Unified Patent Court
Einheitliches Patentgericht
Juridiction unifiée du brevet

Action n°: UPC 252/2023

Revocation action

DECISION

of the Court of First Instance of the Unified Patent Court

Central Division (Section Munich)
delivered on 17 October 2024
concerning EP 2 794 928 B1

HEADNOTES:

1. The Court must examine its international jurisdiction of its own motion when this is required under Union law.

2. Pursuant to Art. 30 of the Brussels I recast Regulation, the UPC may stay proceedings where a related action is pending in a national court. In view of the circumstances of the case the Central Division does not exercise its discretionary power to stay the proceedings.

3. The assessment of novelty within the meaning of Art. 54(1) EPC requires the determination of the whole content of the prior publication. It is decisive whether the subject-matter of the claim with all its features is directly and unambiguously disclosed in the prior art citation.

4. Under the front-loaded system of UPC proceedings, parties are under an obligation to set out their full case as early as possible. Permission for subsequent request to amend under Rule 50.2 RoP in connection with Rule 30.2 RoP is not given as the auxiliary request could and should have been filed earlier.

KEYWORDS:

International jurisdiction. *Lis pendens*. Related actions. Parallel national revocation action. Articles 29-32 Regulation Brussels I recast. Novelty. Inventive step. Subsequent application to amend. Rule 30.2 RoP. Auxiliary requests.

ACT_551180/2023 (UPC_CFI_252/2023)

CLAIMANT:

NanoString Technologies Europe Limited, Suite 2, First Floor, 10 Temple Back - BS1 6FL - Bristol - GB

represented by Daniela Kinkeldey of Bird & Bird.

DEFENDANT:

President and Fellows of Harvard College, 17 Quincy Street - 02138 - Cambridge, MA - US

represented by Axel Berger of Bardehle Pagenberg.

PATENT AT ISSUE

European patent **EP 2 794 928 B1,** hereafter referred to as ´the Patent´.

PANEL/DIVISION

Panel 1 of the Central Division (Section Munich).

DECIDING JUDGES

This decision has been delivered by the presiding judge Ulrike Voß, the legally qualified judge András Kupecz as judge-rapporteur and the technically qualified judge Eric Enderlin.

DATE OF THE ORAL HEARING

18 September 2024.

SUMMARY OF FACTS AND REQUESTS

1 Procedural background and the proceedings before the Central Division

1.1 On 27 July 2023, NanoString Technologies Europe Limited (the 'Claimant') brought the present Revocation action in the Central Division (Section Munich) (´Central Division´) against President and Fellows of Harvard College (the 'Defendant').

1.2 On 29 July 2022 NanoString Technologies Germany GmbH brought a revocation action against the German national part of EP 2 794 928 to the German Federal Patent Court (´BPatG´, the action is referred to as ´the German Revocation action´). The Claimant and NanoString Technologies Germany GmbH have the same parent company: NanoString Technologies, Inc. (USA). After the hearing in the German Revocation action, which was held on 7 May 2024, the BPatG held that the Patent was invalid and revoked the (German part of the) Patent in its entirety. The written grounds for the decision have been submitted in these proceedings as document D60.

1.3 A request for provisional measures by the Defendant and 10x Genomics, Inc. against NanoString Technologies, Inc. and NanoString Technologies Germany GmbH based on the Patent was rejected by the Munich Local Division by order dated 10 October 2023 in case UPC_CFI_17/2023 (ACT_459996/2023) amongst others on the ground that the validity of the Patent was insufficiently certain (D49, p. 35-36).

1.4 The Defendant is also the owner of EP 4 108 782 B1 (EP ´782), which is a (second generation) divisional patent of the Patent. The Local Division Munich in case UPC_CFI_2/2023 (ACT_459746/2023) granted a request for provisional measures based on EP ´782 by order dated 19 September 2023 (submitted in these proceedings as BP4). By order dated 26 February 2024, the Court of Appeal ('CoA') set aside the order of the Local Division on the grounds that, in sum, the CoA on the balance of probabilities, considered it to be more likely than not that the subject matter of EP ´782 will prove to be unpatentable for lack of inventive step over Göransson, document D10 in these proceedings (also referred to as the ´CoA Order in *NanoString/10x Genomics*´). EP ´782 is under opposition at the EPO.

1.5 In the present Revocation action, the Defendant lodged a Preliminary Objection relating to *lis pendens* in view of the German Revocation Action (´PO´). The judge-rapporteur informed the parties by order dated 4 October

2023 that the PO is to be dealt with in the main proceedings (Rule 20.2 RoP). The PO was withdrawn at the oral hearing.

1.6 The Defendant filed a subsequent application to amend the patent in response to the CoA order in *NanoString/10x Genomics*. By order dated 8 March 2024, the judge-rapporteur informed the parties that the panel would decide at the oral hearing whether permission will be granted, should the new auxiliary request and its admissibility become relevant. The Claimant was allowed to submit arguments on the validity of the new auxiliary request so that this could be discussed in case necessary.

1.7 The oral hearing in the present proceedings was originally scheduled for 17 April 2024. After the Claimant´s parent company filed for relief under Chapter 11 of title 11 of the US Bankruptcy Code in February 2024, the hearing in this revocation action was, upon suggestion by the Claimant (with the consent of the Defendant), rescheduled to 18 September 2024. The Claimant informed the Court that the assets of the NanoString group of entities (which includes certain subsidiaries such as the Claimant) have been purchased and that this change in ownership does not affect the present proceedings.

2 The Patent

2.1 EP 2 794 928 B1 entitled "*Compositions and methods for detecting analytes*" was filed on 21 December 2012 (the application as filed was submitted as document D2 in these proceedings). The Patent claims priority to US 201161579265 P of 22 December 2011. The validity of the priority date was not challenged by the Claimant.

2.2 The Patent was granted on 20 February 2019. No opposition was filed. The registered owner of the Patent is the Defendant.

2.3 The Patent is in force in the UPC Contracting Member States Germany (DE), the Netherlands (NL) and France (FR).

2.4 The Claims of the Patent as granted read:

> *1. A method for detecting a plurality of analytes in a sample, comprising:*
>
> *a. contacting the sample with a composition comprising a plurality of detection reagents, wherein each subpopulation of the detection reagents targets at least one different analyte, wherein the analyte is fixed on a solid substrate or support and wherein the solid substrate or support is a chip, a microarray, a blotting membrane or a microscopic slide, and wherein each detection reagent comprises:*
> *at least one probe reagent targeting an analyte and at least one nucleic acid label comprising a plurality of predetermined subsequences, wherein said at least one probe reagent and said at least one nucleic acid label are conjugated together; and wherein at least a portion of said plurality of pre-determined subsequences form an identifier of said at least one probe reagent;*
>
> *b. removing any unbound detection reagents;*
>
> *c. detecting in a temporally-sequential manner said plurality of pre-determined subsequences of said detection reagent, wherein said detection of the subsequences comprises:*
>
> > *i) hybridizing a set of decoder probes with a subsequence of the detection reagents, wherein each subpopulation of said decoder probes comprises an optical detectable label, each optical detectable label generating an optical signal signature corresponding to each subsequence;*
> > *ii) detecting said optical signal signature produced upon the hybridization of said set of decoder probes and obtaining an image;*

iii) removing said optical signal signature produced by the hybridization of said set of decoder probes;
iv) repeating steps (i) through (iii) for other subsequences of said detection reagents, thereby producing a temporal order of optical signal signatures corresponding to the plurality of pre-determined subsequences,
wherein the temporal order of the optical signal signatures corresponding to said plurality of pre-determined subsequences of said detection reagent identifies a subpopulation of the detection reagents and is unique for each subpopulation of the detection reagents; and

d. comparing said temporal order of the optical signal signatures with different identifiers of said at least one probe reagent, wherein an agreement between the temporal order of the optical signal signatures and a particular identifier of said at least one probe reagent identifies the analyte in the sample.

2. The method of claim 1, wherein:

(i) said each subpopulation of the detection reagents targets a set of analytes; and/or
(ii) said detection reagents are present in a soluble phase.

3. The method of claim 1 or claim 2, further comprising processing said sample before said contacting with said plurality of detection reagents.

4. The method of any previous claim, further comprising measuring the intensity of the optical signal signatures generated from each subpopulation of the detection reagents, preferably wherein the intensity of the optical signal signatures generated from each subpopulation of the detection reagents indicates an amount of the analyte, and/or preferably wherein the intensity of the optical signal signatures generated from each subpopulation of the detection reagents is used in identification of the subpopulation of the detection reagents.

5. The method of any previous claim, wherein:

(i) said each subpopulation of the decoder probes comprises a different optical detectable label, each different optical detectable label producing a different optical signal signature; and/or
(ii) said each subpopulation of the decoder probes is at least partially or completely complementary to said subsequence of the detection reagents; and/or

(iii) at least two or more subpopulations of the decoder probes are at least partially or completely complementary to the same subsequence of the detection reagents.

6. The method of any previous claim, wherein said removing of the optical signal signature is performed by washing, heating, photobleaching, displacement, cleavage, enzymatic digestion, quenching, chemical degradation, bleaching, oxidation or any combinations thereof.

7. The method of any previous claim, wherein:

(i) said optical detectable label comprises or is an optical label selected from the group consisting of a small molecule dye, a fluorescent molecule, a fluorescent protein, a quantum dot, Raman label, a chromophore, and any combinations thereof; and/or
(ii) said optical detectable label comprises or is a colourimetric reagent; and/or
(iii) said optical detectable label comprises or is a Raman label.

8. The method of any previous claim, wherein said optical signal signatures comprise signatures of fluorescent colour, visible light, no-colour, Raman label, or any combinations thereof, or wherein said optical signal signatures comprise signatures of one or more fluorescent colours, one or more visible lights, one or more no-colours, one or more Raman labels, or any combinations thereof.

9. The method of any previous claim, wherein said analytes are selected from the group consisting of antigens, receptors, proteins, peptides, sugars, glycoproteins, peptidoglycans, lipids, nucleic acids, oligonucleotides, cells, viruses, and any combinations thereof, preferably wherein said nucleic acids are selected from the group consisting of cellular DNA or RNA, messenger RNA, microRNA, ribosomal RNA, and any combinations thereof.

10. The method of any previous claim, wherein:

(i) said sample is a protein sample immobilized on a solid support, preferably wherein the solid support is a blotting membrane; or
(ii) said sample is a biological sample, preferably wherein said biological sample comprises one or more cells, one or more tissues, one or more fluids or any combinations thereof, and/or preferably (a) wherein said biological sample comprises blood, sputum, cerebrospinal fluid, urine, saliva, sperm, sweat, mucus, nasal discharge, vaginal fluids or any combinations thereof, or (b) wherein said biological sample comprises a biopsy, a surgically removed tissue, a swap or any combinations thereof; or

(iii) said sample comprises an environmental sample, food, food byproduct, soil, an archaeological sample, an extraterrestrial sample, or any combinations thereof.

11. The method of any previous claim, wherein said at least one probe reagent and said at least one nucleic acid label are conjugated together by at least one linker, preferably wherein:

(i) said linker is a bond; and/or
(ii) said linker is a linker molecule, preferably wherein said linker molecule is a polymer, sugar, nucleic acid, peptide, protein, hydrocarbon, lipid, polyethylene glycol, crosslinker, or any combinations thereof; and/or
(iii) said linker is multivalent, preferably wherein when the multivalent linker is an avidin-like molecule, both the probe reagent and the nucleic acid label are biotinylated.

12. The method of claim 11, wherein said linker is a particle, preferably wherein:

(i) said particle is selected from a group consisting of a gold nanoparticle, a magnetic bead or nanoparticle, a polystyrene bead, a nanotube, a nanowire, a microparticle, and any combinations thereof, preferably wherein said particle is a nanoparticle; and/or
(ii) said particle is modified; and/or
(iii) said particle is coated with streptavidin or a derivative thereof; and/or
(iv) said particle is modified with at least one functional group, preferably wherein said at least one functional group is selected from the group consisting of amine, carboxyl, hydroxyl, aldehyde, ketone, tosyl, silanol, chlorine, hydrazine, hydrazide, photoreactive groups, and any combinations thereof.

13. The method of any previous claim, wherein:

(i) said at least one probe reagent is selected from the group consisting of a nucleic acid, an antibody or a portion thereof, an antibody-like molecule, an enzyme, a cell, an antigen, a small molecule, a protein, a peptide, a peptidomimetic, a sugar, a carbohydrate, a lipid, a glycan, a glycoprotein, an aptamer, and any combinations thereof; and/or
(ii) said at least one probe reagent is modified; and/or
(iii) said at least one probe reagent is biotinylated.

14. The method of any previous claim, wherein:

(i) said at least one nucleic acid label is single-stranded, double-stranded, partially double-stranded, a hairpin, linear, circular, branched, a concatemer, or any combinations thereof; and/or
(ii) said at least one nucleic acid label is modified; and/or
(iii) said at least one nucleic acid label is designed for minimal cross-hybridization of bases with each other; and/or
(iv) said at least one nucleic acid label is conjugated to at least one detectable molecule, preferably wherein said at least one detectable molecule is an optical molecule selected from the group consisting of a small molecule dye, a fluorescent protein, a quantum dot, a Raman label, a chromophore, and any combinations thereof.

15. The method of any previous claim, wherein said plurality of pre-determined subsequences are conjugated together by at least one sequence linker, preferably wherein (a) said sequence linker is a bond, and/or (b) said sequence linker is a nucleotidic linker, preferably wherein said nucleotidic linker is single-stranded, double-stranded, partially double-stranded, a hairpin or any combinations thereof, and/or preferably wherein said nucleotidic linker is at least one nucleotide long.

16. The method of any previous claim, wherein:

(i) said detection reagent comprises one probe reagent and a plurality of nucleic acid labels; or
(ii) said detection reagent comprises a plurality of probe reagents and a nucleic acid label; or
(iii) said detection reagent comprises a plurality of probe reagents and a plurality of nucleic acid labels.

17. The method of any previous claim, wherein:

(i) the method is used in immunofluorescence; and/or
(ii) the method is used in immunohistochemistry; and/or
(iii) the method is used in fluorescence in situ hybridization; and/or
(iv) the method is used in western blot.

3 Requests of the Parties

3.1 The Claimant argues that the Patent is invalid based on the grounds that its subject matter is not patentable within the terms of Arts. 52 to 57 EPC (Art. 65(1),(2) UPCA in combination with Art. 138(1)(a) EPC), since it lacks novelty (Art. 54 EPC) and is not based on an inventive step (Art. 56 EPC); the Patent does not disclose the invention in a manner sufficiently clear and complete for it to be carried out by a person skilled in the art (Art. 65(1), (2) UPCA in combination with Art. 138(1)(b) EPC); and that subject matter of the Patent extends beyond the content of the earlier applications as filed (Art. 65(1), (2) UPCA in combination with Art. 138(1)(c) EPC).

3.2 On these grounds, the Claimant requests in the main proceedings (to the extent still relevant):

- to revoke the patent in its entirety for the territory of the UPC member states Germany, France and the Netherlands; and
- to dismiss Proprietor's application to amend the patent in suit and thus reject all Auxiliary Requests 1 to 8
- that the new Auxiliary request 2 is not admitted into the proceedings and should it be admitted to reject it as invalid
- to order the proprietor to pay the costs of the proceedings (Art. 69(1) UPCA).

3.3 The Defendant has put forward various defences including a (conditional) application to amend the Patent which was lodged together with the Defence to Revocation. By submission dated 1 March 2024, the Defendant requested permission from the Court for a subsequent application to amend the Patent in accordance with a new Auxiliary request 2 maintaining the previous main and auxiliary requests.

3.4 The Defendant requests in the main proceedings (to the extent still relevant):

- that the revocation action be rejected
- in the alternative, that the German, the French and the Dutch parts of EP 2 794 928 be upheld to the extent of one of auxiliary requests 1 to 8 (alternatively 9)
- the Claimant be ordered to pay the costs of the proceedings.

3.5 The grounds and defences as brought forward by the parties will, to the extent relevant for this decision, be discussed in detail below.

GROUNDS FOR THE DECISION

4 Summary of the Outcome

4.1 The Central Division comes to the conclusion that claim 1 of the Patent as granted lacks novelty because the claimed subject matter is disclosed directly and unambiguously in the prior art document Göransson. The first Auxiliary request lacks inventive step over Göransson. The skilled person would, starting from Göransson, have had an incentive to transfer the method of Göransson from an *in vitro* to an *in situ* context and would thereby have arrived at the claimed subject matter without inventive skill. Auxiliary requests 2-8 can also not serve as a basis for revoking the Patent only in part. Accordingly, the Patent is revoked in its entirety.

5 Admissibility and International Jurisdiction of the UPC

5.1 The Central Division has no concerns as to the admissibility of this revocation action. The Central Division furthermore establishes that it has (international) jurisdiction and will not stay the proceedings in view of the German Revocation action.

The relevant facts and arguments brought forward by the parties in the withdrawn PO

5.2 In the PO, the Defendant argued that the Central Division (Section Munich) of the Unified Patent Court is not competent to decide on the validity of the German part of the Patent, since there is already a revocation action pending against the Patent at the (competent) BPatG. The Defendant brought forward that the claimant in the German Revocation action, NanoString Technologies Germany GmbH, belongs to the same group of companies and has the same parent company as the Claimant. The Defendant further argued that their interests in the Revocation action are identical to and indissociable from each other. Defendant relied in the PO on Article 29 and, in the alternative, Article 30 of Regulation (EU) No 1215/2012[1] (herein also referred to as "Brussels I recast Regulation"), dealing with *lis pendens* and related actions, respectively, to request a dismissal or alternatively a stay of the action as far as it concerns the German part of the Patent.

1 Regulation (EU) No 1215/2012 of the European Parliament and of the Council of 12 December 2012 on jurisdiction and the recognition and enforcement of judgments in civil and commercial matters (recast), ELI: http://data.europa.eu/eli/reg/2012/1215/2015-02-26.

5.3 In its response to the PO, the Claimant submitted that the Claimant and the plaintiff in the German Revocation action are not to be considered as the "same parties" within the meaning of Article 29 and that there should be no stay pursuant to Article 30 Brussels I recast Regulation.

5.4 At the oral hearing, the Defendant withdrew the PO. Both parties requested the Central Division to accept international jurisdiction, also where it concerns the German part of the Patent, and not to stay the proceedings pending the outcome of the German Proceedings on various grounds, as further discussed below.

Jurisdiction – examination of its own motion

5.5 The Defendant has (unconditionally) withdrawn its PO. The Court furthermore understands the parties´ agreement at the oral hearing as a unanimous wish to submit to the jurisdiction of the UPC (in particular the CD).

5.6 The Court must, however, examine its international jurisdiction of its own motion when this is required under Union law. The rules of Union law on jurisdiction contained in the Brussels I recast Regulation, in accordance with which the Court´s international jurisdiction shall be established (made explicit in Article 34 UPCA), prevail over the UCPA and the RoP (also see Article 20, 24 UPCA) to the extent these rules of Union law are compulsory and require the Court to examine its jurisdiction of its own motion. This is regardless of the possible applicability of Rule 19.7 RoP, in accordance with which the failure to lodge a preliminary objection (which could arguably be equated with the withdrawal of a PO) shall be treated as a submission to the jurisdiction and competence of the Court and regardless of the apparent agreement between the parties to that effect.

International Jurisdiction of the Court for the present Revocation action

5.7 The present action is a patent revocation action. According to Article 24(4) of the Brussels I recast Regulation, the courts of each Member State shall have exclusive jurisdiction in proceedings concerned with the registration or validity of any European patent granted for that Member State. This exclusive jurisdiction is to be examined by the Court of its own motion (Article 27 Brussels I recast Regulation).

5.8 In accordance with Article 71a of Regulation Brussels I recast, a "*common court*" shall be deemed to be a court of a Member State when such a common

court exercises jurisdiction in matters falling within the scope of the Regulation. Article 71b(1) adds that a common court shall have jurisdiction where, under this Regulation, the courts of a Member State party to the instrument establishing the common court would have jurisdiction in a matter governed by that instrument. The UPC is a "*common court*" within the meaning of Article 71a et seq. of Regulation Brussels I recast, see Article 71a(2) sub a Regulation Brussels I recast and Article 1 UPCA, second part.

5.9 Pursuant to Article 32(1) (d) UPCA, the UPC shall have exclusive competence for actions for revocation of (European) patents. In view of this exclusive competence, and since no opt-out from the exclusive competence of the Court in relation to the Patent is in effect (cf. Article 83(3) UPCA), the UPC – as a common court of the Member States to the UPCA – in principle has international jurisdiction based on article 24(4) of Regulation Brussels I recast and is competent in respect of the present Revocation action. This jurisdiction extends to the French, Dutch and German parts of the Patent.

Parallel revocation action in relation to the Patent in Germany

5.10 From the facts as brought forward by the parties in the PO, the Court is aware that the German Revocation action is still pending. The BPatG decided in first instance on 7 May 2024 revoking the German part of the Patent in its entirety. By the time of the oral hearing in the present proceedings, the written grounds had been issued by the BPatG and an appeal had been lodged with the *Bundesgerichtshof* (´BGH´). A (final) decision from the BGH is not to be expected within the next year. As is apparent from the written decision of the BPatG (document D60), the grounds, facts and arguments relied upon by the parties to those proceedings are largely similar to those relied on in the present proceedings.

5.11 In its Order of 17 September 2024 (CoA_227/2024, *Mala Technologies/Nokia Technologies)*, the CoA confirmed that in the light of the objective and purpose of Art. 29 to 32 of the Brussels I recast Regulation which deal with parallel proceedings (i.e. to offer a clear and effective mechanism for resolving cases of *lis pendens* and related actions, see par. 12 of the Order), Article 71c(2) of the Brussels I recast Regulation must be interpreted as meaning that these provisions apply where during the transitional period of Article 83 UPCA, proceedings are pending before the UPC and a national court, also where, as is the case in the present proceedings, the proceedings before the national court were initiated prior to the transitional period (par. 12, 13 of the grounds of the Order).

5.12 The concrete facts and circumstances of the present case as known to the Court based on the submissions from the parties – in essence the existence of parallel proceedings in relation to the Patent in the UPC and in another court of a Member State (Germany) – prompt the Central Division to examine its international jurisdiction in view of Articles 29-32 Regulation Brussels I recast which rules, like Article 24 of Regulation Brussels I recast, are compulsory and have to be applied by the Court of its own motion. The compulsory and *ex officio* nature of these provisions follows from their wording (cf. "*of its own motion*", Article 29) and the object and purpose of these provisions (i.e. to offer a clear and effective mechanism for resolving cases of *lis pendens* and related actions, see CoA above and references to Union law in the CoA Order).

Article 29 (and 31) Brussels I recast Regulation

5.13 In accordance with Article 29 of the Brussels I recast Regulation, where proceedings involving the same cause of action and between the same parties are brought in the courts of different Member States any court other than the court first seised shall decline jurisdiction in favour of that court.

5.14 It is clear that the German Federal Patent Court was seised before the UPC in relation to a revocation action in respect of the (German part of) the same European patent which is the subject of the present Revocation action. The parties to both actions are, however, not the same.

5.15 The CoA in *Mala Technologies/Nokia Technologies*, applying the case law of the (then) ECJ (hereinafter referred to as ´CJEU´) in *Tatry* (CJEU 6 December 1994, C-406/92, ECLI:EU:C:1994:400) and *Drouot* (CJEU 19 May 1998, C351, ECLI:EU:C:1998:242), interpreted and applied Article 29 of the Brussels I recast Regulation such that despite two parties to a UPC and a national revocation action in relation to the same national part of the same European patent being closely related (being part of the same group of companies and having the same parent company) and therefore being in a position to coordinate the initiation of proceedings and their submissions in the proceedings, and notwithstanding the grounds for revocation, arguments and auxiliary requests raised by both parties being largely the same, the parties could not be considered the same party for the purposes of Article 29 Brussels I recast Regulation. They were separate legal entities and there was not such a degree of identity between their interests that a judgment delivered against one of them would have the force of *res judicata* as against

the other. See the CoA in *Mala Technologies/Nokia Technologies,* par. 17-19 of the Order.

5.16 Following the above case law of the CJEU and the UPC CoA and applying this to the present case, the parties are not the same for the purposes of Article 29 Brussels I recast Regulation. NanoString Technologies Germany GmbH (claimant in the German Revocation action) and the Claimant are not the same legal entities. The fact that both parties belong to the same group of companies and have the same parent company is insufficient to conclude that their interests are, even though they may be to a large extent aligned, identical and indissociable. No additional facts have been submitted by the parties to the Court on the basis of which it can be established that there is such a degree of identity between the interests of the parties to both proceedings that a judgment delivered against one of them would have the force of *res judicata* as against the other. Therefore, Article 29 Brussels I recast Regulation is not applicable in the present case.

5.17 It follows from the conclusion reached in relation to Article 29 that Article 31 of the Brussels I recast Regulation also does not apply in this case, since the parties to the proceedings in the German Revocation action are not the same as the parties to the proceedings before the UPC (cf. CoA in *Mala Technologies/Nokia Technologies*, 20-22 of the Order).

Article 30 Brussels I recast Regulation

5.18 Pursuant to Art. 30 of the Brussels I recast Regulation, the UPC may stay proceedings where a related action is pending in a national court. As held by the CoA in *Mala Technologies/Nokia Technologies*, par. 24 of the Order, the objective of this provision is to minimise the possibility of parallel proceedings before different courts and to improve coordination of the exercise of judicial functions within the European Union and to avoid conflicting and contradictory decisions, even where the separate enforcement of each of them is not precluded.

5.19 As was the case in *Mala Technologies/Nokia Technologies*, the present UPC proceedings and the proceedings at the (now) BGH are to be considered as related proceedings for the purposes of Art. 30 of the Brussels I recast Regulation. The parties are (closely) related, both proceedings concern the same national part of the same European patent and the proceedings are largely similar in terms of facts, grounds, arguments and (auxiliary) requests brought forward by the parties.

5.20 However, having regard to the objective of Article 30 Brussels I recast Regulation, in view of the following combination of circumstances, which in important aspects deviates from the circumstances of the case before the CoA in *Mala Technologies/Nokia Technologies*, the Central Division decides not to exercise its discretionary power to stay the proceedings.

- The parties to the present proceedings have unanimously requested the Court to issue a decision, also for the German part of the Patent.
- The parties have explained at the oral hearing that for resolving their dispute, it is important to obtain a decision from the Central Division. This is in particular so because an infringement action is pending in relation to the Patent, also for the German part of the Patent, including a claim for damages. Parties have expressed the wish to have legal certainty as soon as possible.
- The first instance proceedings before the Central Division are already in an advanced stage. The oral hearing has been concluded and the case is ready to be decided. The procedural economical benefits for the Central Division to stay its proceedings at this stage are therefore limited.
- The proceedings at the BGH are still in an early stage. No decision can be expected within the next year.
- If an appeal is filed against the present decision, which is not certain at this point in time, the UPC CoA can be expected to deal with the appeal in approximately one year.
- In the present case, two other national parts of the Patent (the Dutch and the French part) are still in force and are subject of the present Revocation action. The German Revocation action does not affect these parts. The grounds, facts and arguments that the parties have brought forward for these national parts are identical to those brought forward for the German part and thus will have to be considered by this Court at some point in time.
- Staying the action in its entirety risks preventing the parties from obtaining a decision on the (unaffected) national parts within a reasonable time (a fundamental right guaranteed by Article 6 of the European Convention for the Protection of Human Rights and Fundamental Freedoms and Article 47 of the Charter, see in this sense CoA 28 May 2024, UPC_CoA_22/2024 *Carrier/Bitzer*, Headnote 1).
- Staying the action only for the German part of the Patent would have little benefits in terms of procedural economy as the grounds, facts and arguments brought forward by the parties would then have to be considered in any event for the other national parts of the Patent.

- Going forward with the present case may avoid the costs of conducting the proceedings at the BGH and the UPC CoA if the parties settle the case on the basis of this decision by the Central Division.
- There is no risk of a contradictory or conflicting decision with at least the BPatG as the result is the same in both cases (see below).

5.21 For the above reasons, the interests of the parties and procedural economy outweigh the risk that UPC CoA and BGH proceedings may become pending in parallel (and the related risk of contradictory decisions). Accordingly, the Central Division will not stay the present revocation action.

5.22 The Court notes that it would come to the same conclusion if it were to exercise its discretionary power to stay proceedings on the basis of Rule 295(m) RoP (cf. CoA in *Mala Technologies/Nokia Technologies*, 32 of the Order). In view of the facts and circumstances discussed above, also in light of the principles of efficiency and expeditious decisions set out in points 4 and 7 of the Preamble of the RoP and Recital 6 of the UPCA, the Court considers that, in the present situation, it is not in the interest of the proper administration of justice to stay proceedings awaiting the outcome of the appeal proceedings at the BGH.

5.23 In sum, the Court has international jurisdiction and has competence to hear the present Revocation action. The action will not be stayed pending the outcome of the proceedings before the BGH relating to the German part of the Patent.

6 Technical Background

6.1 Before discussing the grounds for invalidity raised by the Claimant in detail, the Central Division finds it useful to provide a brief technical background as follows from the Patent description.

6.2 According to the background section in the description of the Patent:

> *[0003] The need for multiplexing techniques in biology is often driven by the fact that test samples are precious and those analyzing them either do not know in advance precisely what to look for or must extract the most information from any single sample. Hence, it is desirable for clinicians and researcher [sic] to subject each sample to a large set of probes.*
>
> *[0004] Optical readout is common in biology and can be very effective. However, it is typically limited to a relatively small number of available*

fluorophores or chromophores (which are referred to collectively as colours). In practice, multiplexing by fluorescence is often limited to 4 or 5 colours, which by traditional methods implies that at most 4 or 5 probes can be detected in a single sample.

[0005] The common approach to improving multiplexing in optical methods is to increase the number of available colours. To this end, quantum dots have been developed to provide a larger range of colours. However, in reality, it is difficult to use more than 6 quantum dot colours simultaneously. Another approach is to use mixtures or ratio of fluorophores as new colours. Such methods have extended multiplexing to hundreds of analytes, but due to the size of the labels (e.g., microbeads), the technology has thus far been limited to flow-cytometry based analyses. Yet another approach involves nanostrings, which are essentially short strings of strung-up fluorophores creating visible colourful barcodes. Unfortunately, nanostring readout requires very high-resolution imaging and a special flow apparatus. Further, the nanostrings can only be used in a sample where the probes' targets are sparse, or the barcodes will overlap and create a blur.

[0006] A simple workaround for the limited number of colours (e.g., 4 or 5 colours) in optical readouts is to repeat the probing of the same sample with multiple small sets of different probes. For example, the assay can involve probing the sample with 4 different antibodies at a time and imaging after every assay. If the test requires probing the sample with a total of 64 antibodies, the 4-probe procedure would have to be repeated 16 times using the sample. As such, the order of detecting different target analytes in a single sample may need to be prioritized, because some target analytes in the sample can degrade during successive probings. Accordingly, there is still a strong need for accurate and sensitive methods with a high throughput for detection, identification, and/or quantification of target molecules in a sample, e.g., complex mixtures.

6.3 According to the Summary section of the description of the Patent:

[0007] Embodiments provided herein are based on, at least in part, the development of a multiplexed biological assay and readout, in which a multitude of detection reagents comprising one or more probes and/or probe types are applied to a sample, allowing the detection reagents to bind target molecules or analytes, which can then be optically identified in a temporally-sequential manner. In some embodiments, the multitude of detection reagents comprising one or more probes and/or probe types can be applied to a sample simultanesouly [sic]. Accordingly, provided herein are methods for detecting multiple analytes in a sample.

6.4 In relation to the prior art, the description furthermore notes:

> *[0037] To clarify, the compositions and methods described herein are different from the ones described in the US Patent Application No.: US 2007/0231824. The '824 application discusses methods of decoding a sensor array containing immobilized microspheres, wherein the microspheres are immobilized on a solid support (e.g., an array substrate), rather than designed to be in a solution phase. As such, a sample fluid is flowed over the sensor array containing immobilized microspheres. The analytes in the sample fluid then bind to the immobilized microspheres. After binding, the sample fluid is then discarded and the immobilized microspheres are analyzed. Accordingly, the compositions and the methods described in the '824 application cannot be used and detected directly on a sample (e.g., on a tissue sample) or in situ as described herein, e.g., immunofluorescence, immunohistochemistry, fluorescence in situ hybridization, or western blot.*

6.5 From the background section above, it follows that in order to obtain as much information as possible on a variety of analytes (e.g. specific disease-relevant proteins, RNA or DNA) from one sample, e.g. a biopsy sample, it is advantageous to be able to test as many analytes as possible on one sample in so-called "multiplexing" techniques (cf. par. [0003] of the Patent above). Such methods can be performed, for example, by visualising (on the same sample) different analytes with different optical detection probes. With such multiplex approaches, however, there are problems if more analytes than available dyes (also: "colours") are to be detected, for example if only 4 to 5 different dyes are available for multiplex detection, but 6 or more different analytes are to be detected.

6.6 According to the Patent in suit, a known possibility to circumvent the problem of the limited number of available colours was to repeat the test using the same colours for the detection of different analytes with one and the same sample (par. [0006]). By way of example par. [0006] mentions an assay involving probing the sample with 4 different antibodies at a time and imaging after every assay. If the test requires probing the sample with a total of 64 antibodies, the 4-probe procedure would have to be repeated 16 times using the sample. A drawback of this is that some target analytes in the sample can degrade during successive probings resulting in the need to prioritise the order of detecting different target analytes in a single sample.

6.7 Against this background, the Patent furthermore states in par. [0006] that there is a need for accurate and sensitive methods with a high throughput for detection, identification, and/or quantification of target molecules in a

sample, e.g., complex mixtures. Accordingly, the problem underlying the invention is to develop high-throughput optical multiplexing methods for detecting target molecules in a sample. This definition of the underlying problem corresponds to the problem as defined by the CoA in the appeal proceedings relating to EP ´782 (CoA Order in *NanoString/10x Genomics*, 4.b) and in essence to the problem as defined by the BPatG in its decision in the German Revocation action (D60, I.2).

6.8 In order to achieve this aim, the Patent claims a method for detecting a plurality of analytes in a sample having the features as set out below.

7 Claim Features (Main Request, claim 1 as granted)

7.1 The parties agree on the following claim feature breakdown/analysis (see par. 25 statement of Revocation, p. 10 of the Defence to Revocation, submitted in these proceedings as BP5) which is largely adopted by the Central Division (underline added by the CD to highlight particular method steps):

F1 A method for detecting a plurality of analytes in a sample

F2 a. contacting the sample with a composition comprising a plurality of detection reagents,

F2.1 each subpopulation of the detection reagents targets at least one different analyte,

F2.2 the analyte is fixed on a solid substrate or support,

F2.3 the solid substrate or support is a chip, a microarray, a blotting membrane or a microscopic slide,

F2.4 each detection reagent comprises:

F2.4.1 at least one probe reagent targeting an analyte,

F2.4.2 and at least one nucleic acid label comprising a plurality of predetermined subsequences,

F2.4.3 said at least one probe reagent and said at least one nucleic acid label are conjugated together;

F2.4.4 at least a portion of said plurality of pre-determined subsequences form an identifier of said at least one probe reagent;

F3 b. removing any unbound detection reagents;

F4 c. detecting in a temporally sequential manner said plurality of predetermined subsequences of said detection reagent,

F4.1 said detection of the subsequences comprises:

F4.1.1 i) hybridizing a set of decoder probes with a subsequence of the detection reagents

F4.1.1.1 each subpopulation of said decoder probes comprises an optical detectable label, each optical detectable label generating an optical signal signature corresponding to each subsequence;

F4.1.2 ii) detecting said optical signal signature produced upon the hybridization of said set of decoder probes and obtaining an image;

F4.1.3 iii) removing said optical signal signature produced by the hybridization of said set of decoder probes;

F4.1.4 iv) repeating steps (i) through (iii) for other subsequences of said detection reagents, thereby producing a temporal order of optical signal signatures corresponding to the plurality of pre-determined subsequences,

F4.1.4.1 the temporal order of the optical signal signatures corresponding to said plurality of pre-determined subsequences of said detection reagent identifies a subpopulation of the detection reagents;

F4.1.4.2 is unique for each subpopulation of the detection reagents;

F5 d. comparing said temporal order of the optical signal signatures with different identifiers of said at least one probe reagent,

F5.1 an agreement between the temporal order of the optical signal signatures and a particular identifier of said at least one probe reagent identifies the analyte in the sample.

8 Claim Interpretation

8.1 In view of the debate between the parties, several features of claim 1 of the Patent require interpretation.

8.2 As held by this Court in its decisions of 16 July 2024 in cases UPC_CFI_1/2023 and UPC_CFI_14/2023 (par. 6.3-6.8), with reference to the CoA (Order dated 26 February 2024 in UPC_CoA_335/2023, *NanoString/10x Genomics*, p. 26-27 of the original German language version, CoA UPC 13 May 2024, *VusionGroup/Hanshow*), in accordance with Art. 69 EPC and the Protocol on its interpretation, a patent claim is not only the starting point, but the decisive basis for determining the scope of protection of a European patent. The interpretation of a patent claim does not depend solely on the strict, literal meaning of the wording used. Rather, the description and the drawings must always be used as explanatory aids for the interpretation of the patent claim and not only to resolve any ambiguities in the patent claim. However, this does not mean that the patent claim merely serves as a guideline and that its subject-matter also extends to what, after examination of the description and drawings, appears to be the subject-matter for which the patent proprietor seeks protection.

8.3 The patent claim is to be interpreted from the point of view of a person skilled in the art.

8.4 When interpreting a patent claim, the person skilled in the art does not apply a philological understanding, but determines the technical meaning of the terms used with the aid of the description and the drawings. A feature in a patent claim is always to be interpreted in light of the claim as a whole (CoA UPC 13 May 2024, *VusionGroup/Hanshow*, point 29). From the function of the individual features in the context of the patent claim as a whole, it must be deduced which technical function these features actually have individually

and as a whole. The description and the drawings may show that the patent specification defines terms independently and, in this respect, may represent a patent´s own lexicon. Even if terms used in the patent deviate from general usage, it may therefore be that ultimately the meaning of the terms resulting from the patent specification is authoritative.

8.5 In applying these principles, the aim is to combine adequate protection for the patent proprietor with sufficient legal certainty for third parties.

8.6 These principles apply also to the assessment of validity. Accordingly, these principles will also be applied by the Central Division to claim construction in the context of the present Revocation action. The relevant point in time for interpreting a patent claim for the assessment of validity is the filing (or priority) date of the application that led to the patent in suit.

The skilled person

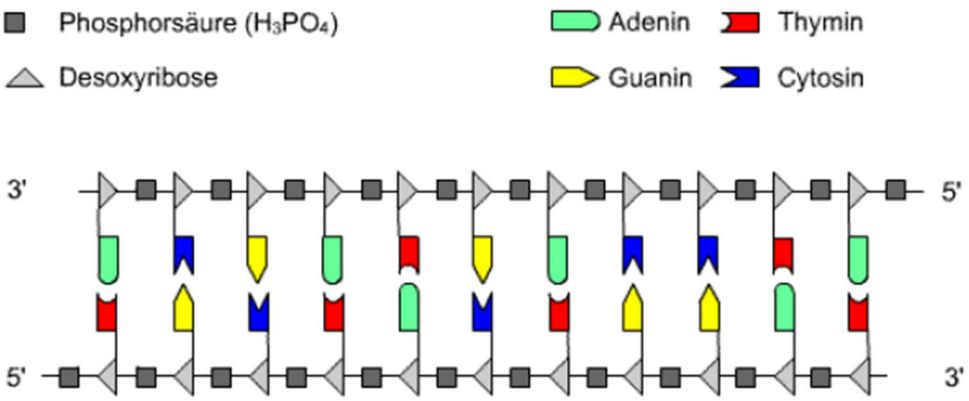
8.7 In the opinion of the Central Division, the skilled person is someone having a degree in biological sciences (or biochemistry) and several years of experience in the field of detection of biomolecules in biological samples. A skilled person having this background will be familiar with both "*in vitro*" and "*in situ*" techniques for the detection of biomolecules.

8.8 The above definition largely corresponds to the definition of the skilled person adopted by the parties. Different from the Defendant, however, the Court does not see the skilled person as having several years of experience only with *in situ* techniques and not with *in vitro* methods. The Patent (see par. [0003]) is generally directed at "*those analyzing*" test samples in biology (the term sample being broadly defined in the Patent, see below) who have a "*need for multiplexing techniques*". In the same sense, still in the same introductory paragraph, the Patent refers to "*clinicians and researcher[s]*" (in general) for whom it is desirable to subject each sample to a large set of probes. No fundamental distinction is made between *in vitro* and *in situ* multiplexing techniques in the Patent. The skilled person must therefore be defined accordingly.

Claim interpretation from the point of view of the above person skilled in the art applying the above principles

General remarks

8.9 In the claimed method, a "*nucleic acid label*" is attached (directly or indirectly) to a probe reagent (together these are called a "*detection reagent*") which are used to detect analytes. The nucleic acid label is "read-out" and decoded in a temporally sequential manner. To this end, the nucleic acid label comprises a plurality of "*predetermined subsequences*" to which "*decoder probes*" can hybridize. "Hybridization" is the formation of a "hybrid" between two separate (but complementary) single-stranded molecules into one single double-stranded molecule. Two hybridized nucleic acid strands can look as follows (Statement of Revocation, par. 73):

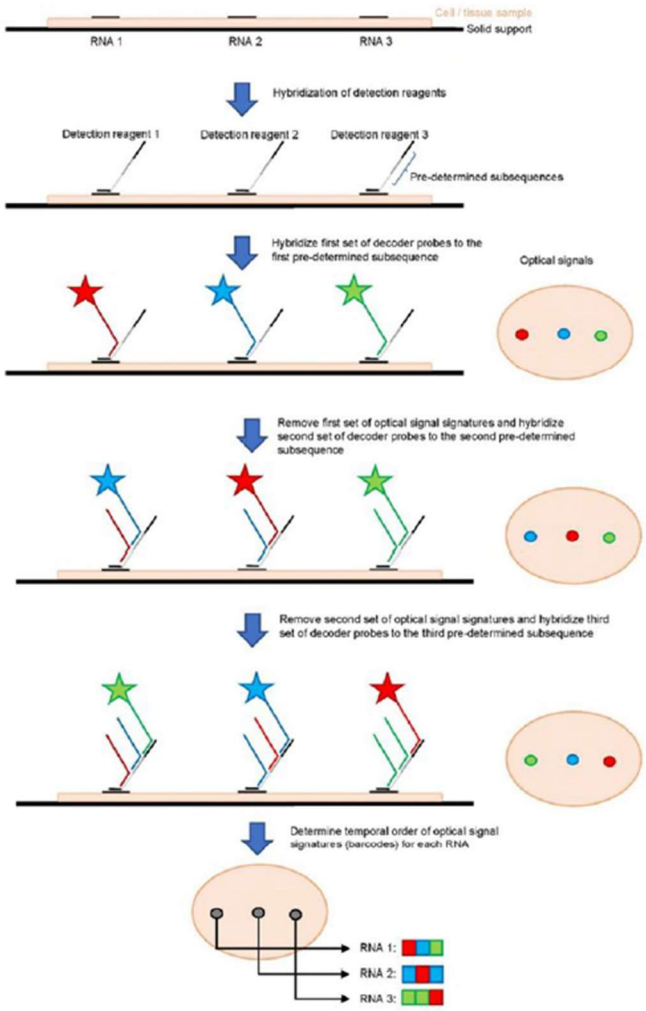


The binding between the two strands is based on base-pairing as shown above. Adenin (´A´) binds to Thymin (´T´), Guanin (´G´) to Cytosin (´C´).

8.10 The decoder probes contain an "*optically detectable label*", e.g. a fluorescent dye (or "colour"). This allows the decoder probes to produce a signal that can be detected ("*signal signature*"). After one "round of detection", the signal signature is removed and another set of decoder probes (having different nucleic acid sequences than the first set of decoder probes) is added. These decoder probes in turn hybridize with the detection reagents on complementary subsequences (but at a different location on the nucleic acid label than during the first "round"), producing new decoder probe signals. The order of the signals produced by multiple runs with different decoder probes makes it possible to identify the corresponding analytes.

8.11 In essence, the method according to the invention results in a particular temporal "barcode" for each analyte. The approach according to the Patent

is summarized graphically in the following figure (p. 12, Defence to Revocation, not (expressly) contested by the Claimant):



<u>The terms "*sample*" and "*analyte*" as used in claim 1 are to be interpreted together.</u>

8.12 The claimed method pertains to detecting a plurality of analytes in a sample (**F1**). The parties are divided over the interpretation of the terms "*sample*" and "*analyte*". The claimed method is a method for detecting a plurality of analytes in a sample. Ultimately, in the last step of the method (cf. **F5**) the analyte in the sample is identified. Even though the Central Division agrees with the Defendant that the "*analyte*" and the "*sample*" are not "identical", the skilled person will not interpret these terms in isolation, but rather together in their mutual context within the claim.

8.13 The Patent description gives a broad definition of the term "*sample*". A sample can be derived "*from any sources*" (par. [0008] and [0213] of the description) and "*…is not limited to biological samples, e.g., collected from organisms, animals or subjects, environmental samples, food, food byproduct, soil, archaeological samples, extraterrestrial samples, or any combinations thereof. For example, a sample can be a protein sample immobilized on a solid support including, e.g., a blotting membrane. In alternative embodiments, a sample can comprise one or more cells, one or more tissues, one or more fluids, or any combinations thereof. In some embodiments, the sample can comprise a tissue sample.*" Accordingly, the term "*sample*" will be interpreted by the skilled person as relating to its origin ("*source*") and/or to its nature (e.g. immobilised proteins, cells or tissue). The description furthermore indicates that the sample can be processed or treated before it is contacted with the plurality of detection reagents (see par. [0011] and [0214] of the description). Such (pre)treatment may involve "*releas[ing] or expos[ing] target analytes from other components of the sample*" (par. [0219]). Numerous ways of processing the sample are mentioned in the description (par. [0049], [0050]), including the "*addition of DNA extraction agents*" and "*isolation of proteins or nucleic acids*". It is therefore clear for the skilled person that a sample which has been processed in a variety of ways before starting the method to detect analytes is also covered by the term "*sample*". It also follows that the term "*sample*" is not limited to a "*(biological) sample comprising one or more cells and/or one or more tissues*" (to the extent the Defendant is arguing this on p. 3 of the Rejoinder, par. 2). The Patent claims nor the description provide any basis for such a narrow interpretation. Also from a technical functional perspective, the skilled person will understand that any sample can qualify as a sample for the purposes of the claimed method, as long as it contains analytes that can be detected/identified using the claimed method.

8.14 The term "*analyte*" is also broadly defined in the Patent (see par. [0008] and [0210] of the description as "*the molecule detected, identified or measured*". Par. [0210] specifies that the analyte "*…can be, but is not limited to, any of the following or any combinations of the following: nucleic acid, peptide, a polypeptide/protein (e.g., a bacterial or viral protein or an antibody), a lipid, a carbohydrate, a glycoprotein, a glycolipid, a small molecule, an organic monomer, sugar, peptidoglycan, a cell, a virus or a drug. Nucleic acids that can be analyzed by the methods herein include: double-stranded DNA, single-stranded DNA, single-stranded DNA hairpins, DNA/RNA hybrids, RNA (e.g. mRNA or miRNA) and RNA hairpins. Generally, a target molecule can be a naturally occurring molecule or a cDNA of a naturally occurring molecule or*

the complement of said cDNA. In other embodiments, a target molecule can be modified, e.g., by mutation or chemical reaction. In some embodiments, a target molecule can be synthetic or recombinant.”). Par. [0212] of the Patent adds that: “*A target molecule or an analyte can be part of a sample that contains other components or can be the sole or major component of the sample. A target molecule or an analyte can be a component of a whole cell, tissue or body fluid, a cell or tissue extract, a fractionated lysate thereof or a substantially purified molecule. The target molecule can be present in solution or attached to a solid substrate, including, for example, to a solid surface such as a chip, microarray, bead or a blotting membrane. According to the invention, the analyte is fixed on a solid substrate or support, wherein the solid substrate or support is a chip, a microarray, a blotting membrane or a microscopic slide. Also the target molecule or analyte can have either a known or unknown structure or sequence.*”

8.15 In the claimed method, the analytes are detected using “*detection reagents*” that “*target*” the analytes (**F2** and **F2.1**) by means of a “*probe reagent*” targeting an analyte (**F2.4.1**). These features do not further define or narrow the skilled person´s understanding of “*analyte*”, also not when seen in their technical functional context. The skilled person understands that the part of the detection reagent that interacts with the target molecule (the “*analyte*”) is the so-called “*probe reagent*” (**F2.4.1**) which is defined in par. [0024] of the description as “*any targeting molecule of interest*”. Par. [0024] adds: “*Examples of the probe reagent can include, but are not limited to, a nucleic acid, an antibody or a portion thereof, an antibody-like molecule, an enzyme, a cell, a virus, an antigen, a small molecule, a protein, a peptide, a peptidomimetic, a sugar, a lipid, a glycoprotein, a peptidoglycan, an aptamer, and any combinations thereof. In some embodiments, the probe reagent can be modified by any means known to one of ordinary skill in the art. By way of example, the probe reagent can be genetically modified, or it can be biotinylated.*” Therefore, the broad definition of “*probe reagent*” provided in the Patent description is congruent with the broad interpretation of “*analyte*”.

<u>At least one nucleic acid label comprising a “plurality” of predetermined subsequences (F2.4.2)</u>

8.16 In addition to a “*probe reagent*” (**F2.4.1**, discussed above), a detection reagent in accordance with the claimed method comprises “*at least one nucleic acid label comprising a <u>plurality of predetermined subsequences</u>*” (**F2.4.2**, underline CD).

8.17 According to the Claimant, the skilled person would interpret the claim such that a detection reagent comprising one pre-determined subsequence is also covered by the claim. In support, the Claimant has referred to par. [0112] of the description which states: "*According to the invention, the nucleic acid label comprises a plurality of predetermined nucleic acid subsequences. In some embodiments, the nucleic acid label or nucleic acid tag can comprise any number of the pre-determined nucleic acid subsequences, e.g., ranging from about 1…*" together with the use of "*Two or more*" pre-determined subsequences in par. [0119].

8.18 According to the Central Division, the skilled person interprets the term "*plurality*" as used in **F2.4.2** in accordance with its plain meaning in common language use, i.e. as "more than one" (or: "*two or more*"). This interpretation is further supported and confirmed by the technical functional context of the claimed method in light of the description.

8.19 The claimed method pertains to the detection of a *plurality* of *analytes* (**F1**, the Central Division notes that it is not in dispute between the parties that "*plurality*" in F1 means "more than one"), by *inter alia* the step of hybridizing a set of decoder probes with a subsequence of the detection reagents which step is repeated for other subsequences of the detection reagents). Accordingly, the claim requires a plurality of, i.e. more than one predetermined subsequence per detection reagent to function. A skilled person will thus appreciate that detection reagents having a nucleic acid label with only one pre-determined subsequence are not covered by the claimed method.

8.20 In the view of the Central Division, an interpretation as advocated by the Claimant would be at odds not only with the wording and context of the claimed method as set out above, but also with the description as a whole, especially the background section, par. [0003]-[0006], wherein the Patent describes the prior art. Therein, it is made clear that optical readout is common in biology but typically limited to a relatively small number of colours. The common approach to improving multiplexing in optical methods is to increase the number of available colours. However, using more than 6 colours simultaneously is difficult in reality. A "*simple workaround*" is, according to the description, to repeat the probing of the same sample with multiple small sets of different probes. As an example, the description mentions probing a sample with 4 different antibodies at a time and imaging after every assay. If the test requires probing the sample with a total of 64

antibodies, the 4-probe procedure would have to be repeated 16 times using the sample. The methods provided in the Patent overcome the need for such successive probings by optically identifying the detection reagents in a temporally-sequential manner by their predetermined subsequences. If only one predetermined subsequence would be available per detection reagent, the method would in essence be identical to the prior art which the Patent tries to distance itself from wherein the sample would have to be probed repeatedly with (sets of) different probes.

8.21 In conclusion, the skilled person would understand from the use of the word "*plurality*" in the claim, in the context of the claimed method and the description as a whole that only embodiments with detection reagents having more than one pre-determined subsequence fall within the scope of the claim.

Does the claimed method require that a detection reagent stays bound to an analyte throughout the method?

8.22 Parties are divided as to whether or not one-and-the-same ("identical") detection reagent with which the sample is contacted in step a (**F2**) of the claimed method has to remain bound throughout the entire detection sequence of feature **F4.1.3** (this is the interpretation according to the Defendant) or whether the claim allows the detection reagents to be removed and replaced with the same detection reagents after the step of removing the optical signal signature (this is the interpretation of the Claimant).

8.23 The Central Division is of the opinion that the skilled person interprets the claimed method such that it does not require that the detection reagent with which the sample is contacted in step a remains bound throughout the detection in accordance with step c and also does not exclude that the same detection reagent is added (or replaced) before another round of detection is carried out in accordance with step c. Nothing in the claim wording, the description, also when read in their technical functional context, excludes this.

8.24 First of all, the wording of the claim does not say that detection reagents may only be added once and/or that the identical detection reagent must remain bound throughout the entire method. Nothing in the Patent description explicitly states that it is necessary that the detection reagent must remain bound.

8.25 Such a requirement also does not follow from **F3** of claim 1. **F3** requires the removal of any unbound detection reagents (step b of the method). This removal can for example be done by washing (see par. [0051], Example 1, par. [0300], line 34. The Patent description does not provide an explicit technical reason for this step of removing the unbound detection reagents. The skilled person, using their common general knowledge to interpret the claim, will understand that the unbound detection reagents are removed because they are of no use in the subsequent detection step c which is carried out to ultimately identify an analyte in the sample (**F5.1**). Detection reagents which are not bound to an analyte cannot contribute to this function (and could possibly create background signal) and therefore these are removed. From these considerations it does not, however, follow that the identical detection reagents which are bound upon starting step c must remain bound throughout each repetition of detection of the subsequences. **F3** is silent where it concerns the possible removal and addition of (the same) detection reagents during the course of step c, in particular before another round of detection (repeating steps (i) through (iii)) in accordance with **F4** (**F4.1.4**).

8.26 The claimed method does not preclude that the detection reagents, after contacting the sample in step a and after a round of detection in accordance with step c are removed, for example together with the removal of the signal signatures. The step of removal of the "*optical signal signature*" in **F4.1.3** is so broadly worded (as opposed to for example specifically and exclusively removing only the decoder probes) that the skilled person would not exclude that the claim (also) covers the situation in which (some of) the detection reagent is removed together with the signal signature. This understanding is confirmed by par. [0074] of the description according to which the "*removal of the signal signatures can be done by any methods known in the art, including, but not limited to, washing, heating, photo-bleaching, displacement, cleavage, enzymatic digestion, quenching, chemical degradation, bleaching, oxidation, and any combinations thereof.*" The skilled person would realise that these methods may include conditions which result in the removal of (bound) detection reagents and would therefore not rule out the possibility of having to add (more of the same, identical) detection reagent when repeating steps i)-iii) in accordance with **F4.1.4**.

8.27 A technical functional perspective confirms the above interpretation. The description states that the methods described can significantly increase the number of different probes (and corresponding analytes) that can be simultaneously detected in a multiplex assay as compared to a traditional

assay wherein each probe is labelled with only one fluorescent label and thus multiplexing is limited by the number of available and practically usable colours. Because the detection reagents are detected and/or imaged in a temporal series of steps, the number of probes (and corresponding analytes) that can be detected in a multiplex assay grows multiplicatively with the number of detection steps in a time series and the number of optical labels being used. By way of example, the description mentions that 3 set of images in which 4 distinct optical labels are used can encode 4 x 4 x 4 = 64 distinct probe reagents (see par. [0040] of the Patent).

8.28 Having this explanation in mind, the skilled person understands that the technical function of step c is to detect the detection reagents (and corresponding analytes) in a temporal series of steps thereby allowing the detection of more detection reagents than there are available colours. To this end, the claimed method requires a plurality of pre-determined subsequences that form an identifier of at least one probe reagent (**F2.4.4**). By in step c repeatedly hybridizing a set of decoder probes having an optical detectable label, a signal signature is generated corresponding to each subsequence. This is repeated in step c.iv for other subsequences whereby a temporal order of optical signature signatures is produced which identifies a subpopulation of the detection reagents (**F4.1.4.1**). Since the temporal order of signal signatures is unique for each subpopulation of the detection reagents (**F4.1.4.2**) it can be used to identify the analyte in the sample which corresponds to the subpopulation of detection reagents (**F5.1**). In other words, the claimed method is based on the detection of a subpopulation of detection reagents that targets an analyte by “reading out” the temporal barcode that is unique for that subpopulation (and thereby the analyte). For the method to function, it is not necessary that one-and-the-same detection reagent remains bound all throughout the method, in particular in the detection step c. The only requirement is that a specific subpopulation of detection reagents that are capable of (via the decoder probes) generating the signal signature(s) corresponding to each subsequence are bound to the analytes in step c, in other words that the same barcodes are read out in each “detection round” of step c. It is therefore not excluded that “fresh” detection reagents (but still the same ones in the sense of having the same barcode, i.e. belonging to the same subpopulation) are added or replaced before starting another round of detection. Regardless of whether the “original” or “fresh” detection reagents are used, the result is that more analytes can be detected than there are colours with less detection rounds.

8.29 The Central Division finds, contrary to the Defendant, that the use of the reference words "*said*" (and "*the*") in feature group **F4**, in particular **F4.1.4**, does not imply that the claimed method is limited to using the identical detection reagent throughout the entire method. First, "*said detection reagent*" in **F4.1.4** refers back to the general definition of detection reagent provided in **F2.4** rather than to the "*plurality of detection reagents*" with which the sample is contacted. Moreover, and more importantly, it follows from an interpretation of these features in the context of the claim in the light of the description and their technical function, as explained above, that the claim is not limited to adding a detection reagent only once and/or that the (same) detection reagent must remain bound throughout the entire method. For the same reason, the circumstance that the claim defines a number of sequential steps does not exclude that before step c, (more of the same) detection reagents are added.

8.30 The use of the wording "*comprising*", which generally has a non-exclusive meaning (as confirmed in par. [0278] of the description of the Patent), confirms for the skilled person that the claim does not exclude a step of (removal and) addition of (the same) detection reagents before the detection of other subsequences of the detection reagents in accordance with step c as set out above.

8.31 Nothing in par. [0052] of the description, which was referred to by the Defendant, excludes the removal and re-adding of the same detection reagents. This paragraph merely describes detecting or decoding in a time series a plurality of the pre-determined subsequences within the nucleic acid labels of any detection reagents that are bound to target analytes in a sample. Par. [0052] further describes that the time period between any two detection steps can be "*of any length*", including hours and longer than 1 day. The skilled person will rather take this as an indication that the time that it might require to add "fresh" detection reagents before another detection step is not an impediment.

8.32 The further argument brought forward by the Defendant that the long incubation time required with a complex biological sample would make the skilled person realise that it would be unpractical to re-add detection reagents cannot be followed (even leaving aside that the claim is not limited to "complex biological samples"). The Central Division notes that the wording of the claim does not contain any limitation as to the incubation time of the sample (referred to as "*contacting*" in the claim, **F2**, step a). The description of the Patent, in par. [0046], discloses a very wide range of incubation times

from "*at least about 30 seconds*" to "*48 hours or longer*". No technical reason is provided nor is it apparent why a limitation as argued by the Defendant would nevertheless be assumed by the skilled person. Therefore, the argument that in practice the skilled person would understand re-incubating with the same detection reagents as excluded from the claim fails.

8.33 In sum, the claim wording, considering the features of the claim the context of the claim as a whole in light of the description and their technical function, does not exclude that before another round of detection (repeating steps (i) through (iii)) in accordance with **F4** (**F4.1.4**), the sample is contacted (again) with the (more of the same) detection reagents. The skilled person would, moreover, not interpret the claim such that the same detection reagent necessarily stays bound to the analyte throughout all the steps of **F4.1.3**.

9 Novelty of the Main Request (Claim 1 as granted)

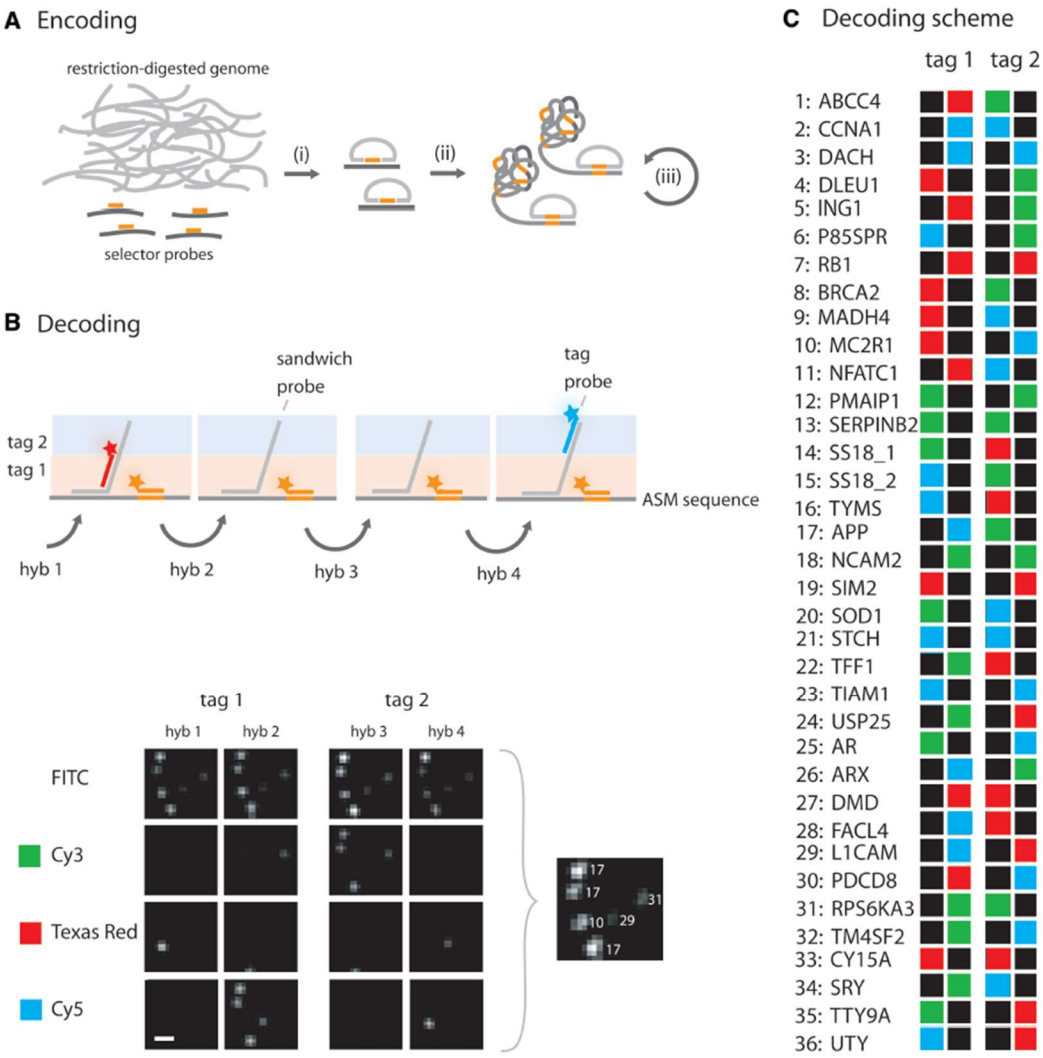
9.1 For the purposes of Article 54 EPC, an invention shall be considered to be new if it does not form part of the state of the art. The state of the art, in accordance with Article 54(2) EPC shall be held to comprise everything made available to the public by means of a written or oral description, by use, or in any other way, before the date of filing of the European patent application (or when applicable the priority date).

9.2 The assessment of novelty within the meaning of Art. 54 (1) EPC requires the determination of the whole content of the prior publication. It is decisive whether the subject-matter of the claim with all its features is directly and unambiguously disclosed in the prior art citation (see UPC CoA, Order of 25 September 2024, UPC_CoA_182/2024, App 21143/2024, *Mammut/Ortovox*, par. 123).

9.3 Applying the above standard to the case at hand, the Central Division comes to the conclusion that the subject matter of claim 1 of the Patent as granted lacks novelty over document D10, Göransson et al.

D10 - Göransson et al. (´Göransson´)

9.4 Göransson is a prior art scientific publication relating to a new random array format together with a decoding scheme for targeted multiplex digital molecular analyses (Abstract, first sentence). Figure 3, which is shown below, depicts the method disclosed in Göransson involving the multiplex encoding and decoding of genomic loci.



9.5 As shown under "A", a genomic sample is prepared by restriction digestion of the sample genome with an appropriate restriction enzyme. (i) probes designed to target specific genomic sequences are added and genomic DNA circles are formed. The DNA circles are either (ii) directly amplified by RCA (rolling-circle amplification), or (iii) enriched for by a process which includes restriction digestion of the RCA products into monomers that can be ligated into new circles to generate amplified single molecules (ASMs). An array is created by random immobilization of the ASMs to a microscopic glass slide.

9.6 As shown under "B" the ASMs that have been immobilized on the array are decoded by sequential hybridizations of sandwich probes (grey), tag probes (red or blue) and a general tag probe (orange). The sandwich probes contain two regions, one complementary to a specific ASM and one region containing the two decoding tags. These decoding tags, denoted tag 1 and tag 2, hybridize with corresponding tag probes. A small 20 x 20 pixel image shows

the labelled ASMs after the different hybridization reactions along with an image showing the identified ASMs. The ASM arrays were decoded in four cycles of hybridization and dehybridization (Göransson, p. 4, left-hand column/p.5, right-hand column).

9.7 "C" shows the decoding scheme used for multiplex decoding of genomic fragments. The names of the gene loci and their corresponding number are listed vertically and the labels from the two tags are illustrated horizontally. Green labels are for the fluorescent dye Cy3, red labels represent Texas Red and blue correspond to Cy5 labelling. Black means no labelling, i.e. absence of a detectable signal (tag probe).

Göransson discloses all features of claim 1 directly and unambiguously

9.8 According to Göransson, ASMs (corresponding to the "*plurality of analytes*" in claim 1 of the Patent) are prepared from a genomic DNA sample. The ASMs are mounted ("*fixed*") on a microscopic glass slide (a "*solid substrate or support*" as required by F2.3) and contacted with a plurality of sandwich probes which target different ASMs (these correspond to the "*detection reagents*" in claim 1) in order to bind each to the other. The sandwich probes contain a part that targets a specific ASM (corresponding to "*a probe reagent targeting an analyte*") which is linked ("*conjugated*") to another part that can hybridize to a "*nucleic acid label comprising a plurality of predetermined subsequences*" (in Göransson referred to as decoding tag 1 and tag 2) to a set of "tag probes" (which are the "*decoder probes*" as defined in claim 1 of the Patent). Each subpopulation of tag probes comprises a detectable tag that produces an "*optical signal signature*" (one of the fluorescent dyes Cy3, Texas Red or Cy5). The signal signatures generated by the hybridization are obtained (see the 20 x 20 pixel image sections in Figure 3) and thus "*detected*". After a first round of detection, the signal signatures are removed by dehybridization (F3), and a new hybridization cycle begins with different sets of decoder probes (corresponding to the detection steps in F4). The resulting "*temporal order of the optical signal signatures*" are compared to a predetermined "*order*" for a particular analyte to "*identify the analyte"* (see "C", the decoding scheme of Göransson).

9.9 There is no dispute between the parties in relation to the disclosure of Göransson so far. Accordingly, there is no dispute between the parties that Göransson discloses all of the features of claim 1, except that – according to the Defendant – Göransson does not disclose the detection of analytes <u>in a sample</u> (F1 and F5.1) and that Göransson also does not disclose that the

detection reagents remain bound to the analyte throughout the detection method.

9.10 The dispute between the parties thus essentially focusses on the interpretation of claim 1 of the Patent rather than on what Göransson actually discloses to the skilled person. According to the Defendant, Göransson does not disclose the detection of analytes "*in a sample*" because the sample is genomic DNA and in Göransson it is not this genomic DNA that is fixed on the slides, but only the ASMs derived from the genomic DNA. The process described in Göransson furthermore, according to the Defendant, makes it impossible to perform *in situ* detection or analysis. Finally, the Defendant argues that claim 1 requires that the detection reagents remain bound to the analyte and that Göransson does not disclose this directly and unambiguously (Göransson rather discloses the dehybridization of the analytes).

9.11 The Central Division does not follow the Defendant´s interpretation of the claimed subject matter and thus comes to the conclusion that Göransson is novelty destroying for claim 1 of the Patent as granted.

9.12 As held above under "*Claim Interpretation*", the terms "*analyte*" and "*sample*" are broadly interpreted. According to the Central Division, these terms include ASMs prepared from genomic DNA and fixed on a microscopic slide as disclosed by Göransson. In Göransson, a genomic DNA sample is (pre)treated such that a collection of ASMs is formed on a microscopic slide (p. 8 left-hand col. under "*Discussion*", "*a random array of all molecules in a sample is created that can be targeted by a series of hybridization reactions to decode the identity of the molecules.*"). As set out above (see par. 8.13), according to the description of the Patent a sample may be pre-treated or processed. This includes pre-treatment by e.g. DNA extraction reagents (par. [0049] of the Patent description). "Extracting" DNA by generating ASMs from a genomic DNA sample, is therefore a way of processing the sample resulting in a processed sample, but there is still a sample "in" which the individual target analytes (in this case the ASMs) can be detected. Such a sample is covered by claim 1.

9.13 Claim 1 of the Patent – in the form as granted – is also not limited to *in situ* detection or analysis, not based on its wording, the context of the claim itself or the description. As follows from the interpretation as provided above, the requirement that the plurality of analytes has to be detected *in* a sample does not constitute such a limitation.

9.14 As furthermore follows from the claim interpretation as set out above, the Central Division does not adopt Defendant´s view that the claim requires that the identical detection reagents must stay bound to the analytes throughout the entire detection method claimed. Regardless of whether or not Göransson discloses directly and unambiguously that all the sandwich probes are dehybridized between two consecutive hybridization and read-out steps (see "*Dehybridization of ASMs*", p. 3, right-hand col. Göransson in combination with Fig. 3 depicted above, washed in a dehybridization buffer containing 50% formamide and 2x SSC buffer at 50 °C for 1 min.), the dehybridization of the analytes and the subsequent addition of "fresh" detection reagents before a new round of detection, as is undisputedly disclosed by Göransson, is not excluded by the claims of the Patent as granted (see par. 8.22 - 8.33 above, also see par. [0075] of the Patent which mentions the use of denaturants such as formamide, used by Göransson, as a way of modifying the decoder probes, i.e. removing the signal signature).

9.15 In conclusion, all features of claim 1 of the Patent as granted are disclosed directly and unambiguously in Göransson. The claimed subject matter therefore lacks novelty.

9.16 Since the Patent cannot be maintained as granted, the condition under which the Defendant has made an application to amend is fulfilled (Defence, p. 39, top). The Court will therefore proceed to consider the admissibility of the application to amend and to assess whether the grounds for revocation brought forward affect the Patent in part or entirely.

10 Application(s) to Amend: Admissibility

10.1 The application to amend lodged with the Defence to Revocation ("DtR"), Auxiliary requests AR1-AR8, is admissible. New AR2, lodged on 6 March 2024, is not admitted into the proceedings.

10.2 The application to amend was made in the Defence to Revocation (Rule 30 RoP which applies *mutatis mutandis* in a revocation action based on Rule 50 RoP). Various amendments were proposed by way of multiple alternative sets of claims (Auxiliary requests 1-8, "**AR1-AR8**"). The Claimant has not argued that the Defendant´s application to amend does not meet the requirements of Rule 30.1 RoP. The Central Division sees no reason to find otherwise. The application to amend is therefore admissible.

10.3 The Court does not give permission for the subsequent application to amend as lodged by the Defendant on 6 March 2024, comprising a new auxiliary request 2, maintaining all the auxiliary requests already proposed in the application to amend that was made in the Statement of Defence. The reason for filing the subsequent application to amend that was provided by the Defendant was the CoA order in *NanoString/10x Genomics*. The reasoning of the CoA in relation to claim construction prompted the Defendant to file "*a further AR emphasizing even more expressly the required persistent binding of the detection reagents to the analytes during the readout of the pre-determined subsequences of the detection reagents.*"

10.4 Under the front-loaded system of UPC proceedings parties are under an obligation to set out their full case as early as possible (Preamble RoP 7, last sentence). The subsequent application to amend was filed late in the proceedings, after closure of the written proceedings and after the interim conference, less than 1.5 months before the (at the time scheduled) oral hearing. The explanation provided by the Defendant as to why it was not possible to set out their full case (by filing the auxiliary request) earlier, i.e. the fact that a CoA order was issued on 26 February 2024 and in particular the claim construction adopted by the CoA, does not justify allowing the new auxiliary request into these proceedings at this stage of the proceedings. Although the Defendant indeed acted swiftly in submitting the application within one week after the CoA order becoming available, the substantive part of the CoA order that triggered the filing of new AR2, i.e. the claim construction issue in relation to the ´persisted binding´, albeit in relation to a different patent (EP ´782), could not have come as a surprise to the Defendant. That the CoA followed the interpretation as argued by the Claimant is not a valid reason. Already in the Statement of Revocation (´SoR´) in the present Revocation action, the Claimant provided its interpretation of the relevant features (par. 91 and footnote 8 and par. 97 footnote 9). In the DtR, the Defendant acknowledged and responded to the issue (DtR p. 16, under b). The Claimant then reiterated and further explained its position in the Reply to the Defence to Revocation (´RtD´, see par. 34-51). Under these circumstances, the Central Division is of the opinion that the Defendant could and should have filed the auxiliary request earlier. New AR2 is filed in response to an issue that was known to the Defendant at the very least since 27 November 2023, the date of the RtD. No satisfactory explanation has been provided why the Defendant waited until 2 March 2024 to file new AR2. This is in violation of the Defendant´s obligation to set out its case as early as possible thereby making it unnecessarily difficult for the Claimant and the

Court to properly deal with the new request. Permission under Rule 50.2 RoP in connection with Rule 30.2 RoP is therefore not given.

10.5 The Claimants have raised several objections against Auxiliary request 1 in relation to the requirements of Articles 84 and 123(2) EPC. It is not necessary for the Central Division to decide on these objections since the proposed claim amendments cannot in any event save the Patent from revocation in its entirety (see below).

11 Auxiliary request 1: Inventive Step

11.1 Auxiliary request 1 cannot serve as a basis to revoke the Patent in part as the subject matter claimed lacks inventive step.

11.2 Claim 1 of Auxiliary request 1 is amended vis-à-vis claim 1 of the Patent as granted in the following way (annotations by the Defendant):

1. *A method used in (i) immunohistochemistry and/or (ii) fluorescence in situ hybridization for detecting a plurality of analytes in a sample, comprising:*

a. contacting the sample with a composition comprising a plurality of detection reagents, wherein each subpopulation of the detection reagents targets at least one different analyte, wherein the analyte is fixed on a solid substrate or support and wherein the solid substrate or support is a chip, a microarray, ~~a blotting membrane~~ or a microscopic slide, and wherein each detection reagent comprises:

at least one probe reagent targeting an analyte and at least one nucleic acid label comprising a plurality of pre-determined subsequences, wherein said at least one probe reagent and said at least one nucleic acid label are conjugated together; and wherein at least a portion of said plurality of pre-determined subsequences form an identifier of said at least one probe reagent;

b. removing any unbound detection reagents;

c. detecting in a temporally-sequential manner said plurality of pre-determined subsequences of said detection reagent, wherein said detection of the subsequences comprises:

i) hybridizing a set of decoder probes with a subsequence of the detection reagents, wherein each subpopulation of said decoder probes comprises an optical detectable label, each optical detectable label generating an optical signal signature corresponding to each subsequence;

ii) detecting said optical signal signature produced upon the hybridization of said set of decoder probes and obtaining an image;

iii) removing said optical signal signature produced by the hybridization of said set of decoder probes;

iv) repeating steps (i) through (iii) for other subsequences of said detection reagents, thereby producing a temporal order of optical signal signatures corresponding to the plurality of pre-determined subsequences, wherein the temporal order of the optical signal signatures corresponding to said plurality of pre-determined subsequences of said detection reagent identifies a subpopulation of the

detection reagents and is unique for each subpopulation of the detection reagents; and

d. comparing said temporal order of the optical signal signatures with different identifiers of said at least one probe reagent, wherein an agreement between the temporal order of the optical signal signatures and a particular identifier of said at least one probe reagent identifies the analyte in the sample; wherein

said sample is a biological sample comprising one or more cells and/or one or more tissues; and wherein

said analytes are selected from the group consisting of proteins, peptides and nucleic acids, wherein said nucleic acids are selected from the group consisting of cellular RNA, messenger RNA, microRNA, ribosomal RNA, and any combinations thereof.

Interpretation of claim 1 of AR1

11.3 The features of AR1 that have been introduced into claim 1 of the Patent as granted are:

- the method is used in *in situ* fluorescence hybridization and/or immunohistochemistry
- the sample is a biological sample comprising one or more cells and/or one or more tissues
- analytes are selected from the group consisting of proteins, peptides and nucleic acids, wherein said nucleic acids are selected from the group consisting of cellular RNA, messenger RNA, microRNA, ribosomal RNA, and any combinations thereof.

11.4 There is no real dispute between the parties about the interpretation of the individual features that have been added to claim 1 of the Patent as granted. The description of the Patent characterises (fluorescence) *in situ* hybridization (FISH) in par. [0236] as a "*technique for detecting (and/or quantifying) the presence of certain cellular DNA or RNA (often ribosomal* RNA*).*" Immunohistochemistry is defined as "*antibody-based staining of cell or tissues for microscopic evaluation*" in par. [0235] of the Patent (also see the dictionary definition in D53). The skilled person is familiar with these methods from their common general knowledge and generally knows how these should be performed. The Patent contains no specific teaching in relation to these methods *per se*.

11.5 In the opinion of the Central Division, the method as claimed in claim 1 of the first Auxiliary Request, by specifying that the method *"is used*" in the context of *in situ* hybridization and/or immunohistochemistry, is limited *vis-à-vis* the claims as granted in that the method must actually be used in an *in situ* context, i.e. for that purpose. In other words, methods that are not used in the context of either of these (well known) *in situ* methods are excluded from the claimed subject matter. This understanding is in line with and further confirmed by the second amendment in Auxiliary request 1 which specifies that the sample is a biological sample comprising one or more cells and/or one or more tissues and the limitation of the analytes.

11.6 The Defendant further argued that the skilled person, in the context of an *in situ* method, to which the claims of AR1 are undisputedly limited, would on the basis of their common general knowledge be aware that significantly longer detection probes (also referred to as "*probe reagents*", the part of the detection reagent that interacts with the analyte of interest), had to be used compared to an *in vitro* method. The "*decoder probes*" (the probes hybridizing the predetermined subsequences) would be much shorter than the detection probes. The likelihood of the detection reagents being "washed away" together with the removal of the signal signature when using such long

detection probes would be next to nil. This knowledge, as the Court understands the argument, would lead to a claim interpretation whereby the skilled person would understand that – in any event in an *in situ* context – (all) the detection reagents with which the sample is contacted in step a of the method would remain bound to "their" analytes throughout the entire detection method.

11.7 The Central Division does not follow the Defendant´s interpretation. Neither the claim nor the description of the Patent contain any information that points in the direction of a limitation for the absolute and/or relative length of probe reagents and decoder probes, specifically for an *in situ* method such as FISH. On the one hand, it is stated in par. [0060] of the description that the decoder probe "*can have a sequence of any length*", whereby 100 nucleotides is mentioned concretely as (the larger end of a) preferred sequence length. Probe reagents, on the other hand, are even much broader defined in the description par. [0087] et seq. including "*an entity (e.g., but not limited to, a molecule, a particle, a composite entity, or a multi-molecular entity) that interacts with or binds to a target molecule*". The probe reagent is thus not even necessarily a nucleic acid, but can for example be a protein (like an antibody in immunohistochemistry). Probe reagents are furthermore not specified by their length, let alone the number of nucleotides, let alone the number of nucleotides relative to the number of nucleotides of a decoder probe.

11.8 In view of the foregoing, even if the Defendant´s contention that the skilled person would, on the basis of their common general knowledge, have used longer probe reagents *in situ* than they would have used in *vitro*, is followed, it cannot be seen that it is <u>required</u> by the claim that the same detection reagent stays bound to "its" analyte throughout the method, also if the method is carried out *in situ*. This analysis does not change when taking into account the article of He *et al*. (Exhibit BP9). It may be so that in an *in situ* method published by employees belonging to the Claimant´s group of companies in October 2022 certain probes and (de)hybridization conditions are used, this does not affect the skilled person´s interpretation of the claims of AR1 at the priority date in accordance with the general principles for claim interpretation as set out above.

11.9 Against the background of this interpretation, the Central Division now will turn to inventive step of Auxiliary Request 1 ("AR1") first as there is no dispute between the parties that the subject matter of Auxiliary Request 1 is novel over Göransson.

Legal framework inventive step

11.10 The Central Division adopts the principles for assessing inventive step as set out by the CoA in CoA *NanoString/10x Genomics* Order and in the Central Division´s decisions of 16 July 2024 in cases UPC_CFI_1/2023 and UPC_CFI_14/2023 (par. 8-2-8.10), also see LD Munich Order dated 27 August 2024 in case UPC_CFI_201/2024, C.4.b).

11.11 According to Article 56 EPC, an invention shall be considered as involving an inventive step if, having regard to the state of the art, it is **not obvious** to a person skilled in the art.

11.12 Whether inventive step is acknowledged is always to be assessed in each individual case and requires a legal evaluation of all relevant facts and circumstances. As held by the Court of Appeal in *NanoString/10x Genomics* (p. 30, fourth par.) the burden of presentation and proof with regard to the facts from which the lack of validity of the patent is derived and other circumstances favourable to the invalidity or revocation lies with the claimant in a revocation action (Art. 54 and 65(1) UPCA, Rules 44(e)-(g), 25.1(b)-(d) RoP). Even though proof of certain facts, if contested, may thus be required, the ultimate assessment of the relevant facts circumstances is a question of law which does not lend itself to the taking of evidence.

11.13 An objective approach must be taken to the assessment of inventive step. The subjective ideas of the applicant or inventor are irrelevant. In principle, it is also irrelevant whether the invention is the result of serendipity or of systematic work involving (potentially costly and laborious) experimentation. It is only relevant what the claimed invention actually contributes to the prior art.

11.14 Inventive step is to be assessed from the point of view of the skilled person on the basis of the state of the art as a whole, including the skilled person´s common general knowledge. The skilled person is assumed to have had access to the entire publicly available art on the relevant date. The decisive factor is whether the claimed subject matter follows from the prior art in such a way that the skilled person would have found it on the basis of their knowledge and skills, for example by obvious modifications of what was already known.

11.15 In order to assess whether or not a claimed invention was obvious to a skilled person, it is first necessary to determine a starting point in the state of the art. There has to be a justification as to why the skilled person would consider a particular part of the state of the art as a realistic starting point. A starting point is realistic if its teaching would have been of interest to a skilled person who, at the priority date of the patent at issue, was seeking to develop a similar product or method to that disclosed in the prior art which thus has a similar **underlying problem** as the claimed invention (cf. Court of Appeal *NanoString/10x Genomics*, p. 34 under "cc" in the German original version, "*Für eine Fachperson, die sich zum Prioritätszeitpunkt des Verfügungspatents vor die Aufgabe gestellt sah war […] D6 von Interesse"*). There can be several realistic starting points. It is not necessary to identify the "most promising" starting point.

11.16 Comparing the claimed subject matter, after interpretation following the guidelines provided above under "claim interpretation", and the prior art, the subsequent question is whether it would be obvious for the skilled person to, starting from a realistic prior art disclosure, in view of the underlying problem, arrive at the claimed solution. If it was not obvious to arrive there, the claimed subject matter meets the requirements of Article 56 EPC.

11.17 In general, a claimed solution is obvious if, starting from the prior art, the skilled person would be motivated (i.e. have an incentive or in German: "*Veranlassung*", see the CoA in NanoString/10x Genomics, p. 34) to consider the claimed solution and to implement it as a next step ("*nächster Schritt*", CoA in NanoString/10x Genomics, p. 35, second par.) in developing the prior art. On the other hand, it may be relevant whether the skilled person would have expected any particular difficulties in taking any next step(s). Depending on the facts and circumstances of the case, it may be allowed to combine prior art disclosures.

11.18 A technical effect or advantage achieved by the claimed subject matter compared to the prior art may be an indication for inventive step. A feature that is selected in an arbitrary way out of several possibilities cannot generally contribute to inventive step.

11.19 The Central Division emphasises that hindsight needs to be avoided. The question of inventive step should not be answered by searching retrospectively, with knowledge of the patented subject matter or solution, for any (combination) prior art disclosures from which that solution could be deduced.

Inventive step over Göransson

11.20 Several prior art disclosures have been relied upon by the Claimant for lack of inventive step of AR1. One of these is Göransson. As discussed above under "novelty" in relation to the Main Request, Göransson discloses all the features of claim 1 of the Patent as granted.

11.21 The finding that Göransson discloses all the features of claim 1 as granted (and hence has many features in common also with claim 1 of AR1) is an indication that Göransson is a realistic starting point for the assessment of inventive step of the subject matter claimed. Furthermore, both the Patent and Göransson relate to (high-throughput) optical methods for the multiplex detection of target molecules in a sample. Therefore, they have the same underlying problem.

11.22 Both Göransson and the Patent address the need to increase the number of analytes that can be identified with a limited number of available "colours". See for the Patent e.g. DtR, p. 10-11 under "*Gist of the Invention*": "*to significantly increase the number of analytes that can be assessed with a limited number of fluorophores*". Cf. Göransson Fig. 3, above, and p. 4, left-hand column under "*Results*": "*Any multiplex molecular analysis utilizing fluorescence for readout is limited by the number of fluorescence spectra that can be resolved. […] By combining the information from several tags, more identities than there is tag probes can be decoded."* Also see p. 8, right-hand col.: *"Regardless of how the tags are introduced, three variables affect the number of identities that can be decoded using the proposed strategy: the number of fluorophores that can be resolved in individual decoding reactions, the numbers of tags used and the number of serial hybridization reactions to the ASMs.*"

11.23 The argument from the Defendant that Göransson is not a suitable starting point for the assessment of inventive step because the fields of cell biology and array technology were not integrated cannot be followed. In the view of the skilled person, who has knowledge of *in vitro* and *in situ* methods, both the Patent and Göransson relate to biological optical multiplexing detection methods. The lack of available fluorophores is moreover a generic issue for all biological multiplex detection methods that make use of such fluorophores. Even though there are differences in relation to the samples and methods used where it concerns ASMs on an array and RNA or proteins in a sample comprising cells or tissues fixed on a slide, the skilled person who

takes note of Göransson would realise that the part of its disclosure relating to the multiplexing problem is not limited to ASMs prepared from genomic DNA randomly spotted on an array. See e.g. Abstract of Göransson, last sentence: "*the target can be any biomolecule which has been encoded into a DNA circle via a molecular probing reaction.*" Likewise, Göransson teaches a "*generic decoding strategy*" (Abstract). So it cannot be said that Göransson´s teaching is confined to ASMs from genomic DNA on an array and will be disregarded by the skilled person who is interested in the detection of biomolecules in other contexts.

11.24 In sum, Göransson and the claimed subject matter have a significant number of technical features in common and relate to a similar underlying problem. Therefore, Göransson is a realistic starting point for the assessment of inventive step.

11.25 Göransson and claim 1 of AR1 differ in that the method is used in *in situ* fluorescence hybridization and/or immunohistochemistry, the sample is a biological sample comprising one or more cells and/or one or more tissues and the analytes are selected from proteins, peptides and certain RNAs. In sum, the claimed method is an *in situ* method for the detection of analytes as specified in the claim whereby more analytes than available colours can be detected.

11.26 Starting from Göransson, it was in the view of the Central Division obvious for the skilled person at the priority date to transfer the method of Göransson to an *in situ* context, for instance in FISH, to detect e.g. RNA or proteins, thereby arriving at the claimed subject matter. The following reasons support this conclusion.

11.27 Göransson explicitly discloses to the skilled person a <u>generic decoding scheme</u> for biomolecules that can be encoded into a DNA circle (cf. Abstract, last sentence, "*The decoding strategy is generic…*") as a solution to a general problem in "*Any multiplex molecular analysis utilizing fluorescence"* (cited above). Göransson furthermore discloses to the skilled person: "*analysis of biomolecules based on a combination of molecular probing and decoding reactions. The biomolecules are first probed with techniques that generate DNA circles upon recognition. ASMs are generated through RCA, and then attached to glass slides in a random pattern. The rolling-circle ASMs include sets of tags that are used for identification following a combinatorial decoding scheme, similar to that used to identify hundreds of thousand bead species in random bead arrays (37). <u>Our approach is generic and can be</u>*

applied for multiplex quantification of ASMs created from any assay that results in circular DNA molecules. We demonstrate our approach for quantitative multiplex analysis by using it to measure relative copy numbers of 31 autosomal and sex chromosome loci, targeted by selector probes (28).." (p.2, left-hand col., last par., underline CD).

11.28 Therefore, taken as a whole, the teaching of Göransson provides a motivation for the skilled person to consider whether the method of Göransson can also be applied to other assays than the random ASM array format that was used to demonstrate the approach for quantitative multiplex analysis.

11.29 Having established this general motivation, the subsequent question is whether the skilled person, without having the benefit of hindsight, *would* indeed as a next step have applied the Göransson method *in situ* (as per the claimed subject matter).

11.30 In this respect, the disclosure of Göransson itself already points the skilled person concretely towards *in situ* application of the methods disclosed therein, see page 2, left-hand col. in the middle: "*The proximity ligation assay has been used to detect proteins, protein modifications and interactions in serum samples and in situ (32–35). Rolling-circle ASMs have been used for readout in several genotyping assays (20,21,36), for detection of protein and protein complexes in situ using proximity ligation (33), and for detecting microbes with padlock probes followed by counting individual rollingcircle ASMs pumped through a microfluidic channel (19)*" (underline CD).

11.31 Reference 33 is the publication of Söderberg *et al.*, submitted in these proceedings as D30. Söderberg *et al.*, discloses combining "*proximity ligation with RCA for localized readout in fixed cells or tissues.*" (Title, p. 995 left-hand col.). It is not in dispute between the parties that in the procedure described by Söderberg *et al.*, proximity ligation rolling circle amplification (RCA) is performed to detect protein analytes *in situ*. According to the Defendant, however, D30 does not teach an *in situ* procedure in which repeated de/re hybridizations would be performed (DtR, p. 46, penultimate paragraph) and therefore the skilled person would not transfer the method of Göransson to an *in situ* context. In the view of the Central Division, this interpretation of the teaching of Göransson ignores the generic character of the coding and decoding method in the context of the multiplexing problem explicitly taught by Göransson. In other words, the skilled person will not see the pointer in Göransson to *in situ* methods separately from the other clear message conveyed by the Göransson publication being that the decoding strategy is

generic and can be applied to *any* biomolecule and ASMs from *any* assay (see above). The skilled person will thus realise that the generic decoding strategy as taught by Göransson can be used as well in other contexts, in particular *in situ*, where the lack of available fluorophores is also an issue.

11.32 The Central Division finds further support for the conclusion that the skilled person would indeed as a next step apply the method from Göransson *in situ* in the PhD thesis of Ida Grundberg, submitted in these proceedings as exhibit D50, which was published in April 2011 and (undisputedly) forms part of the state of the art.

11.33 Grundberg developed a technique involving the use of padlock probes and a proximity ligation assay ("PLA") for detecting and determining ("*genotyping*") point mutations and SNPs ("*single nucleotide polymorphisms*") in genes *in situ*, see title, abstract, and page 27 under the heading "*Padlock probes*". Padlock probes were also used by Grundberg's colleagues Göransson et al. – working in the same laboratory at the time – in the development of their array assay (p. 23, Rejoinder to the reply to the Defence to Revocation).

11.34 On p. 46 of D50, penultimate par., cited by the Claimant in par. 353 of the Reply to the Defence to revocation, markings by Claimant, Grundberg notes that a limitation to the current method design when it comes to multiplexing is the restricted number of fluorophores that can be used. In order to solve that multiplexing problem, Grundberg suggests using the decoding scheme consisting of consecutive hybridization steps as taught by Göransson as a next step (NB reference 133 is to Göransson):

> *"So,* ***what will be the next step to take with this described technique****? Well, the potentials are infinite. What might be the most self-explanatory and natural application is further mutation detection* ***analysis on tissues****. That would especially involve point mutations or other genetic alterations with minor sequence differences, such as deletions or fusion transcripts that other techniques cannot distinguish between. In both paper II and III we explored the multiplex ability of the method and we are convinced* ***that crosshybridization between the padlock probes are not an issue****, which opens up the possibility of detecting multiple mutations in a tissue as a general mutation analysis tool. A limitation with the current method design, when it comes to multiplexing, is the* ***restricted number of fluorophores*** *that can be used in order to not get a spectral overlap that may leads to difficulties in discriminating between signals. However,* ***previous studies have shown that by designing padlock probes with many tag sequences for detection, multiple targets can be detected and discriminated with the use of a decoding scheme consisting of many consecutive hybridization steps[113]****."* (see D50, page 46, penultimate paragraph, emphasis added)

11.35 In the thesis from Grundberg, the skilled person thus finds a further incentive to use the decoding scheme of Göransson *in situ*. The Defendant´s reading of this disclosure in the Grundberg thesis, namely that Grundberg considered the use of a decoding scheme of D10 for detecting the padlock probes in her genotyping and mutation detection assay (and not transferring the sandwich probe setup for detecting analytes *in situ*), Rejoinder p. 23 bottom, is not supported by the disclosure of Grundberg as depicted above in the light of the thesis as a whole. As the title of D50 suggests, Grundberg investigates Genotyping and Mutation Detection *In Situ*. The part of the thesis cited above, relates to the *in situ* use of primary (padlock) probes to detect and discriminate multiple targets using the consecutive hybridization scheme as taught in Göransson, i.e. in a multiplexing method which is to be carried out *in situ*. From this disclosure it rather follows that in a real-world scenario (devoid of any hindsight), the skilled person would have realised that the generic decoding scheme as taught by Göransson would indeed be applicable to *in situ* methods to solve the very problem of having a restricted number of fluorophores that can be used in multiplexing methods.

11.36 Contrary to the Defendant, the Central Division does not find that the skilled person takes from document D39 (Lagunavicius *et al.*) that RCA cannot be used reliably for the *in situ* detection of RNA due to a too low detection efficiency. Leaving aside that neither the claims of the Patent nor the description provide any technical teaching relating to or reporting the (RNA) detection efficiency of the claimed method, in the passage of D39 cited by the Defendant in the DtR, p. 50, bottom, it is indeed remarked by the authors that "*the RCA technique is not suitable for single-copy target examination in a single cell.*" This does, however, not mean that the technique is in general unsuitable for *in situ* RNA detection. In the same paragraph, it is said "*it still can be used for the detection and analysis of high-copy RNA transcripts*". In fact, Lagunavicius *et al.* report under conclusions that "*padlock probe sequence amplification* [was, CD] *successfully applied in vitro and in situ*" and "*individual RNA targets are visualised […] in situ*" (also see Fig. 3). D39 thus provides the skilled person with a further incentive to indeed apply the *in vitro* method as taught by Göransson *in situ* to detect RNA.

11.37 The Central Division also takes the above discussed disclosures as an indication that the skilled person would not have expected any particular technical difficulties in transferring the *in vitro* method as taught by Göransson to an *in situ* application. It is moreover undisputed, at least not sufficiently concretely contested by the Defendant, that at the priority date, it was routine for the skilled person to set up a (multiplex) FISH method for *in*

situ RNA detection (273 SoR et seq., with reference to numerous prior art documents).

11.38 The Defendant nevertheless referred to a number of "problems" that the skilled person would have faced which would have caused the skilled person to not have a reasonable expectation of success even if they would have had an incentive to transfer the method of Göransson from an *in vitro* to an *in situ* context (p. 47 DtR, p. 21-22 R). The doubts that the skilled person would have had were according to the Defendant: the destruction of the sample and analytes; sensitivity of native analytes, especially RNA, to degradation; duration of the procedure with repeated hybridization of the primary probes; change in location of ASMs compared to analyte localization across cycles; separability/distinguishability of multiple analytes occurring in close spatial proximity ("molecular crowding"); autofluorescence and heterogeneity in a cell or tissue sample; sample penetration and distribution of reagents).

11.39 The Central Division finds that the Claimant has in par. 362 RtD, credibly argued that most of the problems raised by the Defendant were problems that were common issues with *any* prior art FISH or IHC application and that those issues were routinely solved by the skilled person. Such problems have no bearing on the expectation of success of transferring the method of Göransson from an *in vitro* to an *in situ* context. Moreover, the fact that none of the problems identified by the Defendant are even mentioned in the Patent as "*in situ* problems", let alone that the Patent provides any solutions for these alleged problems is a strong indication that these problems would be readily addressed by the skilled person should they occur at all (also see below).

11.40 The above applies equally to what according to the Defendant is the "main problem" for transferring the method of Göransson into the *in situ* context which would be the time delay caused by repeatedly hybridizing the primary probe following the teaching of Göransson. As also discussed above in the context of claim interpretation of Auxiliary Request 1, an *in situ* method would require longer probe lengths that would require proportionally longer incubation times (p. 47 DtR). The Defendant refers to BP9, the CosMx Spatial Molecular Imager which has a probe length of 35-50 nucleotides and an incubation time of 16-18 hours. Göransson´s probes have a maximum length of 23 nucleotides and require only one hour to incubate, the Defendant points out.

11.41 First of all, the Central Division notes that the claims of AR1 require (underline CD) "*contacting the sample with a composition comprising a plurality of detection reagents*" (and removing unbound detection reagents) without any indication or limitation as to how long the contacting step should last. In par. [0046] the description of the Patent discloses a wide range of possible contact times being "*at least about 30 seconds, at least about 1 minute, at least about 5 minutes, at least about 10 minutes, at least about 15 minutes, at least about 30 minutes, at least about 1 hour, at least about 2 hours, at least about 3 hours, at least about 4 hours, at least about 6 hours, at least about 8 hours, at least about 10 hours, at least about 12 hours, at least about 24 hours, at least about 48 hours or longer.*" From this the Central Division concludes that the skilled person will be able to determine an appropriate contact time. This is also confirmed by the specification of the Patent in suit, see the last sentence of par. [0046]: "*One of skill in the art can adjust the contact time accordingly.*" Likewise, as discussed above, in par. 11.7, the probe reagents can be of any length. The description adds in par. [0088] "*An ordinary artisan can readily identify appropriate probe reagents for the target molecules or analytes of interest to be detected in various bioassays.*" In view of this information in the Patent, the Central Division concludes that the skilled person, starting from Göransson, would have been able, based on their common general knowledge, to design appropriate probe reagents and contacting times for use *in situ* even if the skilled person would have "stuck" with multiple (re)hybridizations as taught in Göransson (and not excluded by the Patent).

11.42 Based on the foregoing, the Central Division comes to the conclusion that it would have been obvious for the skilled person to, starting from the prior art disclosure of Göransson, arrive at the subject matter of claim 1 of AR1.

11.43 In coming to this conclusion, the Central Division has furthermore taken into account that the claimed subject matter is not limited to nor provides the skilled person with any guidance as to the number of analytes that has to be detected, the time within which this is to be done, the sensitivity of the method that must be reached, the resolution of a spatial location, etc. Such information or guidance is also not to be found in the Patent description. In addition, as stated by the Claimant (in the Statement of Revocation, at par. 191), and not contested by the Defendant, there is not a single experimental example in the Patent of how a FISH method can be carried out with RNA as analyte. Further, there are no experimental examples demonstrating the use of a FFPET (Formalin-Fixed Paraffin-Embedded Tissue used in immunohistochemistry, CD) sample or detection of a particularly high

number of analytes or at least explains under which conditions a particularly high throughput could be realized. The claimed method thus on the one hand includes embodiments wherein the method (arguably) still "works" (i.e. *detects* a plurality of analytes, at least two analytes) but provides none of the advantages relied upon by the Defendant in support of inventive step. On the other hand, the description does not provide sufficient technical information that the above-mentioned problems (which are according to the Defendant specific for *in situ* methods) actually exist, let alone are overcome by the claimed subject matter. In the absence of such a concrete technical teaching or contribution, these "problems" cannot in the view of the Central Division be used as the basis on which to acknowledge inventive step.

11.44 Since the condition that the Patent cannot be maintained in accordance with AR1 is fulfilled, the Central Division will revert to the other auxiliary requests on file.

12 Further Auxiliary Requests AR2-8 and Subclaims

12.1 Turning to the originally filed auxiliary requests, which are formally admissible (see above par. 10.2), **Auxiliary request 2** (´AR2´) submitted by the Defendant is further limited with respect to **F4**, in that the detection of the plurality of predetermined subsequences is performed "*directly on the sample*." Furthermore, an additional limitation of **F6** (compared to claim 1 according to AR1) is proposed in that the sample is a "*biological sample comprising one or more fixed cells*".

12.2 The Central Division finds that these amendments do not render the subject matter of AR2 inventive. The skilled person knows from their common general knowledge that *in situ* methods are normally performed (directly) on cell or tissue samples which are typically fixed on a solid support such as a microscopic slide. There is no inventive (technical) contribution related to these further limitations with respect to **F4** and **F6**.

12.3 **Auxiliary requests 3 and 4**, adding *"at a special location"* to **F4.1.2** and **F4.1.4** and being further restricted to use in FISH, respectively, are further alternatives by which the Defendant wishes to emphasize the *in situ* context of the claimed subject matter (p. 26 Reply to the Defence to the application to amend). As follows from the discussion in relation to AR1, the Central Division finds that performing the method in an *in situ* context, including the well known *in situ* method FISH, was obvious in view of the state of the art

(in particular Göransson). Therefore, these auxiliary requests also cannot render the claimed subject matter inventive for the same reasons as AR1.

12.4 **Auxiliary request 5** has compared to claim 1 of AR1 an additional limitation of **F4.1.3** according to which the removing of the optical signal signature, resulting from hybridization of the decoder probes with the predetermined subsequences, is performed "*by cleavage*". Against the Claimant´s substantiated assertion (with reference to exhibit D54) that cleaving off a fluorescent label was part of the common general knowledge, nothing concrete has been put forward by the Defendant. The subject matter of Auxiliary request 5 therefore lacks inventive step for the same reasons as for AR1. The additional feature does not render the subject-matter of claim 1 inventive.

12.5 In submitting **Auxiliary requests 6 and 7**, specifying in claim 1 the length of the predetermined subsequences and the decoder probes, respectively, the Defendant does not provide any other arguments in defence of patentability compared to the previous Auxiliary Requests. Therefore, these claims lack inventive step for the same reasons and require no separate discussion.

12.6 **Auxiliary request 8** specifies in claim 1 that a plurality of predetermined subsequences is "*at least two*". This request requires no separate discussion as the Central Division has already interpreted a plurality as "at least two" (see par. 8.18 above) and has found a lack of novelty/inventive step on the basis of this interpretation.

13 Conclusion

13.1 In conclusion, the subject matter of claim 1 as granted (Main request) lacks novelty over Göransson. The subject matter of Auxiliary request 1 lacks inventive step over Göransson. Auxiliary requests 2-8 can also not serve as a basis for revoking the Patent only in part. The patent must therefore be revoked in its entirety.

13.2 Since the Patent is revoked in its entirety on the ground of lack of novelty and lack of inventive step, the Central Division does not have to decide on the other grounds for revocation raised by the Claimant.

13.3 The Central Division notes that it comes to the same conclusion as the German Federal Patent Court on essentially similar grounds. Furthermore, this decision is substantively in line with the findings of the CoA in the

NanoString/10x Genomics appeal where many similar issues were dealt with by the CoA.

14 Costs

14.1 In accordance with Article 69 UPCA and Rule 118.5 RoP the Defendant, as the unsuccessful party, the Patent being revoked entirely, has to bear the legal costs of the Claimant.

DECISION

Having heard the parties on all relevant aspects of the case, the Central Division:

1. Revokes European Patent 2 794 928 B1 entirely with effect to the territory of France (FR), Germany (DE) and The Netherlands (NL).

2. The Defendant as the unsuccessful party shall bear the legal costs incurred by the Claimant.

3. Dismisses any further request made.

NAMES AND SIGNATURES	
Judges Presiding judge: Ulrike Voß Ulrike Voß Digital unterschrieben von Ulrike Voß Datum: 2024.10.11 12:21:12 +02'00' Legally qualified judge: András Kupecz (judge-rapporteur) András Ferenc Kupecz Digital unterschrieben von András Ferenc Kupecz Datum: 2024.10.11 11:19:55 +02'00' Technically qualified judge: Eric Enderlin Eric, André Enderlin Signature numérique de Eric, André Enderlin Date : 2024.10.14 13:38:09 +02'00'	**For the Deputy-Registrar** Natalie Gnaß Natalie Gnaß Digital unterschrieben von Natalie Gnaß Datum: 2024.10.14 13:50:54 +02'00'

Information about appeal

An appeal against the present Decision may be lodged at the Court of Appeal, by any party which has been unsuccessful, in whole or in part, in its submissions, within two months of the date of its notification (Art. 73(1) UPCA, R. 220.1(a), 224.1(a) RoP).

Information about enforcement

Art. 82 UPCA, Art. Art. 37(2) UPCS, R. 118.8, 158.2, 354, 355.4 RoP.
An authentic copy of the enforceable decision will be issued by the Deputy-Registrar upon request of the enforcing party, R. 69 RegR.