



(51) International Patent Classification:

C12Q 1/68 (2018.01)

G01N 1/30 (2006.01)

C40B 50/14 (2006.01)

(21) International Application Number:

PCT/US2021/034212

(22) International Filing Date:

26 May 2021 (26.05.2021)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/030,190

26 May 2020 (26.05.2020)

US

63/041,481

19 June 2020 (19.06.2020)

US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

(54) Title: METHOD FOR RESETTING AN ARRAY

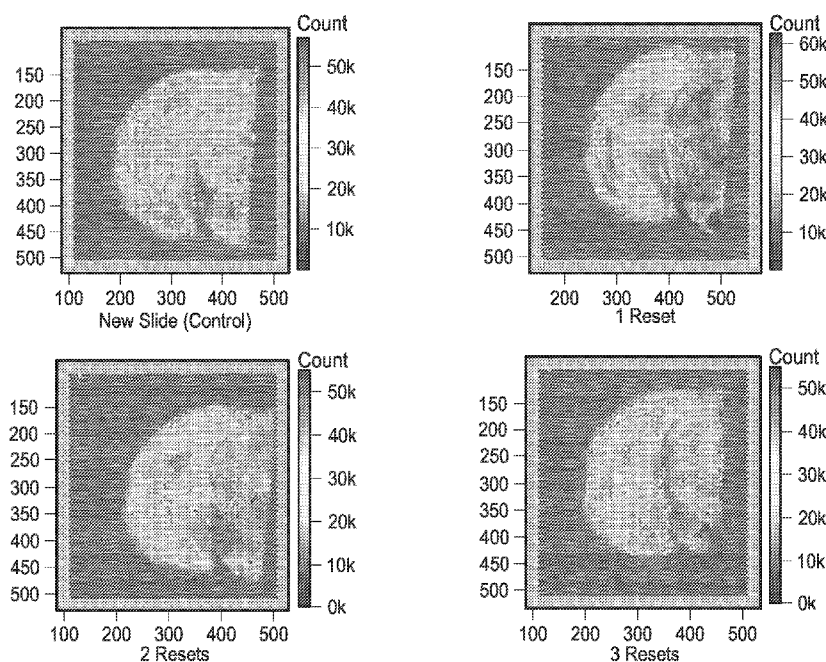


FIG. 12A

(57) Abstract: Provided herein are methods for resetting an array to which a biological sample has been applied that include treating the array with a set of biological sample removal conditions.

Declarations under Rule 4.17:

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:

- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

METHOD FOR RESETTING AN ARRAY

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application Serial Nos. 63/030,190, filed on May 26, 2020 and 63/041,481, filed on June 19, 2020, both of which are
5 hereby incorporated by reference in their entireties.

BACKGROUND

Cells within a tissue of a subject have differences in cell morphology and/or function due to varied analyte levels (e.g., gene and/or protein expression) within the different cells.
10 The specific position of a cell within a tissue (e.g., the cell's position relative to neighboring cells or the cell's position relative to the tissue microenvironment) can affect, e.g., the cell's morphology, differentiation, fate, viability, proliferation, behavior, and signaling and cross-talk with other cells in the tissue.

Spatial heterogeneity has been previously studied using techniques that only provide
15 data for a small handful of analytes in the context of an intact tissue or a portion of a tissue, or provide a lot of analyte data for single cells, but fail to provide information regarding the position of the single cell in a parent biological sample (e.g., tissue sample).

An array may be used to process a biological sample (e.g., tissue sample) for various purposes, such as identification or characterization of an analyte within the biological sample.
20 However, incorrectly placing tissue sample within the capture area and/or placing damaged/folded tissue on the array have been proven to be a common issue when using arrays to study spatial organization of gene expression.

SUMMARY

25 Provided herein are methods of resetting an array, allowing removal of tissue from the array and reprocessing new tissue onto the array without seeing a significant decrease in sequencing metrics.

In one aspect, provided herein is a method for resetting an array, the method including: (a) applying a biological sample to an array wherein the array includes a plurality
30 of capture probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to an analyte from the biological sample, (b) identifying that the biological sample has been applied to the array incorrectly or does not

contain a region of interest, and (c) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, wherein no reverse transcription has been performed prior to step (c), thereby resetting the array.

In another aspect, provided herein is a method for resetting an array to which a biological sample has been applied, the method including: (a) identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest, and (b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, wherein no reverse transcription has been performed on the array, wherein the array includes a plurality of capture probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to an analyte from the biological sample, thereby resetting the array.

In some embodiments, identifying that the biological sample has been applied to the array incorrectly can include identifying that one or more fiducial markers on the array is obscured by the biological sample. In some embodiments, identifying that the biological sample has been applied to the array incorrectly can include identifying that the biological sample is folded. In some embodiments, identifying that the biological sample has been applied to the array incorrectly can include identifying that the biological sample is torn or damaged. In some embodiments, identifying that the biological sample has been applied to the array incorrectly comprises identifying that the biological sample overlaps with a second biological sample. In some embodiments, identifying that the biological sample does not contain the region of interest can include imaging the biological sample after staining and/or immunofluorescence. In some embodiments, an image produced by imaging the biological sample demonstrates an incorrect application of a stain and/or an immunofluorescence antibody. In some embodiments, an image produced by imaging the biological sample demonstrates nonspecific staining of the biological sample.

Also provided herein is a method for resetting an array to which a biological sample has been applied, the method including: treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, wherein no reverse transcription has been performed on the array, wherein the array includes a plurality of capture probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to an analyte from the biological sample, thereby resetting the array.

Provided additionally herein is a method for resetting an array, the method including: (a) applying a biological sample to an array wherein the array includes a plurality of capture

probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to an analyte from the biological sample, and (b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, wherein no reverse transcription has been performed prior to step
5 (b), thereby resetting the array.

In some embodiments, the array can be a tissue optimization array. In some embodiments, treating the array with the set of biological sample removal conditions can include treating the array with a base. In some embodiments, the base can include a base selected from the group consisting of potassium hydroxide and sodium hydroxide. In some
10 embodiments, treating the array with the base can include treating the array with about 40 mM to about 120 mM of the base. In some embodiments, treating the array with the base can include treating the array with about 75 mM to about 85 mM of the base. In some embodiments, treating the array with the base can include treating the array with the base for between about 1 minute and about 20 minutes. In some embodiments, treating the array with
15 the base includes treating the array with the base for about 8 minutes to about 12 minutes. In some embodiments, treating the array with a base can include treating the array with a base for one, two, three, four or five cycles.

In some embodiments, treating the array with the set of biological sample removal conditions further can include washing the array with water one or more times. In some
20 embodiments, the water can be nuclease-free water and/or ultrapure water.

In some embodiments, treating the array with the set of biological sample removal conditions further can include washing the array with a buffer one or more times. In some embodiments, the buffer can be selected from the group consisting of Tris, phosphate buffered saline (PBS), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), TES (2-
25 [(2-Hydroxy-1,1-bis(hydroxymethyl)ethyl)amino]ethanesulfonic acid), and combinations thereof. In some embodiments, the buffer can have a concentration of about 1 mM to about 20 mM. In some embodiments, the buffer can have a concentration of about 8 mM to about 12 mM. In some embodiments, the buffer can have a pH of about 6.0 to about 8.0. In some embodiments, the buffer can have a pH of about 6.5 to about 7.5. In some embodiments, the
30 buffer can have a pH of about 6.8 to about 7.2.

In some embodiments, treating the array with the set of biological sample removal conditions can further include drying the array.

In some embodiments treating the array with the set of biological sample removal conditions, the biological sample is not permeabilized.

In some embodiments, treating the array with the set of biological sample removal conditions can include, sequentially, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying the array.

In some embodiments, treating the array with the set of biological sample removal conditions further can include treating the array with a proteinase. In some embodiments, treating the array with the proteinase precedes treating with the base. In some embodiments, the proteinase can be proteinase K. In some embodiments, treating the array with the proteinase can be for between 10 minutes and 2 hours. In some embodiments, treating the array with the proteinase can be for between 30 minutes and 90 minutes. In some
10 embodiments, treating the array with the proteinase can be for about 55 minutes to about 65 minutes. In some embodiments, during treatment of the array with the proteinase, the biological sample can be incubated at between 40 degrees and 60 degrees Celsius. In some embodiments, during treatment of the array with proteinase, the biological sample can be incubated at between 45 degrees to about 55 degrees Celsius. In some embodiments, treating
15 the array with the proteinase further can include treating the array with a surfactant and a proteinase buffer. In some embodiments, the surfactant can be sodium dodecyl sulfate. In some embodiments, the surfactant can be present in an amount of about 5% w/v to about 20% w/v. In some embodiments, the surfactant can be present in an amount of about 8% w/v to about 10% w/v. In some embodiments, the proteinase buffer can be Tris. In some
20 embodiments, the proteinase buffer can have a concentration of about 1 mM to about 20 mM. In some embodiments, the proteinase buffer can have a concentration of about 8 mM to about 12 mM. In some embodiments, the proteinase buffer can have a pH of about 8.0 to about 10.0. In some embodiments, the proteinase buffer can have a pH of about 8.5 to about 9.5. In some embodiments, the proteinase buffer can have a pH of about 8.8 to about 9.2.

25 In some embodiments, treating the array with the set of biological sample removal conditions can include, sequentially, treating the array with the proteinease, washing the array with water, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying.

30 In some embodiments, the array can include a slide. In some embodiments, the slide can be a glass slide.

In some embodiments, the biological sample can be an animal sample. In some embodiments, the biological sample can be a human sample. In some embodiments, the biological sample can be a rodent sample. In some embodiments, the biological sample can be a breast, brain, heart, small intestine, eye, testes, or kidney sample. In some embodiments,

biological sample can be a cancerous sample or a sample suspected of having cancerous cells. In some embodiments, the biological sample can be a tissue section. In some embodiments, the tissue section can be a fresh frozen tissue section. In some embodiments, the biological sample can be fixed. In some embodiments, the biological sample can be formalin-fixed. In some mebodiments, the biological sample can be fixed using methanol. In some
5 embodiments, the biological sample can be fixed using acetone. In some embodiments, the biological sample can be stained. In some embodiments, the stain can be a histological stain. In some embodiments, the histological stain can be a hematoxylin and eosin stain. In some embodiments, the biological sample can be imaged using immunofluorescence.

10 Also provided herein is a method for capturing an analyte using an array, the method including: (a) resetting an array according to any one or more of the methods described herein, wherein the array is a spatial array and the capture probe further includes a spatial barcode, (b) contacting the spatial array with a biological sample, and (c) capturing an analyte from the biological sample on the spatial array. In some embodiments, the analyte can
15 include RNA, DNA, a protein, a small molecule, or a metabolite. In some embodiments, the method can further include determining (i) all or a portion of a sequence corresponding to the spatial barcode, or a complement thereof, and (ii) all or a portion of a sequence corresponding to the analyte, or a complement thereof.

20 Also provided herein is a method for analyzing capture of a plurality of analytes on a tissue optimization array, the method including (a) resetting a tissue optimization array according to any one of claims 10-65, (b) contacting the tissue optimization array with a biological sample, (c) capturing a plurality of analytes from the biological sample on the tissue optimization array, and (d) analyzing the amount, distribution, and/or diffusion of the plurality of analytes based on the analytes from the biological sample captured on the tissue
25 optimization array. In some embodiments, the plurality of analytes includes RNA, DNA, a protein, a small molecule, a metabolite, or a combination thereof. All publications, patents, patent applications, and information available on the internet and mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, patent application, or item of information was specifically and
30 individually indicated to be incorporated by reference. To the extent publications, patents, patent applications, and items of information incorporated by reference contradict the disclosure contained in the specification, the specification is intended to supersede and/or take precedence over any such contradictory material.

Where values are described in terms of ranges, it should be understood that the description includes the disclosure of all possible sub-ranges within such ranges, as well as specific numerical values that fall within such ranges irrespective of whether a specific numerical value or specific sub-range is expressly stated.

5 The term “each,” when used in reference to a collection of items, is intended to identify an individual item in the collection but does not necessarily refer to every item in the collection, unless expressly stated otherwise, or unless the context of the usage clearly indicates otherwise.

Various embodiments of the features of this disclosure are described herein. However, it should be understood that such embodiments are provided merely by way of example, and numerous variations, changes, and substitutions can occur to those skilled in the art without departing from the scope of this disclosure. It should also be understood that various alternatives to the specific embodiments described herein are also within the scope of this disclosure.

15 **DESCRIPTION OF DRAWINGS**

The following drawings illustrate certain embodiments of the features and advantages of this disclosure. These embodiments are not intended to limit the scope of the appended claims in any manner. Like reference symbols in the drawings indicate like elements.

FIG. 1 shows images of fixed and stained tissue sections on an array. Tissue sections can be extremely thin and delicate, and positioning the tissue sections on an array with minimal folding or tearing of the tissue can be a difficult task. As seen in the images, parts of the tissue sections are not well positioned on the array (e.g., folded, torn, mis-aligned, or obscuring fiducials). A user may wish to remove such a tissue section from an array and either reposition the tissue section or apply a new tissue section to the array without interference or contamination from the first tissue section.

FIG. 2A shows an exemplary workflow for resetting a slide containing multiple arrays.

FIG. 2B shows exemplary images of arrays after application of tissue removal conditions without potassium hydroxide (left) and tissue removal conditions including potassium hydroxide (right).

FIG. 3 shows exemplary images of an array originally in contact with mouse brain tissue (left) and the same array after removing the mouse brain tissue and replacing it with a sample of sectioned human ovarian tumor (right).

FIG. 4 shows exemplary images of four replicates of reset arrays originally in contact with mouse brain tissue (top row). The middle row shows exemplary imaging results after performing spatial analysis on the replicate arrays after resetting the replicate arrays to remove the associated mouse brain tissue and replacing it with sectioned ovarian tumor tissue. The bottom row shows exemplary control array imaging results after performing spatial analysis on arrays with ovarian tumor tissue, which have not been reset.

FIG. 5A-D shows plots and Dunnett's control data for spatial analyte data from control (non-reset) spatial arrays vs. reset spatial arrays for; **FIG. 5A)** Reads Mapped Confidently to Transcriptome, **FIG. 5B)** Fraction of Usable Reads, **FIG. 5C)** Median Genes/Spot and **FIG. 5D)** Median UMI Counts/Spot.

FIG. 6A-B show **FIG. 6A)** gene expression of HPCA, a gene highly expressed in the hippocampus region of mouse brain (indicated with arrows) and **FIG. 6B)** gene expression of HPCA on two arrays comprising ovarian tumor tissue sections: a reset array (left; wherein the array was previously in contact with mouse brain) and a control array (right; wherein the array had not been previously in contact with any other tissue); no detectable expression of mouse HPCA was observed in the reset array, indicating that there was no contamination or interference of mouse HPCA from the mouse brain tissue section when analyzing the ovarian tumor tissue on the reset array.

FIG. 7A-G shows imaging results from a reset array (**FIG. 7B**; previous tissue shown in **FIG. 7A**), new array (**FIG. 7D**), followed by hybridizing a Cy3 labeled-partial Read 1 oligonucleotide to the spots, rinsing and imaging the arrays. The negative control array (**FIG. 7C**) was processed through an entire spatial workflow protocol without any tissue. In the absence of tissue, no gene expression should be detected. Imaging each of the three arrays for 200 milliseconds shows that the overall fluorescence is comparable between the reset array and new array. Both the reset array and the new array demonstrate a similar level of fluorescence (ability to bind the Cy3-partial Read 1 oligonucleotide) as compared to the no tissue, full spatial workflow control array. **FIGs 7E-F** demonstrate the affect of resetting a slide on the probes present on the slide. Blank OCT sections (containing no tissue samples) on array slides were processed through the reset workflow, **FIG. 7F** is exemplary of a reset slide and **FIG. 7E** is exemplary of a slide that was not reset (control). **FIG. 7G** shows the comparative fluorescence intensity of the Cy3 labelled Read 1 oligonucleotide binding to the reset and the control slides, showing minimal reduction in fluorescence and minimal affect of the reset protocol on the probes on the array.

FIG. 8 shows gene expression intensity results for reset arrays when comparing an unstained and unfixed tissue sample (left) to a fixed and stained tissue sample (middle). The control array is an array not previously contacted with tissue (e.g., new array) UMI counts were similar between arrays that were reset with fresh frozen tissue (left), fixed and stained tissue (center), and an array that was not reset (right).

FIG. 9A-C shows **FIG. 9A)** gene expression of MUCL1, a gene highly expressed in an exemplary human breast cancer tissue section. **FIG. 9B** shows gene expression of MUCL1 on an array that originally had human breast cancer tissue on it, was subjected to tissue removal conditions including a single KOH wash, and a mouse brain tissue section was placed on it. Some spatial concentration of MUCL1 was observed on the reset array, indicating that there was some contamination or interference with MUCL1 from the human tissue with the mouse brain tissue of the reset array. **FIG. 9C** shows gene expression on an array that originally had human breast cancer tissue on it, was subjected to tissue removal conditions including two KOH washes, and mouse brain tissue was placed on it. No spatial concentration of MUCL1 was observed on the reset array, indicating that there was no contamination or interference with MUCL1 from the human tissue with the mouse brain tissue of the reset array.

FIG. 10A-F show box plots of control mouse brain data compared to reset arrays, with new human breast cancer or human heart tissue samples placed on the array with regard to: **FIG. 10A)** library quality, **FIG. 10B)** fraction of reads with primer, homopolymer, or switch oligo sequence, **FIG. 10C)** fraction of reads with ribosomal or mitochondrial UMI counts, and **FIG. 10D)** sensitivity. **FIG. 10E** shows overlaid UMAP plots of mouse brain data from a new array and reset arrays (either reset post H&E staining, reset prior to fixation, or a new slide control with no reset). **FIG. 10F** shows mouse brain tissue sections stained with hematoxylin and eosin (upper figures) and gene expression analysis of hippocalcin (HPCA) (lower figures) as determined on a new array and reset arrays (as conditions as found in **FIG. 10E**).

FIG. 11A-G show analysis of immunofluorescence staining on array reset with regard to **FIG. 11A)** immunofluorescence imaging, **FIG. 11B)** UMI count, **FIG. 11C)** library quality, **FIG. 11D)** contamination of primers in the library, and **FIG. 11E)** sensitivity. **FIG. 11F** shows overlaid UMAP plots of mouse brain data from a new (control) array and a reset array, both of which were processed using immunostaining. **FIG. 11G** shows a scatter plot of gene expression data from a new (control) array and a reset array, both of which were processed using immunostaining.

FIG. 12A-D show the effect of resetting an array multiple times with regard to **FIG. 12A)** UMI count, **FIG. 12B)** library quality, **FIG. 12C)** contamination of primers in the library, and **FIG. 12D)** sensitivity.

FIG. 13A-C show the effect of array reset using mouse brain samples using **FIG. 13A)** H&E staining, **FIG. 13B)** fluorescence imaging of cDNA reverse transcribed from captured analytes (time in minutes (m) is time of permeabilization), and **FIG. 13C)** the mean fluorescence intensity from **FIG. 13B)** of a control versus reset array for different tissue permeabilization times.

FIG. 14A-B show the effect of array reset using mouse liver samples using **FIG. 14A)** H&E staining and **FIG. 14B)** fluorescence imaging of cDNA reverse transcribed from captured analytes.

FIG. 15A-B show the effect of array reset using mouse spleen samples using **FIG. 15A)** H&E staining and **FIG. 15B)** fluorescence imaging of cDNA reverse transcribed from captured analytes.

FIG. 16A-E show spatial gene analysis of human heart tissue on a **FIG. 16A)** new (control) array, and reset arrays that originally had **FIG. 16B)** mouse eye tissue, **FIG. 16C)** mouse small intestine tissue, **FIG. 16D)** mouse testes tissue, and **FIG. 16E)** mouse kidney tissue, placed on them.

FIG. 17A-D show spatial gene analysis of mouse brain tissue on **FIG. 17A)** a new (control) array, and reset arrays that originally had **FIG. 17B)** human breast cancer tissue, **FIG. 17C)** human heart tissue, and **FIG. 17D)** human brain tissue, placed on them.

DETAILED DESCRIPTION

Placing a biological sample such as a tissue sample on a location on an array can be challenging. For example, tissue sections which are often around 5-10 μm thick can be difficult to handle. Tissue sections can fold back on themselves, they can tear or be damaged such that proceeding with spatial assays to determine analyte locations within a tissue are compromised. In some cases, after imaging, a tissue sample can be determined not to contain a region of interest (e.g., tumor region or immune cell infiltrate). It would be very beneficial if, once placed on an array, a tissue sample could be removed, repositioned or altogether replaced with another tissue sample without compromising the downstream analysis (e.g., spatial assay). The present disclosure provides methods for repositioning, removing, replacing, or resetting a tissue sample on an array.

Spatial analysis methodologies and compositions described herein can provide a vast amount of analyte and/or expression data for a variety of analytes within a biological sample at high spatial resolution, while retaining native spatial context. Spatial analysis methods and compositions can include, e.g., the use of a capture probe including a spatial barcode (e.g., a nucleic acid sequence that provides information as to the location or position of an analyte within a cell or a tissue sample (e.g., mammalian cell or a mammalian tissue sample) and a capture domain that is capable of binding to an analyte (e.g., a protein and/or a nucleic acid) produced by and/or present in a cell. Spatial analysis methods and compositions can also include the use of a capture probe having a capture domain that captures an intermediate agent for indirect detection of an analyte. For example, the intermediate agent can include a nucleic acid sequence (e.g., a barcode) associated with the intermediate agent. Detection of the intermediate agent is therefore indicative of the analyte in the cell or tissue sample.

Non-limiting aspects of spatial analysis methodologies and compositions are described in U.S. Patent Nos. 10,774,374, 10,724,078, 10,480,022, 10,059,990, 10,041,949, 10,002,316, 9,879,313, 9,783,841, 9,727,810, 9,593,365, 8,951,726, 8,604,182, 7,709,198, U.S. Patent Application Publication Nos. 2020/239946, 2020/080136, 2020/0277663, 2020/024641, 2019/330617, 2019/264268, 2020/256867, 2020/224244, 2019/194709, 2019/161796, 2019/085383, 2019/055594, 2018/216161, 2018/051322, 2018/0245142, 2017/241911, 2017/089811, 2017/067096, 2017/029875, 2017/0016053, 2016/108458, 2015/000854, 2013/171621, WO 2018/091676, WO 2020/176788, Rodriques et al., Science 363(6434):1463-1467, 2019; Lee et al., Nat. Protoc. 10(3):442-458, 2015; Trejo et al., PLoS ONE 14(2):e0212031, 2019; Chen et al., Science 348(6233):aaa6090, 2015; Gao et al., BMC Biol. 15:50, 2017; and Gupta et al., Nature Biotechnol. 36:1197-1202, 2018; the Visium Spatial Gene Expression Reagent Kits User Guide (e.g., Rev C, dated June 2020), and/or the Visium Spatial Tissue Optimization Reagent Kits User Guide (e.g., Rev C, dated July 2020), both of which are available at the 10x Genomics Support Documentation website, and can be used herein in any combination. Further non-limiting aspects of spatial analysis methodologies and compositions are described herein.

Some general terminology that may be used in this disclosure can be found in Section (I)(b) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. Typically, a “barcode” is a label, or identifier, that conveys or is capable of conveying information (e.g., information about an analyte in a sample, a bead, and/or a capture probe). A barcode can be part of an analyte, or independent of an analyte. A barcode can be attached to an analyte. A particular barcode can be unique relative to other barcodes. For the purpose

of this disclosure, an “analyte” can include any biological substance, structure, moiety, or component to be analyzed. The term “target” can similarly refer to an analyte of interest.

Analytes can be broadly classified into one of two groups: nucleic acid analytes, and non-nucleic acid analytes. Examples of non-nucleic acid analytes include, but are not limited to, lipids, carbohydrates, peptides, proteins, glycoproteins (N-linked or O-linked), lipoproteins, phosphoproteins, specific phosphorylated or acetylated variants of proteins, amidation variants of proteins, hydroxylation variants of proteins, methylation variants of proteins, ubiquitylation variants of proteins, sulfation variants of proteins, viral proteins (e.g., viral capsid, viral envelope, viral coat, viral accessory, viral glycoproteins, viral spike, etc.), extracellular and intracellular proteins, antibodies, and antigen binding fragments. In some embodiments, the analyte(s) can be localized to subcellular location(s), including, for example, organelles, e.g., mitochondria, Golgi apparatus, endoplasmic reticulum, chloroplasts, endocytic vesicles, exocytic vesicles, vacuoles, lysosomes, etc. In some embodiments, analyte(s) can be peptides or proteins, including without limitation antibodies and enzymes. Additional examples of analytes can be found in Section (I)(c) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. In some embodiments, an analyte can be detected indirectly, such as through detection of an intermediate agent, for example, a ligation product or an analyte capture agent (e.g., an oligonucleotide-conjugated antibody), such as those described herein.

A “biological sample” is typically obtained from the subject for analysis using any of a variety of techniques including, but not limited to, biopsy, surgery, and laser capture microscopy (LCM), and generally includes cells and/or other biological material from the subject. In some embodiments, a biological sample can be a tissue section. In some embodiments, a biological sample can be a fixed and/or stained biological sample (e.g., a fixed and/or stained tissue section). Non-limiting examples of stains include histological stains (e.g., hematoxylin and/or eosin) and immunological stains (e.g., fluorescent stains). In some embodiments, a biological sample (e.g., a fixed and/or stained biological sample) can be imaged. Biological samples are also described in Section (I)(d) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

In some embodiments, a biological sample is permeabilized with one or more permeabilization reagents. For example, permeabilization of a biological sample can facilitate analyte capture. Exemplary permeabilization agents and conditions are described in Section (I)(d)(ii)(13) or the Exemplary Embodiments Section of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

Array-based spatial analysis methods involve the transfer of one or more analytes from a biological sample to an array of features on a substrate, where each feature is associated with a unique spatial location on the array. Subsequent analysis of the transferred analytes includes determining the identity of the analytes and the spatial location of the analytes within the biological sample. The spatial location of an analyte within the biological sample is determined based on the feature to which the analyte is bound (e.g., directly or indirectly) on the array, and the feature's relative spatial location within the array.

A "capture probe" refers to any molecule capable of capturing (directly or indirectly) and/or labelling an analyte (e.g., an analyte of interest) in a biological sample. In some embodiments, the capture probe is a nucleic acid or a polypeptide. In some embodiments, the capture probe includes a barcode (e.g., a spatial barcode and/or a unique molecular identifier (UMI)) and a capture domain). In some embodiments, a capture probe can include a cleavage domain and/or a functional domain (e.g., a primer-binding site, such as for next-generation sequencing (NGS)). See, e.g., Section (II)(b) (e.g., subsections (i)-(vi)) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. Generation of capture probes can be achieved by any appropriate method, including those described in Section (II)(d)(ii) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

In some embodiments, more than one analyte type (e.g., nucleic acids and proteins) from a biological sample can be detected (e.g., simultaneously or sequentially) using any appropriate multiplexing technique, such as those described in Section (IV) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

In some embodiments, detection of one or more analytes (e.g., protein analytes) can be performed using one or more analyte capture agents. As used herein, an "analyte capture agent" refers to an agent that interacts with an analyte (e.g., an analyte in a biological sample) and with a capture probe (e.g., a capture probe attached to a substrate or a feature) to identify the analyte. In some embodiments, the analyte capture agent includes: (i) an analyte binding moiety (e.g., that binds to an analyte), for example, an antibody or antigen-binding fragment thereof; (ii) analyte binding moiety barcode; and (iii) an analyte capture sequence. As used herein, the term "analyte binding moiety barcode" refers to a barcode that is associated with or otherwise identifies the analyte binding moiety. As used herein, the term "analyte capture sequence" refers to a region or moiety configured to hybridize to, bind to, couple to, or otherwise interact with a capture domain of a capture probe. In some cases, an analyte binding moiety barcode (or portion thereof) may be able to be removed (e.g., cleaved) from

the analyte capture agent. Additional description of analyte capture agents can be found in Section (II)(b)(ix) of WO 2020/176788 and/or Section (II)(b)(viii) U.S. Patent Application Publication No. 2020/0277663.

There are at least two methods to associate a spatial barcode with one or more neighboring cells, such that the spatial barcode identifies the one or more cells, and/or contents of the one or more cells, as associated with a particular spatial location. One method is to promote analytes or analyte proxies (e.g., intermediate agents) out of a cell and towards a spatially-barcoded array (e.g., including spatially-barcoded capture probes). Another method is to cleave spatially-barcoded capture probes from an array and promote the spatially-barcoded capture probes towards and/or into or onto the biological sample.

In some cases, capture probes may be configured to prime, replicate, and consequently yield optionally barcoded extension products from a template (e.g., a DNA or RNA template, such as an analyte or an intermediate agent (e.g., a ligation product or an analyte capture agent), or a portion thereof), or derivatives thereof (see, e.g., Section (II)(b)(vii) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663 regarding extended capture probes). In some cases, capture probes may be configured to form ligation products with a template (e.g., a DNA or RNA template, such as an analyte or an intermediate agent, or portion thereof), thereby creating ligations products that serve as proxies for a template.

As used herein, an “extended capture probe” refers to a capture probe having additional nucleotides added to the terminus (e.g., 3’ or 5’ end) of the capture probe thereby extending the overall length of the capture probe. For example, an “extended 3’ end” indicates additional nucleotides were added to the most 3’ nucleotide of the capture probe to extend the length of the capture probe, for example, by polymerization reactions used to extend nucleic acid molecules including templated polymerization catalyzed by a polymerase (e.g., a DNA polymerase or a reverse transcriptase). In some embodiments, extending the capture probe includes adding to a 3’ end of a capture probe a nucleic acid sequence that is complementary to a nucleic acid sequence of an analyte or intermediate agent specifically bound to the capture domain of the capture probe. In some embodiments, the capture probe is extended using reverse transcription. In some embodiments, the capture probe is extended using one or more DNA polymerases. The extended capture probes include the sequence of the capture probe and the sequence of the spatial barcode of the capture probe.

In some embodiments, extended capture probes are amplified (e.g., in bulk solution or on the array) to yield quantities that are sufficient for downstream analysis, e.g., via DNA

sequencing. In some embodiments, extended capture probes (e.g., DNA molecules) act as templates for an amplification reaction (e.g., a polymerase chain reaction).

Additional variants of spatial analysis methods, including in some embodiments, an imaging step, are described in Section (II)(a) of WO 2020/176788 and/or U.S. Patent

5 Application Publication No. 2020/0277663. Analysis of captured analytes (and/or intermediate agents or portions thereof), for example, including sample removal, extension of capture probes, sequencing (e.g., of a cleaved extended capture probe and/or a cDNA molecule complementary to an extended capture probe), sequencing on the array (e.g., using, for example, in situ hybridization or in situ ligation approaches), temporal analysis, and/or
10 proximity capture, is described in Section (II)(g) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. Some quality control measures are described in Section (II)(h) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

Spatial information can provide information of biological and/or medical importance.

15 For example, the methods and compositions described herein can allow for: identification of one or more biomarkers (e.g., diagnostic, prognostic, and/or for determination of efficacy of a treatment) of a disease or disorder; identification of a candidate drug target for treatment of a disease or disorder; identification (e.g., diagnosis) of a subject as having a disease or disorder; identification of stage and/or prognosis of a disease or disorder in a subject;
20 identification of a subject as having an increased likelihood of developing a disease or disorder; monitoring of progression of a disease or disorder in a subject; determination of efficacy of a treatment of a disease or disorder in a subject; identification of a patient subpopulation for which a treatment is effective for a disease or disorder; modification of a treatment of a subject with a disease or disorder; selection of a subject for participation in a
25 clinical trial; and/or selection of a treatment for a subject with a disease or disorder.

Spatial information can provide information of biological importance. For example, the methods and compositions described herein can allow for: identification of transcriptome and/or proteome expression profiles (e.g., in healthy and/or diseased tissue); identification of multiple analyte types in close proximity (e.g., nearest neighbor analysis); determination of
30 up- and/or down-regulated genes and/or proteins in diseased tissue; characterization of tumor microenvironments; characterization of tumor immune responses; characterization of cells types and their co-localization in tissue; and identification of genetic variants within tissues (e.g., based on gene and/or protein expression profiles associated with specific disease or disorder biomarkers).

Typically, for spatial array-based methods, a substrate functions as a support for direct or indirect attachment of capture probes to features of the array. A “feature” is an entity that acts as a support or repository for various molecular entities used in spatial analysis. In some embodiments, some or all of the features in an array are functionalized for analyte capture.

5 Exemplary substrates are described in Section (II)(c) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. Exemplary features and geometric attributes of an array can be found in Sections (II)(d)(i), (II)(d)(iii), and (II)(d)(iv) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

Generally, analytes and/or intermediate agents (or portions thereof) can be captured
10 when contacting a biological sample with a substrate including capture probes (e.g., a substrate with capture probes embedded, spotted, printed, fabricated on the substrate, or a substrate with features (e.g., beads, wells) comprising capture probes). As used herein, “contact,” “contacted,” and/or “contacting,” a biological sample with a substrate refers to any contact (e.g., direct or indirect) such that capture probes can interact (e.g., bind covalently or
15 non-covalently (e.g., hybridize)) with analytes from the biological sample. Capture can be achieved actively (e.g., using electrophoresis) or passively (e.g., using diffusion). Analyte capture is further described in Section (II)(e) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

In some cases, spatial analysis can be performed by attaching and/or introducing a
20 molecule (e.g., a peptide, a lipid, or a nucleic acid molecule) having a barcode (e.g., a spatial barcode) to a biological sample (e.g., to a cell in a biological sample). In some embodiments, a plurality of molecules (e.g., a plurality of nucleic acid molecules) having a plurality of barcodes (e.g., a plurality of spatial barcodes) are introduced to a biological sample (e.g., to a plurality of cells in a biological sample) for use in spatial analysis. In some embodiments,
25 after attaching and/or introducing a molecule having a barcode to a biological sample, the biological sample can be physically separated (e.g., dissociated) into single cells or cell groups for analysis. Some such methods of spatial analysis are described in Section (III) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663.

In some cases, spatial analysis can be performed by detecting multiple
30 oligonucleotides that hybridize to an analyte. In some instances, for example, spatial analysis can be performed using RNA-templated ligation (RTL). Methods of RTL have been described previously. See, e.g., Credle *et al.*, *Nucleic Acids Res.* 2017 Aug 21;45(14):e128. Typically, RTL includes hybridization of two oligonucleotides to adjacent sequences on an analyte (e.g., an RNA molecule, such as an mRNA molecule). In some instances, the

oligonucleotides are DNA molecules. In some instances, one of the oligonucleotides includes at least two ribonucleic acid bases at the 3' end and/or the other oligonucleotide includes a phosphorylated nucleotide at the 5' end. In some instances, one of the two oligonucleotides includes a capture domain (e.g., a poly(A) sequence, a non-homopolymeric sequence). After hybridization to the analyte, a ligase (e.g., SplintR ligase) ligates the two oligonucleotides together, creating a ligation product. In some instances, the two oligonucleotides hybridize to sequences that are not adjacent to one another. For example, hybridization of the two oligonucleotides creates a gap between the hybridized oligonucleotides. In some instances, a polymerase (e.g., a DNA polymerase) can extend one of the oligonucleotides prior to ligation. After ligation, the ligation product is released from the analyte. In some instances, the ligation product is released using an endonuclease (e.g., RNase H). The released ligation product can then be captured by capture probes (e.g., instead of direct capture of an analyte) on an array, optionally amplified, and sequenced, thus determining the location and optionally the abundance of the analyte in the biological sample.

During analysis of spatial information, sequence information for a spatial barcode associated with an analyte is obtained, and the sequence information can be used to provide information about the spatial distribution of the analyte in the biological sample. Various methods can be used to obtain the spatial information. In some embodiments, specific capture probes and the analytes they capture are associated with specific locations in an array of features on a substrate. For example, specific spatial barcodes can be associated with specific array locations prior to array fabrication, and the sequences of the spatial barcodes can be stored (e.g., in a database) along with specific array location information, so that each spatial barcode uniquely maps to a particular array location.

Alternatively, specific spatial barcodes can be deposited at predetermined locations in an array of features during fabrication such that at each location, only one type of spatial barcode is present so that spatial barcodes are uniquely associated with a single feature of the array. Where necessary, the arrays can be decoded using any of the methods described herein so that spatial barcodes are uniquely associated with array feature locations, and this mapping can be stored as described above.

When sequence information is obtained for capture probes and/or analytes during analysis of spatial information, the locations of the capture probes and/or analytes can be determined by referring to the stored information that uniquely associates each spatial barcode with an array feature location. In this manner, specific capture probes and captured analytes are associated with specific locations in the array of features. Each array feature

location represents a position relative to a coordinate reference point (e.g., an array location, a fiducial marker) for the array. Accordingly, each feature location has an “address” or location in the coordinate space of the array.

Some exemplary spatial analysis workflows are described in the Exemplary Embodiments section of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. See, for example, the Exemplary embodiment starting with “In some non-limiting examples of the workflows described herein, the sample can be immersed...” of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663. See also, e.g., the Visium Spatial Gene Expression Reagent Kits User Guide (e.g., Rev C, dated June 2020), and/or the Visium Spatial Tissue Optimization Reagent Kits User Guide (e.g., Rev C, dated July 2020).

In some embodiments, spatial analysis can be performed using dedicated hardware and/or software, such as any of the systems described in Sections (II)(e)(ii) and/or (V) of WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663, or any of one or more of the devices or methods described in Sections *Control Slide for Imaging, Methods of Using Control Slides and Substrates for, Systems of Using Control Slides and Substrates for Imaging*, and/or *Sample and Array Alignment Devices and Methods, Informational labels* of WO 2020/123320.

Suitable systems for performing spatial analysis can include components such as a chamber (e.g., a flow cell or sealable, fluid-tight chamber) for containing a biological sample. The biological sample can be mounted for example, in a biological sample holder. One or more fluid chambers can be connected to the chamber and/or the sample holder via fluid conduits, and fluids can be delivered into the chamber and/or sample holder via fluidic pumps, vacuum sources, or other devices coupled to the fluid conduits that create a pressure gradient to drive fluid flow. One or more valves can also be connected to fluid conduits to regulate the flow of reagents from reservoirs to the chamber and/or sample holder.

The systems can optionally include a control unit that includes one or more electronic processors, an input interface, an output interface (such as a display), and a storage unit (e.g., a solid state storage medium such as, but not limited to, a magnetic, optical, or other solid state, persistent, writeable and/or re-writeable storage medium). The control unit can optionally be connected to one or more remote devices via a network. The control unit (and components thereof) can generally perform any of the steps and functions described herein. Where the system is connected to a remote device, the remote device (or devices) can perform any of the steps or features described herein. The systems can optionally include one

or more detectors (e.g., CCD, CMOS) used to capture images. The systems can also optionally include one or more light sources (e.g., LED-based, diode-based, lasers) for illuminating a sample, a substrate with features, analytes from a biological sample captured on a substrate, and various control and calibration media.

5 The systems can optionally include software instructions encoded and/or implemented in one or more of tangible storage media and hardware components such as application specific integrated circuits. The software instructions, when executed by a control unit (and in particular, an electronic processor) or an integrated circuit, can cause the control unit, integrated circuit, or other component executing the software instructions to perform any of
10 the method steps or functions described herein.

 In some cases, the systems described herein can detect (e.g., register an image) the biological sample on the array. Exemplary methods to detect the biological sample on an array are described in PCT Application No. 2020/061064 and/or U.S. Patent Application Serial No. 16/951,854.

15 Prior to transferring analytes from the biological sample to the array of features on the substrate, the biological sample can be aligned with the array. Alignment of a biological sample and an array of features including capture probes can facilitate spatial analysis, which can be used to detect differences in analyte presence and/or level within different positions in the biological sample, for example, to generate a three-dimensional map of the analyte
20 presence and/or level. Exemplary methods to generate a two- and/or three-dimensional map of the analyte presence and/or level are described in PCT Application No. 2020/053655 and spatial analysis methods are generally described in WO 2020/061108 and/or U.S. Patent Application Serial No. 16/951,864.

 In some cases, a map of analyte presence and/or level can be aligned to an image of a
25 biological sample using one or more fiducial markers, e.g., objects placed in the field of view of an imaging system which appear in the image produced, as described in the *Substrate Attributes* Section, *Control Slide for Imaging* Section of WO 2020/123320, PCT Application No. 2020/061066, and/or U.S. Patent Application Serial No. 16/951,843. Fiducial markers can be used as a point of reference or measurement scale for alignment (e.g., to align a
30 sample and an array, to align two substrates, to determine a location of a sample or array on a substrate relative to a fiducial marker) and/or for quantitative measurements of sizes and/or distances. Arrays that can be reset using the methods described herein include, for example, tissue optimization arrays and spatial gene expression arrays. In some cases, an array can be a tissue optimization array used to evaluate analyte capture (e.g., by cDNA synthesis using

fluorescent nucleotide analogs). In some cases an array can be a spatial array. Generally, capture probes on a spatial array include spatial barcodes, and capture probes on a tissue optimization array do not, though both include capture domains to capture analytes from a biological sample.

5 Provided herein are methods for resetting an array (e.g., a spatial array or a tissue optimization array). In some embodiments, the first biological sample is fixed, stained and imaged prior to removing the tissue sample from the array (e.g., a spatial array or a tissue optimization array). Also provided herein are methods of capturing an analyte using an array (e.g., a spatial array) that has been reset using any of the methods described herein. Also
10 provided herein are methods for analyzing capture of a plurality of analytes on a tissue optimization array using a tissue optimization array that has been reset using any of the methods described herein. Array-based spatial analysis methods involve the use of a spatial array, where the spatial array includes an array of features on a substrate. In some
15 embodiments, a biological sample (e.g., tissue sample) is contacted with the spatial array, generally allowing the transfer of one or more analytes from the biological sample to the array of features. In some embodiments, before a spatial analysis is performed, a biological
sample is first analyzed using a tissue optimization array to determine the amount or presence of captured analyte for any given sample preparation and/or permeabilization condition.

 In some embodiments, after contacting a biological sample with a substrate that
20 includes an array of features (e.g., including a plurality of capture probes), a removal step can be performed to remove the biological sample from the substrate thereby resetting the array. Typically, array resetting occurs before a capture probe of the plurality of capture probes has been enzymatically extended to include a sequence complementary to all or a part of a
sequence of an analyte from the biological sample. In some workflows, reverse transcription
25 is used to enzymatically extend a capture probe of the plurality of capture probes to include a sequence complementary to all or part of a sequence of an analyte from the biological sample. Accordingly, in some embodiments, resetting an array occurs before reverse
transcription has occurred on the array. In some embodiments, resetting an array occurs
before an extension reaction (e.g., an enzymatic extension reaction) has occurred on the array
30 (e.g., performed on a capture probe). In some embodiments, the biological sample is not permeabilized before the array is reset.

 As used herein, “resetting” an array refers to the removal of a first tissue that was positioned on an array. In some embodiments, resetting an array can be followed by repositioning a first tissue on the array. In some embodiments, an array is reset in order to

position another biological tissue sample on the array (e.g., a second portion of the same biological sample, or a biological sample from a different source, study, or organism). In some embodiments, an array may be reset once. In some embodiments, an array may be reset twice, three times, four times, or five times. In some embodiments, the array is reset in order
5 to be used again, preferably before reverse transcription is performed on the array. In some embodiments, the array is reset in order to be used again, preferably before an extension reaction (e.g., an enzymatic extension reaction) has occurred on the array (e.g., performed on a capture probe).

In some embodiments, a method for resetting an array to which a biological sample
10 has been applied includes treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array.

In some embodiments, a method for resetting an array includes (a) applying a biological sample to an array comprising a plurality of capture probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to
15 an analyte from the biological sample, and (b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, thereby resetting the array.

In some embodiments, a method for resetting an array to which a biological sample has been applied includes (a) identifying that the biological sample has been applied to the
20 array incorrectly or does not contain a region of interest, and (b) treating the array with a set of biological sample removal conditions, thereby resetting the array.

As used herein, identifying that a biological sample has been applied to an array “incorrectly” can include identifying that one or more fiducial markers on the array is obscured by the biological sample, identifying that the biological sample is folded,
25 identifying that the biological sample is torn or damaged, identifying that the biological sample was applied to the wrong array section, identifying that the biological sample overlaps with a second biological sample, or a combination thereof.

In some embodiments, identifying that the biological sample does not contain the region of interest includes imaging the biological sample after staining and/or
30 immunofluorescence. In some cases, an image produced by imaging the biological sample demonstrates an incorrect application of a stain and/or an immunofluorescence antibody. In some cases, an image produced by imaging the biological sample demonstrates nonspecific staining of the biological sample.

In some embodiments, a method for resetting an array includes (a) applying a biological sample to an array including a plurality of capture probes, wherein a capture probe of the plurality of capture probes includes a capture domain that binds specifically to an analyte from the biological sample, (b) identifying that the biological sample has been
5 applied to the array incorrectly or does not contain a region of interest, and (c) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, thereby resetting the array.

In some embodiments of any of the methods described herein, resetting an array is performed before one or more potentially irreversible alterations to the array. In some
10 embodiments, resetting an array occurs before reverse transcription has occurred on the array. In some embodiments, resetting an array occurs before an enzymatic extension reaction has occurred on the array (e.g., performed on a capture probe). In some embodiments, resetting an array occurs before an extension reaction has occurred on the array (e.g., performed on a capture probe).

15 In some embodiments, a biological sample is removed from an array to reset the array. In some embodiments, a method of removing a biological sample from an array comprises treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array.

In some embodiments, resetting an array is performed before the biological sample is
20 imaged; however, it may be easier for a user to identify that the biological sample was incorrectly placed or does not contain a region of interest with a visual aid. For example, it may be easier to identify that the biological sample obscures one or more fiducial markers on the array, or that the biological sample has been folded or torn using a visual aid. As another example, it may be easier to identify that the biological sample does not contain a region of
25 interest after immunofluorescence. Accordingly, in some embodiments, resetting an array is performed after the biological sample is fixed and stained. In some embodiments, resetting an array is performed after the biological sample is fixed. In some embodiments, the biological sample can be fixed in any of the variety of fixatives described in, for example, in Section (I)(d)(ii)(3)-(6) of WO 2020/176788 and/or U.S. Patent Application Publication No.
30 2020/0277663. In some embodiments, the biological sample is stained. In some embodiments, the biological sample can be stained using known staining techniques, including but not limited to, Can-Grunwald, Giemsa, hematoxylin and eosin (H&E), Jenner's, Leishman, Masson's trichrome, Papanicolaou, Romanowsky, silver, Sudan, Wright's, and/or Periodic Acid Schiff (PAS) staining techniques. See, for example, Sections (I)(d)(ii)(3)-(6) of

WO 2020/176788 and/or U.S. Patent Application Publication No. 2020/0277663 for fixing and staining techniques. In some embodiments, resetting an array is performed after the biological sample is evaluated using immunofluorescence. As such, resetting an array can be performed after fixing, immunofluorescence, staining, and/or imaging but prior to performing
5 analyte capture and downstream enzymatic reactions on the captured analyte, for example reverse transcription of a captured mRNA molecule. Once analytes from a biological sample have been captured and extended on the array, the spatial barcodes are associated with the spatial location of the captured analyte in the biological sample. However, staining and/or fixing of a biological sample leaves the spatial barcodes intact thereby allowing for array
10 resetting.

Treating an array (e.g., spatial array or tissue optimization array) to which a biological sample has been applied with a set of biological sample removal conditions can include treating the array with any appropriate reagents, temperatures, or other conditions. Typically, treating an array with a set of biological sample removal conditions includes treating the
15 array with a base. In some embodiments, for example, treating the array with a base is the first part of the set of biological sample removal conditions. In some embodiments, the biological sample on the array is first treated enzymatically and/or chemically to degrade the biological sample prior to treating the array with a base.

In some embodiments, treating an array (e.g., spatial array or tissue optimization
20 array) to which a biological sample has been applied with a set of biological sample removal conditions can include treating enzymatically and/or chemically to degrade the biological sample. For example, treating an array to which a biological sample has been applied with a set of biological sample removal conditions can include treating the array with an enzyme (e.g., a proteinase, e.g., proteinase K) to remove at least a portion of the biological sample
25 from the array (e.g., on a glass slide). In some embodiments, treating an array to which a biological sample has been applied with a set of biological sample removal conditions can include ablation of the biological sample (e.g., laser ablation). In some embodiments, treating an array to which a biological sample has been applied with a set of biological sample removal conditions can include treating the array with a proteinase. In some embodiments,
30 the proteinase is proteinase K. Treating with a proteinase can include any appropriate conditions, e.g., to allow the proteinase to function. In some embodiments, treating with a proteinase can include treating with a buffer (e.g., Tris, phosphate buffered saline (PBS), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), TES (2-[(2-Hydroxy-1,1-bis(hydroxymethyl)ethyl)amino]ethanesulfonic acid), and combinations thereof) at an

appropriate pH (e.g., about pH 8.0 to about 10.0 (e.g., pH about 8.5 to about 9.5, about 8.8 to about 9.2, or about 9.0)) and appropriate concentration (e.g., about 1 mM to about 20 mM (e.g., about 5 mM to about 15 mM, about 8 mM to about 12 mM, or about 10 mM)),
 5 optionally with one or more additional reagents, such as a surfactant (e.g., sodium dodecyl sulfate) at any appropriate concentration (e.g., about 5% to about 15% w/v (e.g., about 8% to about 12% w/v, or about 10% w/v)).

In some embodiments, the array (e.g., spatial array or tissue optimization array) is treated with the proteinease (e.g., proteinase K) for between 10 minutes and 120 minutes (e.g., between 10 minutes and 100 minutes, between 10 minutes and 90 minutes, between 10
 10 minutes and 80 minutes, between 10 minutes and 70 minutes, between 10 minutes and 60 minutes, between 10 minutes and 45 minutes, between 10 minutes and 30 minutes, between 30 minutes and 120 minutes, between 30 minutes and 100 minutes, between 30 minutes and 90 minutes, between 30 minutes and 80 minutes, between 30 minutes and 70 minutes, between 30 minutes and 60 minutes, between 30 minutes and 45 minutes, between 45
 15 minutes and 120 minutes, between 45 minutes and 100 minutes, between 45 minutes and 90 minutes, between 45 minutes and 80 minutes, between 45 minutes and 70 minutes, between 45 minutes and 60 minutes, between 60 minutes and 120 minutes, between 60 minutes and 100 minutes, between 60 minutes and 90 minutes, between 60 minutes and 80 minutes, between 60 minutes and 70 minutes, between 70 minutes and 120 minutes, between 70
 20 minutes and 100 minutes, between 70 minutes and 90 minutes, between 70 minutes and 80 minutes, between 80 minutes and 120 minutes, between 80 minutes and 100 minutes, between 80 minutes and 90 minutes, between 90 minutes and 120 minutes, between 90 minutes and 100 minutes, or between 100 minutes and 120 minutes). In some embodiments, the array is treated with proteinase K for approximately 60 minutes.

25 In some embodiments, the array (e.g., spatial array or tissue optimization array) is incubated during the treatment with a proteinase at a temperature between 40 degrees and 60 degrees (e.g., between 40 degrees and 58 degrees, between 40 degrees and 56 degrees, between 40 degrees and 54 degrees, between 40 degrees and 52 degrees, between 40 degrees and 50 degrees, between 40 degrees and 48 degrees, between 40 degrees and 46 degrees,
 30 between 40 degrees and 44 degrees, between 40 degrees and 42 degrees, between 42 degrees and 60 degrees, between 42 degrees and 58 degrees, between 42 degrees and 56 degrees, between 42 degrees and 54 degrees, between 42 degrees and 52 degrees, between 42 degrees and 50 degrees, between 42 degrees and 48 degrees, between 42 degrees and 46 degrees, between 42 degrees and 44 degrees, between 44 degrees and 60 degrees, between 44 degrees

and 58 degrees, between 44 degrees and 56 degrees, between 44 degrees and 54 degrees, between 44 degrees and 52 degrees, between 44 degrees and 50 degrees, between 44 degrees and 48 degrees, between 44 degrees and 46 degrees, between 46 degrees and 60 degrees, between 46 degrees and 58 degrees, between 46 degrees and 56 degrees, between 46 degrees and 54 degrees, between 46 degrees and 52 degrees, between 46 degrees and 50 degrees, between 46 degrees and 48 degrees, between 48 degrees and 60 degrees, between 48 degrees and 58 degrees, between 48 degrees and 56 degrees, between 48 degrees and 54 degrees, between 48 degrees and 52 degrees, between 48 degrees and 50 degrees, between 50 degrees and 60 degrees, between 50 degrees and 58 degrees, between 50 degrees and 56 degrees, between 50 degrees and 54 degrees, between 50 degrees and 52 degrees, between 52 degrees and 60 degrees, between 52 degrees and 58 degrees, between 52 degrees and 56 degrees, between 52 degrees and 54 degrees, between 54 degrees and 60 degrees, between 54 degrees and 58 degrees, between 54 degrees and 56 degrees, between 56 degrees and 60 degrees, between 56 degrees and 58 degrees, or between 58 degrees and 60 degrees) Celsius. In some embodiments, the array is incubated during the application of a proteinase at a temperature of approximately 50 degrees Celsius.

In some embodiments, treating an array (e.g., spatial array or tissue optimization array) to which a biological sample has been applied with a set of biological sample removal conditions can include treating the array with a base (e.g., soaking the array in a base). In some embodiments, the base can be sodium hydroxide (NaOH), potassium hydroxide (KOH), or a combination thereof. Additional suitable bases that can be used in the methods described herein are known in the art. In some embodiments, the array is treated with the base for between 1 minute and 20 minutes (e.g., between 1 minute and 18 minutes, between 1 minute and 16 minutes, between 1 minute and 14 minutes, between 1 minute and 12 minutes, between 1 minute and 10 minutes, between 1 minute and 8 minutes, between 1 minute and 6 minutes, between 1 minute and 4 minutes, between 1 minute and 2 minutes, between 2 minutes and 20 minutes, between 2 minutes and 18 minutes, between 2 minutes and 16 minutes, between 2 minutes and 14 minutes, between 2 minutes and 12 minutes, between 2 minutes and 10 minutes, between 2 minutes and 8 minutes, between 2 minutes and 6 minutes, between 2 minutes and 4 minutes, between 4 minutes and 20 minutes, between 4 minutes and 18 minutes, between 4 minutes and 16 minutes, between 4 minutes and 14 minutes, between 4 minutes and 12 minutes, between 4 minutes and 10 minutes, between 4 minutes and 8 minutes, between 4 minutes and 6 minutes, between 6 minutes and 20 minutes, between 6 minutes and 18 minutes, between 6 minutes and 16 minutes, between 6 minutes and 14

minutes, between 6 minutes and 12 minutes, between 6 minutes and 10 minutes, between 6 minutes and 8 minutes, between 8 minutes and 20 minutes, between 8 minutes and 18 minutes, between 8 minutes and 16 minutes, between 8 minutes and 14 minutes, between 8 minutes and 12 minutes, between 8 minutes and 10 minutes, between 10 minutes and 20 minutes, between 10 minutes and 18 minutes, between 10 minutes and 16 minutes, between 10 minutes and 14 minutes, between 10 minutes and 12 minutes, between 12 minutes and 20 minutes, between 12 minutes and 18 minutes, between 12 minutes and 16 minutes, between 12 minutes and 14 minutes, between 14 minutes and 20 minutes, between 14 minutes and 18 minutes, between 14 minutes and 16 minutes, between 16 minutes and 20 minutes, between 16 minutes and 18 minutes, or between 18 minutes and 20 minutes). In some embodiments, the array is treated with the base for approximately 5 minutes. In some embodiments, the array is treated with the base for approximately 10 minutes.

In some embodiments, the array (e.g., spatial array or tissue optimization array) is treated with the base at a concentration of approximately 0.08 M. In some embodiments, the array is treated with the base (e.g., potassium hydroxide) at a concentration of about 0.01 M to 0.2 M, including, but not limited to, about 0.01 M, about 0.02 M, about 0.03 M, 0.04 M, about 0.05 M, about 0.06 M, about 0.07 M, about 0.08 M, about 0.09 M, about 0.10 M, about 0.11 M, about 0.12 M, about 0.13 M, about 0.14 M, about 0.15 M, about 0.16 M, about 0.17 M, about 0.18 M, about 0.19 M, or about 0.20 M, or any ranges included therein. In some embodiments, the biological sample is completely removed from the array after the array is treated with the base. In some embodiments, removing the biological sample from the array further comprises rinsing and drying the array. In some embodiments, the array is treated for a second time with base, using any of the times or concentrations of base described herein. In some cases, treating the array with the base can remove or help to remove any nucleic acid (e.g., RNA) hybridized to a capture probe on the array.

In some embodiments, treating an array (e.g., spatial array or tissue optimization array) to which a biological sample has been applied with a set of biological sample removal conditions can include washing the array with water (e.g., nuclease-free water and/or ultrapure water), washing the array with a buffer, and drying, or a combination thereof. A buffer can be any appropriate buffer, for example Tris, phosphate buffered saline (PBS), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), TES (2-[(2-Hydroxy-1,1-bis(hydroxymethyl)ethyl)amino]ethanesulfonic acid), at any appropriate pH (e.g., about 6.0 to about 8.0 (e.g., about 6.5 to about 7.5, about 6.8 to about 7.2, or about 7.0)) and any appropriate concentration (e.g., about 1 mM to about 20 mM (e.g., about 5 mM to about 15

mM, about 8 mM to about 12 mM, or about 10 mM)). Washing the array (e.g., with water or buffer) can include repeatedly washing the array (e.g., 10, 15, 20, or more times). In some embodiments, drying can include centrifugation and/or air drying. For example, in some embodiments, treating an array to which a biological sample has been applied with a set of biological sample removal conditions can include, sequentially, treating the array with a base (e.g., 0.08 M KOH for 10 minutes), optionally treating with a base for a second time (e.g., 0.08 M KOH for 5 minutes), washing with buffer (e.g., 10 mM Tris, pH 7.0, 15 times), washing with water (e.g., nuclease-free water and/or ultrapure water, 20 times), and optionally drying (e.g., via centrifugation or air drying). For example, in some embodiments, treating an array to which a biological sample has been applied with a set of biological sample removal conditions can include, sequentially, treating the array with a proteinase (e.g., at 3.3 mg/mL in 10 mM Tris, pH 9 and 10% sodium dodecyl sulfate) treating the array with a base (e.g., 0.08 M KOH for 10 minutes), optionally treating with a base for a second time (e.g., 0.08 M KOH for 5 minutes), washing with buffer (e.g., 10 mM Tris, pH 7.0, 15 times), washing with water (e.g., nuclease-free water and/or ultrapure water, 20 times), and optionally drying (e.g., via centrifugation or air drying).

A reset array (e.g., spatial array or tissue optimization array) can be stored at room temperature or 4 °C in a sealed container or a dessicator for up to 7 days before placing a new biological sample on the array.

Also provided herein are methods for using of an array (e.g., spatial array or tissue optimization array) reset using any of the methods described herein. In some embodiments, methods for using an array include resetting an array using any of the methods described herein, contacting the array with a biological sample (e.g., a second portion of a biological sample or a biological sample from a different source, study, or organism), and capturing an analyte from the biological sample on the array.

Also provided herein are methods for performing a spatial analysis using a spatial array reset using any of the methods described herein. In some embodiments, methods for performing a spatial analysis include resetting a spatial array using any of the methods described herein, contacting the spatial array with a biological sample (e.g., a second portion of a biological sample or a biological sample from a different source, study, or organism), and capturing an analyte from the biological sample on the spatial array. In some embodiments, the methods can further include determining (i) all or a portion of a sequence corresponding to the spatial barcode, or a complement thereof, and (ii) all or a portion of a sequence corresponding to the analyte, or a complement thereof.

Also provided herein are methods for analyzing analyte capture using a tissue optimization array reset using any of the methods described herein. In some embodiments, methods for analyzing analyte capture include resetting a tissue optimization array using any of the methods described herein, contacting the tissue optimization array with a biological sample (e.g., a second portion of a biological sample or a biological sample from a different source, study, or organism), capturing a plurality of analytes from the biological sample on the tissue optimization array, and analyzing the amount, distribution, diffusion, or a combination thereof, of the analytes.

10 Exemplary Embodiments

Embodiment 1 is a method for resetting an array, the method comprising:

(a) applying a biological sample to an array, wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample;

15 (b) identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest; and

(c) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, thereby resetting the array.

Embodiment 2 is a method for resetting an array to which a biological sample has been applied, the method comprising:

(a) identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest; and

(b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array,

25 wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample, thereby resetting the array.

Embodiment 3 is the method of embodiment 1 or embodiment 2, wherein identifying that the biological sample has been applied to the array incorrectly comprises identifying that one or more fiducial markers on the array is obscured by the biological sample.

Embodiment 4 is the method of any one of embodiments 1-3, wherein identifying that the biological sample has been applied to the array incorrectly comprises identifying that the biological sample is folded.

Embodiment 5 is the method of any one of embodiments 1-4, wherein identifying that the biological sample has been applied to the array incorrectly comprises identifying that the biological sample is torn or damaged.

Embodiment 6 is the method of any one of embodiments 1-5, wherein identifying that
5 the biological sample has been applied to the array incorrectly comprises identifying that the biological sample overlaps with a second biological sample.

Embodiment 7 is the method of any one of embodiments 1-6, wherein identifying that the biological sample does not contain the region of interest comprises imaging the biological sample after staining and/or immunofluorescence.

10 Embodiment 8 is the method of embodiment 7, wherein an image produced by imaging the biological sample demonstrates an incorrect application of a stain and/or an immunofluorescence antibody.

Embodiment 9 is the method of embodiment 7 or embodiment 8, wherein an image produced by imaging the biological sample demonstrates nonspecific staining of the
15 biological sample.

Embodiment 10 is a method for resetting an array to which a biological sample has been applied, the method comprising:

treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array,

20 wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample, thereby resetting the array.

Embodiment 11 is a method for resetting an array, the method comprising:

(a) applying a biological sample to an array wherein the array comprises a plurality of
25 capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample; and

(b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, thereby resetting the array.

Embodiment 12 is the method of any one of embodiments 1-11, wherein the array is a
30 tissue optimization array or a spatial array.

Embodiment 13 is the method of any one of embodiments 1-12, wherein prior to treating the array with the set of biological sample removal conditions, no reverse transcription has been performed on the array.

Embodiment 14 is the method of any one of embodiments 1-12, wherein prior to treating the array with the set of biological sample removal conditions, no enzymatic extension reaction has been performed on the capture probe.

Embodiment 15 is the method of embodiment 14, wherein no extension reaction has
5 been performed on the capture probe.

Embodiment 16 is the method of any one of embodiments 1-15, wherein treating the array with the set of biological sample removal conditions comprises treating the array with a base.

Embodiment 17 is the method of embodiment 16, wherein the base comprises a base
10 selected from the group consisting of potassium hydroxide, sodium hydroxide, and combinations thereof.

Embodiment 18 is the method of embodiment 16 or 17, wherein treating with the base comprises treating the array with about 40 mM to about 120 mM of the base.

Embodiment 19 is the method of any one of embodiments 16-18, wherein treating the
15 array with the base comprises treating the array with about 75 mM to about 85 mM of the base.

Embodiment 20 is the method of any one of embodiments 16-19, wherein treating the array with the base comprises treating the array with the base for between about 1 minute and about 20 minutes.

Embodiment 21 is the method of any one of embodiments 16-20, wherein treating the
20 array with the base comprises treating the array with the base for about 8 minutes to about 12 minutes.

Embodiment 22 is the method of any one of embodiments 16-21, wherein treating the array with a base comprises treating the array with a base for one, two, three, four or five
25 times.

Embodiment 23 is the method of any one of embodiments 16-22, wherein treating the array with the set of biological sample removal conditions further comprises washing the array one or more times.

Embodiment 24 is the method of embodiment 23, wherein the washing comprises
30 water that is nuclease-free water and/or ultrapure water.

Embodiment 25 is the method of any one of embodiments 16-24, wherein treating the array with the set of biological sample removal conditions further comprises washing the array with a buffer one or more times.

Embodiment 26 is the method of embodiment 25, wherein the buffer is selected from the group consisting of Tris, phosphate buffered saline (PBS), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), TES (2-[(2-Hydroxy-1,1-bis(hydroxymethyl)ethyl)amino]ethanesulfonic acid), and combinations thereof.

5 Embodiment 27 is the method of embodiment 25 or 26, wherein the buffer has a concentration of about 1 mM to about 20 mM.

Embodiment 28 is the method of any one of embodiments 25-27, wherein the buffer has a concentration of about 8 mM to about 12 mM.

10 Embodiment 29 is the method of any one of embodiments 25-28, wherein the buffer has a pH of about 6.0 to about 8.0.

Embodiment 30 is the method of any one of embodiments 25-29, wherein the buffer has a pH of about 6.5 to about 7.5.

Embodiment 31 is the method of any one of embodiments 25-30, wherein the buffer has a pH of about 6.8 to about 7.2.

15 Embodiment 32 is the method of any one of embodiments 16-31, wherein treating the array with the set of biological sample removal conditions further comprises drying the array.

Embodiment 33 is the method of any one of embodiments 1-32, wherein, before treating the array with the set of biological sample removal conditions, the biological sample is not permeabilized.

20 Embodiment 34 is the method of embodiment 33, wherein treating the array with the set of biological sample removal conditions comprises, sequentially, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying the array.

25 Embodiment 35 is the method of any one of embodiments 16-34, wherein treating the array with the set of biological sample removal conditions further comprises treating the array with a proteinase.

Embodiment 36 is the method of embodiment 35, wherein treating the array with the proteinase precedes treating with the base.

30 Embodiment 37 is the method of embodiment 35 or 36, wherein the proteinase is proteinase K.

Embodiment 38 is the method of any one of embodiments 35-37, wherein treating the array with the proteinase is for between 10 minutes and 2 hours.

Embodiment 39 is the method of any one of embodiments 35-38, wherein treating the array with the proteinase is for between 30 minutes and 90 minutes.

Embodiment 40 is the method of any one of embodiments 35-38, wherein treating the array with the proteinase is for about 55 minutes to about 65 minutes.

Embodiment 41 is the method of any one of embodiments 35-40, wherein during treatment of the array with the proteinase, the biological sample is incubated at between 40
5 degrees and 60 degrees Celsius.

Embodiment 42 is the method of any one of embodiments 35-40, wherein during treatment of the array with proteinase, the biological sample is incubated at between 45 degrees to about 55 degrees Celsius.

Embodiment 43 is the method of any one of embodiments 35-42, wherein treating the
10 array with the proteinase further comprises treating the array with a surfactant and a proteinase buffer.

Embodiment 44 is the method of embodiment 43, wherein the surfactant is sodium dodecyl sulfate.

Embodiment 45 is the method of embodiment 43 or 44, wherein the surfactant is
15 present in an amount of about 5% w/v to about 20% w/v.

Embodiment 46 is the method of embodiment 43 or 44, wherein the surfactant is present in an amount of about 8% w/v to about 10% w/v.

Embodiment 47 is the method of any one of embodiments 43-46, wherein the proteinase buffer is Tris.

Embodiment 48 is the method of any one of embodiments 43-47, wherein the
20 proteinase buffer has a concentration of about 1 mM to about 20 mM.

Embodiment 49 is the method of any one of embodiments 43-48, wherein the proteinase buffer has a concentration of about 8 mM to about 12 mM.

Embodiment 50 is the method of any one of embodiments 43-49, wherein the
25 proteinase buffer has a pH of about 8.0 to about 10.0.

Embodiment 51 is the method of any one of embodiments 43-49, wherein the proteinase buffer has a pH of about 8.5 to about 9.5.

Embodiment 52 is the method of any one of embodiments 43-49, wherein the proteinase buffer has a pH of about 8.8 to about 9.2.

Embodiment 53 is the method of any one of embodiments 43-52, wherein treating the
30 array with the set of biological sample removal conditions comprises, treating the array with the proteinase, washing the array with water, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying.

Embodiment 54 is the method of any one of embodiments 1-53, wherein the array comprises a slide.

Embodiment 55 is the method of embodiment 54, wherein the slide is a glass slide.

Embodiment 56 is the method of any one of embodiments 1-55, wherein the
5 biological sample is an animal sample.

Embodiment 57 is the method of any one of embodiments 1-55, wherein the biological sample is a human sample.

Embodiment 58 is the method of any one of embodiments 1-55, wherein the biological sample is a rodent sample.

10 Embodiment 59 is the method of any one of embodiments 1-58, wherein the biological sample is a breast, brain, heart, small intestine, eye, testes, or kidney sample.

Embodiment 60 is the method of any one of embodiments 1-59, wherein the biological sample is a cancerous sample or a sample suspected of having cancerous cells.

Embodiment 61 is the method of any one of embodiments 1-60, wherein the
15 biological sample is a tissue section.

Embodiment 62 is the method of embodiment 61, wherein the tissue section is a fresh frozen tissue section.

Embodiment 63 is the method of any one of embodiments 1-62, wherein the biological sample is fixed.

20 Embodiment 64 is the method of any one of embodiments 1-63, wherein the biological sample is formalin-fixed.

Embodiment 65 is the method of any one of embodiments 1-63, wherein the biological sample is fixed using methanol.

Embodiment 66 is the method of any one of embodiments 1-63, wherein the
25 biological sample is fixed using acetone.

Embodiment 67 is the method of any one of embodiments 1-66, wherein the biological sample is stained.

Embodiment 68 is the method of embodiment 67, wherein the stain is a histological stain.

30 Embodiment 69 is the method of embodiment 68, wherein the histological stain is a hematoxylin and eosin stain.

Embodiment 70 is the method of any one of embodiments 1-69, wherein the biological sample is imaged using immunofluorescence.

Embodiment 71 is a method for capturing an analyte using an array, the method comprising:

(a) resetting an array according to any one of embodiments 1-70, wherein the array is a spatial array and the capture probe further comprises a spatial barcode;

5 (b) contacting the spatial array with a biological sample; and

(c) capturing an analyte from the biological sample on the spatial array.

Embodiment 72 is the method of embodiment 71, wherein the analyte comprises RNA, DNA, a protein, a small molecule, or a metabolite.

Embodiment 73 is the method of embodiment 71 or 72, further comprising
10 determining (i) all or a portion of a sequence corresponding to the spatial barcode, or a complement thereof, and (ii) all or a portion of a sequence corresponding to the analyte, or a complement thereof.

Embodiment 74 is a method for analyzing capture of a plurality of analytes on a tissue optimization array, the method comprising:

15 (a) resetting a tissue optimization array according to any one of embodiments 1-70;

(b) contacting the tissue optimization array with a biological sample;

(c) capturing a plurality of analytes from the biological sample on the tissue optimization array; and

(d) analyzing the amount, distribution, and/or diffusion of the plurality of analytes
20 based on the analytes from the biological sample captured on the tissue optimization array.

Embodiment 75 is the method of embodiment 74, wherein the plurality of analytes comprises RNA, DNA, a protein, a small molecule, a metabolite, or a combination thereof.

EXAMPLES

25 **EXAMPLE 1 – Methods for removing a tissue sample from an array**

In a non-limiting example, an array is reset by removing tissue that had been placed the array (**FIG. 1**), using a variety of reagents and consumables. For examples, tissues that were folded when positioned on the array, tissues that covered fiducial markings, tissues that were torn or otherwise compromised and tissues that were not placed in the correct
30 designated area. The reagents and consumables can include proteinase K, Tris buffer, 20% SDS, potassium hydroxide, and a water bath or heat block that can heat up to 50 degrees Celsius. For example, a method for resetting an array can include: (a) soaking a fixed and stained tissue slice on an array for 1 hour in 30 mL of proteinase K buffer (10mM Tris, pH 9,

10% SDS, 3.3mg/mL ProK) at 50°C; (b) removing the array from the proteinase K buffer and rinsing in nuclease-free water; (c) soaking the array for 10 minutes in 30 mL of 0.08M potassium hydroxide; (d) removing the array and rinsing in 10mM Tris, pH 7.0; (e) rinsing the array in nuclease-free water; and (f) spinning down or air drying. See, e.g., **FIG. 2A** for an exemplary workflow.

While tissue removal incubation step (a) may not remove tissue completely and trace amounts of tissue may still remain on the array (**FIG. 2B**, left), in such instances soaking the array in a basic solution such as 0.08M potassium hydroxide has been shown to remove any remaining tissue (**FIG. 2B**, right).

EXAMPLE 2 – Methods for removing a tissue sample from an array

Arrays on a slide are reset prior to tissue permeabilization. When immersing a slide in a solution, the slide is typically completely immersed for about 3 seconds.

Reagent volumes described in this Example can accommodate up to two slides. If resetting two slides, slides are placed back to back so that tissue sections are facing outwards.

A water bath or heat block is preheated to 50 °C to warm 30 mL proteinase K buffer (1 mM Tris, pH 9; 10% SDS, 3.3 mg/mL proteinase K). An array including a tissue sample on a slide is transferred to a 50 mL centrifuge tube containing the warmed proteinase K buffer and incubated for 1 hour at 50 °C. The tube is inverted and some tissue may remain on the array. The slide is immersed in ultrapure water. The slide is transferred to a 50-mL centrifuge tube containing 30 mL 0.08M potassium hydroxide (KOH) and incubated for 10 minutes at room temperature. The tube is inverted. The slide is transferred to a new 50 mL centrifuge tube containing 30 mL 0.08 M KOH and incubated at room temperature for 5 minutes. The slide is transferred to a 50 mL centrifuge tube containing 10 mM Tris, pH 7 and inverted slowly. The slide is immersed in fresh ultrapure water. Excess water is removed using a laboratory wipe on the back of the slide, without touching the active surface of the slide. The slide is dried, optionally for 30 seconds in a slide spinner, or in a 50 mL centrifuge tube centrifuged at 250 relative centrifugal force (rcf) for 30 seconds in a swinging bucket rotor.

The slide, and each array within the slide, is examined for any remaining tissue. If tissue remains, the reset protocol above is repeated.

A slide where tissue is removed, thus resetting the slide, can be stored in a sealed container or dessicator at room temperature or at 4 °C for up to 7 days before placing a new tissue section on one or more of the active arrays on the slide.

EXAMPLE 3 – Resetting an array with a different tissue sample

In a non-limiting example, a tissue sample is removed from an array as described above in Example 1. For this example, the array was originally in contact with mouse brain tissue, wherein the mouse brain tissue was removed, thereby resetting the array and replaced
5 with a section of a human ovarian tumor tissue (**FIG. 3**).

The mouse brain tissue, which was first stained and imaged (**FIG 3**, left panel) and was removed from the array by (a) soaking the fixed and stained tissue slice on the array for 1 hour in 30 mL of proteinase K buffer (10mM Tris, pH9, 10% SDS, 3.3mg/mL ProK) at 50°C; (b) removing the array and rinsing 15 times in nuclease-free water; (c) soaking the array for
10 10 minutes in 30 mL of 0.08M potassium hydroxide; (d) removing the array and rinsing 15 times in 10mM Tris, pH 7.0; (e) rinsing the array 20 times in nuclease-free water; and (f) spinning down or air drying the array. A tissue section from a human ovarian tumor was then placed on the same array, stained and imaged (**FIG 3**, right panel).

FIG. 4 shows exemplary images of replicate experiments where spatial analysis was performed and analyte gene expression information was obtained. **FIG. 4** top row shows
15 four replicates of an array with stained and imaged mouse brain tissue samples. The middle row shows exemplary imaging results after resetting the arrays from the top row by removing the mouse tissues as previously described and replacing the mouse tissue sections with sectioned ovarian tumor tissue followed by spatial analyte analysis of the ovarian tumor
20 tissue samples. The bottom row shows positive control imaging results after performing spatial analyte analysis on ovarian tumor tissue samples that were not reset (i.e., the spatial arrays were new and had not been contacted with tissue prior to the application of the ovarian tumor tissue sections). The reset arrays demonstrate similar spatial analyte data (gene
25 expression intensity) as the control arrays thereby demonstrating negligible or no visible contamination or analyte carry over from the original mouse brain tissue samples to the human ovarian tumor sections on the reset arrays.

FIG. 5A-D show exemplary data analysis and Dunnett's control data demonstrating no significant difference between human ovarian tumor control spatial array analyte determination and that of the reset array data with regards to the A) reads mapped to the
30 human ovarian tumor transcriptome, B) the fraction of usable reads, C) the median of genes per array spot and D) median UMI count per array spot. While there was a slight decrease seen in the median genes and UMIs per spot from the reset arrays vs control arrays (**FIG 5C** and **5D**) it was not significant.

The reset array was also compared to a control array for the potential contamination of the HPCA gene. The hippocalcin gene, or HPCA, is highly expressed in the hippocampus region of mouse brain but not in human ovarian tumors. The results shown in **FIG. 6A** identify the location of the HPCA cluster in mouse brain, HPCA gene expression is not seen in the reset array **FIG. 6B** (left panel) nor in the control (non-reset) array (right panel). As such, there was no detectable contamination noted on the reset array.

EXAMPLE 4 – Effect of the reset protocol on capture probes on an array

In a non-limiting example, experiments were performed to analyze the hybridization of a fluorescently labeled oligonucleotide to the capture probes on three different arrays: (1) an array slide that had fixed and stained tissue on it and was reset, (2) an array that had been processed through the entire spatial analyte localization workflow as described herein, and (3) a new array. An image of the tissue on the control array (which was reset for array (1)) is seen in **FIG. 7A**.

Briefly, the array having fixed and stained tissue was exposed to the previously described reset protocol, and oligonucleotides containing partial Read 1 sequences complexed with Cy3 fluorescent moieties were hybridized to the array. The fluorescently labeled oligonucleotides were also hybridized to the array that had been processed through the entire spatial analyte detection workflow (lacking tissue), as well as a new array.

Fluorescent imaging results from the reset array (**FIG. 7B**) which was processed using the reset protocol, and a new array (**FIG. 7D**), hybridized to Cy3 labelled-partial Read 1 oligonucleotides applied to the arrays, rinsed, and imaged demonstrates that the partial Read 1 portion of the oligonucleotide hybridized to its complementary region on the capture probe on the array. Imaging the three arrays for 200 milliseconds (ms) show that overall fluorescence from the locations of the capture probes are comparable between the reset array and new array. Both the reset array and the new array demonstrate a similar level of fluorescence (ability to bind the Cy3-partial Read 1) as compared to the array that was processed according to the spatial workflows described herein (**FIG. 7C**). The negative fluorescence of the spatial workflow slide provides evidence that once the spatial workflow involving enzymatic actions such as, for example, reverse transcription of mRNA analytes, slide reset is not possible using the tissue removal conditions described in the prior examples.

In experiments to demonstrate the affect of the reset methods on probes affixed to the array slide, blocks of OCT medium without tissue were created and slices places on spatial array slides. Some slides were reset (**FIG. 7E**) and some were not (**FIG. 7F**, control slides),

after which Cy3 labelled-Read 1 oligos were applied to the arrays and binding of the labelled oligos to the probes on the arrays were measured via fluorescence. **FIG. 7G** demonstrates that the fluorescence intensity of the reset versus the control new (non-reset) slides was comparable, as such the oligos on the array slides were not adversely affected by the reset protocol.

EXAMPLE 5 – Fixation Analysis

Reset arrays can be used with both fixed and stained tissue as well as fresh frozen cryostat tissue sections. Breast cancer tissue was originally applied to a spatial array (exemplary tissue shown in **FIG. 9A**). The array was reset, and coronal mouse brain sections, either fixed and stained or fresh frozen sections, were applied to the reset arrays (**FIG. 8**). The reset array on the left of **FIG. 8** shows exemplary imaging results after performing spatial analysis on a cryosectioned tissue that had not been fixed or stained but was reset and mouse brain reapplied to the reset slide. The reset array in the middle image of **FIG. 8** shows exemplary imaging results after performing spatial analysis on a fixed and stained mouse brain section after resetting the array. The control array on the right of **FIG. 8** shows exemplary imaging results after performing spatial analysis of a brain section on a slide that has not been reset. The UMI counts for tissue sections on the reset arrays are similar to the control section on the new array.

MUCL1 is a gene highly expressed in human breast cancer tissue (exemplary expression shown in **FIG. 9A**). The biological sample removal conditions reduced MUCL1 gene expression when 1 KOH wash was used to reset the slide following removal of the original breast cancer tissue (**FIG. 9B**), and no MUCL1 expression was observed when 2 KOH washes were used to reset the slide following removal of the original breast cancer tissue (**FIG. 9C**).

Similarly, when a mouse brain tissue section was applied to a spatial array, the array was reset, and human breast cancer or human heart tissue sections (either fixed and stained or fresh frozen tissue samples), were applied to the reset arrays. Various sequencing metrics were analyzed. **FIGs. 10A-D** show box plots of control mouse brain data compared to the reset arrays having human breast cancer or human heart tissue sections on the arrays, with regard to A) library quality, B) fraction reads with primer, homopolymer, or switch oligo sequence, C) fraction reads with ribosomal or mitochondrial UMI counts, and D) sensitivity. In **FIG. 10A**, the mapping was very consistent between the control and reset slides. In **FIGs. 10B-C**, the fraction reads with primer or homopolymer sequence, or any TSO oligo sequence,

as well as the fraction ribosomal protein UMI counts and fraction mitochondrial UMI counts were consistent between reset and control slides. In **FIG. 10D**, there was no significant difference in median genes in the reset arrays (either fixed and stained or not) and the control arrays, though there was a slight drop in median UMIs for reset slides (about 18% and about 13% for fixed and stained and non-fixed and stained, respectively). The fixed and stained tissue sections and the fresh frozen tissue sections performed about equally on reset arrays. In **FIG. 10E**, overlaid UMAP plots are shown for mouse brain sections analyzed on a new non-reset array and reset arrays (either fixed and stained or not). In **FIG. 10F**, analysis of HPCA is shown for mouse brain sections on a new non-reset array and reset arrays (either fixed and stained or not); in the upper figures, H&E staining is shown, with a box around the hippocampal region, and in the lower figures, gene expression analysis is shown, focused on the boxed hippocampal region. The data in **FIGs. 10A-F** demonstrate that the reset arrays are equally sensitive as a control non-reset array with respect to the fraction of usable reads. There was no significant difference in median genes between reset (pre-fixation or H&E) and control arrays, though there was a slight decrease in median UMIs for the reset arrays.

Example 6 – Immunofluorescence analysis

Resetting arrays is compatible with use of immunofluorescence, both before reset, and when using a new biological sample on an array. Human breast cancer tissue was initially placed on a spatial array and stained with DAPI, an Alexa 647-conjugated anti-CD3 antibody (Biolegend), and an Alexa 488-conjugated anti-CD8 antibody (Biolegend). The array was reset as described in Example 1, and a mouse brain tissue sample was placed on the reset array. The mouse brain tissue was stained with DAPI, an Alexa 555-conjugated anti-NeuN antibody (Abcam), and a FITC-conjugated anti-GFAP antibody (Abcam). There was no difference observed in immunofluorescence images of the reset array (**FIG. 11A**, left) and a non-reset array (control) having mouse brain tissue stained the same way (**FIG. 11A**, right).

Transcript capture and sequencing metrics of the reset array were similar to the control array following removal of an IF-stained biological sample. **FIG. 11B** shows that the UMI count appears similar between reset (top row) and control (bottom row) of replicate samples, with a potentially visible decrease of UMI counts in the reset slides. **FIGs. 11C-E** show box plots of mouse brain tissue on control slides and mouse brain tissue on slides that previously had IF-stained biological samples on them, were reset, and a mouse brain sample placed on the reset array: C) library quality, D) contamination of primers in the library, and E) sensitivity. In **FIG. 11C**, the metrics for mapping, usable reads, and fraction of reads per

spot were very comparable between the control sample (on a non-reset array) and a sample on a reset array. In **FIG. 11D**, the metrics for homopolymer or template switching oligonucleotide (TSO) were very comparable between the control sample (on a non-reset array) and a sample on a reset array. In **FIG. 11E**, no significant difference was observed in median genes between the control sample (on a non-reset array) and a sample on a reset array, though a slight decrease was observed in the number of UMIs detected for the sample on a reset array compared to the control sample (on a non-reset array). In **FIG. 11F**, overlaid UMAP plots are shown for the reset and non-reset (control) arrays. In **FIG. 11G**, a scatter plot of gene expression is shown. Both UMAP and scatter plot data demonstrate good correlation between the reset and non-reset (control) arrays. The data in **FIGs. 11A-G** demonstrate that the reset array provided for similar imaging, library quality and UMI counts as compared to a non-reset array.

Example 7 – Multiple resets

It was determined through experimentation that arrays could be reset multiple times without compromising the array capture probes. A mouse brain tissue sample was evaluated on arrays that had been reset one, two, or three times as in Example 1 and compared to a mouse brain tissue sample on a non-reset array (control). The first tissue set on the arrays was a human breast cancer tissue. The arrays were reset, and for the twice and three-times reset arrays, a human lung tissue sample was placed on the array. The arrays were reset, for the three-times reset array, a human cerebellum tissue sample was placed on the array. The array was reset. All slides were fixed with methanol and stained with hematoxylin and eosin.

Transcript capture and sequencing metrics of the reset arrays were similar to control following multiple resets. **FIG. 12A** shows that the UMI count appears similar for the control and multiple-reset samples, with a potentially visible decrease of UMI counts in the reset slides. **FIGs. 12B-D** show plots of mouse brain tissue on control slides and mouse brain tissue on slides that had been reset one, two, or three times: B) library quality, C) contamination of primers in the library, and D) sensitivity. In **FIG. 12B**, the metrics for mapping, usable reads, and fraction of reads per spot are very comparable between the control sample (on a non-reset array) and samples on reset arrays. In **FIG. 12C**, the metrics for homopolymer or template switching oligonucleotide (TSO) are very comparable between the control sample (on a non-reset array) and samples on reset arrays. In **FIG. 12D**, no significant difference was observed in median genes between the control sample (on a non-reset array) and samples on reset arrays, though a slight decrease was observed in the number

of UMIs detected for the sample on reset arrays compared to the control sample (on a non-reset array). In sum, Figures 12A-D demonstrate that an array can be reset one or more times without substantially impacting library quality, UMI count, and sensitivity.

5 ***Example 8 – Effect of array reset on analyte capture***

Resetting arrays can be performed on tissue optimization arrays, for example, for determining conditions for permeabilization and/or analyte capture following removal of a first biological sample. Three tissues were tested for the effect of reset on permeabilization of the second biological sample and/or the capture of transcripts therefrom on non-spatially
 10 barcoded (i.e., tissue optimization) arrays: mouse brain, mouse liver, and mouse spleen. In each case, the arrays initially had human lung tumor samples covering the entire capture area of the arrays, and the slides were reset as in Example 1, and the new tissues were placed on the slide, stained with H&E, permeabilized, and the transcripts were captured. Capture was evaluated by fluorescence microscopy of reverse-transcribed cDNA using fluorescent
 15 nucleotides.

In **FIG. 13A**, the H&E stained mouse brain samples can be compared to the fluorescence images in **FIG. 13B**, and the mean fluorescence intensity is shown in **FIG. 13C**. In **FIG. 14A**, the H&E stained mouse liver samples can be compared to the fluorescence images in **FIG. 14B**. In **FIG. 15A**, the H&E stained mouse spleen samples can be compared
 20 to the fluorescence images in **FIG. 15B**. In each image, the control samples (on non-reset arrays) are shown on the left, while the samples on reset arrays are shown on the right. While some of the reset fluorescence appeared to be less than that of the control (**FIG. 14B**), or more than the control (**FIG. 15B**), no specific trend was observed in differences in transcript capture between the control samples and samples on reset arrays for the three tissue types.

25

Example 9 – Array reset with different tissue types

Resetting arrays can be performed with multiple tissue types as the initial biological sample. To demonstrate this, different types of fixed and stained mouse or human tissues were originally placed on an array (upper figures in **FIGs. 16B-E** and **17B-D**), and each array
 30 was reset according to Example 1. A new tissue sample was placed on each array, and the sample was analyzed using a spatial gene expression analysis (lower figures in **FIGs. 16B-E** and **17B-D**). Control samples can be seen in **FIG 16A** (human heart tissue) and **17A** (mouse brain tissue) In **FIG. 16A-E**, the reset process is shown mouse eye as the original tissue sample (**FIG. 16B**), mouse small intestine as the original tissue sample (**FIG. 16C**), mouse

testes as the original tissue sample (**FIG. 16D**), and mouse kidney as the original tissue sample (**FIG. 16E**), where human heart tissue was used as the tissue on the reset slides. In **FIG. 17A-D**, the reset process is shown for human breast cancer as the original tissue sample (**FIG. 17B**), human heart as the original tissue sample (**FIG. 17C**), and human brain as the
5 original tissue sample (**FIG. 17D**), where mouse brain tissue was used as the tissue on the reset slides.

For those reset slides where mouse tissue was the original tissue, it was determined that the mouse tissues were removed completely or substantially completely wherein the gene expression of the control versus the reset slides was comparable. The same results were seen
10 when the original tissue was of human origin. It was determined that multiple tissue types could be removed, slides reset, and new, different tissues applied to reset slides without compromising gene expression analysis.

What is claimed is:

1. A method for resetting an array, the method comprising:
 - (a) applying a biological sample to an array, wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample;
 - (b) identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest; and
 - (c) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, thereby resetting the array.
2. A method for resetting an array to which a biological sample has been applied, the method comprising:
 - (a) identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest; and
 - (b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array, wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample, thereby resetting the array.
3. The method of claim 1 or claim 2, wherein identifying that the biological sample has been applied to the array incorrectly or does not contain a region of interest comprises identifying that one or more fiducial markers on the array is obscured by the biological sample, identifying that the biological sample is folded, identifying that the biological sample is torn or damaged, identifying that the biological sample overlaps with a second biological sample, imaging the biological sample after staining and/or immunofluorescence, or a combination thereof.
4. The method of claim 3, wherein an image produced by imaging the biological sample demonstrates an incorrect application of a stain and/or an immunofluorescence antibody, demonstrates nonspecific staining of the biological sample, or a combination thereof.

5. A method for resetting an array to which a biological sample has been applied, the method comprising:
 - treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array,
 - wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample,
 - thereby resetting the array.
6. A method for resetting an array, the method comprising:
 - (a) applying a biological sample to an array wherein the array comprises a plurality of capture probes, wherein a capture probe of the plurality of capture probes comprises a capture domain that binds specifically to an analyte from the biological sample; and
 - (b) treating the array with a set of biological sample removal conditions, such that the biological sample is substantially removed from the array,
 - thereby resetting the array.
7. The method of any one of claims 1-6, wherein the array is a tissue optimization array or a spatial array.
8. The method of any one of claims 1-7, wherein prior to treating the array with the set of biological sample removal conditions, no reverse transcription has been performed on the array.
9. The method of any one of claims 1-8, wherein prior to treating the array with the set of biological sample removal conditions, no enzymatic extension reaction has been performed on the capture probe.
10. The method of claim 9, wherein no extension reaction has been performed on the capture probe.
11. The method of any one of claims 1-10, wherein treating the array with the set of biological sample removal conditions comprises treating the array with a base.

12. The method of claim 11, wherein the base comprises a base selected from the group consisting of potassium hydroxide, sodium hydroxide, and combinations thereof.
13. The method of claim 11 or 12, wherein treating with the base comprises treating the array with about 40 mM to about 120 mM of the base.
14. The method of any one of claims 11-13, wherein treating the array with the set of biological sample removal conditions further comprises washing the array one or more times.
15. The method of any one of claims 11-14, wherein treating the array with the set of biological sample removal conditions further comprises washing the array with a buffer one or more times.
16. The method of claim 15, wherein the buffer is selected from the group consisting of Tris, phosphate buffered saline (PBS), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), TES (2-[(2-Hydroxy-1,1-bis(hydroxymethyl)ethyl)amino]ethanesulfonic acid), and combinations thereof.
17. The method of claim 15 or 16, wherein the buffer has a concentration of about 1 mM to about 20 mM.
18. The method of any one of claims 15-17, wherein the buffer has a pH of about 6.0 to about 8.0.
19. The method of any one of claims 11-18, wherein treating the array with the set of biological sample removal conditions further comprises drying the array.
20. The method of any one of claims 1-19, wherein, before treating the array with the set of biological sample removal conditions, the biological sample is not permeabilized.
21. The method of claim 20, wherein treating the array with the set of biological sample removal conditions comprises, sequentially, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying the array.

22. The method of any one of claims 11-21, wherein treating the array with the set of biological sample removal conditions further comprises treating the array with a proteinase.
23. The method of claim 22, wherein treating the array with the proteinase precedes treating with the base.
24. The method of claim 22 or 23, wherein the proteinase is proteinase K.
25. The method of any one of claims 22-24, wherein treating the array with the set of biological sample removal conditions comprises treating the array with the proteinease, washing the array with water, treating the array with the base, washing the array with the buffer, washing the array with water, and optionally drying.
26. The method of any one of claims 1-25, wherein the biological sample is an animal sample.
27. The method of any one of claims 1-25, wherein the biological sample is a human sample.
28. The method of any one of claims 1-27, wherein the biological sample is a cancerous sample or a sample suspected of having cancerous cells.
29. The method of any one of claims 1-28, wherein the biological sample is a tissue section.
30. The method of claim 29, wherein the tissue section is a fresh frozen tissue section.
31. The method of any one of claims 1-30, wherein the biological sample is fixed.
32. The method of any one of claims 1-31, wherein the biological sample is stained.
33. A method for capturing an analyte using an array, the method comprising:
 - (a) resetting an array according to any one of claims 1-32, wherein the array is a spatial array and the capture probe further comprises a spatial barcode;

- (b) contacting the spatial array with a biological sample; and
- (c) capturing an analyte from the biological sample on the spatial array.

34. The method of claim 33, wherein the analyte comprises RNA, DNA, a protein, a small molecule, or a metabolite.

35. The method of claim 33 or 34, further comprising determining (i) all or a portion of a sequence corresponding to the spatial barcode, or a complement thereof, and (ii) all or a portion of a sequence corresponding to the analyte, or a complement thereof.

36. A method for analyzing capture of a plurality of analytes on a tissue optimization array, the method comprising:

- (a) resetting a tissue optimization array according to any one of claims 1-32;
- (b) contacting the tissue optimization array with a biological sample;
- (c) capturing a plurality of analytes from the biological sample on the tissue optimization array; and
- (d) analyzing the amount, distribution, and/or diffusion of the plurality of analytes based on the analytes from the biological sample captured on the tissue optimization array.

37. The method of claim 36, wherein the plurality of analytes comprises RNA, DNA, a protein, a small molecule, a metabolite, or a combination thereof.

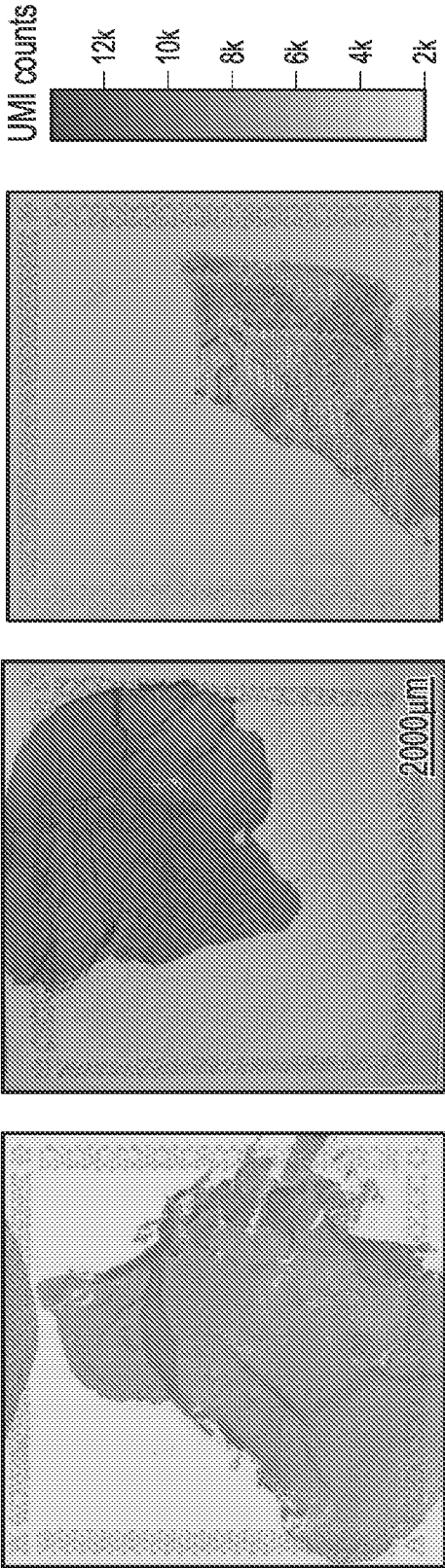


FIG. 1

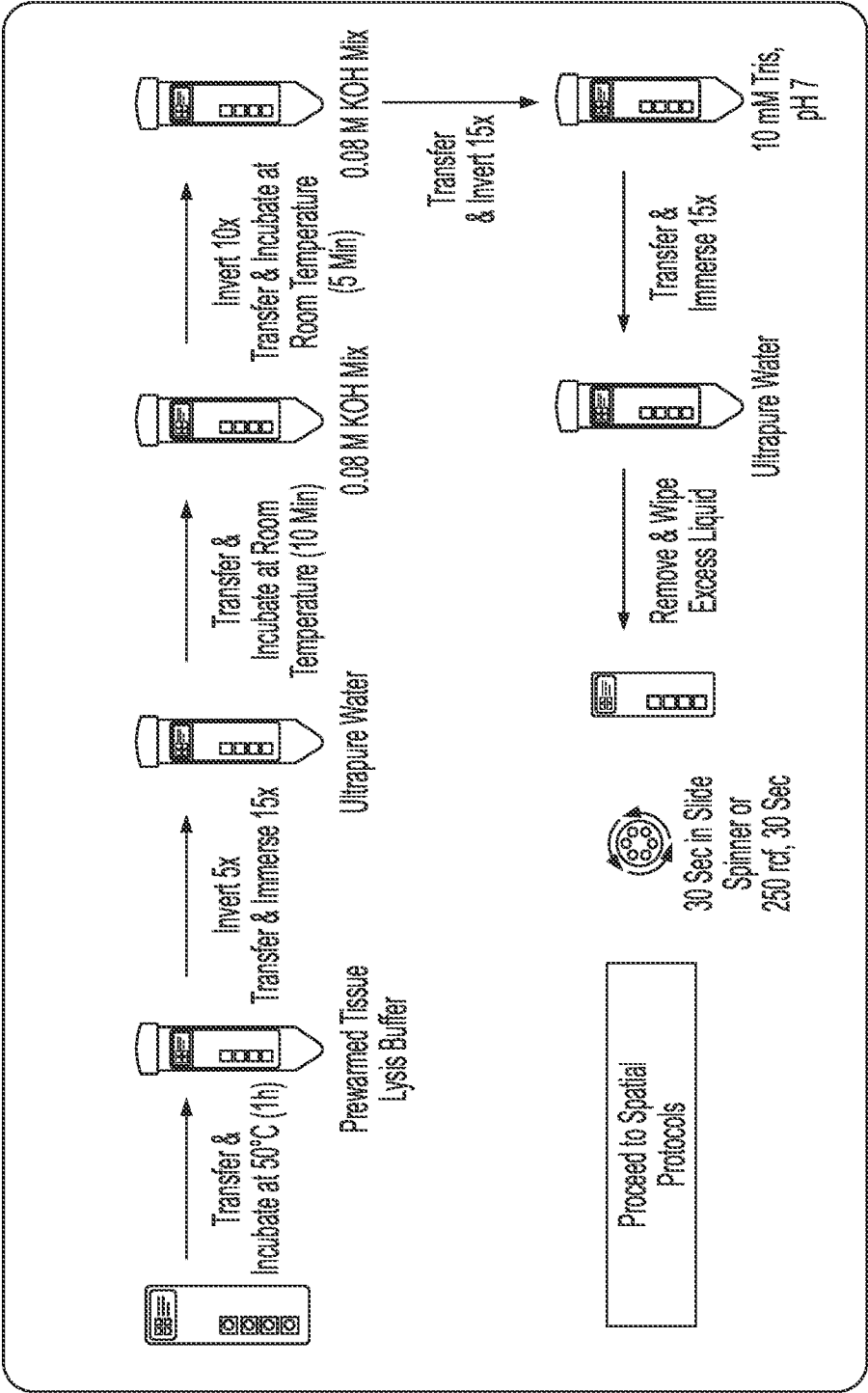


FIG. 2A

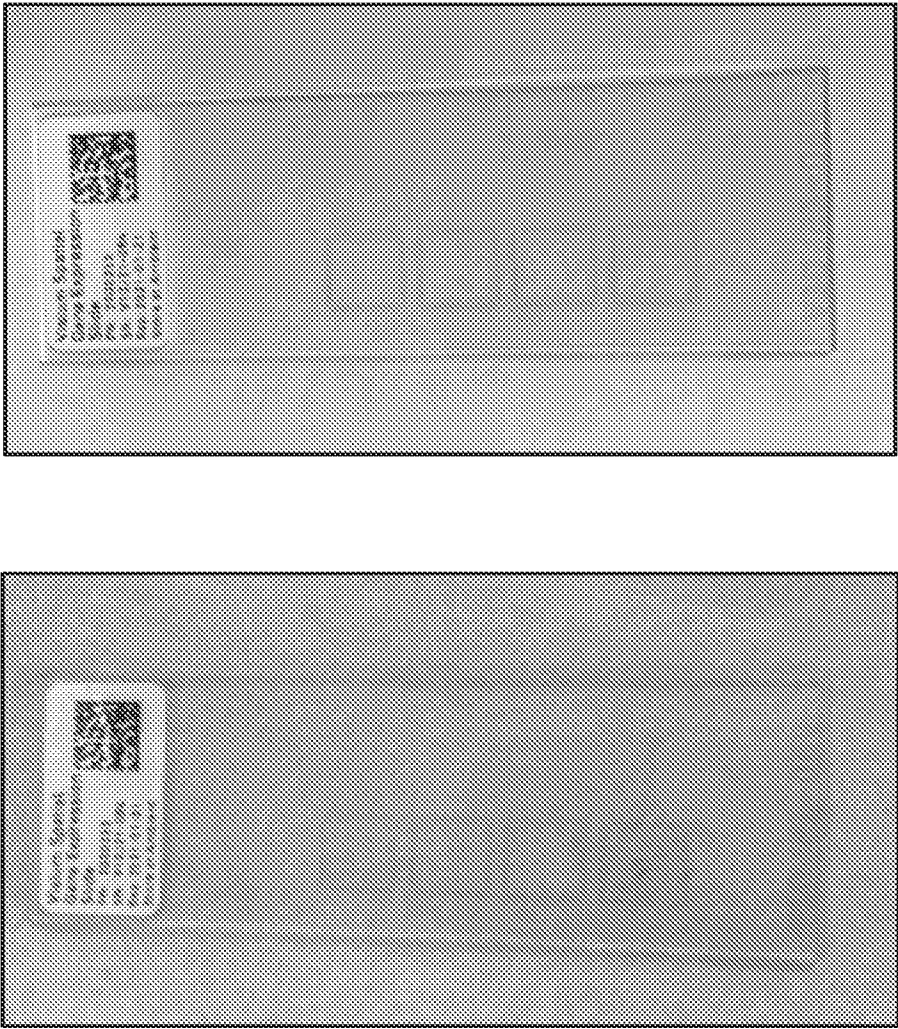


FIG. 2B

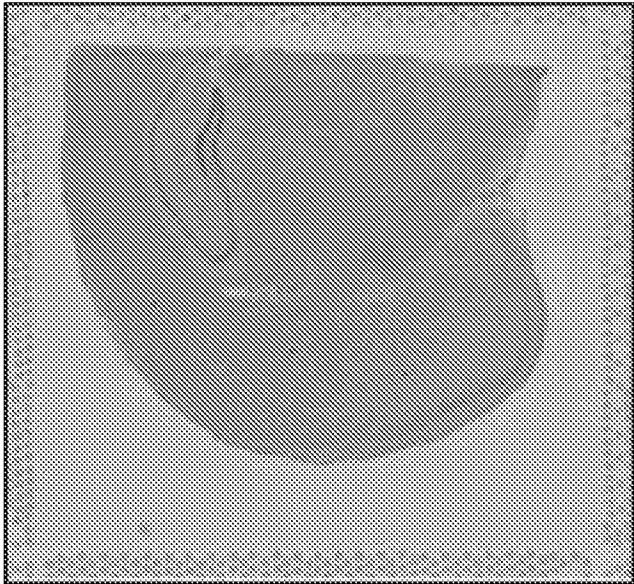
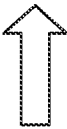


FIG. 3

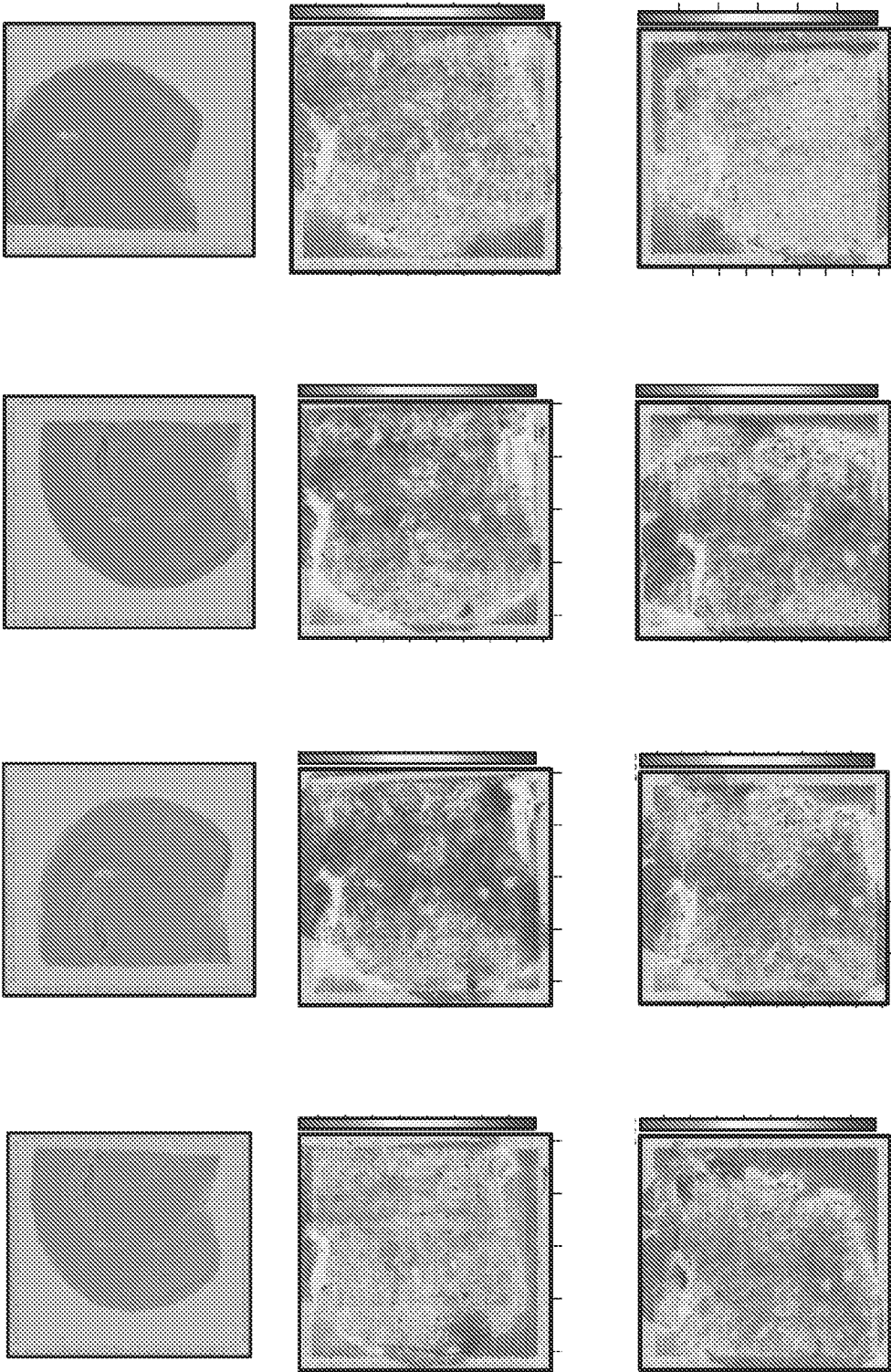


FIG. 4

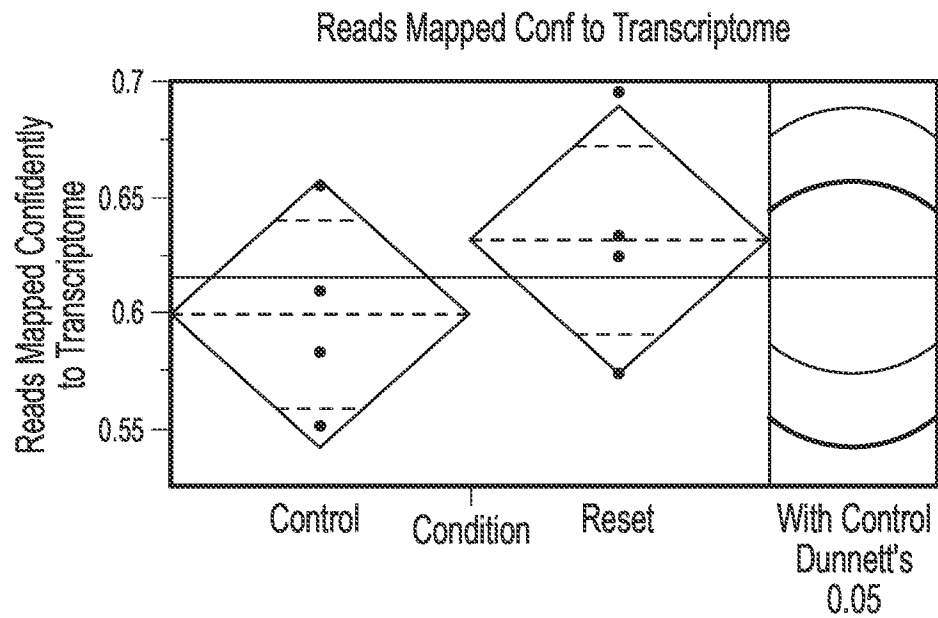


FIG. 5A

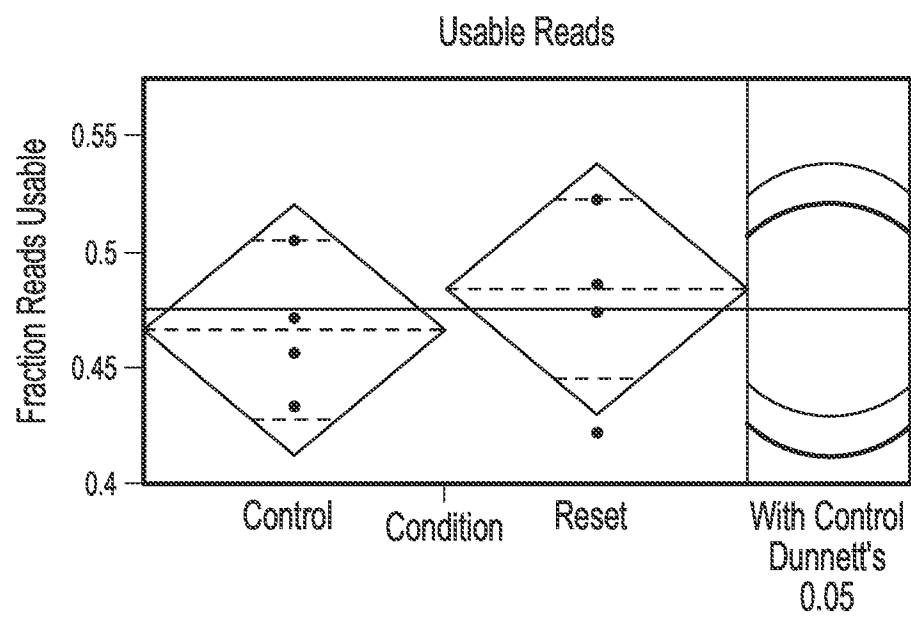


FIG. 5B

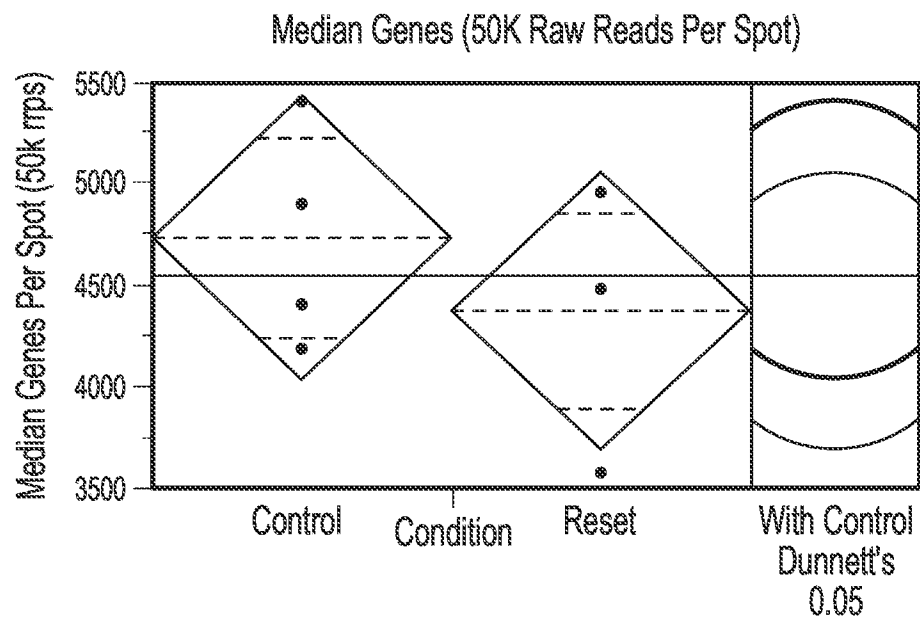


FIG. 5C

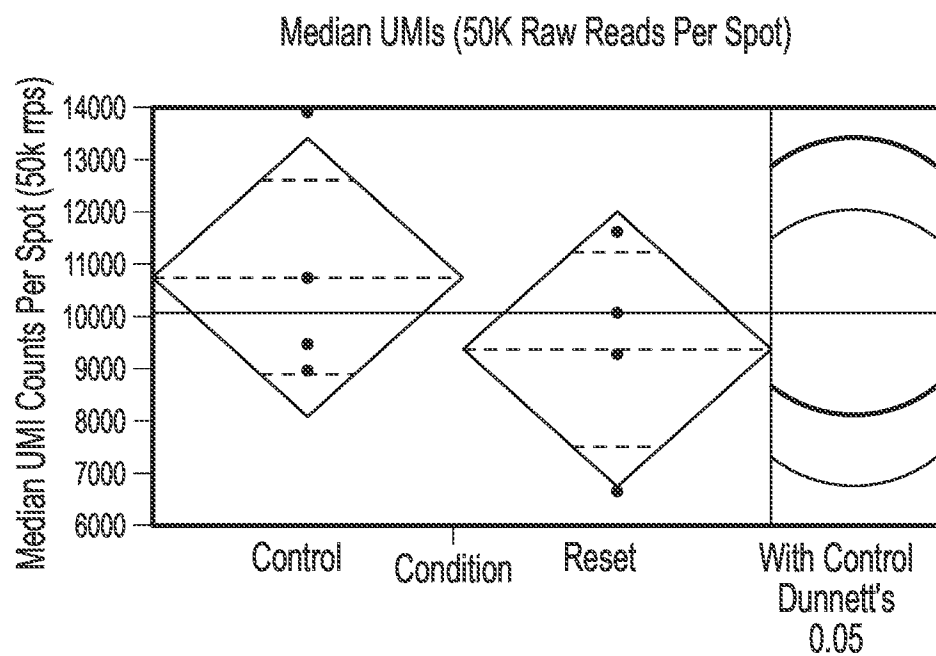


FIG. 5D

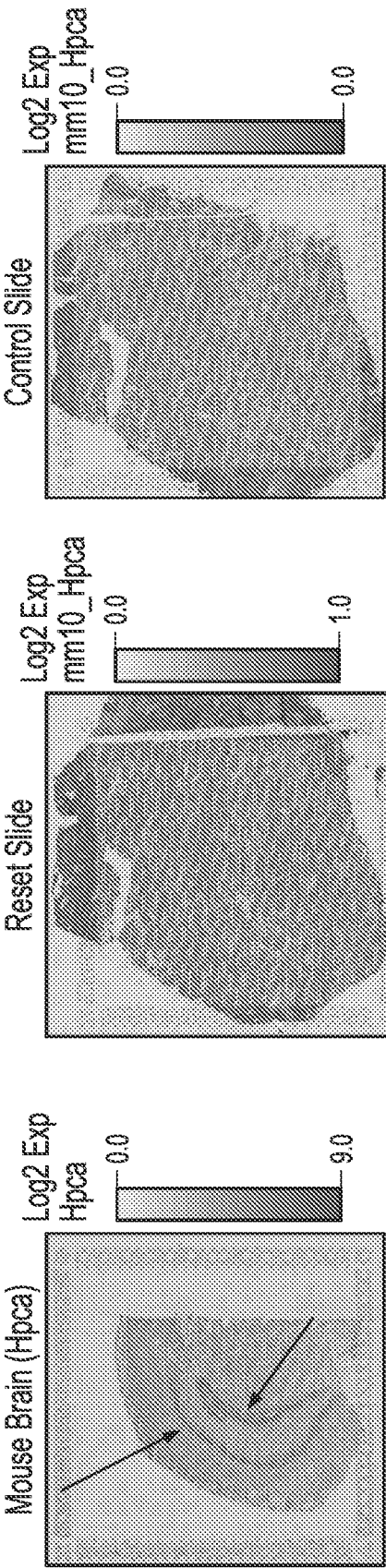


FIG. 6B

FIG. 6A

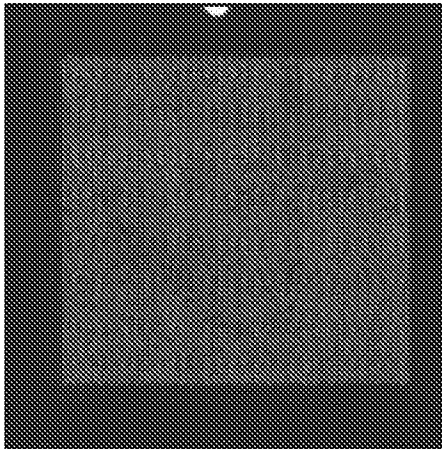


FIG. 7A

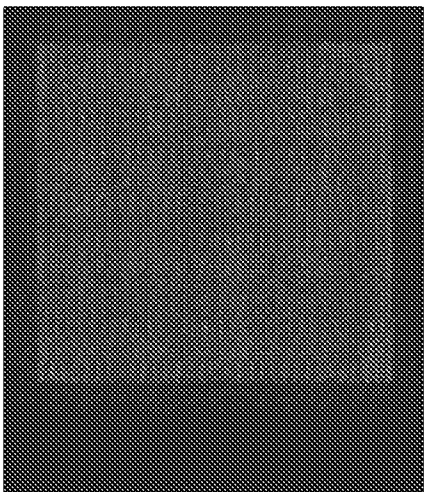


FIG. 7B

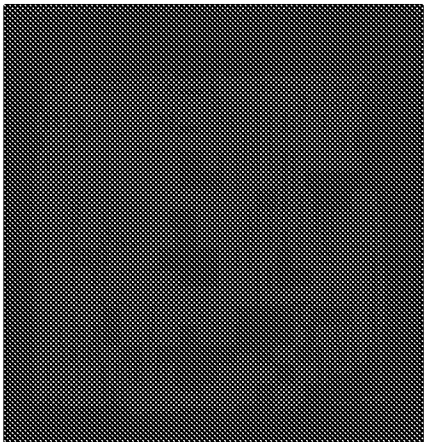


FIG. 7C

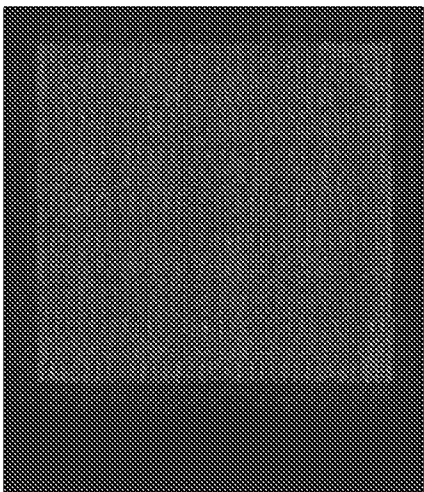


FIG. 7D

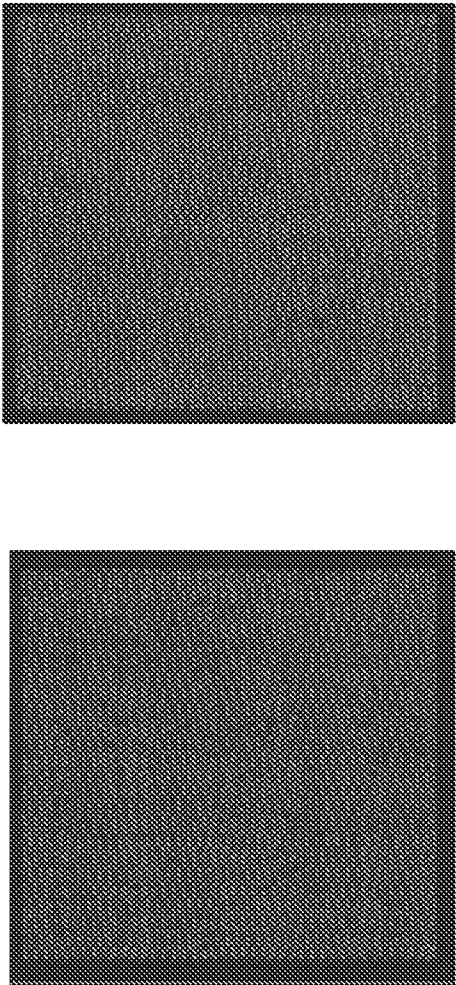


FIG. 7E

FIG. 7F

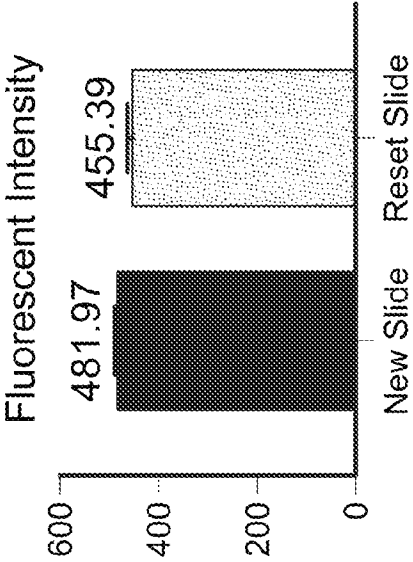


FIG. 7G

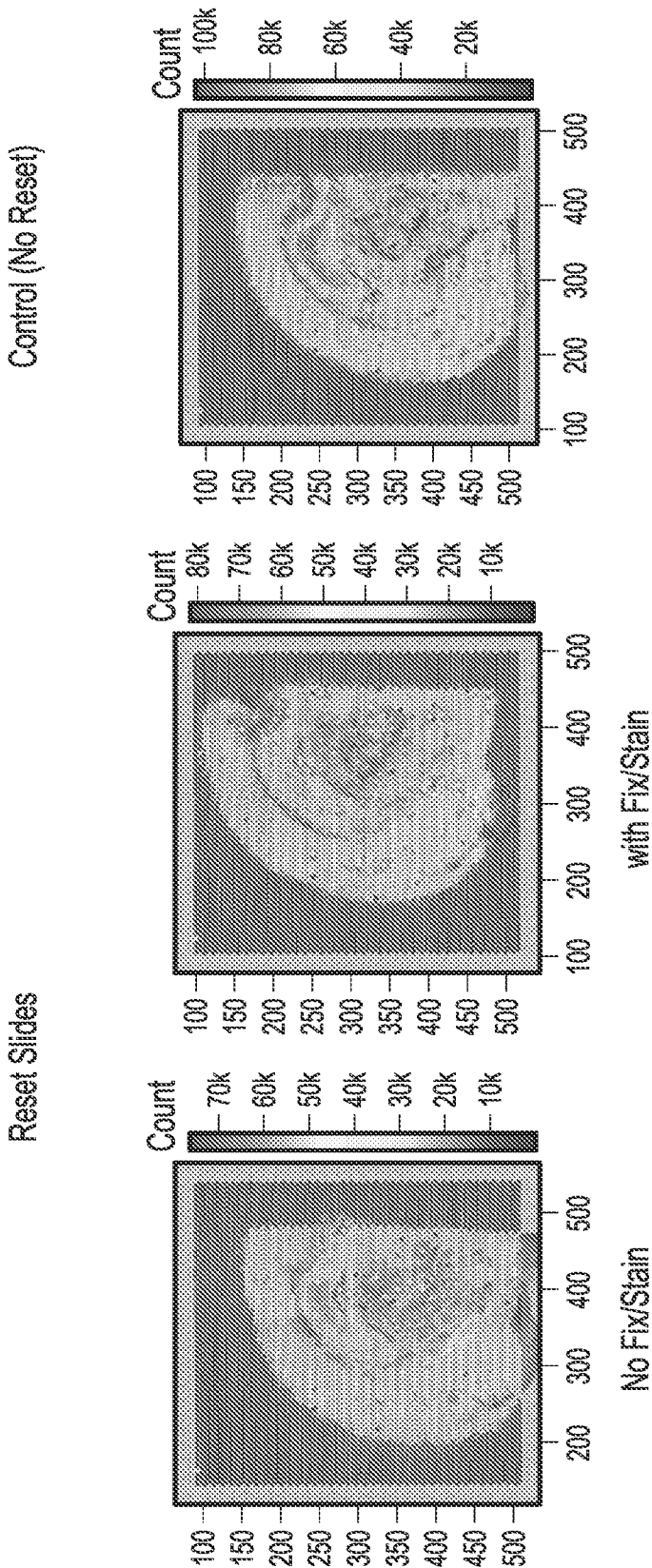


FIG. 8

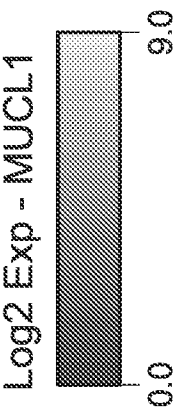
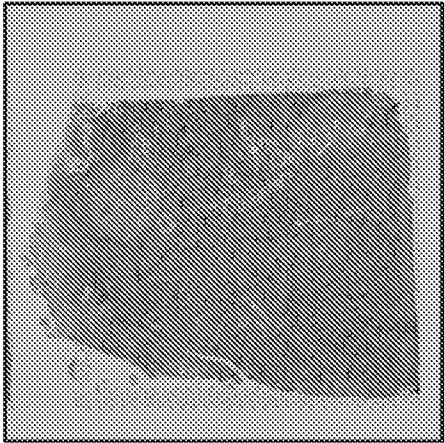


FIG. 9A

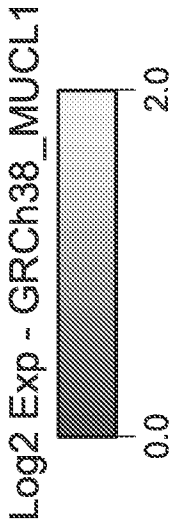
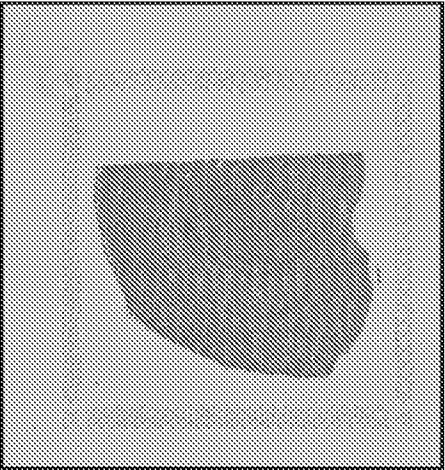


FIG. 9B

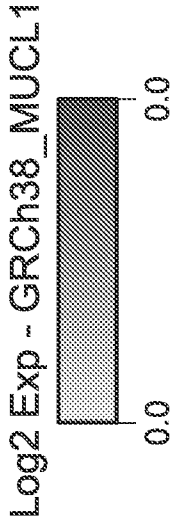
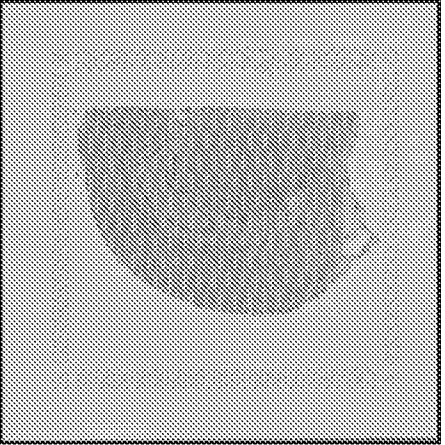


FIG. 9C

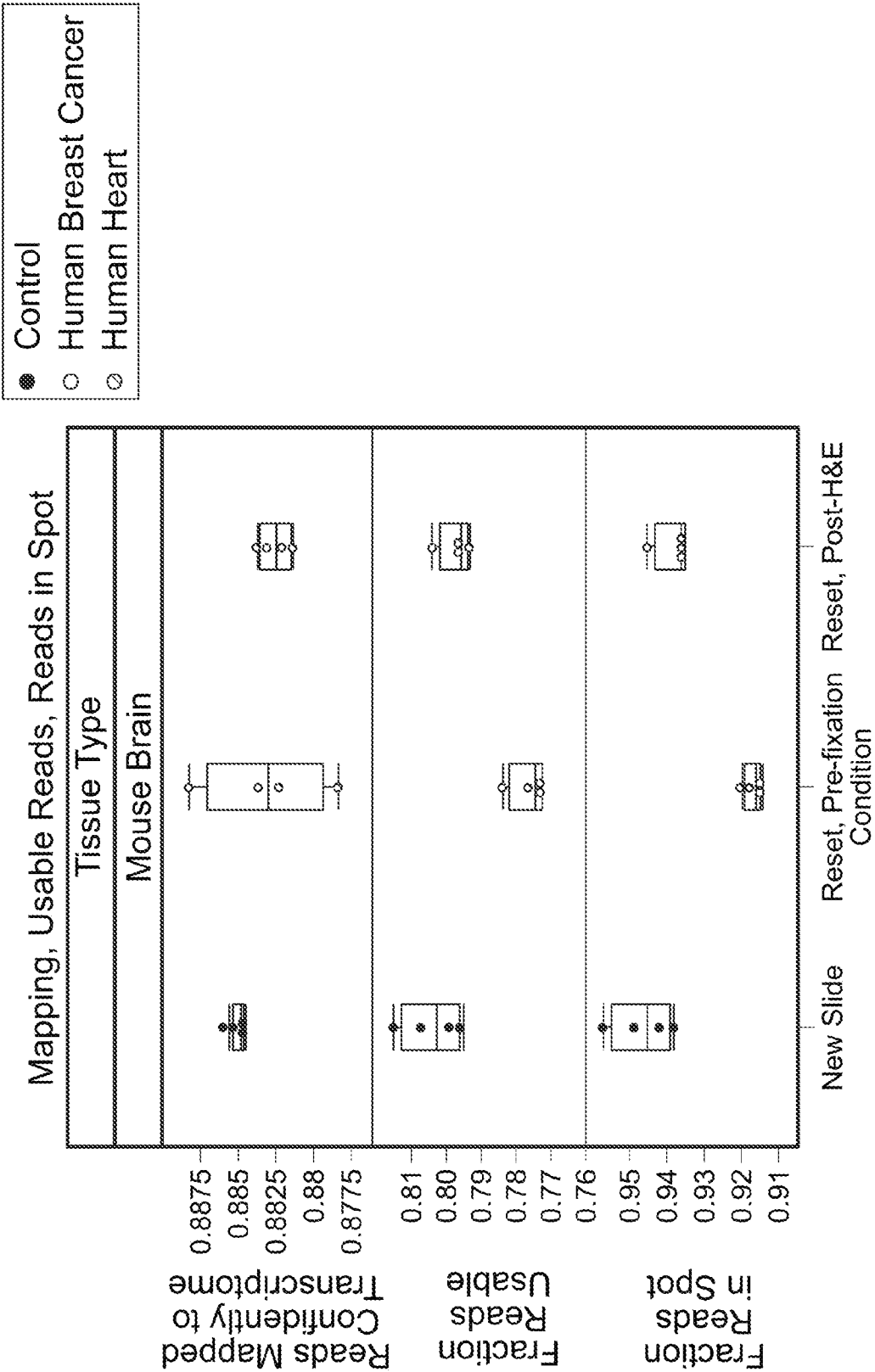


FIG. 10A

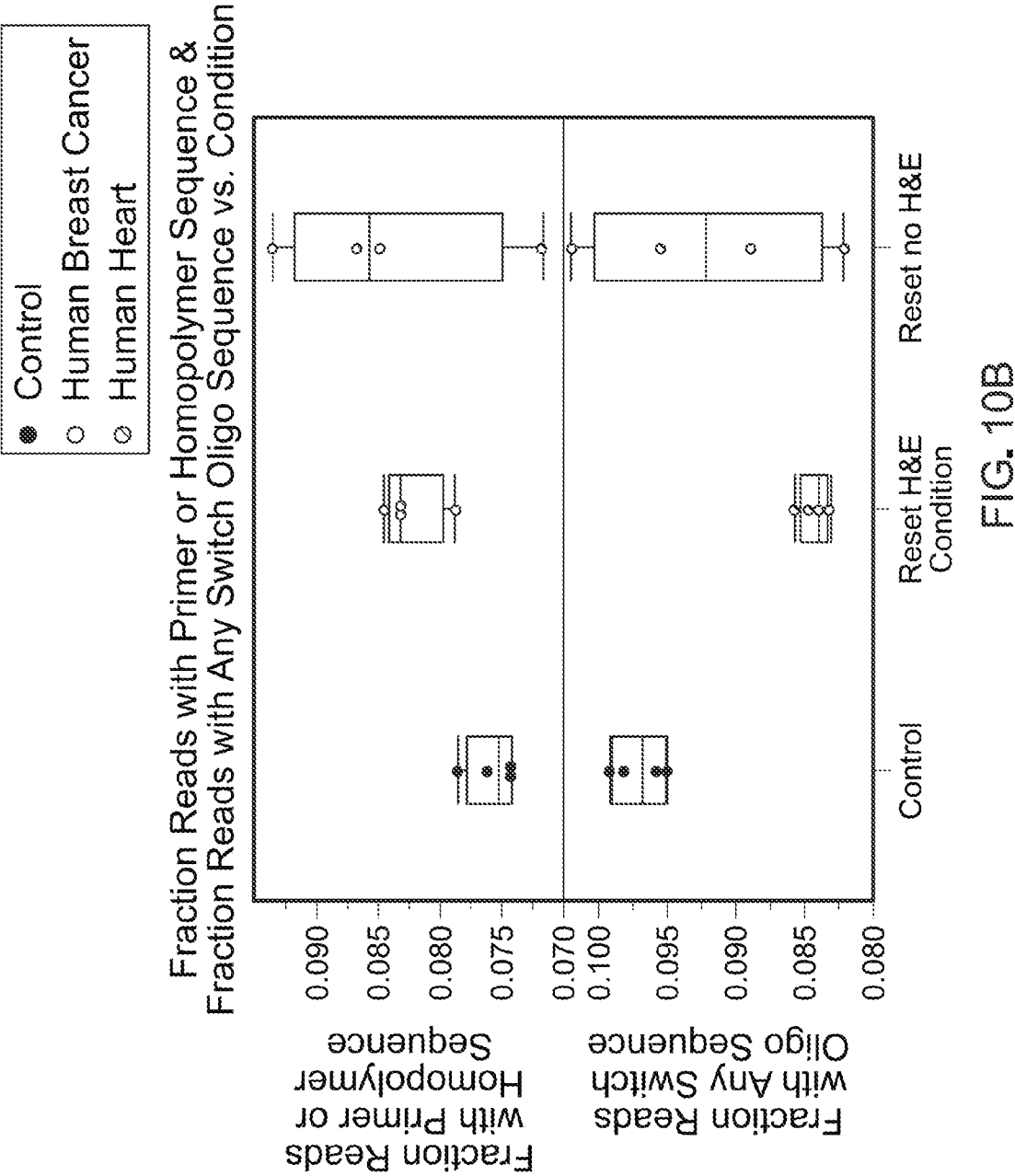


FIG. 10B

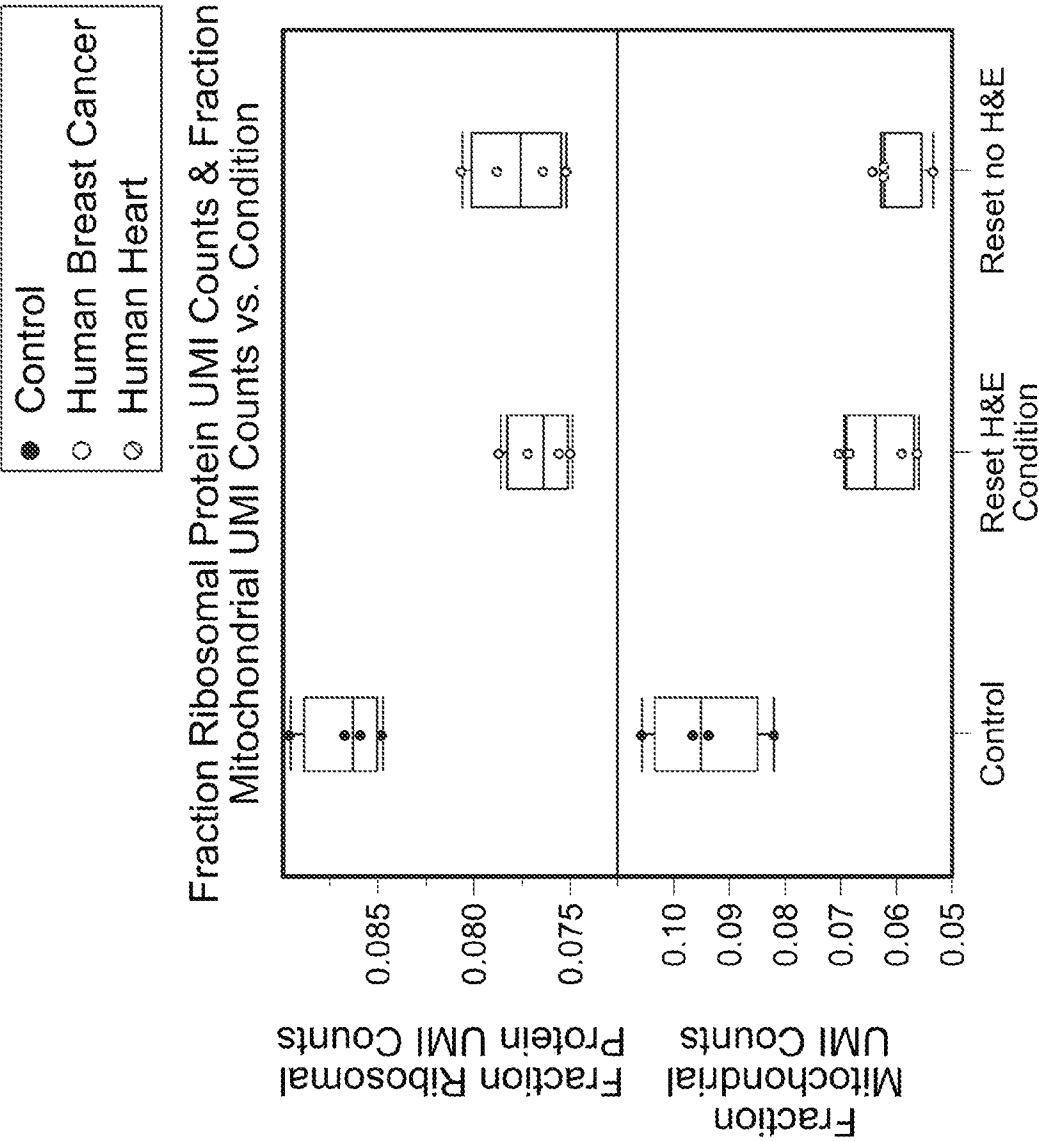


FIG. 10C

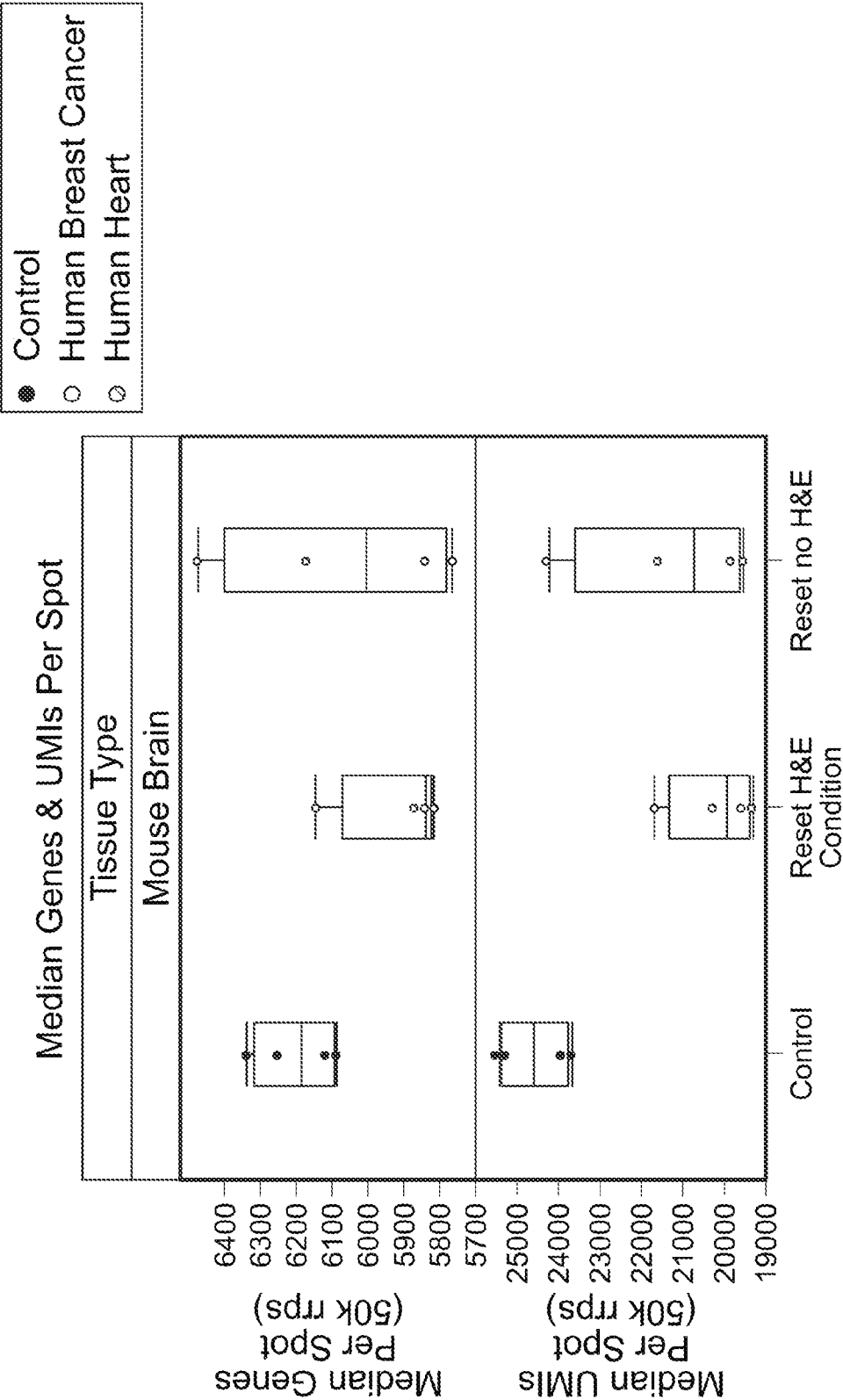


FIG. 10D

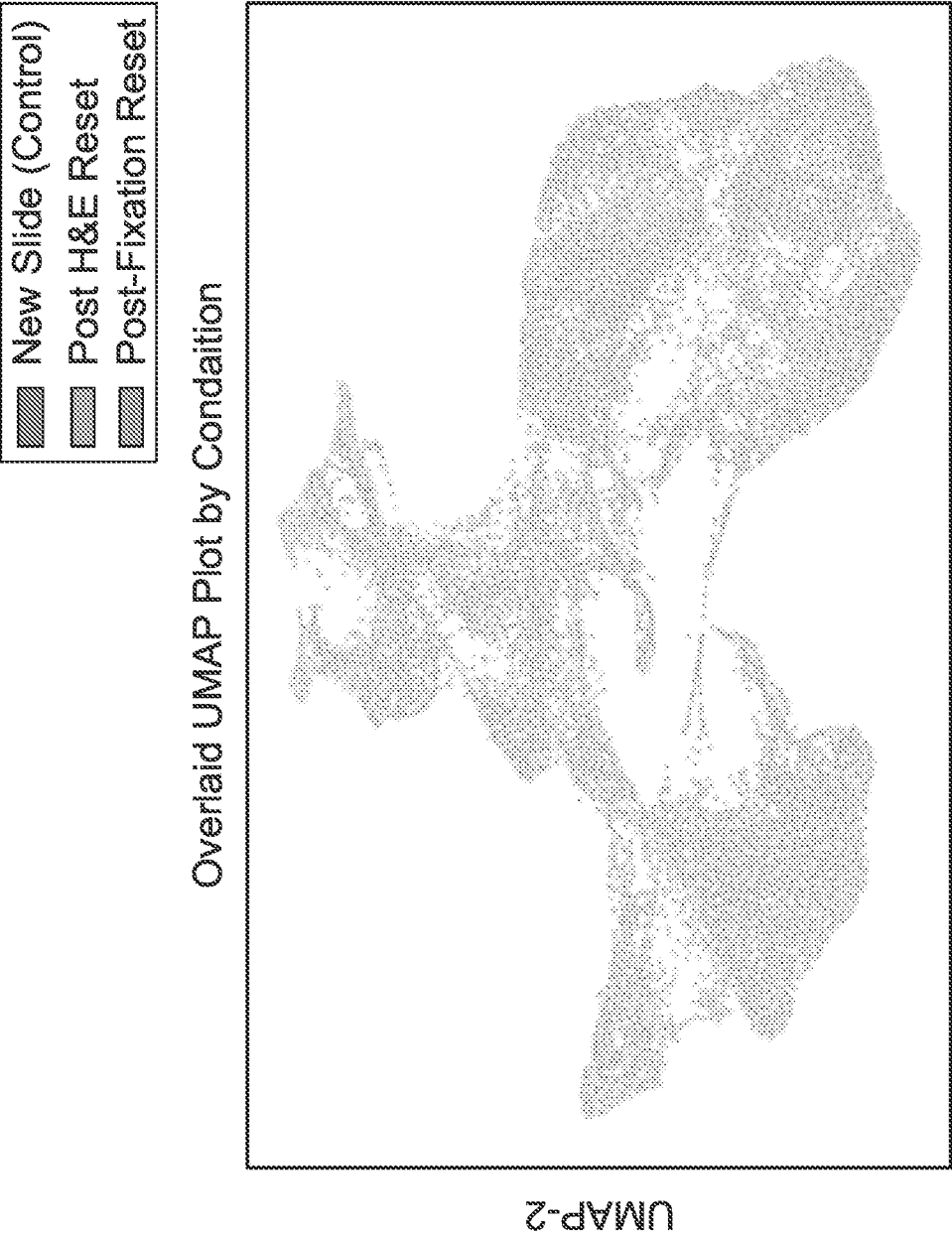
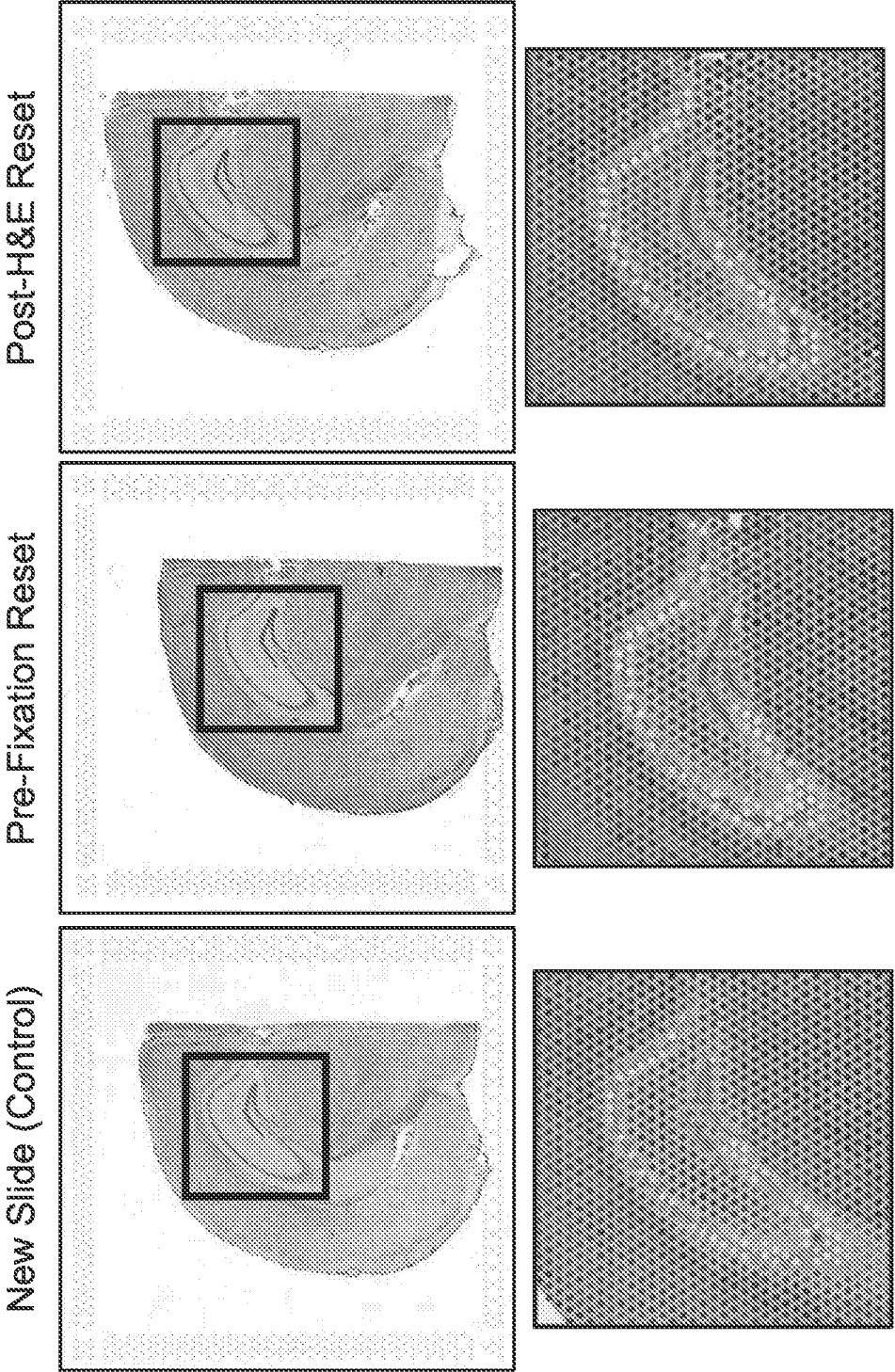


FIG. 10E



Hpca Gene Expression
FIG. 10F

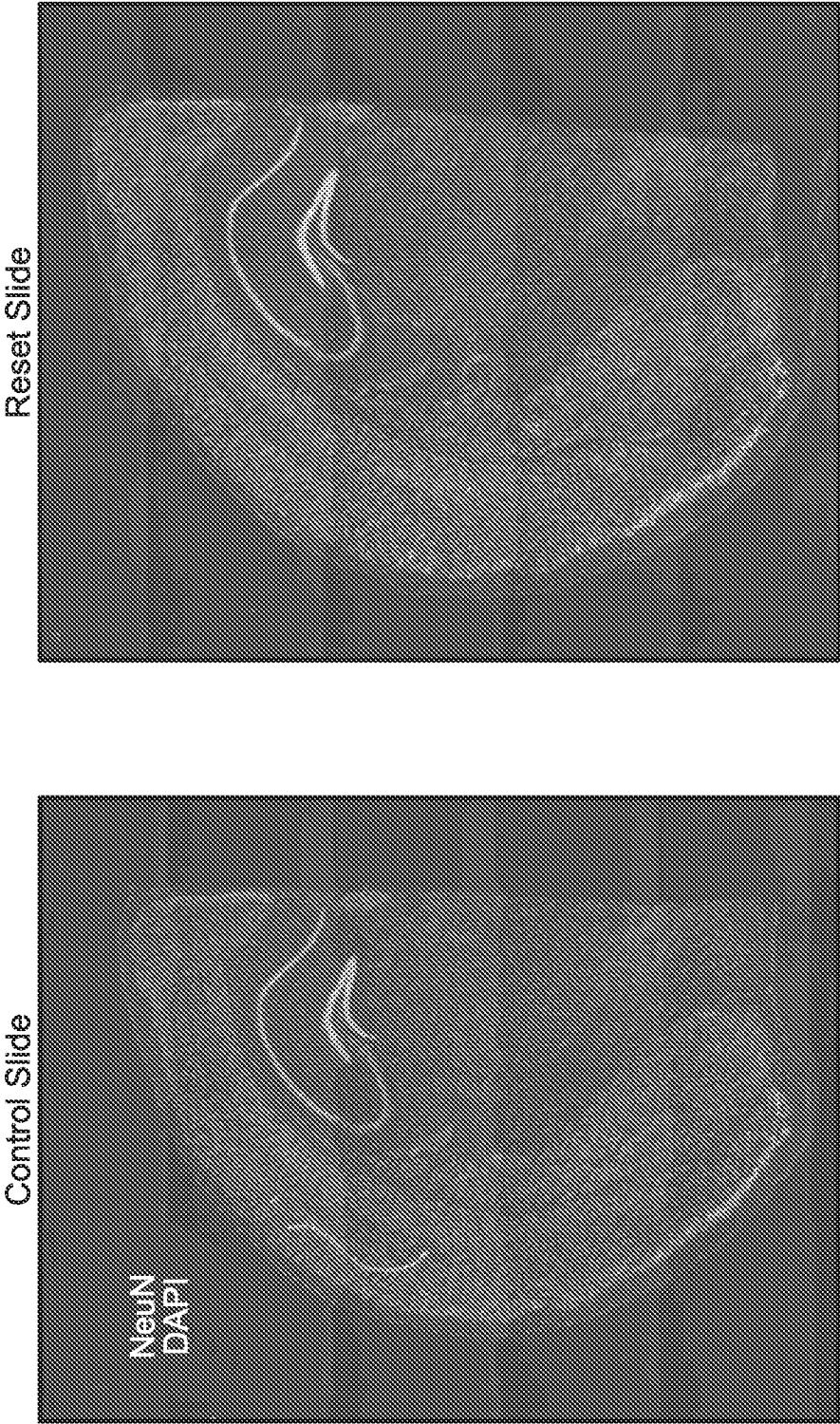


FIG. 11A

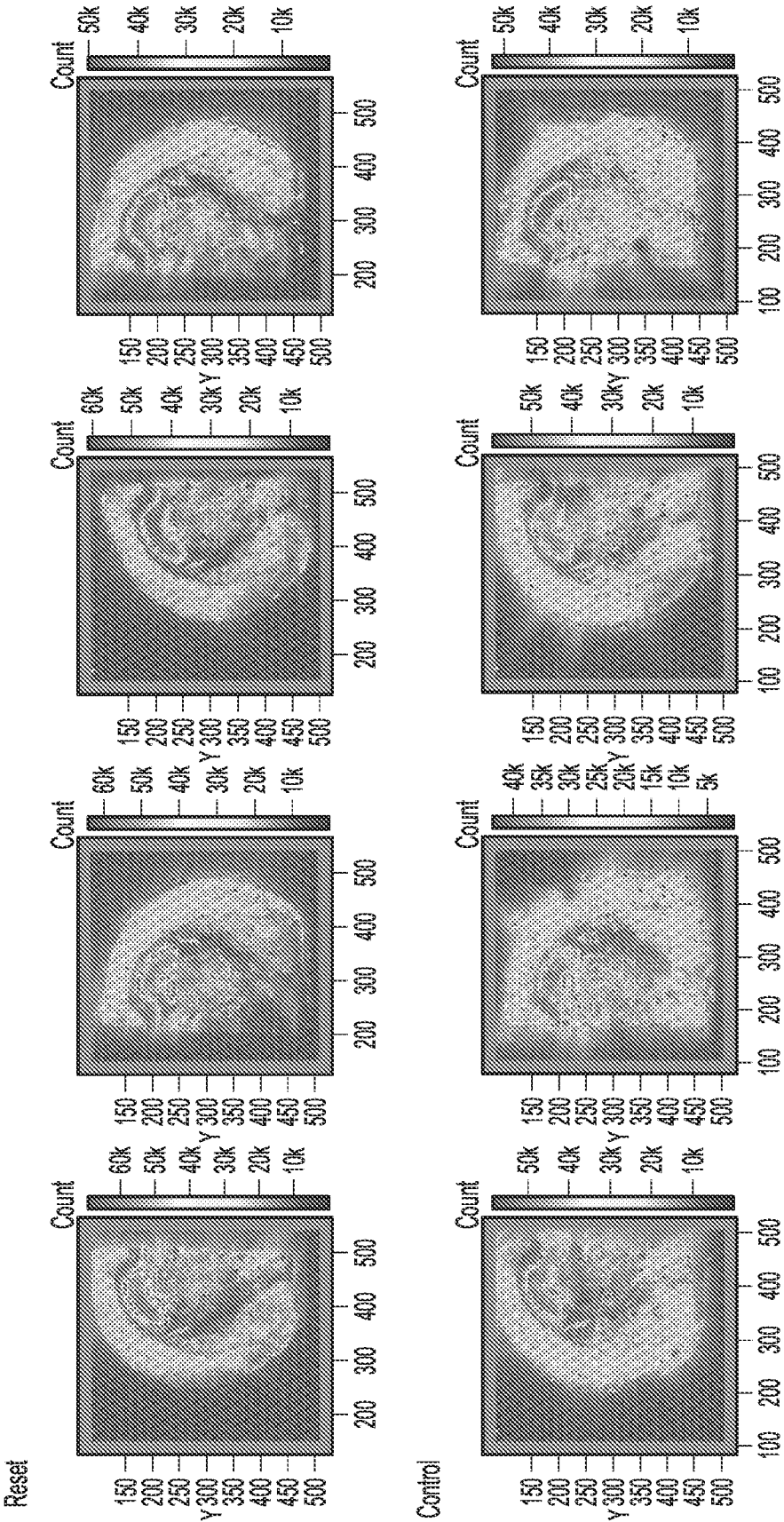
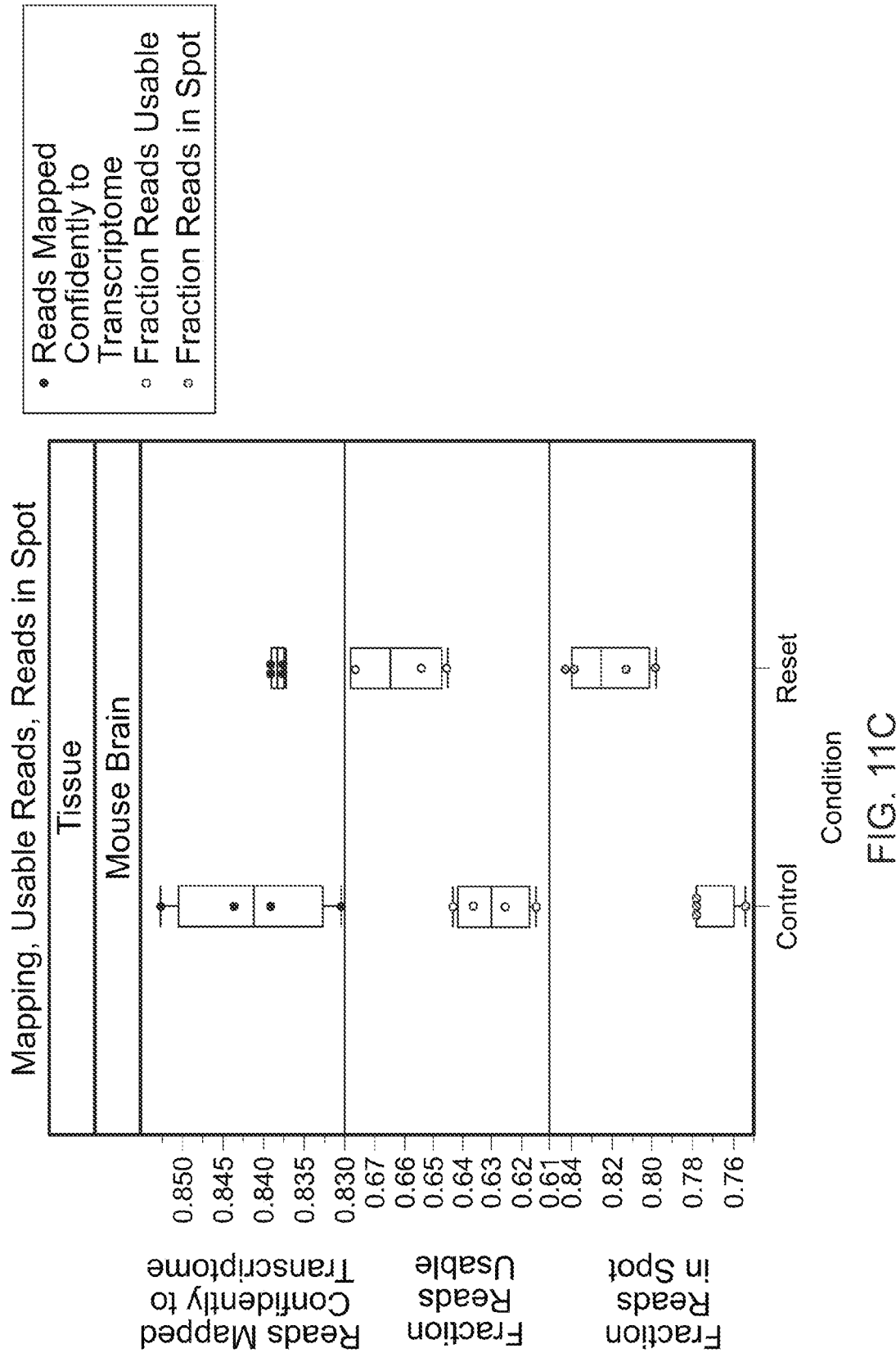


FIG. 11B



- Fraction Reads with Primer or Homopolymer Sequence
- Fraction Reads with Primer or Homopolymer Sequence
- Fraction Reads with any Switch Oligo Sequence
- Fraction Reads with any Switch Oligo Sequence

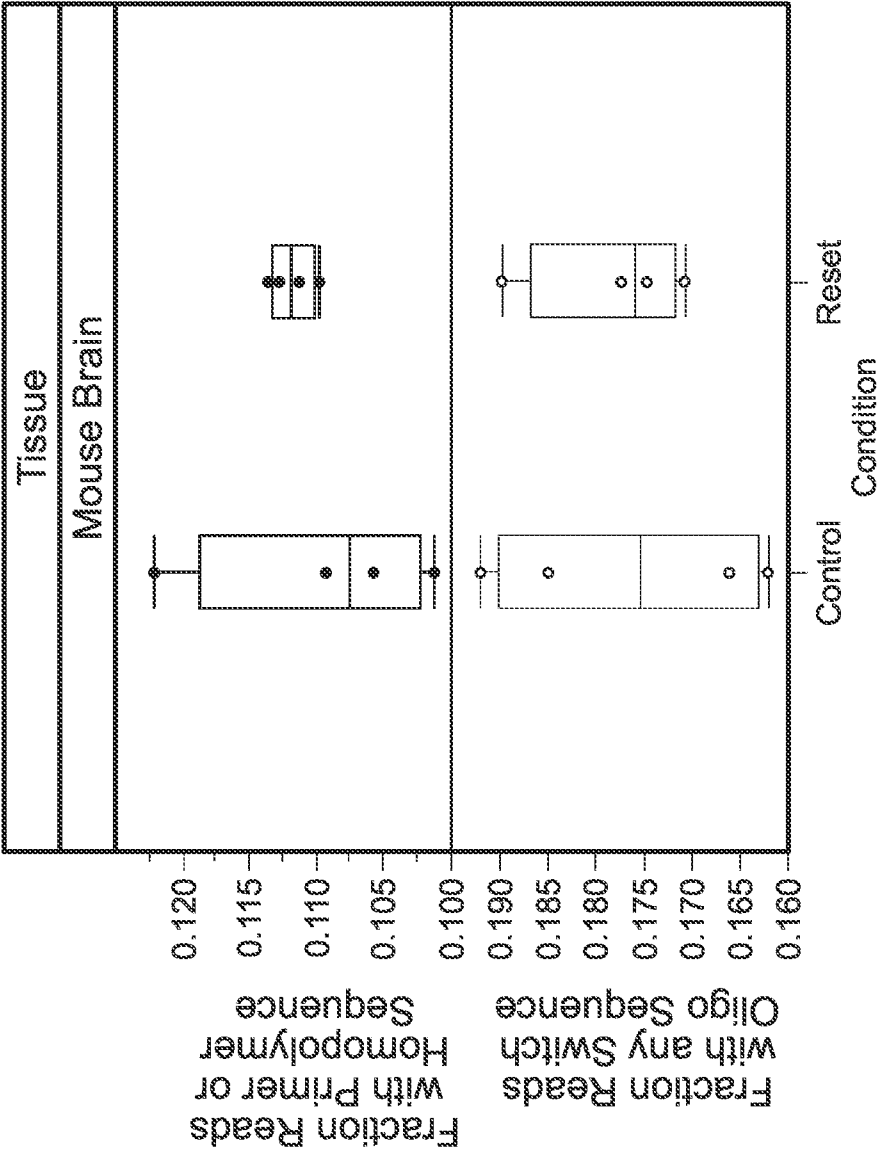


FIG. 11D

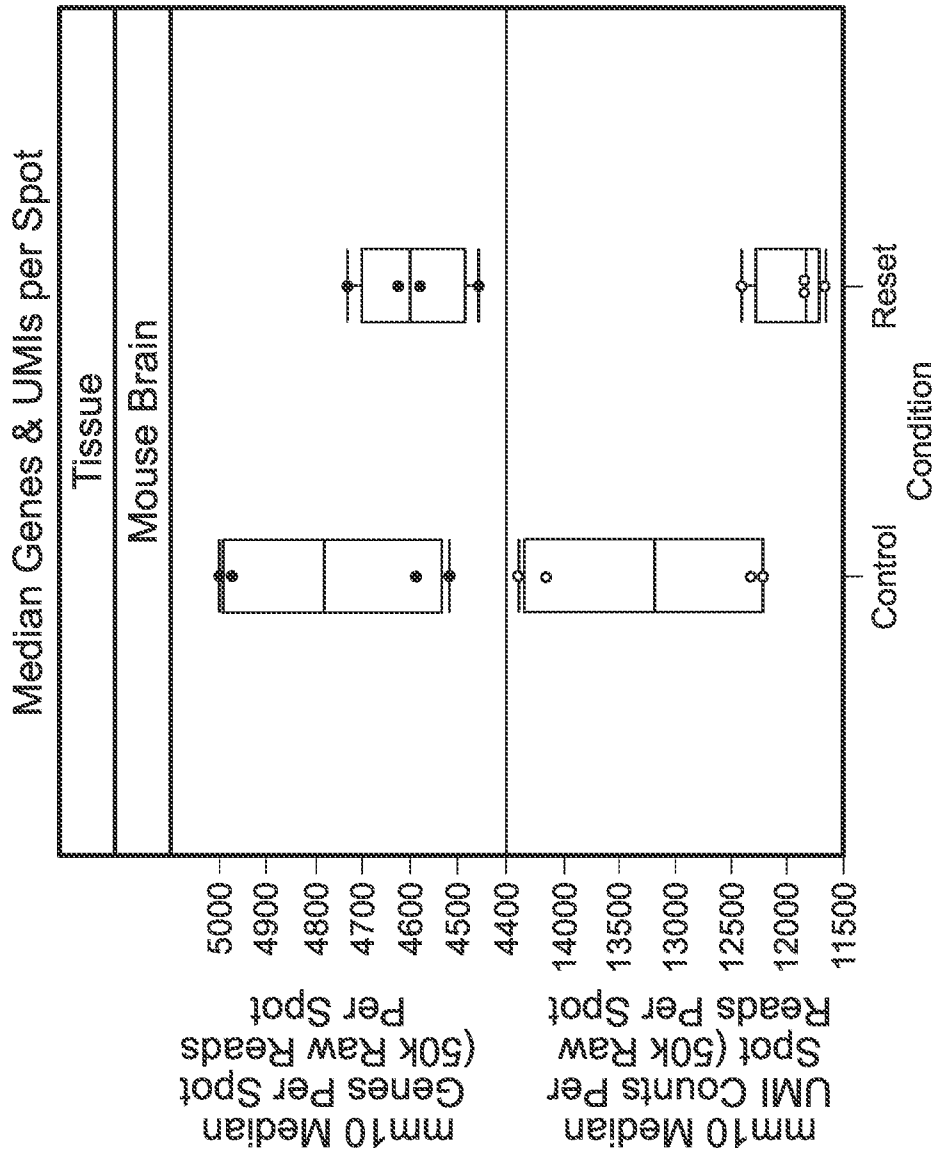


FIG. 11E

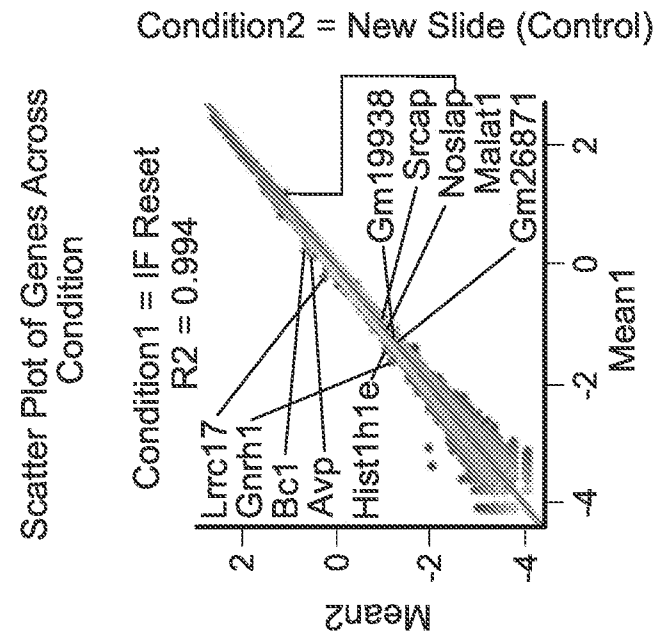


FIG. 11G

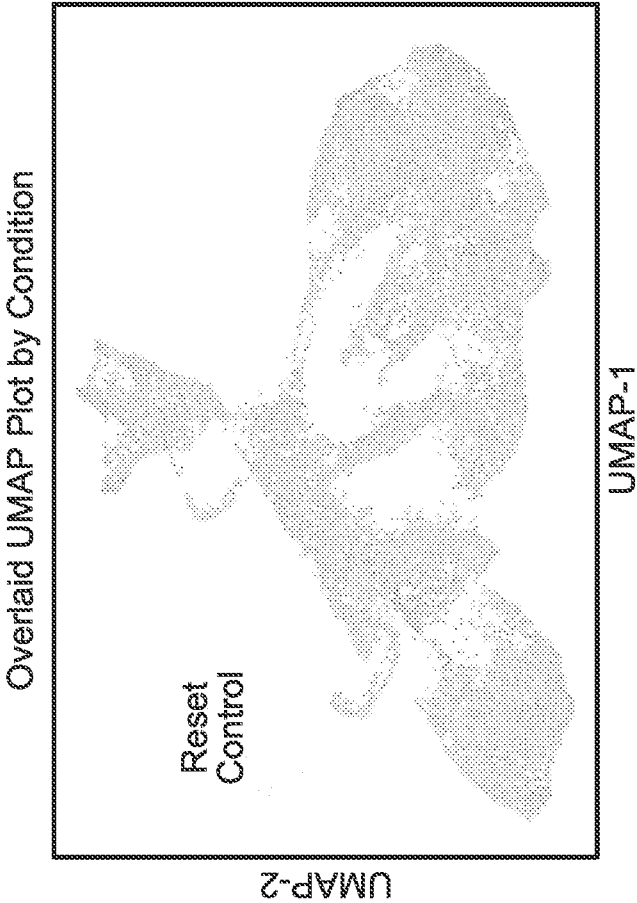


FIG. 11F

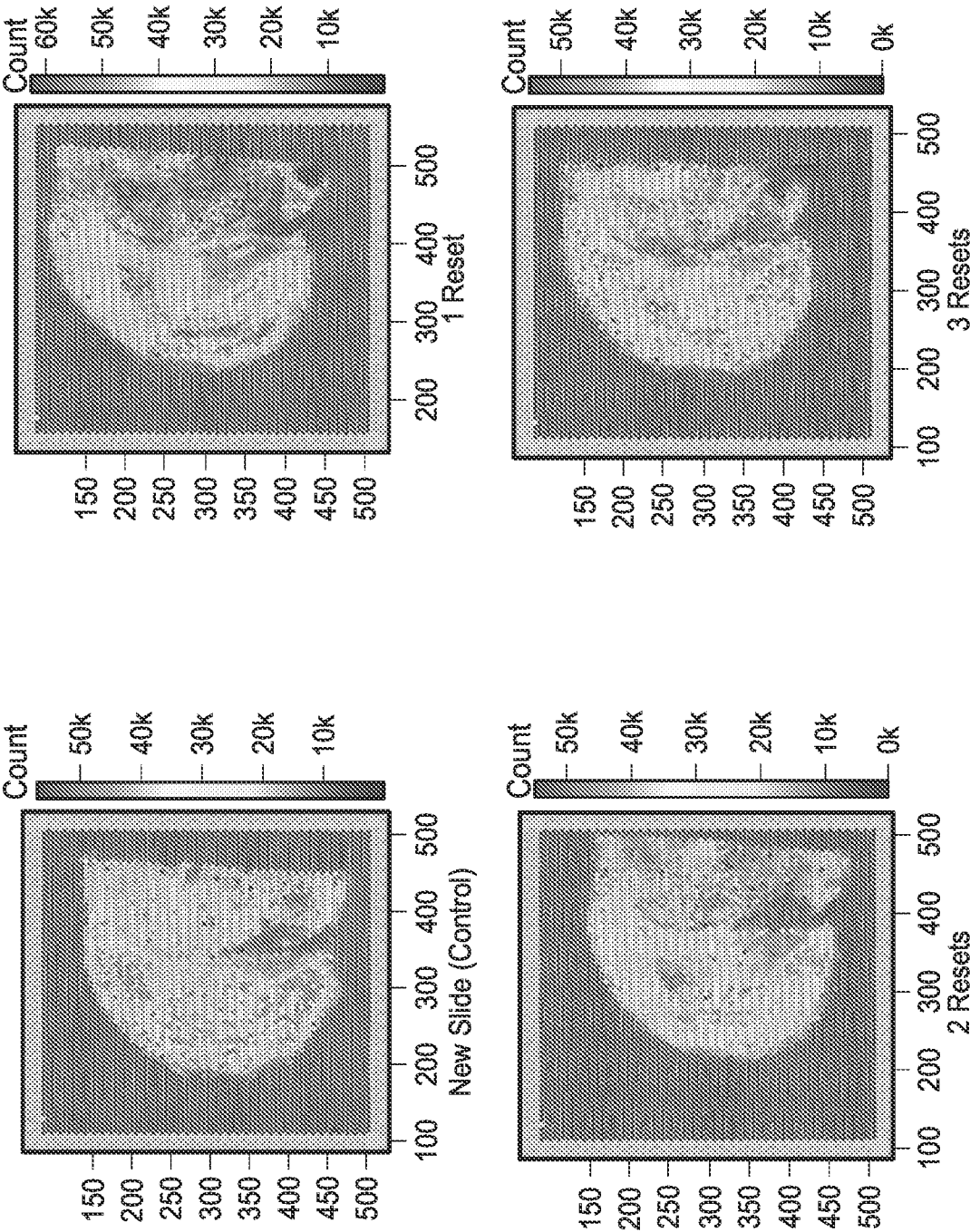


FIG. 12A

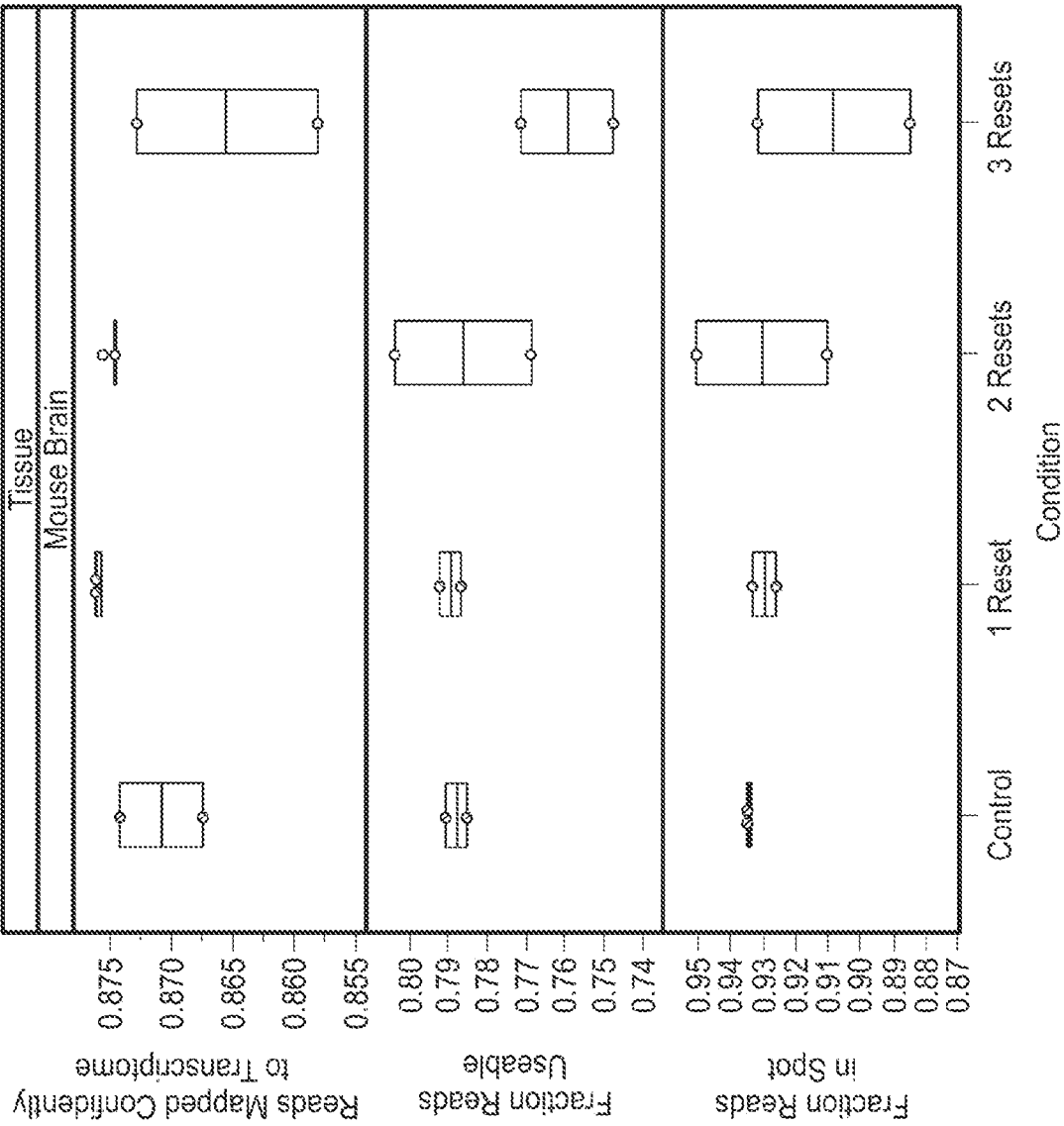


FIG. 12B

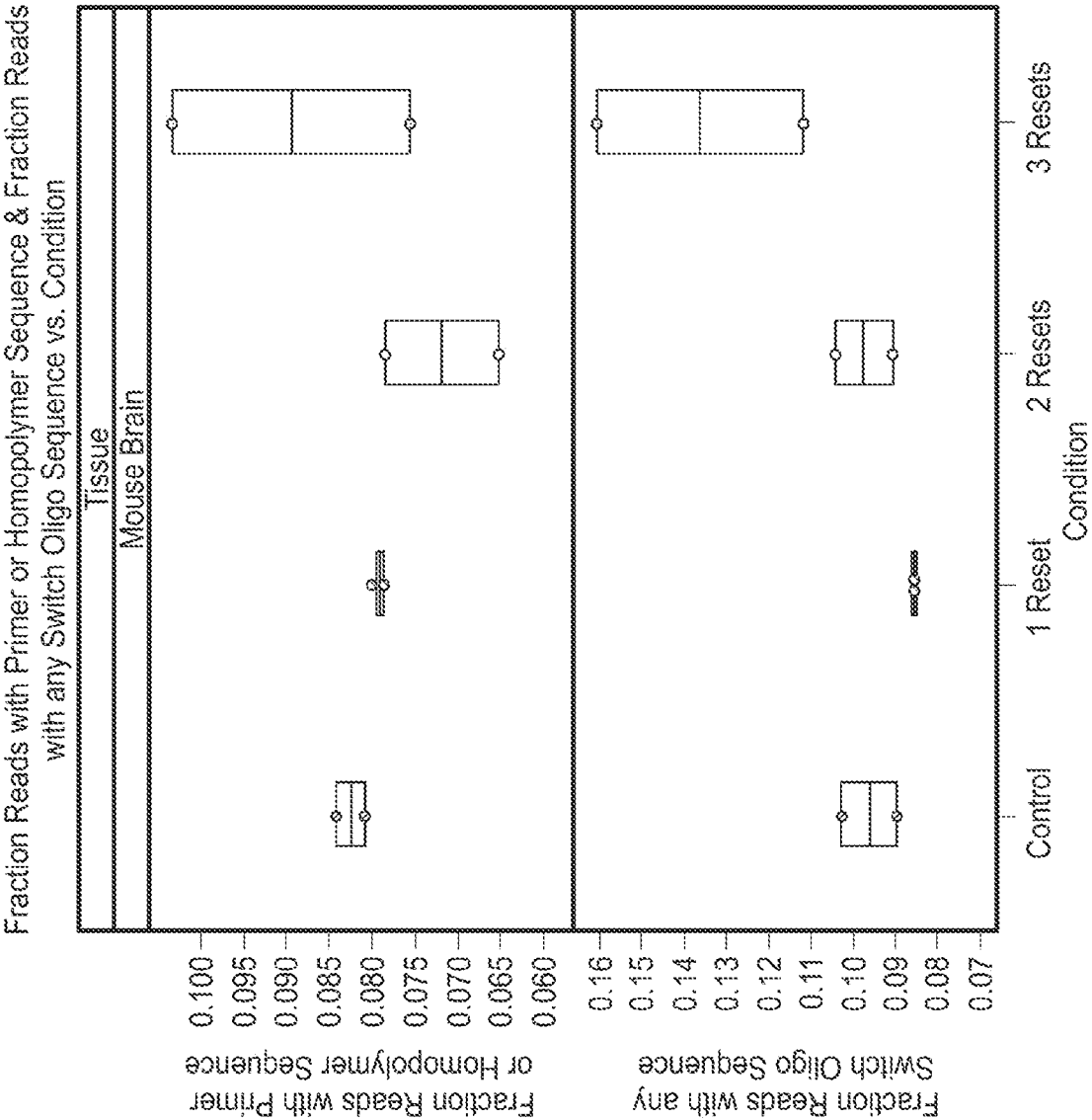


FIG. 12C

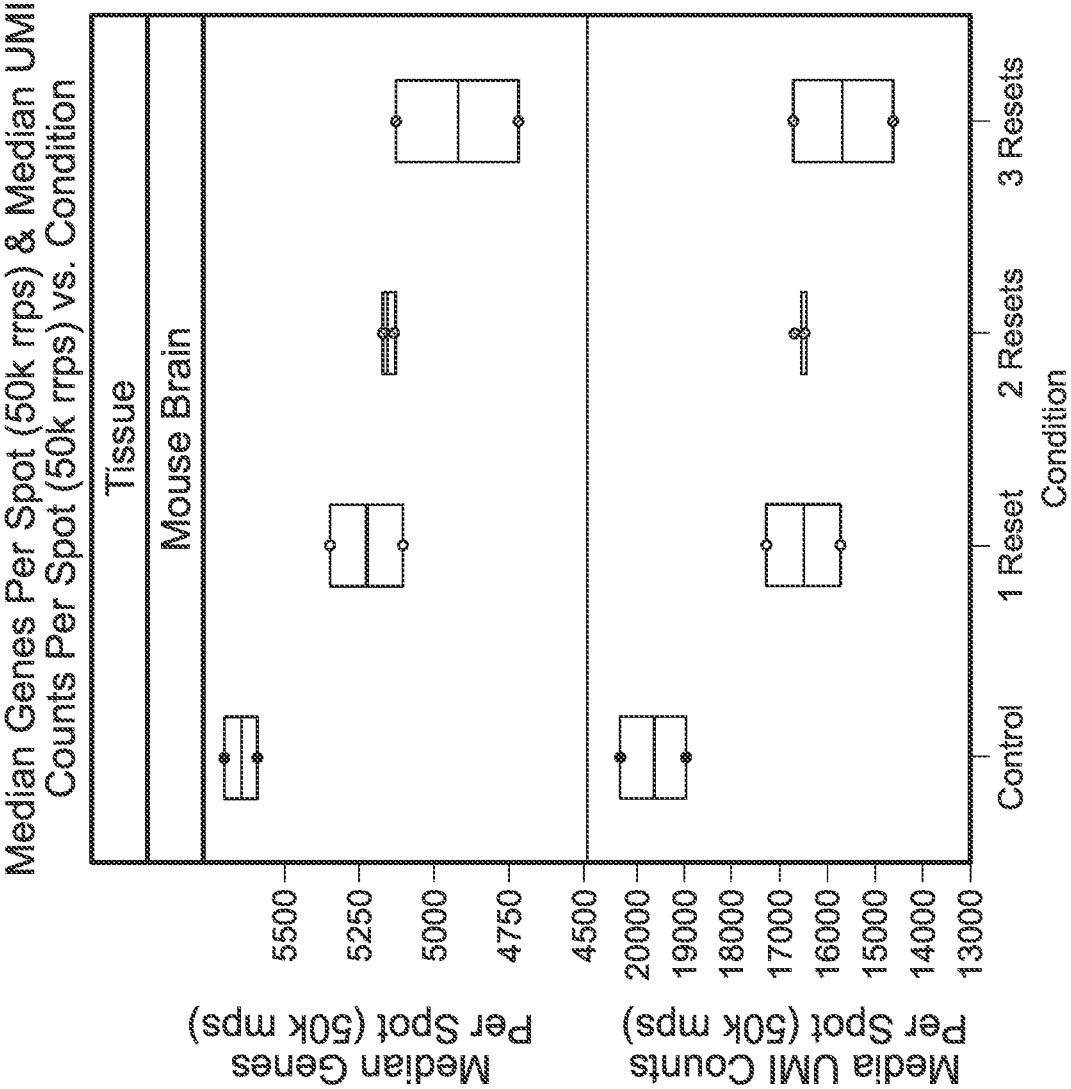


FIG. 12D

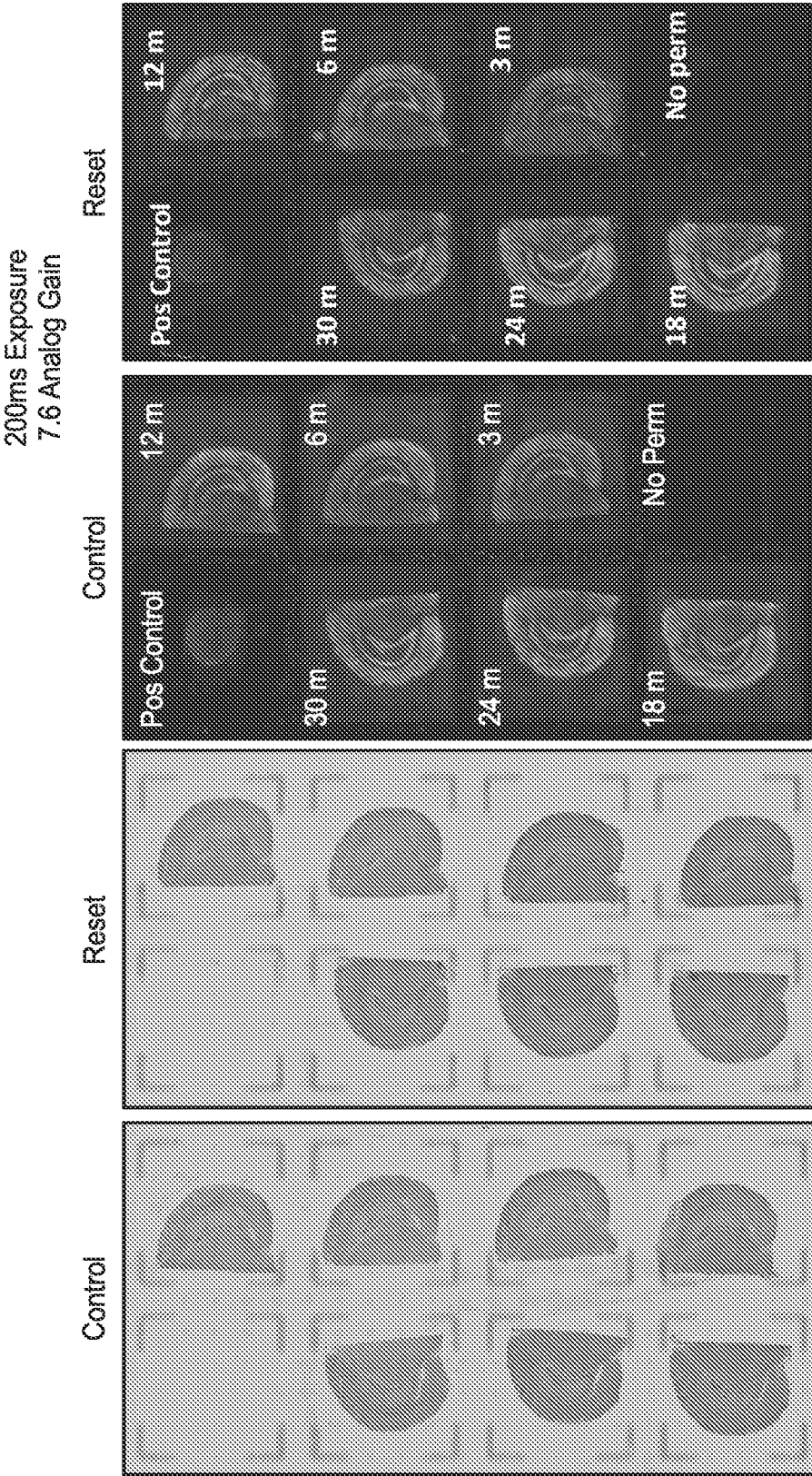


FIG. 13A

FIG. 13B

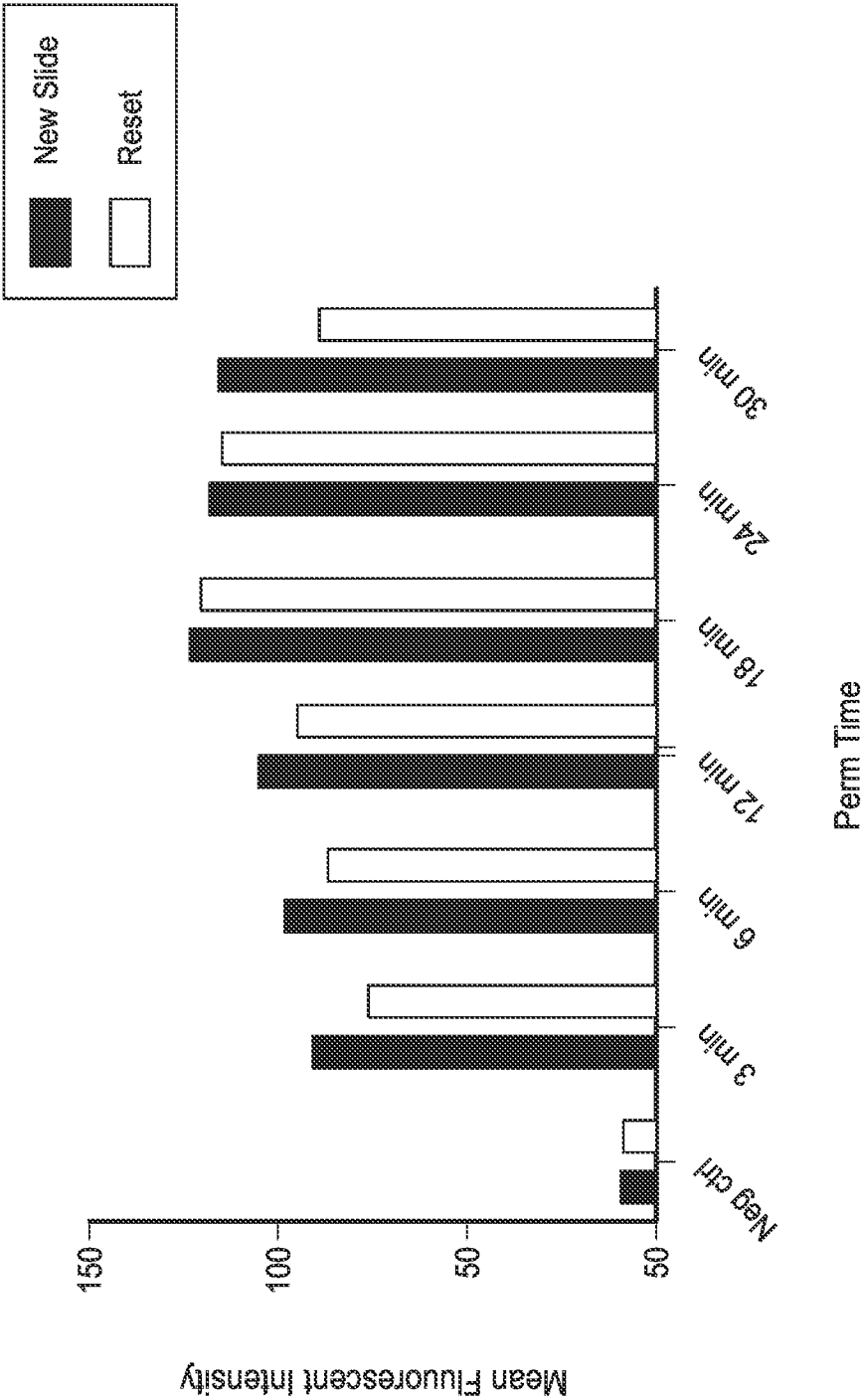


FIG. 13C

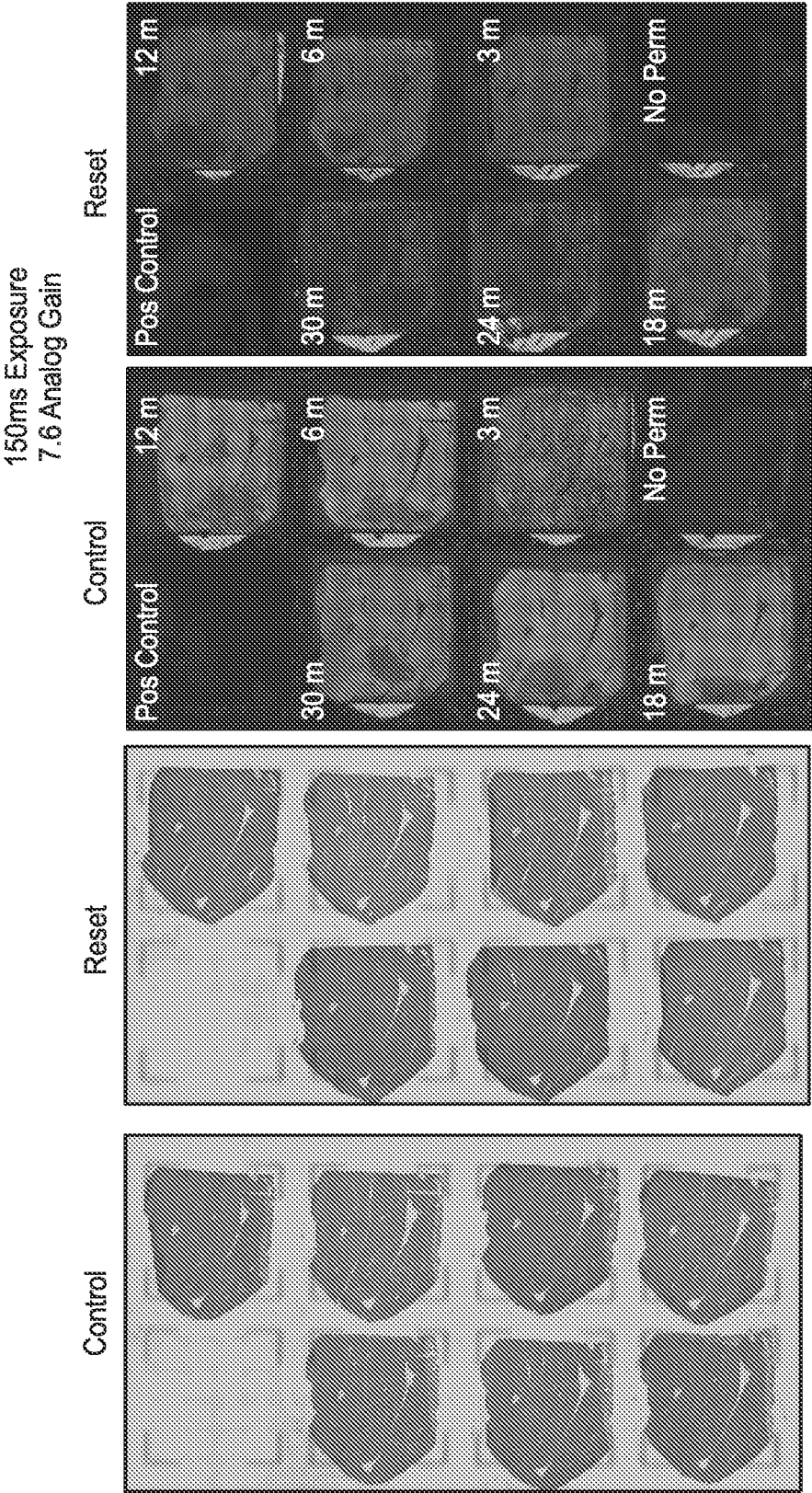


FIG. 14B

FIG. 14A

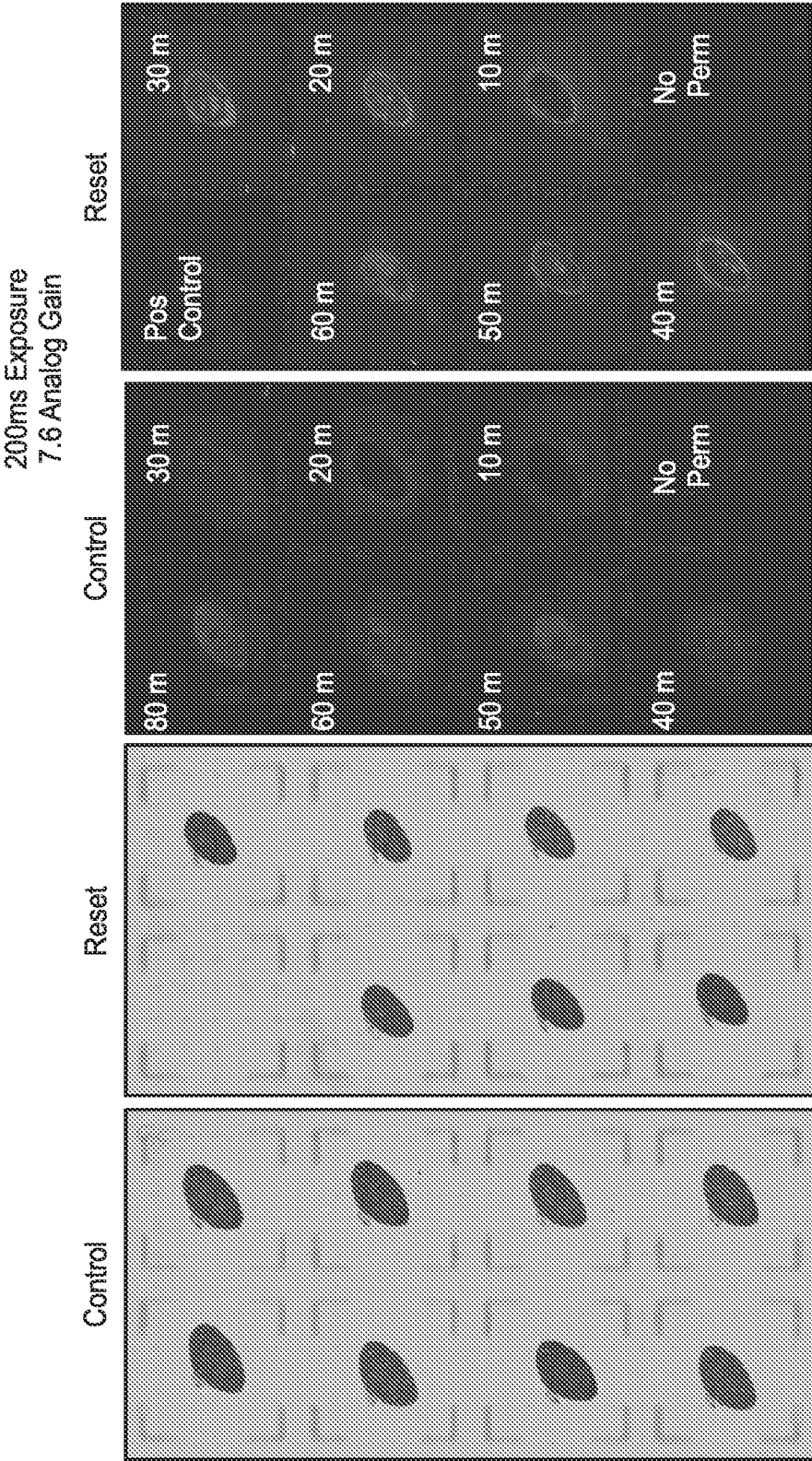


FIG. 15A

FIG. 15B

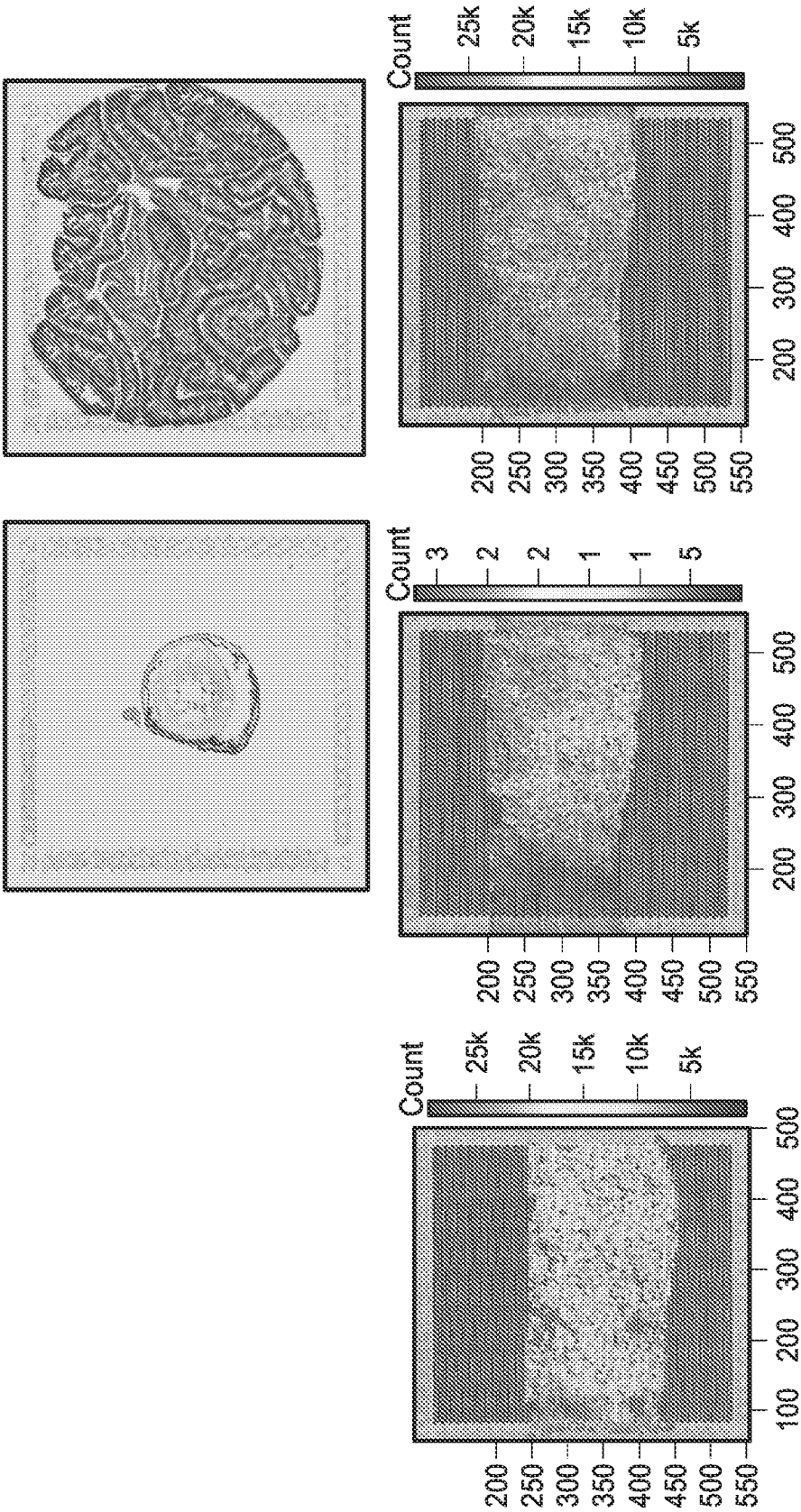


FIG. 16A

FIG. 16B

FIG. 16C

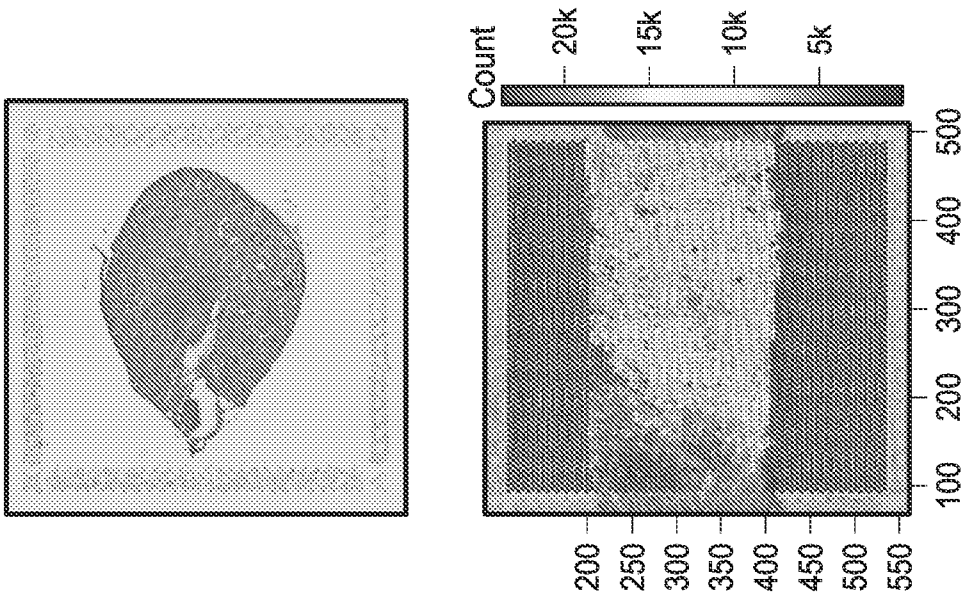


FIG. 16E

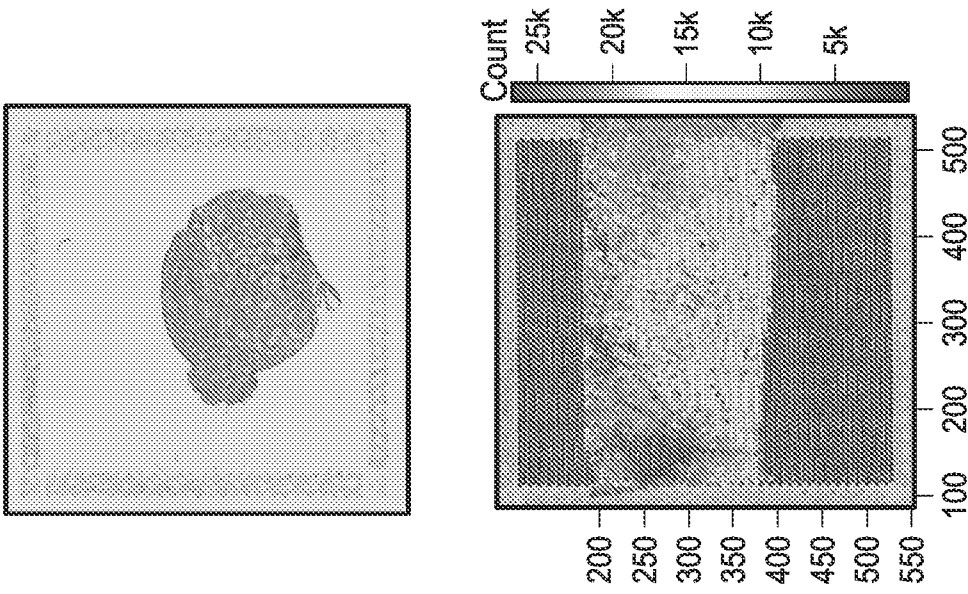


FIG. 16D

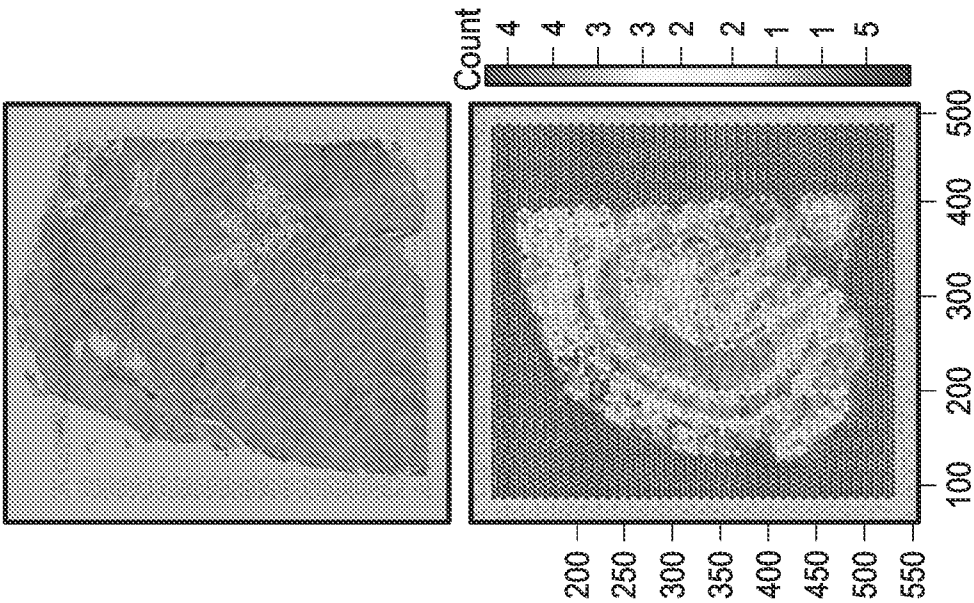


FIG. 17B

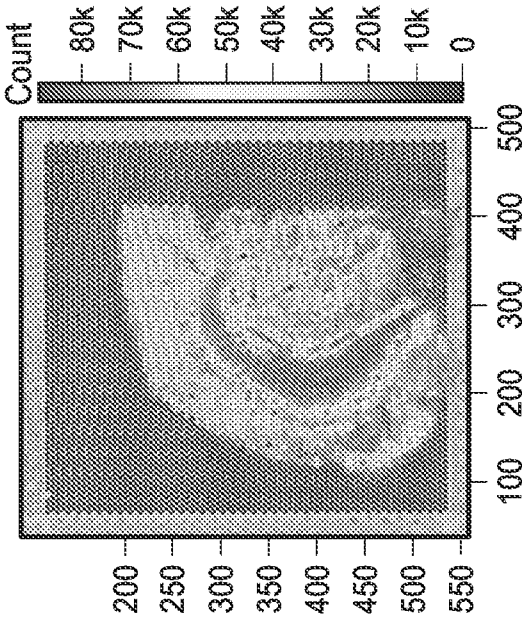


FIG. 17A

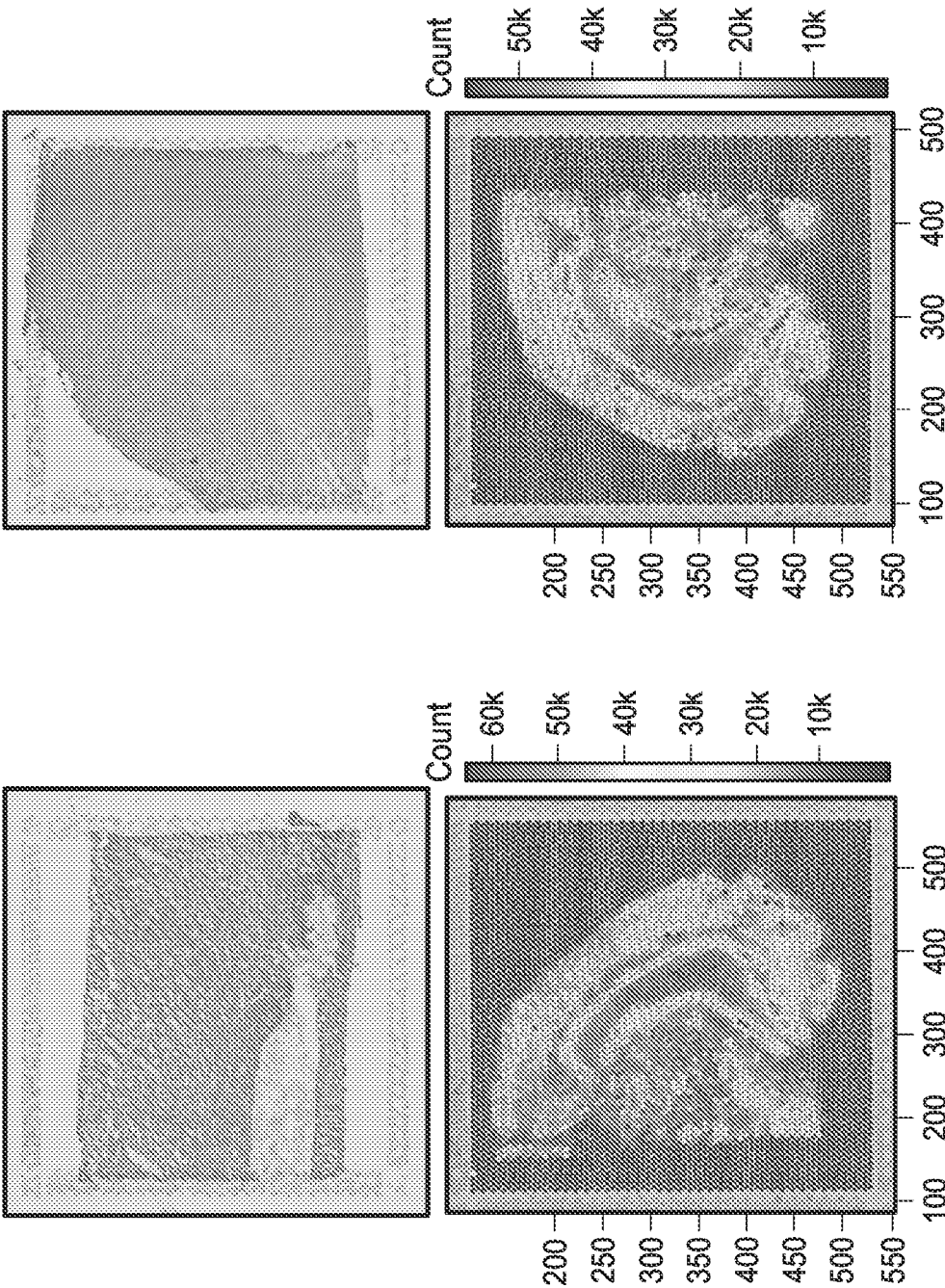


FIG. 17D

FIG. 17C

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2021/034212

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12Q1/68 C40B50/14 G01N1/30
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12Q G01N C40B

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 3 511 423 A1 (SPATIAL TRANSCRIPTOMICS AB [SE]) 17 July 2019 (2019-07-17)	1-11, 13-20, 22-24, 26,29-37
A	abstract, example 6 ----- -/--	25



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search

16 September 2021

Date of mailing of the international search report

27/09/2021

Name and mailing address of the ISA/

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Authorized officer

Lindberg, Pia

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2021/034212

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	10x Genomics: "Visium Spatial Gene Expression Reagent Kits - Tissue Optimization", 1 November 2019 (2019-11-01), pages 1-46, XP055801839, 6230 Stoneridge Mall Road, Pleasanton, CA 94588 USA Retrieved from the Internet: URL:https://assets.ctfassets.net/an68im79xiti/4q03w6959AJFxffSw5lee9/6a2ac61cf6388a72564eeb96bc294967/CG000238_VisiumSpatialTissueOptimizationUserGuide_Rev_A.pdf [retrieved on 2021-05-06]	5-7, 9-11,14, 15,17, 18,26, 29-32
A	pages 10-12, 23 and 34-37 -----	25
X	ZHANG X ET AL: "Stripping custom microRNA microarrays and the lessons learned about probe-slide interactions", ANALYTICAL BIOCHEMISTRY, ACADEMIC PRESS, AMSTERDAM, NL, vol. 386, no. 2, 15 March 2009 (2009-03-15), pages 222-227, XP025942183, ISSN: 0003-2697, DOI: 10.1016/J.AB.2008.12.008 [retrieved on 2009-02-12]	1-12,14, 18-21, 26,27
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X	HU ZHIYUAN ET AL: "High reproducibility using sodium hydroxide-stripped long oligonucleotide DNA microarrays", BIOTECHNIQUES, INFORMA HEALTHCARE, US, vol. 38, no. 1, 1 January 2005 (2005-01-01), pages 121-124, XP002517196, ISSN: 0736-6205, DOI: 10.2144/05381MT02	1-12,14, 15,17, 18,20, 26-28
A	abstract; section "materials and methods" on pages 121-122 -----	25
X	HAHNKE ET AL: "Striptease on glass: Validation of an improved stripping procedure for in situ microarrays", JOURNAL OF BIOTECHNOLOGY, ELSEVIER, AMSTERDAM NL, vol. 128, no. 1, 23 December 2006 (2006-12-23), pages 1-13, XP005734676, ISSN: 0168-1656, DOI: 10.1016/J.JBIOTEC.2006.09.003	1-20,22, 24,26,27
A	abstract; sections 2.2 and 2.5 on pages 3 and 5 -----	25

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2021/034212

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			DK 3511423 T3 07-06-2021
			EP 2909337 A1 26-08-2015
			EP 3511423 A1 17-07-2019
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			WO 2014060483 A1 24-04-2014
