IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

10X GENOMICS, INC., Plaintiff, v. PARSE BIOSCIENCES, INC., Defendant, and THE BOARD OF TRUSTEES OF LELAND STANFORD JUNIOR UNIVERSITY Nominal Defendant.	)	C.A. No. _____ DEMAND FOR JURY TRIAL

COMPLAINT FOR PATENT INFRINGEMENT AND DECLARATORY JUDGMENT FOR PATENT INFRINGEMENT

Plaintiff 10x Genomics, Inc. ("10x" or "Plaintiff") for its Complaint against Defendant Parse Biosciences, Inc. ("Parse"), alleges as follows:

NATURE OF THE ACTION

1. This is an action for infringement of United States Patent Nos. 10,155,981 ("the '981 Patent"), 10,697,013 ("the '013 Patent"), 10,240,197 ("the '197 Patent"), 10,150,995 ("the '995 Patent"), 10,619,207 ("the '207 Patent"), and 10,738,357 ("the '357 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. 10x is a Delaware corporation with its principal place of business at 6230 Stoneridge Mall Road, Pleasanton, California 94588.

3. 10x is a pioneering innovator of genomics and sequencing technologies that are providing life science researchers an unprecedented understanding of biology. By elegantly combining its proprietary hardware, chemistry, and software, 10x has developed and brought to market award-winning products that give single-cell and spatial views of complex biological systems. 10x's products have enabled previously infeasible forms of research in the life sciences in areas of critical importance to human health, including cancer research, neuroscience, immunology, infectious disease, and developmental biology. 10x is the owner of the '981, '013, and '197 Patents, and the exclusive licensee of the '995, '207, and '357 Patents pursuant to an exclusive license agreement with the Board of Trustees of Leland Stanford Junior University ("Stanford University"). 10x is pursuing this action and has the right to join Stanford University, the owner and licensor of the '995, '207, and '357 Patents, as a party in accordance with the terms of its exclusive license agreement with Stanford University.

4. Stanford University is a trust possessing corporate powers that is organized under the laws of the State of California and with its principal place of business at the Office of the President, Building 10 Main Quad, Stanford, California 94305. Stanford University is owner and licensor of the '995, '207, and '357 Patents. Stanford University is named as a nominal defendant in this action for purposes of subject matter jurisdiction only and pursuant to the United States Supreme Court's holding in *Independent Wireless Telegraph 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."

10x requested that Stanford University join as a party in this action, but Stanford University has thus far not agreed to do so. Although Stanford University is named as a nominal defendant, 10x seeks relief realigning Stanford University as a plaintiff.

5. 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.

6. Parse is infringing and will infringe the patents asserted in this action by its manufacture, use, sale, offer to sell, sale, and/or importation into the United States of products, services, and components that are and/or will be used by Parse and its customers to infringe at least Claim 1 of each of the '981, '013, '197, '995, and '207 Patents and Claim 16 of the '357 Patent.

JURISDICTION AND VENUE

7. 10x incorporates and realleges paragraphs 1 to 6 above as if fully set forth herein.

8. This civil action for patent infringement arises under the patent laws of the United States, 35 U.S.C § 1 et seq., including in particular under 35 U.S.C. § 271. This Court has subject matter jurisdiction pursuant to 28 U.S.C. §§ 1331, 1338(a).

9. This Court has personal jurisdiction over Parse, and venue is proper in this district pursuant to 28 U.S.C. § 1400(b), because Parse is a Delaware corporation and thus resides in this district.

10. This Court has personal jurisdiction over nominal defendant Stanford University because Stanford University has substantial contacts with the forum as a consequence of conducting business and activities in Delaware, including having filed lawsuits in this forum.

BACKGROUND

11. 10x incorporates and realleges paragraphs 1 to 10 above as if fully set forth herein.

A. 10x's Groundbreaking Single-Cell Technologies

12. 10x is a life sciences technology company founded in 2012 in Pleasanton, California by Drs. Serge Saxonov and Benjamin Hindson. Since its inception, 10x has focused on building new technologies to enable breakthrough discoveries and accelerate the understanding of biology. To date, 10x has invested hundreds of thousands of hours and over $1 billion in research and development to invent, design, and develop its proprietary line of products for understanding biology at unprecedented resolution and scale. 10x continues to invest significant time and money to further innovate and bring groundbreaking new products and capabilities to market.

13. 10x is a worldwide leader in genomics, the comprehensive study of biological systems at a molecular and cellular level. 10x provides end-to-end solutions for genomic analysis, including instruments, reagent kits, and analysis software that enable researchers to obtain and interpret vast quantities of complex biological data. Since 10x's first commercial launch in 2015, 10x's expanding suite of products has fueled a revolution in genomics, winning wide acclaim and commercial success. 10x has sold more than 3,500 instruments around the world, including at all of the top 100 global research institutions and all of the top 20 global biopharmaceutical companies. In 2021, annual sales of 10x products exceeded $490 million.

14. Over 3,800 scientific articles have been published based on data generated from 10x products, including hundreds of articles in top journals such as *Cell*, *Science*, and *Nature*. This scientific work details the use of 10x products to discover, for example: molecular mechanisms that lead to brain, breast, and lung cancers; how the immune system reacts to COVID-19 infection; and a new type of lung cell that causes cystic fibrosis. The paradigm-changing nature of 10x's

products has led to numerous accolades, including seven 10x products being named to *The Scientist* magazine's Top 10 Innovations list between 2015 and 2021.

15. 10x's Chromium platform has been essential to enabling single-cell genomics—the study of biology at a cell-by-cell resolution and at a massive, system-wide scale, ushering in a single-cell revolution hailed by *Science* magazine as the 2018 "Breakthrough of the Year." Whereas traditional biology relies on "bulk analysis" in which tissue is analyzed as averages across the sample, 10x's breakthrough single-cell products enable researchers to analyze samples on a single cell basis—for millions of cells per experiment—thereby preserving information that is specific to each cell in the sample. 10x's single-cell products do this by "tagging" the molecules of each single cell with a unique nucleic acid barcode, which can then be analyzed to trace the molecule's cellular origin. The Chromium X instrument, which launched in July 2021 and facilitates cost-effective million-cell experiments, is the latest addition to 10x's award-winning platform and was named a Top 10 Innovation in 2021 by *The Scientist* magazine, https://www.the-scientist.com/features/2021-top-10-innovations-69438.

16. A key strength of 10x's Chromium platform lies in its suite of products that use 10x's proprietary molecular assays to probe the various essential constituents of biology—e.g., DNA, RNA, protein, and epigenetics—within a given sample. 10x launched its flagship single-cell product, Chromium Single Cell Gene Expression, in 2016. In addition to providing researchers with the ability to measure gene activity from RNA on a cell-by-cell basis, Single Cell Gene Expression is a versatile product that utilizes 10x's Feature Barcoding technology to enable single-cell protein analysis and single-cell CRISPR screening. 10x's Chromium Single Cell Immune Profiling product, launched in 2017, enables researchers to unravel the vast complexity of adaptive immunity by examining T-cells and B-cells at single cell resolution. 10x's Chromium

Single Cell ATAC and Single Cell Multiome products, launched in 2018 and 2020, respectively, complement RNA measurements by examining DNA chromatin structure and its relation to gene regulation. 10x recently introduced its Chromium Fixed RNA Profiling product, allowing fragile samples to be fixed at the point of sample collection to lock in cell states and vastly increase the number of samples that can be analyzed. Collectively, 10x's suite of products provide researchers with an arsenal of tools to assemble a complete, multi-omic picture of biological systems.

17. 10x's Chromium Single Cell ATAC and Chromium Single Cell Multiome ATAC + Gene Expression products have facilitated significant advancements in genomic research. "ATAC" is an acronym that stands for assay for transposase-accessible chromatin, and was invented by Stanford University researchers to identify transposase-accessible chromatin in a way that allowed for the simultaneous, high-throughput identification of open chromatin regions, nucleosome positioning, and regulatory motifs using sequencing technology. 10x integrated ATAC-seq into its Chromium platform to create its award-winning single cell epigenetics products. The Chromium Single Cell ATAC products allow for evaluation of chromatin accessibility within genomes at a single cell level. The Chromium Single Cell Multiome ATAC + Gene Expression solution allows for the simultaneous profiling of gene expression and open chromatin from the same cell (rather than on different cells within a sample), providing cell-by-cell understanding of transcriptional profiles along with their corresponding gene regulatory environment. Each of 10x's ATAC-seq products have been named a Top 10 Innovation by *The Scientist* magazine, with 10x's Chromium Single Cell ATAC solution making the list in 2019, and the Chromium Single Cell Multiome ATAC + Gene Expression in 2020. Cision PR Newswire, *10x Genomics Recognized on The Scientist's Top 10 Innovations List for Fifth Consecutive Year*

(Dec. 1, 2021), https://www.prnewswire.com/news-releases/10x-genomics-recognized-on-the-scientists-top-10-innovations-list-for-fifth-consecutive-year-301435676.html.

B. Parse's Infringing Evercode Whole Transcriptome ("WT") Products

18. Parse is a single-cell genomics company that has made clear that it intends nothing less than to copy 10x's complete lineup of single-cell products wholesale. Parse currently sells a single-cell gene expression product called Evercode Whole Transcriptome ("WT"). In April 2022, Parse opened up early access programs for two new assays: a targeted single-cell RNA sequencing product and a single-cell CRISPR product. Parse further announced that it plans to launch in the second half of this year early access to a single-cell ATAC-seq product ("Parse Single-Cell ATAC-Seq Product"). *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022), https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach. GenomeWeb noted that these new products "will help Parse compete with 10x Genomics, which already offers solutions for all of the applications Parse is pursuing." *Id.*; *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 (Apr. 13, 2018) (referencing comparison of Parse's SPLiT-seq method to "droplet-based scRNA-seq methods" and using 10x's Chromium v2 as a comparator in Fig. S3); *but see* Fred Hutch Innovation Lab, Twitter, https://twitter.com/hutchinnovation/status/1484326929482219520 (last visited Aug. 24, 2022) (comparing Parse's products to 10x's and noting that Parse's "[c]ell recovery was ~20% compared to 10x's 50-60%," and that Parse's process as "more cumbersome" than 10x as it required "at least 2 full days and a lot of pipetting.").

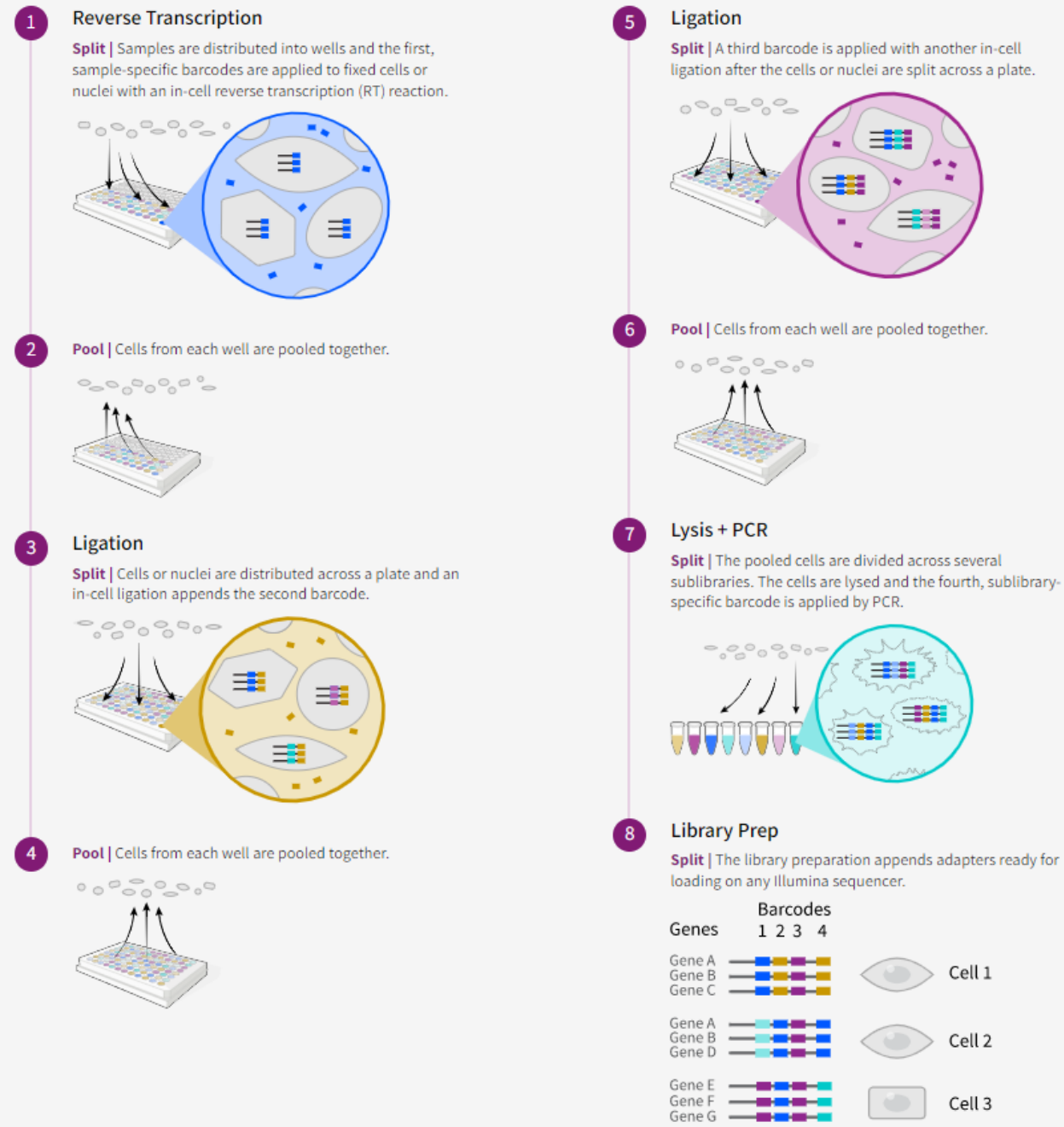
19. On information and belief, Parse copied 10x's single-cell dual-tagging technology to identify the cell and the polynucleotide within that cell despite knowing of the existence of 10x's patents that cover 10x's single-cell dual-tagging technologies, including the '981, '013, and '197

Patents, or deliberately not finding out which of 10x's patents covered 10x's single-cell dual-tagging technologies.

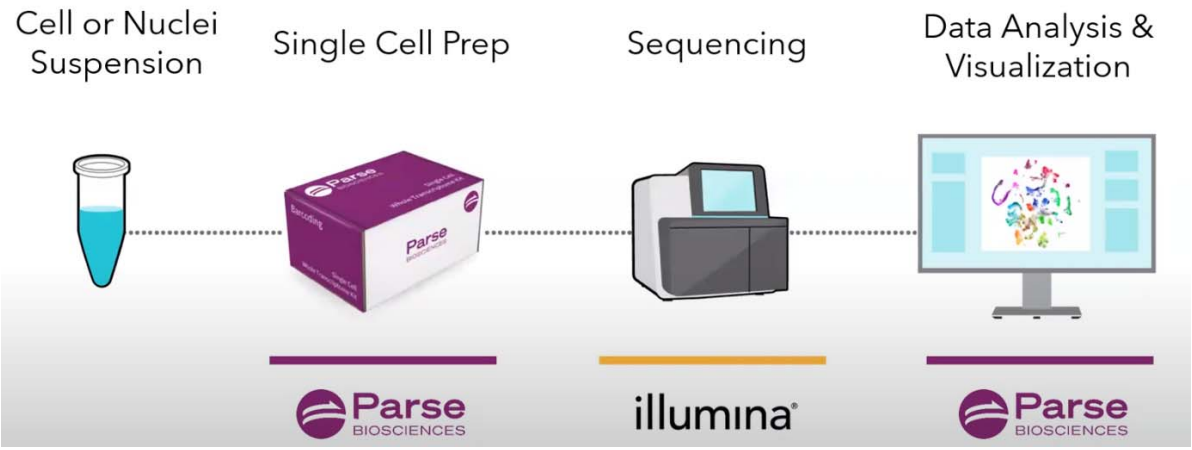
20. On information and belief, Parse provides its Evercode WT kits—including reagents, other consumables, and data analysis software—to its customers. Parse asserts in its publications that its technology is based on a split-pool combinatorial barcoding method called SPLiT-Seq. Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (citing Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 (Apr. 13, 2018)). The first kit launched by Parse purports to enable users to process up to 100,000 single cells and 48 samples. *See* Parse Biosciences, Evercode™ Whole Transcriptome Single Cell for Any Lab, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022). In late 2021, Parse began offering 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, Explore Single Cell, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode™ Whole Transcriptome Mega 1 Million Cells for Your Lab Today, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022). Each of Parse's Evercode WT Products purportedly enable 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 Aug. 24, 2022).

21. On information and belief, Parse purports that its Evercode WT Products are used to convert single cells of nuclei into individualized reaction compartments and that the cells or

nuclei can be paired with unique cellular barcodes and unique molecular indices through a non-automated, labor-intensive manual method of pooling, tagging, re-pooling, re-tagging, etc. *See, e.g.*, Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); 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 (Apr. 13, 2018).



22. On information and belief, Parse claims that its products' barcode tagging allow 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:



Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 6:33; *see also* Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 177 (Apr. 13, 2018); Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022).

23. The "Evercode WT Products" are all products or components that are and/or will be made, used, offered for sale, sold, and/or imported into the United States by or on behalf of Parse in connection with Parse's Evercode WT Products and workflows. The Evercode WT Products include, 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.

24. 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 suite

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.

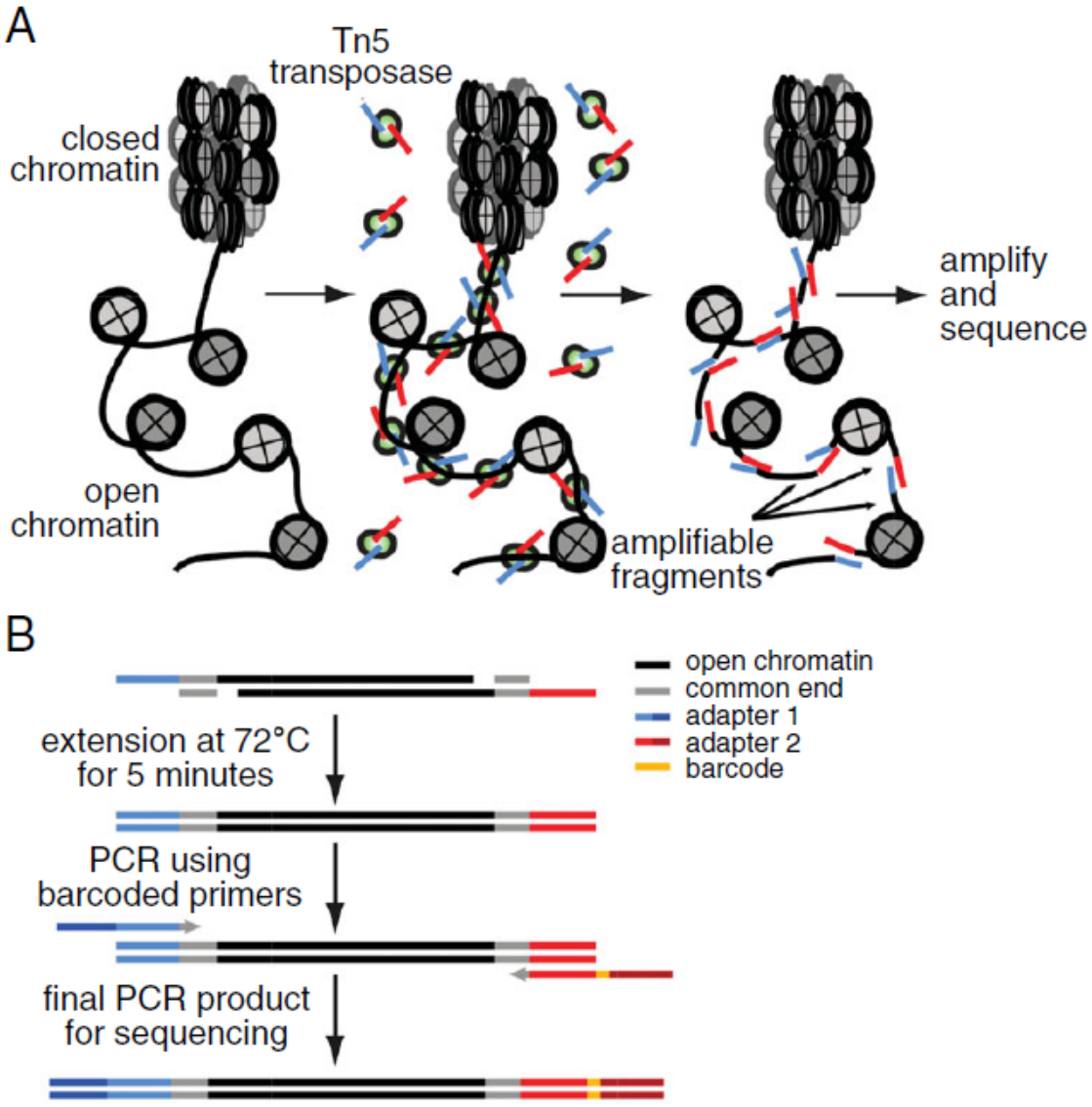
25. On information and belief, Evercode WT Products are and/or will be, presented by Parse to potential and actual customers at seminars, conferences, and meetings (collectively, "Parse Instructional Presentations," and together with "Parse Instructional Materials," "Parse Instructional Materials and 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.

26. In addition, on information and belief, Parse copied 10x's ATAC-seq technologies despite knowing of the existence of 10x's patents that cover 10x's ATAC-seq technologies, including the '995, '207, and '357 Patents, or deliberately not finding out which of 10x's patents covered 10x's ATAC-seq technologies.

27. On information and belief, in or around April 2022, Parse announced its plans to launch, in the second half of 2022, the Parse Single-Cell ATAC-Seq Product (as in the case of the 10x technology described in paragraph 17 above, "ATAC-seq" is an acronym that stands for assay for transposase-accessible chromatin by sequencing). *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022) https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach#.YuvXJbfMKUk. On information and belief, Parse announced on Twitter, "A big

thank you to @genomeweb and @HanAndrewP for covering our new product line, which includes a targeted scRNAseq assay, scCRISPR screen kit, scATAC-seq kit, and an immune profiling kit. Follow us for updates! #scRNAseq #CRISPR #ATACseq #immuneprofiling." Parse Biosciences, Twitter (Apr. 15, 2022), https://twitter.com/ParseBio?ref_src=twsrc%5Egoogle%7Ctwcamp%5Eserp%7Ctwgr%5Eauthor. On information and belief, the Single-Cell ATAC-Seq Product will be an add-on to the Evercode WT Products. *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022) https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach#.YuvXJbfMKUk.

28. Moreover, on information and belief, Parse's Single Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers to perform the ATAC-seq method, namely generating a library of tagged fragments from open chromatin in the nucleus of a cell and sequencing those tagged fragments to obtain a sequencing library of the regions of open chromatin:



ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: An insertional enzyme complex, such as Tn5 transposase (green) loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates a library of fragments that can be PCR amplified and sequenced. (B) During PCR amplification, additional sequences are incorporated into the adaptors, which include common sequencing ends and a sequencing barcode.

Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal*

Epigenomics, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

29. The Parse Single-Cell ATAC-Seq Product are all products or components that have been, are and will be made, used, sold, offered for sale, and/or imported into the United States by or on behalf of Parse in connection with the Parse Single-Cell ATAC-Seq Product kit and workflows. The Parse Single-Cell ATAC-Seq Product includes, 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 Parse Single-Cell ATAC-Seq Product.

30. On information and belief, the Parse Single-Cell ATAC-Seq Product 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 suite information (collectively, "Parse ATAC-Seq Instructional Materials"). On information and belief, the Parse ATAC-Seq Instructional Materials will provide instructions, recommendations, and suggestions to customers on how to use Parse Single-Cell ATAC-Seq Product.

31. On information and belief, the Parse Single-Cell ATAC-Seq Product will be presented by Parse to potential and actual customers at seminars, conferences, and meetings (collectively, "Parse ATAC-Seq Instructional Presentations," and together with Parse ATAC-Seq Instructional Materials, "Parse ATAC-Seq Instructional Materials and Presentations"). On information and belief, the Parse ATAC-Seq Instructional Presentations provide instructions,

recommendations, and suggestions to customers on how to use the Parse Single-Cell ATAC-Seq Product.

THE PATENTS-IN-SUIT

32. 10x incorporates and realleges paragraphs 1 to 31 above as if fully set forth herein.

33. By its manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products, Parse is infringing and will infringe the ’981, ’013, and ’197 Patents. By its manufacture, use, offer for sale, sale, and/or importation into the United States of the Parse Single-Cell ATAC-Seq Product (together with Evercode WT Products, the “Accused Instrumentalities”), Parse is infringing and will infringe the ’995, ’207, and ’357 Patents.

a. The ’981 Patent, entitled “Methods for analyzing nucleic acids from single cells,” is attached as Exhibit 1;

b. The ’013 Patent, entitled “Methods for analyzing nucleic acids from single cells,” is attached as Exhibit 2;

c. The ’197 Patent, entitled “Methods for analyzing nucleic acids from single cells,” is attached as Exhibit 3;

d. The ’995 Patent, entitled “Transposition of Native Chromatin for Personal Epigenomics,” is attached as Exhibit 4;

e. The ’207 Patent, entitled “Transposition of Native Chromatin for Personal Epigenomics,” is attached as Exhibit 5; and

f. The ’357 Patent, entitled “Transposition of Native Chromatin for Personal Epigenomics,” is attached as Exhibit 6.

The ‘981, ’013, ’197, ’995, ’207, and ’357 Patents are referred to collectively as “the Asserted Patents.”

34. The ’981 Patent was duly and legally issued on December 18, 2018, by the United States Patent and Trademark Office. U.S. Application No. 15/677,957, which issued as the ’981 Patent, claims the benefit of Provisional Application Nos. 61/288,792, filed on December 21, 2009, and 61/235,595, filed on August 20, 2009. Sydney Brenner, Gi Mikawa, Robert Osborne, and Andrew Slatter are the named inventors of the ’981 Patent. 10x is the sole legal owner of the ’981 Patent. The assignment abstract and record for the ’981 Patent is attached as Exhibit 7.

35. The ’013 Patent was duly and legally issued on June 30, 2020, by the United States Patent and Trademark Office. U.S. Application No. 16/817,461, which issued as the ’013 Patent, claims the benefit of Provisional Application Nos. 61/288,792, filed on December 21, 2009, and 61/235,595, filed on August 20, 2009. Sydney Brenner, Gi Mikawa, Robert Osborne, and Andrew Slatter are the named inventors of the ’013 Patent. 10x is the sole legal owner of the ’013 Patent. The assignment abstract and record for the ’013 Patent is attached as Exhibit 8.

36. The ’197 Patent was duly and legally issued on March 26, 2019, by the United States Patent and Trademark Office. U.S. Application No. 16/194,047, which issued as the ’197 Patent, claims the benefit of Provisional Application No. 61/288,792, filed on December 21, 2009, and Provisional Application No. 61/235,595, filed on August 20, 2009. Sydney Brenner, Gi Mikawa, Robert Osborne, and Andrew Slatter are the named inventors of the ’197 Patent. 10x is the sole legal owner of the ’197 Patent. The assignment abstract and record for the ’197 Patent is attached as Exhibit 9.

37. The ’995 Patent was duly and legally issued on December 11, 2018, by the United States Patent and Trademark Office. U.S. Application No. 16/043,874, which issued as the ’995 Patent, claims the benefit of Provisional Application No. 61/826,728, filed on May 23, 2013. Paul Giresi, Jason D. Buenrostro, Howard Y. Chang, and William J. Greenleaf are the named inventors

of the ’995 Patent. Stanford University is the sole legal owner of the ’995 Patent. The assignment abstract and record for the ’995 Patent is attached as Exhibit 10. 10x is the exclusive licensee of the ’995 Patent, including the right to sue for acts of infringement and to recover damages.

38. The ’207 Patent was duly and legally issued on April 14, 2020, by the United States Patent and Trademark Office. U.S. Application No. 16/418,889, which issued as the ’207 Patent, claims the benefit of Provisional Application No. 61/826,728, filed on May 23, 2013. Paul Giresi, Jason D. Buenrostro, Howard Y. Chang, and William J. Greenleaf are the named inventors of the ’207 Patent. Stanford University is the sole legal owner of the ’207 Patent. The assignment abstract and record for the ’207 Patent is attached as Exhibit 11. 10x is the exclusive licensee of the ’207 Patent, including the right to sue for acts of infringement and to recover damages.

39. The ’357 Patent was duly and legally issued on August 11, 2020, by the United States Patent and Trademark Office. U.S. Application No. 16/418,796, which issued as the ’357 Patent, claims the benefit of Provisional Application No. 61/826,728, filed on May 23, 2013. Paul Giresi, Jason D. Buenrostro, Howard Y. Chang, and William J. Greenleaf are the named inventors of the ’357 Patent. Stanford University is the sole legal owner of the ’357 Patent. The assignment abstract and record for the ’357 Patent is attached as Exhibit 12. 10x is the exclusive licensee of the ’357 Patent, including the right to sue for acts of infringement and to recover damages.

40. The Asserted Patents describe specific steps and materials—as opposed to the countless other ways one could try to develop a method for nucleic acid analysis, including chromatin analysis—and are neither abstract, nor in any way preempt the field of single-cell nucleic acid analysis or chromatin analysis. The patented subject matter covers specific and concrete methods that remove limitations imposed by older sequencing technologies and are useful in a number of other nucleic acid analyses.

FIRST CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,155,981)

41. 10x incorporates and realleges paragraphs 1 to 40 above as if fully set forth herein.

42. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products directly infringes at least Claim 1 of the '981 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

43. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products indirectly infringes at least Claim 1 of the '981 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse's customers.

44. Claim 1 of the '981 Patent recites:

> A method of analyzing nucleic acids from a plurality of single cells, the method comprising:
>
> (a) providing a sample comprising a plurality of single cells, wherein each single cell of the plurality of single cells comprises a plurality of sample polynucleotides;
>
> (b) generating a plurality of tagged polynucleotides from the plurality of sample polynucleotides, wherein each tagged polynucleotide comprises:
>
> (i) a sequence from a sample polynucleotide of the plurality of sample polynucleotides; and
>
> (ii) a multiplex identifier (MID) sequence comprising:
>
> I. a first tag sequence associated with the single cell from which the sample polynucleotide is derived, wherein the first tag sequence is a different sequence for different single cells in the plurality of single cells; and
>
> II. a second tag sequence distinguishing the sample polynucleotide from other sample polynucleotides derived from the same single cell;

(c) sequencing the plurality of tagged polynucleotides to obtain a plurality of identified polynucleotide sequences;

(d) using the first tag sequence to correlate the identified polynucleotide sequence with the single cell from which the identified polynucleotide sequence is derived; and

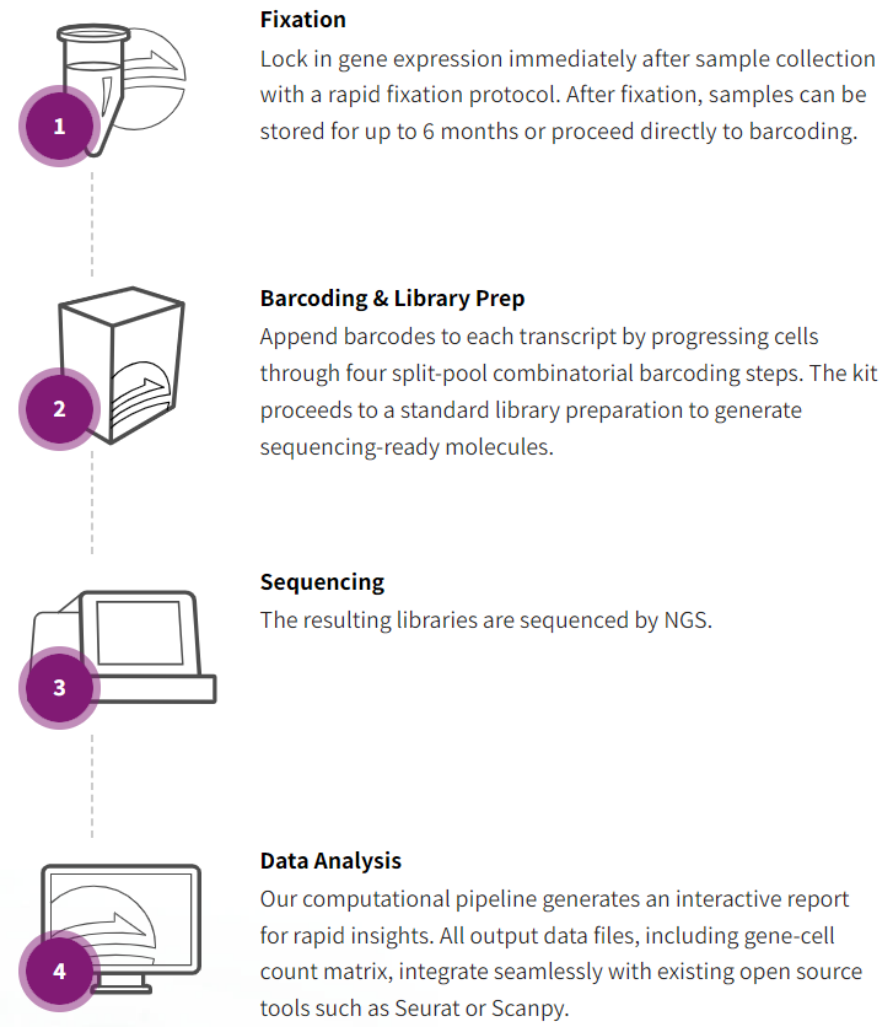
(e) using the second tag sequence to correlate the identified polynucleotide sequence with the sample polynucleotide from which the identified polynucleotide sequence is derived.

45. On information and belief, Parse's use of its Evercode WT Products satisfies each limitation of at least Claim 1 of the '981 Patent.

46. On information and belief, when Parse's customers use the Evercode WT Products in accordance with Parse Instructional Materials and Presentations and in a manner consistent with the available literature, such use satisfies each limitation of at least Claim 1 of the '981 Patent.

47. **Preamble: "Method of analyzing nucleic acids from a plurality of single cells."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers for "method[s] of analyzing nucleic acids from a plurality of single cells." For example, Parse states that "[a]t Parse Biosciences, we are providing researchers with the ability to perform single cell sequencing"; and that "[s]ingle cell insights are accessible to biological researchers in any lab with the Evercode™ combinatorial barcoding approach." Parse Biosciences, https://www.parsebiosciences.com (last visited Aug. 24, 2022); *see also* Parse, Company, https://www.parsebiosciences.com/company (last visited Aug. 24, 2022); Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 177 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021),

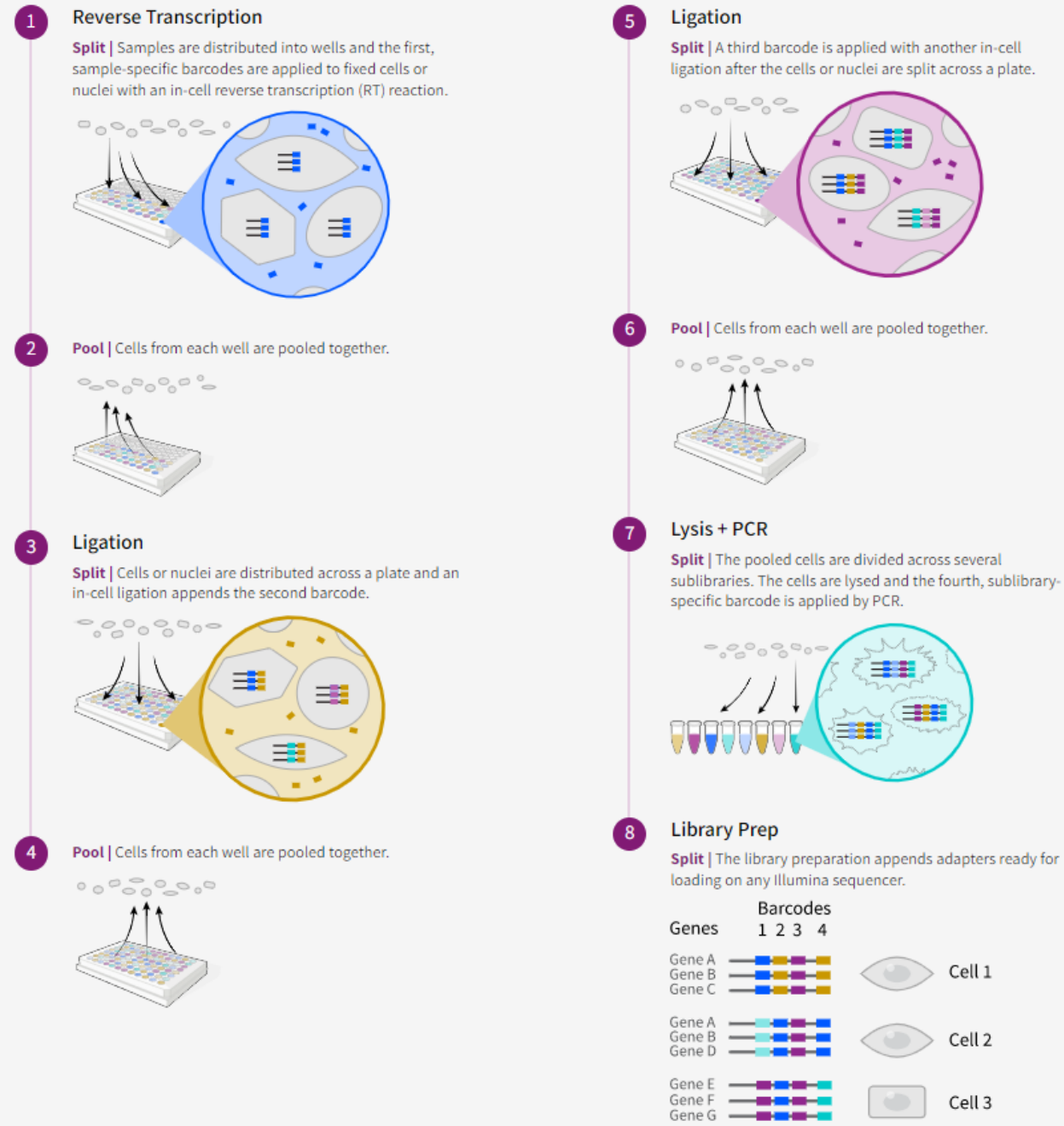
https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. For example, Parse states that its Evercode WT Products are used as follows:



Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited

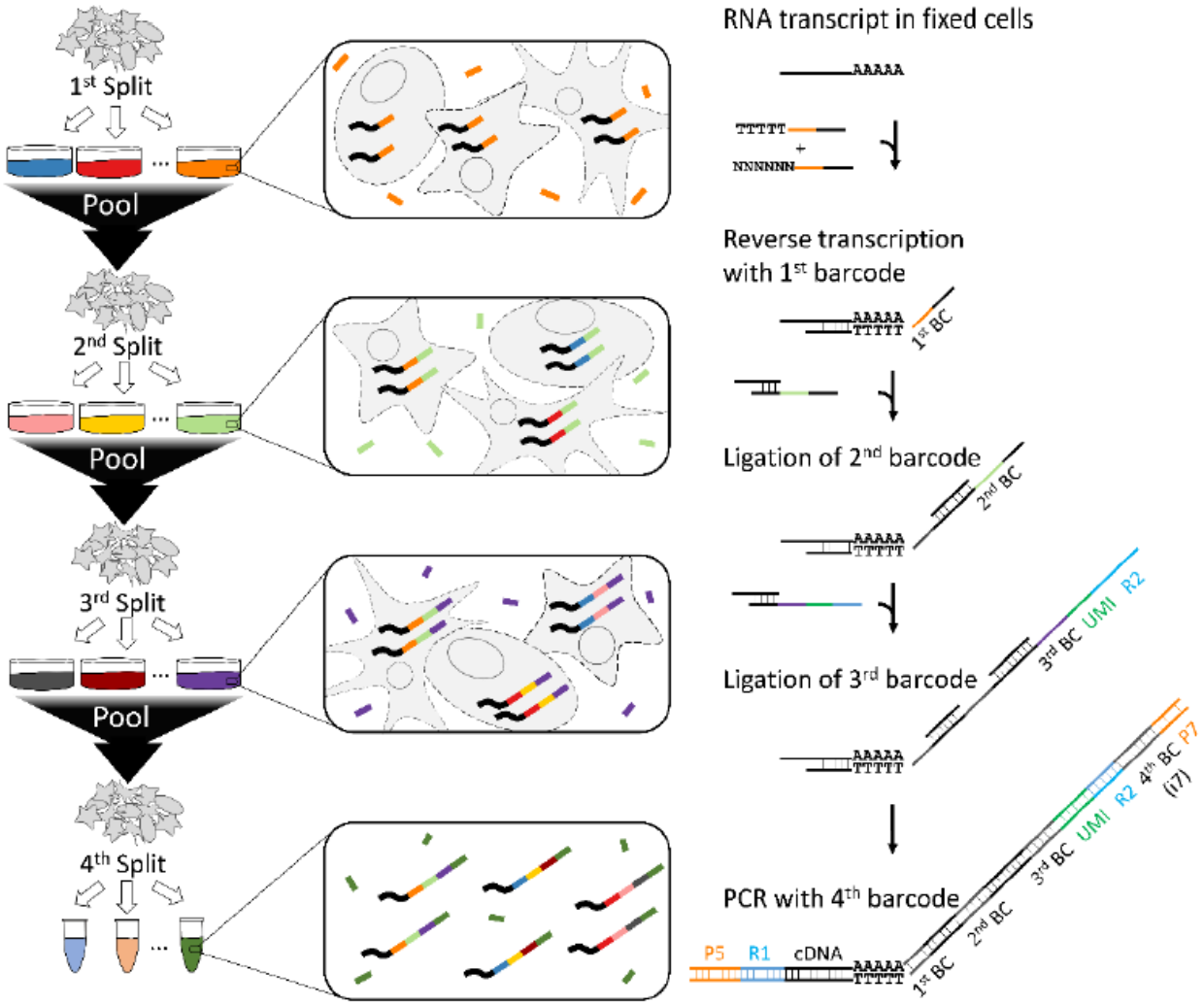
Aug. 24, 2022; *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022).

48. **(a) and (b): "Providing a sample comprising a plurality of single cells, wherein each single cell of the plurality of cells comprises a plurality of sample polynucleotides" and "generating a plurality of tagged polynucleotides from the plurality of sample polynucleotides."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "provid[e] a sample comprising a plurality of single cells, wherein each single cell of the plurality of cells comprises a plurality of sample polynucleotides" and "generating a plurality of tagged polynucleotides from the plurality of sample polynucleotides." For example, Parse states that its Evercode WT Products are used as follows:



Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 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 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

49. **(b): "Wherein each tagged polynucleotide comprises (i) a sequence from a sample polynucleotide of the plurality of sample polynucleotides; and (ii) a multiplex identifier (MID) sequence comprising: I. a first tag sequence associated with the single cell from which the sample polynucleotide is derived, wherein the first tag sequence is a different sequence for different single cells in the plurality of single cells; and II. a second tag sequence distinguishing the sample polynucleotide from other sample polynucleotides derived from the same single cell."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to generate a plurality of tagged polynucleotides "wherein each tagged polynucleotide comprises (i) a sequence from a sample polynucleotide of the plurality of sample polynucleotides; and (ii) a multiplex identifier (MID) sequence comprising: I. a first tag sequence associated with the single cell from which the sample polynucleotide is derived, wherein the first tag sequence is a different sequence for different single cells in the plurality of single cells; and II. a second tag sequence distinguishing the sample polynucleotide from other sample polynucleotides derived from the same single cell." For example, Parse states that "[i]ndividual transcriptomes are uniquely labeled by passing fixed cells or nuclei through four rounds of barcoding. In each round, pooled cells are randomly distributed into different wells, and transcripts are labeled with well-specific barcodes." Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 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 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. For example:



Labeling transcriptomes with split-pool barcoding. 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. After the last round of ligation, cDNA molecules contain a cell-specific combination of barcodes, a unique molecular identifier (UMI), and a universal PCR handle on the 5'end. The bottom scheme shows an exemplary final barcoded cDNA molecule. 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 (Apr. 13, 2018)

Thus, "[i]n the first round of barcoding, cells are distributed [into wells] and cDNA is generated with an in-cell reverse transcription (RT) reaction using well-specific barcoded primers. . . . After this step, cells from all wells are pooled and redistributed into [new wells], where an in-cell ligation

reaction appends a second well-specific barcode to the cDNA. The third-round barcode, which also contains a unique molecular identifier (UMI), is then appended with another round of pooling, splitting, and ligation. After three rounds of barcoding, the cells are pooled and split into sublibraries, and sequencing barcodes are introduced by polymerase chain reaction (PCR). This final step provides a fourth barcode, while also making it possible to sequence different numbers of cells in each sublibrary." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

50. **(c): "Sequencing the plurality of tagged polynucleotide to obtain a plurality of identified polynucleotide sequences."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "sequenc[e] the plurality of tagged polynucleotide to obtain a plurality of identified polynucleotide sequences." For example, Parse states that after preparation of the barcoded library using Parse's Evercode WT Products, "[t]he resulting libraries are sequenced by NGS," including by using an Illumina sequencer. Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited

Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; *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 (Apr. 13, 2018). In addition, Parse states that its barcoded libraries are "sequenced on MiSeq and NextSeq systems (Illumina)," such that "Read 1 cover[s] the transcript sequences"; "Read 2 cover[s] the UMI [unique molecular identifier] and UBC [uniquely barcoded cells] barcode combinations"; and the "index read, serving as the fourth barcode, cover[s] the sublibrary indices introduced after tagmentation." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods at 5–6 (Apr. 13, 2018); *see also* Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

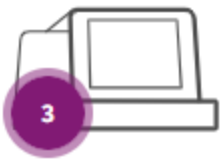
51. **(d) and (e): "Using the first tag sequence to correlate the identified polynucleotide sequence with the single cell from which the identified polynucleotide sequence is derived" and "using the second tag sequence to correlate the identified polynucleotide sequence with the sample polynucleotide from which the identified polynucleotide sequence is derived."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers "to correlate the identified polynucleotide sequence with the single cell from which the identified polynucleotide sequence is derived" by "using the first tag sequence," and "to correlate the identified polynucleotide sequence with the sample polynucleotide from which the identified polynucleotide sequence is derived" by "using the second tag sequence." For example, Parse states that "[a]fter

sequencing, each transcriptome is assembled by combining reads containing the same four-barcode combination"; and that "the sensitivity of SPLiT-seq" in terms of "gene and UMI detection" is "comparable to droplet-based scRNA-seq methods." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods 5–6 & Fig. S3 (Apr. 13, 2018). In addition, Parse states that its barcoded libraries are "sequenced on MiSeq and NextSeq systems (Illumina)," such that "Read 1 cover[s] the transcript sequences"; "Read 2 cover[s] the UMI [unique molecular identifier] and UBC [uniquely barcoded cells] barcode combinations"; and the "index read, serving as the fourth barcode, cover[s] the sublibrary indices introduced after tagmentation." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods at 5–6 (Apr. 13, 2018); *see also* Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. Thus, Parse states that its Evercode WT Products are used as follows:



Barcoding & Library Prep

Append barcodes to each transcript by progressing cells through four split-pool combinatorial barcoding steps. The kit proceeds to a standard library preparation to generate sequencing-ready molecules.



Sequencing

The resulting libraries are sequenced by NGS.



Data Analysis

Our computational pipeline generates an interactive report for rapid insights. All output data files, including gene-cell count matrix, integrate seamlessly with existing open source tools such as Seurat or Scanpy.

Reading in data

```
# The DGE_filtered folder contains the expression matrix, genes, and
adata = sc.read_mtx(mat_path + 'DGE_1M_PBMC.mtx')

adata.write(obj_save_path + 'adata_obj1.h5ad')
# adata = sc.read(obj_save_path + 'adata_obj1.h5ad')

# reading in gene and cell data
gene_data = pd.read_csv(mat_path + 'all_genes_1M_PBMC.csv')
cell_meta = pd.read_csv(mat_path + 'cell_metadata_1M_PBMC.csv')

# find genes with nan values and filter
gene_data = gene_data[gene_data.gene_name.notnull()]
notNa = gene_data.index
notNa = notNa.to_list()

# remove genes with nan values and assign gene names
adata = adata[:,notNa]
adata.var = gene_data
adata.var.set_index('gene_name', inplace=True)
adata.var.index.name = None
adata.var_names_make_unique()

# add cell meta data to anndata object
adata.obs = cell_meta
adata.obs.set_index('bc_wells', inplace=True)
adata.obs.index.name = None
adata.obs_names_make_unique()

sc.pp.filter_cells(adata, min_counts=100)
sc.pp.filter_genes(adata, min_cells=5)
adata.shape
```

Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How to Analyze a 1 Million Cell Data Set Using Scanpy and Harmony*, https://support.parsebiosciences.com/hc/en-us/articles/7704577188500-How-to-analyze-a-1-million-cell-data-set-using-Scanpy-and-Harmony (last visited Aug. 24, 2022); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018), including Experimental Methods at 5–6; Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

52. On information and belief, Parse knew of the ’981 Patent at least as of its receipt of the notice letter sent by 10x to Parse on August 23, 2022 (“10x Notice Letter”). On information and belief, Parse would have known of the ’981 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x’s patents as part of its research.

53. Alternatively, on information and belief, Parse has acted knowingly or has been willfully blind as to the existence of the ’981 Patent, its own infringement, and the infringement

by others. On information and belief, Parse was willfully blind by seeking to copy 10x's product without investigating 10x's patents.

54. On information and belief, Parse has no reasonable basis for believing that the '981 Patent is not infringed.

55. Parse induces infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 1 of the '981 Patent in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

56. On information and belief, Parse's Evercode WT Products are not staple articles of commerce and are not suitable for any substantial use that does not infringe at least Claim 1 of the '981 Patent literally or under the doctrine of equivalents.

57. Parse contributes to the infringement of at least Claim 1 of the '981 Patent under 35 U.S.C. § 271(c), by selling its Evercode WT Products.

58. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 1 of the '981 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against further infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products prior to the expiration of the '981 Patent. 10x does not have an adequate remedy at law.

59. The manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products before the expiration of the '981 Patent caused, causes, and will cause injury to 10x entitling 10x to damages under 35 U.S.C. § 284.

SECOND CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,697,013)

60. 10x incorporates and realleges paragraphs 1 to 59 above as if fully set forth herein.

61. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products directly infringes at least Claim 1 of the '013 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

62. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products indirectly infringes at least Claim 1 of the '013 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse's customers.

63. Claim 1 of the '013 Patent recites:

> A method for multiplexed analysis of nucleic acids from single cells, the method comprising:
>
> (a) providing a sample comprising a plurality of cells, wherein a single cell of the plurality of cells comprises a plurality of sample polynucleotides;
>
> (b) performing combinatorial tagging to generate a plurality of tagged polynucleotides from said plurality of sample polynucleotides and a plurality of oligonucleotide tags, wherein a tagged polynucleotide of the plurality of tagged polynucleotides is generated by:
>
> (A) providing an extension product by primer extension using a first oligonucleotide tag and a sample polynucleotide of said plurality of sample polynucleotides, and
>
> (B) ligating a second oligonucleotide tag to said extension product, and

wherein said tagged polynucleotide of the plurality of tagged polynucleotides comprises:

(i) a sample sequence corresponding to said sample polynucleotide of the plurality of sample polynucleotides;

(ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and

(iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell;

(c) amplifying said tagged polynucleotide, thereby generating a plurality of amplified polynucleotides corresponding to the tagged polynucleotide; and

(d) sequencing said plurality of amplified polynucleotides to determine sequences of the amplified polynucleotides corresponding to the sample sequence, the first tag sequence, and the second tag sequence of the tagged polynucleotide; and

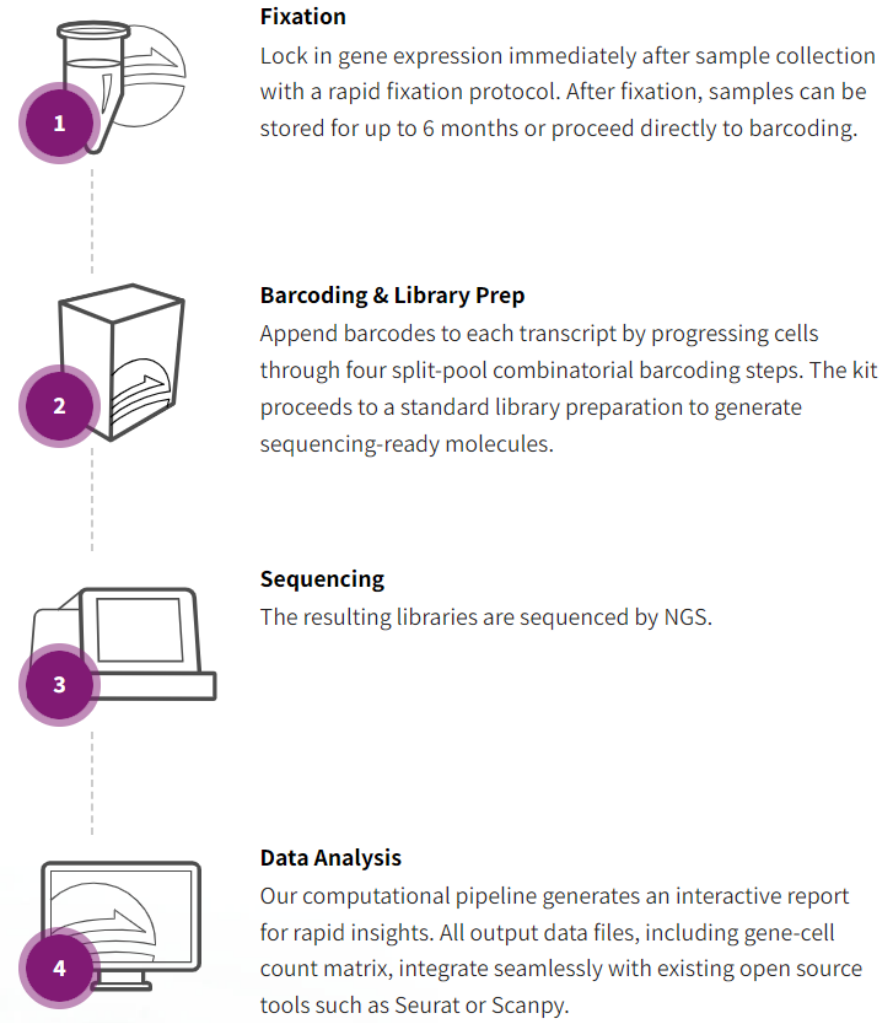
(e) using the sequences determined in step (d) to count sample polynucleotides for multiple different sample polynucleotides of multiple different single cells of said plurality of cells.

64. On information and belief, Parse's use of its Evercode WT Products satisfies each limitation of at least Claim 1 of the '013 Patent.

65. On information and belief, when Parse's customers use the Evercode WT Products in accordance with Parse Instructional Materials and Presentations and in a manner consistent with the available literature, such use satisfies each limitation of at least Claim 1 of the '013 Patent.

66. **Preamble: "Method for multiplexed analysis of nucleic acids from single cells."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers for "method[s] for multiplexed analysis of nucleic acids from single cells." For example, Parse states that "[a]t Parse Biosciences, we are providing researchers with the ability to perform single cell sequencing"; and that "[s]ingle cell

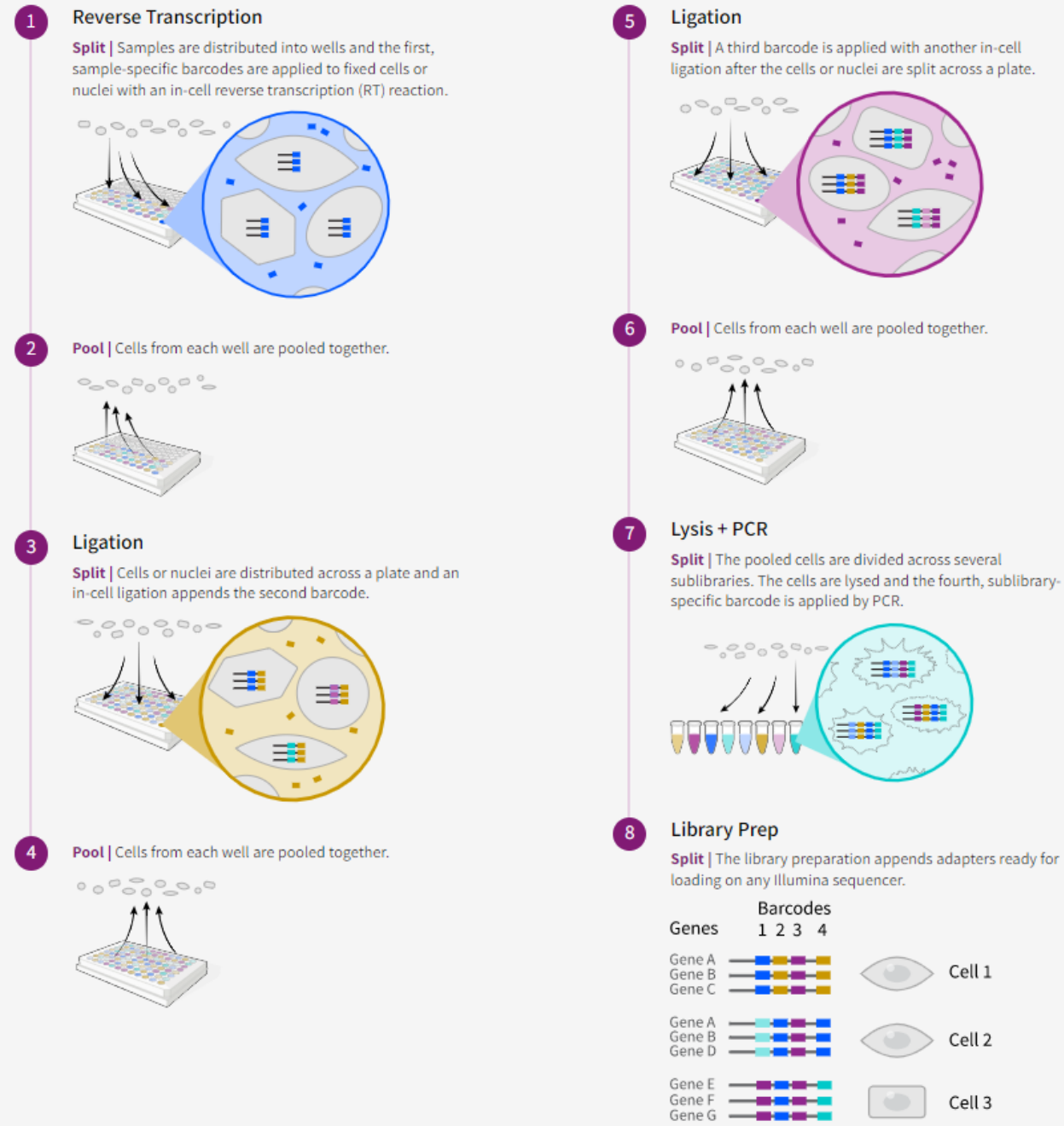
insights are accessible to biological researchers in any lab with the Evercode™ combinatorial barcoding approach." Parse, Company, https://www.parsebiosciences.com/company (last visited Aug. 24, 2022); *see also* Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 177 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. For example, Parse states that its Evercode WT Products are used as follows:



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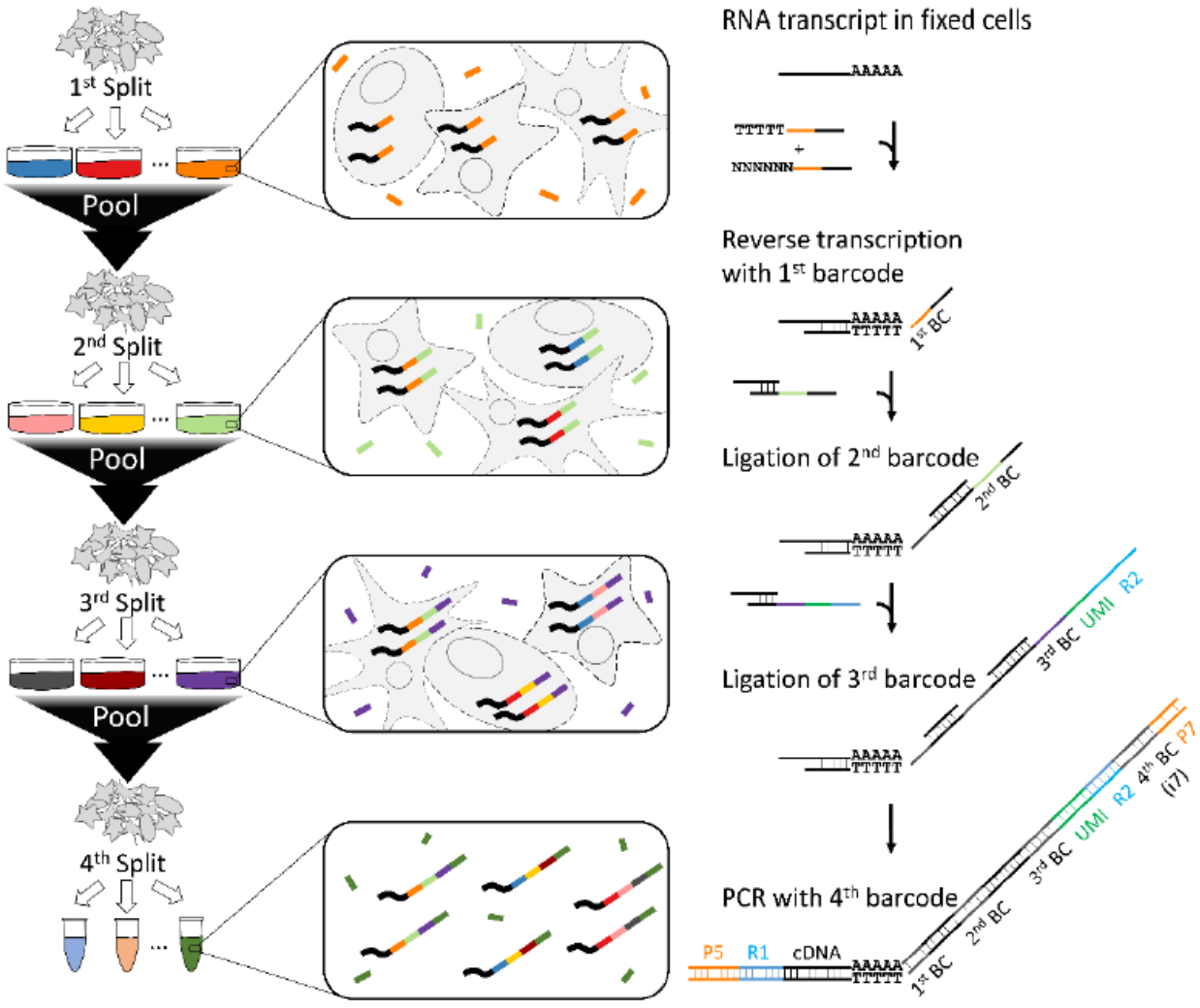
67. **(a) and (b): "Providing a sample comprising a plurality of cells, wherein a single cell of the plurality of cells comprises a plurality of sample polynucleotides" and "performing combinatorial tagging to generate a plurality of tagged polynucleotides from said plurality of sample polynucleotides and a plurality of oligonucleotide tags."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "provid[e] a sample comprising a plurality of cells, wherein a single cell of the plurality of cells comprises a plurality of sample polynucleotides" and "performing combinatorial tagging to generate a plurality of tagged polynucleotides from said plurality of sample polynucleotides and a plurality of oligonucleotide tags." For example, Parse states that its Evercode WT Products are used as follows:



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68. **(b): "Wherein a tagged polynucleotide of the plurality of tagged polynucleotides in generated by: (A) providing an extension product by primer extension using a first oligonucleotide tag and a sample polynucleotide of said plurality of sample polynucleotides, and (B) ligating a second oligonucleotide tag to said extension product," and "wherein said tagged polynucleotide of the plurality of tagged polynucleotides comprises (i) a sample sequence corresponding to said sample polynucleotide of the plurality of sample polynucleotides; (ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and (iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "generate" "a tagged polynucleotide of the plurality of tagged polynucleotides . . . by: (A) providing an extension product by primer extension using a first oligonucleotide tag and a sample polynucleotide of said plurality of sample polynucleotides, and (B) ligating a second oligonucleotide tag to said extension product" and "wherein said tagged polynucleotide of the plurality of tagged polynucleotides comprises (i) a sample sequence corresponding to said sample polynucleotide of the plurality of sample polynucleotides; (ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and (iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell." For example, Parse states that "[i]ndividual transcriptomes are uniquely labeled by passing fixed cells or nuclei through four rounds of barcoding. In each round, pooled cells are randomly distributed into different wells, and transcripts are labeled with well-specific barcodes." Parse Biosciences, Technology,

https://www.parsebiosciences.com/technology (last visited Aug. 24, 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 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. For example:

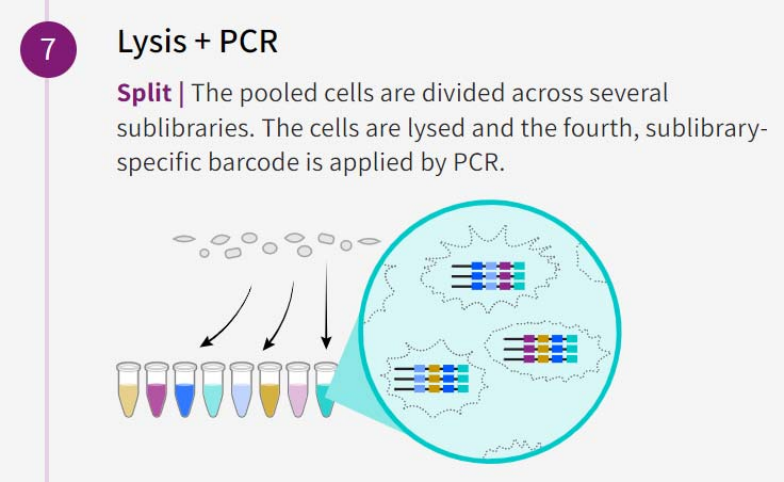


Labeling transcriptomes with split-pool barcoding. In each split-pool round, fixed cells or nuclei are randomly distributed into wells and transcripts are labeled with well-specific barcodes. Barcoded RT primers are used in the first round. Second and third round barcodes are appended to cDNA through ligation. After the last round of ligation, cDNA molecules contain a cell-specific combination of barcodes, a unique molecular identifier (UMI), and a universal PCR handle on the

> 5'end. The bottom scheme shows an exemplary final barcoded cDNA molecule. 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 (Apr. 13, 2018)

Thus, "[i]n the first round of barcoding, cells are distributed [into wells] and cDNA is generated with an in-cell reverse transcription (RT) reaction using well-specific barcoded primers. . . . After this step, cells from all wells are pooled and redistributed into [new wells], where an in-cell ligation reaction appends a second well-specific barcode to the cDNA. The third-round barcode, which also contains a unique molecular identifier (UMI), is then appended with another round of pooling, splitting, and ligation. After three rounds of barcoding, the cells are pooled and split into sublibraries, and sequencing barcodes are introduced by polymerase chain reaction (PCR). This final step provides a fourth barcode, while also making it possible to sequence different numbers of cells in each sublibrary." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

69. **(c): "Amplifying said tagged polynucleotide, thereby generating a plurality of amplified polynucleotides corresponding to the tagged polynucleotide."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "amplify[] said tagged polynucleotide, thereby generating a plurality of amplified polynucleotides corresponding to the tagged polynucleotide." For example, Parse states that its Evercode WT Products are used as follows:



Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); *see also* Parse, Single Cell Sequencing with Split Pool Barcoding Video, YouTube (Jan. 26, 2021), https://www.youtube.com/watch?v=HVx4UBweNH4 at 1:40.

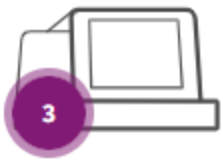
70. **(d): "Sequencing said plurality of amplified polynucleotides to determine sequences of the amplified polynucleotides corresponding to the sample sequence, the first tag sequence, and the second tag sequence of the tagged polynucleotide."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "sequenc[e] said plurality of amplified polynucleotides to determine sequences of the amplified polynucleotides corresponding to the sample sequence, the first tag sequence, and the second tag sequence of the tagged polynucleotide." For example, Parse states that after preparation of the barcoded library using Parse's Evercode WT Products, "[t]he resulting libraries are sequenced by NGS," including by using an Illumina sequencer. Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last

visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; *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 (Apr. 13, 2018). In addition, Parse states that its barcoded libraries are "sequenced on MiSeq and NextSeq systems (Illumina)," such that "Read 1 cover[s] the transcript sequences"; "Read 2 cover[s] the UMI [unique molecular identifier] and UBC [uniquely barcoded cells] barcode combinations"; and the "index read, serving as the fourth barcode, cover[s] the sublibrary indices introduced after tagmentation." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods at 5–6 (Apr. 13, 2018); *see also* Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. Parse also states that "[a]fter sequencing, each transcriptome is assembled by combining reads containing the same four-barcode combination"; and that "the sensitivity of SPLiT-seq" in terms of "gene and UMI detection" is "comparable to droplet-based scRNA-seq methods." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods 5–6 & Fig. S3 (Apr. 13, 2018). Thus, Parse states that its Evercode WT Products are used as follows:



Barcoding & Library Prep

Append barcodes to each transcript by progressing cells through four split-pool combinatorial barcoding steps. The kit proceeds to a standard library preparation to generate sequencing-ready molecules.



Sequencing

The resulting libraries are sequenced by NGS.



Data Analysis

Our computational pipeline generates an interactive report for rapid insights. All output data files, including gene-cell count matrix, integrate seamlessly with existing open source tools such as Seurat or Scanpy.

Reading in data

```
# The DGE_filtered folder contains the expression matrix, genes, and
adata = sc.read_mtx(mat_path + 'DGE_1M_PBMC.mtx')

adata.write(obj_save_path + 'adata_obj1.h5ad')
# adata = sc.read(obj_save_path + 'adata_obj1.h5ad')

# reading in gene and cell data
gene_data = pd.read_csv(mat_path + 'all_genes_1M_PBMC.csv')
cell_meta = pd.read_csv(mat_path + 'cell_metadata_1M_PBMC.csv')

# find genes with nan values and filter
gene_data = gene_data[gene_data.gene_name.notnull()]
notNa = gene_data.index
notNa = notNa.to_list()

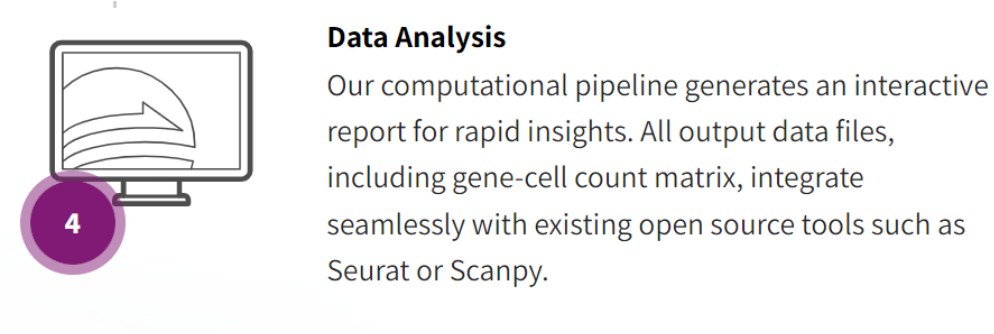
# remove genes with nan values and assign gene names
adata = adata[:,notNa]
adata.var = gene_data
adata.var.set_index('gene_name', inplace=True)
adata.var.index.name = None
adata.var_names_make_unique()

# add cell meta data to anndata object
adata.obs = cell_meta
adata.obs.set_index('bc_wells', inplace=True)
adata.obs.index.name = None
adata.obs_names_make_unique()

sc.pp.filter_cells(adata, min_counts=100)
sc.pp.filter_genes(adata, min_cells=5)
adata.shape
```

Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How to Analyze a 1 Million Cell Data Set Using Scanpy and Harmony*, https://support.parsebiosciences.com/hc/en-us/articles/7704577188500-How-to-analyze-a-1-million-cell-data-set-using-Scanpy-and-Harmony (last visited Aug. 24, 2022); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018), including Experimental Methods at 5–6; Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

71. **(e): "Using the sequences determined in step (d) to count sample polynucleotides for multiple different sample polynucleotides of multiple different single cells of said plurality of cells."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers "to count sample polynucleotides for multiple different sample polynucleotides of multiple different single cells of said plurality of cells" by "using the sequences determined in step (d) [the sequencing step]." For example, Parse states that its Evercode WT Products are used as follows:



Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 176–77 (Apr. 13, 2018); *id*., Suppl. Materials at 5–6.

72. On information and belief, Parse knew of the ’013 Patent at least as of its receipt of the 10x Notice Letter. On information and belief, Parse would have known of the ’013 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x’s patents as part of its research.

73. Alternatively, on information and belief, Parse has acted knowingly or has been willfully blind as to the existence of the ’013 Patent, its own infringement, and the infringement by others. On information and belief, Parse was willfully blind by seeking to copy 10x’s product without investigating 10x’s patents.

74. On information and belief, Parse has no reasonable basis for believing that the '013 Patent is not infringed.

75. Parse induces infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 1 of the '013 Patent in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

76. On information and belief, Parse's Evercode WT Products are not staple articles of commerce and are not suitable for any substantial use that does not infringe at least Claim 1 of the '013 Patent literally or under the doctrine of equivalents.

77. Parse contributes to the infringement of at least Claim 1 of the '013 Patent under 35 U.S.C. § 271(c), by selling its Evercode WT Products.

78. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 1 of the '013 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against further infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products prior to the expiration of the '013 Patent. 10x does not have an adequate remedy at law.

79. The manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products before the expiration of the '013 Patent causes or will cause injury to 10x entitling 10x to damages under 35 U.S.C. § 284.

THIRD CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,240,197)

80. 10x incorporates and realleges paragraphs 1 to 79 above as if fully set forth herein.

81. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products directly infringes at least Claim 1 of the '197 Patent, literally or equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

82. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Evercode WT Products indirectly infringes at least Claim 1 of the '197 Patent, literally or equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse's customers.

83. Claim 1 of the '197 Patent recites:

A method of counting nucleic acids in a sample, the method comprising:

(a) providing a sample comprising a plurality of cells, wherein a cell of the plurality of cells comprises a plurality of sample polynucleotides;

(b) generating a plurality of tagged polynucleotides from the plurality of sample polynucleotides of said cell and a plurality of oligonucleotide tags, wherein a tagged polynucleotide of the plurality of tagged polynucleotides comprises:

(i) a sample sequence from a sample polynucleotide of the plurality of sample polynucleotides;

(ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and

(iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell;

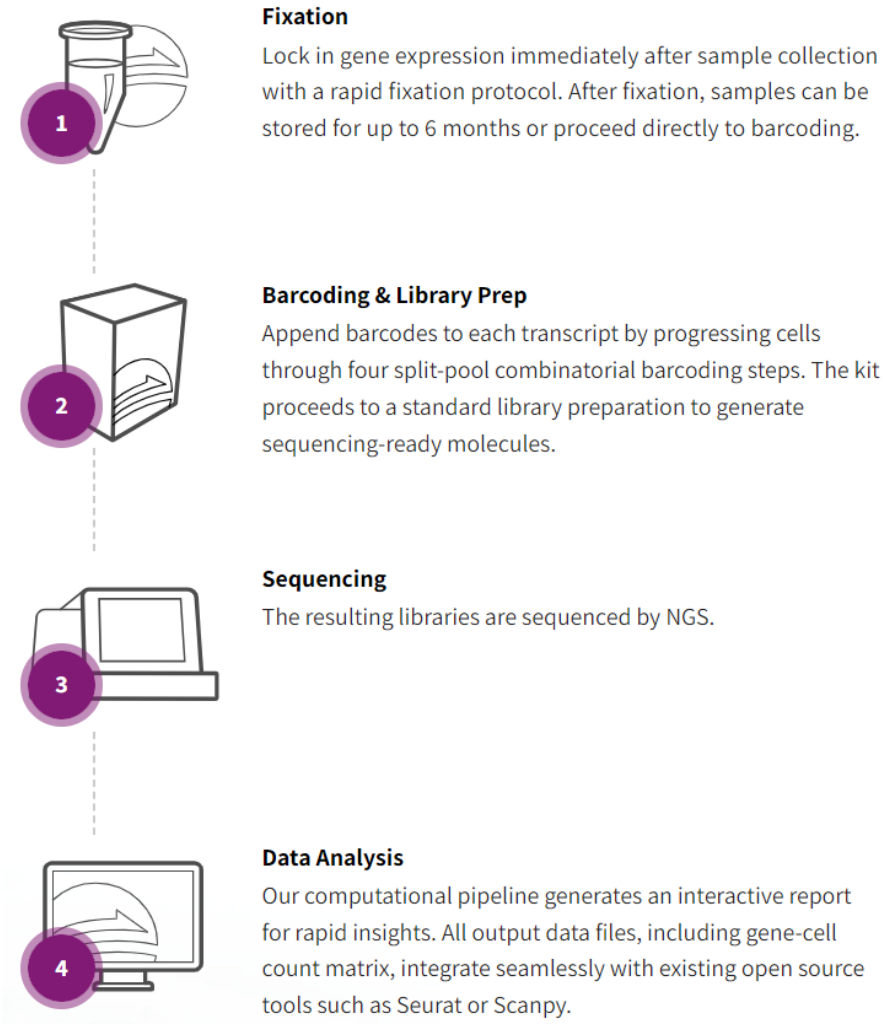
(c) sequencing the tagged polynucleotide to determine the sample sequence, the first tag sequence, and the second tag sequence; and

(d) using the first tag sequence and the second tag sequence to count a number of sample polynucleotides in said plurality of sample polynucleotides of said cell.

84. On information and belief, Parse's use of its Evercode WT Products satisfies each limitation of at least Claim 1 of the '197 Patent.

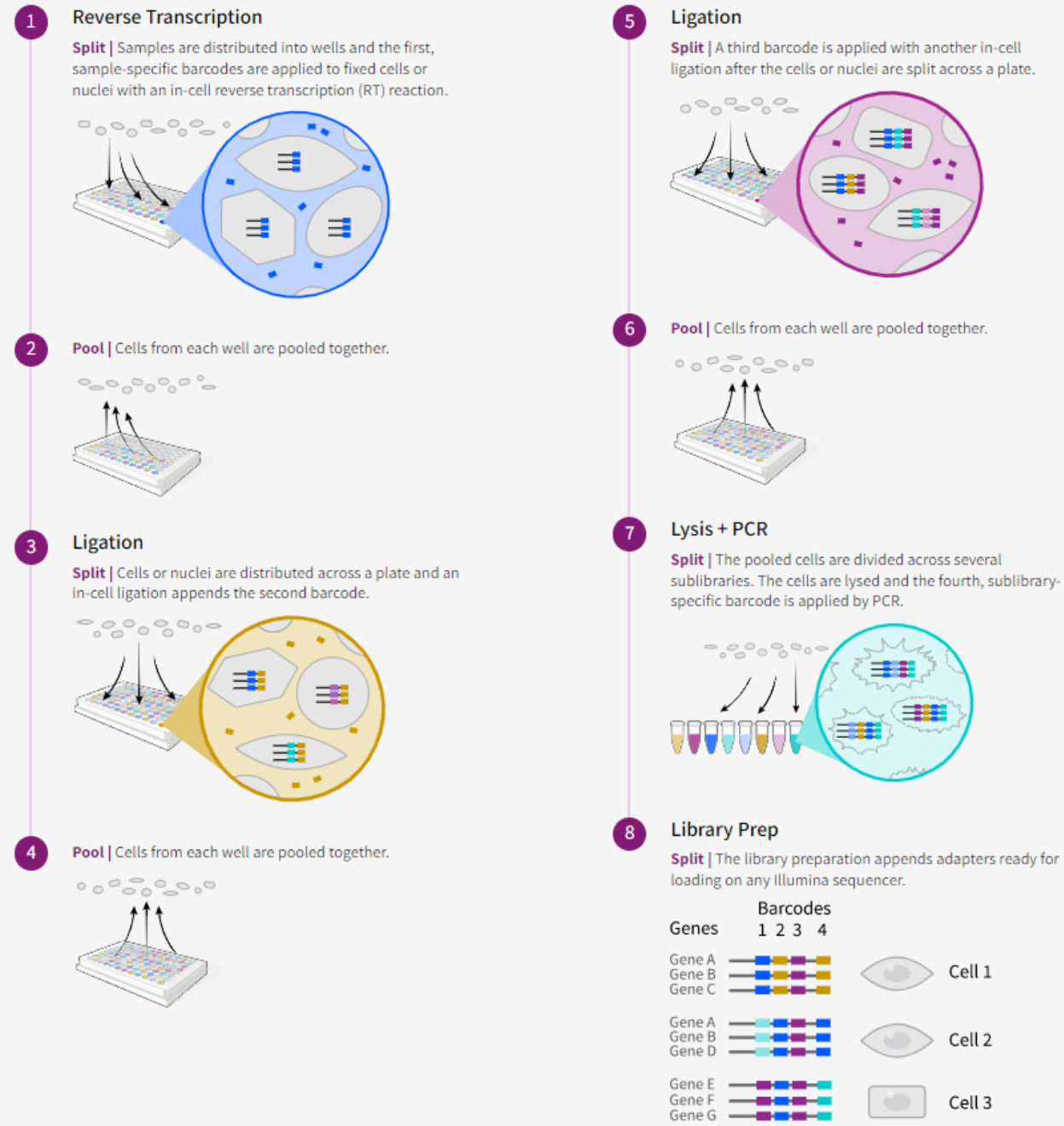
85. On information and belief, when Parse's customers use the Evercode WT Products in accordance with Parse Instructional Materials and Presentations and in a manner consistent with the available literature, such use satisfies each limitation of at least Claim 1 of the '197 Patent.

86. **Preamble: "Method of counting nucleic acids in a sample."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers for "method[s] of counting nucleic acids in a sample." For example, Parse states that its Evercode WT Products are used as follows:



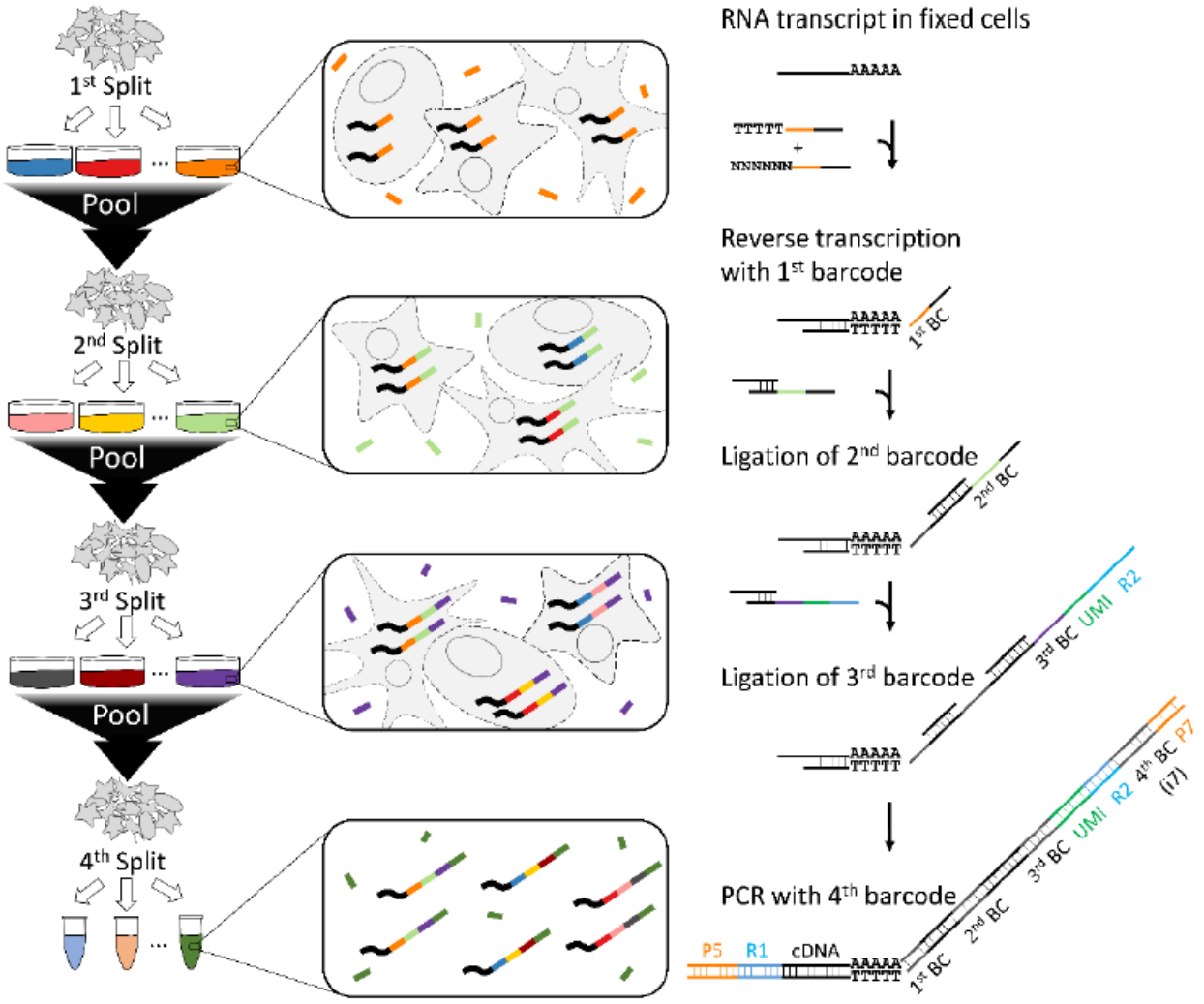
Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022).

87. **(a) and (b): "Providing a sample comprising a plurality of cells, wherein a cell of the plurality of cells comprises a plurality of sample polynucleotides" and "generating a plurality of tagged polynucleotides from the plurality of sample polynucleotides of said cell and a plurality of oligonucleotide tags."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "provid[e] a sample comprising a plurality of cells, wherein a cell of the plurality of cells comprises a plurality of sample polynucleotides" and to "generat[e] a plurality of tagged polynucleotides from the plurality of sample polynucleotides of said cell and a plurality of oligonucleotide tags." For example, Parse's Evercode WT Products are used as follows:



Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 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 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

88. **(b): "Wherein a tagged polynucleotide of the plurality of tagged polynucleotides comprises: (i) a sample sequence from a sample polynucleotide of the plurality of sample polynucleotides; (ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and (iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to generate "a tagged polynucleotide of the plurality of tagged polynucleotides" that "comprises: (i) a sample sequence from a sample polynucleotide of the plurality of sample polynucleotides; (ii) a first tag sequence distinguishing said sample polynucleotide from sample polynucleotides from other cells; and (iii) a second tag sequence distinguishing said sample polynucleotide from other sample polynucleotides from said cell a plurality of tagged polynucleotides " For example, Parse states that "[i]ndividual transcriptomes are uniquely labeled by passing fixed cells or nuclei through four rounds of barcoding. In each round, pooled cells are randomly distributed into different wells, and transcripts are labeled with well-specific barcodes." Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 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 (Apr. 13, 2018); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. For example:



Labeling transcriptomes with split-pool barcoding. 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. After the last round of ligation, cDNA molecules contain a cell-specific combination of barcodes, a unique molecular identifier (UMI), and a universal PCR handle on the 5'end. The bottom scheme shows an exemplary final barcoded cDNA molecule. 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 (Apr. 13, 2018)

Thus, "[i]n the first round of barcoding, cells are distributed [into wells] and cDNA is generated with an in-cell reverse transcription (RT) reaction using well-specific barcoded primers. . . . After this step, cells from all wells are pooled and redistributed into [new wells], where an in-cell ligation

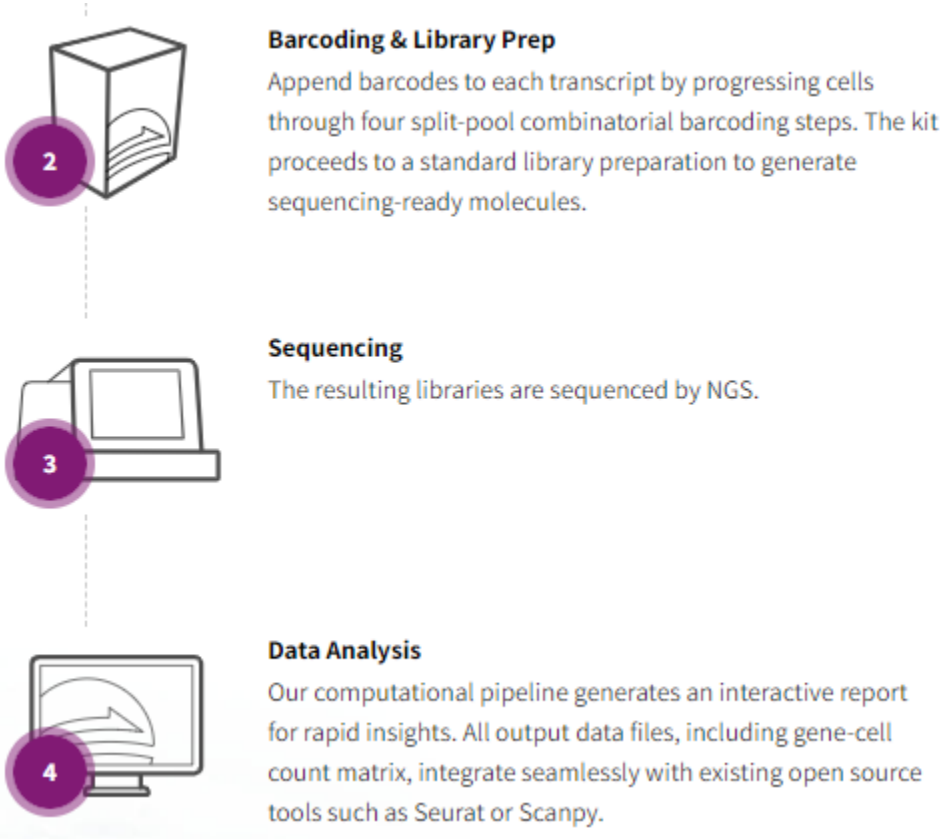
reaction appends a second well-specific barcode to the cDNA. The third-round barcode, which also contains a unique molecular identifier (UMI), is then appended with another round of pooling, splitting, and ligation. After three rounds of barcoding, the cells are pooled and split into sublibraries, and sequencing barcodes are introduced by polymerase chain reaction (PCR). This final step provides a fourth barcode, while also making it possible to sequence different numbers of cells in each sublibrary." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

89. **(c): "Sequencing the tagged polynucleotide to determine the sample sequence, the first tag sequence, and the second tag sequence."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "sequenc[e] the tagged polynucleotide to determine the sample sequence, the first tag sequence, and the second tag sequence." For example, Parse states that after preparation of the barcoded library using Parse's Evercode WT Products, "[t]he resulting libraries are sequenced by NGS," including by using an Illumina sequencer. Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited

Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; *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 (Apr. 13, 2018). In addition, Parse states that its barcoded libraries are "sequenced on MiSeq and NextSeq systems (Illumina)," such that "Read 1 cover[s] the transcript sequences"; "Read 2 cover[s] the UMI [unique molecular identifier] and UBC [uniquely barcoded cells] barcode combinations"; and the "index read, serving as the fourth barcode, cover[s] the sublibrary indices introduced after tagmentation." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods at 5–6 (Apr. 13, 2018); *see also* Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

90. **(d): "Using the first tag sequence and the second tag sequence to count a number of sample polynucleotides in said plurality of sample polynucleotides of said cell."** On information and belief, in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Evercode WT Products are and will be used by Parse and its customers to "us[e] the first tag sequence and the second tag sequence to count a number of sample polynucleotides in said plurality of sample polynucleotides of said cell." For example, Parse states that "[a]fter sequencing, each transcriptome is assembled by combining reads containing the same four-barcode combination"; and that "the sensitivity of SPLiT-seq" in terms of "gene and UMI detection" is "comparable to droplet-based scRNA-seq methods." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods 5–6 &

Fig. S3 (Apr. 13, 2018). In addition, Parse states that its barcoded libraries are "sequenced on MiSeq and NextSeq systems (Illumina)," such that "Read 1 cover[s] the transcript sequences"; "Read 2 cover[s] the UMI [unique molecular identifier] and UBC [uniquely barcoded cells] barcode combinations"; and the "index read, serving as the fourth barcode, cover[s] the sublibrary indices introduced after tagmentation." Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials at Experimental Methods at 5–6 (Apr. 13, 2018); *see also* Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16. Thus, Parse states that its Evercode WT Products are used as follows:



Reading in data

```
# The DGE_filtered folder contains the expression matrix, genes, and
adata = sc.read_mtx(mat_path + 'DGE_1M_PBMC.mtx')

adata.write(obj_save_path + 'adata_obj1.h5ad')
# adata = sc.read(obj_save_path + 'adata_obj1.h5ad')

# reading in gene and cell data
gene_data = pd.read_csv(mat_path + 'all_genes_1M_PBMC.csv')
cell_meta = pd.read_csv(mat_path + 'cell_metadata_1M_PBMC.csv')

# find genes with nan values and filter
gene_data = gene_data[gene_data.gene_name.notnull()]
notNa = gene_data.index
notNa = notNa.to_list()

# remove genes with nan values and assign gene names
adata = adata[:,notNa]
adata.var = gene_data
adata.var.set_index('gene_name', inplace=True)
adata.var.index.name = None
adata.var_names_make_unique()

# add cell meta data to anndata object
adata.obs = cell_meta
adata.obs.set_index('bc_wells', inplace=True)
adata.obs.index.name = None
adata.obs_names_make_unique()

sc.pp.filter_cells(adata, min_counts=100)
sc.pp.filter_genes(adata, min_cells=5)
adata.shape
```

Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How to Analyze a 1 Million Cell Data Set Using Scanpy and Harmony*, https://support.parsebiosciences.com/hc/en-us/articles/7704577188500-How-to-analyze-a-1-million-cell-data-set-using-Scanpy-and-Harmony (last visited Aug. 24, 2022); *see also* Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176 & Suppl. Materials (Apr. 13, 2018), including Experimental Methods at 5–6; Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16.

91. On information and belief, Parse knew of the ’197 Patent at least as of its receipt of the 10x Notice Letter. On information and belief, Parse would have known of the ’197 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x’s patents as part of its research.

92. Alternatively, on information and belief, Parse has acted knowingly or has been willfully blind as to the existence of the ’197 Patent, its own infringement, and the infringement by others. On information and belief, Parse was willfully blind by seeking to copy 10x’s product without investigating 10x’s patents.

93. On information and belief, Parse has no reasonable basis for believing that the '197 Patent is not infringed.

94. Parse induces infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 1 of the '197 Patent in accordance with the Parse Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

95. On information and belief, Parse's Evercode WT Products are not staple articles of commerce and are not suitable for any substantial use that does not infringe at least Claim 1 of the '197 Patent literally or under the doctrine of equivalents.

96. Parse contributes to the infringement of at least Claim 1 of the '197 Patent under 35 U.S.C. § 271(c), by selling its Evercode WT Products.

97. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 1 of the '197 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against further infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products prior to the expiration of the '197 Patent. 10x does not have an adequate remedy at law.

98. The manufacture, use, offer for sale, sale, and/or importation into the United States of the Evercode WT Products before the expiration of the '197 Patent caused, causes, and will cause injury to 10x entitling 10x to damages under 35 U.S.C. § 284.

FOURTH CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,150,995)

99. 10x incorporates and realleges paragraphs 1 to 98 above as if fully set forth herein.

100. Pursuant to license agreements with Stanford University, 10x obtained an exclusive license to the ’995 Patent.

101. Parse’s manufacture and use of the Parse Single-Cell ATAC-Seq Product directly infringes at least Claim 1 of the ’995 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

102. Parse’s manufacture, use, offer for sale, sale, and/or importation into the United States of the Parse Single-Cell ATAC-Seq Product will directly infringe at least Claim 1 of the ’995 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

103. Parse’s manufacture, use, offer for sale, sale, and/or importation into the United States of the Parse Single-Cell ATAC-Seq Product will indirectly infringe at least Claim 1 of the ’995 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse’s customers.

104. Claim 1 of the ’995 Patent recites:

A method for analyzing a biological sample, comprising:

(a) contacting chromatin of a genome region of said biological sample with an insertional enzyme complex to produce tagged nucleic acid molecules, wherein said insertional enzyme complex does not comprise an antibody specific to a protein that is part of said chromatin; and

(b) performing a nucleic acid assay on said tagged nucleic acid molecules or derivatives thereof, to provide sequence information of said tagged nucleic acid molecules or derivatives thereof.

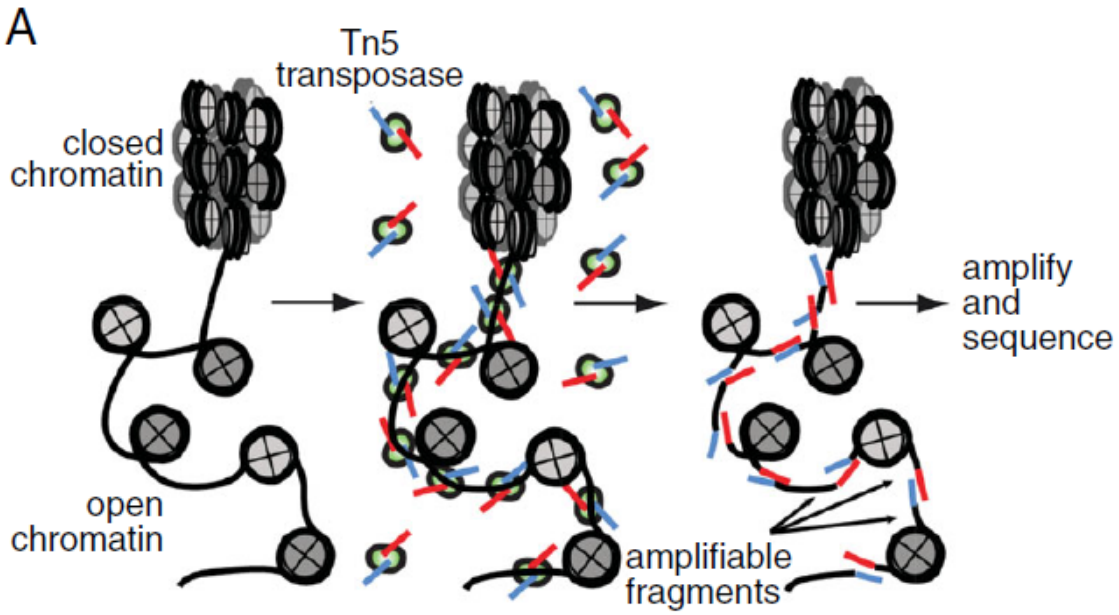
105. On information and belief, Parse’s use of the Parse Single-Cell ATAC-Seq Product satisfies each limitation of at least Claim 1 of the ’995 Patent.

106. On information and belief, when Parse's customers use the Parse Single-Cell ATAC-Seq Product in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, such use will satisfy each limitation of at least Claim 1 of the '995 Patent.

107. **Preamble: "Method for analyzing a biological sample."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers for "method[s] for analyzing a biological sample." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods to assay for transposase-accessible chromatin in a biological sample by sequencing. *See, e.g.*, Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

108. (**a): "Contacting chromatin of a genome region of said biological sample with an insertional enzyme complex to produce tagged nucleic acid molecules, wherein said insertional enzyme complex does not comprise an antibody specific to a protein that is part of said chromatin."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its

customers for "contacting chromatin of a genome region of said biological sample with an insertional enzyme complex to produce tagged nucleic acid molecules, wherein said insertional enzyme complex does not comprise an antibody specific to a protein that is part of said chromatin." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which require using an insertional enzyme complex to tag and fragment (i.e., tagment) the open chromatin of the genomic regions in the nucleus of the sample cells without any antibody specific to a protein that is part of said chromatin, such as an antibody that binds to a specific transcription factor.

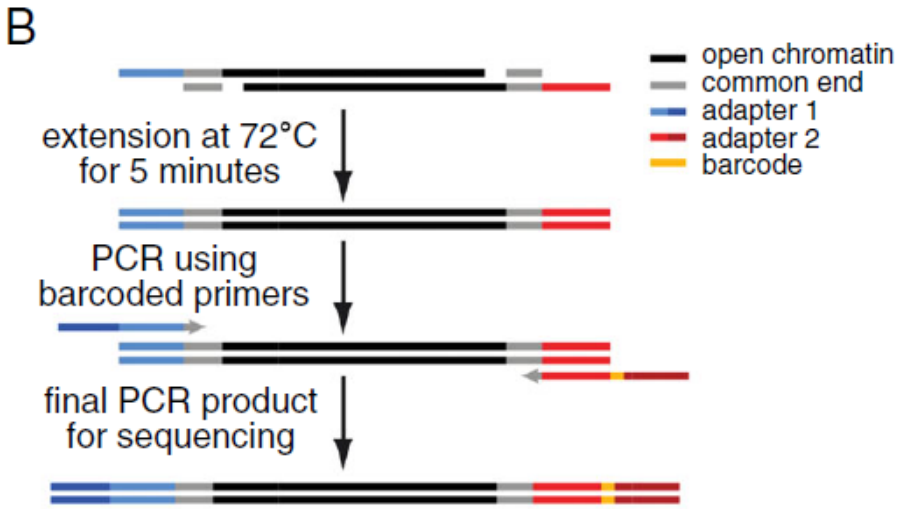


ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: An insertional enzyme complex, such as Tn5 transposase (green) loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates a library of fragments that can be PCR amplified and sequenced.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal*

Epigenomics, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

109. **(b): "Performing a nucleic acid assay on said tagged nucleic acid molecules or derivatives thereof, to provide sequence information of said tagged nucleic acid molecules or derivatives thereof."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers for "performing a nucleic acid assay on said tagged nucleic acid molecules or derivatives thereof, to provide sequence information of said tagged nucleic acid molecules or derivatives thereof." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which require sequencing the library of tagged fragments from open chromatin.



ATAC-seq is a probe of open chromatin state. (B) The generated library of fragments can be PCR amplified and sequenced. During PCR amplification, additional sequences are incorporated into the adaptors, which include common sequencing ends and a sequencing barcode.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022). On information and belief, the Parse Single-Cell ATAC-Seq Product will be an add-on to the Evercode WT Products, which, together or separately, can be used to incorporate common sequencing ends and sequencing barcodes to the generated library of tagged fragments from open chromatin, which then can be "sequenced by NGS," including by using an Illumina sequencer. *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022) https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach#.YuvXJbfMKUk; *see also* Parse Biosciences, Evercode Whole Transcriptome

Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How Do I Process My Data?*, https://support.parsebiosciences.com/hc/en-us/articles/360052845451-How-do-I-process-my-data- (last visited Aug. 24, 2022); Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 176 (Apr. 13, 2018).

110. On information and belief, Parse knew of the ’995 Patent at least as of its receipt of the 10x Notice Letter. On information and belief, Parse would have known of the ’995 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x’s patents as part of its research.

111. Alternatively, on information and belief, Parse acts knowingly or and is willfully blind as to the existence of the ’995 Patent, its own infringement, and the infringement by others. On information and belief, Parse was willfully blind by seeking to copy 10x’s product without investigating 10x’s patents.

112. On information and belief, Parse has no reasonable basis for believing that the ’995 Patent is not infringed.

113. Parse will induce infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 1 of the '995 Patent in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

114. On information and belief, Parse's Single-Cell ATAC-Seq Product will not be a staple article of commerce and will not be suitable for any substantial use that will not infringe at least Claim 1 of the '995 Patent literally or under the doctrine of equivalents.

115. Parse will contribute to the infringement of at least Claim 1 of the '995 Patent under 35 U.S.C. § 271(c), by selling its Single-Cell ATAC-Seq Kit.

116. 10x is entitled to judgment that Parse infringes at least Claim 1 of the '995 Patent by its manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '995 Patent.

117. 10x is entitled to declaratory judgment that Parse will infringe at least Claim 1 of the '995 Patent by its manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '995 Patent.

118. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 1 of the '995 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against any infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell

ATAC-Seq Product prior to the expiration of the '995 Patent. 10x would have no adequate remedy at law.

FIFTH CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,619,207)

119. 10x incorporates and realleges paragraphs 1 to 118 above as if fully set forth herein.

120. Pursuant to license agreements with Stanford University, 10x obtained an exclusive license to the '207 Patent.

121. Parse's manufacture and use of the Parse Single-Cell ATAC-Seq Product directly infringes at least Claim 1 of the '207 Patent, literally or equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

122. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Single-Cell ATAC-Seq Product will directly infringe at least Claim 1 of the '207 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

123. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Single-Cell ATAC-Seq Product will indirectly infringe at least Claim 1 of the '207 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse's customers.

124. Claim 1 of the '207 Patent recites:

A method for generating a sequencing library from a plurality of cells, comprising:

a) lysing a plurality of cells to provide a plurality of cell nuclei, wherein the plurality of cell nuclei comprises chromatin;

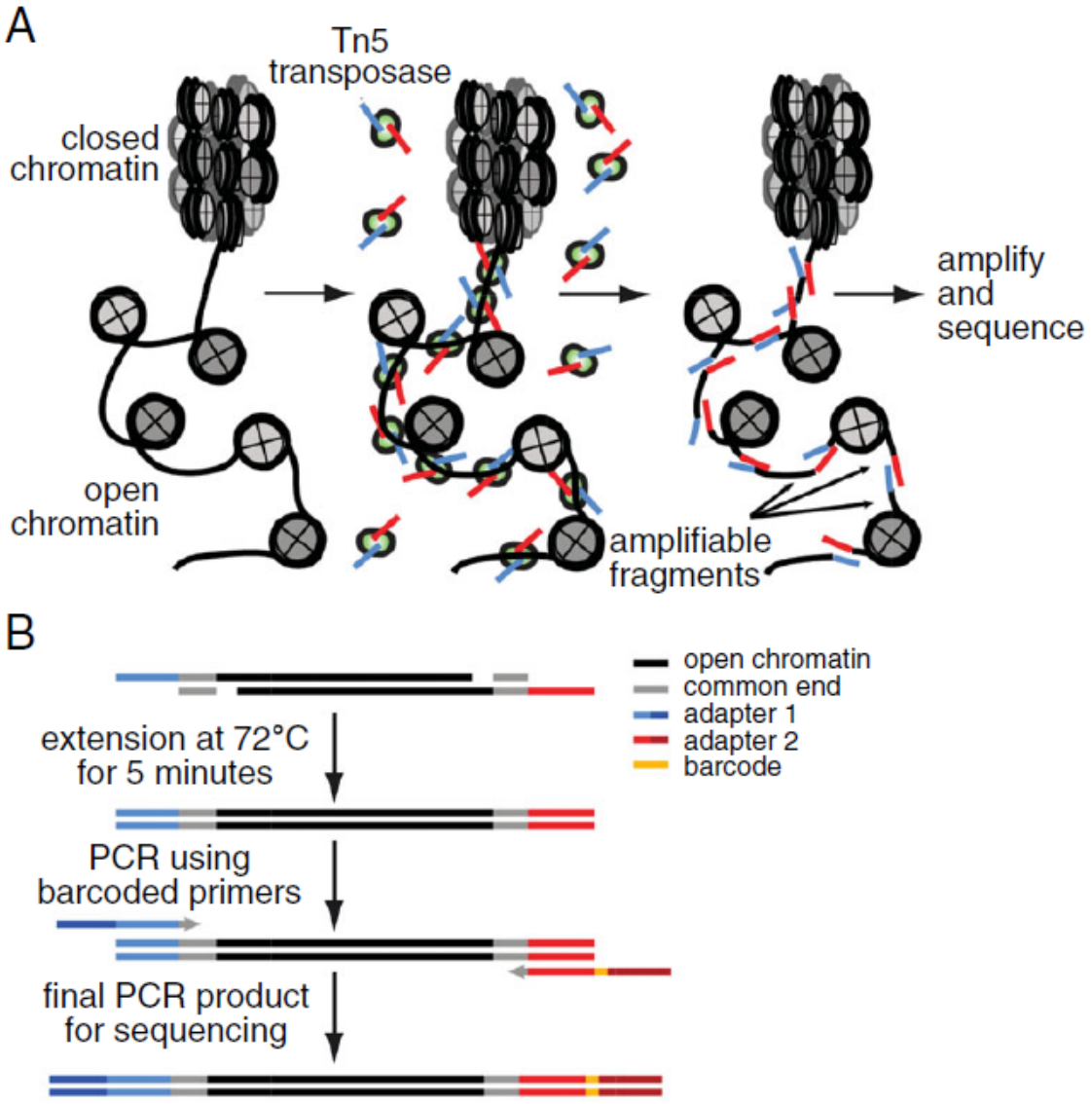
b) contacting a cell nucleus of the plurality of cell nuclei with a transposase complex such that polynucleotides of the cell nucleus are tagmented at regions of open chromatin to produce a plurality of tagged fragments; and

c) performing one or more nucleic acid reactions on the tagged fragment to produce a sequencing library.

125. On information and belief, Parse's use of Single-Cell ATAC-Seq Product satisfies each limitation of at least Claim 1 of the '207 Patent.

126. On information and belief, when Parse's customers use the Single-Cell ATAC-Seq Product in accordance with Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, such use will satisfy each limitation of at least Claim 1 of the '207 Patent.

127. **Preamble: "Method for generating a sequencing library from a plurality of cells."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product has been, are, or will be used by Parse and will be used by its customers for "method for generating a sequencing library from a plurality of cells." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods to generate a sequencing library of open chromatin from sample cells by assaying for transposase-accessible chromatin by sequencing. *See, e.g.*, Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).



ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: Transposase (green), loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates sequence library fragments that can be PCR amplified. (B) During PCR amplification, additional sequences are incorporated into the adaptors, which include common sequencing ends and a sequencing barcode.

Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf,

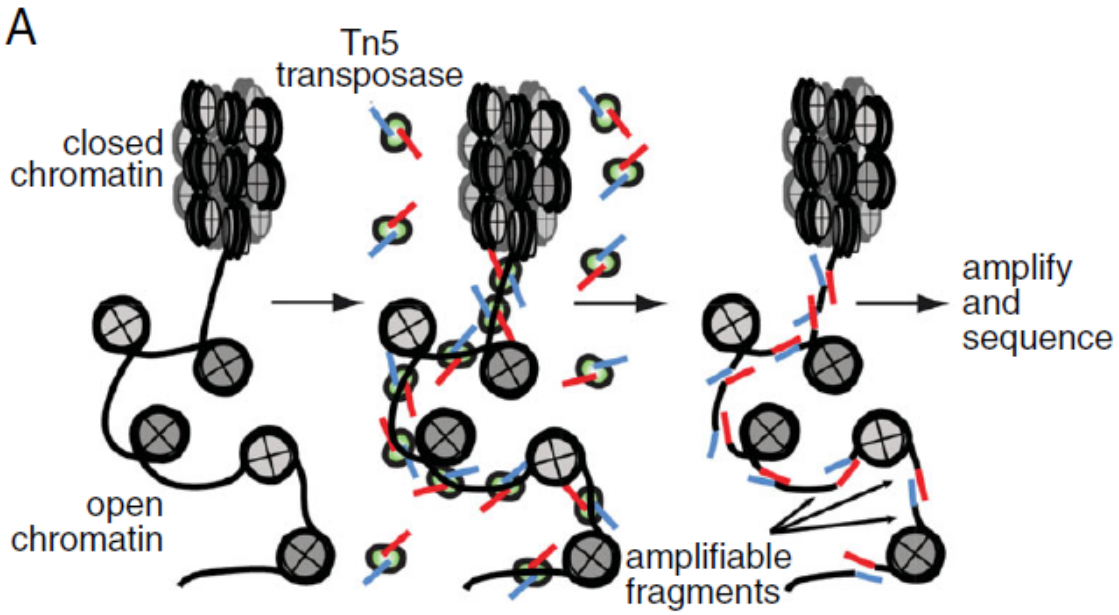
Chromatin accessibility and the regulatory epigenome, 20 Nature Reviews 207, 208–210 (Apr. 2019). On information and belief, the Parse Single-Cell ATAC-Seq Product is an add-on to the Evercode WT Products, which, together or separately, can be used to incorporate common sequencing ends and sequencing barcodes to the generated library of tagged fragments from open chromatin, which then can be "sequenced by NGS," including by using an Illumina sequencer. *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022) https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach#.YuvXJbfMKUk; *see also* Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How Do I Process My Data?*, https://support.parsebiosciences.com/hc/en-us/articles/360052845451-How-do-I-process-my-data- (last visited Aug. 24, 2022); Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 176 (Apr. 13, 2018).

128. **(a): "Lysing a plurality of cells to provide a plurality of cell nuclei, wherein the plurality of cell nuclei comprises chromatin."** On information and belief, in accordance with

the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers for "lysing a plurality of cells to provide a plurality of cell nuclei, wherein the plurality of cell nuclei comprises chromatin." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which require accessing the chromatin-containing nuclei of sample cells by lysing the sample cells. *See, e.g.*, Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

129. **(b): "Contacting a cell nucleus of the plurality of cell nuclei with a transposase complex such that polynucleotides of the cell nucleus are tagmented at regions of open chromatin to produce a plurality of tagged fragments."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers for "contacting a cell nucleus of the plurality of cell nuclei with a transposase complex such that polynucleotides of the cell nucleus are tagmented at regions of open chromatin to produce a plurality of tagged fragments." For example, Parse's Single-Cell ATAC-Seq Product is and will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which use a transposase complex to tag and fragment (i.e.,

tagment) the open chromatin of the genomic regions in the nucleus of the sample cells to produce a library of tagged fragments from open chromatin.

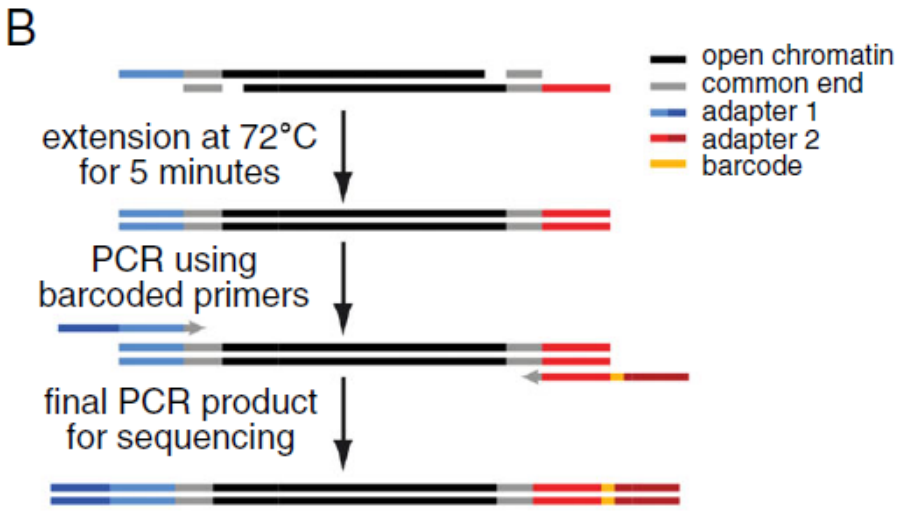


ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: An insertional enzyme complex, such as Tn5 transposase (green) loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates a library of fragments that can be PCR amplified and sequenced.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

130. **(c): "Performing one or more nucleic acid reactions on the tagged fragment to produce a sequencing library."** On information and belief, in accordance with the Parse ATAC-

Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers for "performing one or more nucleic acid reactions on the tagged fragment to produce a sequencing library." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which require sequencing the library of tagged fragments from open chromatin to generate a sequencing library.



ATAC-seq is a probe of open chromatin state. (B) The generated library of fragments can be PCR amplified and sequenced. During PCR amplification, additional sequences are incorporated into the adaptors, which include common sequencing ends and a sequencing barcode.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022). On information and belief, the Parse Single-Cell ATAC-Seq Product is an add-on to the

Evercode WT Products, which, together or separately, can be used to incorporate common sequencing ends and sequencing barcodes to the generated library of tagged fragments from open chromatin, which then can be "sequenced by NGS," including by using an Illumina sequencer. *See* Andrew P. Han, *Parse Biosciences Expands Single-Cell Product Line, Global Reach* (Apr. 14, 2022) https://www.genomeweb.com/sequencing/parse-biosciences-expands-single-cell-product-line-global-reach#.YuvXJbfMKUk; *see also* Parse Biosciences, Evercode Whole Transcriptome Mini, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mini (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome, https://www.parsebiosciences.com/products/evercode-whole-transcriptome (last visited Aug. 24, 2022); Parse Biosciences, Evercode Whole Transcriptome Mega, https://www.parsebiosciences.com/products/evercode-whole-transcriptome-mega (last visited Aug. 24, 2022); Parse Biosciences, *How Do I Process My Data?*, https://support.parsebiosciences.com/hc/en-us/articles/360052845451-How-do-I-process-my-data- (last visited Aug. 24, 2022); Parse Biosciences, Technology, https://www.parsebiosciences.com/technology (last visited Aug. 24, 2022); Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 11:16; Rosenberg et al., *Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding*, 360 Science 176, 176 (Apr. 13, 2018).

131. On information and belief, Parse knew of the '207 Patent at least as of its receipt of the 10x Notice Letter. On information and belief, Parse would have known of the '207 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x's patents as part of its research.

132. Alternatively, on information and belief, Parse acts knowingly and is willfully blind as to the existence of the '207 Patent, its own infringement, and the infringement by others. On information and belief, Parse was willfully blind by seeking to copy 10x's product without investigating 10x's patents.

133. On information and belief, Parse has no reasonable basis for believing that the '207 Patent is not infringed.

134. Parse will induce infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 1 of the '207 Patent in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

135. On information and belief, Parse's Single-Cell ATAC-Seq Product will not be a staple article of commerce and will not be suitable for any substantial use that will not infringe at least Claim 1 of the '207 Patent literally or under the doctrine of equivalents.

136. Parse will contribute to the infringement of at least Claim 1 of the '207 Patent under 35 U.S.C. § 271(c), by selling its Single-Cell ATAC-Seq Kit.

137. 10x is entitled to a judgment that Parse infringes at least Claim 1 of the '207 Patent by its manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '207 Patent.

138. 10x is entitled to a declaratory judgment that Parse will infringe at least Claim 1 of the '207 Patent by its manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '207 Patent.

139. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 1 of the '207 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against any infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '207 Patent. 10x would have no adequate remedy at law.

SIXTH CAUSE OF ACTION
(INFRINGEMENT OF U.S. PATENT NO. 10,738,357)

140. 10x incorporates and realleges paragraphs 1 to 139 above as if fully set forth herein.

141. Pursuant to license agreements with Stanford University, 10x obtained an exclusive license to the '357 Patent.

142. Parse's manufacture and use of the Parse Single-Cell ATAC-Seq Product directly infringes at least Claim 1 of the '357 Patent, literally or equivalents, under 35 U.S.C. §§ 271(a), (f), (g).

143. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Single-Cell ATAC-Seq Product will directly infringe at least Claim 16 of the '357 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(a), (f).

144. Parse's manufacture, use, offer for sale, sale, and/or importation into the United States of its Single-Cell ATAC-Seq Product will indirectly infringe at least Claim 16 of the '357 Patent, literally or by equivalents, under 35 U.S.C. §§ 271(b), (c) based on an underlying act of direct infringement by Parse's customers.

145. Claim 16 of the ’357 Patent recites:

A composition comprising:

a permeabilized cell nucleus comprising:

(a) an insertional enzyme complex comprising a transposase enzyme; and

(b) a plurality of tagged nucleic acid fragments, wherein each tagged nucleic acid fragment comprises a first sequencing adapter and a second sequencing adapter;

wherein each tagged nucleic acid fragment is derived from a region of open chromatin.

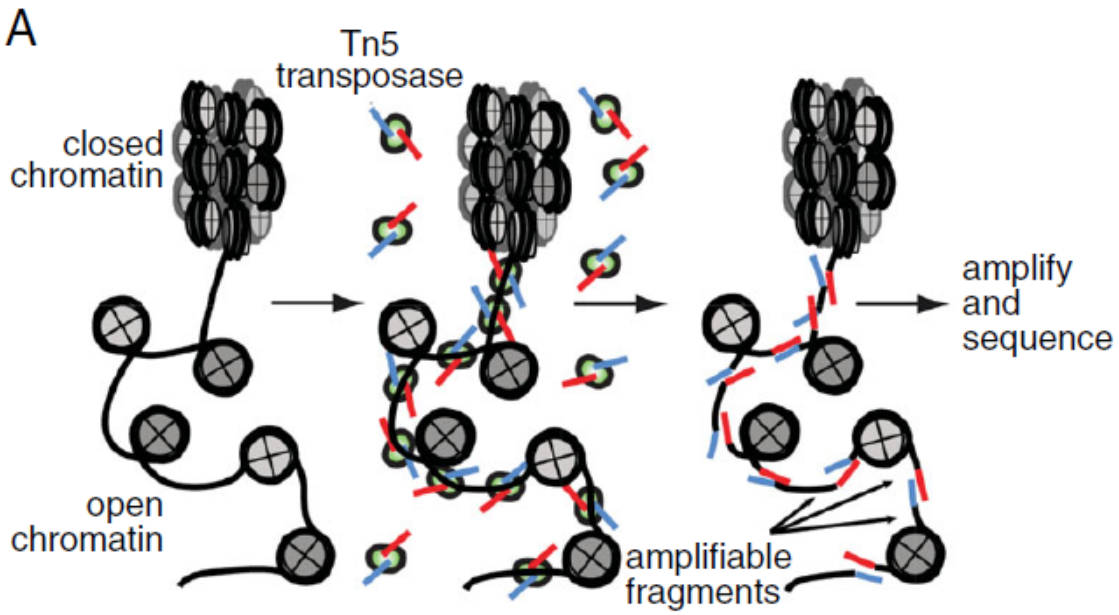
146. On information and belief, Parse’s use of Single-Cell ATAC-Seq Product satisfies each limitation of at least Claim 16 of the ’357 Patent.

147. On information and belief, when Parse’s customers use the Single-Cell ATAC-Seq Product in accordance with Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, such use will satisfy each limitation of at least Claim 16 of the ’357 Patent.

148. **(Preamble): “Composition comprising a permeabilized cell nucleus.”** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse’s Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers to create “a composition comprising a permeablized cell nucleus.” For example, Parse’s Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which require generating a permeabilized cell nucleus in order to assay the open chromatin in the nucleus of the sample cells. *See, e.g.*, Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal*

Regulatory Analysis and Personal Epigenomics, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

149. **(a): "An insertional enzyme complex comprising a transposase enzyme."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers to create a permeablized cell nucleus composition with "an insertional enzyme complex comprising a transposase enzyme." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which use a transposase enzyme linked to sequence adaptors as an insertional enzyme complex.

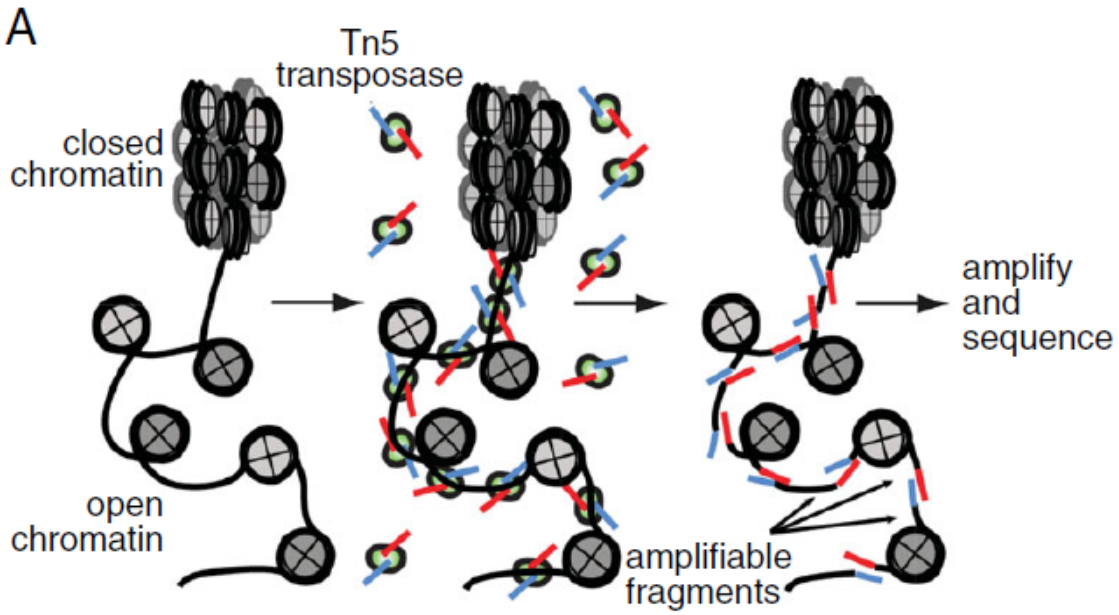


ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: An insertional enzyme complex, such as Tn5 transposase (green) loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates a library of fragments that can be PCR amplified and sequenced.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al., *Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics*, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

150. **(b): "A plurality of tagged nucleic acid fragments, wherein each tagged nucleic acid fragment comprises a first sequencing adapter and a second sequencing adapter" and "wherein each tagged nucleic acid fragment is derived from a region of open chromatin."** On information and belief, in accordance with the Parse ATAC-Seq Instructional Materials and

Presentations and in a manner consistent with the available literature, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers to create a permeablized cell nucleus composition with "a plurality of tagged nucleic acid fragments, wherein each tagged nucleic acid fragment comprises a first sequencing adapter and a second sequencing adapter." For example, Parse's Single-Cell ATAC-Seq Product is or will be used by Parse and will be used by its customers, as its name states, for ATAC-seq methods, which use a transposase complex with two sequencing adaptors to tag and fragment (i.e., tagment) the open chromatin of the genomic regions in the nucleus of the sample cells to produce a library of tagged fragments with two adaptors, such that each tagged fragment is derived from a region of open chromatin.



ATAC-seq is a probe of open chromatin state. (A) ATAC-seq library preparation schematic: An insertional enzyme complex, such as Tn5 transposase (green) loaded with sequence adaptors (red and blue), inserts only in regions of open chromatin (nucleosomes in gray) and generates a library of fragments that can be PCR amplified and sequenced.

See, e.g., Buenrostro et al., *ATAC-Seq: A Method for Assaying Chromatin Accessibility Genome Wide*, 109 Current Protocols in Molecular Biology 21.29.1, 21.29.2 (Jan. 2015); Buenrostro et al.,

Transposition of Native Chromatin for Multimodal Regulatory Analysis and Personal Epigenomics, 10(12) Nature Methods 1213 (2013); *see also* Klemm, Shipony, & Greenleaf, *Chromatin accessibility and the regulatory epigenome*, 20 Nature Reviews 207, 208–210 (Apr. 2019); Wikipedia, ATAC-seq, https://en.wikipedia.org/wiki/ATAC-seq (last visited Aug. 24, 2022).

151. On information and belief, Parse knew of the '357 Patent at least as of its receipt of the 10x Notice Letter. On information and belief, Parse would have known of the '357 Patent before receiving the 10x Notice Letter because it set out to copy 10x products and would have been aware of 10x's patents as part of its research.

152. Alternatively, on information and belief, Parse acts knowingly and is willfully blind as to the existence of the '357 Patent, its own infringement, and the infringement by others. On information and belief, Parse was willfully blind by seeking to copy 10x's product without investigating 10x's patents.

153. On information and belief, Parse has no reasonable basis for believing that the '357 Patent is not infringed.

154. Parse will induce infringement under 35 U.S.C. § 271(b) no later than the date of the 10x Notice Letter by, without authorization, actively instructing, recommending, encouraging, and/or suggesting its customers practice at least Claim 16 of the '357 Patent in accordance with the Parse ATAC-Seq Instructional Materials and Presentations and in a manner consistent with the available literature. *See, e.g.*, Decode Science, Parse Biosciences Introduces Single Cell 3.0, YouTube (Nov. 17, 2021), https://www.youtube.com/watch?v=GP3zx0-D_Yg at 1:39 (identifying some of Parse's end users, i.e., direct infringers).

155. On information and belief, Parse's Single-Cell ATAC-Seq Product will not be a staple article of commerce and will not be suitable for any substantial use that will not infringe at least Claim 16 of the '357 Patent literally or under the doctrine of equivalents.

156. Parse will contribute to the infringement of at least Claim 16 of the '357 Patent under 35 U.S.C. § 271(c), by selling its Single-Cell ATAC-Seq Kit.

157. 10x is entitled to a judgment, that Parse infringes at least Claim 16 of the '357 Patent by manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '357 Patent.

158. 10x is entitled to a declaratory judgment, that Parse infringes at least Claim 16 of the '357 Patent by manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '357 Patent.

159. 10x will be irreparably harmed if Parse is not enjoined from infringing or actively inducing or contributing to infringement of at least Claim 16 of the '357 Patent. Pursuant to 35 U.S.C. § 283, 10x is entitled to a permanent injunction against any infringement, including the manufacture, use, offer for sale, sale, and/or importation into the United States of the Single-Cell ATAC-Seq Product prior to the expiration of the '357 Patent. 10x would have no adequate remedy at law.

PRAYER FOR RELIEF

WHEREFORE, 10x respectfully requests that the Court enter the following relief in its favor and against Parse:

A. A judgment that Parse infringes at least Claim 1 of the '981 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f), (g).

B. A judgment that Parse infringes at least Claim 1 of the '013 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f), (g).

C. A judgment that Parse infringes at least Claim 1 of the '197 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f), (g).

D. A judgment that Parse infringes at least Claim 1 of the '995 Patent under 35 U.S.C. §§ 271(a), (f), (g).

E. A declaratory judgment that Parse will infringe at least Claim 1 of the '995 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f), (g).

F. A judgment that Parse infringes at least Claim 1 of the '207 Patent under 35 U.S.C. §§ 271(a), (f), (g).

G. A declaratory judgment that Parse will infringe at least Claim 1 of the '207 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f), (g).

H. A judgment that Parse infringes at least Claim 16 of the '357 Patent under 35 U.S.C. §§ 271(a), (f), (g).

I. A declaratory judgment that Parse will infringe at least Claim 16 of the '357 Patent under 35 U.S.C. §§ 271(a), (b), (c), (f).

J. An injunction enjoining the aforesaid acts of infringement by Parse, its officers, agents, servants, employees, attorneys, parent and subsidiary entities, assigns and successors in interest, and those persons acting in concert with them, including related individuals and entities,

customers, representatives, distributors, and dealers. In the alternative, if the Court finds that an injunction is not warranted, 10x requests an award of post-judgment royalty to compensate for future infringement;

K. An award of all monetary relief adequate to compensate for damages resulting from Parse's infringement, including lost profits but in no event less than a reasonable royalty under 35 U.S.C. § 284 for Parse's infringement, including all pre-judgment and post-judgment interest at the maximum rate allowed by law;

L. A judgment awarding 10x such other and further relief as the Court may deem just, reasonable, and proper.

DEMAND FOR JURY TRIAL

10x demands a jury trial on all issues so triable.

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