent Technologies, Inc.

Opponents:
Mathys & Squire LLP
James Poole Limited
Becton, Dickinson and Company

Headword:
confidence of allele calls/AGILENT TECHNOLOGIES

Relevant legal provisions:
EPC Art. 76(1), 112a(2)
EPC R. 106

Keyword:
Divisional application - subject-matter extends beyond content of earlier application (yes)
Obligation to raise objections - objection dismissed

Decisions cited:
G 0003/89, G 0011/91, G 0002/10

Catchword:

Europäisches Patentamt
European Patent Office
Office européen des brevets

Beschwerdekammern

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Case Number: T 1360/21 - 3.3.08

D E C I S I O N
of Technical Board of Appeal 3.3.08
of 9 March 2023

Appellant: (Patent Proprietor)	Agilent Technologies, Inc. 5301 Stevens Creek Boulevard Santa Clara, CA 95051 (US)
Representative:	Grünecker Patent- und Rechtsanwälte PartG mbB Leopoldstraße 4 80802 München (DE)
Respondent: (Opponent 1)	Mathys & Squire LLP The Shard 32 London Bridge Street London SE1 9SG (GB)
Representative:	Griffin, Philippa Jane Mathys & Squire The Shard 32 London Bridge Street London SE1 9SG (GB)
Respondent: (Opponent 2)	James Poole Limited One Southampton Row London WC1B 5HA (GB)
Respondent: (Opponent 3)	Becton, Dickinson and Company One Becton Drive Franklin Lakes, New Jersey 07417-1880 (US)
Representative:	Carpmaels & Ransford LLP One Southampton Row London WC1B 5HA (GB)

Decision under appeal: **Decision of the Opposition Division of the European Patent Office posted on 18 June 2021 revoking European patent No. 3115468 pursuant to Article 101(3)(b) EPC**

Composition of the Board:

Chair T. Sommerfeld
Members: B. Claes
R. Winkelhofer

Summary of Facts and Submissions

I. The appeal of the patent proprietor (appellant) lies from the decision of the opposition division revoking European patent No. 3 115 468 (patent), entitled "*Increasing confidence of allele calls with molecular counting*", granted on European patent application No. 16170857.3, filed as a divisional application of the earlier European patent application No. 13164430.4 (parent application), itself a divisional of the earlier application No. 11810645.9 (grandparent application). The grandparent application was filed as an international patent application published as WO 2012/038839.

II. Three oppositions were filed against the patent, and the opposition proceedings were based on the grounds for opposition in Article 100(a) EPC, in relation to novelty (Article 54 EPC) and inventive step (Article 56 EPC), and Article 100(b) and (c) EPC. The opposition division decided that the claims of a main request and 90 auxiliary requests related to added subject-matter contrary to, *inter alia*, Article 76(1) EPC and revoked the patent for this reason.

III. With the statement of grounds of appeal, the appellant maintained all claim requests on which the decision under appeal was based and argued that the claims of the main request and all 90 auxiliary requests had a basis in the grandparent application.

IV. Opponents 1 and 2 (respondents I and II, respectively) replied to the appeal.

V. In a communication pursuant to Article 15(1) RPBA, the board's preliminary opinion was expressed that claim 1 of the main request and each of auxiliary requests 1 to 90 did not comply with the requirements of Article 76(1) EPC.

VI. Oral proceedings were held with all parties except opponent 3 (respondent III) being represented. The appellant argued that the sets of claims of all requests complied with the requirements of Articles 76(1) and 123(2) EPC. The respondents considered none of these requests to comply with the requirements of Articles 76(1) and 123(2) EPC.

The appellant raised the following objection under Rule 106 EPC in conjunction with Article 112a(2) EPC.

"Written Submission during Oral Proceedings on March 9, 2022 in T1360/21 submitted by the Patent Proprietor (Appellant)

- Appellant presented arguments concerning the Main Request (MR) from about 9 am to about 10:05 am
- At the beginning of the pleading, Appellant indicated that they will focus initially on the arguments relevant for preliminary opinion given by the Board of Appeal (BoA), but assume that they will be given the chance to elaborate in a second round, in particular after the Respondents presented their arguments
- At about 10:05 am BoA announced a about 15 min break before the Respondents will be given to opportunity to respond
- After the break BoA indicted [*sic*] that they still consider the MR and all ARs to contravene Art. 123(2) and 76 EPC; debate was not explicitly closed on MR

- Respondents were not given the floor
- Appellant asked for brief break, which was granted by BoA
- After the break Appellant intended to present further arguments on MR, which was not allowed by BoA, despite that debate on MR had not been closed
- Appellant also pointed out during oral proceedings that debate on MR had not been closed
- This constitutes a procedural defect, which was objected to by the Appellant in oral proceedings and in writing herewith and which has been dismissed by the BoA"

VII. The appellant requested that the decision under appeal be set aside and amended such that the set of claims of the main request or, alternatively, of auxiliary requests 1 to 90 be held to comply with the requirements of Article 76(1) and 123(2) EPC, i.e. the patent be maintained on that basis.

The respondents requested that the appeal be dismissed and that the auxiliary requests not be considered.

Reasons for the Decision

Main request - claim 1 - added subject-matter (Article 76(1) EPC)

1. The claim results from a combination of independent claim 1 and dependent claim 4 as granted. Reference to features in claim 1 of the main request is in accordance with the feature numbering adhered to by the parties and in the decision under appeal (see point 4.1.1 of the Reasons for the decision).

Claim 1 of the main request, including the respective feature numbering (here (i) to (vii)), reads:

"1. A method for determining the minimum number of individual polynucleotide molecules originating from the same genomic region of the same original sample that have been sequenced in a particular sequence analysis configuration or process, including:

(i) attaching a degenerate base region (DBR) to starting polynucleotide molecules;

(ii) amplifying the DBR-attached starting polynucleotide molecules;

(iii) sequencing the amplified polynucleotide molecules, wherein the sequence of the DBR as well as a portion of the polynucleotide is obtained;

(iv) determining the number of different DBRs attached to a polynucleotide of interest; and

(v) using the number of different DBR sequences present in the sequencing run to determine the minimum number of individual polynucleotide molecules originating from the same genomic region of the same original sample that have been sequenced in the particular sequence analysis configuration or process;

(vi) wherein the method includes pooling polynucleotide molecules from a plurality of original samples, wherein the polynucleotide molecules derived from each original sample include a multiplex identifier (MID) tag, wherein each original sample is correlated with a unique MID such that the original sample from which each tagged polynucleotide molecule was derived can be determined, and

(vii) including determining a statistical value for an allele call in a genotyping assay that cannot be derived from the read number alone."

2. The opposition division concluded, *inter alia*, that the grandparent application did not directly and unambiguously disclose the combination of the pooling step (vi) in a method for determining the *minimum* number of individual polynucleotide molecules as referred to in the preamble and step v) referred to in the claim. The claim thus failed to meet the requirements of Article 76(1) EPC.

3. Any amendment to a European patent application or a European patent (Article 123(2) EPC) can only be made within the limits of what a skilled person would derive directly and unambiguously, using common general knowledge, and seen objectively and relative to the date of filing, from the whole of these documents as filed (see decisions G 3/89, OJ EPO 1993, 117; G 11/91, OJ 1993, 125 and G 2/10, OJ 2012, 376 referring to this test as gold standard). When determining whether the subject-matter of a divisional application extends beyond the content of the earlier application as filed (Article 76(1), second sentence, EPC), the same principles apply for extension of subject-matter under Article 123(2) EPC.

4. The first paragraph under the heading "Summary of the invention" in the description of the grandparent application reads:

(page 1, line 29 to page 2, line 8)
"*Aspects of the present invention include methods and compositions for determining the number of individual polynucleotide molecules originating from the same genomic region of the same original sample that have been sequenced in a particular sequence analysis configuration or process. In these aspects of the*

invention, a degenerate base region (DBR) is attached [(i)] *to the starting polynucleotide molecules that are subsequently sequenced* [(iii)] *(e.g., after certain process steps are performed, e.g., amplification* [(ii)] *and/or enrichment). The number of different DBR sequences* [(iv)] *present in a sequencing run can be used to determine/estimate the number of individual polynucleotide molecules originating from the same genomic region of the same original sample* [(v) without reference to 'minimum number'] *that have been sequenced in a particular sequence analysis configuration or process. DBRs can be used to improve the analysis of many different nucleic acid sequencing applications. For example, DBRs enable the determination of a statistical value for an allele call* [(vii)] *in genotyping assays that cannot be derived from the read number alone*." (Emphasis added; the respective features in the claim are added in square brackets)

5. The board concurs with the appellant that this paragraph may serve as disclosure of a method for determining the number of individual polynucleotide molecules originating from the same genomic region of the same original sample (i.e. the combination of features (i) to (iv) and (vii) of the claim). However, it fails to disclose the combination with two particular further features of the claimed subject-matter: i.e. the pooling step (vi) and the provision in the preamble of the claim and feature (v) that the determined number of individual polynucleotide molecules originating from the same genomic region of the same original sample that has been sequenced is the "minimum" number.

6. The appellant referred to a number of passages in the description of the grandparent application as

disclosing the pooling step (vi). For ease of reference, the passages referred to are reproduced here with emphasis added:

(page 2, lines 9 to 22)
"I*n certain embodiments, aspects of the subject invention are drawn to methods of determining the number of starting polynucleotide molecules sequenced from multiple different samples. In certain embodiments, the method includes: (1) attaching an adapter to starting polynucleotide molecules in multiple different samples, where the adapter for each sample includes: a unique MID specific for the sample; and a degenerate base region (DBR) (e.g., a DBR with at least one nucleotide base selected from: R, Y, S, W, K, M, B, D, H, V, N, and modified versions thereof); (2) pooling the multiple different adapter-attached samples to generate a pooled sample; (3) amplifying the adapter-attached polynucleotides in the pooled sample; (4) sequencing a plurality of the amplified adapter-attached polynucleotides, where the sequence of the MID, the DBR and at least a portion of the polynucleotide is obtained for each of the plurality of adapter-attached polynucleotides; and (5) determining the number of distinct DBR sequences present in the plurality of sequenced adapter-attached polynucleotides from each sample to determine or estimate the number of starting polynucleotides from each sample that were sequenced in the sequencing step.*"

(page 7, lines 13 to 17)
"*For example, a nucleic acid sample may be a pool of polynucleotides derived from different sources, (e.g., polynucleotides derived from different individuals, different tissues or cells, or polynucleotides isolated at different time points), where the polynucleotides*

from each different source are tagged with a unique MID."

(page 17, lines 8 to 14)
"*DBRs also find use in performing genetic analyses on pooled polynucleotide samples in which each polynucleotide in the pooled sample includes a MID specific for its sample of origin (described in detail below). This allows a user to determine the sequence coverage of a specific polynucleotide species (or multiple species) from each of the samples of origin that were combined to generate the pooled sample. Thus, embodiments of the present invention include sequence analysis of polynucleotides in a pooled sample, where each polynucleotide contains a MID and a DBR.*"

(page 18, lines 20 to 31)
"*... the nucleic acid sample is a pool of nucleic acids extracted from a plurality of sources (e.g., a pool of nucleic acids from a plurality of organisms, tissues, cells, subjects, etc. (...)*
In certain embodiments, nucleic acid fragments that are to be pooled with nucleic acid fragments derived from a plurality of sources (e.g., a plurality of organisms, tissues, cells, subjects, etc.), where by "plurality" is meant two or more. In such embodiments, the nucleic acids derived from each source include a multiplex identifier (MID) such that the source from which each tagged nucleic acid fragment was derived can be determined."

(page 31, lines 5 to 33)
"*Another application of DBRs is in performing genetic analyses on pooled polynucleotide samples in which each polynucleotide in the pooled sample includes a MID specific for its sample of origin (described in detail*

above). This allows a user to determine the sequence coverage of a specific polynucleotide species (or multiple species) from each of the samples of origin that were combined to generate the pooled sample. This provides a mechanism to make sure that the polynucleotides from each starting sample in the pooled sample are represented adequately. (...)
Pooled sample analyses using MIDs and DBRs finds us [sic] *in numerous genetic analyses, including making allele calls, error correction of sequences, relative and quantitative gene expression analyses, and the like. It is noted that in analyzing polynucleotides in a pooled sample according to aspects of the present invention, it is important to maintain both the MID and DBR domains in each step of the workflow being employed, as loss of one or the other domain will negatively impact the confidence in the results obtained.*
It is further noted that the use of MID and DBR domains in genetic analysis is especially powerful when combined with next-generation sequencing (NGS) platforms, many of which provide sequence data for each individual polynucleotide present in the sample to be sequenced. In contrast to conventional sequencing approaches in which individual clones of polynucleotides are sequenced independently, NGS platforms provide sequences for multiple different polynucleotides in a sample simultaneously. This difference allows for sample-specific statistical analyses to be done which are not constrained by having to clone and independently sequence each polynucleotide. Thus, the MID/DBR domain analyses described herein synergize with NGS platforms, providing improved statistical approaches to analyze the very large amounts of sequence data from pooled samples."

7. The board concurs with the appellant that a basis can be identified in the grandparent application for the step corresponding to feature (vi) of the claimed method (pooling step) and a combination of it with methods for determining the number of individual polynucleotide molecules originating from the same genomic region of the same original sample, i.e. the combination of features (i) to (iv) and (vii) of the claim, on page 1, line 29 to page 2, line 8 (see point 5. above).

8. As to the parts of the grandparent application on which the appellant relies in support of the disclosure of the pooling step (vi), these are either kept general without specific reference to the aim of determining the number of individual polynucleotide molecules (see the passages on pages 7 and 18 reproduced in point 6.) or (as in the paragraphs on pages 2, 17 and 31 reproduced in point 6.) refer to the aim "*to determine or estimate the number of starting polynucleotides from each sample*" (page 2) or "*to determine the sequence coverage of a specific polynucleotide species (or multiple species) from each of the samples of origin*" (pages 17 and 31). These passages are therefore either explicitly (page 2) or implicitly ("gene coverage", pages 17 and 31) in the context of "*determining the number of individual polynucleotide molecules*" (emphasis added), as is the basic method, which is disclosed on page 1, line 29 to page 2, line 8 of the grandparent application (see point 5. above).

9. The board cannot, however, concur with the appellant that because the passages on pages 17 and 31 on pooling step (vi) teach that the use of DBRs in accordance with the overall technical teaching of the application

"allows" determining the sequence coverage, the determination of the number of individual polynucleotide molecules referred to in these passages constituted an optional embodiment. On the contrary, these passages in fact frame the use of pooled polynucleotide samples including a MID specific for its sample of origin in the very aim of the basic methods for determining the number of individual polynucleotide molecules originating from the same genomic region of the same original sample (combination of features (i) to (iv) and (vii) of the claim disclosed on page 1, line 29 to page 2, line 8, see point 5. above).

10. The sole disclosure of the notion "minimum number" in the grandparent application is in the following passage:

(page 19, lines 14 to 26)
"*Aspects of the present invention include methods and compositions for determining or estimating the number of individual polynucleotide molecules originating from the same genomic region of the same original sample that have been sequenced in a particular sequence analysis configuration or process. In these aspects of the invention, a degenerate base region (DBR) is attached to the starting polynucleotide molecules that are subsequently sequenced (e.g., after certain process steps are performed, e.g., amplification and/or enrichment, e.g., PCR). As detailed below, evaluating the number (and in some cases, the combination) of different DBR sequences present in a sequencing run allows the establishment of the number (or minimum number) of different starting polynucleotides that have been sequenced for a particular polynucleotide (or region of interest; ROI). This number can be used, for example, to give a*

statistical measure of confidence in allele calls, thus increasing the confidence in making such allele determinations (e.g., when calling homozygous alleles)." (Emphasis added)

11. The passages relating to pooling step (vi) in the grandparent application are, also in this context, either kept general without specific reference to the aim of determining the number of individual polynucleotide molecules or are in the context of "*determining the number of individual polynucleotide molecules*" (emphasis added), as is the aim of the general method disclosed on page 1, line 29 to page 2, line 8 of the grandparent application (see point 7.), and the above-quoted passage on page 19 lacks any reference to a method for establishing the number (or minimum number) of different starting polynucleotides sequenced for a particular polynucleotide including a step of pooling samples. Therefore, the skilled person would not directly and unambiguously derive from the passage on page 19 a disclosure of the method in claim 1 combining the "pooling" step disclosures also with the feature of the determination of the *minimum* number of individual polynucleotide molecules.

12. The appellant argued that the skilled person would realise that typically any pool of DBRs used in the disclosed method still had some redundancy, i.e. multiple copies of a specific DBR sequence, and that thus collisions could never be completely ruled out. Reference was made to the following disclosure on page 23 of the grandparent application:

(page 23, lines 22 to 34)
"*It is noted here that in many embodiments, it is not possible to conclude that polynucleotides having*

identical DBR sequences are derived from the same parent polynucleotide molecule, as multiple identical DBRs may be present in the DBR-attached polynucleotides. For example, if an adapter population that contains a DBR of two N bases is used to tag a sample containing more that [sic] *16 polynucleotides, a subset of the tagged polynucleotides will have identical DBRs, and thus it will not be possible to determine that their sequences were derived from different parent polynucleotide molecules.*
One exemplary way to determine more accurately the actual number of starting or parent molecules would be to increase the degeneracy of DBRs (i.e., to increase the number of unique sequences in the DBR used to label the particular sample of interest) so that every single molecule is likely to have a different DBR. In any event we can, in exemplary methods, either use the number of observed DBRs or else the probability distribution of the expected number of reads likely to produce the observed number of DBRs."

13. The appellant submitted that the skilled person understood from the fundamental principles underlying the invention that the general challenge of a collision always existed and that the determined number of individual polynucleotide molecules always constituted an approximation of the actual number, which might be greater. Consequently, the skilled person understood that the determined number was always a minimum number, and this understanding spilled over to all disclosed embodiments of the invention.

14. Any reference in the grandparent application to the use of DBRs in performing "genetic analyses" on pooled polynucleotide samples was thus understood by the skilled person in accordance with the invention to

refer to the use of DBRs for determining the minimum number of individual polynucleotide molecules. The pooling step (vi) and the feature of determining the minimum number of individual polynucleotides originating from the same genomic region of the same original sample did not therefore constitute different embodiments.

15. This argument is not persuasive. In fact, the passage referred to on page 23 does not directly and unambiguously establish the skilled person's understanding of the disclosure of the grandparent application that the minimum number of individual polynucleotide sequences is always equivalent to or inherently the number of individual polynucleotide sequences. Indeed, from the cited passage, the skilled person is, by the same token, equally cautioned to provide for a sufficiently high DBR degeneracy so that collision would be minimised or would not occur when aiming at determining the number of individual polynucleotide molecules. Consequently, the board disagrees with the appellant that the skilled person understood that the determined number was always a minimum number and that this understanding spilled over to all disclosed embodiments of the invention, including those relating to pooling step (vi).

16. The board accordingly agrees with the opposition division that claim 1 of the main request relates to added subject-matter contrary to Article 76(1) EPC.

Auxiliary requests

Admittance

17. The respondents requested that the auxiliary requests not be considered in appeal and that the board thus overturn the opposition divisions decision to admit these requests in the opposition proceedings. In view of the board's conclusion on the issue of added subject-matter (see points 19. and 20. below), there is no need to deal with this question.

Amendments (Articles 76(1) EPC)

18. Compared to claim 1 of the main request (see point 1.), **auxiliary requests 1 to 42** include one or more of the following additional features (numbering as referred to by the appellant when filing these auxiliary requests with the submission of 23 September 2019, pages 6 to 9):

- amendment C: "to increase the confidence in an allele call"
- amendment D: "based on the minimum number of individual polynucleotide molecules"
- amendment E: "using a probability distribution ..."
- amendment F: "using maximum likelihood estimation ..."
- amendment G: the features of dependent claims 11 and 12 as granted
- amendment H: the features of dependent claim 13 as granted
- amendment I: "PCR reaction"
- amendment J: "... removed or inactivated ..."
- amendment K:"... inactivated ..."
- amendments L to N: "... first, second or third cycle", "... first cycle" or "... third cycle", respectively
- amendment 0: "wherein DBR-containing primer is part of a PCR primer pair ..."

- amendment P: DBR-containing primer with higher Tm, second set of primers with lower Tm

Dependent claims 11 to 13 (see amendments G and H) of the patent as granted read:

"11. A method as claimed in claim 1, wherein the DBR is present in a nucleic acid synthesis primer, such that the DBR is added to a target polynucleotide when the primer is used in a polymerization reaction.

12. A method as claimed in claim 11, wherein the nucleic acid synthesis primer is a PCR primer.

13. A method as claimed in claim 12, including determining the number of starting molecules used as templates for a PCR reaction."

The following chart (submitted with the same submission) provides an overview of which auxiliary request (AR) includes which additional feature(s):

Auxiliary Claim Request (AR)	Amendments to claim 1															
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
	Claim 4 → Claim 1	"from a plurality of sources"	"to increase the confidence in an allele call"	"based on the minimum number of individual polynucleotide molecules"	"using probability distribution..."	"using maximum likelihood estimation..."	claims 11+12→ claim 1	claim 13→ claim 1	"PCR reaction"	"...removed or inactivated..."	"...inactivated..."	"...first, second or third cycle..."	"...first cycle..."	"...third cycle..."	"wherein DBR-containing primer is part of a PCR primer pair..."	DBR-containing primer with higher Tm, second set of primers with lower Tm
MR	•															
AR1	•		•													
AR2	•		•	•												
AR3	•				•	•										
AR4	•					•										
AR5	•		•		•	•										
AR6	•		•			•										
AR7	•						•									
AR8	•						•	•								
AR9	•						•		•							
AR10	•						•		•	•		•				
AR11	•						•		•	•			•			
AR12	•						•		•	•				•		
AR13	•						•		•	•		•			•	
AR14	•						•		•	•			•		•	
AR15	•						•		•	•				•	•	
AR16	•						•		•		•	•				
AR17	•						•		•		•		•			
AR18	•						•		•		•			•		
AR19	•						•		•		•	•			•	
AR20	•						•		•		•		•		•	
AR21	•						•		•		•			•	•	
AR22	•						•		•			•				•
AR23	•						•		•				•			•
AR24	•						•		•					•		•
AR25	•		•			•	•									
AR26	•		•			•	•	•								
AR27	•		•			•	•		•							
AR28	•		•			•	•		•	•		•				
AR29	•		•			•	•		•	•			•			
AR30	•		•			•	•		•	•				•		
AR31	•		•			•	•		•	•		•			•	
AR32	•		•			•	•		•	•			•		•	
AR33	•		•			•	•		•	•				•	•	
AR34	•		•			•	•		•		•	•				
AR35	•		•			•	•		•		•		•			
AR36	•		•			•	•		•		•			•		
AR37	•		•			•	•		•		•	•			•	
AR38	•		•			•	•		•		•		•		•	
AR39	•		•			•	•		•		•			•	•	
AR40	•		•			•	•		•			•				•
AR41	•		•			•	•		•				•			•
AR42	•		•			•	•		•					•		•

Auxiliary requests 43 to 85 were filed by the appellant with the submission of 26 March 2021.

Claim 1 of **auxiliary request 43** differs from claim 1 of the main request (see point 1. above) by the fourfold replacement of the wording "original sample(s)" in feature (vi) with the wording "source(s)".

Claim 1 of **auxiliary requests 44 to 85** equally includes the same fourfold amendment in feature (vi) as auxiliary request 43 and further includes the same amendments C to P as included in auxiliary requests 1 to 42 filed on 23 September 2019 (see chart above).

Auxiliary requests 86 to 89 were filed with the submission of 22 July 2020.

Claim 1 of **auxiliary request 86** differs from claim 1 of the main request (see point 1. above) by the insertion of the wording "prior to sequencing" at the end of the wording "wherein the method includes pooling polynucleotide molecules from a plurality of original samples" in feature (vi) and the addition of the following wording at the end of the claim:

", wherein the DBR is added to the starting polynucleotides as part of an adapter,
wherein the DBR comprises at least one degenerate nucleotide base selected from the group consisting of (i)-(xi): (i) A or G, (ii) C or T, (iii) G or C, (iv) A or T, (v) G or T, (vi) A or C, (vii) C or G or T, (viii) A or G or T, (ix) A or C or T, (x) A or C or G and (xi) any base,
wherein the attaching comprises attaching the adapter to the starting polynucleotide molecules in each original sample and the adapter comprises the unique MID,
and wherein the sequencing comprises obtaining the sequence of the MID."

Claim 1 of **auxiliary request 87** differs from claim 1 of auxiliary request 86 in that it recites "a plurality of <u>different</u> original samples" in feature vi) (emphasis indicates the insertion). Claim 1 of **auxiliary**

request 88 differs from claim 1 of auxiliary request 86 in that the feature "and wherein the sequencing comprises obtaining the sequence of the MID" is deleted. Similar to claim 1 of auxiliary request 87, claim 1 of **auxiliary request 89** recites "a plurality of different original samples" in combination with all features of auxiliary request 88.

Claim 1 of **auxiliary request 90** (filed with the submission of 20 May 2021) is identical to previously filed auxiliary request 87 in all aspects, with the only exception that the first "wherein" clause in feature (vi) is amended to "wherein the method includes pooling polynucleotide molecules from a plurality of different original samples prior to sequencing and amplifying" (emphasis indicates the insertion).

Auxiliary requests 1 to 42 and 44 to 89

19. The appellant has not submitted dedicated arguments for these auxiliary requests but merely referred to the reasons submitted why the claims of the main request did not relate to added subject-matter. However, the board's reasoning on why the claims of the main request related to added subject-matter apply *mutatis mutandis* also to the claims of these auxiliary requests. The amendments in these requests thus do not comply with Article 76(1) EPC.

Auxiliary requests 43 and 90

20. The board's considerations in points 11. and 15. above equally apply to these requests. These auxiliary requests thus equally do not comply with the requirements of Article 76(1) EPC.

Objection under Rule 106 EPC in conjunction with Article 112a(2) EPC

21. During the oral proceedings, the appellant raised an objection under Rule 106 EPC in conjunction with Article 112a(2)(c) EPC (see section VI.).

22. The objection concerns the board's refusal of the appellant's wish to present further arguments under Article 76(1) EPC on claim 1 of the main request after the Chair had announced - after deliberation on the matter - the view of the board that the requirements of Article 76(1) EPC were not fulfilled and after a subsequent break at the request of the appellant (see section VIII. for the text of the objection).

23. In the appellant's view, the debate on the main request had not been concluded. Thus, the refusal of their wish to present further arguments constituted a violation of the right to be heard as guaranteed in Article 113(1) EPC.

24. As acknowledged by the appellant in their written objection, at the beginning of the oral proceedings they had been given, for more than an hour, the opportunity to present arguments on the requirements of Article 76(1) EPC for claim 1 of the main request. Furthermore, as also acknowledged in the written objection, in their pleading, the appellant had focused on the arguments as outlined in the (negative) preliminary opinion of the board (see points 15 to 20 of the communication pursuant to Article 15(1) RPBA and section V. above).

25. The appellant thus had presented their arguments at length in a first round of pleading. These arguments

did not, after deliberation, convince the board to overhaul its view on Article 76(1) EPC, as expressed in the communication pursuant to Article 15(1) RPBA. Thus, the appellant's right to be heard was not compromised in any way.

26. The mere fact that there has been no need to give the floor to the respondents also during the oral proceedings on the requirements of Article 76(1) EPC for claim 1 of the main request does not have any bearing in this context. Contrary to what is seemingly argued by the appellant, there is no absolute right to be given a second round of pleading, in particular where no further arguments have been brought forward by the board or another party, as in the case in hand. The appellant, in the first round, had been given the opportunity to present everything they deemed fit, without being interrupted or cut short.

27. Therefore, the objection under Rule 106 EPC in conjunction with Article 112a(2) EPC had to be dismissed.

Order

For these reasons it is decided that:

The appeal is dismissed.

The Registrar: The Chair:

B. Brückner T. Sommerfeld

Decision electronically authenticated