IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

SCALE BIOSCIENCES, INC., Plaintiff, v. PARSE BIOSCIENCES, INC., Defendant, and ROCHE SEQUENCING SOLUTIONS, INC., Nominal Defendant.	)	C.A. No. _____ **DEMAND FOR JURY TRIAL**

COMPLAINT

Plaintiff Scale Biosciences, Inc. ("ScaleBio") for its Complaint against Defendant Parse Biosciences, Inc. ("Parse" or "Defendant"), alleges as follows:

NATURE OF THE ACTION

1. This is an action for infringement of United States Patent Nos. 10,626,442 (the "'442 Patent"), 10,982,256 (the "'256 Patent") and 11,512,341 (the "'341 Patent") (collectively, the "Asserted Patents"). This action arises under the patent laws of the United States, Title 35, United States Code, including 35 U.S.C. § 271, and the Declaratory Judgment Act, Title 28, United States Code, including §§ 2201, 2202.

THE PARTIES

2. ScaleBio is a Delaware corporation with its principal place of business at 3210 Merryfield Row, San Diego, California 92121. Pursuant to a license agreement with Roche Sequencing Solutions, Inc. ("RSS") and certain of its affiliates, ScaleBio is the exclusive licensee of the Asserted Patents in the research field and is a co-exclusive licensee of the Asserted Patents

in the diagnostic field. ScaleBio is commencing this action and has the right to join RSS as a party in accordance with the terms of its license agreement with RSS and its affiliates.

3. On information and belief, RSS is a Delaware corporation with its principal place of business at 4300 Hacienda Drive, Pleasanton, California 94588. RSS is the sole assignee and the true and legal owner of the Asserted Patents. RSS is named as nominal defendant in this action for purposes of subject matter jurisdiction only, pursuant to the Supreme Court's holding in *Independent Wireless Co. v. Radio Corp. of America*, 269 U.S. 459, 468 (1926) that "[i]f the owner of a patent, being within the jurisdiction, refuses or is unable to join an exclusive licensee as coplaintiff, the licensee may make him a party defendant by process, and he will be lined up by the court in the party character which he should assume." ScaleBio has requested that RSS join as a party in this action, but RSS has thus far not agreed to do so. Accordingly, RSS is named as a nominal defendant and ScaleBio seeks relief realigning RSS as a plaintiff.

4. On information and belief, Parse is a Delaware corporation with its principal place of business at 201 Elliott Avenue W, Suite 290, Seattle, Washington 98119.

JURISDICTION AND VENUE

5. This civil action for patent infringement arises under the Patent Laws of the United States, 35 U.S.C § 1 *et seq.* and in addition seeks declaratory relief pursuant to 28 U.S.C. §§ 2201 and 2202.

6. This Court has subject matter jurisdiction pursuant to 28 U.S.C. §§ 1331 and 1338(a).

7. This Court has personal jurisdiction over Parse because Parse is a Delaware corporation and thus resides in this district.

8. This Court has personal jurisdiction over RSS because RSS is a Delaware corporation and thus resides in this district.

9. Venue is proper in this district under 28 U.S.C. § 1400(b).

BACKGROUND

A. Plaintiff's Pioneering Single-Cell Sequencing Technology

10. ScaleBio (formerly known as SC Bio, Inc.) was founded in 2019 by a multidisciplinary team of scientists and technologists, with expertise in next generation sequencing, genomics, proteomics, and bioinformatics. Its founders share a common mission to develop, democratize and make accessible this important technology for the broader research community to support a broad range of applications including epigenomics, transcriptomics, proteomics, and multi-omics.

11. RSS is a branch of the diagnostics division of the Roche group focusing on making next-generation sequencing simple and accessible enough for routine use in research and medical laboratories. The revolutionary technology patented by RSS and licensed to ScaleBio is enabling the creation of critical research and diagnostic tools and techniques that are poised to deliver on the promise of personalized medicine.

12. Dr. Garry Nolan, the inventor of the Asserted Patents and a co-founder of ScaleBio, devised the invention disclosed and claimed in the Asserted Patents to address the need for a method that would identify multiple target molecules in cells of a complex cell population while retaining cell specific information regarding those target molecules at large scale without requiring additional, expensive laboratory equipment. By using the cell or nucleus as its own reaction vessel in which to attach barcode label components to target molecules for sequencing, Dr. Nolan's invention eliminates the need for specialized equipment to separate cells prior to sequencing and allows single-cell sequencing to proceed at vastly greater scale than prior methods.

13. Moreover, Dr. Nolan's innovative development of single-cell combinatorial barcoding removed previous constraints that had limited the number of cells and molecular targets

that could be measured in a single assay. Previous methods which relied on fluorescent sorting were inherently limited by the fluorescent spectra available to individually label targets. Other prior art tagging methods were similarly limited by the number of unique tags available. The combinatorial barcoding technique invented by Dr. Nolan, on the other hand, is not so limited and allows for vastly greater numbers of cells and target molecules to be analyzed. For example, Dr. Nolan's use of a split pool approach to perform barcoding steps so as to create cell-specific labels on multiple target molecules of cells in a mixed cell population was a novel, unconventional and pathbreaking innovation.

14. Licensing that innovative technology from RSS, ScaleBio has developed and brought to market single cell sequencing library preparation technology, reagents, and software that enable scalable, easy-to-adopt, extensible, cost-effective single-cell analysis and that make single-cell sequencing accessible to the larger scientific community across a broad range of systems, sample types, and applications.

15. ScaleBio's technology leverages split-pool barcoding and combinatorial indexing methods so as to use the cell or nucleus as a compartment for barcoding steps in order to provide a simple, scalable single-cell sequencing workflow. ScaleBio's single cell sequencing product provides single-cell combinatorial indexing applications and workflows, including single-cell transcriptome profiling for high throughput analyses which utilize the invention of the Asserted Patents. ScaleBio's single cell sequencing product frees researchers from the constraints of expensive and proprietary compartmentalization instruments and makes this important technology more accessible to a larger community of researchers.

B. Parse's Infringing Products

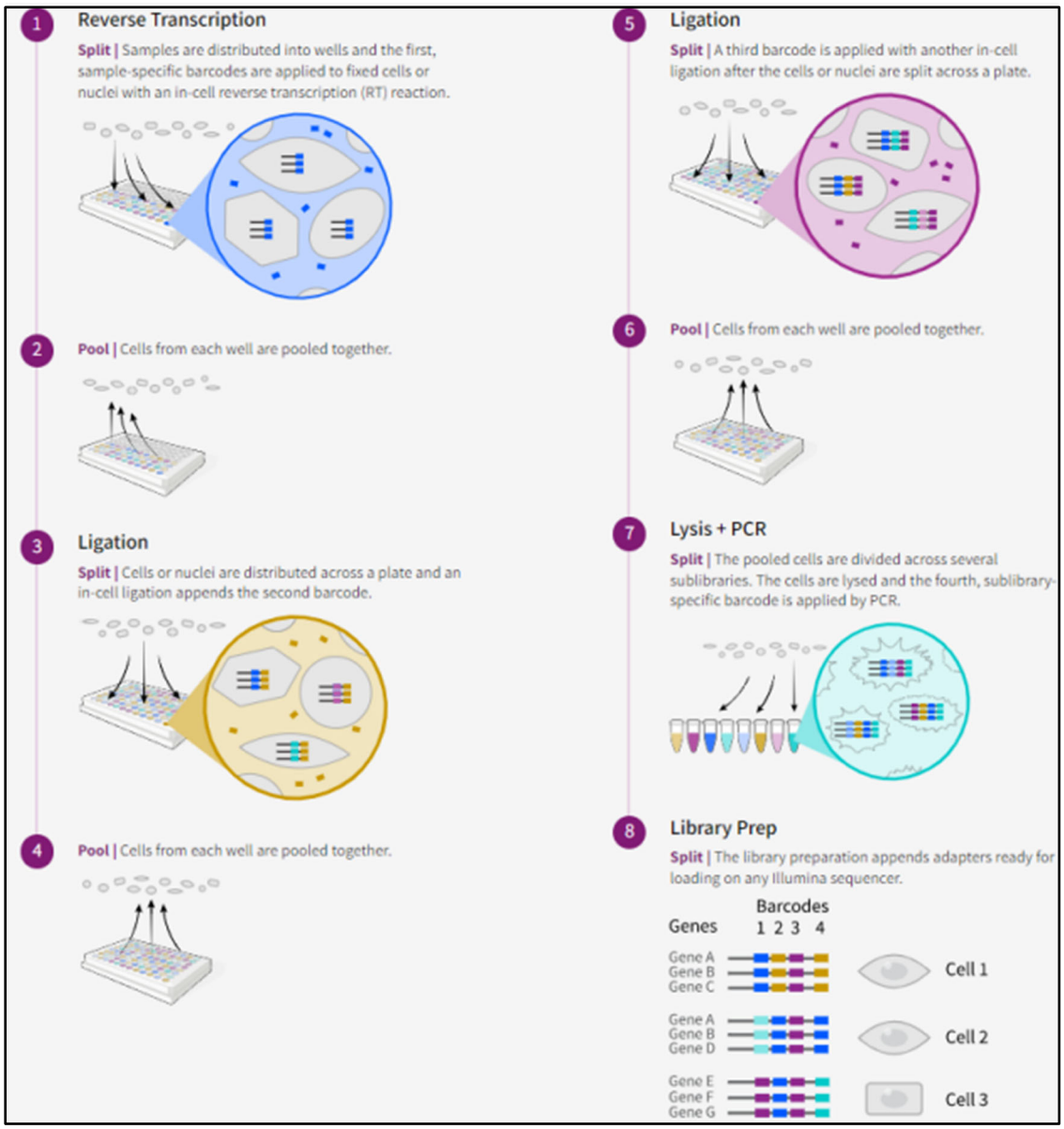
16. Parse (formerly known as "Split Biosciences" or "Split Bio") is a single-cell genomics company that has seized a critical early market share by misappropriating Plaintiff's

groundbreaking licensed technology. Parse sells a line of single-cell gene expression products, initially marketed under the name "Single Cell Whole Transcriptome" and more recently commercialized under the designation "Evercode Whole Transcriptome" or "Evercode WT," which exploit Plaintiff's licensed technology to achieve combinatorial barcoding steps within the cell itself. Parse has marketed its Evercode WT kits in two versions—v1 and v2—and has offered each version in three configurations designed to process different numbers of cells and samples—Evercode WT Mini, Evercode WT, and Evercode WT Mega. Parse's single cell gene expression products are collectively referred to herein as the "Accused Products" or "Evercode WT Products" and include all the aforementioned kits including, for example and without limitation, reagents, other consumables, and data analysis software used or provided by Parse in connection with its kits, along with instruction manuals for how to use the Evercode WT Products, and any other Parse products having substantially the same functions and uses.

17. On information and belief, Parse provides its Evercode WT Products—including reagents, other consumables, and data analysis software—to its customers. Parse asserts in its publications that its technology is based on a split-pool combinatorial barcoding method called SPLiT-Seq. Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (referencing Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176 (2018)) (last visited Dec. 14, 2022). The first configuration, which Parse launched commercially on or about February 18, 2021, purports to enable users to process up to 100,000 single cells and 48 samples. *See* Parse Biosciences, *Evercode™ WT v2 Resolve More Biology*, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Dec. 14, 2022). In late 2021, Parse began offering additional configurations: its Evercode WT Mini kit that purports to enable users to process up to 10,000

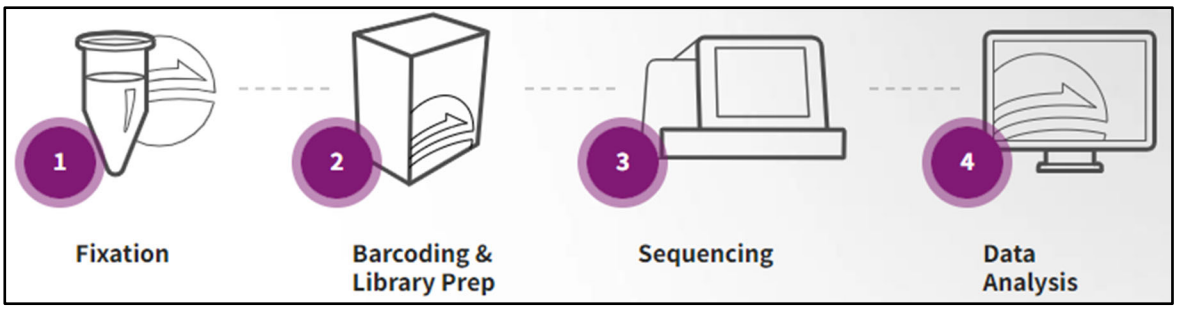
single cells and its Evercode WT Mega kit that purports to enable users to process up to one million single cells. *See* Parse Biosciences, *Evercode™ WT Mini v2 Explore Single Cell*, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Dec. 14, 2022); Parse Biosciences, *Evercode™ WT Mega v2 1 Million Cells for Your Lab Today*, https://www.parsebiosciences.com/products/evercode-whole-transcriptomemega (last visited Dec. 14, 2022). Each of Parse's Evercode WT Products purportedly enables users to analyze molecular signatures at the single-cell level. *See, e.g.*, Parse Biosciences, https://www.parsebiosciences.com ("Single cell insights are accessible to biological researchers in any lab with the Evercode™ combinatorial barcoding approach.") (last visited Dec. 14, 2022).

18. On information and belief, Parse purports that its Evercode WT Products are used to convert single cells or nuclei into individualized reaction compartments and that the cells or nuclei can be paired with unique cellular barcodes and unique molecular indices through a nonautomated method of pooling, tagging, re-pooling, re-tagging, etc. *See, e.g.*, Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 177, Suppl. Materials Fig. S1 (2018);



Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022).

19. On information and belief, Parse claims that its products' barcode tagging allows the user to track a molecule of interest and the cell of origin of that molecule, and as a result detect and quantify the level of the molecule of interest by sequencing:



Parse Biosciences, https://www.parsebiosciences.com (last visited Dec. 14, 2022); *see also* Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 177 (2018).

20. On information and belief, the Evercode WT Products are and/or will be, marketed, offered for sale, and sold by Parse to potential and actual customers with material including technical brochures, instructional information, dataset examples, tutorials, and support information (collectively, "Parse Instructional Materials"). Such materials can be found for example on Parse's website (parsebiosciences.com), Parse's YouTube channel (https://www.youtube.com/channel/UCnV6KzlTvt8JYX2idK7nY1A/videos), and Parse's Vimeo channel (https://vimeo.com/504880645). On information and belief, the Parse Instructional Materials provide instructions, recommendations, and suggestions to customers on how to use Parse's Evercode WT Products.

21. On information and belief, Evercode WT Products are and/or will be, presented by Parse to potential and actual customers at seminars, conferences, and meetings (collectively, "Parse Instructional Presentations," and together with "Parse Instructional Materials," "Parse Instructional Materials and Presentations"). On information and belief, the Parse Instructional Presentations provide instructions, recommendations, and suggestions to customers on how to use Parse's Evercode WT Products.

THE ASSERTED PATENTS

22. RSS is the owner by assignment of the'442 Patent, titled "Methods of Identifying Multiple Epitopes in Cells," which was duly and legally issued by the United States Patent and Trademark Office on April 21, 2020. The '442 Patent issued from U.S. Application No. 15/597,917, filed on May 17, 2017, and claims priority to U.S. Application No. 13/981,711, filed on January 31, 2012 as International Application No. PCT/US2012/023411, and to U.S. Provisional Application Nos. 61/437,854, filed on January 31, 2011 and 61/444,067, filed on February 17, 2011. A true and correct copy of the '442 Patent is attached hereto as Exhibit A.

23. RSS is the owner by assignment of the '256 Patent, titled "Methods of Identifying Multiple Epitopes in Cells," which was duly and legally issued by the United States Patent and Trademark Office on April 20, 2021. The '256 Patent issued from U.S. Application No. 16/147,250, filed on September 28, 2018, and claims priority to U.S. Application No. 13/981,711, filed on January 31, 2012 as International Application No. PCT/US2012/023411, and to U.S. Provisional Application Nos. 61/437,854, filed on January 31, 2011 and 61/444,067, filed on February 17, 2011. A true and correct copy of the '256 Patent is attached hereto as Exhibit B.

24. RSS is the owner by assignment of the '341 Patent, titled "Methods of Identifying Multiple Epitopes in Cells," which was duly and legally issued by the United States Patent and Trademark Office on November 29, 2022. The '341 Patent issued from U.S. Application No. 17/870,641, filed on July 21, 2022, and ultimately claims priority to U.S. Application No. 13/981,711, filed on January 31, 2012 as International Application No. PCT/US2012/023411, and to U.S. Provisional Application Nos. 61/437,854, filed on January 31, 2011 and 61/444,067, filed on February 17, 2011. A true and correct copy of the '341 Patent is attached hereto as Exhibit C.

25. Parse has been on notice of the ’256 Patent and its infringement thereof since at least on or about June 10, 2021, when it received a letter from ScaleBio of that date identifying Parse’s infringement of the ’256 Patent by its use and commercialization of Accused Products.

26. Parse has been on notice of the ’442 Patent and its infringement thereof since at least on or about March 1, 2022, when it received a letter from ScaleBio’s counsel of that date identifying Parse’s infringement of the ’442 Patent by its use and commercialization of Accused Products.

COUNT I
(DIRECT INFRINGEMENT OF U.S. PATENT NO. 10,626,442)

27. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

28. On information and belief, Parse’s officers, employees and agents have used the Accused Products in the United States for purposes of customer support and training, product development, quality control and comparative testing.

29. Claim 1 of the ’442 Patent recites:

> A method of uniquely labeling target molecules within a plurality of cells, the method comprising:
>
> (a) coupling a common linker sequence to target molecules within the plurality of cells;
>
> (b) dividing the plurality of cells into at least two primary reaction volumes, the at least two primary reaction volumes comprising a first primary reaction volume and a second primary reaction volume;
>
> (c) providing primary nucleic acid tags to the at least two primary reaction volumes, wherein the primary nucleic acid tags provided to the first reaction volume are different from the primary nucleic acid tags provided to a second reaction volume;
>
> (d) coupling the common linker sequences within each of the at least two primary reaction volumes with the provided primary nucleic acid tags; (e) pooling the at least two primary reaction volumes;

(e) splitting the combined primary reaction volumes into at least two secondary reaction volumes, the at least two secondary reaction volumes comprising a first secondary reaction volume and a second secondary reaction volume;

(f) providing secondary nucleic acid tags to each of the at least two secondary reaction volumes, wherein the secondary nucleic acid tags provided to the first secondary reaction volume are different from the secondary nucleic acid tags provided to the second reaction volume; and

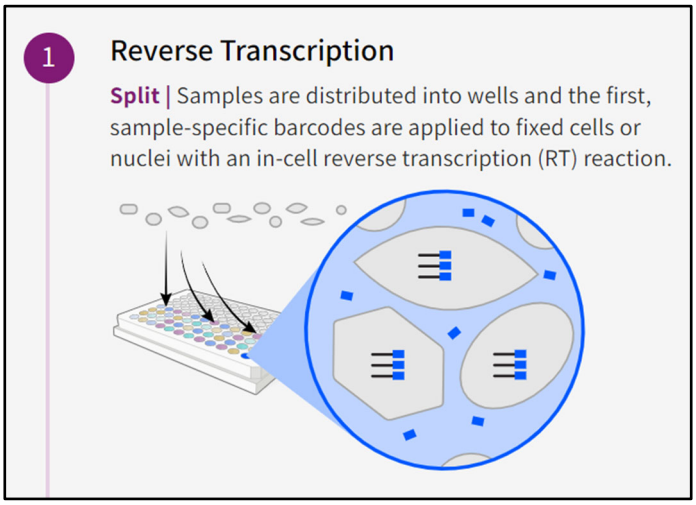
(g) coupling the target molecules within each of the at least two secondary reaction volumes with the provided secondary nucleic acid tags.

30. Use of the Accused Products in accordance with their accompanying directions directly infringes at least Claim 1 of the '442 Patent, literally or by equivalents, under 35 U.S.C. § 271(a).

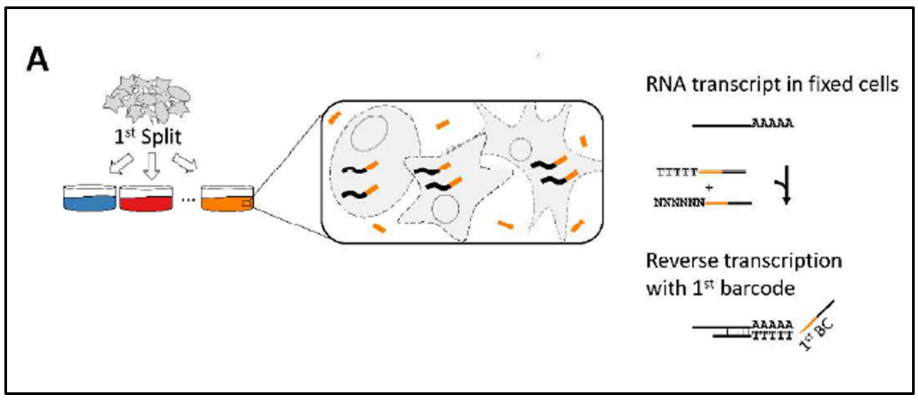
31. **Preamble: "A method of uniquely labeling target molecules within a plurality of cells, the method comprising"** Use of the Accused Products in accordance with their directions performs "[a] method of uniquely labeling target molecules within a plurality of cells." For example, Parse states that "[t]he Evercode™ Whole Transcriptome technology, originally based on the split-pool combinatorial barcoding method published in Science and known widely as SPLiT-Seq, is accessible to any standard biology lab." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). The SPLiT-seq method "labels the cellular origin of RNA through combinatorial barcoding." Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018); *see also id.* ("In SPLiT-seq, individual transcriptomes are uniquely labeled…."); Parse Biosciences, *Evercode™ WT v2 Resolve More Biology*, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Dec. 14, 2022) ("Append barcodes to each transcript by progressing cells through four split-pool combinatorial barcoding steps."). Parse further states that its Evercode WT Products can "[p]rofile anywhere from 10,000 to 1 million cells." Parse Biosciences, https://www.parsebiosciences.com

(last visited Dec. 14, 2022). Thus, use of the Evercode WT Products "uniquely label[s]" genomic "transcripts" (i.e., target molecules) across a population of "10,000 to 1 million cells" (i.e., a plurality).

32. **(a): "coupling a common linker sequence to target molecules within the plurality of cells"** Use of the Accused Products in accordance with their directions performs a first step that includes "coupling a common linker sequence to target molecules within the plurality of cells." For example, Parse states that the first step in the Evercode WT Products workflow is "appl[ying]" "sample-specific barcodes … to fixed cells or nuclei with an in-cell reverse transcription (RT) reaction":

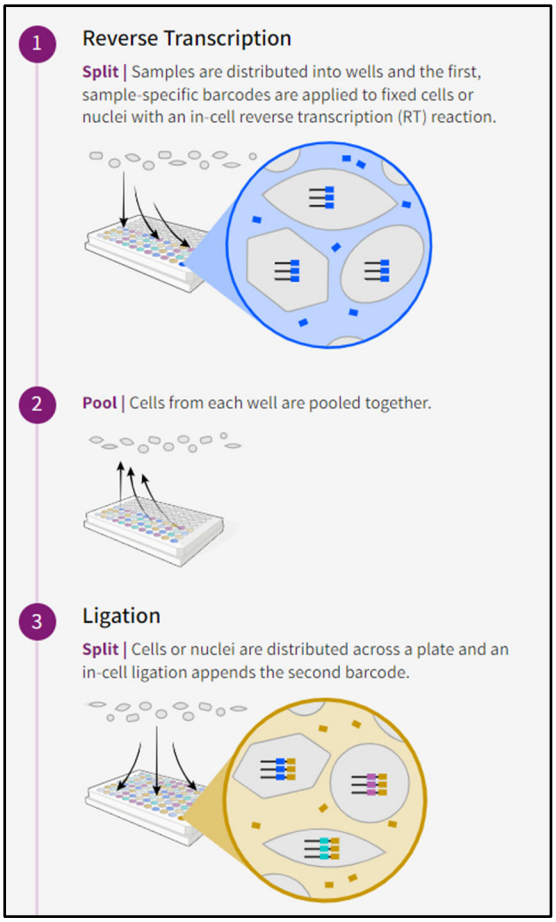


Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Suppl. Materials 2 (2018) ("The first round of barcoding occurs through an *in situ* reverse transcription (RT) reaction. … Both random hexamer and anchored poly(dT)15 barcoded RT primers were used in each well."). Upon information and belief, the first barcoding step in the Evercode WT Products workflow is further illustrated below:



Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. S1A (2018). Thus, in the workflow directed for the Accused Products, "barcoded RT primers" (which ***include*** a common linker sequence) are coupled with "RNA transcripts in fixed cells" through "reverse transcription."

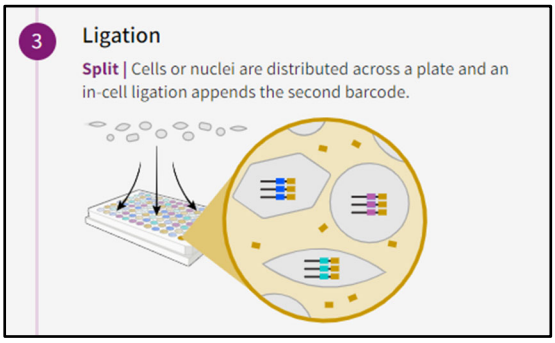
33. **(b): "dividing the plurality of cells into at least two primary reaction volumes, the at least two primary reaction volumes comprising a first primary reaction volume and a second primary reaction volume"** Use of the Accused Products in accordance with their directions comprises "dividing the plurality of cells into at least two primary reaction volumes, the at least two primary reaction volumes comprising a first primary reaction volume and a second primary reaction volume." For example, Parse states that, in the Evercode WT Products workflow, after the "in-cell reverse transcription," "[c]ells from each well are pooled together" and then, in the "split" step, "[c]ells or nuclei are distributed across a plate":



Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 177 (2018) ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with well-specific barcodes."). Thus, in the Evercode WT Products workflow, the cells are divided (or split) into at least two reaction volumes (i.e., two or more wells of the plate).

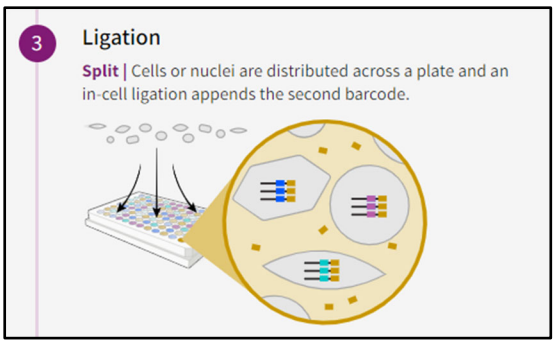
34. **(c): "providing primary nucleic acid tags to the at least two primary reaction volumes, wherein the primary nucleic acid tags provided to the first reaction volume are different from the primary nucleic acid tags provided to a second reaction volume"** Use of the Accused Products in accordance with their directions comprises "providing primary nucleic acid tags to the at least two primary reaction volumes, wherein the primary nucleic acid tags

provided to the first reaction volume are different from the primary nucleic acid tags provided to a second reaction volume." For example, Parse states that, in the Evercode WT Products workflow, after the cells or nuclei have been split across a plate, "an in-cell ligation appends the second barcode":



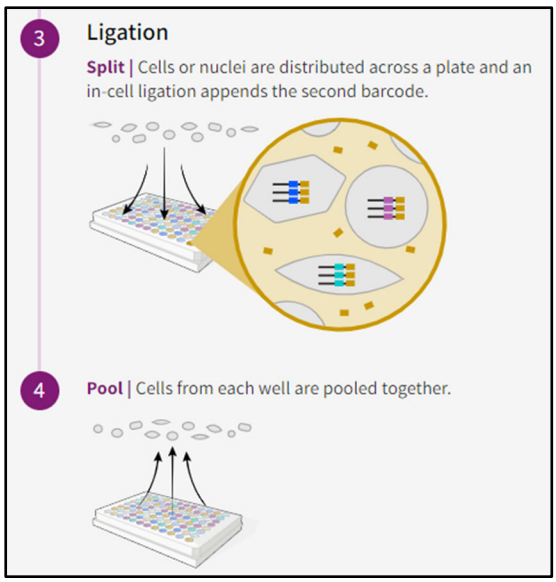
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 177 (2018) ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with ***well-specific*** barcodes."). Thus, in the Evercode WT Products workflow, "well-specific barcodes" are provided to the reaction volumes (i.e., the reaction volumes in the individual wells are provided with a specific nucleic acid tag that comprises a well-specific second barcode so that the tag in each well is different from the tags in the other wells).

35. **(d): "coupling the common linker sequences within each of the at least two primary reaction volumes with the provided primary nucleic acid tags"** Use of the Accused Products in accordance with their directions comprises "coupling the common linker sequences within each of the at least two primary reaction volumes with the provided primary nucleic acid tags." For example, Parse states that, in the Evercode WT Products workflow, after the cells or nuclei have been split across a plate, "an in-cell ligation appends the second barcode":



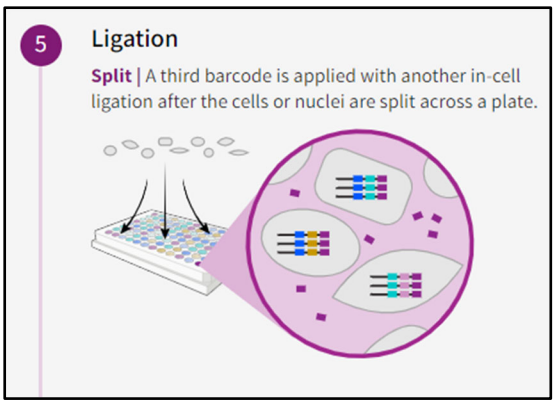
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 177 (2018) ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with well-specific barcodes. … Second- and third-round barcodes are appended to cDNA through ligation."). Thus, in the Evercode WT Products workflow, the first ligation barcoding round ligates (i.e., couples) the primary nucleic acid tag (comprising the second barcode in the Evercode WT Products workflow) to the previously coupled DNA linker.

36. **(e): "pooling the at least two primary reaction volumes"** Use of the Accused Products in accordance with their directions comprises "pooling the at least two primary reaction volumes." For example, Parse states that, in the Evercode WT Products workflow, after the "in-cell ligation appends the second barcode," "[c]ells from each well are pooled together":



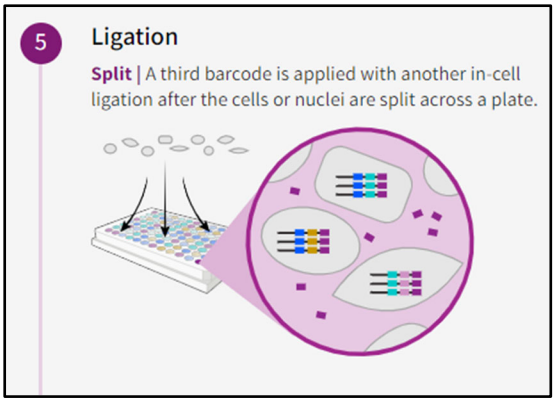
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. 1A & Suppl. Materials Fig. S1.A (2018). Thus, in the Evercode WT Products workflow, the reaction volumes (i.e., the "cells from each well") are pooled.

37. **(f): "splitting the combined primary reaction volumes into at least two secondary reaction volumes, the at least two secondary reaction volumes comprising a first secondary reaction volume and a second secondary reaction volume"** Use of the Accused Products in accordance with their directions comprises "splitting the combined primary reaction volumes into at least two secondary reaction volumes, the at least two secondary reaction volumes comprising a first secondary reaction volume and a second secondary reaction volume." For example, Parse states that, in the Evercode WT Products workflow, "[a] third barcode is applied with another in-cell ligation after the cells or nuclei are split across a plate":



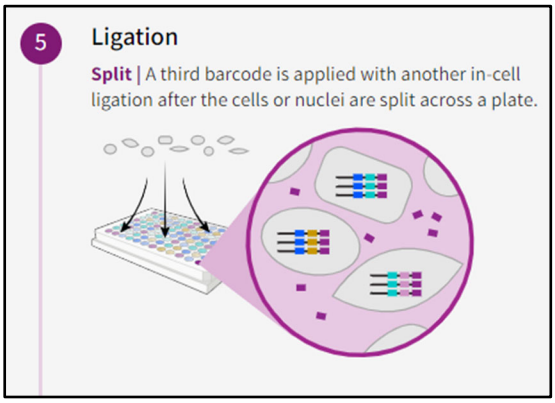
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. 1A & Suppl. Materials Fig. S1.A (2018). Thus, in the Evercode WT Products workflow, the cells from each well of the plate (i.e., the reaction volumes) are pooled together before being re-distributed into the wells of a new plate.

38. **(g): "providing secondary nucleic acid tags to each of the at least two secondary reaction volumes, wherein the secondary nucleic acid tags provided to the first secondary reaction volume are different from the secondary nucleic acid tags provided to the second reaction volume"** Use of the Accused Products in accordance with their directions comprises "providing secondary nucleic acid tags to each of the at least two secondary reaction volumes, wherein the secondary nucleic acid tags provided to the first secondary reaction volume are different from the secondary nucleic acid tags provided to the second reaction volume." For example, Parse states that, in the Evercode WT Products workflow, "[a] third barcode is applied with another in-cell ligation after the cells or nuclei are split across a plate":



Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. 1A & Suppl. Materials Fig. S1.A (2018). Thus, in the Evercode WT Products workflow, the previously pooled cells are split into at least two volumes (i.e., the wells of a plate) after being pooled.

39. **(h):** "**coupling the target molecules within each of the at least two secondary reaction volumes with the provided secondary nucleic acid tags**" Use of the Accused Products in accordance with their directions comprises "coupling the target molecules within each of the at least two secondary reaction volumes with the provided secondary nucleic acid tags." For example, Parse states that, in the Evercode WT Products workflow, "[a] third barcode is applied with another in-cell ligation after the cells or nuclei are split across a plate":



Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. 1A & Suppl. Materials Fig. S1.A (2018) ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with well-specific barcodes."). Thus, in the Evercode WT Products workflow, "well-specific barcodes" are provided to the reaction volumes (i.e., the reaction volumes in the individual wells are provided with a nucleic acid tag that comprises a well-specific third barcode that is different from the tags in other wells).

40. Use of the Accused Products by customers and end users in accordance with the accompanying directions and use of the Accused Products by Parse in the course of customer support and training, product development, quality control and comparative testing directly infringes the '442 Patent under 35 U.S.C. § 271(a).

41. As a result of Parse's direct infringement of the '442 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

42. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's direct infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

43. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '442 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

44. Parse's direct infringement of the '442 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT II
(INDIRECT INFRINGEMENT OF U.S. PATENT NO. 10,626,442)

45. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

46. On information and belief, Parse had knowledge of the '442 Patent at least as early as March of 2022 upon receipt of the March 1, 2022 letter from ScaleBio's counsel.

47. On information and belief, Parse knew and should have known that use of the Accused Products in accordance with their accompanying directions infringes the '442 Patent, at least because this was expressly set forth in correspondence from ScaleBio's counsel. Alternatively, on information and belief, Parse has been willfully blind as to infringement of the '442 Patent by use of the Accused Products.

48. Parse has committed, and continues to commit, affirmative acts that actively induce infringement of the '442 Patent by including instructions that explicitly guide customers and end users to use the Accused Products in an infringing manner, by demonstrating infringing use in the course of customer training and support, and by presentations to the public, including via Parse Instructional Materials.

49. Parse's sale and offer for sale of the Accused Products with the accompanying directions induces infringement of the '442 Patent by customers and other end users under 35 U.S.C. § 271(b).

50. The Accused Products have no substantial use other than for uniquely labeling target molecules within a plurality of cells in a manner that infringes the '442 Patent.

51. On information and belief, Parse knew that the Accused Products were especially made or especially adapted for use by customers and end users for uniquely labeling target molecules within a plurality of cells in a manner that infringes the '442 Patent and that its Accused Products are not a staple article or commodity of commerce suitable for substantial non-infringing use.

52. Parse's sale and offer for sale of the Accused Products contributes to infringement of the '442 Patent under 35 U.S.C. § 271(c).

53. As a result of Parse's indirect infringement of the '442 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

54. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's indirect infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

55. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '442 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

56. Parse's indirect infringement of the '442 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT III
(DECLARATORY JUDGMENT OF INDIRECT INFRINGEMENT OF U.S. PATENT NO. 10,626,442)

57. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

58. In the event the Court construes the claims of the ’442 Patent so as to encompass use of the Accused Products, any further sale or offer for sale by Parse of the Accused Products with knowledge of the Court’s ruling will constitute induced and contributory infringement of the ’442 Patent.

59. Plaintiff will seek monetary damages in an amount adequate to compensate for any indirect infringement by Parse but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse’s infringing activities are enjoined by this Court.

60. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the ’442 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

COUNT IV
(DIRECT INFRINGEMENT OF U.S. PATENT NO. 10,982,256)

61. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

62. Claim 1 of the ’256 Patent recites:

> A method for identifying whether a plurality of nucleic acid targets is present in a plurality of cells comprising:

(a) binding to the nucleic acid targets in the plurality of cells a plurality of unique binding agent (UBA) nucleic acid tags;

(b) extending the UBAs bound to the targets, and

(c) [1] assembling cell originating barcodes (COB) on the extended UBAs by subsequently adding multiple assayable polymer subunit (APS) oligonucleotides to each of the extended UBAs in the plurality of cells in an ordered manner during successive rounds of split pool synthesis

[2] wherein the APS oligonucleotides in each round anneal to the APS from a previous round and are covalently linked to the adjacently annealed APS to create unique codes that represent the identities of individual cells in which the tags are bound, and

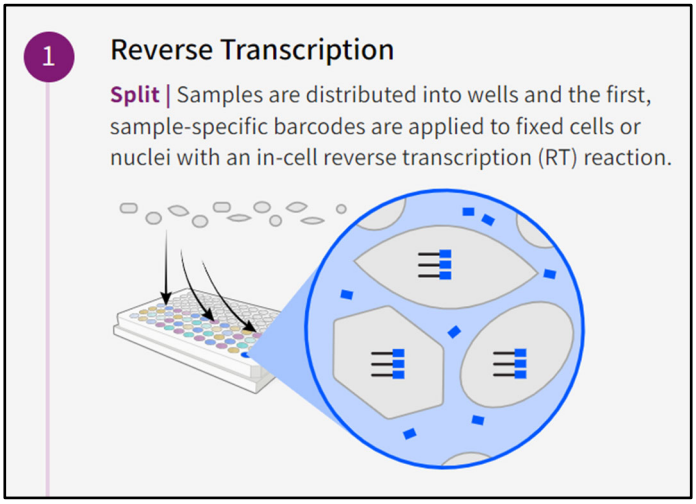
[3] wherein the method does not include a step of isolating each cell in the plurality of cells.

63. Use of the Accused Products in accordance with their accompanying directions directly infringes at least Claim 1 of the '256 Patent, literally or by equivalents, under 35 U.S.C. § 271(a).

64. **Preamble: "A method for identifying whether a plurality of nucleic acid targets is present in a plurality of cells"** Use of the Accused Products in accordance with their directions performs "[a] method for identifying whether a plurality of nucleic acid targets is present in a plurality of cells." For example, Parse states that "[t]he Evercode™ Whole Transcriptome technology, originally based on the split-pool combinatorial barcoding method published in Science and known widely as SPLiT-Seq, is accessible to any standard biology lab." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). The SPLiT-seq method "labels the cellular origin of RNA through combinatorial barcoding." Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018); *see also id.* ("In SPLiT-seq, individual transcriptomes are uniquely labeled…."); Parse Biosciences, *Evercode™ WT v2 Resolve More Biology*, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited

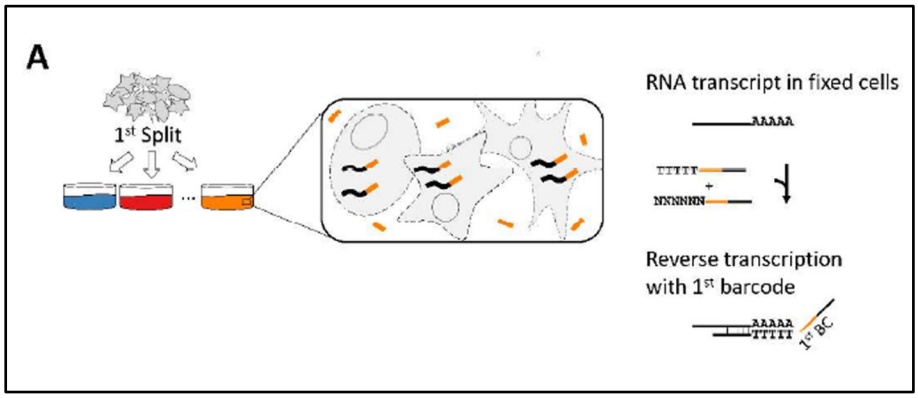
Dec. 14, 2022) ("Append barcodes to each transcript by progressing cells through four split-pool combinatorial barcoding steps."). Parse states that use of the Evercode WT Products allows for "gene and transcript detection that outperforms droplet-based methods." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). Parse further states that its Evercode WT Products can "[p]rofile anywhere from 10,000 to 1 million cells." Parse Biosciences, https://www.parsebiosciences.com (last visited Dec. 14, 2022). Thus, use of the Evercode WT Products "detect[s]" multiple genomic "transcripts" (i.e., a plurality of nucleic acid targets) across a population of "10,000 to 1 million cells" (i.e., a plurality).

65. **(a): "binding to the nucleic acid targets in the plurality of cells a plurality of unique binding agent (UBA) nucleic acid tags"** Use of the Accused Products in accordance with their directions performs a first step that includes "binding to the nucleic acid targets in the plurality of cells a plurality of unique binding agent (UBA) nucleic acid tags." For example, Parse states that the first step in the Evercode WT Products workflow is "appl[ying]" "sample-specific barcodes … to fixed cells or nuclei with an in-cell reverse transcription (RT) reaction":



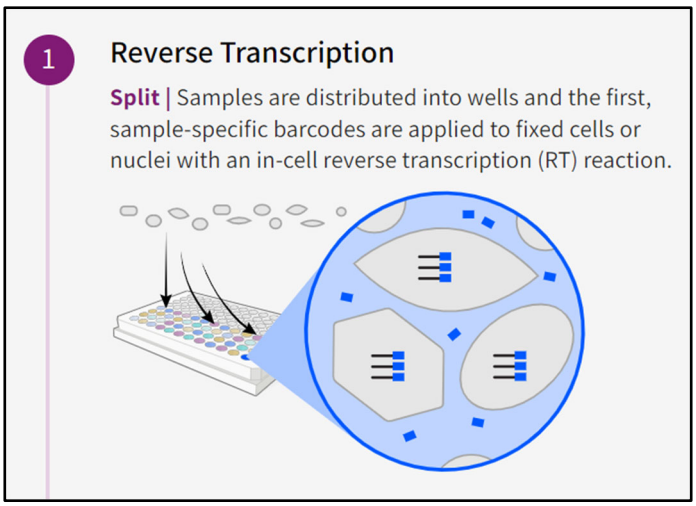
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal*

cord with split-pool barcoding, 360 Science 176, Suppl. Materials 2 (2018) ("The first round of barcoding occurs through an *in situ* reverse transcription (RT) reaction. … Both random hexamer and anchored poly(dT)15 barcoded RT primers were used in each well."). Upon information and belief, the first barcoding step in the Evercode WT Products workflow is further illustrated below:



Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Fig. S1A (2018). Thus, in the Evercode WT Products workflow, the first round of barcoding occurs through an "in situ reverse transcription (RT) reaction," in which "sample-specific barcodes" (i.e., attached to "random hexamer and anchored poly(dT)15 barcoded RT primers") bind to mRNA targets in a plurality of cells during the reverse transcription process. The poly(dT)15 barcoded RT primer acts as a unique binding agent ("UBA"), as it binds to at least one part of the mRNA target (i.e., polyA portion of mRNA).

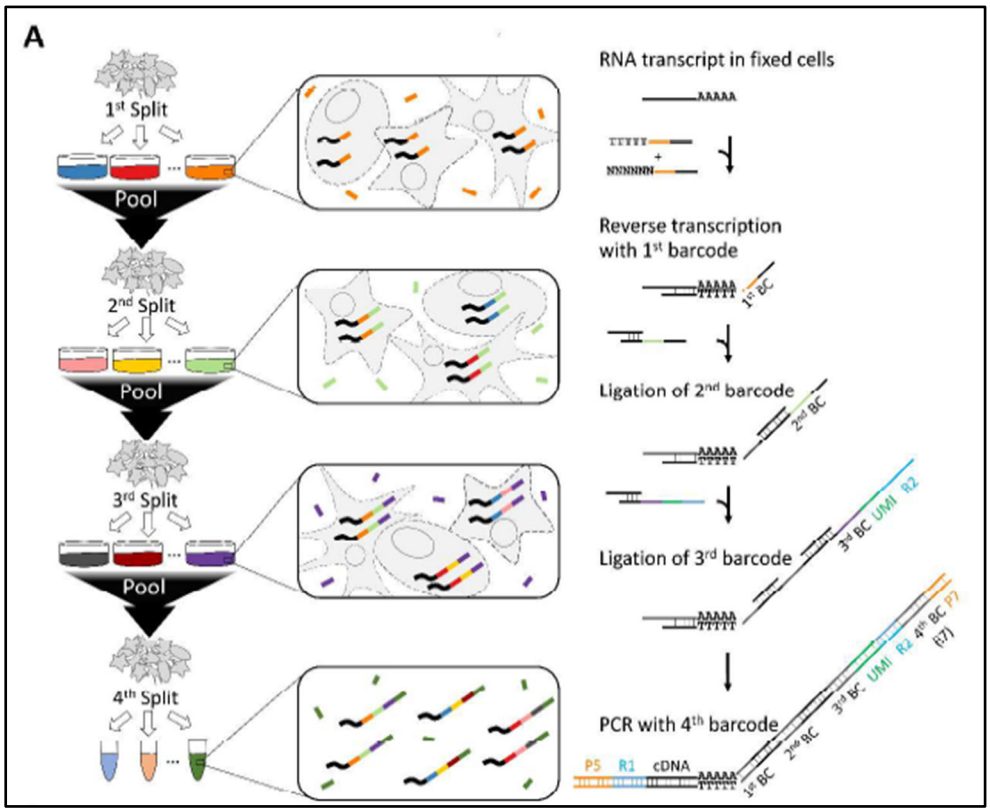
66. **(b): "extending the UBAs bound to the targets"** Use of the Accused Products in accordance with their directions comprises "extending the UBAs bound to the targets." For example, Parse states that, in the Evercode WT Products workflow, "sample-specific barcodes are applied to fixed cells or nuclei with an in-cell reverse transcription (RT) reaction":



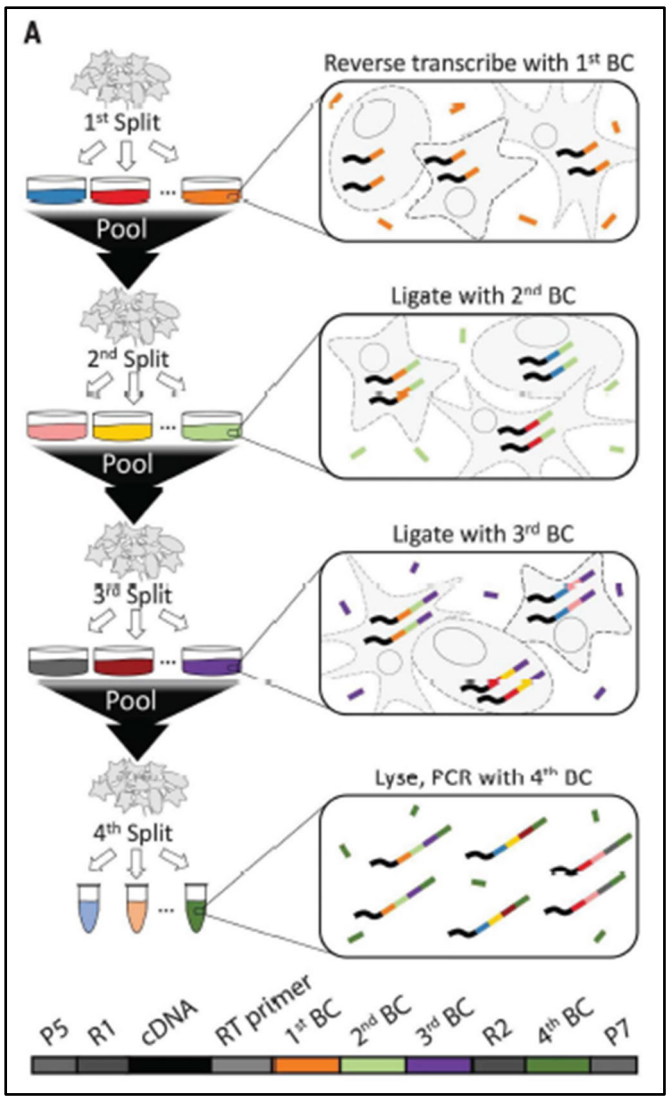
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Suppl. Materials 2 (2018) ("The first round of barcoding occurs through an *in situ* reverse transcription (RT) reaction."). Thus, in the Evercode WT Products workflow, the reverse transcription primers (i.e., the UBAs) are extended by virtue of the in-cell reverse transcription reaction.

67. **(c.1): "assembling cell originating barcodes (COB) on the extended UBAs by subsequently adding multiple assayable polymer subunit (APS) oligonucleotides to each of the extended UBAs in the plurality of cells in an ordered manner during successive rounds of split pool synthesis"** Use of the Accused Products in accordance with their directions comprises "assembling cell originating barcodes (COB) on the extended UBAs by subsequently adding multiple assayable polymer subunit (APS) oligonucleotides to each of the extended UBAs in the plurality of cells in an ordered manner during successive rounds of split pool synthesis." For example, Parse states that the Evercode WT Products utilize "combinatorial barcoding technology." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last

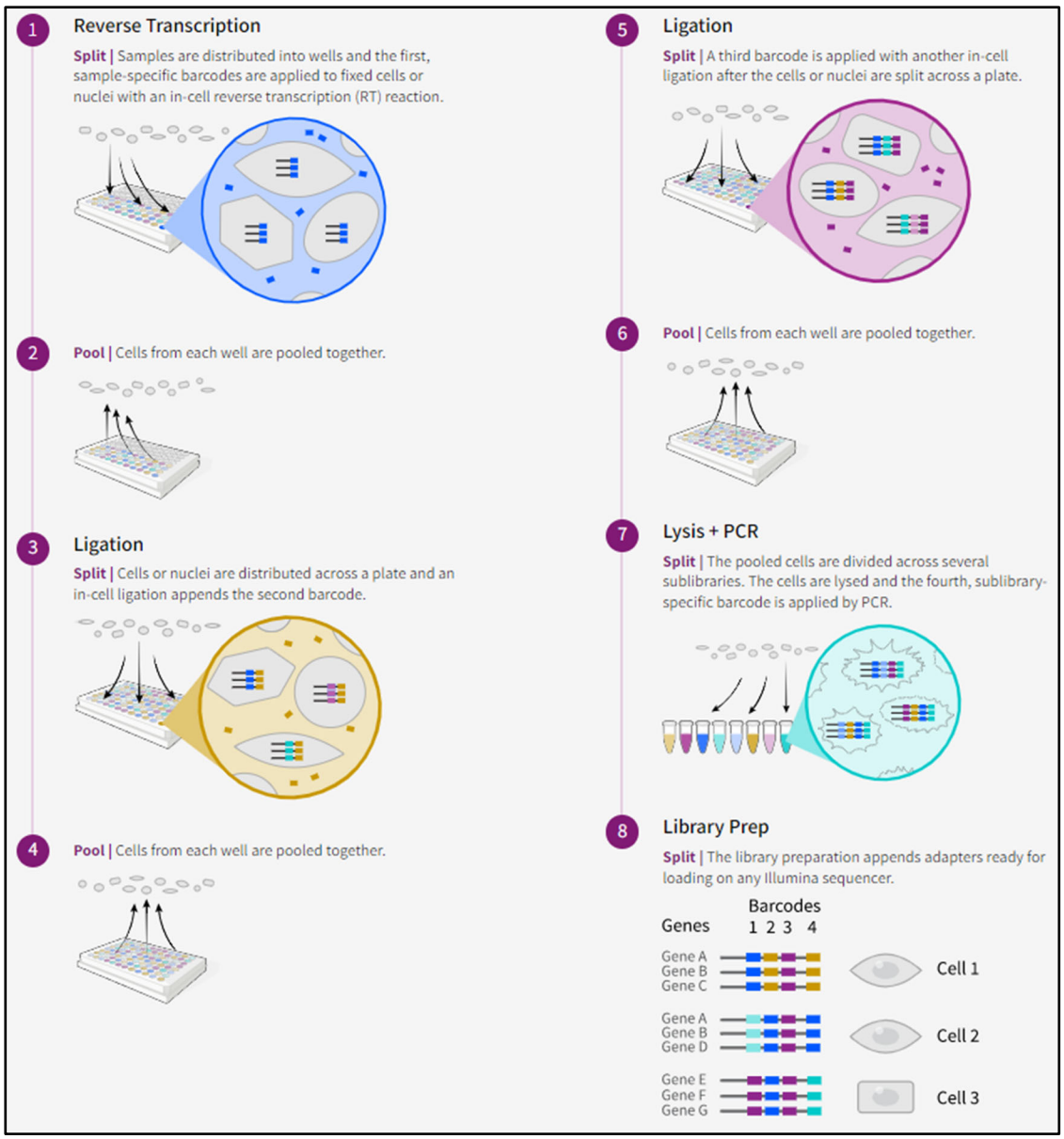
visited Dec. 14, 2022). Use of this "combinatorial barcoding technology" results in a "cell-specific combination of barcodes":



Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Suppl. Materials Fig. S1 (2018); *see also*

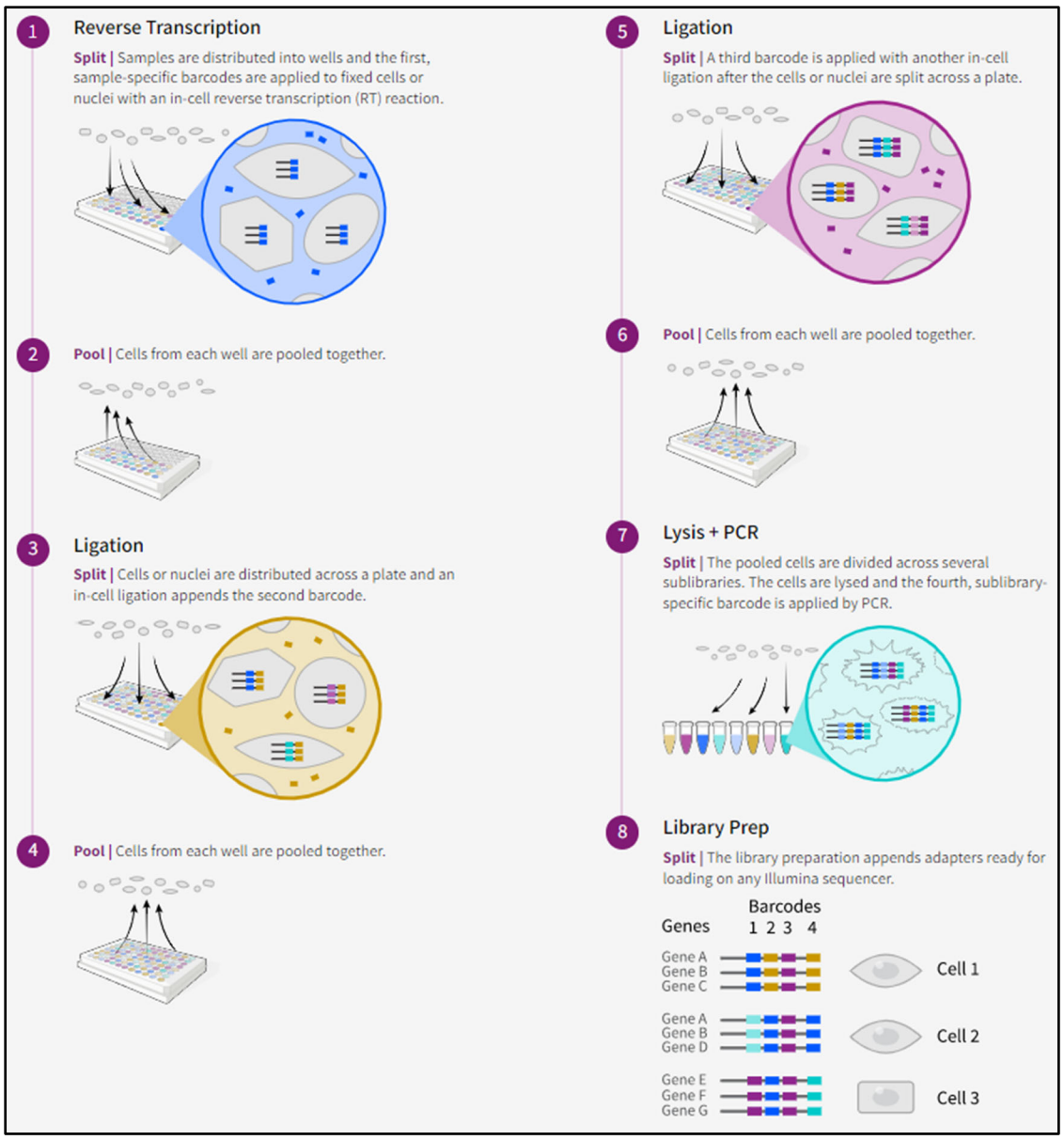


id. at Fig. 1A ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with well-specific barcodes. Barcoded RT primers are used in the first round. Second- and third-round barcodes are appended to cDNA through ligation.");



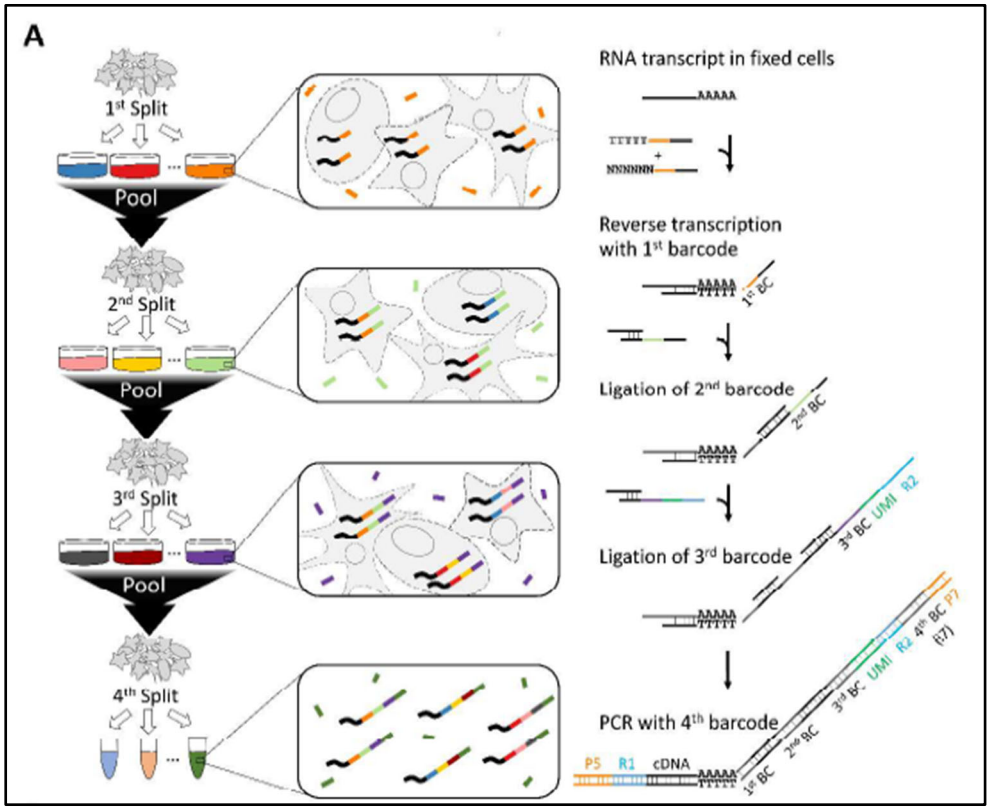
Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). Thus, in the Evercode WT Products workflow, the nucleic acid tags encoding a barcode act as assayable polymer subunits ("APS"), and the first tag is added to the extended reverse transcription primer (i.e., the UBA) and then subsequent tags are added to previously added tags during successive rounds of split-pool synthesis (i.e., each tag is added subsequent to the one added prior). Combined after the successive rounds, these nucleic acid tags make up a unique sequence of barcodes (i.e., the COB).

68. **(c.2): "wherein the APS oligonucleotides in each round anneal to the APS from a previous round and are covalently linked to the adjacently annealed APS to create unique codes that represent the identities of individual cells in which the tags are bound"** Use of the Accused Products in accordance with their directions further comprises a process "wherein the APS oligonucleotides in each round anneal to the APS from a previous round and are covalently linked to the adjacently annealed APS to create unique codes that represent the identities of individual cells in which the tags are bound." For example, Parse states that the nucleic acid tags encoding the barcodes are "ligat[ed]" to "append" barcodes sequentially:

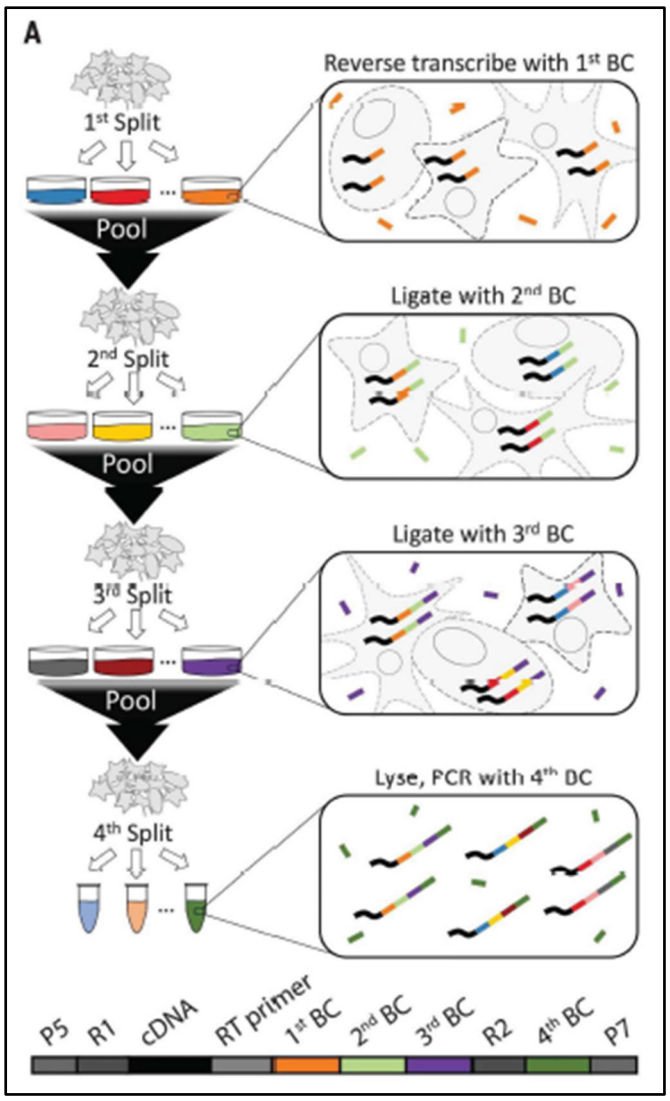


Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). The tags are initially appended to one another by virtue of a region of complementarity between them. *See* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Suppl. Materials 3 (2018) ("The second and third barcoding round consist of a ligation reaction. Each round uses a different set of 96 well barcoding plates (Table S1). Ligation rounds have a universal linker strand with partial complementarity to a second strand containing the unique well-specific barcode sequence added to each well. These

strands were annealed together prior to cellular barcoding to create a DNA molecule with three distinct functional domains: a 5' overhang that is complementary to the 3' overhang present on the cDNA molecule (may originate from RT primer or previous barcoding round), a unique well-specific barcode sequence, and a 3' overhang complementary to the 5' overhang present on the DNA molecule to be subsequently ligated (Fig. S1A)."). The result of the sequential addition of the tags encoding barcodes is a "cell-specific combination of barcodes":



Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, Suppl. Materials Fig. S1A (2018); *see also*



id. at Fig. 1A ("In each split-pool round, fixed cells or nuclei are randomly distributed into wells, and transcripts are labeled with well-specific barcodes. Barcoded RT primers are used in the first round. Second- and third-round barcodes are appended to cDNA through ligation."); *id.* at 176 ("To facilitate scalable profiling of single cells, we developed split-pool ligation based transcriptome sequencing (SPLiT-seq)."). Thus, in the Evercode WT Products workflow, the tags encoding the barcodes are annealed to the previously added tag through ligation (i.e., covalent linkage). The result of these successive rounds of split-pool synthesis is a "cell-specific combination of barcodes" that allows for "profiling of single cells."

69. **(c.3): "wherein the method does not include a step of isolating each cell in the plurality of cells"** Use of the Accused Products in accordance with their directions comprises a process that "does not include a step of isolating each cell in the plurality of cells." The SPLiT-seq method utilized by Parse's Evercode WT Products "does not require partitioning single cells into individual compartments (droplets, microwells, or wells) but relies on the cells themselves as compartments." Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018). Thus, the Evercode WT Products workflow does not involve cell isolation.

70. Use of the Accused Products by customers and end users in accordance with the accompanying directions and use of the Accused Products by Parse in the course of customer support and training, product development, quality control and comparative testing directly infringes the '256 Patent under 35 U.S.C. § 271(a).

71. As a result of Parse's direct infringement of the '256 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

72. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's direct infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

73. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '256 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

74. Parse's direct infringement of the '256 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT V
(INDIRECT INFRINGEMENT OF U.S. PATENT NO. 10,982,256)

75. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

76. On information and belief, Parse had knowledge of the '256 Patent at least as early as June of 2021 upon receipt of the June 10, 2021 letter from ScaleBio.

77. On information and belief, Parse knew and should have known that use of the Accused Products in accordance with their accompanying directions infringes the '256 Patent, at least because this was expressly set forth in the initial correspondence from ScaleBio and in subsequent correspondence from ScaleBio's counsel. Alternatively, on information and belief, Parse has been willfully blind as to infringement of the '256 Patent by use of the Accused Products.

78. Parse has committed, and continues to commit, affirmative acts that actively induce infringement of the '256 Patent by including instructions that explicitly guide customers and end users to use the Accused Products in an infringing manner, by demonstrating infringing use in the course of customer training and support, and by presentations to the public including via Parse Instructional Materials.

79. Parse's sale and offer for sale of the Accused Products with the accompanying directions induces infringement of the '256 Patent by customers and other end users under 35 U.S.C. § 271(b).

80. The Accused Products have no substantial use other than for identifying whether a plurality of nucleic acid targets is present in a plurality of cells in a manner that infringes the '256 Patent.

81. On information and belief, Parse knew that the Accused Products were especially made or especially adapted for use by customers and end users for identifying whether a plurality of nucleic acid targets is present in a plurality of cells in a manner that infringes the '256 Patent and that its Accused Products are not a staple article or commodity of commerce suitable for substantial non-infringing use.

82. Parse's sale and offer for sale of the Accused Products contributes to infringement of the '256 Patent under 35 U.S.C. § 271(c).

83. As a result of Parse's indirect infringement of the '256 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

84. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's indirect infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

85. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '256 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

86. Parse's indirect infringement of the '256 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT VI
(DECLARATORY JUDGMENT OF INDIRECT INFRINGEMENT OF U.S. PATENT NO. 10,982,256)

87. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

88. In the event the Court construes the claims of the '256 Patent so as to encompass use of the Accused Products, any further sale or offer for sale by Parse of the Accused Products with knowledge of the Court's ruling will constitute induced and contributory infringement of the '256 Patent.

89. Plaintiff will seek monetary damages in an amount adequate to compensate for any indirect infringement by Parse but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

90. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '256 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

COUNT VII
(DIRECT INFRINGEMENT OF U.S. PATENT NO. 11,512,341)

91. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

92. Claim 1 of the ’341 Patent recites:

A method of barcoding cDNA in cells or cell compartments, the method comprising:

(a) producing cDNA in the cells or cell compartments; and

(b) adding oligonucleotide barcodes onto the cDNA in the cells or compartments by a method comprising at least two barcoding steps that comprise:

(i) splitting the cells or cell compartments and adding assayable oligonucleotide subunits to the cDNA while the cells or cell compartments are split; and then

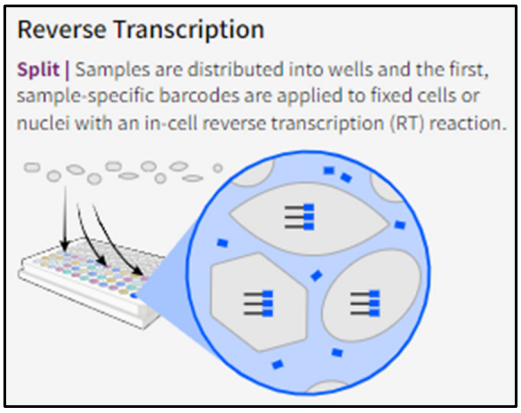
(ii) pooling the cells.

93. Use of the Accused Products in accordance with their accompanying directions directly infringes at least Claim 1 of the ’341 Patent, literally or by equivalents, under 35 U.S.C. § 271(a).

94. **Preamble: “A method of barcoding cDNA in cells or cell compartments, the method comprising”** Use of the Accused Products in accordance with their directions performs “[a] method of barcoding cDNA in cells or cell compartments.” For example, “[t]he Evercode™ Whole Transcriptome technology, originally based on the split-pool combinatorial barcoding method published in Science and known widely as SPLiT-Seq, is accessible to any standard biology lab.” Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022). The SPLiT-seq method “labels the cellular origin of RNA through combinatorial barcoding.” Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018); *see also id.* (“In SPLiT-seq, individual transcriptomes are uniquely labeled….”); Parse Biosciences, *Evercode™ WT v2 Resolve More Biology*, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Dec. 14, 2022) (“Append barcodes to each transcript by progressing cells through four split-pool combinatorial barcoding steps.”). Parse further states that its Evercode WT Products can “[p]rofile anywhere from 10,000 to 1 million cells.” Parse

Biosciences, https://www.parsebiosciences.com (last visited Dec. 14, 2022). Moreover, Parse highlights that its Evercode WT Products "convert[] each cell … into an individualized reaction compartment" because "[c]ombinatorial barcoding happens within cells themselves." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022).

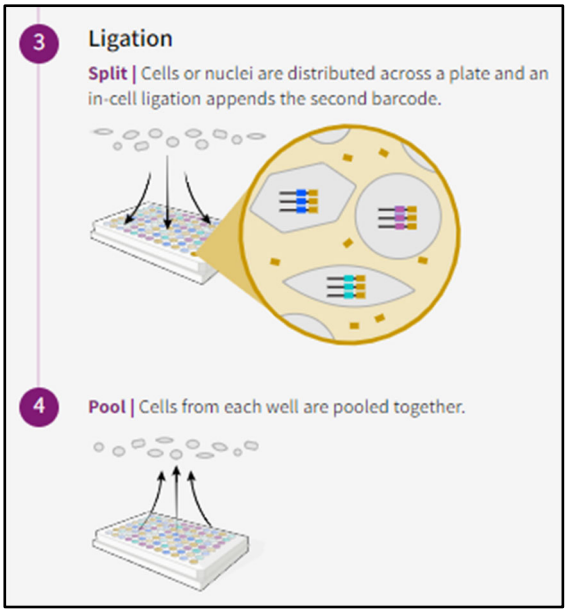
95. **(a): "producing cDNA in the cells or cell compartments"** Use of the Accused Products in accordance with their directions performs a first step that includes "producing cDNA in the cells or cell compartments." For example, in the first step of the SPLiT-seq method utilized by Parse for its Evercode WT Products, "cells are distributed into a 96-well plate, and cDNA is generated with an in-cell reverse transcription (RT) reaction using well-specific barcoded primers." Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018); *see also*

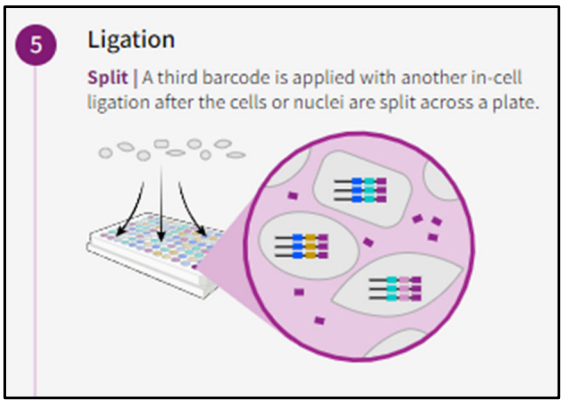


Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022).

96. **(b): "adding oligonucleotide barcodes onto the cDNA in the cells or compartments by a method comprising at least two barcoding steps that comprise (i) splitting the cells or cell compartments and adding assayable oligonucleotide subunits to the cDNA**

while the cells or cell compartments are split and then" Use of the Accused Products in accordance with their directions comprises "adding oligonucleotide barcodes onto the cDNA in the cells or compartments by a method comprising at least two barcoding steps that comprise (i) splitting the cells or cell compartments and adding assayable oligonucleotide subunits to the cDNA while the cells or cell compartments are split."

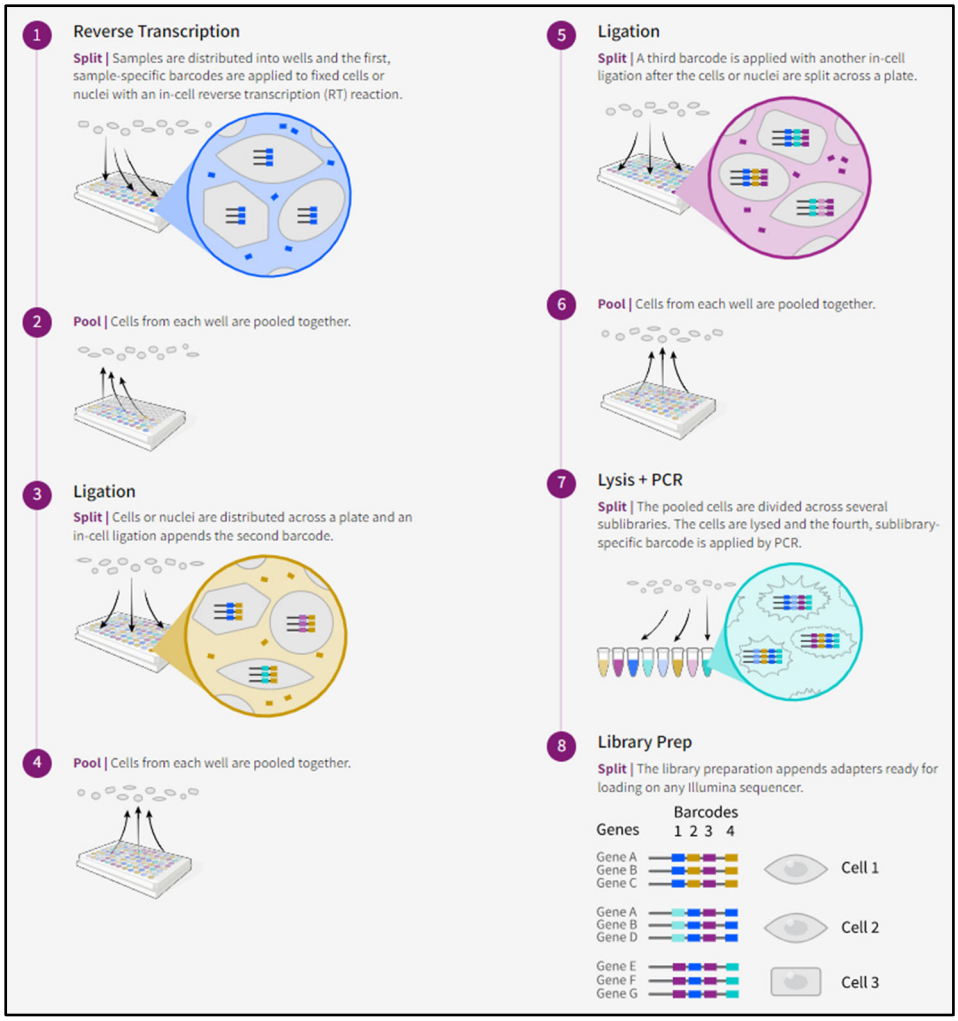




For example, Parse states that after the first round of barcoding through reverse transcription, "[c]ells or nuclei are distributed across a plate, and an in-cell ligation reaction appends the second barcode." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding*, 360 Science 176, 176 (2018) ("[C]ells from all wells are pooled and redistributed into a new 96-well plate, where an in-cell ligation reaction appends a second well-specific barcode to the cDNA."). Parse further states that "[a] third barcode is applied with another in-cell ligation after the cells or nuclei are split across a plate." Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse brain and spinal*

cord with split-pool barcoding, 360 Science 176, 176 (2018) ("The third-round barcode … is then appended with another round of pooling, splitting, and ligation.").

97. **(b)(ii): "pooling the cells"** Use of the Accused Products in accordance with their directions comprises "pooling the cells" after each of the round of appending barcodes while the cells are split.



For example, Parse states that "[c]ells from each well are pooled together" after each of the barcoding rounds. Parse Biosciences, *Technology*, https://www.parsebiosciences.com/technology (last visited Dec. 14, 2022); *see also* Rosenberg et al., *Single-cell profiling of the developing mouse*

brain and spinal cord with split-pool barcoding, 360 Science 176, 176 (2018) ("After three rounds of barcoding, the cells are pooled….").

98. Use of the Accused Products by customers and end users in accordance with the accompanying directions and use of the Accused Products by Parse in the course of customer support and training, product development, quality control and comparative testing directly infringes the '341 Patent under 35 U.S.C. § 271(a).

99. As a result of Parse's direct infringement of the '341 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

100. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's direct infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

101. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '341 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

102. Parse's direct infringement of the '341 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT VIII
(INDIRECT INFRINGEMENT OF U.S. PATENT NO. 11,512,341)

103. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

104. On information and belief, in the exercise of due diligence, Parse has been monitoring the family from which the ’442 and ’256 Patents issued and had knowledge of the ’341 Patent shortly after its issuance on November 29, 2022.

105. On information and belief, Parse knew and should have known that use of the Accused Products in accordance with their accompanying directions infringes the ’341 Patent. Alternatively, on information and belief, Parse has been willfully blind as to infringement of the ’341 Patent by use of the Accused Products.

106. Parse has committed, and continues to commit, affirmative acts that actively induce infringement of the ’341 Patent by including instructions that explicitly guide customers and end users to use the Accused Products in an infringing manner, by demonstrating infringing use in the course of customer training and support, and by presentations to the public including via Parse Instructional Materials.

107. Parse’s sale and offer for sale of the Accused Products with the accompanying directions induces infringement of the ’341 Patent by customers and other end users under 35 U.S.C. § 271(b).

108. The Accused Products have no substantial use other than for barcoding cDNA in cells or cell compartments in a manner that infringes the ’341 Patent.

109. On information and belief, Parse knew that the Accused Products were especially made or especially adapted for use by customers and end users for barcoding cDNA in cells or cell compartments in a manner that infringes the ’341 Patent and that its Accused Products are not a staple article or commodity of commerce suitable for substantial non-infringing use.

110. Parse’s sale and offer for sale of the Accused Products contributes to infringement of the ’341 Patent under 35 U.S.C. § 271(c).

111. As a result of Parse's indirect infringement of the '341 Patent, Plaintiff has been and continues to be injured by Parse's unauthorized use of Plaintiff's patented and exclusively licensed intellectual property.

112. Plaintiff seeks monetary damages in an amount adequate to compensate for Parse's indirect infringement but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

113. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '341 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

114. Parse's indirect infringement of the '341 Patent has been and continues to be willful and deliberate, entitling Plaintiff to increased damages under 35 U.S.C. § 284 and reasonable attorneys' fees under 35 U.S.C. § 285.

COUNT IX
(DECLARATORY JUDGMENT OF INDIRECT INFRINGEMENT OF U.S. PATENT NO. 11,512,341)

115. The allegations in the foregoing paragraphs of this Complaint are incorporated by reference herein and realleged as if restated and set forth in full.

116. Parse will have knowledge of the '341 Patent at least from the date it is served with this Complaint with its appended exhibits.

117. In the event the Court construes the claims of the '341 Patent so as to encompass use of the Accused Products, any further sale or offer for sale by Parse of the Accused Products with knowledge of the Court's ruling will constitute induced and contributory infringement of the '341 Patent.

118. Plaintiff will seek monetary damages in an amount adequate to compensate for any indirect infringement by Parse but in no event less than a reasonable royalty for the use made of the invention by Parse, together with interest and costs as fixed by the Court, and Plaintiff will continue to suffer damages in the future unless Parse's infringing activities are enjoined by this Court.

119. Unless a permanent injunction is issued enjoining Parse and its agents, servants, employees, representatives, affiliates, and all others acting in privity or in active concert therewith from infringing the '341 Patent, Plaintiff will be greatly and irreparably harmed in a manner for which damages are an inadequate remedy.

REQUEST FOR RELIEF

WHEREFORE, Plaintiff respectfully requests that the Court:

a. declare, adjudge and decree that use of the Accused Products by Parse, its customers and other end users directly infringes the Asserted Patents and that Parse's use, distribution, sale and offer for sale of the Accused Products with their accompanying instructions induces and contributes to infringement of the Asserted Patents;

b. award compensatory damages as provided by law, including damages adequate to compensate for infringement arising from Parse's use, sale and offer for sale of the Accused Products, in an amount to be determined at trial, including all pre-judgment and post-judgment interest and costs at the maximum rate allowed by law;

c. issue a permanent injunction pursuant to 35 U.S.C. § 283 and 35 U.S.C. § 1331 restraining and enjoining Parse and its affiliates, subsidiaries, directors, officers, agents, servants, employees, attorneys, assigns and successors in interest, and all persons acting in privity or in concert with them, including related individuals and entities, customers, representatives, distributors, and dealers, from further acts that infringe, induce infringement, or contribute to

infringement of the Asserted Patents. In the alternative, if the Court finds that an injunction is not warranted, Plaintiff requests an award of post-judgment royalties to compensate for future infringement;

d. declare, adjudge and decree that this case is exceptional and award Plaintiff its reasonable attorneys' fees and costs pursuant to 35 U.S.C. § 285;

e. declare, adjudge and decree that Parse's infringement has been willful and that the damages will be increased under 35 U.S.C. § 284 up to three times the amount found or measured; and

f. award such other and further relief as the Court may deem just, reasonable, and proper.

DEMAND FOR JURY TRIAL

Pursuant to Rule 38(b) of the Federal Rules of Civil Procedure, Plaintiff demands a trial by jury of all issues triable of right by jury.

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Dated: December 14, 2022