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(54) **SINGLE CELL SECRETOME ANALYSIS**(71) Applicant: **Becton, Dickinson and Company**, Franklin Lakes, NJ (US)(72) Inventors: **Hye-Won Song**, San Jose, CA (US); **Jody Martin**, San Jose, CA (US)(73) Assignee: **BECTON, DICKINSON AND COMPANY**, Franklin Lakes, NJ (US)

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None

See application file for complete search history.

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Primary Examiner — Brian Gangle*Assistant Examiner* — Andrea K McCollum(74) *Attorney, Agent, or Firm* — Dickinson Wright PLLC(57) **ABSTRACT**

Systems, methods, compositions, and kits for measuring secreted factors from cells are disclosed herein, including those capable of determining single cell secretion activity and protein expression and/or gene expression simultaneously. Disclosed herein include solid supports comprising a plurality of capture probes capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. Also disclosed herein include secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe. A secreted factor-binding reagent can comprise a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

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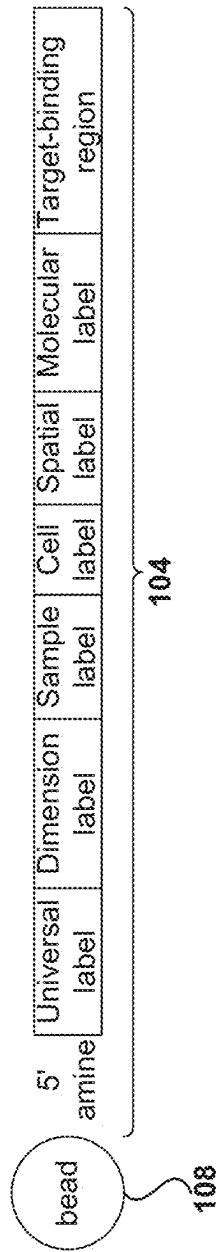


FIG. 1

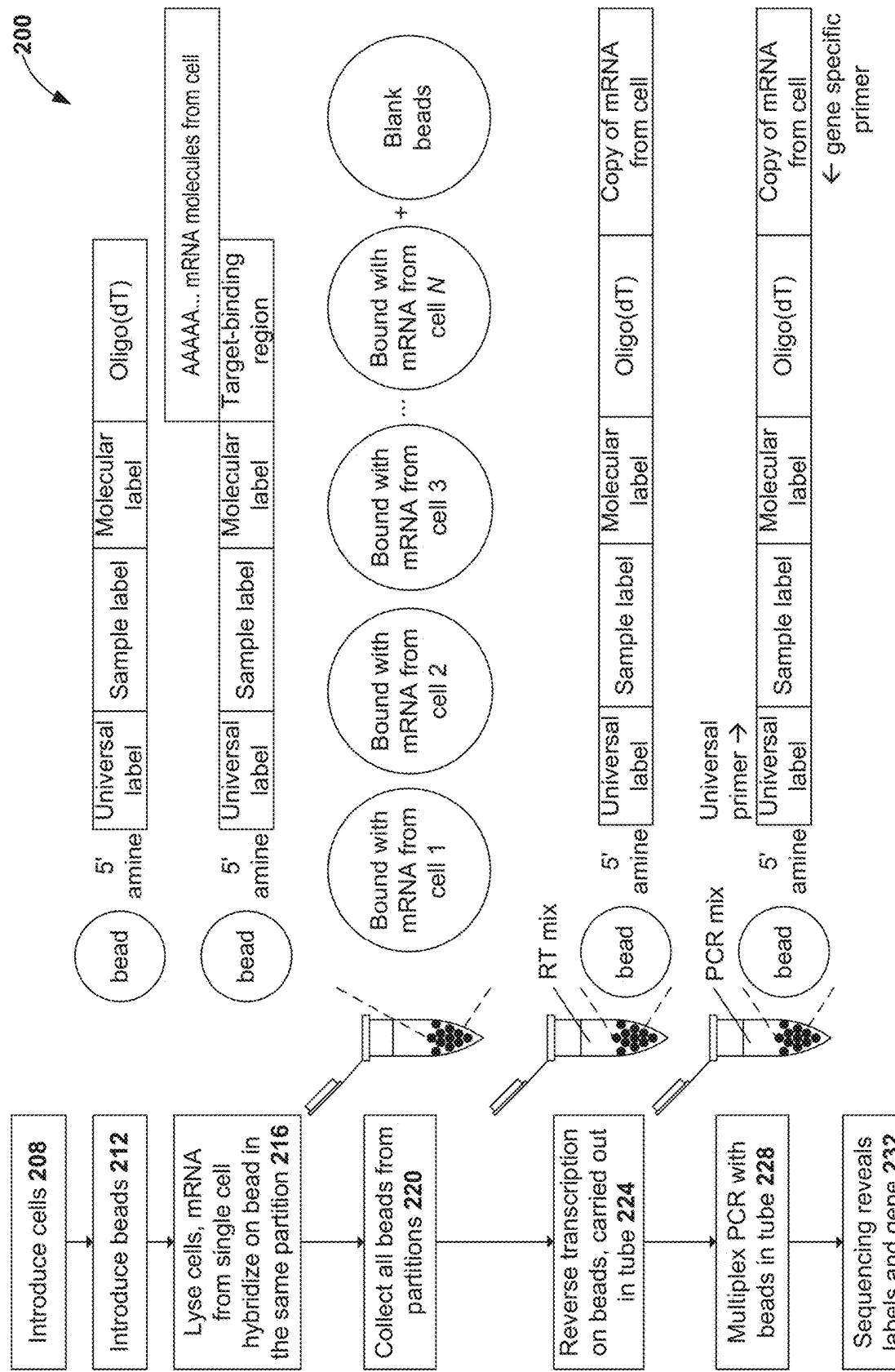
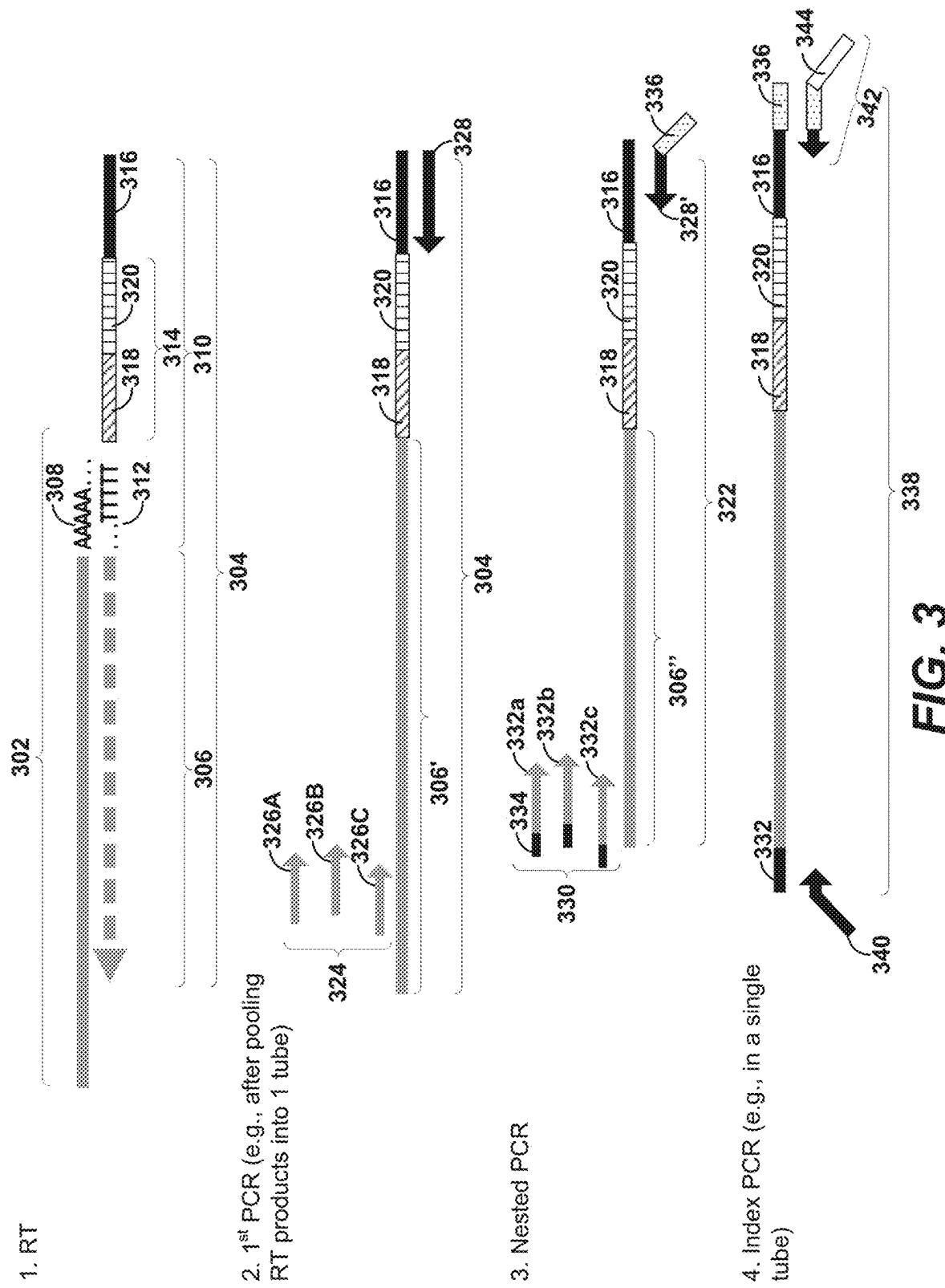


FIG. 2

**FIG. 3**

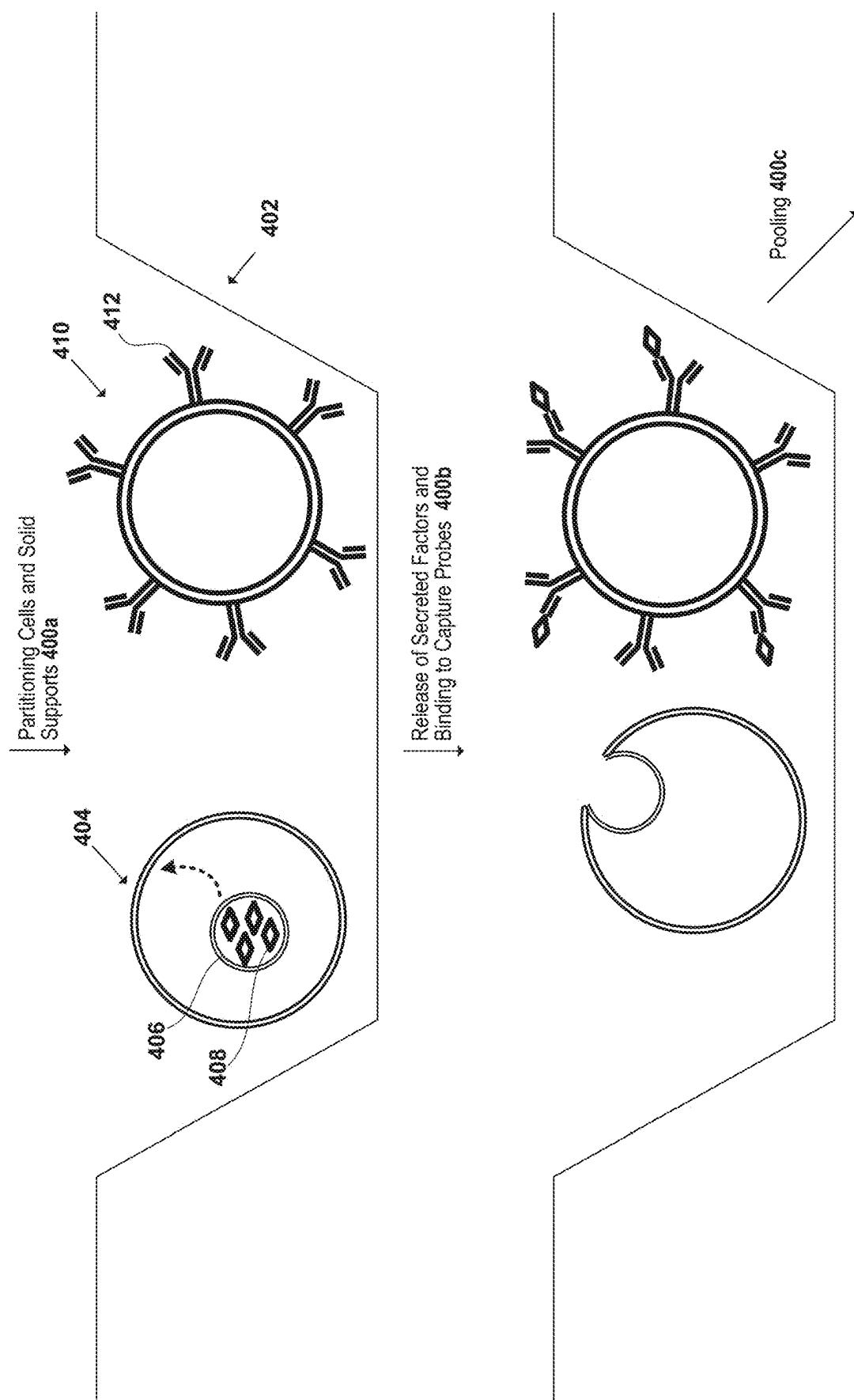
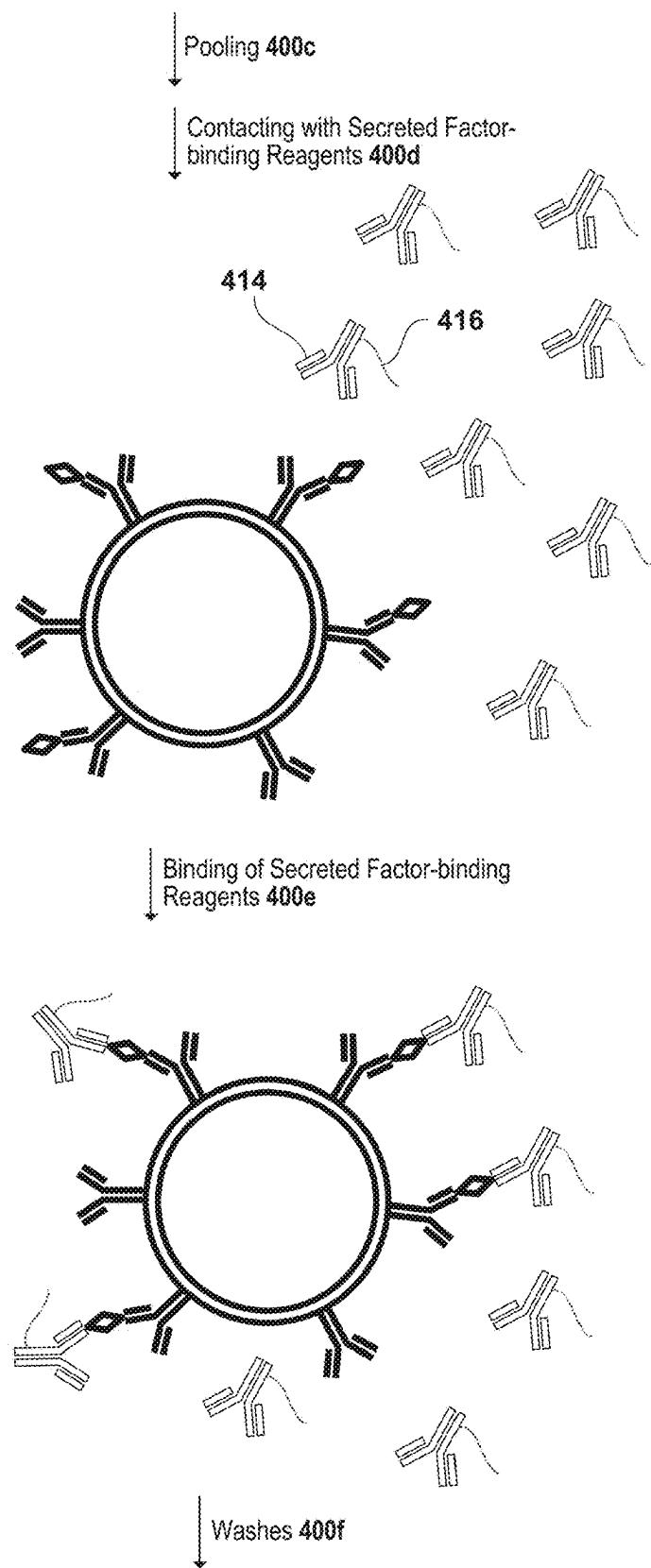
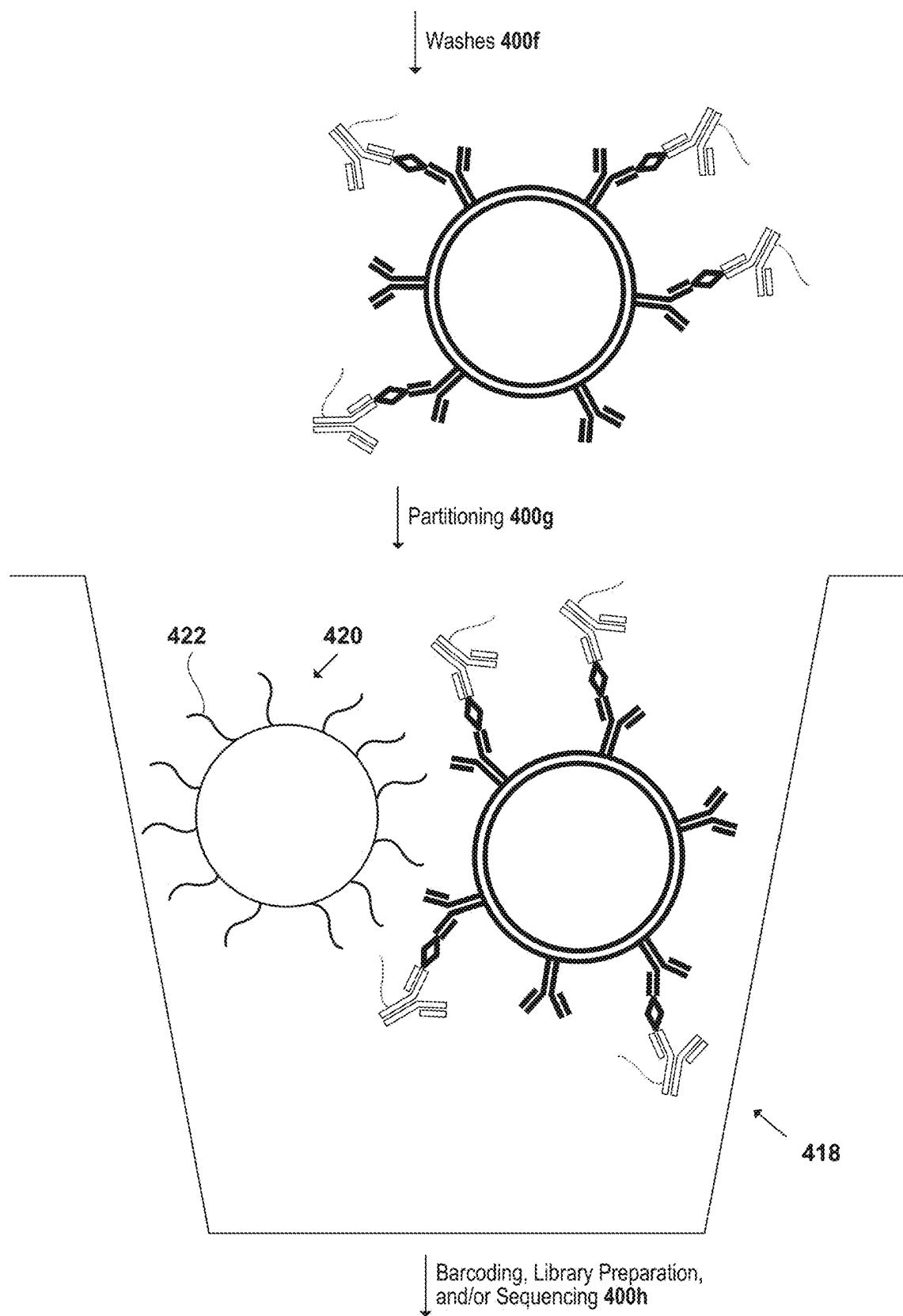
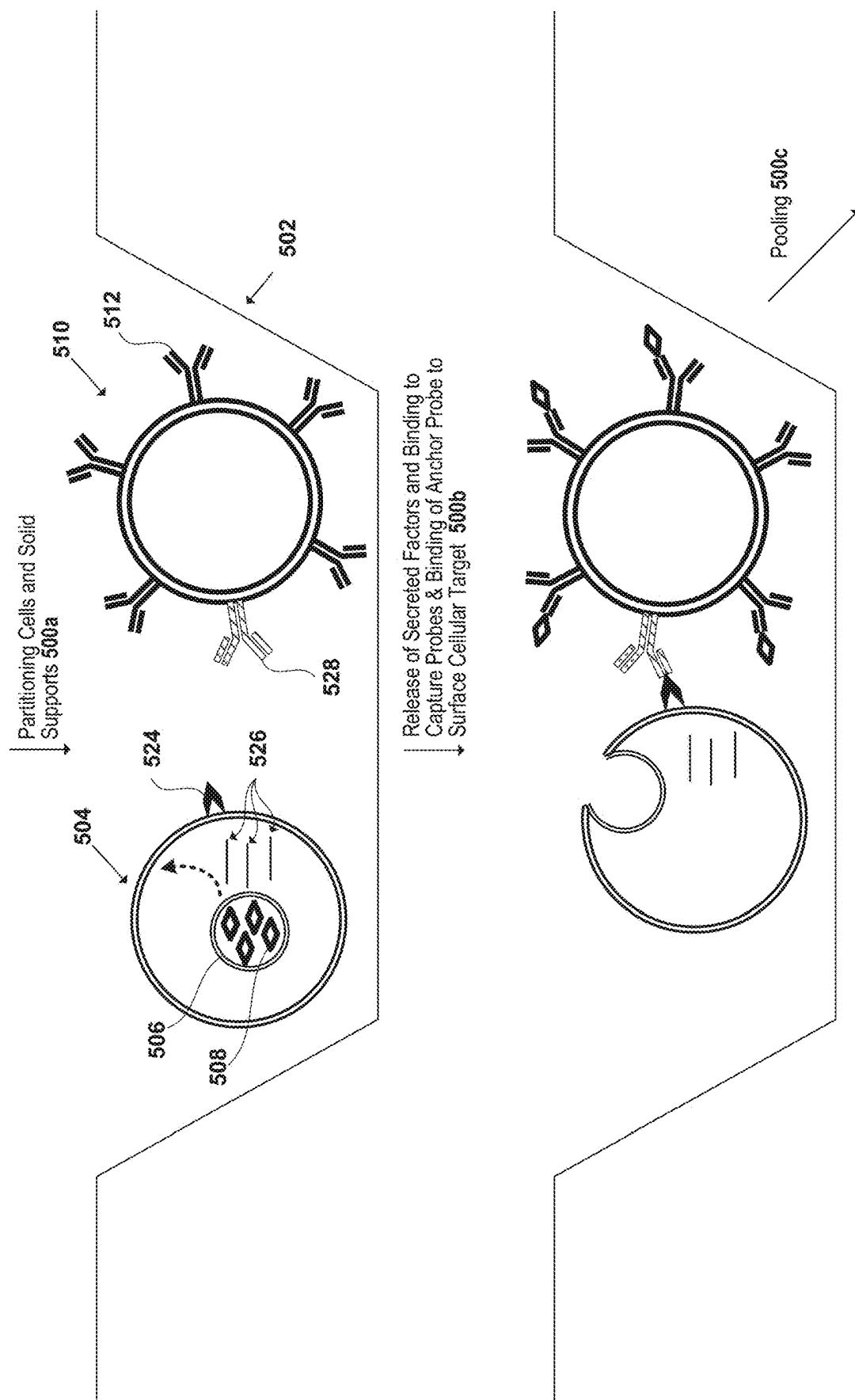
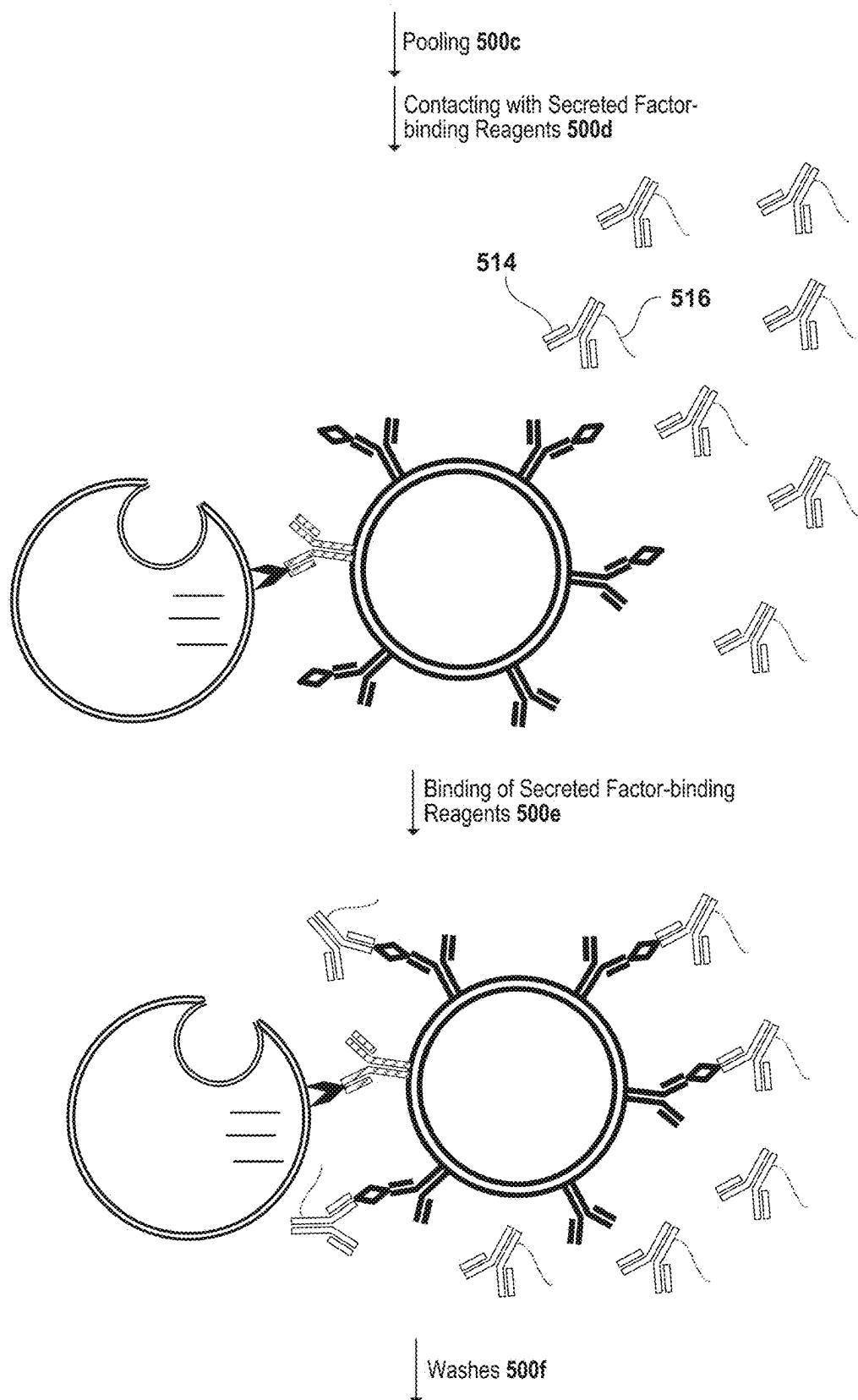


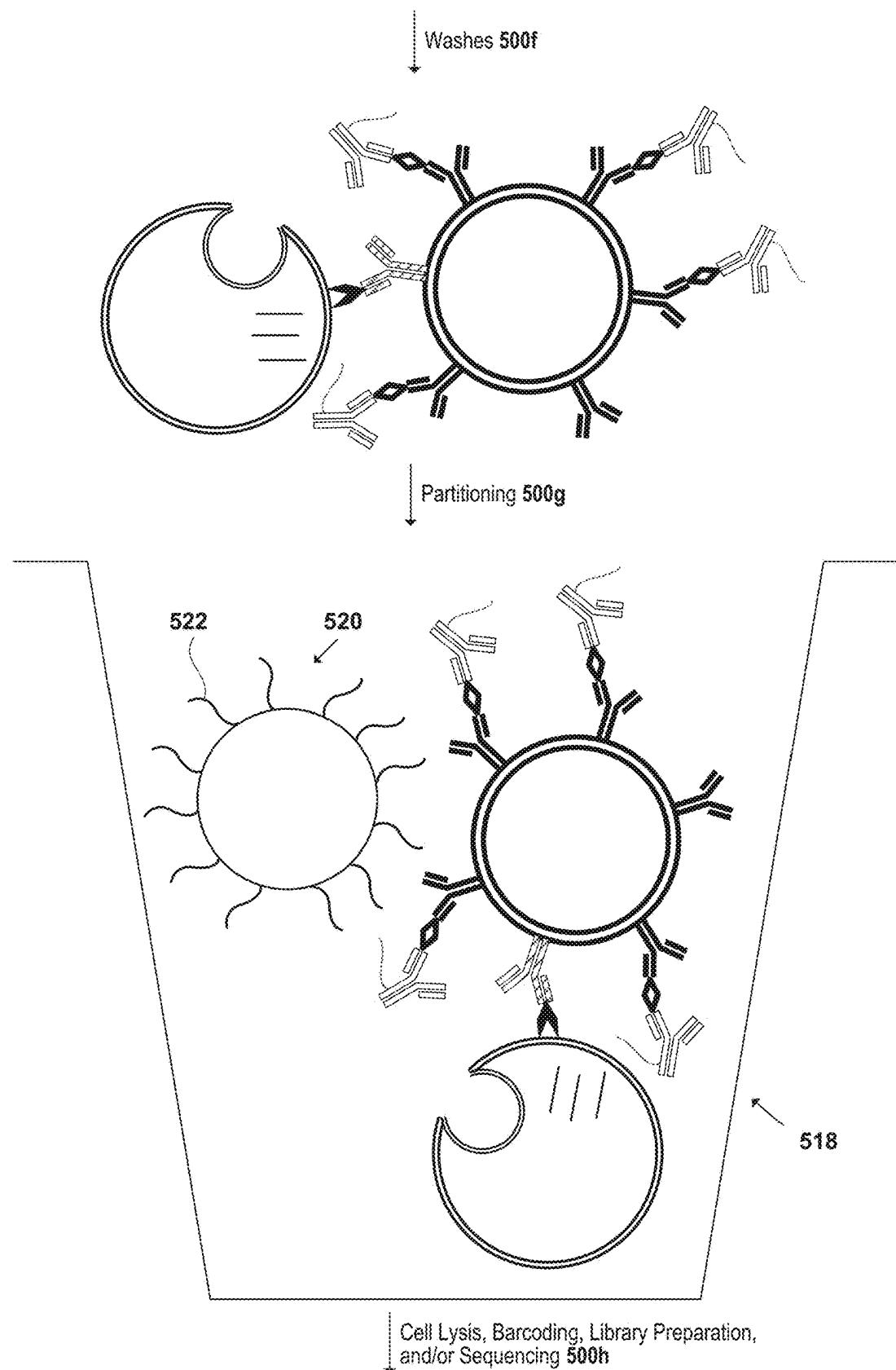
FIG. 4A

**FIG. 4B**

**FIG. 4C**

**FIG. 5A**

**FIG. 5B**

**FIG. 5C**

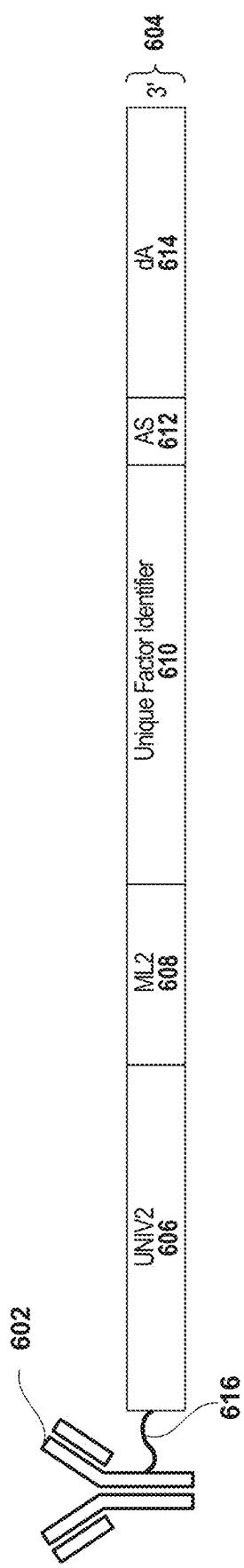


FIG. 6

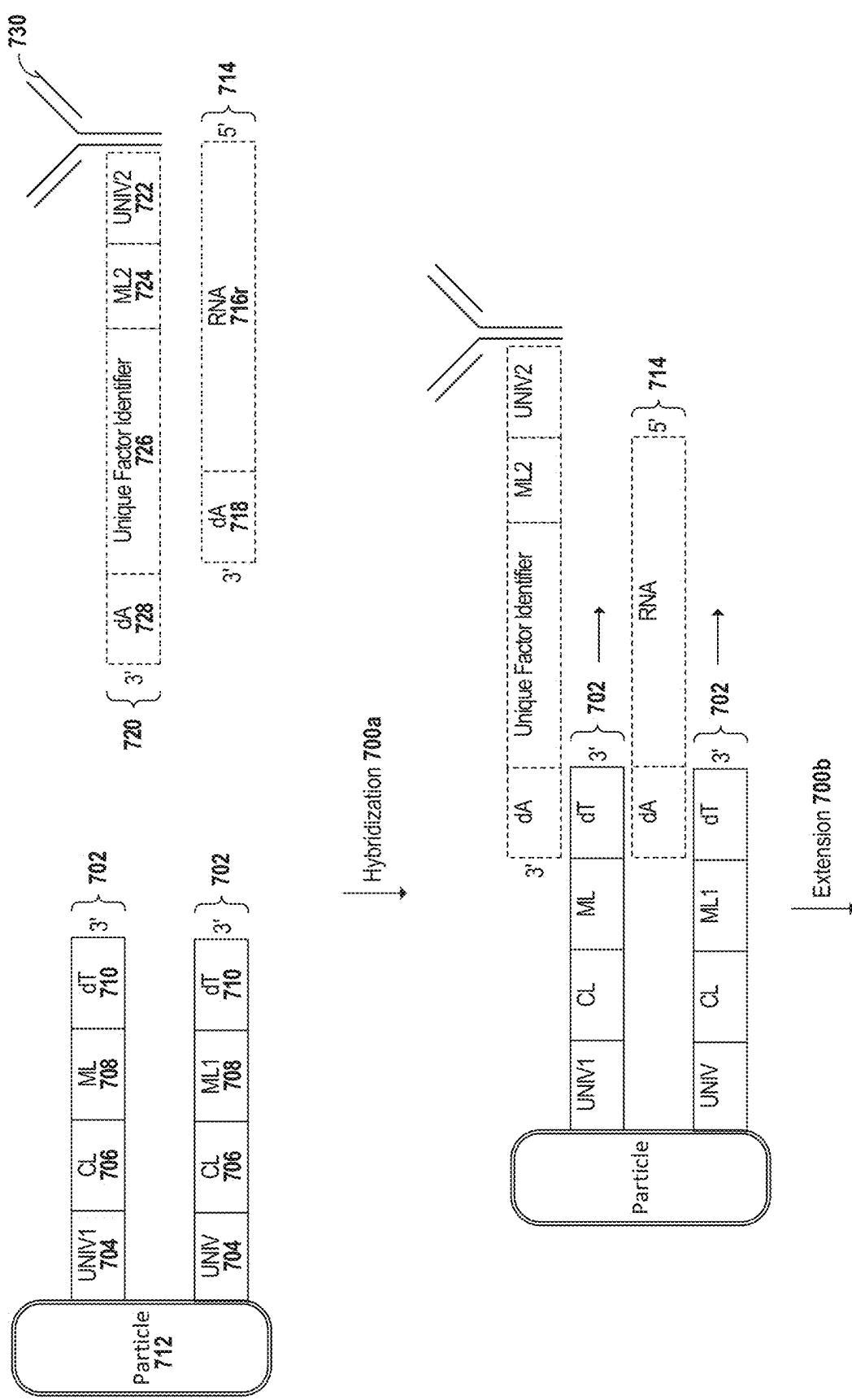


FIG. 7A

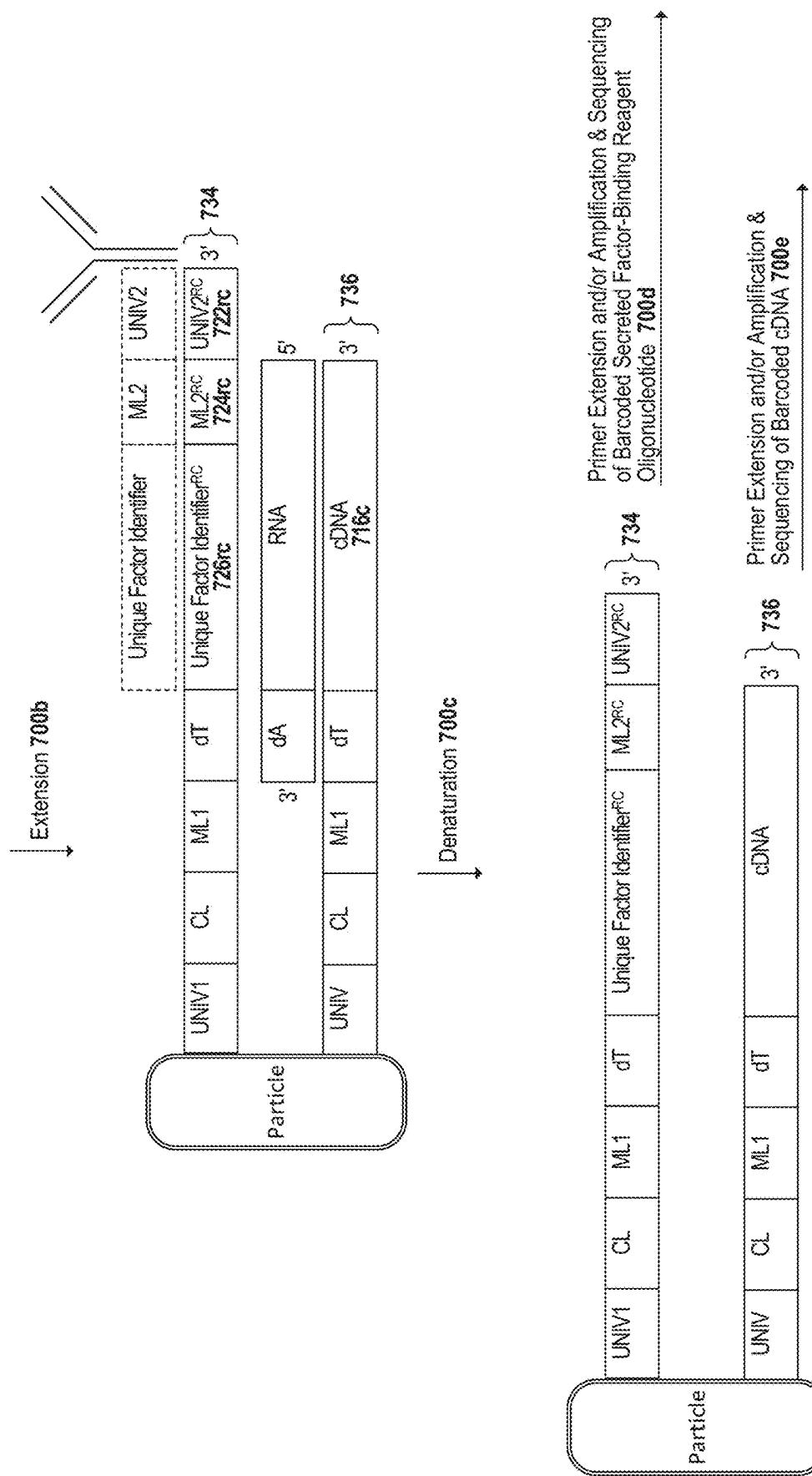


FIG. 7B

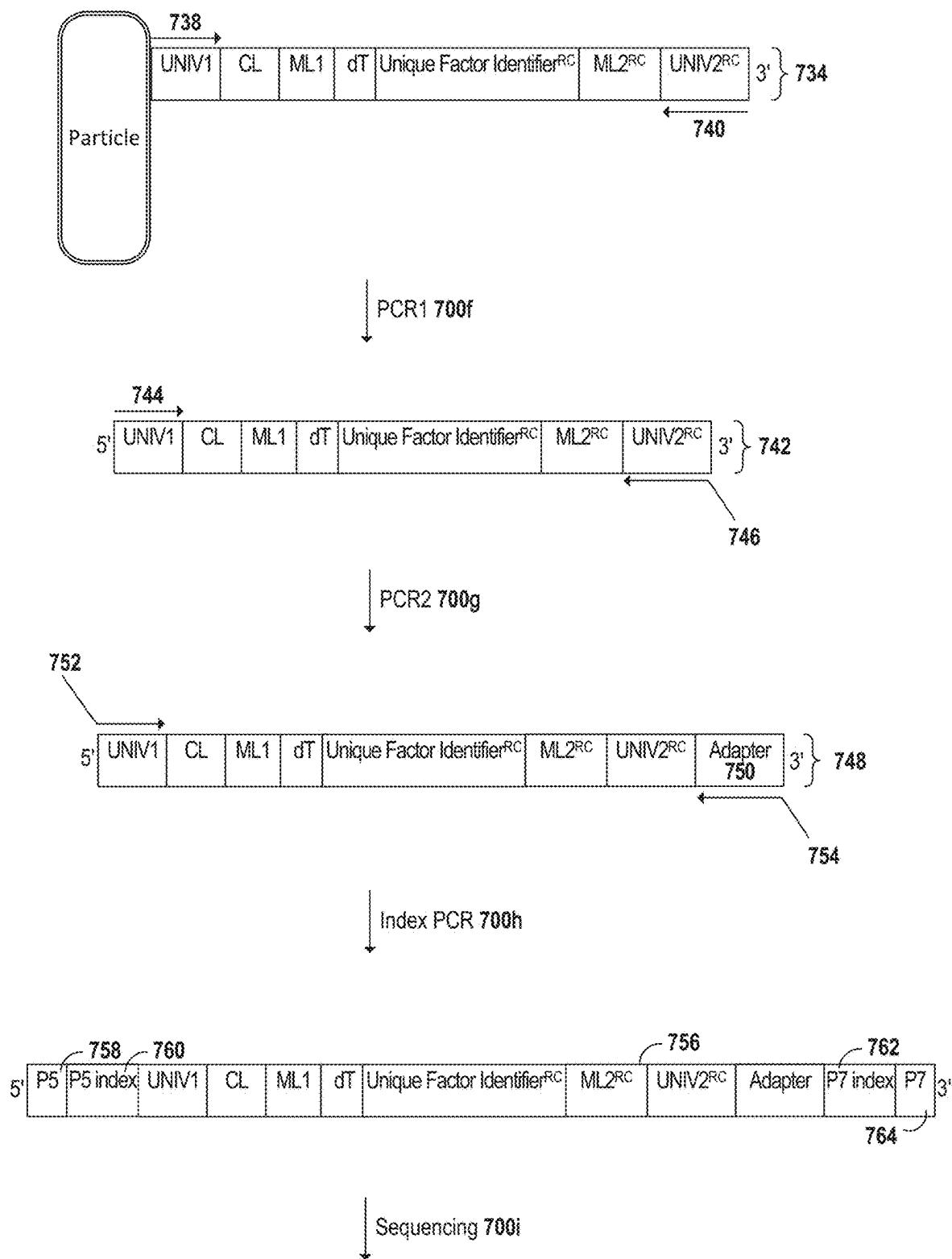
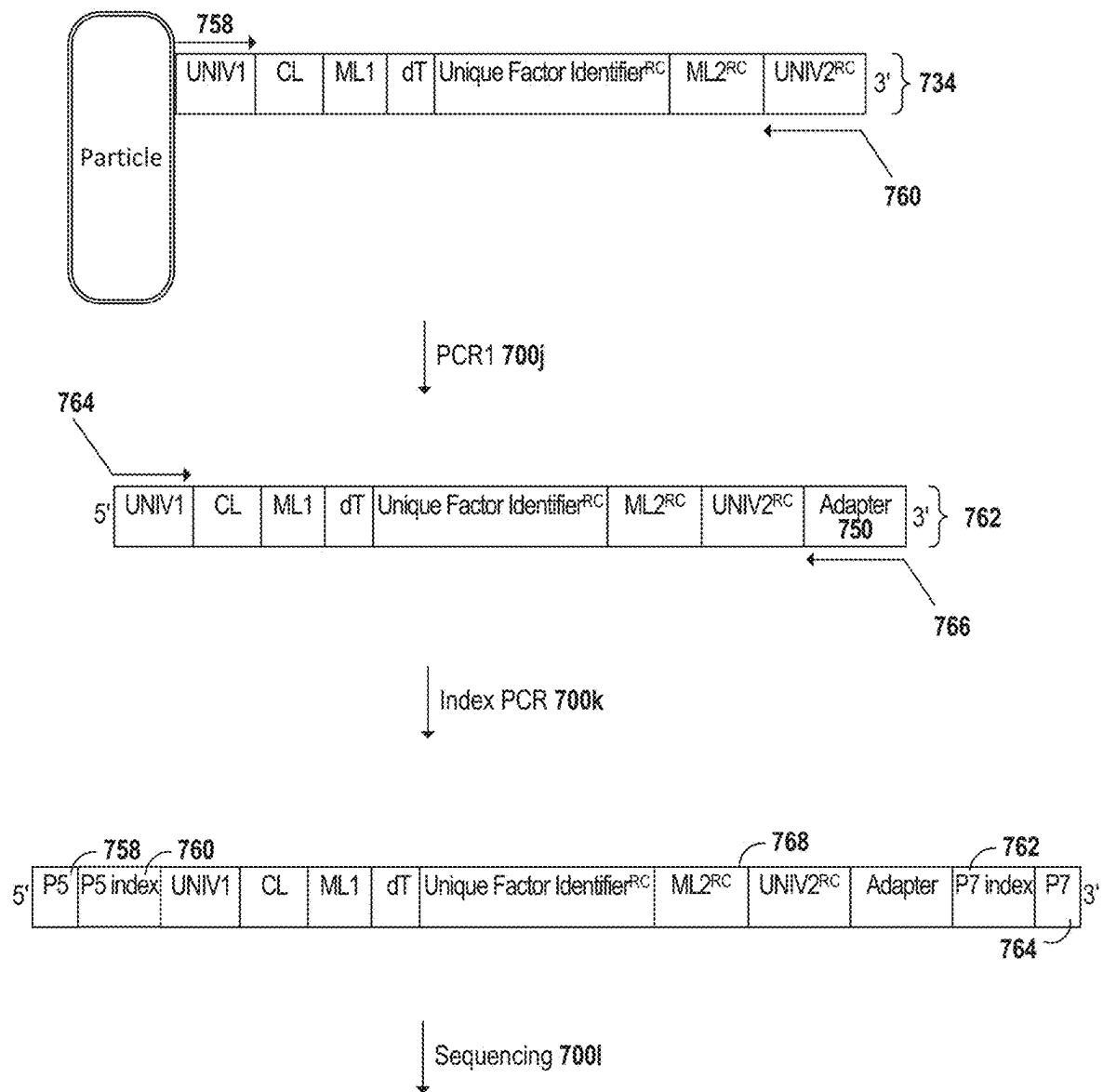


FIG. 7C

**FIG. 7D**

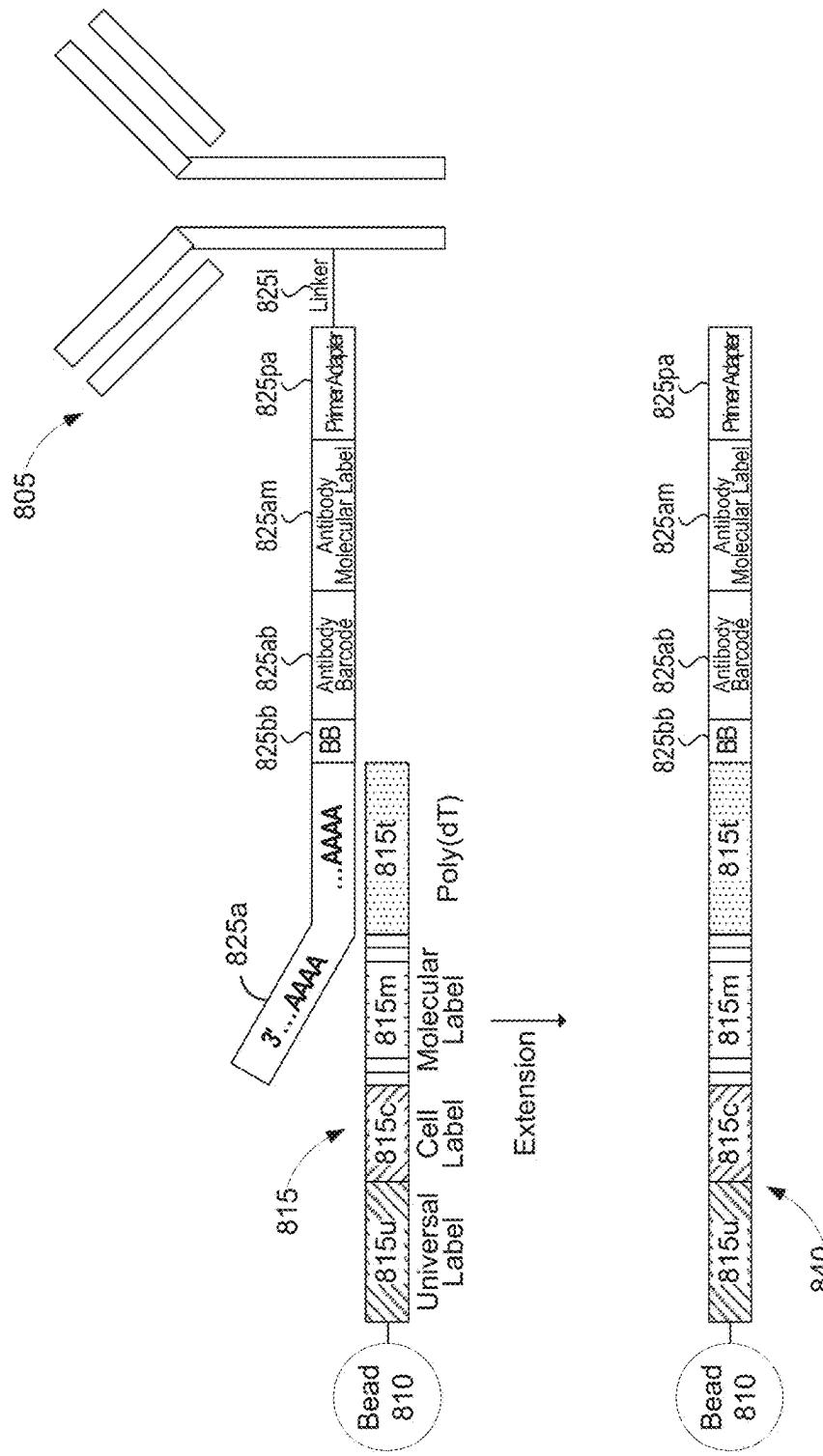


FIG. 8

1**SINGLE CELL SECRETOME ANALYSIS****RELATED APPLICATIONS**

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Patent Application Ser. No. 63/125,629, filed Dec. 15, 2020, the content of this related application is incorporated herein by reference in its entirety for all purposes.

BACKGROUND**Field**

The present disclosure relates generally to the field of molecular biology, for example determining the secreted molecule profiles of cells using molecular barcoding.

Description of the Related Art

Current technology allows measurement of gene expression of single cells in a massively parallel manner (e.g., >10000 cells) by attaching cell specific oligonucleotide barcodes to poly(A) mRNA molecules from individual cells as each of the cells is co-localized with a barcoded reagent bead in a compartment. Gene expression may affect protein expression and the secretion of molecules. Protein-protein interaction may affect gene expression and protein expression as well as secretion of molecules by cells. Cytokines and other molecules released by the cell are of keen interest to immunologists and other cell biologists. Traditional methods for detecting and measuring secreted proteins are typically measured in bulk (rather than at the single cell level). For example, currently available methods include bead-based assays and ELISA for studying secreted factors in bulk. Therefore, single cell quantification and cellular phenotype analysis are missing in the data. As with the comparison of flow cytometry to traditional western blots, there is tremendous value in studying the individual cells from a heterogenous mixture of cells. There is an increasing need to correlate specific secretion activity with complex cell phenotype. Currently available methods for detecting secreted proteins have a limitation on the number of proteins that can be detected due to the number of fluorescence markers that can be used in the microscope or flow cytometry analysis. Moreover, such methods are less quantitative than desired due to limitations in measuring fluorescence intensity differences. There is a need for systems and methods that can quantitatively analyze the number of copies of a secreted factor secreted by a single cell. There is a need for systems and methods that can quantitatively analyze the number of copies of a secreted factor secreted by a single cell and simultaneously measure protein expression and/or gene expression.

SUMMARY

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell. The method can comprise: contacting one or more single cells with a first plurality of first solid supports, the one or more single cells are capable of secreting a plurality of secreted factors, each first solid support comprises a plurality of capture probes capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the first solid support with a plurality of secreted factor-binding

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reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof.

In some embodiments, contacting one or more single cells with a first plurality of first solid supports comprises: partitioning the one or more single cells and the first plurality of first solid supports to a plurality of first partitions, a first partition of the plurality of first partitions comprises a single cell of the one or more single cells and a single first solid support of the first plurality of first solid supports. In some embodiments, the method comprises, prior to contacting the first solid support with a plurality of secreted factor-binding reagents: pooling the single first solid supports from each first partition of the plurality of first partitions to generate a second plurality of first solid supports. In some embodiments, contacting the first solid support with a plurality of secreted factor-binding reagents comprises contacting the second plurality of first solid supports with the plurality of secreted factor-binding reagents. In some embodiments, the method comprises, after contacting the second plurality of first solid supports with the plurality of secreted factor-binding reagents, removing one or more secreted factor-binding reagents of the plurality of secreted factor-binding reagents that are not contacted with the second plurality of first solid supports to generate a third plurality of first solid supports. In some embodiments, removing the one or more secreted factor-binding reagents not contacted with the second plurality of first solid supports comprises: removing the one or more secreted factor-binding reagents not contacted with the respective at least one of the secreted factor bound by a capture probe. In some embodiments, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization comprises: partitioning the third plurality of first solid supports to a plurality of second partitions, a second partition of the plurality of second partitions comprises a single first solid support from the third plurality of first solid supports; and in the second partition comprising the single first solid support, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization.

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell and the number of copies of a nucleic acid target in a single cell. The method can comprise: contacting one or more single

cells with a first plurality of second solid supports to form one or more single cells associated with a second solid support, the one or more single cells comprise a surface cellular target and copies of a nucleic acid target, the one or more single cells are capable of secreting a plurality of secreted factors, each second solid support comprises a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to the surface cellular target, and the capture probe is capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the copies of a nucleic acid target to generate a plurality of barcoded nucleic acid molecules each comprising a sequence complementary to at least a portion of the nucleic acid target and the first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded nucleic acid molecules, or products thereof, to determine the copy number of the nucleic acid target in each of the one or more single cells. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells (e.g., T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof).

In some embodiments, contacting one or more single cells with a first plurality of second solid supports to form one or more single cells associated with a second solid support comprises: partitioning the one or more single cells and the plurality of second solid supports to a plurality of first partitions, a first partition of the plurality of first partitions comprises a single cell of the one or more single cells and a single second solid support of the plurality of second solid supports, the single cell is capable of becoming associated with a second solid support via the anchor probe binding to the surface cellular target. In some embodiments, the method comprises, prior to contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents: pooling the single cells associated with a second solid support from each first partition of the plurality of first partitions to generate a first plurality of single cells associated with a second solid support.

In some embodiments, contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents comprises contacting the

first plurality of single cells associated with a second solid support with the plurality of secreted factor-binding reagents. In some embodiments, the method comprises, after contacting the first plurality of single cells associated with a second solid support with the plurality of secreted factor-binding reagents, removing one or more secreted factor-binding reagents of the plurality of secreted factor-binding reagents that are not contacted with the first plurality of single cells associated with a second solid support to generate a second plurality of single cells associated with a second solid support. In some embodiments, removing the one or more secreted factor-binding reagents not contacted with the first plurality of single cells associated with a second solid support comprises: removing the one or more secreted factor-binding reagents not contacted with the respective at least one of the secreted factor bound by a capture probe.

The method can comprise: prior to contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization: partitioning the second plurality of single cells associated with a second solid support to a plurality of second partitions, a second partition of the plurality of second partitions comprises a single cell and a single second solid support from the second plurality of single cells associated with a second solid support; in the second partition comprising the single cell and the single second solid support, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization. In some embodiments, the method comprises lysing the single cell in the second partition. Lysing the single cell can comprise heating the sample, contacting the sample with a detergent, changing the pH of the sample, or any combination thereof.

The at least one secreted factor can comprise a lymphokine, an interleukin, a chemokine, or any combination thereof. For example, the secreted factor can be a cytokine, a hormone, a molecular toxin, or any combination thereof. In some embodiments, the at least one secreted factor comprises a nerve growth factor, a hepatic growth factor, a fibroblast growth factor, a vascular endothelial growth factor, a platelet-derived growth factor, a transforming growth factor, an osteoinductive factor, an interferon, a colony stimulating factor, or any combination thereof. The at least one secreted factor can comprise angiogenin, angiopoietin-1, angiopoietin-2, bNGF, cathepsin S, Galectin-7, GCP-2, G-CSF, GM-CSF, PAI-1, PDGF-AA, PDGF-BB, PDGF-AB, PIGF, PIGF-2, SDF-1, Tie2, VEGF-A, VEGF-C, VEGF-D, VEGF-R1, VEGF-R2, VEGF-R3, 6Ckine, angiopoietin-1, angiopoietin-2, BLC, BRAK, CD186, ENA-78, Eotaxin-1, Eotaxin-2, Eotaxin-3, EpCAM, GDF-15, GM-CSF, GRO, HCC-4, I-309, IFN- γ , IL-1 α , IL-1 β , IL-1R4 (ST2), IL-2, IL-2R, IL-3, IL-3Ra, IL-5, IL-6, IL-6R, IL-7, IL-8, IL-8 RB, IL-11, IL-12, IL-12p40, IL-12p70, IL-13, IL-13 R1, IL-13R2, IL-15, IL-15Ra, IL-16, IL-17, IL-17C, IL-17E, IL-17F, IL-17R, IL-18, IL-18BPa, IL-18 Ra, IL-20, IL-23, IL-27, IL-28, IL-31, IL-33, IP-10, I-TAC, LIF, LIX, LRP6, MadCAM-1, MCP-1, MCP-2, MCP-3, MCP-4, M-CSF, MIF, MIG, MIP-1 gamma, MIP-1 α , MIP-1 β , MIP-1 δ , MIP-3 α , MIP-3 β , MPIF-1, PARC, PF4, RANTES, Resistin, SCF, SCYB16, TACI, TARC, TSLP, TNF- α , TNF-R1, TRAIL-R4, TREM-1, Activin A, Amphiregulin, Axl, BDNF, BMP4, cathepsin S, EGF, FGF-1, FGF-2, FGF-7, FGF-21, Follistatin, Galectin-7, Gas6, GDF-15, HB-EGF, HGF, IGFBP-1, IGFBP-3, LAP, NGF R, NrCAM, NT-3, NT-4, PAI-1, TGF- α , TGF- β , TGF- β 3, TRAIL-R4,

ADAMTS1, cathepsin S, FGF-2, Folistatin, Galectin-7, GCP-2, GDF-15, IGFBP-6, LIF, MMP-9, pro-MMP9, RANK, RANKL, RANTES, SDF-1, CXCR4, or any combination thereof.

In some embodiments, the secreted factor-binding reagent and the capture probe are capable of binding to distinct epitopes of the same secreted factor. In some embodiments, one or more of the secreted factor-binding reagents, the capture probe, and the anchor probe comprise an antibody or fragment thereof. In some embodiments, the antibody or fragment thereof comprises a monoclonal antibody. In some embodiments, the antibody or fragment thereof comprises a Fab, a Fab', a F(ab')₂, a Fv, a scFv, a dsFv, a diabody, a triabody, a tetrabody, a multispecific antibody formed from antibody fragments, a single-domain antibody (sdAb), a single chain comprising complementary scFvs (tandem scFvs) or bispecific tandem scFvs, an Fv construct, a disulfide-linked Fv, a dual variable domain immunoglobulin (DVD-Ig) binding protein or a nanobody, an aptamer, an affibody, an affilin, an affitin, an affimer, an alphabody, an anticalin, an avimer, a DARPin, a Fynomeric, a Kunitz domain peptide, a monobody, or any combination thereof. In some embodiments, the capture probe and/or the anchor probe is conjugated to the first solid support and/or the second solid support by a 1,3-dipolar cycloaddition reaction, a hetero-Diels-Alder reaction, a nucleophilic substitution reaction, a non-aldol type carbonyl reaction, an addition to carbon-carbon multiple bond, an oxidation reaction, a click reaction, or any combination thereof.

The surface cellular target can comprise a carbohydrate, a lipid, a protein, an extracellular protein, a cell-surface protein, a cell marker, a B-cell receptor, a T-cell receptor, a major histocompatibility complex, a tumor antigen, a receptor, an intracellular protein, or any combination thereof. For example, the surface cellular target can comprise a carbohydrate, a lipid, a protein, or any combination thereof. In some embodiments, the surface cellular target comprises CD1a, CD1b, CD1c, CD1d, CD1e, CD2, CD3, CD3d, CD3e, CD3g, CD4, CD5, CD6, CD7, CD8a, CD8b, CD9, CD10, CD11a, CD11b, CD11c, CD11d, CDw12, CD13, CD14, CD15, CD15u, CD15s, CD15su, CD16, CD16b, CD17, CD18, CD19, CD20, CD21, CD22, CD23, CD24, CD25, CD26, CD27, CD28, CD29, CD30, CD31, CD32, CD33, CD34, CD35, CD36, CD37, CD38, CD39, CD40, CD41, CD42a, CD42b, CD42c, CD42d, CD43, CD44, CD45, CD45RA, CD45RB, CD45RC, CD45RO, CD46, CD47, CD48, CD49a, CD49b, CD49c, CD49d, CD49e, CD49f, CD50, CD51, CD52, CD53, CD54, CD55, CD56, CD57, CD58, CD59, CD60a, CD60b, CD60c, CD61, CD62E, CD62L, CD62P, CD63, CD64, CD65, CD65s, CD66a, CD66b, CD66c, CD66d, CD66e, CD66f, CD68, CD69, CD70, CD71, CD72, CD73, CD74, CD75, CD75s, CD77, CD79a, CD79b, CD80, CD81, CD82, CD83, CD84, CD85a, CD85d, CD85j, CD85k, CD86, CD87, CD88, CD89, CD90, CD91, CD92, CD93, CD94, CD95, CD96, CD97, CD98, CD99, CD99R, CD100, CD101, CD102, CD103, CD104, CD105, CD106, CD107a, CD107b, CD108, CD109, CD110, CD111, CD112, CD113, CD114, CD115, CD116, CD117, CD118, CD119, CD120a, CD120b, CD121a, CD121b, CD122, CD123, CD124, CD125, CD126, CD127, CD129, CD130, CD131, CD132, CD133, CD134, CD135, CD136, CD137, CD138, CD139, CD140a, CD140b, CD141, CD142, CD143, CD144, CDw145, CD146, CD147, CD148, CDw149, CD150, CD151, CD152, CD153, CD154, CD155, CD156a, CD156b, CD156c, CD157, CD158e, CD158i, CD158k, CD159a, CD159c, CD160, CD161, CD162, CD163, CD164, CD165, CD166,

CD167a, CD167b, CD168, CD169, CD170, CD171, CD172a, CD172b, CD172g, CD173, CD174, CD175, CD175s, CD176, CD177, CD178, CD179a, CD179b, CD180, CD181, CD182, CD183, CD184, CD185, CD186, 5 CD191, CD192, CD193, CD194, CD195, CD196, CD197, CDw198, CD199, CD200, CD201, CD202b, CD203c, CD204, CD205, CD206, CD207, CD208, CD209, CD210, CDw210b, CD212, CD213a1, CD213a2, CD215, CD217a, CD218a, CD218b, CD220, CD221, CD222, CD223, 10 CD224, CD225, CD226, CD227, CD228, CD229, CD230, CD231, CD232, CD233, CD234, CD235a, CD235b, CD236, CD236R, CD238, CD239, CD240CE, CD240DCE, CD240D, CD241, CD242, CD243, CD244, CD245, CD246, CD247, CD248, CD249, CD252, CD253, CD254, CD256, 15 CD266, CD267, CD268, CD269, CD270, CD271, CD272, CD273, CD274, CD275, CD276, CD277, CD278, CD279, CD280, CD281, CD282, CD283, CD284, CD286, CD289, CD290, CD292, CDw293, CD294, CD295, CD296, CD297, CD298, CD299, CD300a, CD300c, CD300e, CD301, 20 CD302, CD303, CD304, CD305, CD306, CD307a, CD307b, CD307c, CD307d, CD307e, CD308, CD309, CD312, CD314, CD315, CD316, CD317, CD318, CD319, CD320, CD321, CD322, CD324, CD325, CD326, CD327, CD328, CD329, CD331, CD332, CD333, CD334, CD335, 25 CD336, CD337, CD338, CD339, CD340, CD344, CD349, CD350, CD351, CD352, CD353, CD354, CD355, CD357, CD358, CD360, CD361, CD362, CD363, CD364, CD365, CD366, CD367, CD368, CD369, CD370, CD371, BCMA, a HLA protein, β 2-microglobulin, or any combination thereof.

In some embodiments, the plurality of oligonucleotide barcodes are associated with a third solid support, and a second partition of the plurality of second partitions comprises a single third solid support. In some embodiments, the first partition and/or second partition is a well or a droplet. 35 In some embodiments, each oligonucleotide barcode comprises a first universal sequence. In some embodiments, the oligonucleotide barcode comprises a target-binding region comprising a capture sequence. In some embodiments, the target-binding region comprises a poly(dT) region. In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises a sequence complementary to the capture sequence configured to capture the secreted factor-binding reagent specific oligonucleotide. In some embodiments, the sequence complementary to the capture sequence comprises a poly(dA) region. In some embodiments, the plurality of barcoded secreted factor-binding reagent specific oligonucleotides comprise a complement of the first universal sequence. In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises a second universal sequence.

In some embodiments, obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, comprises: 40 amplifying the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, using a primer capable of hybridizing to the first universal sequence, or a complement thereof, and a primer capable of hybridizing to the second universal sequence, or a complement thereof, to generate a plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides; and obtaining sequencing data of the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof.

45 The secreted factor-binding reagent specific oligonucleotide can comprise a second molecular label. In some embodiments, at least ten of the plurality of secreted factor-

binding reagent specific oligonucleotides comprise different second molecular label sequences. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are identical. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are different.

In some embodiments, the number of unique first molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the number of unique second molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the method comprises determining the number of copies of the at least one secreted factor secreted by each of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof.

In some embodiments, the method comprises determining the number of copies of the at least one secreted factor secreted by each of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof. In some embodiments, obtaining the sequence information comprises attaching sequencing adaptors to the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof.

In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises an alignment sequence adjacent to the poly(dA) region. The alignment sequence can be, one or more nucleotides in length, or two or more nucleotides in length. For example, the alignment sequence can (a) comprises a guanine, a cytosine, a thymine, a uracil, or a combination thereof; (b) comprises a poly(dT) sequence, a poly(dG) sequence, a poly(dC) sequence, a poly(dU) sequence, or a combination thereof; and/or (c) is 5' to the poly(dA) region.

In some embodiments, the secreted factor-binding reagent specific oligonucleotide is associated with the secreted factor-binding reagent through a linker. In some embodiments, the linker comprises a carbon chain. The carbon chain can comprise 2-30 carbons (e.g., 12 carbons). In some embodiments, the linker comprises 5' amino modifier C12 (5AmMC12), or a derivative thereof. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is configured to be detachable from the secreted factor-binding reagent. For example, the method can comprise dissociating the secreted factor-binding reagent specific oligonucleotide from the secreted factor-binding reagent.

In some embodiments, determining the copy number of the nucleic acid target in each of the one or more single cells comprises determining the copy number of the nucleic acid

target in each of the one or more single cells based on the number of first molecular labels with distinct sequences, complements thereof, or a combination thereof, associated with the plurality of barcoded nucleic acid molecules, or products thereof.

In some embodiments, the method comprises: contacting random primers with the plurality of barcoded nucleic acid molecules, each of the random primers comprises a third universal sequence, or a complement thereof; and extending the random primers hybridized to the plurality of barcoded nucleic acid molecules to generate a plurality of extension products. In some embodiments, the method comprises amplifying the plurality of extension products using primers capable of hybridizing to the first universal sequence or complements thereof, and primers capable of hybridizing the third universal sequence or complements thereof, thereby generating a first plurality of barcoded amplicons. In some embodiments, amplifying the plurality of extension products comprises adding sequences of binding sites of sequencing primers and/or sequencing adaptors, complementary sequences thereof, and/or portions thereof, to the plurality of extension products. In some embodiments, the method comprises determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the first plurality of barcoded amplicons, or products thereof.

In some embodiments, determining the copy number of the nucleic acid target in each of the one or more single cells comprises determining the number of each of the plurality of nucleic acid targets in each of the one or more single cells based on the number of the first molecular labels with distinct sequences associated with barcoded amplicons of the first plurality of barcoded amplicons comprising a sequence of the each of the plurality of nucleic acid targets. In some embodiments, the sequence of the each of the plurality of nucleic acid targets comprises a subsequence of the each of the plurality of nucleic acid targets. In some embodiments, the sequence of the nucleic acid target in the first plurality of barcoded amplicons comprises a subsequence of the nucleic acid target.

In some embodiments, the method comprises amplifying the first plurality of barcoded amplicons using primers capable of hybridizing to the first universal sequence or complements thereof, and primers capable of hybridizing the third universal sequence or complements thereof, thereby generating a second plurality of barcoded amplicons. In some embodiments, amplifying the first plurality of barcoded amplicons comprises adding sequences of binding sites of sequencing primers and/or sequencing adaptors, complementary sequences thereof, and/or portions thereof, to the first plurality of barcoded amplicons. In some embodiments, the method comprises determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the second plurality of barcoded amplicons, or products thereof. In some embodiments, the first plurality of barcoded amplicons and/or the second plurality of barcoded amplicons comprise whole transcriptome amplification (WTA) products.

In some embodiments, the method comprises synthesizing a third plurality of barcoded amplicons using the plurality of barcoded nucleic acid molecules as templates to generate a third plurality of barcoded amplicons. In some embodiments, synthesizing a third plurality of barcoded amplicons comprises performing (1) PCR amplification of the plurality of the barcoded nucleic acid molecules; (2)

PCR amplification using primers capable of hybridizing to the first universal sequence, or a complement thereof, and a target-specific primer; or both. In some embodiments, the method comprises obtaining sequence information of the third plurality of barcoded amplicons, or products thereof. Obtaining the sequence information can comprise attaching sequencing adaptors to the third plurality of barcoded amplicons, or products thereof. The method can comprise determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the third plurality of barcoded amplicons, or products thereof.

In some embodiments, the nucleic acid target comprises a nucleic acid molecule. In some embodiments, the nucleic acid molecule comprises ribonucleic acid (RNA), messenger RNA (mRNA), microRNA, small interfering RNA (siRNA), RNA degradation product, RNA comprising a poly(A) tail, a sample indexing oligonucleotide, a cellular component-binding reagent specific oligonucleotide, or any combination thereof. In some embodiments, extending the plurality of oligonucleotide barcodes comprising extending the plurality of oligonucleotide barcodes using a reverse transcriptase and/or a DNA polymerase lacking at least one of 5' to 3' exonuclease activity and 3' to 5' exonuclease activity. In some embodiments, the DNA polymerase comprises a Klenow Fragment. In some embodiments, the reverse transcriptase comprises a viral reverse transcriptase (e.g., a murine leukemia virus (MLV) reverse transcriptase or a Moloney murine leukemia virus (MMLV) reverse transcriptase).

In some embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence are the same. In some embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence are different. In some embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence comprise the binding sites of sequencing primers and/or a sequencing adaptor, complementary sequences thereof, and/or portions thereof. In some embodiments, the sequencing adaptors comprise a P5 sequence, a P7 sequence, complementary sequences thereof, and/or portions thereof. In some embodiments, the sequencing primers comprise a Read 1 sequencing primer, a Read 2 sequencing primer, complementary sequences thereof, and/or portions thereof. In some embodiments, at least 10 of the plurality of oligonucleotide barcodes comprise different first molecular label sequences. In some embodiments, the plurality of oligonucleotide barcodes each comprise a cell label. In some embodiments, each cell label of the plurality of oligonucleotide barcodes comprises at least 6 nucleotides. In some embodiments, oligonucleotide barcodes associated with the same third solid support comprise the same cell label. In some embodiments, oligonucleotide barcodes associated with different third solid supports comprise different cell labels.

In some embodiments, the first solid support, second solid support, and/or third solid support comprises a synthetic particle or a planar surface. In some embodiments, at least one of the plurality of oligonucleotide barcodes is immobilized or partially immobilized on the synthetic particle, or the at least one of the plurality of oligonucleotide barcodes is enclosed or partially enclosed in the synthetic particle. The synthetic particle can be disruptable. The synthetic particle can comprise a bead. The bead can comprise: a sepharose bead, a streptavidin bead, an agarose bead, a magnetic bead, a conjugated bead, a protein A conjugated bead, a protein G conjugated bead, a protein A/G conjugated

bead, a protein L conjugated bead, an oligo(dT) conjugated bead, a silica bead, a silica-like bead, an anti-biotin micro-bead, an anti-fluorochrome microbead, or any combination thereof; a material selected from the group consisting of polydimethylsiloxane (PDMS), polystyrene, glass, polypropylene, agarose, gelatin, hydrogel, paramagnetic, ceramic, plastic, glass, methylstyrene, acrylic polymer, titanium, latex, sepharose, cellulose, nylon, silicone, and any combination thereof; or a disruptable hydrogel particle.

10 In some embodiments, each of the plurality of oligonucleotide barcodes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

15 In some embodiments, each of the plurality of anchor probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

20 In some embodiments, each of the plurality of capture probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

25 In some embodiments, the first solid support and/or the second solid support is sized and shaped to approximate a cell. In some embodiments, the first solid support and/or the second solid support has the dimensions of a cell. In some embodiments, the cell is a mammalian cell, a yeast cell, an insect cell, a plant cell, a bacterial cell, or any combination thereof.

30 Disclosed herein include compositions (e.g., kits). The composition can comprise: a first solid support comprising a plurality of capture probes capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

35 Disclosed herein include compositions (e.g., kits). The composition can comprise: a second solid support comprising a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to a surface cellular target, and the capture probe is capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

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In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises a second molecular label sequence (e.g., 2-20 nucleotides in length). In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are identical. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are different.

In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises a second universal sequence. In some embodiments, the second universal sequence comprises a binding site of a sequencing primers and/or a sequencing adaptor, complementary sequences thereof, and/or portions thereof. In some embodiments, the sequencing adaptor comprises a P5 sequence, a P7 sequence, complementary sequences thereof, and/or portions thereof. In some embodiments, the sequencing primer comprises a Read 1 sequencing primer, a Read 2 sequencing primer, complementary sequences thereof, and/or portions thereof.

In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises a poly(dA) region. In some embodiments, the secreted factor-binding reagent specific oligonucleotide comprises an alignment sequence adjacent to the poly(dA) region. The alignment sequence can be one or more nucleotides in length, or two or more nucleotides in length. The alignment sequence can (a) comprises a guanine, a cytosine, a thymine, a uracil, or a combination thereof; (b) comprises a poly(dT) sequence, a poly(dG) sequence, a poly(dC) sequence, a poly(dU) sequence, or a combination thereof; and/or (c) is 5' to the poly(dA) region.

In some embodiments, the secreted factor-binding reagent specific oligonucleotide is associated with the secreted factor-binding reagent through a linker. In some embodiments, the linker comprises a carbon chain. The carbon chain can comprise 2-30 carbons (e.g., 12 carbons). In some embodiments, the linker comprises 5' amino modifier C12 (5AmMC12), or a derivative thereof. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is attached to the secreted factor-binding reagent. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is covalently attached to the secreted factor-binding reagent. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is non-covalently attached to the secreted factor-binding reagent. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is conjugated to the secreted factor-binding reagent. In some embodiments, the secreted factor-binding reagent specific oligonucleotide is conjugated to the secreted factor-binding reagent through a chemical group, such as a UV photocleavable group, a streptavidin, a biotin, an amine, or a combination thereof.

The secreted factor can comprise a lymphokine, an interleukin, a chemokine, or any combination thereof. For example, the secreted factor can comprise a cytokine, a hormone, a molecular toxin, or any combination thereof. In some embodiments, the secreted factor comprises a nerve growth factor, a hepatic growth factor, a fibroblast growth factor, a vascular endothelial growth factor, a platelet-derived growth factor, a transforming growth factor, an osteoinductive factor, an interferon, a colony stimulating factor, or any combination thereof.

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In some embodiments, the secreted factor-binding reagents and the capture probe are capable of binding to distinct epitopes of the same secreted factor. In some embodiments, one or more of the secreted factor-binding reagents, the capture probe, and the anchor probe comprise an antibody or fragment thereof. In some embodiments, the antibody or fragment thereof comprises a monoclonal antibody. In some embodiments, the antibody or fragment thereof comprises a Fab, a Fab', a F(ab')₂, a Fv, a scFv, a dsFv, a diabody, a triabody, a tetrabody, a multispecific antibody formed from antibody fragments, a single-domain antibody (sdAb), a single chain comprising complementary scFvs (tandem scFvs) or bispecific tandem scFvs, an Fv construct, a disulfide-linked Fv, a dual variable domain immunoglobulin (DVD-Ig) binding protein or a nanobody, an aptamer, an affibody, an affilin, an affitin, an affimer, an alphabody, an anticalin, an avimer, a DARPin, a Fynomeric, a Kunitz domain peptide, a monobody, or any combination thereof. In some embodiments, the capture probe and/or the anchor probe is conjugated to the first solid support and/or the second solid support by a 1,3-dipolar cycloaddition reaction, a hetero-Diels-Alder reaction, a nucleophilic substitution reaction, a non-aldol type carbonyl reaction, an addition to carbon-carbon multiple bond, an oxidation reaction, a click reaction, or any combination thereof.

In some embodiments, the surface cellular target comprises a carbohydrate, a lipid, a protein, an extracellular protein, a cell-surface protein, a cell marker, a B-cell receptor, a T-cell receptor, a major histocompatibility complex, a tumor antigen, a receptor, an intracellular protein, or any combination thereof. For example, the surface cellular target can comprise a carbohydrate, a lipid, a protein, or any combination thereof.

In some embodiments, the composition comprises a DNA polymerase (e.g., a Klenow Fragment) lacking at least one of 5' to 3' exonuclease activity and 3' to 5' exonuclease activity. In some embodiments, the composition comprises a reverse transcriptase, such as a viral reverse transcriptase. The composition can comprise a buffer, a cartridge, or both.

In some embodiments, the composition comprises a plurality of oligonucleotide barcodes, each oligonucleotide barcode of the plurality of oligonucleotide barcodes comprises a target-binding region. The target-binding region can comprise a poly(dA) region, a poly(dT) region, a random sequence, a gene-specific sequence, or any combination thereof. In some embodiments, the plurality of oligonucleotide barcodes each comprise a molecular label. The molecular label can comprise at least 6 nucleotides. In some embodiments, at least 10 of the plurality of oligonucleotide barcodes comprise different molecular label sequences. In some embodiments, the plurality of oligonucleotide barcodes are associated with a third solid support. In some embodiments, the plurality of oligonucleotide barcodes each comprise a cell label. In some embodiments, oligonucleotide barcodes of the plurality of oligonucleotide barcodes associated with the same third solid support comprise the same cell label. In some embodiments, oligonucleotide barcodes of the plurality of oligonucleotide barcodes associated with different third solid supports comprise different cell labels.

In some embodiments, the first solid support, second solid support, and/or third solid support comprises a synthetic particle or a planar surface. The at least one of the plurality of oligonucleotide barcodes can be immobilized or partially immobilized on the synthetic particle, or the at least one of the plurality of oligonucleotide barcodes is enclosed or

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partially enclosed in the synthetic particle. The synthetic particle can be disruptable, e.g., a disruptable hydrogel particle.

In some embodiments, each of the plurality of oligonucleotide barcodes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

In some embodiments, each of the plurality of anchor probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

In some embodiments, each of the plurality of capture probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

In some embodiments, the first solid support and/or the second solid support is sized and shaped to approximate a cell. In some embodiments, the first solid support and/or the second solid support has the dimensions of a cell. In some embodiments, the cell is a mammalian cell, a yeast cell, an insect cell, a plant cell, a bacterial cell, or any combination thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 illustrates a non-limiting exemplary barcode.

FIG. 2 shows a non-limiting exemplary workflow of barcoding and digital counting.

FIG. 3 is a schematic illustration showing a non-limiting exemplary process for generating an indexed library of targets barcoded at the 3'-ends from a plurality of targets.

FIGS. 4A-4C show a schematic illustration of a non-limiting exemplary workflow for measurement of the number of copies of one or more secreted factors secreted by a single cell.

FIGS. 5A-5C show a schematic illustration of a non-limiting exemplary workflow for simultaneous measurement of secreted factors and gene expression of single cells.

FIG. 6 shows a non-limiting exemplary design of a secreted factor-binding reagent specific oligonucleotide (antibody oligonucleotide illustrated here) that is associated with a secreted factor-binding reagent (antibody illustrated here).

FIGS. 7A-7D show a schematic illustration of a non-limiting exemplary workflow for simultaneous measurement of the number of copies of a secreted factor and a nucleic acid target.

FIG. 8 shows a schematic illustration of a non-limiting exemplary workflow of barcoding of a binding reagent

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oligonucleotide (antibody oligonucleotide illustrated here) that is associated with a binding reagent (antibody illustrated here).

DETAILED DESCRIPTION

In the following detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be utilized, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It will be readily understood that the aspects of the present disclosure, as generally described herein, and illustrated in the Figures, can be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein and made part of the disclosure herein.

All patents, published patent applications, other publications, and sequences from GenBank, and other databases referred to herein are incorporated by reference in their entirety with respect to the related technology.

Quantifying small numbers of nucleic acids, for example messenger ribonucleotide acid (mRNA) molecules, is clinically important for determining, for example, the genes that are expressed in a cell at different stages of development or under different environmental conditions. However, it can also be very challenging to determine the absolute number of nucleic acid molecules (e.g., mRNA molecules), especially when the number of molecules is very small. One method to determine the absolute number of molecules in a sample is digital polymerase chain reaction (PCR). Ideally, PCR produces an identical copy of a molecule at each cycle. However, PCR can have disadvantages such that each molecule replicates with a stochastic probability, and this probability varies by PCR cycle and gene sequence, resulting in amplification bias and inaccurate gene expression measurements. Stochastic barcodes with unique molecular labels (also referred to as molecular indexes (MIs)) can be used to count the number of molecules and correct for amplification bias. Stochastic barcoding, such as the PreciseTM assay (Cellular Research, Inc. (Palo Alto, CA)) and RhapsodyTM assay (Becton, Dickinson and Company (Franklin Lakes, NJ)), can correct for bias induced by PCR and library preparation steps by using molecular labels (MLs) to label mRNAs during reverse transcription (RT).

The PreciseTM assay can utilize a non-depleting pool of stochastic barcodes with large number, for example 6561 to 65536, unique molecular label sequences on poly(T) oligonucleotides to hybridize to all poly(A)-mRNAs in a sample during the RT step. A stochastic barcode can comprise a universal PCR priming site. During RT, target gene molecules react randomly with stochastic barcodes. Each target molecule can hybridize to a stochastic barcode resulting to generate stochastically barcoded complementary ribonucleotide acid (cDNA) molecules. After labeling, stochastically barcoded cDNA molecules from microwells of a microwell plate can be pooled into a single tube for PCR amplification and sequencing. Raw sequencing data can be analyzed to produce the number of reads, the number of stochastic barcodes with unique molecular label sequences, and the numbers of mRNA molecules.

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell.

The method can comprise: contacting one or more single cells with a first plurality of first solid supports, the one or more single cells are capable of secreting a plurality of secreted factors, each first solid support comprises a plurality of capture probes capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the first solid support with a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof.

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell and the number of copies of a nucleic acid target in a single cell. The method can comprise: contacting one or more single cells with a first plurality of second solid supports to form one or more single cells associated with a second solid support, the one or more single cells comprise a surface cellular target and copies of a nucleic acid target, the one or more single cells are capable of secreting a plurality of secreted factors, each second solid support comprises a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to the surface cellular target, and the capture probe is capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the copies of a nucleic acid target to generate a plurality of barcoded nucleic acid molecules each comprising a sequence complementary to at least a portion of the nucleic acid target and the first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to

generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded nucleic acid molecules, or products thereof, to determine the copy number of the nucleic acid target in each of the one or more single cells. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof.

Disclosed herein include compositions (e.g., kits). The composition can comprise: a first solid support comprising a plurality of capture probes capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

Disclosed herein include compositions (e.g., kits). The composition can comprise: a second solid support comprising a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to a surface cellular target, and the capture probe is capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the present disclosure belongs. See, e.g., Singleton et al., Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, NY 1994); Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press (Cold Spring Harbor, NY 1989). For purposes of the present disclosure, the following terms are defined below.

As used herein, the term "adaptor" can mean a sequence to facilitate amplification or sequencing of associated nucleic acids. The associated nucleic acids can comprise target nucleic acids. The associated nucleic acids can comprise one or more of spatial labels, target labels, sample labels, indexing label, or barcode sequences (e.g., molecular labels). The adaptors can be linear. The adaptors can be pre-adenylated adaptors. The adaptors can be double- or single-stranded. One or more adaptor can be located on the 5' or 3' end of a nucleic acid. When the adaptors comprise known sequences on the 5' and 3' ends, the known sequences can be the same or different sequences. An adaptor located on the 5' and/or 3' ends of a polynucleotide can be capable of hybridizing to one or more oligonucleotides immobilized on a surface. An adaptor can, in some embodiments, com-

prise a universal sequence. A universal sequence can be a region of nucleotide sequence that is common to two or more nucleic acid molecules. The two or more nucleic acid molecules can also have regions of different sequence. Thus, for example, the 5' adaptors can comprise identical and/or universal nucleic acid sequences and the 3' adaptors can comprise identical and/or universal sequences. A universal sequence that may be present in different members of a plurality of nucleic acid molecules can allow the replication or amplification of multiple different sequences using a single universal primer that is complementary to the universal sequence. Similarly, at least one, two (e.g., a pair) or more universal sequences that may be present in different members of a collection of nucleic acid molecules can allow the replication or amplification of multiple different sequences using at least one, two (e.g., a pair) or more single universal primers that are complementary to the universal sequences. Thus, a universal primer includes a sequence that can hybridize to such a universal sequence. The target nucleic acid sequence-bearing molecules may be modified to attach universal adaptors (e.g., non-target nucleic acid sequences) to one or both ends of the different target nucleic acid sequences. The one or more universal primers attached to the target nucleic acid can provide sites for hybridization of universal primers. The one or more universal primers attached to the target nucleic acid can be the same or different from each other.

As used herein the term “associated” or “associated with” can mean that two or more species are identifiable as being co-located at a point in time. An association can mean that two or more species are or were within a similar container. An association can be an informatics association. For example, digital information regarding two or more species can be stored and can be used to determine that one or more of the species were co-located at a point in time. An association can also be a physical association. In some embodiments, two or more associated species are “tethered”, “attached”, or “immobilized” to one another or to a common solid or semisolid surface. An association may refer to covalent or non-covalent means for attaching labels to solid or semi-solid supports such as beads. An association may be a covalent bond between a target and a label. An association can comprise hybridization between two molecules (such as a target molecule and a label).

As used herein, the term “complementary” can refer to the capacity for precise pairing between two nucleotides. For example, if a nucleotide at a given position of a nucleic acid is capable of hydrogen bonding with a nucleotide of another nucleic acid, then the two nucleic acids are considered to be complementary to one another at that position. Complementarity between two single-stranded nucleic acid molecules may be “partial,” in which only some of the nucleotides bind, or it may be complete when total complementarity exists between the single-stranded molecules. A first nucleotide sequence can be said to be the “complement” of a second sequence if the first nucleotide sequence is complementary to the second nucleotide sequence. A first nucleotide sequence can be said to be the “reverse complement” of a second sequence, if the first nucleotide sequence is complementary to a sequence that is the reverse (i.e., the order of the nucleotides is reversed) of the second sequence. As used herein, a “complementary” sequence can refer to a “complement” or a “reverse complement” of a sequence. It is understood from the disclosure that if a molecule can hybridize to another molecule it may be complementary, or partially complementary, to the molecule that is hybridizing.

As used herein, the term “digital counting” can refer to a method for estimating a number of target molecules in a sample. Digital counting can include the step of determining a number of unique labels that have been associated with targets in a sample. This methodology, which can be stochastic in nature, transforms the problem of counting molecules from one of locating and identifying identical molecules to a series of yes/no digital questions regarding detection of a set of predefined labels.

- 10 As used herein, the term “label” or “labels” can refer to nucleic acid codes associated with a target within a sample. A label can be, for example, a nucleic acid label. A label can be an entirely or partially amplifiable label. A label can be a portion of a native nucleic acid that is identifiable as distinct. A label can be a known sequence. A label can comprise a junction of nucleic acid sequences, for example a junction of a native and non-native sequence. As used herein, the term “label” can be used interchangeably with the terms, “index”, “tag,” or “label-tag.” Labels can convey information. For example, in various embodiments, labels can be used to determine an identity of a sample, a source of a sample, an identity of a cell, and/or a target.

As used herein, the term “non-depleting reservoirs” can refer to a pool of barcodes (e.g., stochastic barcodes) made up of many different labels. A non-depleting reservoir can comprise large numbers of different barcodes such that when the non-depleting reservoir is associated with a pool of targets each target is likely to be associated with a unique barcode. The uniqueness of each labeled target molecule can be determined by the statistics of random choice, and depends on the number of copies of identical target molecules in the collection compared to the diversity of labels. The size of the resulting set of labeled target molecules can be determined by the stochastic nature of the barcoding process, and analysis of the number of barcodes detected then allows calculation of the number of target molecules present in the original collection or sample. When the ratio of the number of copies of a target molecule present to the number of unique barcodes is low, the labeled target molecules are highly unique (i.e., there is a very low probability that more than one target molecule will have been labeled with a given label).

As used herein, the term “nucleic acid” refers to a polynucleotide sequence, or fragment thereof. A nucleic acid can comprise nucleotides. A nucleic acid can be exogenous or endogenous to a cell. A nucleic acid can exist in a cell-free environment. A nucleic acid can be a gene or fragment thereof. A nucleic acid can be DNA. A nucleic acid can be RNA. A nucleic acid can comprise one or more analogs (e.g., altered backbone, sugar, or nucleobase). Some non-limiting examples of analogs include: 5-bromouracil, peptide nucleic acid, xeno nucleic acid, morpholinos, locked nucleic acids, glycol nucleic acids, threose nucleic acids, dideoxynucleotides, cordycepin, 7-deaza-GTP, fluorophores (e.g., rhodamine or fluorescein linked to the sugar), thiol containing nucleotides, biotin linked nucleotides, fluorescent base analogs, CpG islands, methyl-7-guanosine, methylated nucleotides, inosine, thiouridine, pseudouridine, dihydrouridine, queuosine, and wyosine. “Nucleic acid”, “polynucleotide”, “target polynucleotide”, and “target nucleic acid” can be used interchangeably.

A nucleic acid can comprise one or more modifications (e.g., a base modification, a backbone modification), to provide the nucleic acid with a new or enhanced feature (e.g., improved stability). A nucleic acid can comprise a nucleic acid affinity tag. A nucleoside can be a base-sugar

combination. The base portion of the nucleoside can be a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides can be nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to the 2', the 3', or the 5' hydroxyl moiety of the sugar. In forming nucleic acids, the phosphate groups can covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn, the respective ends of this linear polymeric compound can be further joined to form a circular compound; however, linear compounds are generally suitable. In addition, linear compounds may have internal nucleotide base complementarity and may therefore fold in a manner as to produce a fully or partially double-stranded compound. Within nucleic acids, the phosphate groups can commonly be referred to as forming the internucleoside backbone of the nucleic acid. The linkage or backbone can be a 3' to 5' phosphodiester linkage.

A nucleic acid can comprise a modified backbone and/or modified internucleoside linkages. Modified backbones can include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. Suitable modified nucleic acid backbones containing a phosphorus atom therein can include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkyl phosphotriesters, methyl and other alkyl phosphonate such as 3'-alkylene phosphonates, 5'-alkylene phosphonates, chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkyl phosphoramidates, phosphorodiamidates, thionophosphoramidates, thioalkylphosphonates, thioalkylphosphotriesters, selenophosphates, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', a 5' to 5' or a 2' to 2' linkage.

A nucleic acid can comprise polynucleotide backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatomic and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These can include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH₂ component parts.

A nucleic acid can comprise a nucleic acid mimetic. The term "mimetic" can be intended to include polynucleotides wherein only the furanose ring or both the furanose ring and the internucleotide linkage are replaced with non-furanose groups, replacement of only the furanose ring can also be referred as being a sugar surrogate. The heterocyclic base moiety or a modified heterocyclic base moiety can be maintained for hybridization with an appropriate target nucleic acid. One such nucleic acid can be a peptide nucleic acid (PNA). In a PNA, the sugar-backbone of a polynucleotide can be replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleotides can be retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. The backbone in PNA compounds can comprise two or more

linked aminoethylglycine units which gives PNA an amide containing backbone. The heterocyclic base moieties can be bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone.

- 5 A nucleic acid can comprise a morpholino backbone structure. For example, a nucleic acid can comprise a 6-membered morpholino ring in place of a ribose ring. In some of these embodiments, a phosphorodiamidate or other non-phosphodiester internucleoside linkage can replace a 10 phosphodiester linkage.
- 15 A nucleic acid can comprise linked morpholino units (e.g., morpholino nucleic acid) having heterocyclic bases attached to the morpholino ring. Linking groups can link the morpholino monomeric units in a morpholino nucleic acid.
- 15 Non-ionic morpholino-based oligomeric compounds can have less undesired interactions with cellular proteins. Morpholino-based polynucleotides can be nonionic mimics of nucleic acids. A variety of compounds within the morpholino class can be joined using different linking groups. A 20 further class of polynucleotide mimetic can be referred to as cyclohexenyl nucleic acids (CeNA). The furanose ring normally present in a nucleic acid molecule can be replaced with a cyclohexenyl ring. CeNA DMT protected phosphoramidite monomers can be prepared and used for oligomeric 25 compound synthesis using phosphoramidite chemistry. The incorporation of CeNA monomers into a nucleic acid chain can increase the stability of a DNA/RNA hybrid. CeNA oligoadenylylates can form complexes with nucleic acid complements with similar stability to the native complexes.
- 30 A further modification can include Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 4' carbon atom of the sugar ring thereby forming a 2'-C, 4'-C-oxymethylene linkage thereby forming a bicyclic sugar moiety. The linkage can be a methylene (—CH₂), group 35 bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNA and LNA analogs can display very high duplex thermal stabilities with complementary nucleic acid (T_m=+3 to +10° C.), stability towards 3'-exonucleolytic degradation and good solubility properties.
- 40 A nucleic acid may also include nucleobase (often referred to simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases can include the purine bases, (e.g., adenine (A) and guanine (G)), and the pyrimidine bases, (e.g., thymine (T), cytosine (C) and uracil (U)). Modified nucleobases can include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives 45 of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (—C≡C—CH₃) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 50 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-aminoadenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Modified nucleobases can include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido(5,4-b)(1,4)benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido(5,4-b)(1,4)benzothiazin-2(3H)-one), 55 G-clamps such as a substituted phenoxazine cytidine (e.g., 9-(2-aminoethoxy)-H-pyrimido(5,4-b)(1,4)benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido(5,4-b)(1,4)

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benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g., 9-(2-aminoethoxy)-H-pyrimido (5,4-(b) (1,4)benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido(4,5-b)indol-2-one), pyridoindole cytidine (H-pyrido(3',2':4,5)pyrrolo[2,3-d]pyrimidin-2-one).

As used herein, the term "sample" can refer to a composition comprising targets. Suitable samples for analysis by the disclosed methods, devices, and systems include cells, tissues, organs, or organisms.

As used herein, the term "sampling device" or "device" can refer to a device which may take a section of a sample and/or place the section on a substrate. A sample device can refer to, for example, a fluorescence activated cell sorting (FACS) machine, a cell sorter machine, a biopsy needle, a biopsy device, a tissue sectioning device, a microfluidic device, a blade grid, and/or a microtome.

As used herein, the term "solid support" can refer to discrete solid or semi-solid surfaces to which a plurality of barcodes (e.g., stochastic barcodes) may be attached. A solid support may encompass any type of solid, porous, or hollow sphere, ball, bearing, cylinder, or other similar configuration composed of plastic, ceramic, metal, or polymeric material (e.g., hydrogel) onto which a nucleic acid may be immobilized (e.g., covalently or non-covalently). A solid support may comprise a discrete particle that may be spherical (e.g., microspheres) or have a non-spherical or irregular shape, such as cubic, cuboid, pyramidal, cylindrical, conical, oblong, or disc-shaped, and the like. A bead can be non-spherical in shape. A plurality of solid supports spaced in an array may not comprise a substrate. A solid support may be used interchangeably with the term "bead."

As used herein, the term "stochastic barcode" can refer to a polynucleotide sequence comprising labels of the present disclosure. A stochastic barcode can be a polynucleotide sequence that can be used for stochastic barcoding. Stochastic barcodes can be used to quantify targets within a sample. Stochastic barcodes can be used to control for errors which may occur after a label is associated with a target. For example, a stochastic barcode can be used to assess amplification or sequencing errors. A stochastic barcode associated with a target can be called a stochastic barcode-target or stochastic barcode-tag-target.

As used herein, the term "gene-specific stochastic barcode" can refer to a polynucleotide sequence comprising labels and a target-binding region that is gene-specific. A stochastic barcode can be a polynucleotide sequence that can be used for stochastic barcoding. Stochastic barcodes can be used to quantify targets within a sample. Stochastic barcodes can be used to control for errors which may occur after a label is associated with a target. For example, a stochastic barcode can be used to assess amplification or sequencing errors. A stochastic barcode associated with a target can be called a stochastic barcode-target or stochastic barcode-tag-target.

As used herein, the term "stochastic barcoding" can refer to the random labeling (e.g., barcoding) of nucleic acids. Stochastic barcoding can utilize a recursive Poisson strategy to associate and quantify labels associated with targets. As used herein, the term "stochastic barcoding" can be used interchangeably with "stochastic labeling."

As used here, the term "target" can refer to a composition which can be associated with a barcode (e.g., a stochastic barcode). Exemplary suitable targets for analysis by the disclosed methods, devices, and systems include oligonucleotides, DNA, RNA, mRNA, microRNA, tRNA, and the like. Targets can be single or double stranded. In some embodiments, targets can be proteins, peptides, or polypeptides. In

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some embodiments, targets are lipids. As used herein, "target" can be used interchangeably with "species."

As used herein, the term "reverse transcriptases" can refer to a group of enzymes having reverse transcriptase activity (i.e., that catalyze synthesis of DNA from an RNA template). In general, such enzymes include, but are not limited to, retroviral reverse transcriptase, retrotransposon reverse transcriptase, retroplasmid reverse transcriptases, retror reverse transcriptases, bacterial reverse transcriptases, group II intron-derived reverse transcriptase, and mutants, variants or derivatives thereof. Non-retroviral reverse transcriptases include non-LTR retrotransposon reverse transcriptases, retroplasmid reverse transcriptases, retror reverse transcriptases, and group II intron reverse transcriptases. Examples of group II intron reverse transcriptases include the *Lactococcus lactis* LI.LtrB intron reverse transcriptase, the *Thermosynechococcus elongatus* Tel4c intron reverse transcriptase, or the *Geobacillus stearothermophilus* GsI-IIIC intron reverse transcriptase. Other classes of reverse transcriptases can include many classes of non-retroviral reverse transcriptases (i.e., retrons, group II introns, and diversity-generating retroelements among others).

The terms "universal adaptor primer," "universal primer adaptor" or "universal adaptor sequence" are used interchangeably to refer to a nucleotide sequence that can be used to hybridize to barcodes (e.g., stochastic barcodes) to generate gene-specific barcodes. A universal adaptor sequence can, for example, be a known sequence that is universal across all barcodes used in methods of the disclosure. For example, when multiple targets are being labeled using the methods disclosed herein, each of the target-specific sequences may be linked to the same universal adaptor sequence. In some embodiments, more than one universal adaptor sequences may be used in the methods disclosed herein. For example, when multiple targets are being labeled using the methods disclosed herein, at least two of the target-specific sequences are linked to different universal adaptor sequences. A universal adaptor primer and its complement may be included in two oligonucleotides, one of which comprises a target-specific sequence and the other comprises a barcode. For example, a universal adaptor sequence may be part of an oligonucleotide comprising a target-specific sequence to generate a nucleotide sequence that is complementary to a target nucleic acid. A second oligonucleotide comprising a barcode and a complementary sequence of the universal adaptor sequence may hybridize with the nucleotide sequence and generate a target-specific barcode (e.g., a target-specific stochastic barcode). In some embodiments, a universal adaptor primer has a sequence that is different from a universal PCR primer used in the methods of this disclosure.

Barcodes

Barcode, such as stochastic barcoding, has been described in, for example, Fu et al., *Proc Natl Acad Sci U.S.A.*, 2011 May 31, 108(22):9026-31; U.S. Patent Application Publication No. US2011/0160078; Fan et al., *Science*, 2015 Feb. 6, 347(6222):1258367; US Patent Application Publication No. US2015/0299784; and PCT Application Publication No. WO2015/031691; the content of each of these, including any supporting or supplemental information or material, is incorporated herein by reference in its entirety. In some embodiments, the barcode disclosed herein can be a stochastic barcode which can be a polynucleotide sequence that may be used to stochastically label (e.g., barcode, tag) a target. Barcodes can be referred to stochastic barcodes if the ratio of the number of different barcode sequences of the stochastic barcodes and the number of

occurrence of any of the targets to be labeled can be, or be about, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 50:1, 60:1, 70:1, 80:1, 90:1, 100:1, or a number or a range between any two of these values. A target can be an mRNA species comprising mRNA molecules with identical or nearly identical sequences. Barcodes can be referred to as stochastic barcodes if the ratio of the number of different barcode sequences of the stochastic barcodes and the number of occurrence of any of the targets to be labeled is at least, or is at most, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 50:1, 60:1, 70:1, 80:1, 90:1, or 100:1. Barcode sequences of stochastic barcodes can be referred to as molecular labels.

A barcode, for example a stochastic barcode, can comprise one or more labels. Exemplary labels can include a universal label, a cell label, a barcode sequence (e.g., a molecular label), a sample label, a plate label, a spatial label, and/or a pre-spatial label. FIG. 1 illustrates an exemplary barcode 104 with a spatial label. The barcode 104 can comprise a 5' amine that may link the barcode to a solid support 105. The barcode can comprise a universal label, a dimension label, a spatial label, a cell label, and/or a molecular label. The order of different labels (including but not limited to the universal label, the dimension label, the spatial label, the cell label, and the molecule label) in the barcode can vary. For example, as shown in FIG. 1, the universal label may be the 5'-most label, and the molecular label may be the 3'-most label. The spatial label, dimension label, and the cell label may be in any order. In some embodiments, the universal label, the spatial label, the dimension label, the cell label, and the molecular label are in any order. The barcode can comprise a target-binding region. The target-binding region can interact with a target (e.g., target nucleic acid, RNA, mRNA, DNA) in a sample. For example, a target-binding region can comprise an oligo (dT) sequence which can interact with poly(A) tails of mRNAs. In some instances, the labels of the barcode (e.g., universal label, dimension label, spatial label, cell label, and barcode sequence) may be separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 or more nucleotides.

A label, for example the cell label, can comprise a unique set of nucleic acid sub-sequences of defined length, e.g., seven nucleotides each (equivalent to the number of bits used in some Hamming error correction codes), which can be designed to provide error correction capability. The set of error correction sub-sequences comprise seven nucleotide sequences can be designed such that any pairwise combination of sequences in the set exhibits a defined "genetic distance" (or number of mismatched bases), for example, a set of error correction sub-sequences can be designed to exhibit a genetic distance of three nucleotides. In this case, review of the error correction sequences in the set of sequence data for labeled target nucleic acid molecules (described more fully below) can allow one to detect or correct amplification or sequencing errors. In some embodiments, the length of the nucleic acid sub-sequences used for creating error correction codes can vary, for example, they can be, or be about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 31, 40, 50, or a number or a range between any two of these values, nucleotides in length. In some embodiments, nucleic acid sub-sequences of other lengths can be used for creating error correction codes.

The barcode can comprise a target-binding region. The target-binding region can interact with a target in a sample.

The target can be, or comprise, ribonucleic acids (RNAs), messenger RNAs (mRNAs), microRNAs, small interfering RNAs (siRNAs), RNA degradation products, RNAs each comprising a poly(A) tail, or any combination thereof. In some embodiments, the plurality of targets can include deoxyribonucleic acids (DNAs).

In some embodiments, a target-binding region can comprise an oligo(dT) sequence which can interact with poly(A) tails of mRNAs. One or more of the labels of the barcode 10 (e.g., the universal label, the dimension label, the spatial label, the cell label, and the barcode sequences (e.g., molecular label)) can be separated by a spacer from another one or two of the remaining labels of the barcode. The spacer can be, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20, or more nucleotides. In some embodiments, none of the labels of the barcode is separated by spacer.

Universal Labels

A barcode can comprise one or more universal labels. In 20 some embodiments, the one or more universal labels can be the same for all barcodes in the set of barcodes attached to a given solid support. In some embodiments, the one or more universal labels can be the same for all barcodes attached to a plurality of beads. In some embodiments, a universal label 25 can comprise a nucleic acid sequence that is capable of hybridizing to a sequencing primer. Sequencing primers can be used for sequencing barcodes comprising a universal label. Sequencing primers (e.g., universal sequencing primers) can comprise sequencing primers associated with high-throughput sequencing platforms. In some embodiments, a universal label can comprise a nucleic acid sequence that is capable of hybridizing to a PCR primer. In some embodiments, the universal label can comprise a nucleic acid sequence that is capable of hybridizing to a sequencing 30 primer and a PCR primer. The nucleic acid sequence of the universal label that is capable of hybridizing to a sequencing or PCR primer can be referred to as a primer binding site. A universal label can comprise a sequence that can be used to initiate transcription of the barcode. A universal label can 35 comprise a sequence that can be used for extension of the barcode or a region within the barcode. A universal label can be, or be about, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. For example, a universal label can 40 comprise at least about 10 nucleotides. A universal label can be at least, or be at most, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides in length. In some embodiments, a cleavable linker or modified nucleotide can be part of the universal label sequence to enable the barcode 45 to be cleaved off from the support.

Dimension Labels

A barcode can comprise one or more dimension labels. In some embodiments, a dimension label can comprise a nucleic acid sequence that provides information about a dimension in which the labeling (e.g., stochastic labeling) occurred. For example, a dimension label can provide information about the time at which a target was barcoded. A dimension label can be associated with a time of barcoding (e.g., stochastic barcoding) in a sample. A dimension label 55 can be activated at the time of labeling. Different dimension labels can be activated at different times. The dimension label provides information about the order in which targets, groups of targets, and/or samples were barcoded. For example, a population of cells can be barcoded at the G0 phase of the cell cycle. The cells can be pulsed again with barcodes (e.g., stochastic barcodes) at the G1 phase of the cell cycle. The cells can be pulsed again with barcodes at the 60 65

S phase of the cell cycle, and so on. Barcodes at each pulse (e.g., each phase of the cell cycle), can comprise different dimension labels. In this way, the dimension label provides information about which targets were labelled at which phase of the cell cycle. Dimension labels can interrogate many different biological times. Exemplary biological times can include, but are not limited to, the cell cycle, transcription (e.g., transcription initiation), and transcript degradation. In another example, a sample (e.g., a cell, a population of cells) can be labeled before and/or after treatment with a drug and/or therapy. The changes in the number of copies of distinct targets can be indicative of the sample's response to the drug and/or therapy.

A dimension label can be activatable. An activatable dimension label can be activated at a specific time point. The activatable label can be, for example, constitutively activated (e.g., not turned off). The activatable dimension label can be, for example, reversibly activated (e.g., the activatable dimension label can be turned on and turned off). The dimension label can be, for example, reversibly activatable at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more times. The dimension label can be reversibly activatable, for example, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more times. In some embodiments, the dimension label can be activated with fluorescence, light, a chemical event (e.g., cleavage, ligation of another molecule, addition of modifications (e.g., pegylated, sumoylated, acetylated, methylated, deacetylated, demethylated), a photochemical event (e.g., photocaging), and introduction of a non-natural nucleotide.

The dimension label can, in some embodiments, be identical for all barcodes (e.g., stochastic barcodes) attached to a given solid support (e.g., a bead), but different for different solid supports (e.g., beads). In some embodiments, at least 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99% or 100%, of barcodes on the same solid support can comprise the same dimension label. In some embodiments, at least 60% of barcodes on the same solid support can comprise the same dimension label. In some embodiments, at least 95% of barcodes on the same solid support can comprise the same dimension label.

There can be as many as 10^6 or more unique dimension label sequences represented in a plurality of solid supports (e.g., beads). A dimension label can be, or be about 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. A dimension label can be at least, or be at most, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300, nucleotides in length. A dimension label can comprise between about 5 to about 200 nucleotides. A dimension label can comprise between about 10 to about 150 nucleotides. A dimension label can comprise between about 20 to about 125 nucleotides in length.

Spatial Labels

A barcode can comprise one or more spatial labels. In some embodiments, a spatial label can comprise a nucleic acid sequence that provides information about the spatial orientation of a target molecule which is associated with the barcode. A spatial label can be associated with a coordinate in a sample. The coordinate can be a fixed coordinate. For example, a coordinate can be fixed in reference to a substrate. A spatial label can be in reference to a two or three-dimensional grid. A coordinate can be fixed in reference to a landmark. The landmark can be identifiable in space. A landmark can be a structure which can be imaged. A landmark can be a biological structure, for example an anatomical landmark. A landmark can be a cellular landmark, for instance an organelle. A landmark can be a

non-natural landmark such as a structure with an identifiable identifier such as a color code, bar code, magnetic property, fluorescents, radioactivity, or a unique size or shape. A spatial label can be associated with a physical partition (e.g., a well, a container, or a droplet). In some embodiments, multiple spatial labels are used together to encode one or more positions in space.

The spatial label can be identical for all barcodes attached to a given solid support (e.g., a bead), but different for different solid supports (e.g., beads). In some embodiments, the percentage of barcodes on the same solid support comprising the same spatial label can be, or be about, 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99%, or 100%. In some embodiments, at least 60% of barcodes on the same solid support can comprise the same spatial label. In some embodiments, at least 95% of barcodes on the same solid support can comprise the same spatial label.

There can be as many as 10^6 or more unique spatial label sequences represented in a plurality of solid supports (e.g., beads). A spatial label can be, or be about, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. A spatial label can be at least or at most 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides in length. A spatial label can comprise between about 5 to about 200 nucleotides. A spatial label can comprise between about 10 to about 150 nucleotides. A spatial label can comprise between about 20 to about 125 nucleotides in length.

Cell Labels

A barcode (e.g., a stochastic barcode) can comprise one or more cell labels. In some embodiments, a cell label can comprise a nucleic acid sequence that provides information for determining which target nucleic acid originated from which cell. In some embodiments, the cell label is identical for all barcodes attached to a given solid support (e.g., a bead), but different for different solid supports (e.g., beads). In some embodiments, the percentage of barcodes on the same solid support comprising the same cell label can be, or be about 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99%, 100%, or a number or a range between any two of these values. In some embodiments, the percentage of barcodes on the same solid support comprising the same cell label can be, or be about 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99%, or 100%. For example, at least 60% of barcodes on the same solid support can comprise the same cell label. As another example, at least 95% of barcodes on the same solid support can comprise the same cell label.

There can be as many as 10^6 or more unique cell label sequences represented in a plurality of solid supports (e.g., beads). A cell label can be, or be about, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. A cell label can be at least, or be at most, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides in length. For example, a cell label can comprise between about 5 to about 200 nucleotides. As another example, a cell label can comprise between about 10 to about 150 nucleotides. As yet another example, a cell label can comprise between about 20 to about 125 nucleotides in length.

Barcode Sequences

A barcode can comprise one or more barcode sequences. In some embodiments, a barcode sequence can comprise a nucleic acid sequence that provides identifying information

for the specific type of target nucleic acid species hybridized to the barcode. A barcode sequence can comprise a nucleic acid sequence that provides a counter (e.g., that provides a rough approximation) for the specific occurrence of the target nucleic acid species hybridized to the barcode (e.g., target-binding region).

In some embodiments, a diverse set of barcode sequences are attached to a given solid support (e.g., a bead). In some embodiments, there can be, or be about, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or a number or a range between any two of these values, unique molecular label sequences. For example, a plurality of barcodes can comprise about 6561 barcode sequences with distinct sequences. As another example, a plurality of barcodes can comprise about 65536 barcode sequences with distinct sequences. In some embodiments, there can be at least, or be at most, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , or 10^9 , unique barcode sequences. The unique molecular label sequences can be attached to a given solid support (e.g., a bead). In some embodiments, the unique molecular label sequence is partially or entirely encompassed by a particle (e.g., a hydrogel bead).

The length of a barcode can be different in different implementations. For example, a barcode can be, or be about, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. As another example, a barcode can be at least, or be at most, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides in length.

Molecular Labels

A barcode (e.g., a stochastic barcode) can comprise one or more molecular labels. Molecular labels can include barcode sequences. In some embodiments, a molecular label can comprise a nucleic acid sequence that provides identifying information for the specific type of target nucleic acid species hybridized to the barcode. A molecular label can comprise a nucleic acid sequence that provides a counter for the specific occurrence of the target nucleic acid species hybridized to the barcode (e.g., target-binding region).

In some embodiments, a diverse set of molecular labels are attached to a given solid support (e.g., a bead). In some embodiments, there can be, or be about, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or a number or a range between any two of these values, of unique molecular label sequences. For example, a plurality of barcodes can comprise about 6561 molecular labels with distinct sequences. As another example, a plurality of barcodes can comprise about 65536 molecular labels with distinct sequences. In some embodiments, there can be at least, or be at most, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , or 10^9 , unique molecular label sequences. Barcodes with unique molecular label sequences can be attached to a given solid support (e.g., a bead).

For barcoding (e.g., stochastic barcoding) using a plurality of stochastic barcodes, the ratio of the number of different molecular label sequences and the number of occurrence of any of the targets can be, or be about, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 50:1, 60:1, 70:1, 80:1, 90:1, 100:1, or a number or a range between any two of these values. A target can be an mRNA species comprising mRNA molecules with identical or nearly identical sequences. In some embodiments, the ratio of the number of different molecular label sequences and the number of occurrence of any of the targets is at least, or is at most, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 50:1, 60:1, 70:1, 80:1, 90:1, or 100:1.

A molecular label can be, or be about, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. A molecular label can be at least, or be at most, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides in length.

Target-Binding Region

A barcode can comprise one or more target binding regions, such as capture probes. In some embodiments, a target-binding region can hybridize with a target of interest. 10 In some embodiments, the target binding regions can comprise a nucleic acid sequence that hybridizes specifically to a target (e.g., target nucleic acid, target molecule, e.g., a cellular nucleic acid to be analyzed), for example to a specific gene sequence. In some embodiments, a target binding region can comprise a nucleic acid sequence that can attach (e.g., hybridize) to a specific location of a specific target nucleic acid. In some embodiments, the target binding region can comprise a nucleic acid sequence that is capable of specific hybridization to a restriction enzyme site overhang (e.g., an EcoRI sticky-end overhang). The barcode can then ligate to any nucleic acid molecule comprising a sequence complementary to the restriction site overhang.

In some embodiments, a target binding region can comprise a non-specific target nucleic acid sequence. A non-specific target nucleic acid sequence can refer to a sequence that can bind to multiple target nucleic acids, independent of the specific sequence of the target nucleic acid. For example, target binding region can comprise a random multimer sequence, a poly(dA) sequence, a poly(dT) sequence, a poly(dG) sequence, a poly(dC) sequence, or a combination thereof. For example, the target binding region can be an oligo(dT) sequence that hybridizes to the poly(A) tail on mRNA molecules. A random multimer sequence can be, for example, a random dimer, trimer, quaternary, pentamer, hexamer, septamer, octamer, nonamer, decamer, or higher multimer sequence of any length. In some embodiments, the target binding region is the same for all barcodes attached to a given bead. In some embodiments, the target binding regions for the plurality of barcodes attached to a given bead can comprise two or more different target binding sequences. A target binding region can be, or be about, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or a number or a range between any two of these values, nucleotides in length. A target binding region can be at most about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more nucleotides in length. For example, an mRNA molecule can be reverse transcribed using a reverse transcriptase, such as Moloney murine leukemia virus (MMLV) reverse transcriptase, to generate a cDNA molecule with a poly(dC) tail. A barcode can include a target binding region with a poly(dG) tail. Upon base pairing between the poly(dG) tail of the barcode and the poly(dC) tail of the cDNA molecule, the reverse transcriptase switches template strands, from cellular RNA molecule to the barcode, and continues replication to the 5' end of the barcode. By doing so, the resulting cDNA molecule contains the sequence of the barcode (such as the molecular label) on the 3' end of the cDNA molecule.

In some embodiments, a target-binding region can comprise an oligo(dT) which can hybridize with mRNAs comprising polyadenylated ends. A target-binding region can be gene-specific. For example, a target-binding region can be configured to hybridize to a specific region of a target. A target-binding region can be, or be about, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or a number or a range between any two of these values, nucleotides in length. A target-binding region can be at least, or be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9,

10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 27, 28, 29, or 30, nucleotides in length. A target-binding region can be about 5-30 nucleotides in length. When a barcode comprises a gene-specific target-binding region, the barcode can be referred to herein as a gene-specific barcode.

Orientation Property

A stochastic barcode (e.g., a stochastic barcode) can comprise one or more orientation properties which can be used to orient (e.g., align) the barcodes. A barcode can comprise a moiety for isoelectric focusing. Different barcodes can comprise different isoelectric focusing points. When these barcodes are introduced to a sample, the sample can undergo isoelectric focusing in order to orient the barcodes into a known way. In this way, the orientation property can be used to develop a known map of barcodes in a sample. Exemplary orientation properties can include, electrophoretic mobility (e.g., based on size of the barcode), isoelectric point, spin, conductivity, and/or self-assembly. For example, barcodes with an orientation property of self-assembly, can self-assemble into a specific orientation (e.g., nucleic acid nanostructure) upon activation.

Affinity Property

A barcode (e.g., a stochastic barcode) can comprise one or more affinity properties. For example, a spatial label can comprise an affinity property. An affinity property can include a chemical and/or biological moiety that can facilitate binding of the barcode to another entity (e.g., cell receptor). For example, an affinity property can comprise an antibody, for example, an antibody specific for a specific moiety (e.g., receptor) on a sample. In some embodiments, the antibody can guide the barcode to a specific cell type or molecule. Targets at and/or near the specific cell type or molecule can be labeled (e.g., stochastically labeled). The affinity property can, in some embodiments, provide spatial information in addition to the nucleotide sequence of the spatial label because the antibody can guide the barcode to a specific location. The antibody can be a therapeutic antibody, for example a monoclonal antibody or a polyclonal antibody. The antibody can be humanized or chimeric. The antibody can be a naked antibody or a fusion antibody.

The antibody can be a full-length (i.e., naturally occurring or formed by normal immunoglobulin gene fragment recombinatorial processes) immunoglobulin molecule (e.g., an IgG antibody) or an immunologically active (i.e., specifically binding) portion of an immunoglobulin molecule, like an antibody fragment.

The antibody fragment can be, for example, a portion of an antibody such as F(ab')2, Fab', Fab, Fv, sFv and the like. In some embodiments, the antibody fragment can bind with the same antigen that is recognized by the full-length antibody. The antibody fragment can include isolated fragments consisting of the variable regions of antibodies, such as the "Fv" fragments consisting of the variable regions of the heavy and light chains and recombinant single chain polypeptide molecules in which light and heavy variable regions are connected by a peptide linker ("scFv proteins"). Exemplary antibodies can include, but are not limited to, antibodies for cancer cells, antibodies for viruses, antibodies that bind to cell surface receptors (CD8, CD34, CD45), and therapeutic antibodies.

Universal Adaptor Primer

A barcode can comprise one or more universal adaptor primers. For example, a gene-specific barcode, such as a gene-specific stochastic barcode, can comprise a universal adaptor primer. A universal adaptor primer can refer to a nucleotide sequence that is universal across all barcodes. A universal adaptor primer can be used for building gene-

specific barcodes. A universal adaptor primer can be, or be about, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 27, 28, 29, 30, or a number or a range between any two of these nucleotides in length.

5 A universal adaptor primer can be at least, or be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 27, 28, 29, or 30 nucleotides in length. A universal adaptor primer can be from 5-30 nucleotides in length.

Linker

When a barcode comprises more than one of a type of label (e.g., more than one cell label or more than one barcode sequence, such as one molecular label), the labels may be interspersed with a linker label sequence. A linker label sequence can be at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more nucleotides in length. A linker label sequence can be at most about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50 or more nucleotides in length. In some instances, a linker label sequence is 12 nucleotides in length. A linker label sequence can be used to facilitate the synthesis of the barcode. The linker label can comprise an error-correcting (e.g., Hamming) code.

Solid Supports

Barcodes, such as stochastic barcodes, disclosed herein can, in some embodiments, be associated with a solid support. The solid support can be, for example, a synthetic particle. In some embodiments, some or all of the barcode sequences, such as molecular labels for stochastic barcodes (e.g., the first barcode sequences) of a plurality of barcodes (e.g., the first plurality of barcodes) on a solid support differ by at least one nucleotide. The cell labels of the barcodes on the same solid support can be the same. The cell labels of the barcodes on different solid supports can differ by at least one nucleotide. For example, first cell labels of a first plurality of barcodes on a first solid support can have the same sequence, and second cell labels of a second plurality of barcodes on a second solid support can have the same sequence. The first cell labels of the first plurality of barcodes on the first solid support and the second cell labels of the second plurality of barcodes on the second solid support can differ by at least one nucleotide. A cell label can be, for example, about 5-20 nucleotides long. A barcode sequence can be, for example, about 5-20 nucleotides long. The synthetic particle can be, for example, a bead.

45 The bead can be, for example, a silica gel bead, a controlled pore glass bead, a magnetic bead, a Dynabead, a Sephadex/Sephadose bead, a cellulose bead, a polystyrene bead, or any combination thereof. The bead can comprise a material such as polydimethylsiloxane (PDMS), polystyrene, glass, polypropylene, agarose, gelatin, hydrogel, paramagnetic, ceramic, plastic, glass, methylstyrene, acrylic polymer, titanium, latex, Sephadose, cellulose, nylon, silicone, or any combination thereof.

In some embodiments, the bead can be a polymeric bead, 55 for example a deformable bead or a gel bead, functionalized with barcodes or stochastic barcodes (such as gel beads from 10x Genomics (San Francisco, CA). In some implementation, a gel bead can comprise a polymer based gels. Gel beads can be generated, for example, by encapsulating one or more polymeric precursors into droplets. Upon exposure of the polymeric precursors to an accelerator (e.g., tetramethylethylenediamine (TEMED)), a gel bead may be generated.

In some embodiments, the particle can be disruptable 60 (e.g., dissolvable, degradable). For example, the polymeric bead can dissolve, melt, or degrade, for example, under a desired condition. The desired condition can include an

environmental condition. The desired condition may result in the polymeric bead dissolving, melting, or degrading in a controlled manner. A gel bead may dissolve, melt, or degrade due to a chemical stimulus, a physical stimulus, a biological stimulus, a thermal stimulus, a magnetic stimulus, an electric stimulus, a light stimulus, or any combination thereof.

Analytes and/or reagents, such as oligonucleotide barcodes, for example, may be coupled/immobilized to the interior surface of a gel bead (e.g., the interior accessible via diffusion of an oligonucleotide barcode and/or materials used to generate an oligonucleotide barcode) and/or the outer surface of a gel bead or any other microcapsule described herein. Coupling/immobilization may be via any form of chemical bonding (e.g., covalent bond, ionic bond) or physical phenomena (e.g., Van der Waals forces, dipole-dipole interactions, etc.). In some embodiments, coupling/immobilization of a reagent to a gel bead or any other microcapsule described herein may be reversible, such as, for example, via a labile moiety (e.g., via a chemical cross-linker, including chemical cross-linkers described herein). Upon application of a stimulus, the labile moiety may be cleaved and the immobilized reagent set free. In some embodiments, the labile moiety is a disulfide bond. For example, in the case where an oligonucleotide barcode is immobilized to a gel bead via a disulfide bond, exposure of the disulfide bond to a reducing agent can cleave the disulfide bond and free the oligonucleotide barcode from the bead. The labile moiety may be included as part of a gel bead or microcapsule, as part of a chemical linker that links a reagent or analyte to a gel bead or microcapsule, and/or as part of a reagent or analyte. In some embodiments, at least one barcode of the plurality of barcodes can be immobilized on the particle, partially immobilized on the particle, enclosed in the particle, partially enclosed in the particle, or any combination thereof.

In some embodiments, a gel bead can comprise a wide range of different polymers including but not limited to: polymers, heat sensitive polymers, photosensitive polymers, magnetic polymers, pH sensitive polymers, salt-sensitive polymers, chemically sensitive polymers, polyelectrolytes, polysaccharides, peptides, proteins, and/or plastics. Polymers may include but are not limited to materials such as poly(N-isopropylacrylamide) (PNIPAAm), poly(styrene sulfonate) (PSS), poly(allyl amine) (PAAm), poly(acrylic acid) (PAA), poly(ethylene imine) (PEI), poly(diallyldimethyl-ammonium chloride) (PDADMAC), poly(pyrrrole) (PPy), poly(vinylpyrrolidone) (PVON), poly(vinyl pyridine) (PVP), poly(methacrylic acid) (PMAA), poly(methyl methacrylate) (PMMA), polystyrene (PS), poly(tetrahydrofuran) (PTHF), poly(phthaladehyde) (PTHF), poly(hexyl viologen) (PHV), poly(L-lysine) (PLL), poly(L-arginine) (PARG), poly(lactic-co-glycolic acid) (PLGA).

Numerous chemical stimuli can be used to trigger the disruption, dissolution, or degradation of the beads. Examples of these chemical changes may include, but are not limited to pH-mediated changes to the bead wall, disintegration of the bead wall via chemical cleavage of cross-link bonds, triggered depolymerization of the bead wall, and bead wall switching reactions. Bulk changes may also be used to trigger disruption of the beads.

Bulk or physical changes to the microcapsule through various stimuli also offer many advantages in designing capsules to release reagents. Bulk or physical changes occur on a macroscopic scale, in which bead rupture is the result of mechano-physical forces induced by a stimulus. These

processes may include, but are not limited to pressure induced rupture, bead wall melting, or changes in the porosity of the bead wall.

Biological stimuli may also be used to trigger disruption, dissolution, or degradation of beads. Generally, biological triggers resemble chemical triggers, but many examples use biomolecules, or molecules commonly found in living systems such as enzymes, peptides, saccharides, fatty acids, nucleic acids and the like. For example, beads may comprise polymers with peptide cross-links that are sensitive to cleavage by specific proteases. More specifically, one example may comprise a microcapsule comprising GFLGK peptide cross links. Upon addition of a biological trigger such as the protease Cathepsin B, the peptide cross links of the shell well are cleaved and the contents of the beads are released. In other cases, the proteases may be heat-activated. In another example, beads comprise a shell wall comprising cellulose. Addition of the hydrolytic enzyme chitosan serves as biologic trigger for cleavage of cellulosic bonds, depolymerization of the shell wall, and release of its inner contents.

The beads may also be induced to release their contents upon the application of a thermal stimulus. A change in temperature can cause a variety changes to the beads. A change in heat may cause melting of a bead such that the bead wall disintegrates. In other cases, the heat may increase the internal pressure of the inner components of the bead such that the bead ruptures or explodes. In still other cases, the heat may transform the bead into a shrunken dehydrated state. The heat may also act upon heat-sensitive polymers within the wall of a bead to cause disruption of the bead.

Inclusion of magnetic nanoparticles to the bead wall of microcapsules may allow triggered rupture of the beads as well as guide the beads in an array. A device of this disclosure may comprise magnetic beads for either purpose. In one example, incorporation of Fe_3O_4 nanoparticles into polyelectrolyte containing beads triggers rupture in the presence of an oscillating magnetic field stimulus.

A bead may also be disrupted, dissolved, or degraded as the result of electrical stimulation. Similar to magnetic particles described in the previous section, electrically sensitive beads can allow for both triggered rupture of the beads as well as other functions such as alignment in an electric field, electrical conductivity or redox reactions. In one example, beads containing electrically sensitive material are aligned in an electric field such that release of inner reagents can be controlled. In other examples, electrical fields may induce redox reactions within the bead wall itself that may increase porosity.

A light stimulus may also be used to disrupt the beads. Numerous light triggers are possible and may include systems that use various molecules such as nanoparticles and chromophores capable of absorbing photons of specific ranges of wavelengths. For example, metal oxide coatings can be used as capsule triggers. UV irradiation of polyelectrolyte capsules coated with SiO_2 may result in disintegration of the bead wall. In yet another example, photo switchable materials such as azobenzene groups may be incorporated in the bead wall. Upon the application of UV or visible light, chemicals such as these undergo a reversible cis-to-trans isomerization upon absorption of photons. In this aspect, incorporation of photon switches result in a bead wall that may disintegrate or become more porous upon the application of a light trigger.

For example, in a non-limiting example of barcoding (e.g., stochastic barcoding) illustrated in FIG. 2, after introducing cells such as single cells onto a plurality of microw-

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ells of a microwell array at block 208, beads can be introduced onto the plurality of microwells of the microwell array at block 212. Each microwell can comprise one bead. The beads can comprise a plurality of barcodes. A barcode can comprise a 5' amine region attached to a bead. The barcode can comprise a universal label, a barcode sequence (e.g., a molecular label), a target-binding region, or any combination thereof.

The barcodes disclosed herein can be associated with (e.g., attached to) a solid support (e.g., a bead). The barcodes associated with a solid support can each comprise a barcode sequence selected from a group comprising at least 100 or 1000 barcode sequences with unique sequences. In some embodiments, different barcodes associated with a solid support can comprise barcode with different sequences. In some embodiments, a percentage of barcodes associated with a solid support comprises the same cell label. For example, the percentage can be, or be about 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99%, 100%, or a number or a range between any two of these values. As another example, the percentage can be at least, or be at most 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99%, or 100%. In some embodiments, barcodes associated with a solid support can have the same cell label. The barcodes associated with different solid supports can have different cell labels selected from a group comprising at least 100 or 1000 cell labels with unique sequences.

The barcodes disclosed herein can be associated to (e.g., attached to) a solid support (e.g., a bead). In some embodiments, barcoding the plurality of targets in the sample can be performed with a solid support including a plurality of synthetic particles associated with the plurality of barcodes. In some embodiments, the solid support can include a plurality of synthetic particles associated with the plurality of barcodes. The spatial labels of the plurality of barcodes on different solid supports can differ by at least one nucleotide. The solid support can, for example, include the plurality of barcodes in two dimensions or three dimensions. The synthetic particles can be beads. The beads can be silica gel beads, controlled pore glass beads, magnetic beads, Dynabeads, Sephadex/Sephadose beads, cellulose beads, polystyrene beads, or any combination thereof. The solid support can include a polymer, a matrix, a hydrogel, a needle array device, an antibody, or any combination thereof. In some embodiments, the solid supports can be free floating. In some embodiments, the solid supports can be embedded in a semi-solid or solid array. The barcodes may not be associated with solid supports. The barcodes can be individual nucleotides. The barcodes can be associated with a substrate.

As used herein, the terms "tethered," "attached," and "immobilized," are used interchangeably, and can refer to covalent or non-covalent means for attaching barcodes to a solid support. Any of a variety of different solid supports can be used as solid supports for attaching pre-synthesized barcodes or for *in situ* solid-phase synthesis of barcode.

In some embodiments, the solid support is a bead. The bead can comprise one or more types of solid, porous, or hollow sphere, ball, bearing, cylinder, or other similar configuration which a nucleic acid can be immobilized (e.g., covalently or non-covalently). The bead can be, for example, composed of plastic, ceramic, metal, polymeric material, or any combination thereof. A bead can be, or comprise, a discrete particle that is spherical (e.g., microspheres) or have a non-spherical or irregular shape, such as cubic, cuboid,

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pyramidal, cylindrical, conical, oblong, or disc-shaped, and the like. In some embodiments, a bead can be non-spherical in shape.

Beads can comprise a variety of materials including, but not limited to, paramagnetic materials (e.g., magnesium, molybdenum, lithium, and tantalum), superparamagnetic materials (e.g., ferrite (Fe_3O_4 ; magnetite) nanoparticles), ferromagnetic materials (e.g., iron, nickel, cobalt, some alloys thereof, and some rare earth metal compounds), 10 ceramic, plastic, glass, polystyrene, silica, methylstyrene, acrylic polymers, titanium, latex, Sepharose, agarose, hydrogel, polymer, cellulose, nylon, or any combination thereof.

In some embodiments, the bead (e.g., the bead to which the labels are attached) is a hydrogel bead. In some embodiments, the bead comprises hydrogel.

Some embodiments disclosed herein include one or more particles (for example, beads). Each of the particles can comprise a plurality of oligonucleotides (e.g., barcodes). Each of the plurality of oligonucleotides can comprise a 20 barcode sequence (e.g., a molecular label sequence), a cell label, and a target-binding region (e.g., an oligo(dT) sequence, a gene-specific sequence, a random multimer, or a combination thereof). The cell label sequence of each of the plurality of oligonucleotides can be the same. The cell 25 label sequences of oligonucleotides on different particles can be different such that the oligonucleotides on different particles can be identified. The number of different cell label sequences can be different in different implementations. In some embodiments, the number of cell label sequences can be 30 be, or be about 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000, 10^6 , 10^7 , 10^8 , 10^9 , a number or a range between any two of these values, or more. In some embodiments, the number of cell label sequences can be at least, or be at most 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000, 10^6 , 10^7 , 10^8 , or 10^9 . In some embodiments, 35 no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, or more of the plurality of the particles include oligonucleotides with the same cell sequence. In some embodiment, the plurality of particles that include oligonucleotides with the same cell sequence can be at most 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, or more. In some embodiments, none of the plurality of the particles has the same cell label sequence.

The plurality of oligonucleotides on each particle can comprise different barcode sequences (e.g., molecular labels). In some embodiments, the number of barcode sequences can be, or be about 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000, 10^6 , 10^7 , 10^8 , 10^9 , or a number or a range between any two of these values. In some embodiments, the number of barcode sequences can be at least, or be at most 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000, 10^6 , 10^7 , 10^8 , or 10^9 . For example, at least 100 of the plurality of oligonucleotides comprise different barcode sequences. As another example, in a single particle, at least 100, 500, 1000, 5000, 10000, 15000, 20000, 50000, a number or a range between any two of these values, or more of the plurality of oligonucleotides

comprise different barcode sequences. Some embodiments provide a plurality of the particles comprising barcodes. In some embodiments, the ratio of an occurrence (or a copy or a number) of a target to be labeled and the different barcode sequences can be at least 1:1, 1:2, 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:11, 1:12, 1:13, 1:14, 1:15, 1:16, 1:17, 1:18, 1:19, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90, or more. In some embodiments, each of the plurality of oligonucleotides further comprises a sample label, a universal label, or both. The particle can be, for example, a nanoparticle or microparticle.

The size of the beads can vary. For example, the diameter of the bead can range from 0.1 micrometer to 50 micrometer. In some embodiments, the diameter of the bead can be, or be about, 0.1, 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50 micrometer, or a number or a range between any two of these values.

The diameter of the bead can be related to the diameter of the wells of the substrate. In some embodiments, the diameter of the bead can be, or be about, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, or a number or a range between any two of these values, longer or shorter than the diameter of the well. The diameter of the beads can be related to the diameter of a cell (e.g., a single cell entrapped by a well of the substrate). In some embodiments, the diameter of the bead can be at least, or be at most, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, or 100% longer or shorter than the diameter of the well. The diameter of the beads can be related to the diameter of a cell (e.g., a single cell entrapped by a well of the substrate). In some embodiments, the diameter of the bead can be, or be about, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, 200%, 250%, 300%, or a number or a range between any two of these values, longer or shorter than the diameter of the cell. In some embodiments, the diameter of the beads can be at least, or be at most, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, 200%, 250%, or 300% longer or shorter than the diameter of the cell.

A bead can be attached to and/or embedded in a substrate. A bead can be attached to and/or embedded in a gel, hydrogel, polymer and/or matrix. The spatial position of a bead within a substrate (e.g., gel, matrix, scaffold, or polymer) can be identified using the spatial label present on the barcode on the bead which can serve as a location address.

Examples of beads can include, but are not limited to, streptavidin beads, agarose beads, magnetic beads, Dynabeads®, MACS® microbeads, antibody conjugated beads (e.g., anti-immunoglobulin microbeads), protein A conjugated beads, protein G conjugated beads, protein A/G conjugated beads, protein L conjugated beads, oligo(dT) conjugated beads, silica beads, silica-like beads, anti-biotin microbeads, anti-fluorochrome microbeads, and BcMag™ Carboxyl-Terminated Magnetic Beads.

A bead can be associated with (e.g., impregnated with) quantum dots or fluorescent dyes to make it fluorescent in one fluorescence optical channel or multiple optical channels. A bead can be associated with iron oxide or chromium oxide to make it paramagnetic or ferromagnetic. Beads can be identifiable. For example, a bead can be imaged using a camera. A bead can have a detectable code associated with the bead. For example, a bead can comprise a barcode. A bead can change size, for example, due to swelling in an organic or inorganic solution. A bead can be hydrophobic. A bead can be hydrophilic. A bead can be biocompatible.

A solid support (e.g., a bead) can be visualized. The solid support can comprise a visualizing tag (e.g., fluorescent

dye). A solid support (e.g., a bead) can be etched with an identifier (e.g., a number). The identifier can be visualized through imaging the beads.

A solid support can comprise an insoluble, semi-soluble, or insoluble material. A solid support can be referred to as “functionalized” when it includes a linker, a scaffold, a building block, or other reactive moiety attached thereto, whereas a solid support may be “nonfunctionalized” when it lacks such a reactive moiety attached thereto. The solid support can be employed free in solution, such as in a microtiter well format; in a flow-through format, such as in a column; or in a dipstick.

The solid support can comprise a membrane, paper, plastic, coated surface, flat surface, glass, slide, chip, or any combination thereof. A solid support can take the form of resins, gels, microspheres, or other geometric configurations. A solid support can comprise silica chips, microparticles, nanoparticles, plates, arrays, capillaries, flat supports such as glass fiber filters, glass surfaces, metal surfaces (steel, gold silver, aluminum, silicon and copper), glass supports, plastic supports, silicon supports, chips, filters, membranes, microwell plates, slides, plastic materials including multiwell plates or membranes (e.g., formed of polyethylene, polypropylene, polyamide, polyvinylidene fluoride), and/or wafers, combs, pins or needles (e.g., arrays of pins suitable for combinatorial synthesis or analysis) or beads in an array of pits or nanoliter wells of flat surfaces such as wafers (e.g., silicon wafers), wafers with pits with or without filter bottoms.

The solid support can comprise a polymer matrix (e.g., gel, hydrogel). The polymer matrix may be able to permeate intracellular space (e.g., around organelles). The polymer matrix may be able to be pumped throughout the circulatory system.

35 Substrates and Microwell Array

As used herein, a substrate can refer to a type of solid support. A substrate can refer to a solid support that can comprise barcodes or stochastic barcodes of the disclosure. A substrate can, for example, comprise a plurality of microwells. For example, a substrate can be a well array comprising two or more microwells. In some embodiments, a microwell can comprise a small reaction chamber of defined volume. In some embodiments, a microwell can entrap one or more cells. In some embodiments, a microwell can entrap only one cell. In some embodiments, a microwell can entrap one or more solid supports. In some embodiments, a microwell can entrap only one solid support. In some embodiments, a microwell entraps a single cell and a single solid support (e.g., a bead). A microwell can comprise barcode reagents of the disclosure.

Methods of Barcoding

The disclosure provides for methods for estimating the number of distinct targets at distinct locations in a physical sample (e.g., tissue, organ, tumor, cell). The methods can comprise placing barcodes (e.g., stochastic barcodes) in close proximity with the sample, lysing the sample, associating distinct targets with the barcodes, amplifying the targets and/or digitally counting the targets. The method can further comprise analyzing and/or visualizing the information obtained from the spatial labels on the barcodes. In some embodiments, a method comprises visualizing the plurality of targets in the sample. Mapping the plurality of targets onto the map of the sample can include generating a two dimensional map or a three dimensional map of the sample. The two dimensional map and the three dimensional map can be generated prior to or after barcoding (e.g., stochastically barcoding) the plurality of targets in the

sample. Visualizing the plurality of targets in the sample can include mapping the plurality of targets onto a map of the sample. Mapping the plurality of targets onto the map of the sample can include generating a two dimensional map or a three dimensional map of the sample. The two dimensional map and the three dimensional map can be generated prior to or after barcoding the plurality of targets in the sample. In some embodiments, the two dimensional map and the three dimensional map can be generated before or after lysing the sample. Lysing the sample before or after generating the two dimensional map or the three dimensional map can include heating the sample, contacting the sample with a detergent, changing the pH of the sample, or any combination thereof.

In some embodiments, barcoding the plurality of targets comprises hybridizing a plurality of barcodes with a plurality of targets to create barcoded targets (e.g., stochastically barcoded targets). Barcoding the plurality of targets can comprise generating an indexed library of the barcoded targets. Generating an indexed library of the barcoded targets can be performed with a solid support comprising the plurality of barcodes (e.g., stochastic barcodes).

Contacting a Sample and a Barcode

The disclosure provides for methods for contacting a sample (e.g., cells) to a substrate of the disclosure. A sample comprising, for example, a cell, organ, or tissue thin section, can be contacted to barcodes (e.g., stochastic barcodes). The cells can be contacted, for example, by gravity flow wherein the cells can settle and create a monolayer. The sample can be a tissue thin section. The thin section can be placed on the substrate. The sample can be one-dimensional (e.g., forms a planar surface). The sample (e.g., cells) can be spread across the substrate, for example, by growing/culturing the cells on the substrate.

When barcodes are in close proximity to targets, the targets can hybridize to the barcode. The barcodes can be contacted at a non-depletable ratio such that each distinct target can associate with a distinct barcode of the disclosure. To ensure efficient association between the target and the barcode, the targets can be cross-linked to barcode.

Cell Lysis

Following the distribution of cells and barcodes, the cells can be lysed to liberate the target molecules. Cell lysis can be accomplished by any of a variety of means, for example, by chemical or biochemical means, by osmotic shock, or by means of thermal lysis, mechanical lysis, or optical lysis. Cells can be lysed by addition of a cell lysis buffer comprising a detergent (e.g., SDS, Li dodecyl sulfate, Triton X-100, Tween-20, or NP-40), an organic solvent (e.g., methanol or acetone), or digestive enzymes (e.g., proteinase K, pepsin, or trypsin), or any combination thereof. To increase the association of a target and a barcode, the rate of the diffusion of the target molecules can be altered by for example, reducing the temperature and/or increasing the viscosity of the lysate.

In some embodiments, the sample can be lysed using a filter paper. The filter paper can be soaked with a lysis buffer on top of the filter paper. The filter paper can be applied to the sample with pressure which can facilitate lysis of the sample and hybridization of the targets of the sample to the substrate.

In some embodiments, lysis can be performed by mechanical lysis, heat lysis, optical lysis, and/or chemical lysis. Chemical lysis can include the use of digestive enzymes such as proteinase K, pepsin, and trypsin. Lysis can be performed by the addition of a lysis buffer to the substrate. A lysis buffer can comprise Tris HCl. A lysis buffer can comprise at least about 0.01, 0.05, 0.1, 0.5, or 1 M or

more Tris HCl. A lysis buffer can comprise at most about 0.01, 0.05, 0.1, 0.5, or 1 M or more Tris HCl. A lysis buffer can comprise about 0.1 M Tris HCl. The pH of the lysis buffer can be at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more. The pH of the lysis buffer can be at most about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more. In some embodiments, the pH of the lysis buffer is about 7.5. The lysis buffer can comprise a salt (e.g., LiCl). The concentration of salt in the lysis buffer can be at least about 0.1, 0.5, or 1 M or more. The concentration of salt in the lysis buffer can be at most about 0.1, 0.5, or 1 M or more. In some embodiments, the concentration of salt in the lysis buffer is about 0.5M. The lysis buffer can comprise a detergent (e.g., SDS, Li dodecyl sulfate, triton X, tween, NP-40). The concentration of the detergent in the lysis buffer can be at least about 0.0001%, 0.0005%, 0.001%, 0.005%, 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, or 7%, or more. The concentration of the detergent in the lysis buffer can be at most about 0.0001%, 0.0005%, 0.001%, 0.005%, 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, or 7%, or more. In some embodiments, the concentration of the detergent in the lysis buffer is about 1% Li dodecyl sulfate. The time used in the method for lysis can be dependent on the amount of detergent used. In some embodiments, the more detergent used, the less time needed for lysis. The lysis buffer can comprise a chelating agent (e.g., EDTA and EGTA). The concentration of a chelating agent in the lysis buffer can be at least about 1, 5, 10, 15, 20, 25, or 30 mM or more. The concentration of a chelating agent in the lysis buffer can be at most about 1, 5, 10, 15, 20, 25, or 30 mM or more. In some embodiments, the concentration of chelating agent in the lysis buffer is about 10 mM. The lysis buffer can comprise a reducing reagent (e.g., beta-mercaptoethanol, DTT). The concentration of the reducing reagent in the lysis buffer can be at least about 1, 5, 10, 15, or 20 mM or more. The concentration of the reducing reagent in the lysis buffer can be at most about 1, 5, 10, 15, or 20 mM or more. In some embodiments, the concentration of reducing reagent in the lysis buffer is about 5 mM. In some embodiments, a lysis buffer can comprise about 0.1M TrisHCl, about pH 7.5, about 0.5M LiCl, about 1% lithium dodecyl sulfate, about 10 mM EDTA, and about 5 mM DTT.

Lysis can be performed at a temperature of about 4, 10, 15, 20, 25, or 30° C. Lysis can be performed for about 1, 5, 10, 15, or 20 or more minutes. A lysed cell can comprise at least about 100000, 200000, 300000, 400000, 500000, 600000, or 700000 or more target nucleic acid molecules. A lysed cell can comprise at most about 100000, 200000, 300000, 400000, 500000, 600000, or 700000 or more target nucleic acid molecules.

Attachment of Barcodes to Target Nucleic Acid Molecules

Following lysis of the cells and release of nucleic acid molecules therefrom, the nucleic acid molecules can randomly associate with the barcodes of the co-localized solid support. Association can comprise hybridization of a barcode's target recognition region to a complementary portion of the target nucleic acid molecule (e.g., oligo(dT) of the barcode can interact with a poly(A) tail of a target). The assay conditions used for hybridization (e.g., buffer pH, ionic strength, temperature, etc.) can be chosen to promote formation of specific, stable hybrids. In some embodiments, the nucleic acid molecules released from the lysed cells can associate with the plurality of probes on the substrate (e.g., hybridize with the probes on the substrate). When the probes comprise oligo(dT), mRNA molecules can hybridize to the probes and be reverse transcribed. The oligo(dT) portion of the oligonucleotide can act as a primer for first strand

synthesis of the cDNA molecule. For example, in a non-limiting example of barcoding illustrated in FIG. 2, at block 216, mRNA molecules can hybridize to barcodes on beads. For example, single-stranded nucleotide fragments can hybridize to the target-binding regions of barcodes.

Attachment can further comprise ligation of a barcode's target recognition region and a portion of the target nucleic acid molecule. For example, the target binding region can comprise a nucleic acid sequence that can be capable of specific hybridization to a restriction site overhang (e.g., an EcoRI sticky-end overhang). The assay procedure can further comprise treating the target nucleic acids with a restriction enzyme (e.g., EcoRI) to create a restriction site overhang. The barcode can then be ligated to any nucleic acid molecule comprising a sequence complementary to the restriction site overhang. A ligase (e.g., T4 DNA ligase) can be used to join the two fragments.

For example, in a non-limiting example of barcoding illustrated in FIG. 2, at block 220, the labeled targets from a plurality of cells (or a plurality of samples) (e.g., target-barcode molecules) can be subsequently pooled, for example, into a tube. The labeled targets can be pooled by, for example, retrieving the barcodes and/or the beads to which the target-barcode molecules are attached.

The retrieval of solid support-based collections of attached target-barcode molecules can be implemented by use of magnetic beads and an externally-applied magnetic field. Once the target-barcode molecules have been pooled, all further processing can proceed in a single reaction vessel. Further processing can include, for example, reverse transcription reactions, amplification reactions, cleavage reactions, dissociation reactions, and/or nucleic acid extension reactions. Further processing reactions can be performed within the microwells, that is, without first pooling the labeled target nucleic acid molecules from a plurality of cells.

Reverse Transcription or Nucleic Acid Extension

The disclosure provides for a method to create a target-barcode conjugate using reverse transcription (e.g., at block 224 of FIG. 2) or nucleic acid extension. The target-barcode conjugate can comprise the barcode and a complementary sequence of all or a portion of the target nucleic acid (i.e., a barcoded cDNA molecule, such as a stochastically barcoded cDNA molecule). Reverse transcription of the associated RNA molecule can occur by the addition of a reverse transcription primer along with the reverse transcriptase. The reverse transcription primer can be an oligo(dT) primer, a random hexanucleotide primer, or a target-specific oligonucleotide primer. Oligo(dT) primers can be, or can be about, 12-18 nucleotides in length and bind to the endogenous poly(A) tail at the 3' end of mammalian mRNA. Random hexanucleotide primers can bind to mRNA at a variety of complementary sites. Target-specific oligonucleotide primers typically selectively prime the mRNA of interest.

In some embodiments, reverse transcription of an mRNA molecule to a labeled-RNA molecule can occur by the addition of a reverse transcription primer. In some embodiments, the reverse transcription primer is an oligo(dT) primer, random hexanucleotide primer, or a target-specific oligonucleotide primer. Generally, oligo(dT) primers are 12-18 nucleotides in length and bind to the endogenous poly(A) tail at the 3' end of mammalian mRNA. Random hexanucleotide primers can bind to mRNA at a variety of complementary sites. Target-specific oligonucleotide primers typically selectively prime the mRNA of interest.

In some embodiments, a target is a cDNA molecule. For example, an mRNA molecule can be reverse transcribed using a reverse transcriptase, such as Moloney murine leukemia virus (MMLV) reverse transcriptase, to generate a cDNA molecule with a poly(dC) tail. A barcode can include a target binding region with a poly(dG) tail. Upon base pairing between the poly(dG) tail of the barcode and the poly(dC) tail of the cDNA molecule, the reverse transcriptase switches template strands, from cellular RNA molecule to the barcode, and continues replication to the 5' end of the barcode. By doing so, the resulting cDNA molecule contains the sequence of the barcode (such as the molecular label) on the 3' end of the cDNA molecule.

Reverse transcription can occur repeatedly to produce multiple labeled-cDNA molecules. The methods disclosed herein can comprise conducting at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 reverse transcription reactions. The method can comprise conducting at least about 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 reverse transcription reactions.

Amplification

One or more nucleic acid amplification reactions (e.g., at block 228 of FIG. 2) can be performed to create multiple copies of the labeled target nucleic acid molecules. Amplification can be performed in a multiplexed manner, wherein multiple target nucleic acid sequences are amplified simultaneously. The amplification reaction can be used to add sequencing adaptors to the nucleic acid molecules. The amplification reactions can comprise amplifying at least a portion of a sample label, if present. The amplification reactions can comprise amplifying at least a portion of the cellular label and/or barcode sequence (e.g., a molecular label). The amplification reactions can comprise amplifying at least a portion of a sample tag, a cell label, a spatial label, a barcode sequence (e.g., a molecular label), a target nucleic acid, or a combination thereof. The amplification reactions can comprise amplifying 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 100%, or a range or a number between any two of these values, of the plurality of nucleic acids. The method can further comprise conducting one or more cDNA synthesis reactions to produce one or more cDNA copies of target-barcode molecules comprising a sample label, a cell label, a spatial label, and/or a barcode sequence (e.g., a molecular label).

In some embodiments, amplification can be performed using a polymerase chain reaction (PCR). As used herein, PCR can refer to a reaction for the *in vitro* amplification of specific DNA sequences by the simultaneous primer extension of complementary strands of DNA. As used herein, PCR can encompass derivative forms of the reaction, including but not limited to, RT-PCR, real-time PCR, nested PCR, quantitative PCR, multiplexed PCR, digital PCR, and assembly PCR.

Amplification of the labeled nucleic acids can comprise non-PCR based methods. Examples of non-PCR based methods include, but are not limited to, multiple displacement amplification (MDA), transcription-mediated amplification (TMA), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), real-time SDA, rolling circle amplification, or circle-to-circle amplification. Other non-PCR-based amplification methods include multiple cycles of DNA-dependent RNA polymerase-driven RNA transcription amplification or RNA-directed DNA synthesis and transcription to amplify DNA or RNA targets, a ligase chain reaction (LCR), and a Qβ

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replicase ($\text{Q}\beta$) method, use of palindromic probes, strand displacement amplification, oligonucleotide-driven amplification using a restriction endonuclease, an amplification method in which a primer is hybridized to a nucleic acid sequence and the resulting duplex is cleaved prior to the extension reaction and amplification, strand displacement amplification using a nucleic acid polymerase lacking 5' exonuclease activity, rolling circle amplification, and ramification extension amplification (RAM). In some embodiments, the amplification does not produce circularized transcripts.

In some embodiments, the methods disclosed herein further comprise conducting a polymerase chain reaction on the labeled nucleic acid (e.g., labeled-RNA, labeled-DNA, labeled-cDNA) to produce a labeled amplicon (e.g., a stochastically labeled amplicon). The labeled amplicon can be double-stranded molecule. The double-stranded molecule can comprise a double-stranded RNA molecule, a double-stranded DNA molecule, or a RNA molecule hybridized to a DNA molecule. One or both of the strands of the double-stranded molecule can comprise a sample label, a spatial label, a cell label, and/or a barcode sequence (e.g., a molecular label). The labeled amplicon can be a single-stranded molecule. The single-stranded molecule can comprise DNA, RNA, or a combination thereof. The nucleic acids of the disclosure can comprise synthetic or altered nucleic acids.

Amplification can comprise use of one or more non-natural nucleotides. Non-natural nucleotides can comprise photolabile or triggerable nucleotides. Examples of non-natural nucleotides can include, but are not limited to, peptide nucleic acid (PNA), morpholino and locked nucleic acid (LNA), as well as glycol nucleic acid (GNA) and threose nucleic acid (TNA). Non-natural nucleotides can be added to one or more cycles of an amplification reaction. The addition of the non-natural nucleotides can be used to identify products as specific cycles or time points in the amplification reaction.

Conducting the one or more amplification reactions can comprise the use of one or more primers. The one or more primers can comprise, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 or more nucleotides. The one or more primers can comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 or more nucleotides. The one or more primers can comprise less than 12-15 nucleotides. The one or more primers can anneal to at least a portion of the plurality of labeled targets (e.g., stochastically labeled targets). The one or more primers can anneal to the 3' end or 5' end of the plurality of labeled targets. The one or more primers can anneal to an internal region of the plurality of labeled targets. The internal region can be at least about 50, 100, 150, 200, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 650, 700, 750, 800, 850, 900 or 1000 nucleotides from the 3' ends the plurality of labeled targets. The one or more primers can comprise a fixed panel of primers. The one or more primers can comprise at least one or more custom primers. The one or more primers can comprise at least one or more control primers. The one or more primers can comprise at least one or more gene-specific primers.

The one or more primers can comprise a universal primer. The universal primer can anneal to a universal primer binding site. The one or more custom primers can anneal to a first sample label, a second sample label, a spatial label, a cell label, a barcode sequence (e.g., a molecular label), a target, or any combination thereof. The one or more primers

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can comprise a universal primer and a custom primer. The custom primer can be designed to amplify one or more targets. The targets can comprise a subset of the total nucleic acids in one or more samples. The targets can comprise a subset of the total labeled targets in one or more samples. The one or more primers can comprise at least 96 or more custom primers. The one or more primers can comprise at least 960 or more custom primers. The one or more primers can comprise at least 9600 or more custom primers. The one or more custom primers can anneal to two or more different labeled nucleic acids. The two or more different labeled nucleic acids can correspond to one or more genes.

Any amplification scheme can be used in the methods of the present disclosure. For example, in one scheme, the first round PCR can amplify molecules attached to the bead using a gene specific primer and a primer against the universal Illumina sequencing primer 1 sequence. The second round of PCR can amplify the first PCR products using a nested gene specific primer flanked by Illumina sequencing primer 2 sequence, and a primer against the universal Illumina sequencing primer 1 sequence. The third round of PCR adds P5 and P7 and sample index to turn PCR products into an Illumina sequencing library. Sequencing using 150 bp \times 2 sequencing can reveal the cell label and barcode sequence (e.g., molecular label) on read 1, the gene on read 2, and the sample index on index 1 read.

In some embodiments, nucleic acids can be removed from the substrate using chemical cleavage. For example, a chemical group or a modified base present in a nucleic acid can be used to facilitate its removal from a solid support. For example, an enzyme can be used to remove a nucleic acid from a substrate. For example, a nucleic acid can be removed from a substrate through a restriction endonuclease digestion. For example, treatment of a nucleic acid containing a dUTP or ddUTP with uracil-d-glycosylase (UDG) can be used to remove a nucleic acid from a substrate. For example, a nucleic acid can be removed from a substrate using an enzyme that performs nucleotide excision, such as a base excision repair enzyme, such as an apurinic/aprimidinic (AP) endonuclease. In some embodiments, a nucleic acid can be removed from a substrate using a photocleavable group and light. In some embodiments, a cleavable linker can be used to remove a nucleic acid from the substrate. For example, the cleavable linker can comprise at least one of biotin/avidin, biotin/streptavidin, biotin/neutravidin, Ig-protein A, a photolabile linker, acid or base labile linker group, or an aptamer.

When the probes are gene-specific, the molecules can hybridize to the probes and be reverse transcribed and/or amplified. In some embodiments, after the nucleic acid has been synthesized (e.g., reverse transcribed), it can be amplified. Amplification can be performed in a multiplex manner, wherein multiple target nucleic acid sequences are amplified simultaneously. Amplification can add sequencing adaptors to the nucleic acid.

In some embodiments, amplification can be performed on the substrate, for example, with bridge amplification. cDNAs can be homopolymer tailed in order to generate a compatible end for bridge amplification using oligo(dT) probes on the substrate. In bridge amplification, the primer that is complementary to the 3' end of the template nucleic acid can be the first primer of each pair that is covalently attached to the solid particle. When a sample containing the template nucleic acid is contacted with the particle and a single thermal cycle is performed, the template molecule can be annealed to the first primer and the first primer is elongated in the forward direction by addition of nucleotides

to form a duplex molecule consisting of the template molecule and a newly formed DNA strand that is complementary to the template. In the heating step of the next cycle, the duplex molecule can be denatured, releasing the template molecule from the particle and leaving the complementary DNA strand attached to the particle through the first primer. In the annealing stage of the annealing and elongation step that follows, the complementary strand can hybridize to the second primer, which is complementary to a segment of the complementary strand at a location removed from the first primer. This hybridization can cause the complementary strand to form a bridge between the first and second primers secured to the first primer by a covalent bond and to the second primer by hybridization. In the elongation stage, the second primer can be elongated in the reverse direction by the addition of nucleotides in the same reaction mixture, thereby converting the bridge to a double-stranded bridge. The next cycle then begins, and the double-stranded bridge can be denatured to yield two single-stranded nucleic acid molecules, each having one end attached to the particle surface via the first and second primers, respectively, with the other end of each unattached. In the annealing and elongation step of this second cycle, each strand can hybridize to a further complementary primer, previously unused, on the same particle, to form new single-strand bridges. The two previously unused primers that are now hybridized elongate to convert the two new bridges to double-strand bridges.

The amplification reactions can comprise amplifying at least 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, or 100% of the plurality of nucleic acids.

Amplification of the labeled nucleic acids can comprise PCR-based methods or non-PCR based methods. Amplification of the labeled nucleic acids can comprise exponential amplification of the labeled nucleic acids. Amplification of the labeled nucleic acids can comprise linear amplification of the labeled nucleic acids. Amplification can be performed by polymerase chain reaction (PCR). PCR can refer to a reaction for the *in vitro* amplification of specific DNA sequences by the simultaneous primer extension of complementary strands of DNA. PCR can encompass derivative forms of the reaction, including but not limited to, RT-PCR, real-time PCR, nested PCR, quantitative PCR, multiplexed PCR, digital PCR, suppression PCR, semi-suppressive PCR and assembly PCR.

In some embodiments, amplification of the labeled nucleic acids comprises non-PCR based methods. Examples of non-PCR based methods include, but are not limited to, multiple displacement amplification (MDA), transcription-mediated amplification (TMA), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), real-time SDA, rolling circle amplification, or circle-to-circle amplification. Other non-PCR-based amplification methods include multiple cycles of DNA-dependent RNA polymerase-driven RNA transcription amplification or RNA-directed DNA synthesis and transcription to amplify DNA or RNA targets, a ligase chain reaction (LCR), a Q β replicase (Q β), use of palindromic probes, strand displacement amplification, oligonucleotide-driven amplification using a restriction endonuclease, an amplification method in which a primer is hybridized to a nucleic acid sequence and the resulting duplex is cleaved prior to the extension reaction and amplification, strand displacement amplification using a

nucleic acid polymerase lacking 5' exonuclease activity, rolling circle amplification, and/or ramification extension amplification (RAM).

In some embodiments, the methods disclosed herein further comprise conducting a nested polymerase chain reaction on the amplified amplicon (e.g., target). The amplicon can be double-stranded molecule. The double-stranded molecule can comprise a double-stranded RNA molecule, a double-stranded DNA molecule, or a RNA molecule hybridized to a DNA molecule. One or both of the strands of the double-stranded molecule can comprise a sample tag or molecular identifier label. Alternatively, the amplicon can be a single-stranded molecule. The single-stranded molecule can comprise DNA, RNA, or a combination thereof. The nucleic acids of the present invention can comprise synthetic or altered nucleic acids.

In some embodiments, the method comprises repeatedly amplifying the labeled nucleic acid to produce multiple amplicons. The methods disclosed herein can comprise 20 conducting at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amplification reactions. Alternatively, the method comprises conducting at least about 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amplification reactions.

Amplification can further comprise adding one or more control nucleic acids to one or more samples comprising a plurality of nucleic acids. Amplification can further comprise adding one or more control nucleic acids to a plurality of nucleic acids. The control nucleic acids can comprise a 30 control label.

Amplification can comprise use of one or more non-natural nucleotides. Non-natural nucleotides can comprise photolabile and/or triggerable nucleotides. Examples of non-natural nucleotides include, but are not limited to, peptide 35 nucleic acid (PNA), morpholino and locked nucleic acid (LNA), as well as glycol nucleic acid (GNA) and threose nucleic acid (TNA). Non-natural nucleotides can be added to one or more cycles of an amplification reaction. The addition of the non-natural nucleotides can be used to identify 40 products as specific cycles or time points in the amplification reaction.

Conducting the one or more amplification reactions can comprise the use of one or more primers. The one or more primers can comprise one or more oligonucleotides. The one or more oligonucleotides can comprise at least about 7-9 nucleotides. The one or more oligonucleotides can comprise less than 12-15 nucleotides. The one or more primers can anneal to at least a portion of the plurality of labeled nucleic acids. The one or more primers can anneal to the 3' end and/or 5' end of the plurality of labeled nucleic acids. The one or more primers can anneal to an internal region of the plurality of labeled nucleic acids. The internal region can be at least about 50, 100, 150, 200, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 650, 700, 750, 800, 850, 900 or 1000 nucleotides from the 3' ends the plurality of labeled nucleic acids. The one or more primers can comprise a fixed panel of primers. The one or more primers can comprise at least one or more custom primers. The one or more primers can comprise at least one or more control primers. The one or more primers can comprise at least one or more housekeeping gene primers. The one or more primers can comprise a universal primer. The universal 60 primer can anneal to a universal primer binding site. The one or more custom primers can anneal to the first sample tag, the second sample tag, the molecular identifier label, the

nucleic acid or a product thereof. The one or more primers can comprise a universal primer and a custom primer. The custom primer can be designed to amplify one or more target nucleic acids. The target nucleic acids can comprise a subset of the total nucleic acids in one or more samples. In some embodiments, the primers are the probes attached to the array of the disclosure.

In some embodiments, barcoding (e.g., stochastically barcoding) the plurality of targets in the sample further comprises generating an indexed library of the barcoded targets (e.g., stochastically barcoded targets) or barcoded fragments of the targets. The barcode sequences of different barcodes (e.g., the molecular labels of different stochastic barcodes) can be different from one another. Generating an indexed library of the barcoded targets includes generating a plurality of indexed polynucleotides from the plurality of targets in the sample. For example, for an indexed library of the barcoded targets comprising a first indexed target and a second indexed target, the label region of the first indexed polynucleotide can differ from the label region of the second indexed polynucleotide by, by about, by at least, or by at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, or a number or a range between any two of these values, nucleotides. In some embodiments, generating an indexed library of the barcoded targets includes contacting a plurality of targets, for example mRNA molecules, with a plurality of oligonucleotides including a poly(T) region and a label region; and conducting a first strand synthesis using a reverse transcriptase to produce single-strand labeled cDNA molecules each comprising a cDNA region and a label region, wherein the plurality of targets includes at least two mRNA molecules of different sequences and the plurality of oligonucleotides includes at least two oligonucleotides of different sequences. Generating an indexed library of the barcoded targets can further comprise amplifying the single-strand labeled cDNA molecules to produce double-strand labeled cDNA molecules; and conducting nested PCR on the double-strand labeled cDNA molecules to produce labeled amplicons. In some embodiments, the method can include generating an adaptor-labeled amplicon.

Barcodeing (e.g., stochastic barcoding) can include using nucleic acid barcodes or tags to label individual nucleic acid (e.g., DNA or RNA) molecules. In some embodiments, it involves adding DNA barcodes or tags to cDNA molecules as they are generated from mRNA. Nested PCR can be performed to minimize PCR amplification bias. Adaptors can be added for sequencing using, for example, next generation sequencing (NGS). The sequencing results can be used to determine cell labels, molecular labels, and sequences of nucleotide fragments of the one or more copies of the targets, for example at block 232 of FIG. 2.

FIG. 3 is a schematic illustration showing a non-limiting exemplary process of generating an indexed library of the barcoded targets (e.g., stochastically barcoded targets), such as barcoded mRNAs or fragments thereof. As shown in step 1, the reverse transcription process can encode each mRNA molecule with a unique molecular label sequence, a cell label sequence, and a universal PCR site. In particular, RNA molecules 302 can be reverse transcribed to produce labeled cDNA molecules 304, including a cDNA region 306, by hybridization (e.g., stochastic hybridization) of a set of barcodes (e.g., stochastic barcodes) 310 to the poly(A) tail region 308 of the RNA molecules 302. Each of the barcodes 310 can comprise a target-binding region, for example a poly(dT) region 312, a label region 314 (e.g., a barcode sequence or a molecule), and a universal PCR region 316.

In some embodiments, the cell label sequence can include 3 to 20 nucleotides. In some embodiments, the molecular label sequence can include 3 to 20 nucleotides. In some embodiments, each of the plurality of stochastic barcodes 5 further comprises one or more of a universal label and a cell label, wherein universal labels are the same for the plurality of stochastic barcodes on the solid support and cell labels are the same for the plurality of stochastic barcodes on the solid support. In some embodiments, the universal label can 10 include 3 to 20 nucleotides. In some embodiments, the cell label comprises 3 to 20 nucleotides.

In some embodiments, the label region 314 can include a barcode sequence or a molecular label 318 and a cell label 320. In some embodiments, the label region 314 can include 15 one or more of a universal label, a dimension label, and a cell label. The barcode sequence or molecular label 318 can be, can be about, can be at least, or can be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length. The cell label 320 can be, can be about, can be at least, or can be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length. The universal label can be, can be about, can be at least, or can be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length. Universal labels can be the same for the plurality of stochastic barcodes on the solid support and cell labels are the same for the plurality of stochastic barcodes on the solid support. The dimension label can be, can be about, can be at least, or can be at most 25 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length. Universal labels can be the same for the plurality of stochastic barcodes on the solid support and cell labels are the same for the plurality of stochastic barcodes on the solid support. The dimension label can be, can be about, can be at least, or can be at most 30 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length.

In some embodiments, the label region 314 can comprise, comprise about, comprise at least, or comprise at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, or a number or a range between any of these values, different labels, such as 35 a barcode sequence or a molecular label 318 and a cell label 320. Each label can be, can be about, can be at least, or can be at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, or a number or a range between any of these values, of nucleotides in length. A set of barcodes or stochastic barcodes 310 can contain, contain about, contain 40 at least, or can be at most, 10, 20, 40, 50, 70, 80, 90, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{20} , or a number or a range between any of these values, barcodes or stochastic barcodes 310. And the set of 45 barcodes or stochastic barcodes 310 can, for example, each contain a unique label region 314. The labeled cDNA molecules 304 can be purified to remove excess barcodes or stochastic barcodes 310. Purification can comprise Ampure bead purification.

50 As shown in step 2, products from the reverse transcription process in step 1 can be pooled into 1 tube and PCR amplified with a 1st PCR primer pool and a 1st universal PCR primer. Pooling is possible because of the unique label region 314. In particular, the labeled cDNA molecules 304 can be amplified to produce nested PCR labeled amplicons 322. Amplification can comprise multiplex PCR amplification. Amplification can comprise a multiplex PCR amplification with 96 multiplex primers in a single reaction volume. In some embodiments, multiplex PCR amplification can 55 utilize, utilize about, utilize at least, or utilize at most, 10, 20, 40, 50, 70, 80, 90, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{20} , or a number or a range

between any of these values, multiplex primers in a single reaction volume. Amplification can comprise using a 1st PCR primer pool 324 comprising custom primers 326A-C targeting specific genes and a universal primer 328. The custom primers 326 can hybridize to a region within the cDNA portion 306 of the labeled cDNA molecule 304. The universal primer 328 can hybridize to the universal PCR region 316 of the labeled cDNA molecule 304.

As shown in step 3 of FIG. 3, products from PCR amplification in step 2 can be amplified with a nested PCR primers pool and a 2nd universal PCR primer. Nested PCR can minimize PCR amplification bias. In particular, the nested PCR labeled amplicons 322 can be further amplified by nested PCR. The nested PCR can comprise multiplex PCR with nested PCR primers pool 330 of nested PCR primers 332a-c and a 2nd universal PCR primer 328' in a single reaction volume. The nested PCR primer pool 328 can contain, contain about, contain at least, or contain at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, or a number or a range between any of these values, different nested PCR primers 330. The nested PCR primers 332 can contain an adaptor 334 and hybridize to a region within the cDNA portion 306' of the labeled amplicon 322. The universal primer 328' can contain an adaptor 336 and hybridize to the universal PCR region 316 of the labeled amplicon 322. Thus, step 3 produces adaptor-labeled amplicon 338. In some embodiments, nested PCR primers 332 and the 2nd universal PCR primer 328' may not contain the adaptors 334 and 336. The adaptors 334 and 336 can instead be ligated to the products of nested PCR to produce adaptor-labeled amplicon 338.

As shown in step 4, PCR products from step 3 can be PCR amplified for sequencing using library amplification primers. In particular, the adaptors 334 and 336 can be used to conduct one or more additional assays on the adaptor-labeled amplicon 338. The adaptors 334 and 336 can be hybridized to primers 340 and 342. The one or more primers 340 and 342 can be PCR amplification primers. The one or more primers 340 and 342 can be sequencing primers. The one or more adaptors 334 and 336 can be used for further amplification of the adaptor-labeled amplicons 338. The one or more adaptors 334 and 336 can be used for sequencing the adaptor-labeled amplicon 338. The primer 342 can contain a plate index 344 so that amplicons generated using the same set of barcodes or stochastic barcodes 310 can be sequenced in one sequencing reaction using next generation sequencing (NGS).

Methods and Compositions for Single Cell Secretomics

There are provided, in some embodiments, systems, methods, compositions, and kits for single cell secretomics. The methods and compositions disclosed herein can determine the number of copies of one or more secreted factors secreted by a single cell (e.g., secretomics, secreted factor profiling). There are provided, in some embodiments, compositions and methods for single cell secretome analysis. Some embodiments described herein employ antibodies capable of binding secreted factors, and said antibodies can be associated with oligonucleotides. In some embodiments, the methods and compositions provided herein are compatible with single cell analysis systems, workflows, and platforms (e.g., BD Rhapsody). There is a need for compositions and methods for analyzing the secretome profile of individual cells. Currently available methods of secretome profiling (e.g., fluorescence- or microarray chip-based) are high-cost and low-throughput, and are less quantitative than the secretome profiling methods and compositions provided

herein. In some embodiments, secreted proteins of single cells are captured by synthetic beads (a cell mimic) with multiple antibodies (specific for said secreted proteins) conjugated thereto. In some embodiments, said beads can then be probed with secreted factor binding-reagents as described herein. Said secreted factor binding-reagents can comprise a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. Barcoding and sequence analysis of said secreted factor-binding reagent specific oligonucleotides as described herein can enable high-throughput single cell secretome analysis.

There are provided, in some embodiments solid supports (e.g., beads, first solid supports, second solid supports) that are cell-sized. Said solid supports can comprise a functional surface for antibody conjugation (e.g., conjugation of antibodies versus secreted proteins). The method can comprise incubation of single cells with said antibody-coated solid support. The incubation can take place in partitions (e.g., wells). Partition size can be optimized to capture most of secreted proteins. The time, media, and/or temperature of incubation can be varied depending on the needs of the user. Cells can, depending on the embodiment, die during the incubation; however, in some such embodiments, the secretome information is still valuable. Thus, the compositions and methods provided herein can still acquire useful secretome information even in cases of cell death. The solid supports can be collected from said partitions and stained with the secreted factor-binding reagents provided herein. The staining can be multiplexed. In some embodiments provided herein, flow Abs can be also added for sorting to enrich certain secretomic types. In some embodiments, solid supports are stained with antibodies comprising a detectable moiety that enable the sorting of solid supports by flow cytometry for one or more desired properties. The method can comprise washing of unbound the secreted factor-binding reagents. The solid supports can be loaded into a plurality of partitions (e.g., wells, droplets, partitions of a single cell analysis platform such as BD Rhapsody). A single partition of the plurality of partitions can comprise a single solid support. A single partition of the plurality of partitions can comprise a plurality of oligonucleotide barcodes. A single partition of the plurality of partitions can comprise a barcoding particle (e.g., a single third solid support as described herein). Barcoding of barcoded secreted factor-binding reagent specific oligonucleotides with said oligonucleotide barcodes can be performed as described herein. Library generation and obtaining the sequence information can yield secretome data.

There are provided, in some embodiments, compositions and methods for simultaneous high-throughput single cell secretome and transcriptome analysis. In some such embodiments, the solid support (e.g. second solid support) comprises a plurality of capture probes and a plurality of anchor probes. Each of the plurality of anchor probes can be capable of specifically binding to a surface cellular target to form single cells associated with a second solid support. Barcoding and sequence analysis of said secreted factor-binding reagent specific oligonucleotides as well as the nucleic acid targets of the associated single cells as described herein can enable high-throughput single cell secretome and transcriptome analysis. In some embodiments, single cell secretome analysis and single cell protein profiling can be performed using the compositions and methods provided herein. In some embodiments, compositions and methods for simultaneous single cell secretome analysis, transcriptome analysis, and protein profiling are described. Embodiments of using

AbOs to determine protein expression profiles in single cells and tracking sample origins have been described in U.S. patent application Ser. No. 15/715,028, published as U.S. Patent Application Publication No. 2018/0088112, and U.S. patent application Ser. No. 15/937,713; the content of each is incorporated by reference herein in its entirety.

In some embodiments, the solid support (e.g., bead, first solid support, second solid support) comprising a plurality of capture probes (e.g., multiple different antibodies for secreted protein) is a cell mimic. A single cell and one of said solid supports can located in a partition (e.g., well) of a plurality of partitions (e.g., a culture plate) with media so secreted proteins will be captured by capture probes on the solid support from the given cell. Then the solid support can be stained with secreted factor binding reagents that can detect the captured proteins and those solid supports can be loaded onto a plurality of partitions (e.g., wells, droplets, partitions of a single cell analysis platform such as BD Rhapsody) for library generation. Said secreted factor binding-reagents can comprise a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The secreted factor-binding reagent specific oligonucleotide library can be sequenced and generate the secretome information of single cells. Currently available methods for detecting secreted proteins have a limitation on the number of proteins that can be detected due to the number of fluorescence markers that can be used in the microscope or flow cytometry analysis. The compositions and methods provided herein remove this limitation and can enable detection of secreted proteins with as many pairs of capture probe/secreted factor-binding reagent needed by the user. Moreover, as described therein, the disclosed methods can comprise the capture of both secreted protein and single cells for the analysis of the transcriptome and secretome of a single cell. Systems, methods, compositions, and kits for measuring secreted factors from cells employing (i) bispecific probes comprising anchor probe(s) capable of specifically binding to a surface cellular target of a cell and capture probe(s) capable of specifically binding to a secreted factor secreted by a cell that is associated with the capture probe, and/or (ii) secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe, are described in the U.S. Patent Application No. 62/962,927, filed Jan. 17, 2020, entitled "METHODS AND COMPOSITIONS FOR SINGLE CELL SECRETOMICS", the content of which is incorporated herein by reference in its entirety.

Currently available methods of single cell secretome profiling, such as those using fluorescence detection on microarray chips, suffer from the deficiencies of being less quantitative due to the fluorescence intensity differences and low potential to capture transcriptome of given cell. The limitations of fluorescence intensity difference-based methods and low number of secreted proteins that can be detected from a given cell are solved with the methods and compositions provided herein, in some embodiments, by utilizing the sequence analysis of secreted factor-binding reagent specific oligonucleotides, which are not limited by fluorescent markers and are more quantitative due to the ability to count the number of molecules (instead of fluorescent intensity).

Cytokines and other proteins released by the cell are of keen interest to immunologists and other cell biologists. Traditional methods for detecting and measuring secreted proteins are typically measured in bulk (rather than at the single cell level). For example, currently available methods

include bead-based assays and ELISA for studying secreted factors in bulk. Therefore, single cell quantification and cellular phenotype analysis are missing in the data. As with the comparison of flow cytometry to traditional western blots, there is tremendous value in studying the individual cells from a heterogenous mixture of cells. The methods and compositions provided herein enable detection and relative quantification of secreted proteins of individual cells in a heterogeneous mixture. Oligonucleotide barcoded detection probes (e.g., secreted factor-binding reagent specific oligonucleotides) can be optimized for single cell genomics analysis. The secreted factor analysis methods provided herein can be compatible with other analyses techniques for single cell multiomics platforms. Disclosed herein include methods and compositions enabling rapid adoption of single-cell secretomic assays across a flexible portfolio of targets without the need for specialized instrumentation. In some embodiments, the methods disclosed herein can provide the ability to assay secreted proteins without compromising cell-viability, and thus can enable the sorting of live cells based on their protein secretion profile. Additionally, the methods provided herein enable a broader suite of single cell omic data downstream of cell preparation.

The use of an oligo-barcode detection probe (e.g., an secreted factor binding reagent) as provided herein enables, for the first time, the ability to assess secreted factors from individual cells simultaneously with surface proteins (e.g., cellular component targets) and intracellular transcript (mRNA). The methods and compositions provided herein enable, for the first time, single cell secretion analysis on single cell genomic platforms.

In some embodiments of the methods and compositions provided herein, a DNA cellular component binding reagent specific oligonucleotide (e.g., an antibody oligonucleotide) is hybridized to an oligonucleotide barcode and extended to enable a separate, but parallel workflow for protein quantitation and mRNA quantitation from the same beads, as described in U.S. application Ser. No. 17/147,272, the content of which is incorporated herein by reference in its entirety. Some embodiments of the methods and compositions provided herein employ the separate, but parallel workflow concept described in U.S. application Ser. No. 17/147,272; for example, in some embodiments, a secreted factor-binding reagent specific oligonucleotide (e.g., an antibody oligonucleotide) is hybridized to an oligonucleotide barcode and extended to enable a separate, but parallel workflow for secreted factor quantitation and mRNA quantitation from the same beads.

In some embodiments of the methods and compositions provided herein, the oligonucleotide barcode comprises a cleavage region (comprising, for example, one or more cleavage sites such as a non-canonical nucleotide (e.g., deoxyuridine) or a restriction enzyme recognition sequence) as described in U.S. application Ser. No. 17/147,283, the content of which is incorporated herein by reference in its entirety.

FIG. 6 shows a non-limiting exemplary design of a secreted factor binding reagent specific oligonucleotide (antibody oligonucleotide illustrated here) that is associated with a secreted factor-binding reagent (antibody illustrated here). The secreted factor-binding reagent specific oligonucleotide 604 can be associated with secreted factor-binding reagent 602 through linker 616. The secreted factor-binding reagent specific oligonucleotide 604 can be detached from the secreted factor-binding reagent 602 using chemical, optical or other means. The secreted factor-binding reagent specific oligonucleotide 604 can be an mRNA

mimic. The secreted factor-binding reagent specific oligonucleotide **604** can include a second universal sequence **606** (e.g., a primer adapter), a second molecular label **608** (e.g., a unique molecular label sequence), an antibody barcode **610** (e.g., a unique factor identifier sequence), an alignment sequence **612**, and a poly(A) tail **614**.

FIGS. 4A-4C show a schematic illustration of a non-limiting exemplary workflow for measurement of the number of copies of one or more secreted factors secreted by a single cell. The workflow can comprise analysis of cells **404** (e.g., T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof) with first plurality of first solid supports **410** (e.g., beads). The workflow can comprise contacting cells **404** with first solid supports **410**. The workflow can comprise partitioning **400a** the cells **404** and the first solid supports **410** to a plurality of first partitions **402**. A first partition **402** (e.g., a well, a droplet) of the plurality of first partitions can comprise a single cell **404** and a single first solid support **410**. A cell **404** can comprise secretory vesicles **406** comprising unreleased secretory factors **408**. A cell **404** can capable of secreting a plurality of secreted factors **408**. A first solid support **410** can comprise capture probes **412** capable of specifically binding to at least one of the plurality of secreted factors **408** secreted by a single cell **404**. The workflow can comprise an incubation **400b** comprising secretion of secreted factors and binding thereof to capture probes. The workflow can comprise pooling **400c** of the single first solid supports **410** from each first partition **402** (to generate a second plurality of first solid supports). The workflow can comprise contacting **400d** the first solid support **410** with a plurality of secreted factor-binding reagents **414** each capable of specifically binding to a secreted factor bound by a capture probe. Each of the plurality of secreted factor-binding reagents can comprise a secreted factor-binding reagent specific oligonucleotide **416** comprising a unique factor identifier sequence for the secreted factor-binding reagent. The workflow can comprise an incubation **400e** comprising binding of the secreted factor-binding reagents **414** to secreted factor **408** bound by a capture probe **412**. The workflow can comprise one or more washes **400f** comprising removal of secreted factor-binding reagents **414** that are not bound to secreted factor **408** bound by a capture probe **412** (to generate a third plurality of first solid supports). The workflow can comprise partitioning **400g** the first solid supports **410** to a plurality of second partitions **418**. A second partition **418** (e.g., a well, a droplet) of the plurality of second partitions can comprise a single first solid support **410** and a single third solid support **420**. Third solid support **420** can comprise a plurality of oligonucleotide barcodes **422**. Oligonucleotide barcodes **422** can comprise a first molecular label and/or cellular label. The workflow can comprise contacting oligonucleotide barcodes **422** with the secreted factor-binding reagent specific oligonucleotides **416** for hybridization. The workflow can comprise barcoding, library preparation, and/or sequencing **400h** as described herein. For example, the workflow can comprise extending oligonucleotide barcodes **422** hybridized to the secreted factor-binding reagent specific oligonucleotides **416** to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise obtaining sequence information of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of a secreted factor **408** secreted by each of the one

or more single cells **404**. The workflow can comprise performing the steps with a plurality of cells (e.g., in bulk).

FIGS. 5A-5C show a schematic illustration of a non-limiting exemplary workflow for measuring the number of copies of a secreted factor secreted by a single cell and the number of copies of a nucleic acid target in a single cell. The workflow can comprise analysis of cells **504** (e.g., T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof) with first plurality of second solid supports **510** (e.g., beads). The workflow can comprise contacting cells **504** with second solid supports **510**. The workflow can comprise partitioning **500a** the cells **504** and the second solid supports **510** to a plurality of first partitions **502**. A first partition **502** (e.g., a well, a droplet) of the plurality of first partitions can comprise a single cell **504** and a single second solid support **510**. A cell **504** can comprise secretory vesicles **506** comprising unreleased secretory factors **508**. A cell **504** can capable of secreting a plurality of secreted factors **508**. A second solid support **510** can comprise capture probes **512** capable of specifically binding to at least one of the plurality of secreted factors **508** secreted by a single cell **504**. Cells **504** can comprise a surface cellular target **524** and copies of a nucleic acid target **526**. The second solid support **510** can comprise anchor probes **528** capable of specifically binding to the surface cellular target **524**. The single cell **504** can be capable of becoming associated with a second solid support **510** via the anchor probe **528** binding to the surface cellular target **524**. The workflow can comprise an incubation **500b** comprising secretion of secreted factors and binding thereof to capture probes and the single cell **504** becoming associated with a second solid support **510** via the anchor probe **528** binding to the surface cellular target **524**. The workflow can comprise pooling **500c** of single cells associated with a second solid support from each first partition **502** (to generate a first plurality of single cells associated with a second solid support). The workflow can comprise contacting **500d** the single cells associated with a second solid support with a plurality of secreted factor-binding reagents **514** each capable of specifically binding to a secreted factor bound by a capture probe. Each of the plurality of secreted factor-binding reagents can comprise a secreted factor-binding reagent specific oligonucleotide **516** comprising a unique factor identifier sequence for the secreted factor-binding reagent. The workflow can comprise an incubation **500e** comprising binding of the secreted factor-binding reagents **514** to secreted factor **508** bound by a capture probe **512**. The workflow can comprise one or more washes **500f** comprising removal of secreted factor-binding reagents **514** that are not bound to secreted factor **508** bound by a capture probe **512** (to generate a second plurality of single cells associated with a second solid support). The workflow can comprise partitioning **500g** single cells associated with a second solid support to a plurality of second partitions **518**. A second partition **518** (e.g., a well, a droplet) of the plurality of second partitions can comprise a single cells associated with a second solid support and a single third solid support **520**. Third solid support **520** can comprise a plurality of oligonucleotide barcodes **522**. Oligonucleotide barcodes **522** can comprise a first molecular label and/or cellular label. The workflow can comprise contacting oligonucleotide barcodes **522** with the secreted factor-binding reagent specific oligonucleotides **516** for hybridization. The workflow can comprise cell lysis barcoding, library preparation, and/or sequencing **500h** as described herein. For example, the workflow can comprise extending oligonucleotide barcodes **522** hybridized to the secreted factor-binding

reagent specific oligonucleotides **516** to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The workflow can comprise lysing the single cell **504** to release copies of the nucleic acid target **526** contained therein. The workflow can comprise contacting oligonucleotide barcodes **522** with the copies of the nucleic acid target **526** for hybridization. The workflow can comprise extending the plurality of oligonucleotide barcodes **522** hybridized to the copies of a nucleic acid target **526** to generate a plurality of barcoded nucleic acid molecules each comprising a sequence complementary to at least a portion of the nucleic acid target and the first molecular label. The method can comprise obtaining sequence information of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of a secreted factor **508** secreted by each of the one or more single cells **504**. The workflow can comprise obtaining sequence information of the plurality of barcoded nucleic acid molecules, or products thereof, to determine the copy number of the nucleic acid target **526** in each of the one or more single cells **504**. The workflow can comprise performing the steps with a plurality of cells (e.g., in bulk).

Some embodiments disclosed herein provide a plurality of compositions each comprising a secreted factor binding reagent (such as a protein binding reagent). The secreted factor binding reagent can be conjugated with an oligonucleotide, wherein the oligonucleotide comprises a unique factor identifier for the secreted factor binding reagent that it is conjugated with. The unique factor identifiers can be, for example, a nucleotide sequence having any suitable length, for example, from about 4 nucleotides to about 200 nucleotides. In some embodiments, the unique factor identifier is a nucleotide sequence of 25 nucleotides to about 45 nucleotides in length. In some embodiments, the unique factor identifier can have a length that is, is about, is less than, is greater than, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 200 nucleotides, or a range that is between any two of the above values.

In some embodiments, the unique factor identifiers are selected from a diverse set of unique factor identifiers. The diverse set of unique factor identifiers can comprise, or comprise about, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or a number or a range between any two of these values, different unique factor identifiers. The diverse set of unique factor identifiers can comprise at least, or comprise at most, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, or 5000, different unique factor identifiers. In some embodiments, the set of unique factor identifiers is designed to have minimal sequence homology to the DNA or RNA sequences of the sample to be analyzed. In some embodiments, the sequences of the set of unique factor identifiers are different from each other, or the complement thereof, by, or by about, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides, or a number or a range between any two of these values. In some embodiments, the sequences of the set of unique factor identifiers are different from each other, or the complement thereof, by at least, or by at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides. In some embodiments, the sequences of the set of unique factor identifiers are different from each other, or the complement thereof, by at least 3%, at least 5%, at least 8%, at least 10%, at least 15%, at least 20%, or more.

Any suitable secreted factor binding reagents, anchor probes, and capture probes are contemplated in this disclosure, such as protein binding reagents, antibodies or fragments thereof, aptamers, small molecules, ligands, peptides, oligonucleotides, etc., or any combination thereof. The secreted factor binding reagents, anchor probes, and/or capture probes can be polyclonal antibodies, monoclonal antibodies, recombinant antibodies, single chain antibody (sc-Ab), or fragments thereof, such as Fab, Fv, etc. In some embodiments, the plurality of secreted factor binding reagents can comprise, or comprise about, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or a number or a range between any two of these values, different secreted factor binding reagents. In some embodiments, the plurality of secreted factor binding reagents can comprise at least, or comprise at most, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or 5000, different secreted factor binding reagents. In some embodiments, the plurality of anchor probes can comprise about, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or a number or a range between any two of these values, different anchor probes. In some embodiments, the plurality of anchor probes can comprise at least, or comprise at most, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or 5000, different anchor probes. In some embodiments, the plurality of capture probes can comprise, or comprise about, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 5000, or a number or a range between any two of these values, different capture probes. In some embodiments, the plurality of capture probes can comprise at least, or comprise at most, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, or 5000, different capture probes.

The oligonucleotide can be conjugated with the secreted factor binding reagent through various mechanisms. In some embodiments, the oligonucleotide can be conjugated with the secreted factor binding reagent covalently. In some embodiment, the oligonucleotide can be conjugated with the secreted factor binding reagent non-covalently. In some embodiments, the oligonucleotide is conjugated with the secreted factor binding reagent through a linker. The linker can be, for example, cleavable or detachable from the secreted factor binding reagent and/or the oligonucleotide. In some embodiments, the linker can comprise a chemical group that reversibly attaches the oligonucleotide to the secreted factor binding reagents. The chemical group can be conjugated to the linker, for example, through an amine group. In some embodiments, the linker can comprise a chemical group that forms a stable bond with another chemical group conjugated to the secreted factor binding reagent. For example, the chemical group can be a UV photocleavable group, a disulfide bond, a streptavidin, a biotin, an amine, etc. In some embodiments, the chemical group can be conjugated to the secreted factor binding reagent through a primary amine on an amino acid, such as lysine, or the N-terminus. Commercially available conjugation kits, such as the Protein-Oligo Conjugation Kit (Solu-link, Inc., San Diego, California), the Thunder-Link® oligo conjugation system (Innova Biosciences, Cambridge, United Kingdom), etc., can be used to conjugate the oligonucleotide to the secreted factor binding reagent.

The oligonucleotide can be conjugated to any suitable site of the secreted factor binding reagent (e.g., a protein binding reagent), as long as it does not interfere with the specific binding between the secreted factor binding reagent and its

secreted factor. In some embodiments, the secreted factor binding reagent is a protein, such as an antibody. In some embodiments, the secreted factor binding reagent is not an antibody. In some embodiments, the oligonucleotide can be conjugated to the antibody anywhere other than the antigen-binding site, for example, the Fc region, the C_H1 domain, the C_H2 domain, the C_H3 domain, the C_L domain, etc. Methods of conjugating oligonucleotides to binding reagents (e.g., antibodies) have been previously disclosed, for example, in U.S. Pat. No. 6,531,283, the content of which is hereby expressly incorporated by reference in its entirety. Stoichiometry of oligonucleotide to secreted factor binding reagent can be varied. To increase the sensitivity of detecting the secreted factor binding reagent specific oligonucleotide in sequencing, it may be advantageous to increase the ratio of oligonucleotide to secreted factor binding reagent during conjugation. In some embodiments, each secreted factor binding reagent can be conjugated with a single oligonucleotide molecule. In some embodiments, each secreted factor binding reagent can be conjugated with more than one oligonucleotide molecule, for example, at least, or at most, 2, 3, 4, 5, 10, 20, 30, 40, 50, 100, 1000, or a number or a range between any two of these values, oligonucleotide molecules wherein each of the oligonucleotide molecule comprises the same, or different, unique factor identifiers. In some embodiments, each secreted factor binding reagent can be conjugated with more than one oligonucleotide molecule, for example, at least, or at most, 2, 3, 4, 5, 10, 20, 30, 40, 50, 100, 1000, oligonucleotide molecules, wherein each of the oligonucleotide molecule comprises the same, or different, unique factor identifiers.

In some embodiments, the plurality of secreted factor binding reagents are capable of specifically binding to a plurality of secreted factors in a sample, such as a single cell, a plurality of cells, a tissue sample, a tumor sample, a blood sample, or the like. In some embodiments, the plurality of secreted factors can comprise, or comprise about, 2, 3, 4, 5, 10, 20, 30, 40, 50, 100, 1000, 10000, or a number or a range between any two of these values, different secreted factors. In some embodiments, the plurality of secreted factors can comprise at least, or comprise at most, 2, 3, 4, 5, 10, 20, 30, 40, 50, 100, 1000, 10000, different secreted factors.

In some embodiments, the secreted factor binding reagent specific oligonucleotide can comprise a nucleotide sequence of, or a nucleotide sequence of about, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 128, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, or a number or a range between any two of these values, nucleotides in length. In some embodiments, the secreted factor binding reagent specific oligonucleotide comprises a nucleotide sequence of at least, or of at most, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 128, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780,

790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000, nucleotides in length.

Oligonucleotide-Conjugated Antibodies

Some embodiments disclosed herein provide a plurality of compositions each comprising a cellular component binding reagent (such as a protein binding reagent) that is conjugated with an oligonucleotide, wherein the oligonucleotide comprises a unique identifier for the cellular component binding reagent that it is conjugated with. Cellular component binding reagents (such as barcoded antibodies) and their uses (such as sample indexing of cells) have been described in U.S. Patent Application Publication No. US2018/0088112 and U.S. Patent Application Publication No. US2018/0346970; the content of each of these is incorporated herein by reference in its entirety. There are provided, in some embodiments provided herein, secreted factor-binding reagents capable of specifically binding to a secreted factor. Secreted factor-binding reagents can comprise a secreted factor-binding reagent specific oligonucleotide. There are provided, in some embodiments, methods for simultaneous quantitative analysis of a plurality of cellular component targets (e.g., protein targets) and copies of a secreted factor secreted by a single cell. The methods and systems described herein can be used with methods and systems using antibodies associated with (e.g., attached to or conjugated with) oligonucleotides (also referred to herein as AbOs or AbO-oligos). Embodiments of using AbOs to determine protein expression profiles in single cells and tracking sample origins have been described in U.S. patent application Ser. No. 15/715,028, published as U.S. Patent Application Publication No. 2018/0088112, and U.S. patent application Ser. No. 15/937,713; the content of each is incorporated by reference herein in its entirety.

Unique Molecular Label Sequence

In some embodiments, the methods and compositions provided herein comprise an oligonucleotide associated with a cellular component-binding reagent (e.g., antibody oligonucleotide ("AbOligo" or "AbO"), binding reagent oligonucleotide, cellular component-binding reagent specific oligonucleotides, sample indexing oligonucleotides) as described in U.S. application Ser. No. 16/747,737, filed on Jan. 21, 2020, the content of which is incorporated herein by reference in its entirety. In some embodiments, the oligonucleotide associated with a cellular component-binding reagent (e.g., antibody oligonucleotide ("AbOligo" or "AbO"), binding reagent oligonucleotide, a secreted factor-binding reagent specific oligonucleotide, cellular component-binding reagent specific oligonucleotides, sample indexing oligonucleotides) comprises a unique molecular label sequence (also referred to as a molecular index (MI), "molecular barcode," or Unique Molecular Identifier (UMI)). In some embodiments, binding reagent oligonucleotide species comprising molecule barcodes as described herein reduce bias by increasing sensitivity, decreasing relative standard error, or increasing sensitivity and/or reducing standard error. The molecule barcode can comprise a unique sequence, so that when multiple sample nucleic acids (which can be the same and/or different from each other) are associated one-to-one with molecule barcodes, different sample nucleic acids can differentiated from each other by the molecule barcodes. As such, even if a sample comprises two nucleic acids having the same sequence, each of these two nucleic acids can be labeled with a different molecule barcode, so that nucleic acids in the population can be quantified, even after amplification. The molecule barcode can comprise a nucleic acid sequence of at least 5

nucleotides, for example at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides, including ranges between any two of the listed values, for example 5-50, 5-45, 5-40, 5-35, 5-30, 5-25, 5-20, 5-15, 5-14, 5-13, 5-12, 5-11, 5-10, 5-9, 5-8, 5-7, 5-6, 6-50, 6-45, 6-40, 6-35, 6-30, 6-25, 6-20, 6-15, 6-14, 6-13, 6-12, 6-11, 6-10, 6-9, 6-8, 6-7, 7-50, 7-45, 7-40, 7-35, 7-30, 7-25, 7-20, 7-15, 7-14, 7-13, 7-12, 7-11, 7-10, 7-9, 7-8, 8-50, 8-45, 8-40, 8-35, 8-30, 8-25, 8-20, 8-15, 8-14, 8-13, 8-12, 8-11, 8-10, 8-9, 9-50, 9-45, 9-40, 9-35, 9-30, 9-25, 9-20, 9-15, 9-14, 9-13, 9-12, 9-11, 9-10, 10-50, 10-45, 10-40, 10-35, 10-30, 10-25, 10-20, 10-15, 10-14, 10-13, 10-12, or 10-11 nucleotides. In some embodiments, the nucleic acid sequence of the molecule barcode comprises a unique sequence, for example, so that each unique oligonucleotide species in a composition comprises a different molecule barcode. In some embodiments, two or more unique oligonucleotide species can comprise the same molecule barcode, but still differ from each other. For example, if the unique oligonucleotide species include sample barcodes, each unique oligonucleotide species with a particular sample barcode can comprise a different molecule barcode. In some embodiments, a composition comprising unique oligonucleotide species comprises a molecule barcode diversity of at least 1000 different molecule barcodes, and thus at least 1000 unique oligonucleotide species. In some embodiments, a composition comprising unique oligonucleotide species comprises a molecule barcode diversity of at least 6,500 different molecule barcodes, and thus at least 6,500 unique oligonucleotide species. In some embodiments, a composition comprising unique oligonucleotide species comprises a molecule barcode diversity of at least 65,000 different molecule barcodes, and thus at least 65,000 unique oligonucleotide species.

In some embodiments, the unique molecular label sequence is positioned 5' of the unique identifier sequence without any intervening sequences between the unique molecular label sequence and the unique identifier sequence. In some embodiments, the unique molecular label sequence is positioned 5' of a spacer, which is positioned 5' of the unique identifier sequence, so that a spacer is between the unique molecular label sequence and the unique identifier sequence. In some embodiments, the unique identifier sequence is positioned 5' of the unique molecular label sequence without any intervening sequences between the unique identifier sequence and the unique molecular label sequence. In some embodiments, the unique identifier sequence is positioned 5' of a spacer, which is positioned 5' of the unique molecular label sequence, so that a spacer is between the unique identifier sequence and the unique molecular label sequence.

The unique molecular label sequence can comprise a nucleic acid sequence of at least 3 nucleotides, for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50 nucleotides, including ranges between any two of the listed values, for example 3-50, 3-45, 3-40, 3-35, 3-30, 3-25, 3-20, 3-15, 3-14, 3-13, 3-12, 3-11, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-50, 4-45, 4-40, 4-35, 4-30, 4-25, 4-20, 4-15, 4-14, 4-13, 4-12, 4-11, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-50, 5-45, 5-40, 5-35, 5-30, 5-25, 5-20, 5-15, 5-14, 5-13, 5-12, 5-11, 5-10, 5-9, 5-8, 5-7, 5-6, 6-50, 6-45, 6-40, 6-35, 6-30, 6-25, 6-20, 6-15, 6-14, 6-13, 6-12, 6-11, 6-10, 6-9, 6-8, 6-7, 7-50, 7-45, 7-40, 7-35, 7-30, 7-25, 7-20, 7-15, 7-14, 7-13, 7-12, 7-11, 7-10, 7-9, 7-8, 8-50, 8-45, 8-40, 8-35, 8-30, 8-25, 8-20,

8-15, 8-14, 8-13, 8-12, 8-11, 8-10, 8-9, 9-50, 9-45, 9-40,
9-35, 9-30, 9-25, 9-20, 9-15, 9-14, 9-13, 9-12, 9-11, 9-10,
10-50, 10-45, 10-40, 10-35, 10-30, 10-25, 10-20, 10-15,
10-14, 10-13, 10-12, or 10-11 nucleotides. In some embodiments,
5 the unique molecular label sequence is 2-20 nucleotides in length.

In some embodiments, the unique molecular label sequence of the binding reagent oligonucleotide comprises the sequence of at least three repeats of the doublets “VN” and/or “NV” (in which each “V” is any of A, C, or G, and in which “N” is any of A, G, C, or T), for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. Examples of multiple repeats of the doublet “VN” include VN, VNVN, VNVNVN, and VNVNVNVN. It is noted that while the formulas “VN” and “NV” describe constraints on the base content, not every V or every N has to be the same or different. For example, if the molecule barcodes of unique oligonucleotide species in a composition comprised VNVNVN, one molecule barcode can comprise the sequence ACGGCA, while another molecule barcode can comprise the sequence ATACAT, while another molecule barcode could comprise the sequence ATACAC. It is noted that any number of repeats of the doublet “VN” would have a T content of no more than 50%. In some embodiments, at least 95% of the unique oligonucleotide species of a composition comprising at least 1000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99% of the unique oligonucleotide species of a composition comprising at least 1000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99.9% of the unique oligonucleotide species of a composition comprising at least 1000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 95% of the unique oligonucleotide species of a composition comprising at least 6500 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99% of the unique oligonucleotide species of a composition comprising at least 6500 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99.9% of the unique oligonucleotide species of a composition comprising at least 6500 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 95% of the unique oligonucleotide species of a composition comprising at least 65,000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values.

otide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99% of the unique oligonucleotide species of a composition comprising at least 65,000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, at least 99.9% of the unique oligonucleotide species of a composition comprising at least 65,000 unique oligonucleotide species comprise molecule barcodes comprising at least three repeats of the doublets “VN” and/or “NV,” for example at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 repeats, including ranges between any two of the listed values. In some embodiments, the composition consists of or consists essentially of at least 1000, 6500, or 65,000 unique oligonucleotide species that each have a molecule barcode comprising the sequence VNVNVN. In some embodiments, the composition consists of or consists essentially of at least 1000, 6500, or 65,000 unique oligonucleotide species that each has a molecule barcode comprising the sequence VNVNVNVN. In some embodiments, at least 95%, 99%, or 99.9% of the barcode regions of the composition as described herein comprise at least three repeats of the doublets “VN” and/or “NV,” as described herein. In some embodiments, unique molecular label sequences comprising repeated “doublets “VN” and/or “NV” can yield low bias, while providing a compromise between reducing bias and maintaining a relatively large quantity of available nucleotide sequences, so that relatively high diversity can be obtained in a relatively short sequence, while still minimizing bias. In some embodiments, unique molecular label sequences comprising repeated “doublets “VN” and/or “NV” can reduce bias by increasing sensitivity, decreasing relative standard error, or increasing sensitivity and reducing standard error. In some embodiments, unique molecular label sequences comprising repeated “doublets “VN” and/or “NV” improve informatics analysis by serving as a geomarker. In some embodiments, the repeated doublets “VN” and/or “NV” described herein reduce the incidence of homopolymers within the unique molecular label sequences. In some embodiments, the repeated doublets “VN” and/or “NV” described herein break up homopolymers.

In some embodiments, the sample indexing oligonucleotide comprises a first molecular label sequence. In some embodiments, the first molecular label sequences of at least two sample indexing oligonucleotides are different, and the sample indexing sequences of the at least two sample indexing oligonucleotides are identical. In some embodiments, the first molecular label sequences of at least two sample indexing oligonucleotides are different, and the sample indexing sequences of the at least two sample indexing oligonucleotides are different. In some embodiments, the cellular component-binding reagent specific oligonucleotide comprises a second molecular label sequence. In some embodiments, the second molecular label sequences of at least two cellular component-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two cellular component-binding reagent specific oligonucleotides are identical. In some embodiments, the second molecular label sequences of at least two cellular component-binding reagent specific oligonucleotides are different, and the unique identifier

sequences of the at least two cellular component-binding reagent specific oligonucleotides are different. In some embodiments, the number of unique second molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data indicates the number of copies of the at least one cellular component target in the one or more of the plurality of cells. In some embodiment, a combination (e.g., minimum, average, and maximum) of (1) the number of unique first molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data and (2) the number of unique second molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data indicates the number of copies of the at least one cellular component target in the one or more of the plurality of cells.

Alignment Sequence

In some embodiments, the binding reagent oligonucleotide comprises an alignment sequence (e.g., the alignment sequence 825bb) adjacent to the poly(dA) region. The alignment sequence can be 1 or more nucleotides in length. The alignment sequence can be 2 nucleotides in length. The alignment sequence can comprise a guanine, a cytosine, a thymine, a uracil, or a combination thereof. The alignment sequence can comprise a poly(dT) region, a poly(dG) region, a poly(dC) region, a poly(dU) region, or a combination thereof. In some embodiments, the alignment sequence is 5' to the poly(dA) region. Advantageously, in some embodiments, the presence of the alignment sequence enables the poly(A) tail of each of the binding reagent oligonucleotides to have the same length, leading to greater uniformity of performance. In some embodiments, the percentage of binding reagent oligonucleotides with an identical poly(dA) region length within a plurality of binding reagent oligonucleotides, each of which comprise an alignment sequence, can be, or be about, 80%, 90%, 91%, 93%, 95%, 97%, 99.9%, 99.99%, or 100%, or a number or a range between any two of these values. In some embodiments, the percentage of binding reagent oligonucleotides with an identical poly(dA) region length within the plurality of binding reagent oligonucleotides, each of which comprise an alignment sequence, can be at least, or be at most, 80%, 90%, 91%, 93%, 95%, 97%, 99.9%, 99.99%, or 100%.

The length of the alignment sequence can be different in different implementations. In some embodiments, the length of the alignment sequence can be, or can be about, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or a number or a range between any two of these values. In some embodiments, the length of the alignment sequence can be at least, or can be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100. The number of

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guanine(s), cytosine(s), thymine(s), or uracil(s) in the alignment sequence can be different in different implementations. The number of guanine(s), cytosine(s), thymine(s), or uracil (s) can be, or can be about, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or a number or a range between any two of these values. The number of guanine(s), cytosine(s), thymine(s), or uracil(s) can be at least, or can be at most, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100. In some embodiments, the sample indexing oligonucleotide comprises an alignment sequence. In some embodiments, the cellular component-binding reagent specific oligonucleotide and/or secreted factor-binding reagent specific oligonucleotide comprises an alignment sequence.

Linker

The binding reagent oligonucleotide (e.g., secreted factor-binding reagent specific oligonucleotide) can be conjugated with the cellular component binding reagent through various mechanisms. In some embodiments, the binding reagent oligonucleotide can be conjugated with the cellular component binding reagent covalently. In some embodiments, the binding reagent oligonucleotide can be conjugated with the cellular component binding reagent non-covalently. In some embodiments, the binding reagent oligonucleotide is conjugated with the cellular component binding reagent through a linker. In some embodiments, the binding reagent oligonucleotide can comprise the linker. The linker can comprise a chemical group. The chemical group can be reversibly, or irreversibly, attached to the molecule of the cellular component binding reagent. The chemical group can be selected from the group consisting of a UV photocleavable group, a disulfide bond, a streptavidin, a biotin, an amine, and any combination thereof. The linker can comprise a carbon chain. The carbon chain can comprise, for example, 5-50 carbon atoms. The carbon chain can have different numbers of carbon atoms in different embodiments. In some embodiments, the number of carbon atoms in the carbon chain can be, or can be about, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or a number or a range between any two of these values. In some embodiments, the number of carbon atoms in the carbon chain can be at least, or can be at most, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or a number or a range between any two of these values. In some embodiments, the carbon chain comprises 2-30 carbons. In some embodiments, the carbon chain comprises 12 carbons. In some embodiments, amino modifiers employed for binding reagent oligonucleotide can be conjugated to the cellular component binding reagent. In some embodiments, the linker comprises 5' amino modifier C6 (5AmMC6). In some embodiments, the linker comprises 5' amino modifier C12 (5AmMC12). In some embodiments, the linker comprises a derivative of 5AmMC12. In some embodiments, a longer linker achieves a higher efficiency of conjugation. In some embodiments, a longer linker achieves a higher efficiency of

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modification prior to conjugation. In some embodiments, increasing the distance between the functional amine and the DNA sequence yields a higher efficiency of conjugation. In some embodiments, increasing the distance between the functional amine and the DNA sequence yields a higher efficiency of modification prior to conjugation. In some embodiments, the use of 5AmMC12 as a linker yields a higher efficiency of modification (prior to conjugation) than the use of 5AmMC6 as a linker. In some embodiments the use of 5AmMC12 as a linker yields a higher efficiency of conjugation than the use of 5AmMC6 as a linker. In some embodiments, the sample indexing oligonucleotide is associated with the cellular component-binding reagent through a linker. In some embodiments, the cellular component-binding reagent specific oligonucleotide and/or secreted factor-binding reagent specific oligonucleotide is associated with the cellular component-binding reagent through a linker.

Antibody-Specific Barcode Sequence

Disclosed herein, in several embodiments, are improvements to the design of the unique identifier sequence (e.g., antibody-specific barcode sequence) of a binding reagent oligonucleotide (e.g., secreted factor-binding reagent specific oligonucleotide). In some embodiments the unique identifier sequence (e.g., sample indexing sequence, unique factor identifier sequence, a unique identifier sequence of a cellular component-binding reagent specific oligonucleotide) is designed to have a Hamming distance greater than 3. In some embodiments, the Hamming distance of the unique identifier sequence can be, or be about, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or a number or a range between any two of these values. In some embodiments, the unique identifier sequences has a GC content in the range of 40% to 60% and does not have a predicted secondary structure (e.g., hairpin). In some embodiments, the unique identifier sequence does not comprise any sequences predicted in silico to bind to the mouse and/or human transcripts. In some embodiments, the unique identifier sequence does not comprise any sequences predicted in silico to bind to Rhapsody™ and/or SCMK system primers. In some embodiments, the unique identifier sequence does not comprise homopolymers.

Primer Adapter

In some embodiments, the binding reagent oligonucleotide (e.g., secreted factor-binding reagent specific oligonucleotide) comprises a primer adapter. In some embodiments, the primer adapter comprises the sequence of a first universal primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof. In some embodiments, the first universal primer comprises an amplification primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof. In some embodiments, the first universal primer comprises a sequencing primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof. In some embodiments, the sequencing primer comprises an Illumina sequencing primer. In some embodiments, the sequencing primer comprises a portion of an Illumina sequencing primer. In some embodiments, the sequencing primer comprises a P7 sequencing primer or a portion of P7 sequencing primer. In some embodiments, the primer adapter comprises an adapter for Illumina P7 or a partial adapter for Illumina P7. In some embodiments, the amplification primer is an Illumina P7 sequence or a subsequence thereof. In some embodiments, the sequencing primer is an Illumina R2 sequence or a subsequence thereof. In some embodiments, the first universal primer is 5-50 nucleotides in length. In some embodiments, The primer adapter can comprise a

nucleic acid sequence of at least 5 nucleotides, for example at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides, including ranges between any two of the listed values, for example 5-50, 5-45, 5-40, 5-35, 5-30, 5-25, 5-20, 5-15, 5-14, 5-13, 5-12, 5-11, 5-10, 5-9, 5-8, 5-7, 5-6, 6-50, 6-45, 6-40, 6-35, 6-30, 6-25, 6-20, 6-15, 6-14, 6-13, 6-12, 6-11, 6-10, 6-9, 6-8, 6-7, 7-50, 7-45, 7-40, 7-35, 7-30, 7-25, 7-20, 7-15, 7-14, 7-13, 7-12, 7-11, 7-10, 7-9, 7-8, 8-50, 8-45, 8-40, 8-35, 8-30, 8-25, 8-20, 8-15, 8-14, 8-13, 8-12, 8-11, 8-10, 8-9, 9-50, 9-45, 9-40, 9-35, 9-30, 9-25, 9-20, 9-15, 9-14, 9-13, 9-12, 9-11, 9-10, 10-50, 10-45, 10-40, 10-35, 10-30, 10-25, 10-20, 10-15, 10-14, 10-13, 10-12, or 10-11 nucleotides. The primer adapter can comprise a nucleic acid sequence of at least 5 nucleotides of the sequence of a first universal primer, an amplification primer, a sequencing primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof, for example at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides, including ranges between any two of the listed values, for example 5-50, 5-45, 5-40, 5-35, 5-30, 5-25, 5-20, 5-15, 5-14, 5-13, 5-12, 5-11, 5-10, 5-9, 5-8, 5-7, 5-6, 6-50, 6-45, 6-40, 6-35, 6-30, 6-25, 6-20, 6-15, 6-14, 6-13, 6-12, 6-11, 6-10, 6-9, 6-8, 6-7, 7-50, 7-45, 7-40, 7-35, 7-30, 7-25, 7-20, 7-15, 7-14, 7-13, 7-12, 7-11, 7-10, 7-9, 7-8, 8-50, 8-45, 8-40, 8-35, 8-30, 8-25, 8-20, 8-15, 8-14, 8-13, 8-12, 8-11, 8-10, 8-9, 9-50, 9-45, 9-40, 9-35, 9-30, 9-25, 9-20, 9-15, 9-14, 9-13, 9-12, 9-11, 9-10, 10-50, 10-45, 10-40, 10-35, 10-30, 10-25, 10-20, 10-15, 10-14, 10-13, 10-12, or 10-11 nucleotides of the sequence of a first universal primer, an amplification primer, a sequencing primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof.

A conventional amplification workflow for sequencing library preparation can employ three rounds of PCR, such as, for example: a first round ("PCR 1") employing a target-specific primer and a primer against the universal Illumina sequencing primer 1 sequence; a second round ("PCR 2") using a nested target-specific primer flanked by Illumina sequencing primer 2 sequence, and a primer against the universal Illumina sequencing primer 1 sequence; and a third round ("PCR 3") adding Illumina P5 and P7 and sample index. Advantageously, in some embodiments, the primer adapter disclosed herein enables a shorter and simpler workflow in library preparation as compared to if the starting template (e.g., a sample indexing oligonucleotide attached to a bead) does not have a primer adapter. In some embodiments, the primer adapter reduces pre-sequencing PCR amplification of a template by one round (as compared to if the template does not comprise a primer adapter). In some embodiments, the primer adapter reduces pre-sequencing PCR amplification of the template to one round (as compared to if the template does not comprise a primer adapter). In some embodiments, a template comprising the primer adapter does not require a PCR amplification step for attachment of Illumina sequencing adapters that would require pre-sequencing if the template did not comprise a primer adapter. In some embodiments, the primer adapter sequence (or a subsequence thereof) is not part of the sequencing readout of a sequencing template comprising a primer adapter sequence and therefore does not affect read quality of a template comprising a primer adapter. In some embodiments, a template comprising the primer adapter has

decreased sequencing diversity as compared to if the template does not comprise a primer adapter.

In some embodiments, the sample indexing oligonucleotide comprises a primer adapter. In some embodiments, replicating a sample indexing oligonucleotide, a barcoded sample indexing oligonucleotide, or a product thereof, comprises using a first universal primer, a first primer comprising the sequence of the first universal primer, or a combination thereof, to generate a plurality of replicated sample indexing oligonucleotides. In some embodiments, replicating a sample indexing oligonucleotide, a barcoded sample indexing oligonucleotide, or a product thereof, comprises using a first universal primer, a first primer comprising the sequence of the first universal primer, a second universal primer, a second primer comprising the sequence of the second universal primer, or a combination thereof, to generate the plurality of replicated sample indexing oligonucleotides. In some embodiments, the cellular component-binding reagent specific oligonucleotide and/or secreted factor-binding reagent specific oligonucleotide comprises a primer adapter, the sequence of a first universal primer, a complementary sequence thereof, a partial sequence thereof, or a combination thereof.

Binding Reagent Oligonucleotide Barcoding

FIG. 8 shows a schematic illustration of a non-limiting exemplary workflow of barcoding of a binding reagent oligonucleotide **825** (antibody oligonucleotide illustrated here, e.g., secreted factor-binding reagent specific oligonucleotide) that is associated with a binding reagent **805** (antibody illustrated here, such as, for example, a secreted factor-binding reagent). The binding reagent oligonucleotide **825** can be associated with binding reagent **805** through linker **8251**. The binding reagent oligonucleotide **825** can be detached from the binding reagent using chemical, optical or other means. The binding reagent oligonucleotide **825** can be an mRNA mimic. The binding reagent oligonucleotide **825** can include a primer adapter **825pa**, an antibody molecular label **825am** (e.g., a unique molecular label sequence), an antibody barcode **825ab** (e.g., a unique identifier sequence), an alignment sequence **825bb**, and a poly(A) tail **825a**. In some embodiments, the primer adapter **825pa** comprises the sequence of a first universal primer, a complimentary sequence thereof, a partial sequence thereof, or a combination thereof. In some embodiments, the primer adapter **825pa** can be the same for all or some of binding reagent oligonucleotides **825**. In some embodiments, the antibody barcode **825ab** can be the same for all or some of binding reagent oligonucleotides **825**. In some embodiments, the antibody barcode **825ab** of different binding reagent oligonucleotides **825** are different. In some embodiments, the antibody molecular label **825am** of different binding reagent oligonucleotides **825** are different.

The binding reagent oligonucleotides **825** can be barcoded using a plurality of barcodes **815** (e.g., barcodes **815** associated with a particle, such as a bead **810**) to create a plurality of barcoded binding reagent oligonucleotides **840**. In some embodiments, a barcode **815** can include a poly(dT) region **815t** for binding to a binding reagent oligonucleotide **825**, optionally a molecular label **815m** (e.g., for determining the number of occurrences of the binding reagent oligonucleotides), a cell label **815c**, and a universal label **815u**. In some embodiments the barcode **815** is hybridized to the poly(dT) region **815t** of binding reagent oligonucleotides **825**. In some embodiments barcoded binding reagent oligonucleotides **840** are generated by extending (e.g., by reverse transcription) the barcode **815** hybridized to the binding reagent oligonucleotide **825**. In some embodiments,

barcoded binding reagent oligonucleotides **840** comprise primer adapter **825pa**, an antibody molecular label **825am** (e.g., a unique molecular label sequence), an antibody barcode **825ab** (e.g., a unique identifier sequence), an alignment sequence **825bb**, poly(dT) region **815t**, molecular label **815m**, cell label **815c**, and universal label **815u**.

In some embodiments, the barcoded binding reagent oligonucleotides disclosed herein comprises two unique molecular label sequences: a molecular label sequence derived from the barcode (e.g., molecular label **815m**) and a molecular label sequence derived from a binding reagent oligonucleotide (e.g., antibody molecular label **825am**, the first molecular label sequence of a sample indexing oligonucleotide, the second molecular label sequence of a cellular component-binding reagent specific oligonucleotide, the molecular label of a secreted factor-binding reagent specific oligonucleotide). As used herein, “dual molecular indexing” refers to methods and compositions disclosed herein employing barcoded binding reagent oligonucleotides (or products thereof) that comprise a first unique molecular label sequence and second unique molecular label sequence (or complementary sequences thereof). In some embodiments, the methods of sample identification and of quantitative analysis of cellular component targets disclosed herein can comprise obtaining the sequence of information of the barcode molecular label sequence and/or the binding reagent oligonucleotide molecular label sequence. In some embodiments, the number of barcode molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data indicates the number of copies of the at least one cellular component target in the one or more of the plurality of cells. In some embodiments, the number of binding reagent oligonucleotide molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data indicates the number of copies of the at least one cellular component target in the one or more of the plurality of cells. In some embodiments, the number of both the binding reagent oligonucleotide molecular label sequences and barcode molecular label sequences associated with the unique identifier sequence for the cellular component-binding reagent capable of specifically binding to the at least one cellular component target in the sequencing data indicates the number of copies of the at least one cellular component target in the one or more of the plurality of cells.

The use of PCR to amplify the amount of material before starting the sequencing protocol adds the potential for artifacts, such as artifactual recombination during amplification occurs when premature termination products prime a subsequent round of synthesis). In some embodiments, the methods of dual molecular indexing provided herein allow the identification of PCR chimeras given sufficient sequencing depth. Additionally, in some embodiments, the addition of the unique molecular label sequence to the binding reagent oligonucleotide increases stochastic labelling complexity. Thus, in some embodiments, the presence of the unique molecular label sequence in the binding reagent oligonucleotide can overcome UMI diversity limitations. In some embodiments the methods of dual molecular indexing provided herein decrease the number of cellular component targets flagged as “saturated” during post-sequencing molecular coverage calculations by at least about 2% (e.g., 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 40%,

50%, 75%, 100%, 150%, 200%, 250%, 500%, 1000%, or higher and overlapping ranges therein) compared to if the methods and compositions are not used.

Probes, Binding Reagents, and Solid Supports

5 The first solid support and/or the second solid support can be sized and shaped to approximate a cell. In some embodiments, the first solid support and/or the second solid support has the dimensions of a cell (e.g., a mammalian cell, a yeast cell, an insect cell, a plant cell, a bacterial cell, or any 10 combination thereof). The first solid support, second solid support, and/or third solid support can comprise a synthetic particle or a planar surface. At least one of the plurality of oligonucleotide barcodes can be immobilized or partially immobilized on the synthetic particle. At least one of the 15 plurality of oligonucleotide barcodes can be enclosed or partially enclosed in the synthetic particle. The synthetic particle can be disruptable. The synthetic particle can comprise a bead. The bead can comprise: a sepharose bead, a streptavidin bead, an agarose bead, a magnetic bead, a 20 conjugated bead, a protein A conjugated bead, a protein G conjugated bead, a protein A/G conjugated bead, a protein L conjugated bead, an oligo(dT) conjugated bead, a silica bead, a silica-like bead, an anti-biotin microbead, an anti-fluorochrome microbead, or any combination thereof; a 25 material selected from the group consisting of polydimethylsiloxane (PDMS), polystyrene, glass, polypropylene, agarose, gelatin, hydrogel, paramagnetic, ceramic, plastic, glass, methylstyrene, acrylic polymer, titanium, latex, sepharose, cellulose, nylon, silicone, and any combination thereof; or a disruptable hydrogel particle.

In some embodiments, each of the plurality of oligonucleotide barcodes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

40 In some embodiments, each of the plurality of anchor probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

45 In some embodiments, each of the plurality of capture probes comprises a linker functional group, the synthetic particle comprises a solid support functional group, and the support functional group and the linker functional group are associated with each other. The linker functional group and the support functional group can be individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.

50 The secreted factor-binding reagent and the capture probe can be capable of binding to distinct epitopes of the same secreted factor. In some embodiments, one or more of the secreted factor-binding reagents, the capture probe, and the anchor probe comprise an antibody or fragment thereof. The antibody or fragment thereof can comprise a monoclonal antibody. The antibody or fragment thereof can comprise a Fab, a Fab', a F(ab')₂, a Fv, a scFv, a dsFv, a diabody, a 55 triabody, a tetrabody, a multispecific antibody formed from antibody fragments, a single-domain antibody (sdAb), a

single chain comprising complementary scFvs (tandem scFvs) or bispecific tandem scFvs, an Fv construct, a disulfide-linked Fv, a dual variable domain immunoglobulin (DVD-Ig) binding protein or a nanobody, an aptamer, an affibody, an affilin, an affitin, an affimer, an alphabody, an anticalin, an avimer, a DARPin, a Fynomeric, a Kunitz domain peptide, a monobody, or any combination thereof. The capture probe and/or the anchor probe can be conjugated to the first solid support and/or the second solid support by a 1,3-dipolar cycloaddition reaction, a hetero-Diels-Alder reaction, a nucleophilic substitution reaction, a non-aldol type carbonyl reaction, an addition to carbon-carbon multiple bond, an oxidation reaction, a click reaction, or any combination thereof.

The at least one secreted factor can comprise a lymphokine, an interleukin, a chemokine, or any combination thereof. The at least one secreted factor can comprise a cytokine, a hormone, a molecular toxin, or any combination thereof. The at least one secreted factor can comprise a nerve growth factor, a hepatic growth factor, a fibroblast growth factor, a vascular endothelial growth factor, a platelet-derived growth factor, a transforming growth factor, an osteoinductive factor, an interferon, a colony stimulating factor, or any combination thereof. The at least one secreted factor can comprise angiogenin, angiopoietin-1, angiopoietin-2, bNGF, cathepsin S, Galectin-7, GCP-2, G-CSF, GM-CSF, PAI-1, PDGF-AA, PDGF-BB, PDGF-AB, PIGF, PIGF-2, SDF-1, Tie2, VEGF-A, VEGF-C, VEGF-D, VEGF-R1, VEGF-R2, VEGF-R3, 6Ckine, angiopoietin-1, angiopoietin-2, BLC, BRAK, CD186, ENA-78, Eotaxin-1, Eotaxin-2, Eotaxin-3, EpCAM, GDF-15, GM-CSF, GRO, HCC-4, I-309, IFN- γ , IL-1 α , IL-1 β , IL-1R4 (ST2), IL-2, IL-2R, IL-3, IL-3Ra, IL-5, IL-6, IL-6R, IL-7, IL-8, IL-8RB, IL-11, IL-12, IL-12p40, IL-12p70, IL-13, IL-13 R1, IL-13R2, IL-15, IL-15Ra, IL-16, IL-17, IL-17C, IL-17E, IL-17F, IL-17R, IL-18, IL-18BPa, IL-18 Ra, IL-20, IL-23, IL-27, IL-28, IL-31, IL-33, IP-10, I-TAC, LIF, LIX, LRP6, MadCAM-1, MCP-1, MCP-2, MCP-3, MCP-4, M-CSF, MIF, MIG, MIP-1 gamma, MIP-1 α , MIP-1 β , MIP-1 δ , MIP-3 α , MIP-3 β , MPIF-1, PARC, PF4, RANTES, Resistin, SCF, SCYB16, TACI, TARC, TSLP, TNF- α , TNF-R1, TRAIL-R4, TREM-1, Activin A, Amphiregulin, Axl, BDNF, BMP4, cathepsin S, EGF, FGF-1, FGF-2, FGF-7, FGF-21, Follistatin, Galectin-7, Gash, GDF-15, HB-EGF, HGF, IGFBP-1, IGFBP-3, LAP, NGF R, NrCAM, NT-3, NT-4, PAI-1, TGF- α , TGF- β , TGF- β 3, TRAIL-R4, ADAMTS1, cathepsin S, FGF-2, Follistatin, Galectin-7, GCP-2, GDF-15, IGFBP-6, LIF, MMP-9, pro-MMP9, RANK, RANKL, RANTES, SDF-1, CXCR4, or any combination thereof.

The surface cellular target can comprise a carbohydrate, a lipid, a protein, an extracellular protein, a cell-surface protein, a cell marker, a B-cell receptor, a T-cell receptor, a major histocompatibility complex, a tumor antigen, a receptor, an intracellular protein, or any combination thereof. The surface cellular target can comprise a carbohydrate, a lipid, a protein, or any combination thereof. The surface cellular target can comprise CD1a, CD1b, CD1c, CD1d, CD1e, CD2, CD3, CD3d, CD3e, CD3g, CD4, CD5, CD6, CD7, CD8a, CD8b, CD9, CD10, CD11a, CD11b, CD11c, CD11d, CDw12, CD13, CD14, CD15, CD15u, CD15s, CD15su, CD16, CD16b, CD17, CD18, CD19, CD20, CD21, CD22, CD23, CD24, CD25, CD26, CD27, CD28, CD29, CD30, CD31, CD32, CD33, CD34, CD35, CD36, CD37, CD38, CD39, CD40, CD41, CD42a, CD42b, CD42c, CD42d, CD43, CD44, CD45, CD45RA, CD45RB, CD45RC, CD45RO, CD46, CD47, CD48, CD49a, CD49b, CD49c, CD49d, CD49e, CD49f, CD50, CD51, CD52, CD53, CD54,

CD55, CD56, CD57, CD58, CD59, CD60a, CD60b, CD60c, CD61, CD62E, CD62L, CD62P, CD63, CD64, CD65, CD65s, CD66a, CD66b, CD66c, CD66d, CD66e, CD66f, CD68, CD69, CD70, CD71, CD72, CD73, CD74, CD75, 5 CD75s, CD77, CD79a, CD79b, CD80, CD81, CD82, CD83, CD84, CD85a, CD85d, CD85j, CD85k, CD86, CD87, CD88, CD89, CD90, CD91, CD92, CD93, CD94, CD95, CD96, CD97, CD98, CD99, CD99R, CD100, CD101, CD102, CD103, CD104, CD105, CD106, CD107a, 10 CD107b, CD108, CD109, CD110, CD111, CD112, CD113, CD114, CD115, CD116, CD117, CD118, CD119, CD120a, CD120b, CD121a, CD121b, CD122, CD123, CD124, CD125, CD126, CD127, CD129, CD130, CD131, CD132, CD133, CD134, CD135, CD136, CD137, CD138, CD139, 15 CD140a, CD140b, CD141, CD142, CD143, CD144, CDw145, CD146, CD147, CD148, CDw149, CD150, CD151, CD152, CD153, CD154, CD155, CD156a, CD156b, CD156c, CD157, CD158e, CD158i, CD158k, CD159a, CD159c, CD160, CD161, CD162, CD163, 20 CD164, CD165, CD166, CD167a, CD167b, CD168, CD169, CD170, CD171, CD172a, CD172b, CD172g, CD173, CD174, CD175, CD175s, CD176, CD177, CD178, CD179a, CD179b, CD180, CD181, CD182, CD183, CD184, CD185, CD186, CD191, CD192, CD193, CD194, 25 CD195, CD196, CD197, CDw198, CD199, CD200, CD201, CD202b, CD203c, CD204, CD205, CD206, CD207, CD208, CD209, CD210, CDw210b, CD212, CD213a1, CD213a2, CD215, CD217a, CD218a, CD218b, CD220, CD221, CD222, CD223, CD224, CD225, CD226, CD227, 30 CD228, CD229, CD230, CD231, CD232, CD233, CD234, CD235a, CD235b, CD236, CD236R, CD238, CD239, CD240CE, CD240DCE, CD240D, CD241, CD242, CD243, CD244, CD245, CD246, CD247, CD248, CD249, CD252, CD253, CD254, CD256, CD266, CD267, CD268, CD269, 35 CD270, CD271, CD272, CD273, CD274, CD275, CD276, CD277, CD278, CD279, CD280, CD281, CD282, CD283, CD284, CD286, CD289, CD290, CD292, CDw293, CD294, CD295, CD296, CD297, CD298, CD299, CD300a, CD300c, CD300e, CD301, CD302, CD303, CD304, 40 CD305, CD306, CD307a, CD307b, CD307c, CD307d, CD307e, CD308, CD309, CD312, CD314, CD315, CD316, CD317, CD318, CD319, CD320, CD321, CD322, CD324, CD325, CD326, CD327, CD328, CD329, CD331, CD332, CD333, CD334, CD335, CD336, CD337, CD338, CD339, 45 CD340, CD344, CD349, CD350, CD351, CD352, CD353, CD354, CD355, CD357, CD358, CD360, CD361, CD362, CD363, CD364, CD365, CD366, CD367, CD368, CD369, CD370, CD371, BCMA, a HLA protein, β 2-microglobulin, or any combination thereof.

50 Methods for Simultaneous Single Cell Secretome and Transcriptome Analysis

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell. The method can comprise: contacting one or more single cells with a first plurality of first solid supports, the one or more single cells are capable of secreting a plurality of secreted factors, each first solid support comprises a plurality of capture probes capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the first solid support with a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a

plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof.

In some embodiments, contacting one or more single cells with a first plurality of first solid supports comprises: partitioning the one or more single cells and the first plurality of first solid supports to a plurality of first partitions, a first partition of the plurality of first partitions comprises a single cell of the one or more single cells and a single first solid support of the first plurality of first solid supports.

In some embodiments, the method comprises, prior to contacting the first solid support with a plurality of secreted factor-binding reagents: pooling the single first solid supports from each first partition of the plurality of first partitions to generate a second plurality of first solid supports. In some embodiments, contacting the first solid support with a plurality of secreted factor-binding reagents comprises contacting the second plurality of first solid supports with the plurality of secreted factor-binding reagents.

In some embodiments, the method comprises, after contacting the second plurality of first solid supports with the plurality of secreted factor-binding reagents, removing one or more secreted factor-binding reagents of the plurality of secreted factor-binding reagents that are not contacted with the second plurality of first solid supports to generate a third plurality of first solid supports. In some embodiments, removing the one or more secreted factor-binding reagents not contacted with the second plurality of first solid supports comprises: removing the one or more secreted factor-binding reagents not contacted with the respective at least one of the secreted factor bound by a capture probe.

In some embodiments, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization comprises: partitioning the third plurality of first solid supports to a plurality of second partitions, a second partition of the plurality of second partitions comprises a single first solid support from the third plurality of first solid supports; and in the second partition comprising the single first solid support, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides for hybridization.

Disclosed herein include methods of measuring the number of copies of a secreted factor secreted by a single cell and the number of copies of a nucleic acid target in a single cell. The method can comprise: contacting one or more single cells with a first plurality of second solid supports to form one or more single cells associated with a second solid support, the one or more single cells comprise a surface cellular target and copies of a nucleic acid target, the one or more single cells are capable of secreting a plurality of

secreted factors, each second solid support comprises a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to the surface cellular target, and the capture probe is capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell. The method can comprise: contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent. The method can comprise: contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization, the oligonucleotide barcodes each comprise a first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the copies of a nucleic acid target to generate a plurality of barcoded nucleic acid molecules each comprising a sequence complementary to at least a portion of the nucleic acid target and the first molecular label. The method can comprise: extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to at least a portion of the unique factor identifier sequence and the first molecular label. The method can comprise: obtaining sequence information of the plurality of barcoded nucleic acid molecules, or products thereof, to determine the copy number of the nucleic acid target in each of the one or more single cells. The method can comprise: obtaining sequence information of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, to determine the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, normal cells, fetal cells, maternal cells, or a mixture thereof.

In some embodiments, contacting one or more single cells with a first plurality of second solid supports to form one or more single cells associated with a second solid support comprises: partitioning the one or more single cells and the plurality of second solid supports to a plurality of first partitions, a first partition of the plurality of first partitions comprises a single cell of the one or more single cells and a single second solid support of the plurality of second solid supports, the single cell is capable of becoming associated with a second solid support via the anchor probe binding to the surface cellular target.

In some embodiments, the method comprises, prior to contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents: pooling the single cells associated with a second solid support from each first partition of the plurality of first partitions to generate a first plurality of single cells associated with a second solid support. In some embodiments, contacting the one or more single cells associated with a second solid support with a plurality of secreted factor-binding reagents comprises contacting the first plurality of single cells associated with a second solid support with the plurality of secreted factor-binding reagents.

In some embodiments, the method comprises, after contacting the first plurality of single cells associated with a

second solid support with the plurality of secreted factor-binding reagents, removing one or more secreted factor-binding reagents of the plurality of secreted factor-binding reagents that are not contacted with the first plurality of single cells associated with a second solid support to generate a second plurality of single cells associated with a second solid support. In some embodiments, removing the one or more secreted factor-binding reagents not contacted with the first plurality of single cells associated with a second solid support comprises: removing the one or more secreted factor-binding reagents not contacted with the respective at least one of the secreted factor bound by a capture probe.

The method can comprise: prior to contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization: partitioning the second plurality of single cells associated with a second solid support to a plurality of second partitions, a second partition of the plurality of second partitions comprises a single cell and a single second solid support from the second plurality of single cells associated with a second solid support; in the second partition comprising the single cell and the single second solid support, contacting a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target for hybridization. The method can comprise lysing the single cell in the second partition. Lysing the single cell can comprise heating the sample, contacting the sample with a detergent, changing the pH of the sample, or any combination thereof.

FIGS. 7A-7D show a schematic illustration of a non-limiting exemplary workflow for simultaneous measurement of the number of copies of a secreted factor and a nucleic acid target. A barcode (e.g., a stochastic barcode, an oligonucleotide barcode 702) can comprise a target binding region (e.g., a poly(dT) 710) that can bind to nucleic acid targets (e.g., poly-adenylated RNA transcripts 714 or other nucleic acid targets, such as for example, secreted factor-binding reagent specific oligonucleotide 720, whether associated with antibodies or have dissociated from antibodies) via a poly(dA) tail 718, or other nucleic acid targets, for labeling or barcoding (e.g., unique labeling). The target-binding region can comprise a gene-specific sequence, an oligo(dT) sequence, a random multimer, or any combination thereof. The oligonucleotide barcode 702 can also comprise a number of labels. The oligonucleotide barcode 702 can include first molecular label (ML) 708 and a sample label (e.g., partition label, cell label (CL) 706) for labeling the transcripts and/or tracking sample origins of the RNA transcripts (or nucleic acid targets, such as for example, antibody oligonucleotides, whether associated with antibodies or have dissociated from antibodies), respectively, along with one or more additional sequences flanking the first molecular label 708/cell label 706 region of each barcode 702 for subsequent reactions, such as, for example, a first universal sequence 704 (e.g., Read 1 sequence). The repertoire of sequences of the molecular labels in the oligonucleotide barcodes per sample can be sufficiently large for stochastic labeling of RNA transcripts. The sample label can be, for example, a partition label, and/or a cell label. In some embodiments the barcode is associated with a solid support (e.g., a particle 712). A plurality of barcodes 702 can be associated with particle 712. In some embodiments, the particle is a bead. The bead can be a polymeric bead, for example a deformable bead or a gel bead, functionalized with barcodes or stochastic barcodes (such as gel beads from 10x Genomics (San

Francisco, CA)). In some implementation, a gel bead can comprise a polymer-based gels. Gel beads can be generated, for example, by encapsulating one or more polymeric precursors into droplets. Upon exposure of the polymeric precursors to an accelerator (e.g., tetramethylethylenediamine (TEMED)), a gel bead may be generated. Poly-adenylated RNA transcripts 714 can comprise RNA sequence 716r and poly(dA) tail 718. Secreted factor-binding reagent specific oligonucleotide 720 can comprise a second universal sequence 722, a molecular label (e.g., a second molecular label 724) a unique factor identifier sequence 726, a sequence complementary to the target binding region (e.g., a poly(A) tail 728), or complements thereof. In some embodiments secreted factor binding reagent specific oligonucleotide 720 is associated with a secreted factor-binding reagent (e.g., antibody 730).

The workflow can comprise hybridization 700a of the secreted factor binding reagent specific oligonucleotide 720 and oligonucleotide barcode 702. The workflow can comprise hybridization 700a of the poly-adenylated RNA transcript 714 and oligonucleotide barcode 702. The workflow can comprise extending 700b the oligonucleotide barcode 702 hybridized to the secreted factor binding reagent specific oligonucleotide 720 to generate a barcoded secreted factor binding reagent specific oligonucleotide 734 comprising a complement of the unique factor identifier sequence 726rc, a complement of the second molecular label 724rc, and a complement of the second universal sequence 722rc. In some embodiments, the extension reaction 700b can comprise extending the oligonucleotide barcode 702 hybridized to the poly-adenylated RNA transcript 714 to generate a barcoded nucleic acid molecule 736 comprising cDNA 1416c (the reverse complementary sequence of RNA sequence 716r). The workflow can comprise denaturation 700c (e.g., with use of heating and/or chemicals). The workflow can comprise downstream 700d primer extension, amplification and/or sequencing of barcoded secreted factor binding reagent specific oligonucleotides as described herein. The workflow can comprise downstream 700e primer extension, amplification and/or sequencing of barcoded cDNAs as described herein.

Barcoded secreted factor binding reagent specific oligonucleotide 734 can serve as a template for one or more extension reactions (e.g., random priming and extension) and/or amplification reactions (e.g., PCR). For example, barcoded secreted factor binding reagent specific oligonucleotide 734 can undergo a first round of amplification (“PCR1”) 700f employing amplification primers 738 and 740 that can anneal to first universal sequence and second universal sequence (or complements thereof), respectively. PCR1 700f can generate first amplified barcoded secreted factor binding reagent specific oligonucleotide 742. PCR1 700f can comprise 1-30 cycles (e.g., 15 cycles). First amplified barcoded secreted factor binding reagent specific oligonucleotide 742 can undergo a second round of amplification (“PCR2”) 700g employing amplification primers 744 and 746 that can anneal to first universal sequence and second universal sequence (or complements thereof), respectively. PCR2 700g can generate second amplified barcoded secreted factor binding reagent specific oligonucleotide 748. PCR2 700g can add sequencing adapter 750 via an overhang in primer 746. PCR2 700g can comprise 1-30 cycles (e.g., 15 cycles). The workflow can comprise library amplification (“Index PCR”) 700h. Index PCR 700h can comprise library amplification of second amplified barcoded secreted factor binding reagent specific oligonucleotide 748 with sequencing library amplification primers 752

and 754. Sequencing library amplification primers 752 and 754 can anneal to first universal sequence and second universal sequence (or complements thereof) and/or sequencing adapter 750. Library PCR 700*h* can add sequencing adapters (e.g., P5 758 and P7 764) and sample index 760 and/or 762 (e.g., i5, i7) via overhangs in sequencing library amplification primers 752 and 754. Library PCR amplicons 756 can be sequenced and subjected to downstream methods of the disclosure. Sequencing 700*i* using 150 bp×2 sequencing can reveal the cell label, the first molecular label and/or unique factor identifier sequence (or a partial sequence of the unique factor identifier sequence) on read 1, the unique factor identifier sequence (or a partial sequence of the unique factor identifier sequence) and/or the second molecular label on read 2, and a sample index on index 1 read and/or index 2 read.

In some embodiments, barcoded secreted factor binding reagent specific oligonucleotide 734 can undergo a first round of amplification ("PCR1") 700*j* employing amplification primers 758 and 760 that can anneal to first universal sequence and second universal sequence (or complements thereof), respectively. PCR1 700*j* can generate first amplified barcoded secreted factor binding reagent specific oligonucleotide 762. PCR1 700*j* can comprise 1-30 cycles (e.g., 15 cycles). PCR1 700*j* can add sequencing adapter 750 via an overhang in primer 760. The workflow can comprise library amplification ("Index PCR") 700*k*. Index PCR 700*k* can comprise library amplification of first amplified barcoded secreted factor binding reagent specific oligonucleotide 762 with sequencing library amplification primers 764 and 766. Sequencing library amplification primers 764 and 766 can anneal to first universal sequence and second universal sequence (or complements thereof) and/or sequencing adapter 750. Library PCR 700*k* can add sequencing adapters (e.g., P5 758 and P7 764) and sample index 760 and/or 762 (e.g., i5, i7) via overhangs in sequencing library amplification primers 764 and 766. Library PCR amplicons 768 can be sequenced and subjected to downstream methods of the disclosure. Sequencing 700*l* using 150 bp×2 sequencing can reveal the cell label, the first molecular label and/or unique factor identifier sequence (or a partial sequence of the unique factor identifier sequence) on read 1, the unique factor identifier sequence (or a partial sequence of the unique factor identifier sequence) and/or the second molecular label on read 2, and a sample index on index 1 read and/or index 2 read.

In some embodiments, the plurality of oligonucleotide barcodes are associated with a third solid support. A second partition of the plurality of second partitions can comprise a single third solid support. The first partition and/or second partition can be a well or a droplet. Each oligonucleotide barcode can comprise a first universal sequence. The oligonucleotide barcode can comprise a target-binding region comprising a capture sequence. The target-binding region can comprise a poly(dT) region. The secreted factor-binding reagent specific oligonucleotide can comprise a sequence complementary to the capture sequence configured to capture the secreted factor-binding reagent specific oligonucleotide. The sequence complementary to the capture sequence can comprise a poly(dA) region. In some embodiments, the plurality of barcoded secreted factor-binding reagent specific oligonucleotides comprise a complement of the first universal sequence. The secreted factor-binding reagent specific oligonucleotide can comprise a second universal sequence.

In some embodiments, obtaining sequence information of the plurality of barcoded secreted factor-binding reagent

specific oligonucleotides, or products thereof, comprises: amplifying the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof, using a primer capable of hybridizing to the first universal sequence, or a complement thereof, and a primer capable of hybridizing to the second universal sequence, or a complement thereof, to generate a plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides; and obtaining sequencing data of the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof.

The secreted factor-binding reagent specific oligonucleotide can comprise a second molecular label. In some embodiments, at least ten of the plurality of secreted factor-binding reagent specific oligonucleotides comprise different second molecular label sequences. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are identical. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are different. In some embodiments, the number of unique first molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the number of unique second molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by each of the one or more single cells. In some embodiments, the method comprises determining the number of copies of the at least one secreted factor secreted by each of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof. In some embodiments, the method comprises determining the number of copies of the at least one secreted factor secreted by each of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof. In some embodiments, obtaining the sequence information comprises attaching sequencing adaptors to the plurality of barcoded secreted factor-binding reagent specific oligonucleotides, or products thereof. The secreted factor-binding reagent specific oligonucleotide can be configured to be detachable from the secreted factor-binding reagent. The method can comprise dissociating the secreted factor-binding reagent specific oligonucleotide from the secreted factor-binding reagent.

Determining the copy number of the nucleic acid target in each of the one or more single cells can comprise determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences, complements thereof, or a combination thereof, associated with the plurality of barcoded nucleic acid molecules, or products

thereof. The method can comprise: contacting random primers with the plurality of barcoded nucleic acid molecules, each of the random primers comprises a third universal sequence, or a complement thereof; and extending the random primers hybridized to the plurality of barcoded nucleic acid molecules to generate a plurality of extension products. The method can comprise amplifying the plurality of extension products using primers capable of hybridizing to the first universal sequence or complements thereof, and primers capable of hybridizing the third universal sequence or complements thereof, thereby generating a first plurality of barcoded amplicons. Amplifying the plurality of extension products can comprise adding sequences of binding sites of sequencing primers and/or sequencing adaptors, complementary sequences thereof, and/or portions thereof, to the plurality of extension products. The method can comprise determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the first plurality of barcoded amplicons, or products thereof. Determining the copy number of the nucleic acid target in each of the one or more single cells can comprise determining the number of each of the plurality of nucleic acid targets in each of the one or more single cells based on the number of the first molecular labels with distinct sequences associated with barcoded amplicons of the first plurality of barcoded amplicons comprising a sequence of the each of the plurality of nucleic acid targets. The sequence of the each of the plurality of nucleic acid targets can comprise a subsequence of the each of the plurality of nucleic acid targets. The sequence of the nucleic acid target in the first plurality of barcoded amplicons can comprise a subsequence of the nucleic acid target.

The method can comprise amplifying the first plurality of barcoded amplicons using primers capable of hybridizing to the first universal sequence or complements thereof, and primers capable of hybridizing the third universal sequence or complements thereof, thereby generating a second plurality of barcoded amplicons. Amplifying the first plurality of barcoded amplicons can comprise adding sequences of binding sites of sequencing primers and/or sequencing adaptors, complementary sequences thereof, and/or portions thereof, to the first plurality of barcoded amplicons. The method can comprise determining the copy number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the second plurality of barcoded amplicons, or products thereof. In some embodiments, the first plurality of barcoded amplicons and/or the second plurality of barcoded amplicons comprise whole transcriptome amplification (WTA) products.

The method can comprise synthesizing a third plurality of barcoded amplicons using the plurality of barcoded nucleic acid molecules as templates to generate a third plurality of barcoded amplicons. Synthesizing a third plurality of barcoded amplicons can comprise performing polymerase chain reaction (PCR) amplification of the plurality of the barcoded nucleic acid molecules. Synthesizing a third plurality of barcoded amplicons can comprise PCR amplification using primers capable of hybridizing to the first universal sequence, or a complement thereof, and a target-specific primer. The method can comprise obtaining sequence information of the third plurality of barcoded amplicons, or products thereof. Obtaining the sequence information can comprise attaching sequencing adaptors to the third plurality of barcoded amplicons, or products thereof. The method can comprise determining the copy

number of the nucleic acid target in each of the one or more single cells based on the number of first molecular labels with distinct sequences associated with the third plurality of barcoded amplicons, or products thereof.

5 The nucleic acid target can comprise a nucleic acid molecule. The nucleic acid molecule can comprise ribonucleic acid (RNA), messenger RNA (mRNA), microRNA, small interfering RNA (siRNA), RNA degradation product, RNA comprising a poly(A) tail, a sample indexing oligo-
10 nucleotide, a cellular component-binding reagent specific oligonucleotide, or any combination thereof. In some embodiments, extending the plurality of oligonucleotide barcodes comprising extending the plurality of oligonucleotide barcodes using a reverse transcriptase and/or a DNA
15 polymerase lacking at least one of 5' to 3' exonuclease activity and 3' to 5' exonuclease activity. The DNA polymerase can comprise a Klenow Fragment. The reverse transcriptase can comprise a viral reverse transcriptase (e.g., a murine leukemia virus (MLV) reverse transcriptase or a
20 Moloney murine leukemia virus (MMLV) reverse transcriptase). In some embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence are the same. In some embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence are different. In some
25 embodiments, the first universal sequence, the second universal sequence, and/or the third universal sequence comprise the binding sites of sequencing primers and/or a sequencing adaptor, complementary sequences thereof, and/or portions thereof. In some embodiments, the sequencing adaptors comprise a P5 sequence, a P7 sequence, complementary sequences thereof, and/or portions thereof. In some
30 embodiments, the sequencing primers comprise a Read 1 sequencing primer, a Read 2 sequencing primer, complementary sequences thereof, and/or portions thereof. In some
35 embodiments, at least 10 of the plurality of oligonucleotide barcodes comprise different first molecular label sequences. In some embodiments, the plurality of oligonucleotide barcodes each comprise a cell label. Each cell label of the
40 plurality of oligonucleotide barcodes can comprise at least 6 nucleotides. In some embodiments, oligonucleotide barcodes associated with the same third solid support comprise the same cell label. In some embodiments, oligonucleotide barcodes associated with different third solid supports comprise different cell labels.

Compositions and Kits

Disclosed herein include compositions (e.g., kits). The composition can comprise: a first solid support comprising a plurality of capture probes capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

Disclosed herein include compositions (e.g., kits). The composition can comprise: a second solid support comprising a plurality of capture probes and a plurality of anchor probes, each of the plurality of anchor probes is capable of specifically binding to a surface cellular target, and the capture probe is capable of specifically binding to at least one of a plurality of secreted factors secreted by a single cell; and a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, each of the plurality of secreted factor-

binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent.

The secreted factor-binding reagent specific oligonucleotide can comprise a second molecular label sequence. The second molecular label sequence can be 2-20 nucleotides in length. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and wherein the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are identical. In some embodiments, the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and wherein the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are different.

The secreted factor-binding reagent specific oligonucleotide can comprise a second universal sequence. The second universal sequence can comprise a binding site of a sequencing primers and/or sequencing adaptor, complementary sequences thereof, and/or portions thereof. The sequencing adaptor can comprise a P5 sequence, a P7 sequence, complementary sequences thereof, and/or portions thereof. The sequencing primer can comprise a Read 1 sequencing primer, a Read 2 sequencing primer, complementary sequences thereof, and/or portions thereof.

The cellular component-binding reagent specific oligonucleotide can comprise a poly(dA) region. The secreted factor-binding reagent specific oligonucleotide can comprise an alignment sequence adjacent to the poly(dA) region. The alignment sequence can be one or more nucleotides in length. The alignment sequence can be two or more nucleotides in length. The alignment sequence can comprise a guanine, a cytosine, a thymine, a uracil, or a combination thereof. The alignment sequence can comprise a poly(dT) sequence, a poly(dG) sequence, a poly(dC) sequence, a poly(dU) sequence, or a combination thereof. The alignment sequence can be 5' to the poly(dA) region.

The secreted factor-binding reagent specific oligonucleotide can be associated with the secreted factor-binding reagent through a linker. The linker can comprise a carbon chain. The carbon chain can comprise 2-30 carbons. The carbon chain can comprise 12 carbons. The linker can comprise 5' amino modifier C12 (5AmMC12), or a derivative thereof. The secreted factor-binding reagent specific oligonucleotide can be attached to the secreted factor-binding reagent. The secreted factor-binding reagent specific oligonucleotide can be covalently attached to the secreted factor-binding reagent. The secreted factor-binding reagent specific oligonucleotide can be non-covalently attached to the secreted factor-binding reagent. The secreted factor-binding reagent specific oligonucleotide can be conjugated to the secreted factor-binding reagent. The secreted factor-binding reagent specific oligonucleotide can be conjugated to the secreted factor-binding reagent through a chemical group selected from the group consisting of a UV photo-cleavable group, a streptavidin, a biotin, an amine, and a combination thereof.

The composition can comprise a DNA polymerase (e.g., a Klenow Fragment) lacking at least one of 5' to 3' exonuclease activity and 3' to 5' exonuclease activity. The composition can comprise a reverse transcriptase, such as a viral reverse transcriptase (e.g., murine leukemia virus (MLV) reverse transcriptase or a Moloney murine leukemia virus (MMLV) reverse transcriptase). The composition can comprise a buffer, a cartridge, or both. The composition can

comprise a plurality of oligonucleotide barcodes. The plurality of oligonucleotide barcodes are associated with a third solid support. The composition can comprise third solid supports.

5 Terminology

In at least some of the previously described embodiments, one or more elements used in an embodiment can interchangeably be used in another embodiment unless such a replacement is not technically feasible. It will be appreciated by those skilled in the art that various other omissions, additions and modifications may be made to the methods and structures described above without departing from the scope of the claimed subject matter. All such modifications and changes are intended to fall within the scope of the subject matter, as defined by the appended claims.

One skilled in the art will appreciate that, for this and other processes and methods disclosed herein, the functions performed in the processes and methods can be implemented in differing order. Furthermore, the outlined steps and operations are only provided as examples, and some of the steps and operations can be optional, combined into fewer steps and operations, or expanded into additional steps and operations without detracting from the essence of the disclosed embodiments.

25 With respect to the use of substantially any plural and/or singular terms herein, those having skill in the art can translate from the plural to the singular and/or from the singular to the plural as is appropriate to the context and/or application. The various singular/plural permutations may 30 be expressly set forth herein for sake of clarity. As used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise. Any reference to "or" herein is intended to encompass "and/or" unless otherwise stated.

It will be understood by those within the art that, in general, terms used herein, and especially in the appended claims (e.g., bodies of the appended claims) are generally intended as "open" terms (e.g., the term "including" should 40 be interpreted as "including but not limited to," the term "having" should be interpreted as "having at least," the term "includes" should be interpreted as "includes but is not limited to," etc.). It will be further understood by those within the art that if a specific number of an introduced claim recitation is intended, such an intent will be explicitly recited in the claim, and in the absence of such recitation no such intent is present. For example, as an aid to understanding, the following appended claims may contain usage of the introductory phrases "at least one" and "one or more" to introduce claim recitations. However, the use of such phrases should not be construed to imply that the introduction of a claim recitation by the indefinite articles "a" or "an" 45 limits any particular claim containing such introduced claim recitation to embodiments containing only one such recitation, even when the same claim includes the introductory phrases "one or more" or "at least one" and indefinite articles such as "a" or "an" (e.g., "a" and/or "an" should be interpreted to mean "at least one" or "one or more"); the same holds true for the use of definite articles used to introduce claim recitations. In addition, even if a specific number of an introduced claim recitation is explicitly recited, those skilled in the art will recognize that such recitation should be interpreted to mean at least the recited number (e.g., the bare recitation of "two recitations," without other modifiers, means at least two recitations, or two or more recitations). Furthermore, in those instances where a convention analogous to "at least one of A, B, and C, etc."

is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (e.g., "a system having at least one of A, B, and C" would include but not be limited to systems that have A alone, B alone, C alone, A and B together, A and C together, B and C together, and/or A, B, and C together, etc.). In those instances where a convention analogous to "at least one of A, B, or C, etc." is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (e.g., "a system having at least one of A, B, or C" would include but not be limited to systems that have A alone, B alone, C alone, A and B together, A and C together, B and C together, and/or A, B, and C together, etc.). It will be further understood by those within the art that virtually any disjunctive word and/or phrase presenting two or more alternative terms, whether in the description, claims, or drawings, should be understood to contemplate the possibilities of including one of the terms, either of the terms, or both terms. For example, the phrase "A or B" will be understood to include the possibilities of "A" or "B" or "A and B."

In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

As will be understood by one skilled in the art, for any and all purposes, such as in terms of providing a written description, all ranges disclosed herein also encompass any and all possible sub-ranges and combinations of sub-ranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, etc. As will also be understood by one skilled in the art all language such as "up to," "at least," "greater than," "less than," and the like include the number recited and refer to ranges which can be subsequently broken down into sub-ranges as discussed above. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 articles refers to groups having 1, 2, or 3 articles. Similarly, a group having 1-5 articles refers to groups having 1, 2, 3, 4, or 5 articles, and so forth.

From the foregoing, it will be appreciated that various embodiments of the present disclosure have been described herein for purposes of illustration, and that various modifications may be made without departing from the scope and spirit of the present disclosure. Accordingly, the various embodiments disclosed herein are not intended to be limiting, with the true scope and spirit being indicated by the following claims.

What is claimed is:

1. A method for measuring the number of copies of a secreted factor secreted by one or more single cells, comprising:

contacting one or more single cells with a first plurality of capturing synthetic particles, wherein the one or more single cells are capable of secreting a plurality of secreted factors, wherein each capturing synthetic particle comprises a plurality of capture probes capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell,
wherein contacting one or more single cells with a first plurality of capturing synthetic particles comprises partitioning the one or more single cells and the first

plurality of capturing synthetic particles to a plurality of first partitions, wherein a first partition of the plurality of first partitions comprises a single cell of the one or more single cells and a single capturing synthetic particle of the first plurality of capturing synthetic particles;

pooling the single capturing synthetic particles from each first partition of the plurality of first partitions to generate a second plurality of capturing synthetic particles;

contacting the second plurality of capturing synthetic particles with a plurality of secreted factor-binding reagents each capable of specifically binding to a secreted factor bound by a capture probe, wherein each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent;

hybridizing a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides, wherein the oligonucleotide barcodes each comprise a first molecular label;

extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to the unique factor identifier sequence and the first molecular label; and

obtaining sequencing data of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides to determine the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells.

2. The method of claim 1, comprising, after contacting the second plurality of capturing synthetic particles with the plurality of secreted factor-binding reagents, removing one or more secreted factor-binding reagents of the plurality of secreted factor-binding reagents that are not bound with the second plurality of capturing synthetic particles to generate a third plurality of capturing synthetic particles, wherein removing the one or more secreted factor-binding reagents not bound with the second plurality of capturing synthetic particles comprises: removing the one or more secreted factor-binding reagents not bound with the respective at least one of the secreted factor bound by a capture probe.

3. The method of claim 2, wherein hybridizing a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides comprises:

partitioning the third plurality of capturing synthetic particles to a plurality of second partitions, wherein a second partition of the plurality of second partitions comprises a single capturing synthetic particle from the third plurality of capturing synthetic particles; and
in the second partition comprising the single capturing synthetic particle, hybridizing a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides.

4. The method of claim 1, wherein the one or more single cells comprises T cells, B cells, tumor cells, myeloid cells, blood cells, or a mixture thereof.

5. The method of claim 1, wherein the at least one secreted factor comprises a cytokine, a hormone, a molecular toxin, or any combination thereof.

6. The method of claim 1, wherein the secreted factor-binding reagent and the capture probe are capable of binding to distinct epitopes of the same secreted factor.

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7. The method of claim 1, wherein one or more of the secreted factor-binding reagents and the capture probe comprise an antibody or fragment thereof.

8. A method for measuring the number of copies of a secreted factor secreted by one or more single cells and the number of copies of a nucleic acid target in one or more single cells, comprising:

contacting one or more single cells with a first plurality of dual capturing synthetic particles to form one or more single cells associated with a dual capturing synthetic particle, wherein the one or more single cells comprise a surface cellular target and copies of a nucleic acid target, wherein the one or more single cells are capable of secreting a plurality of secreted factors, wherein each dual capturing synthetic particle comprises a plurality of capture probes and a plurality of anchor probes, wherein each of the plurality of anchor probes is capable of specifically binding to the surface cellular target, and wherein the capture probe is capable of specifically binding to at least one of the plurality of secreted factors secreted by a single cell;

contacting the one or more single cells associated with a dual capturing synthetic particle with a plurality of secreted factor-binding reagents capable of specifically binding to a secreted factor bound by a capture probe, wherein each of the plurality of secreted factor-binding reagents comprises a secreted factor-binding reagent specific oligonucleotide comprising a unique factor identifier sequence for the secreted factor-binding reagent;

hybridizing a plurality of oligonucleotide barcodes with the secreted factor-binding reagent specific oligonucleotides and the copies of the nucleic acid target, wherein the oligonucleotide barcodes each comprise a first molecular label;

extending the plurality of oligonucleotide barcodes hybridized to the copies of a nucleic acid target to generate a plurality of barcoded nucleic acid molecules each comprising a sequence complementary to at least a portion of the nucleic acid target and the first molecular label;

extending the plurality of oligonucleotide barcodes hybridized to the secreted factor-binding reagent specific oligonucleotides to generate a plurality of barcoded secreted factor-binding reagent specific oligonucleotides each comprising a sequence complementary to the unique factor identifier sequence and the first molecular label;

obtaining sequencing data of the plurality of barcoded nucleic acid molecules to determine the copy number of the nucleic acid target in at least one of the one or more single cells; and

obtaining sequencing data of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides to determine the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells.

9. The method of claim 3, wherein the plurality of oligonucleotide barcodes are associated with a barcoding synthetic particle, wherein the first partition and/or second partition is a well or a droplet, and wherein a second partition of the plurality of second partitions comprises a single barcoding synthetic particle.

10. The method of claim 1, wherein each oligonucleotide barcode comprises a first universal primer sequence, and wherein the plurality of barcoded secreted factor-binding

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reagent specific oligonucleotides comprise a complement of the first universal primer sequence.

11. The method of claim 10, wherein the secreted factor-binding reagent specific oligonucleotide comprises a second universal primer sequence, and wherein obtaining sequencing data of the plurality of barcoded secreted factor-binding reagent specific oligonucleotides comprises:

amplifying the plurality of barcoded secreted factor-binding reagent specific oligonucleotides using a primer capable of hybridizing to the first universal primer sequence, or a complement thereof, and a primer capable of hybridizing to the second universal primer sequence, or a complement thereof, to generate a plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides; and
obtaining sequencing data of the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides.

12. The method of claim 1, wherein the secreted factor-binding reagent specific oligonucleotide comprises a second molecular label, and wherein: (i) the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and wherein the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are identical; or (ii) the second molecular label sequences of at least two secreted factor-binding reagent specific oligonucleotides are different, and wherein the unique identifier sequences of the at least two secreted factor-binding reagent specific oligonucleotides are different.

13. The method of claim 1, wherein the number of distinct first molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells.

14. The method of claim 12, wherein the number of distinct second molecular label sequences associated with the unique factor identifier sequence for the secreted factor-binding reagent capable of specifically binding to the at least one secreted factor in the sequencing data indicates the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells.

15. The method of claim 1, comprising determining the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of barcoded secreted factor-binding reagent specific oligonucleotides in the sequencing data.

16. The method of claim 11, comprising determining the number of copies of the at least one secreted factor secreted by at least one of the one or more single cells based on the number of first molecular labels and/or second molecular labels with distinct sequences associated with the plurality of amplified barcoded secreted factor-binding reagent specific oligonucleotides in the sequencing data.

17. The method of claim 1, wherein the capturing synthetic particle has the dimensions of a cell, wherein the cell is a mammalian cell, a yeast cell, an insect cell, a plant cell, or a bacterial cell.

18. The method of claim 8, wherein the surface cellular target comprises a carbohydrate, a lipid, a protein, or any combination thereof.