

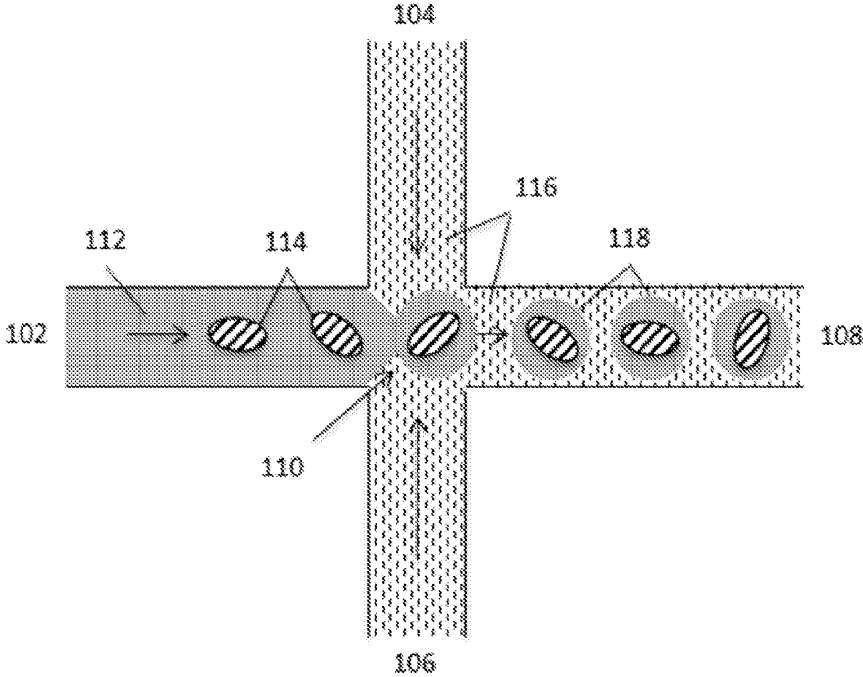


FIG. 1

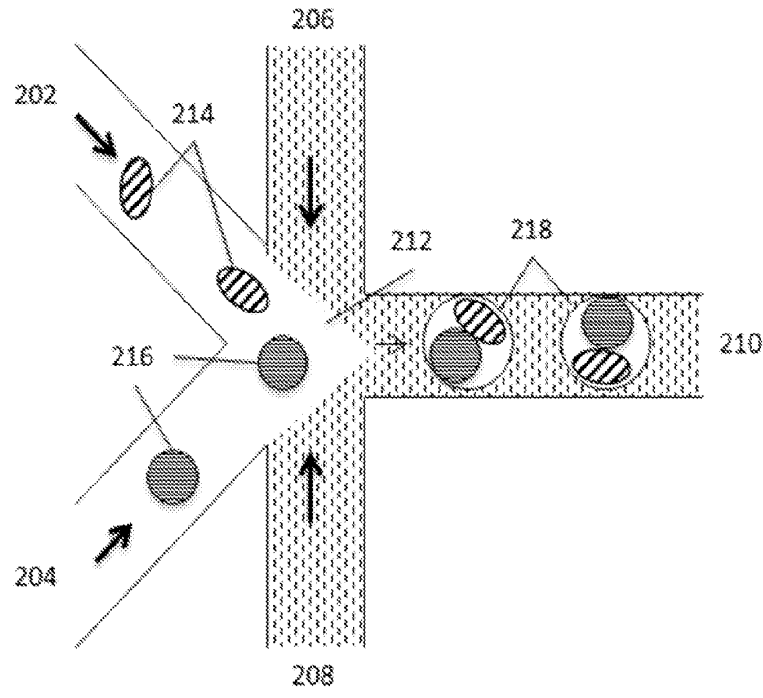


FIG. 2

FIG. 3A

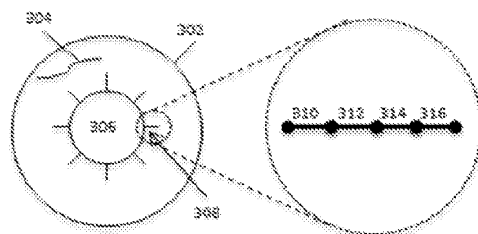


FIG. 3B



FIG. 3C

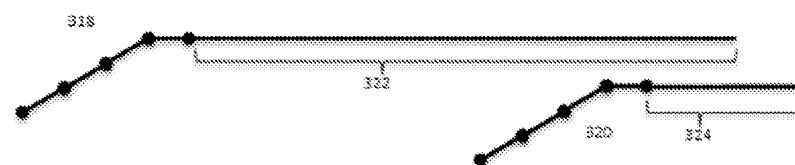


FIG. 3D

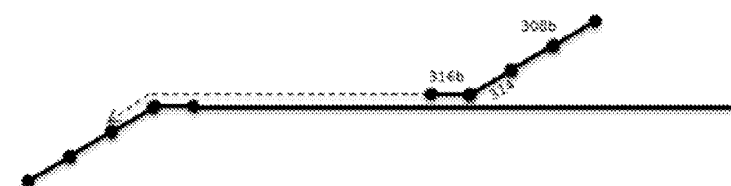
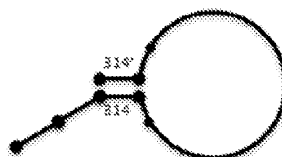


FIG. 3E



FIG. 3F



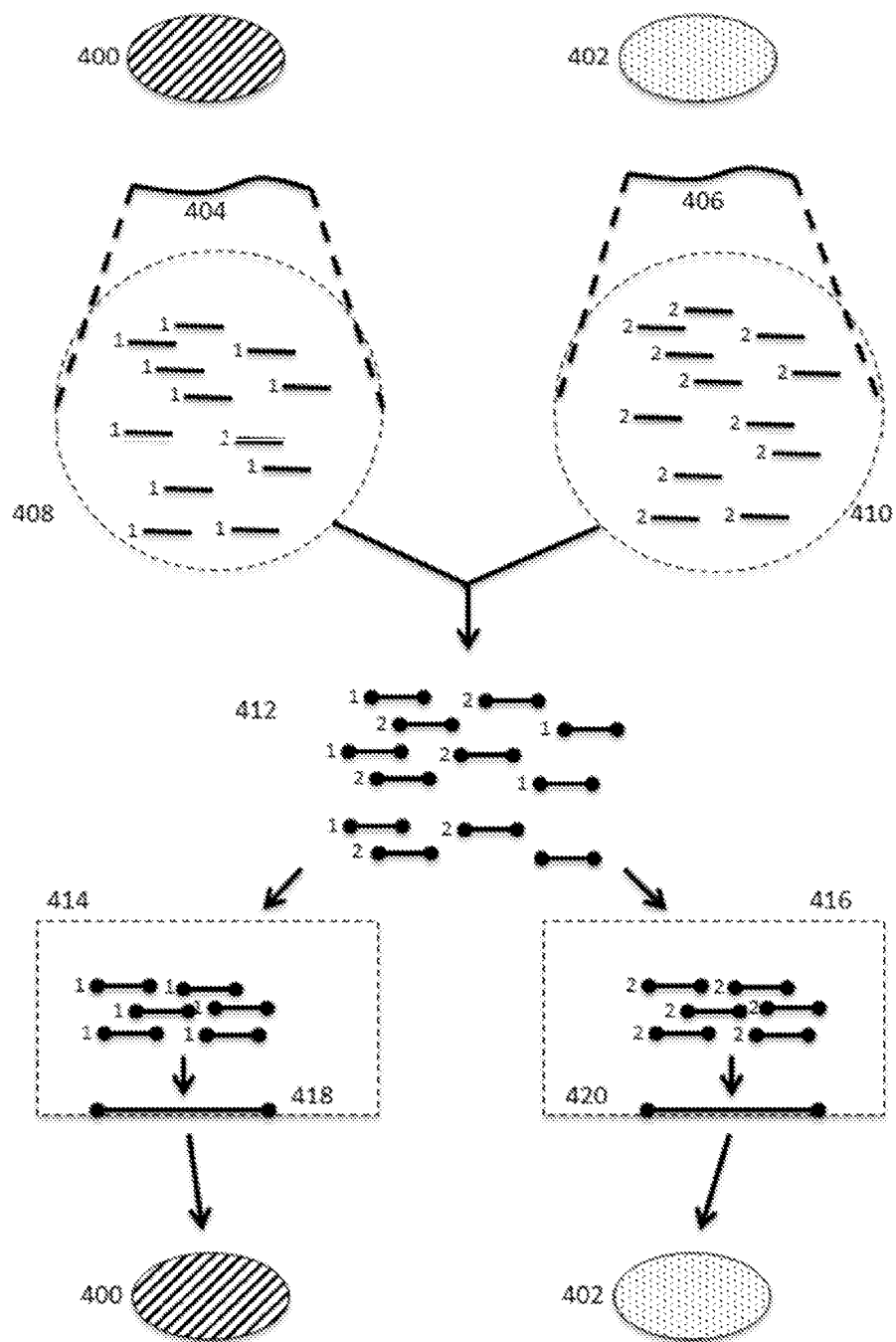


FIG. 4

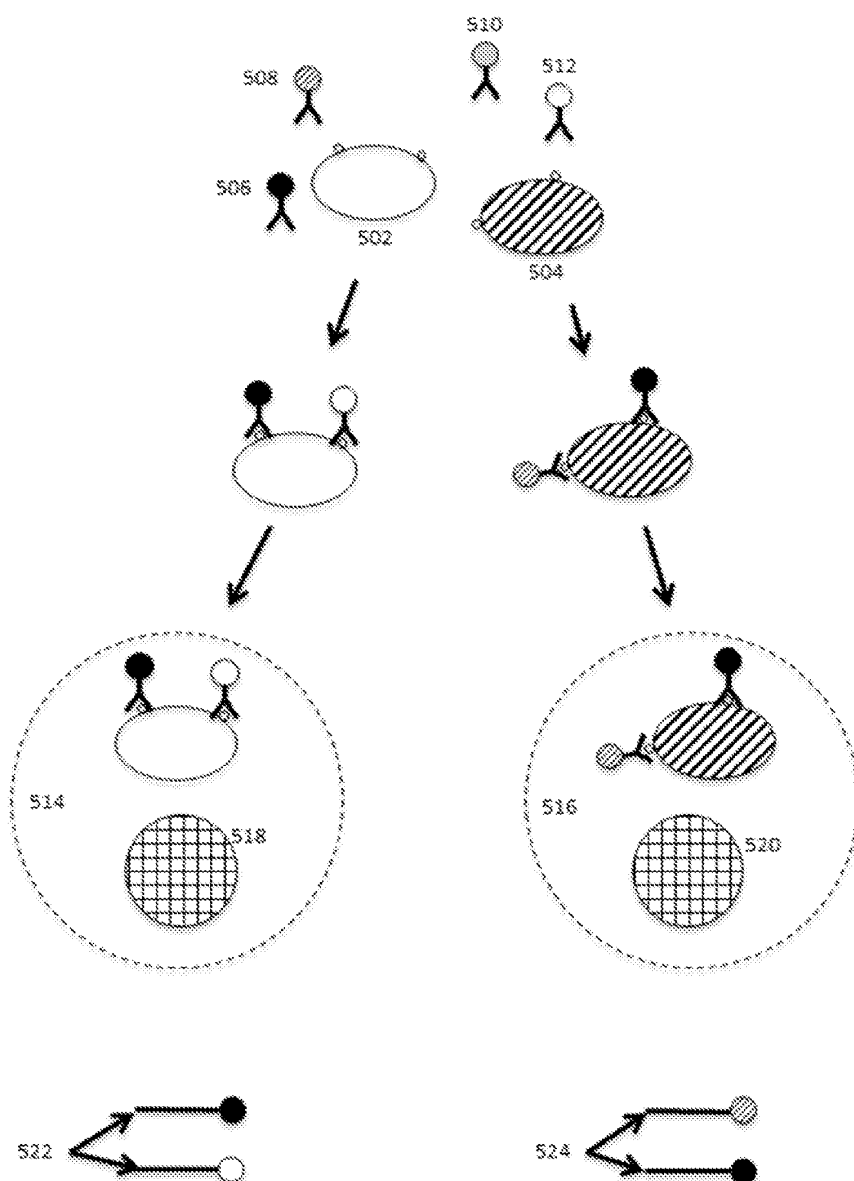


FIG. 5

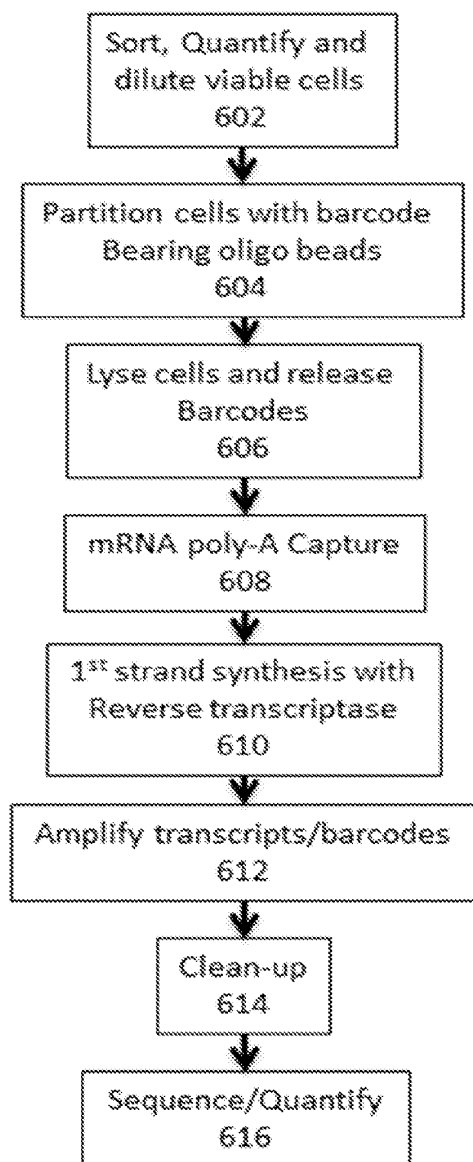


FIG. 6

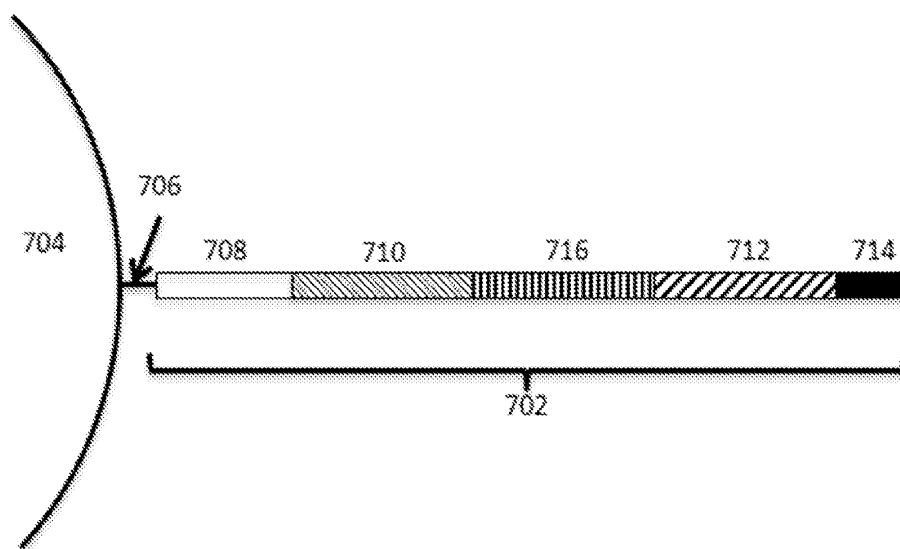


FIG. 7

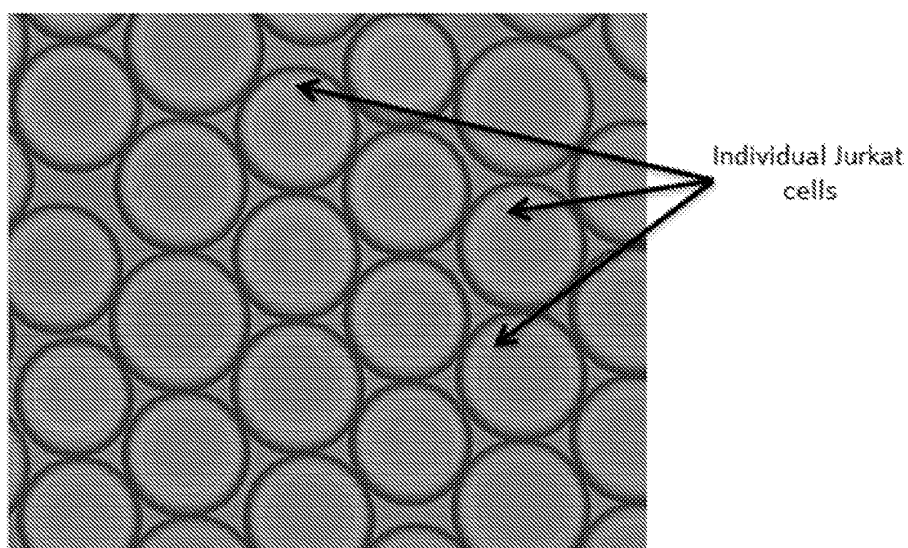
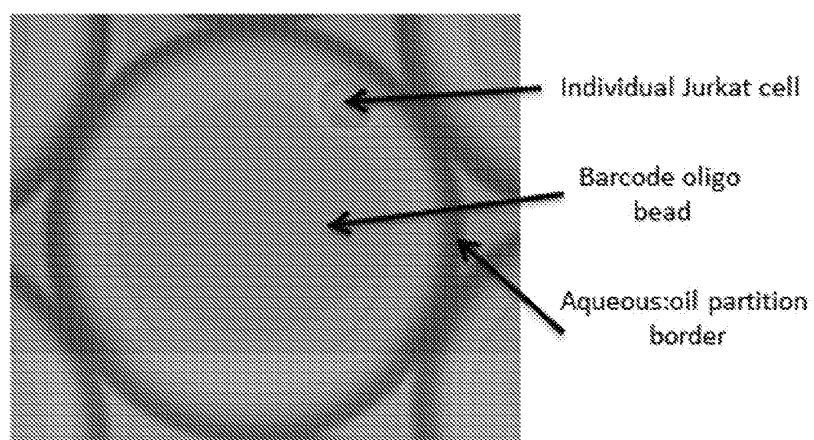


FIG. 8

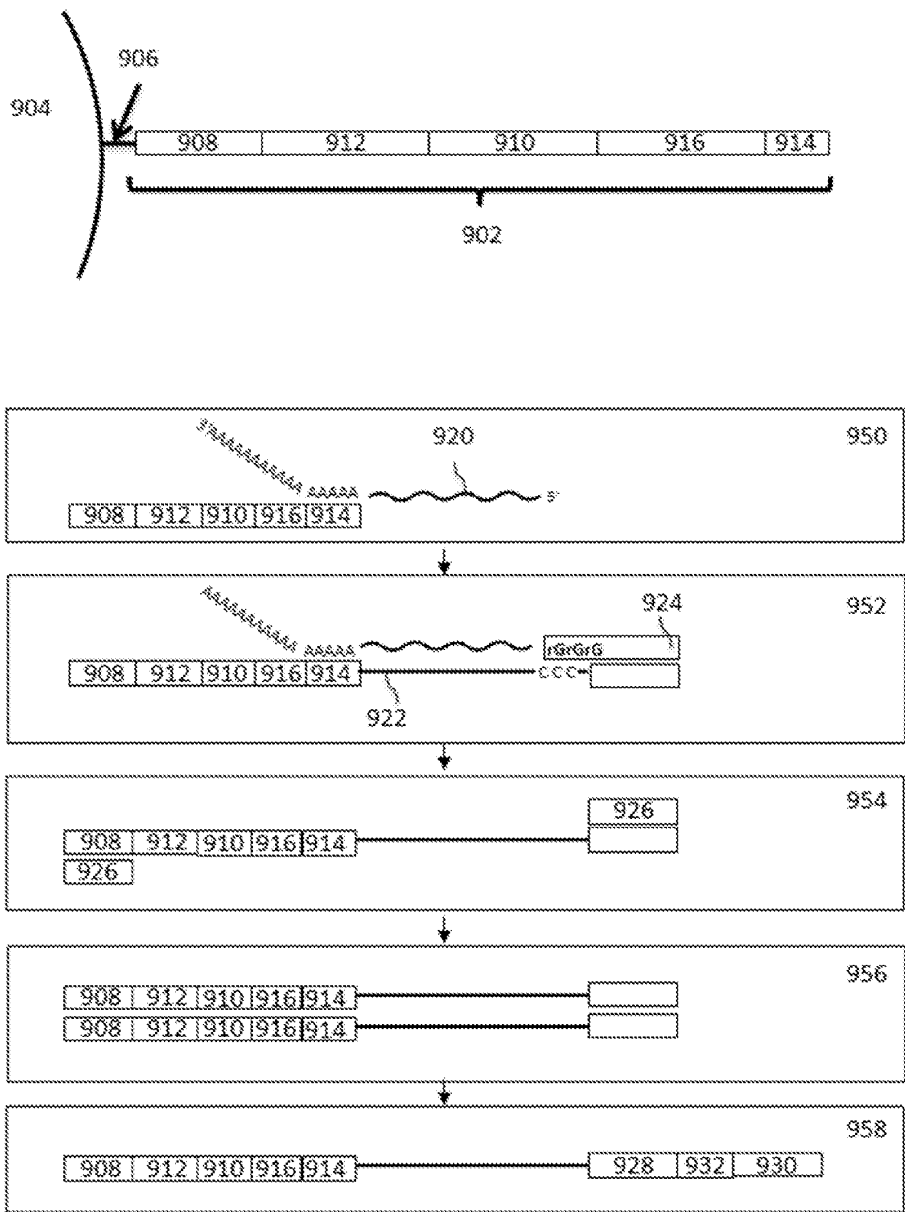


FIG. 9A

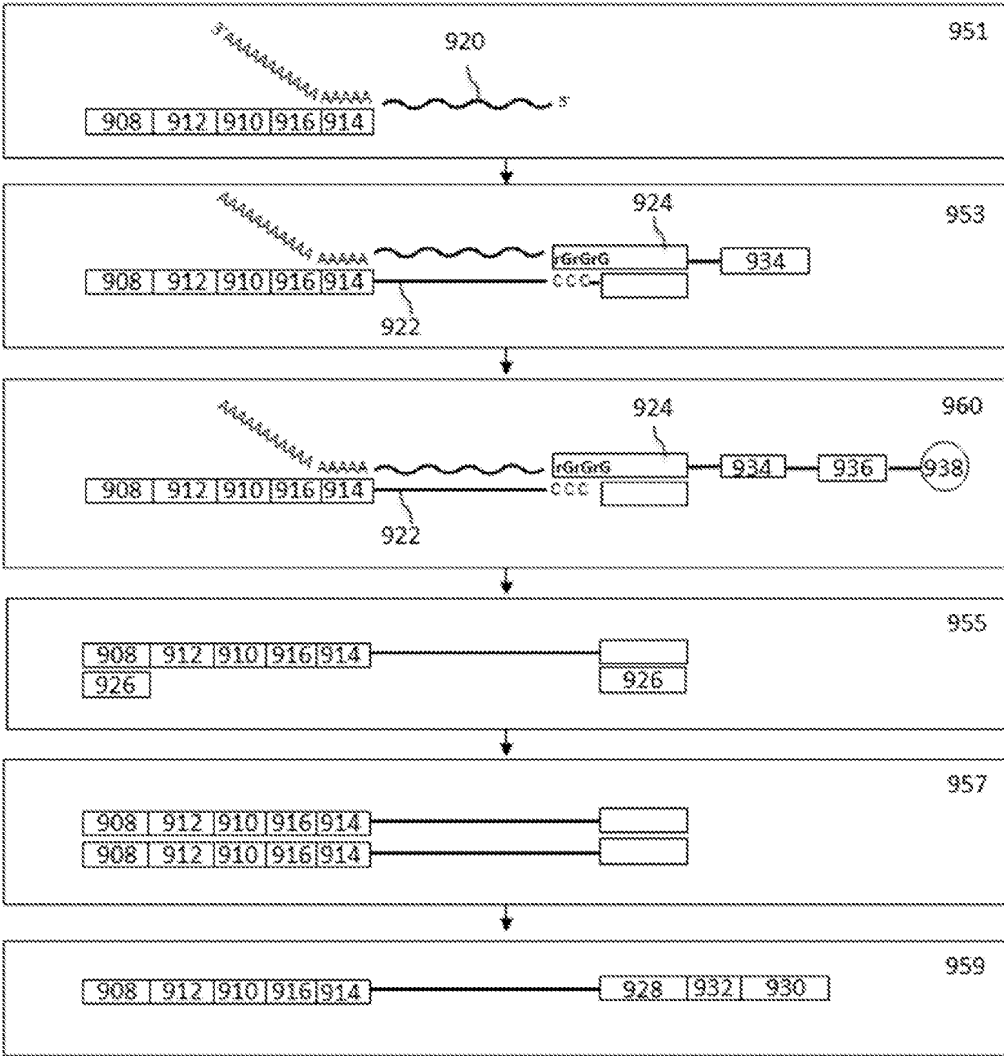


FIG. 9B

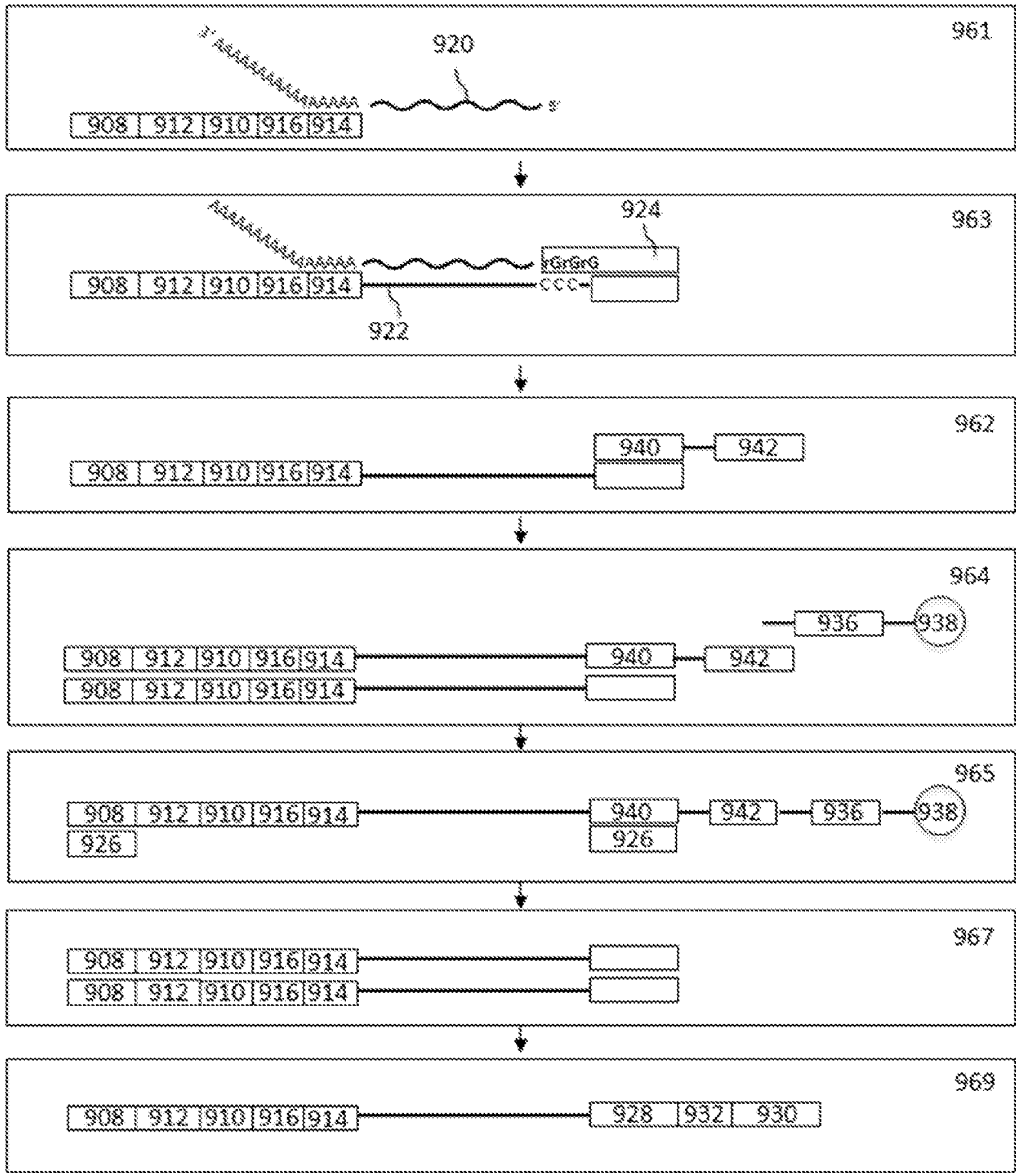


FIG. 9C

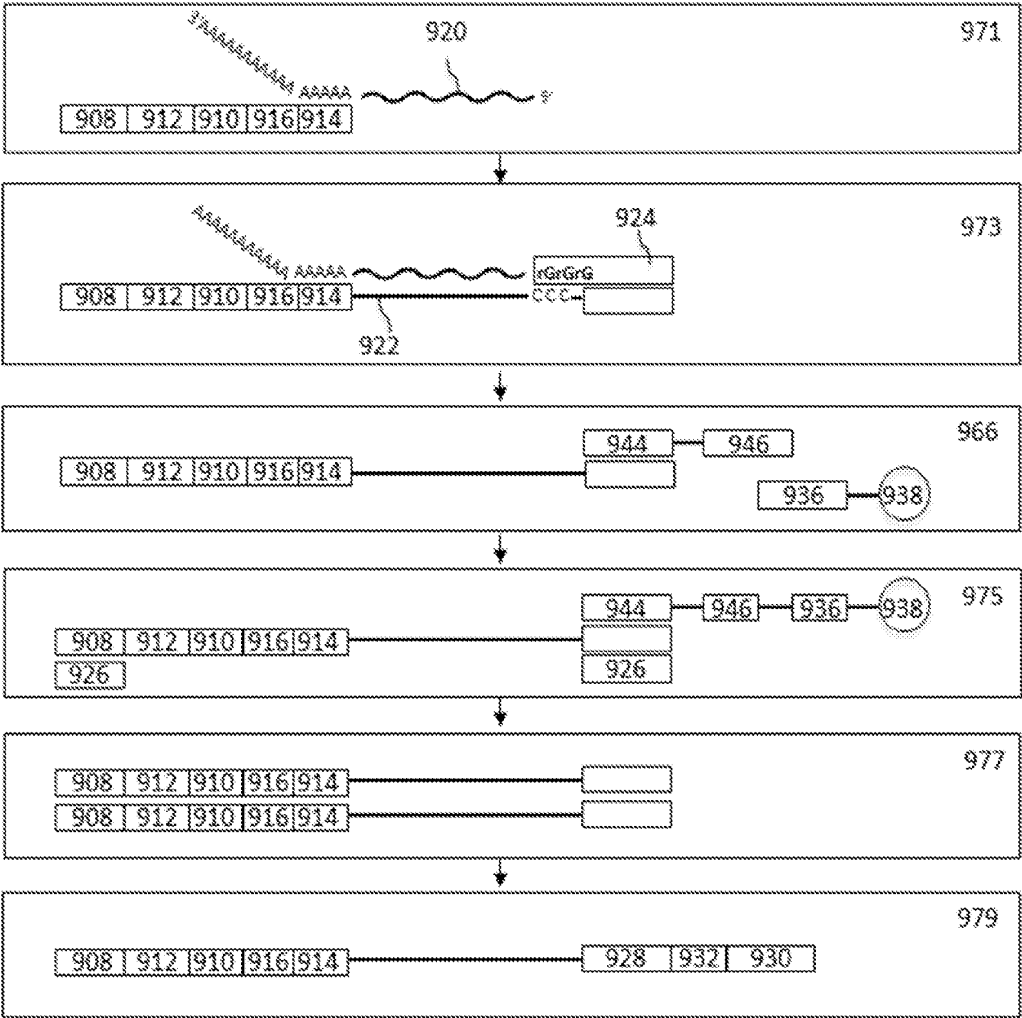


FIG. 9D

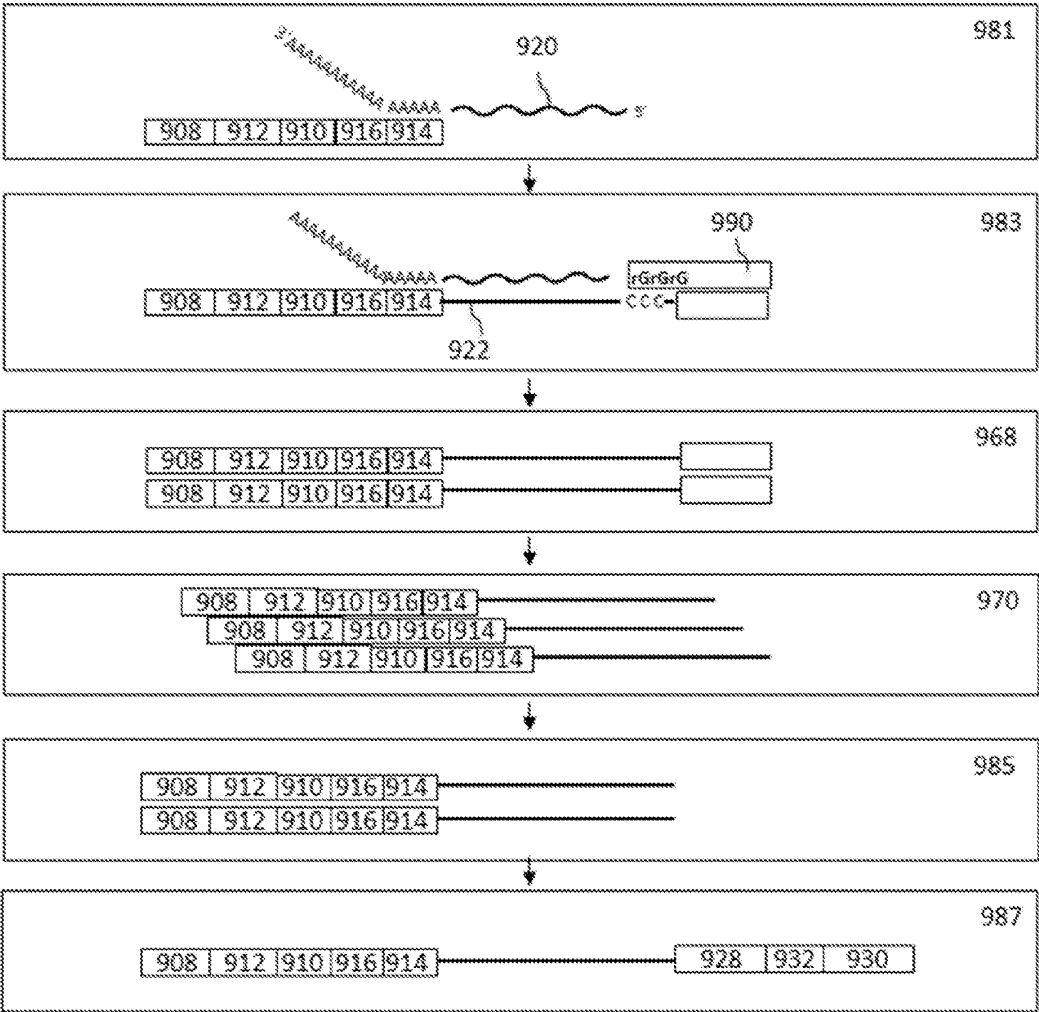


FIG. 9E

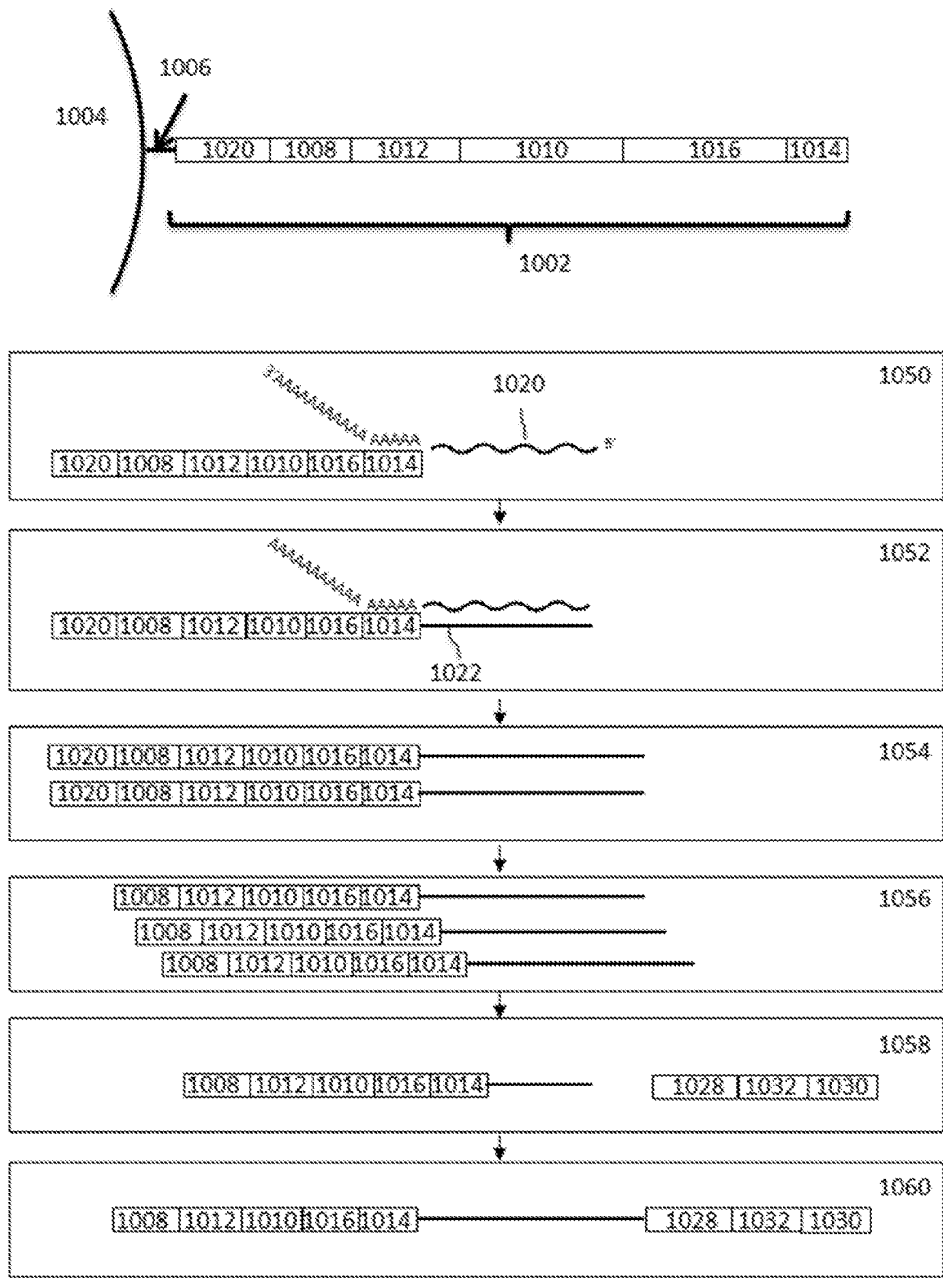


FIG. 10

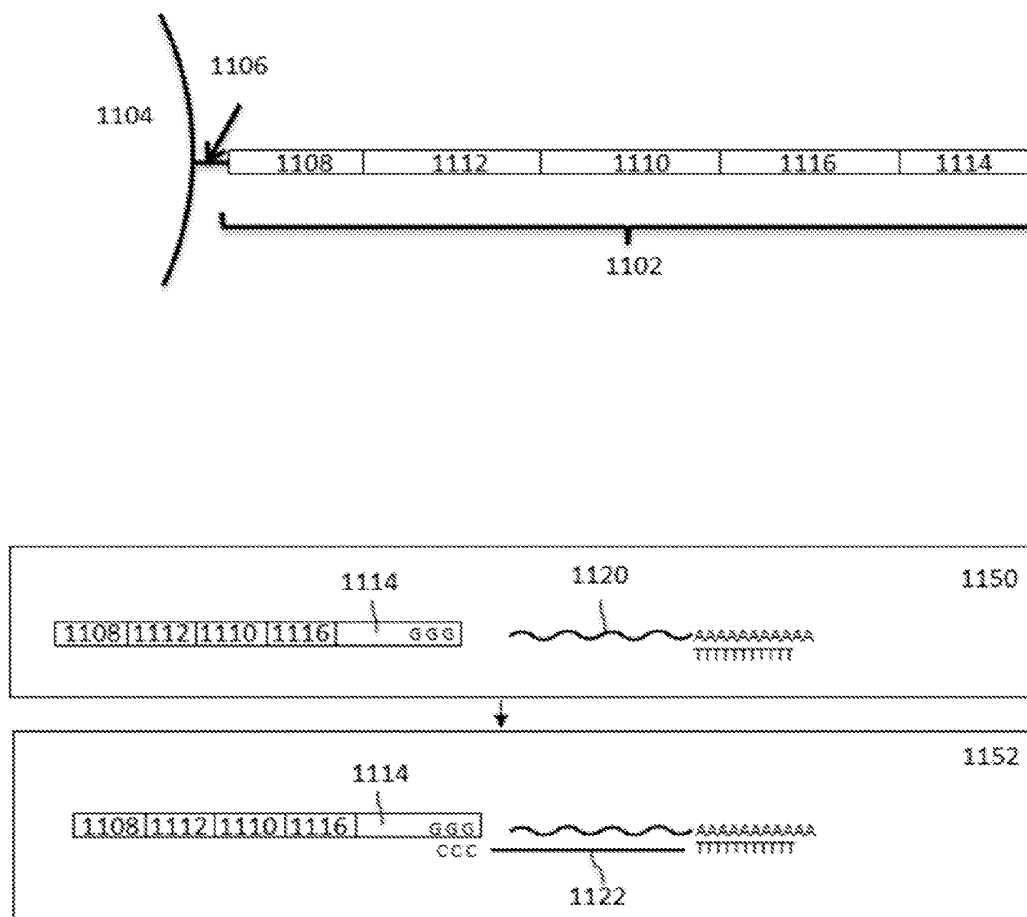


FIG. 11

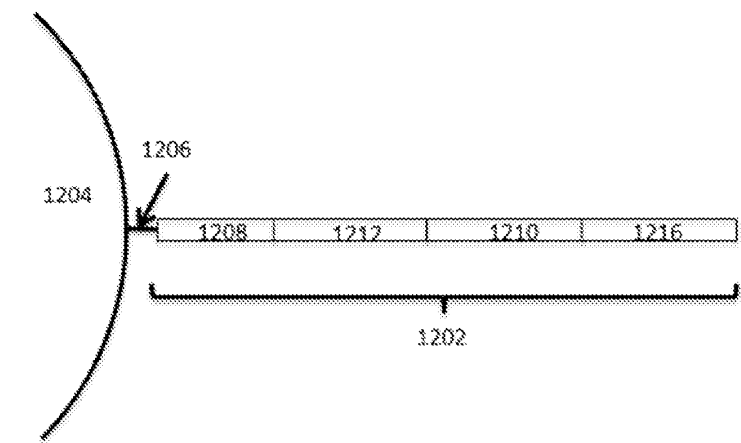


FIG. 12A

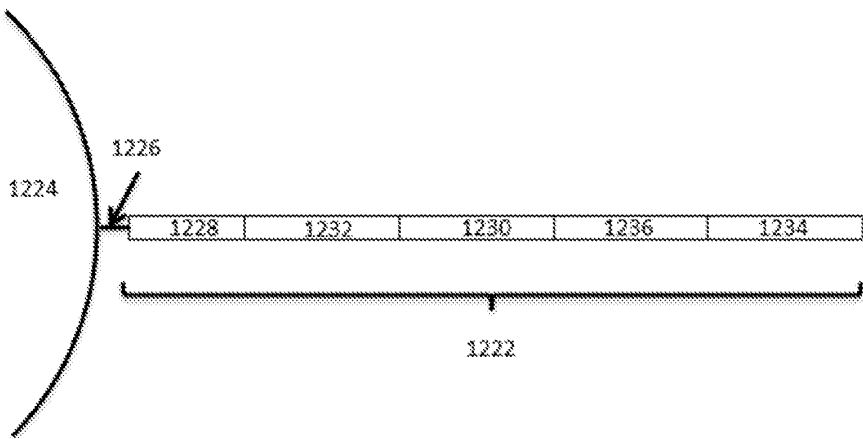


FIG. 12B

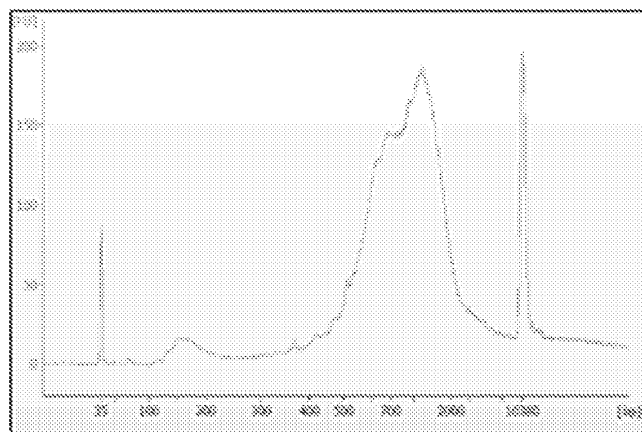


FIG. 13A

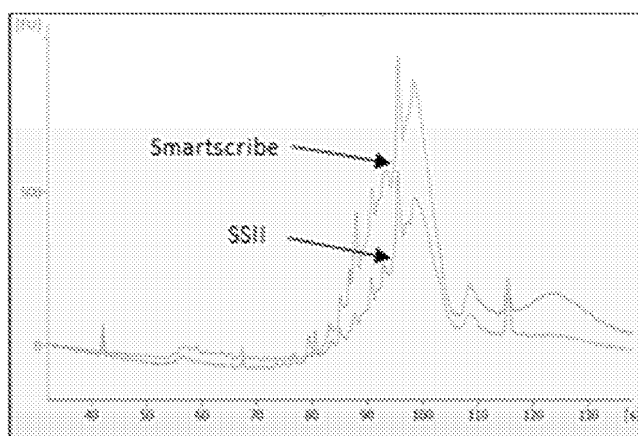


FIG. 13B

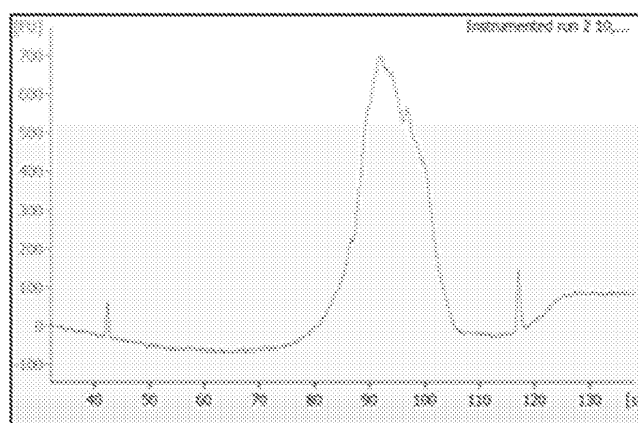


FIG. 13C

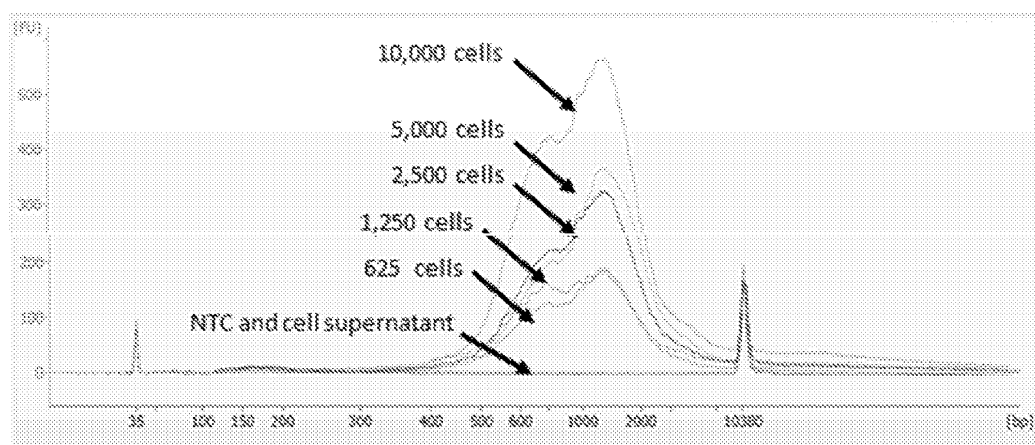


FIG. 14A

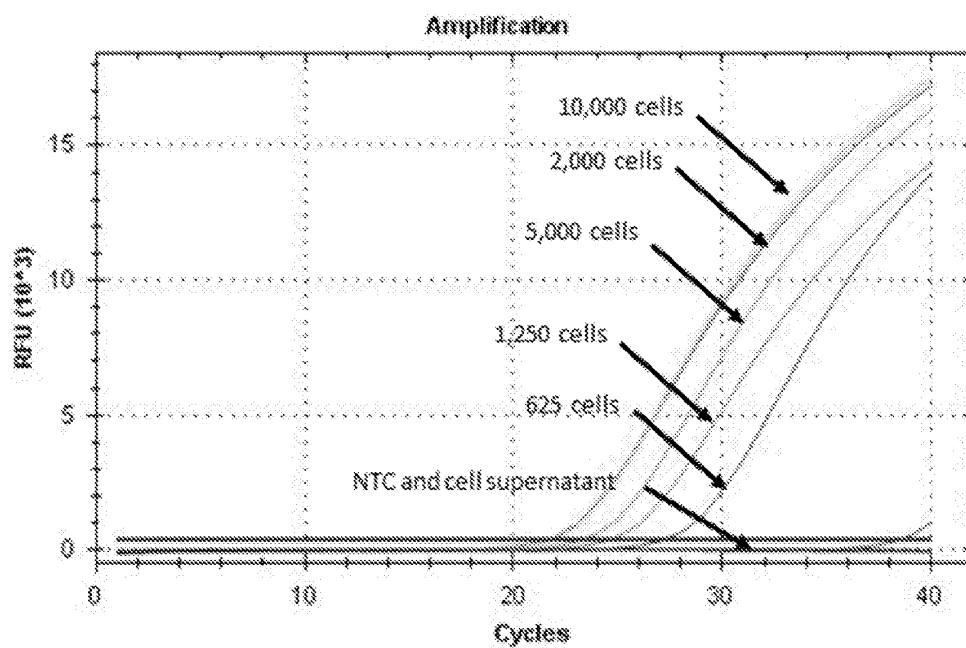


FIG. 14B

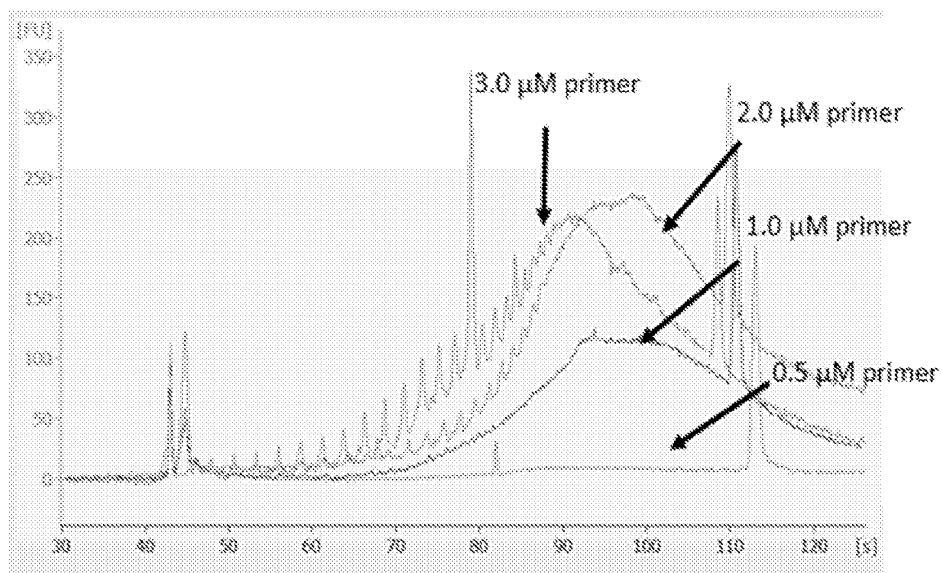


FIG. 15

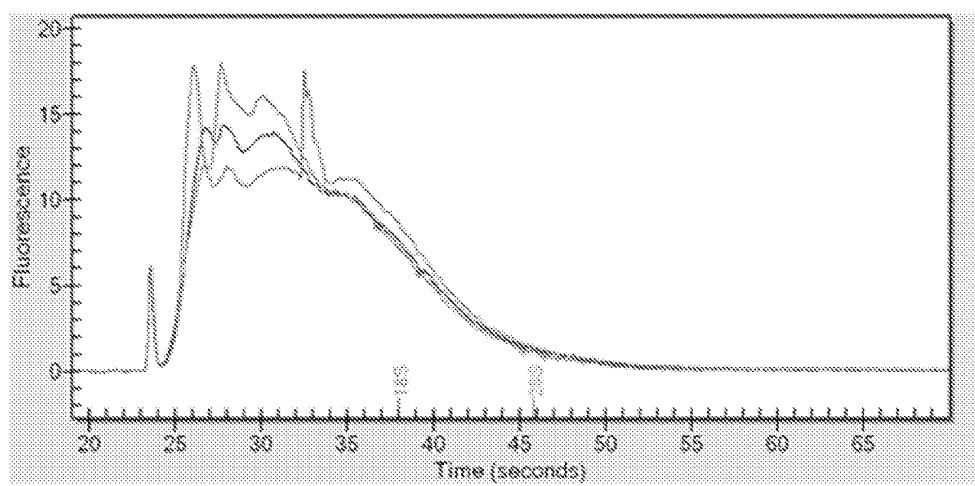


FIG. 16

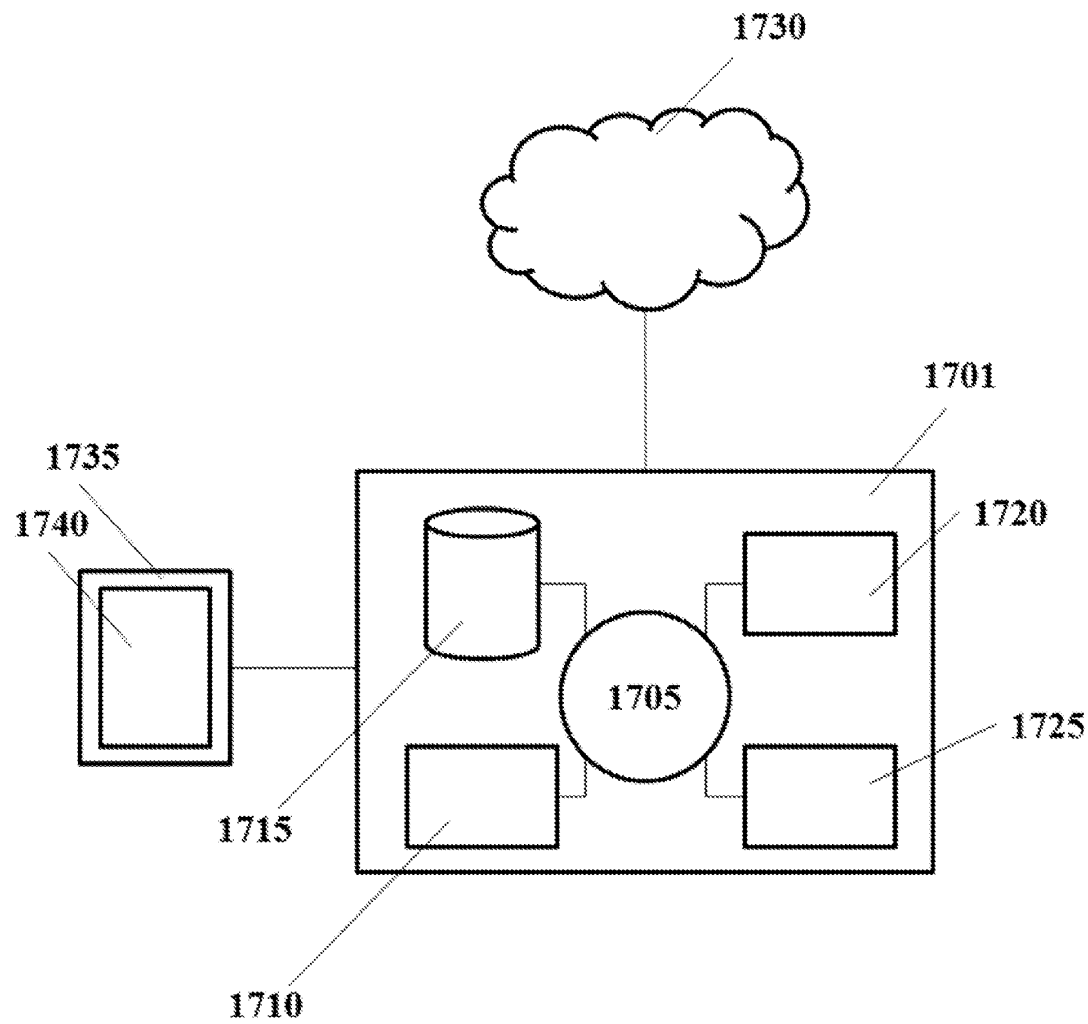


FIG. 17

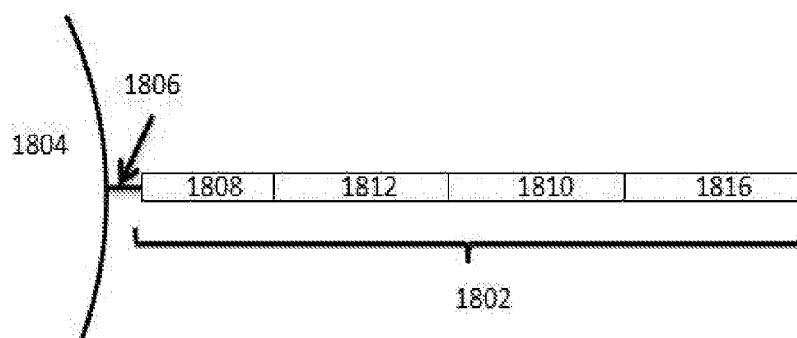


FIG. 18

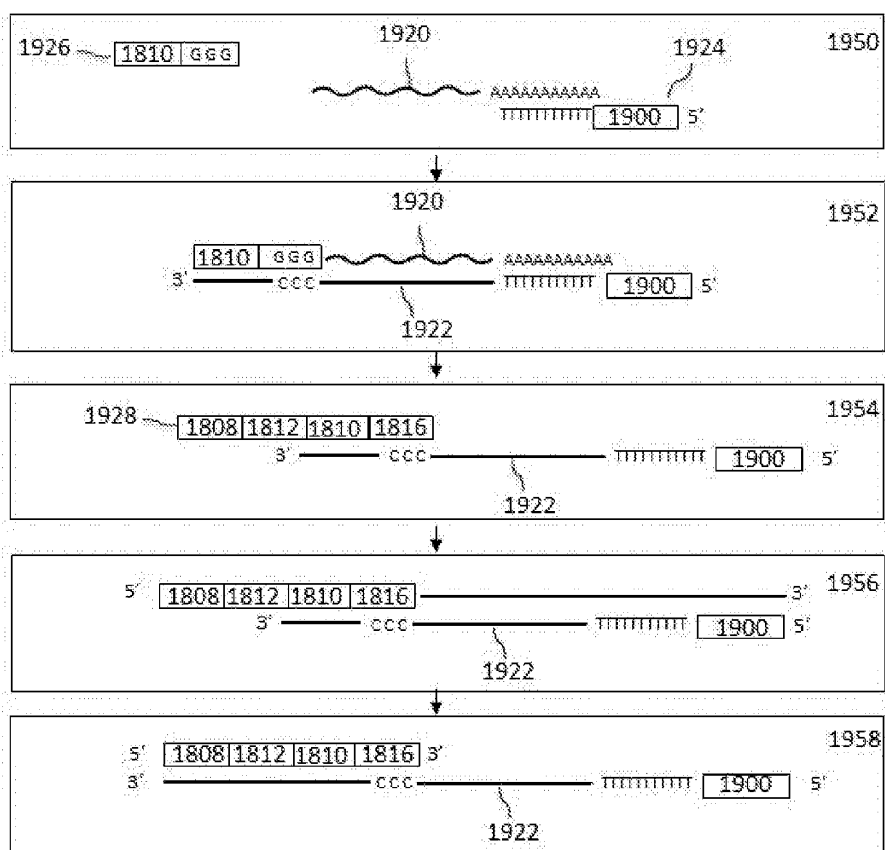


FIG. 19

2000



Providing a partition comprising a cell and at least one labeling agent, wherein said at least one labeling agent is (i) capable of binding to a cell surface feature of said cell and (ii) is coupled to a reporter oligonucleotide comprising a nucleic acid barcode sequence that permits identification of said at least one labeling agent, wherein said partition comprises an anchor oligonucleotide that is capable of interacting with said reporter oligonucleotide barcode;

2010

In said partition, synthesizing a nucleic acid molecule comprising at least a portion of said nucleic acid barcode sequence or a complement thereof;

2020

Subjecting said nucleic acid molecule to sequencing to identify said labeling agent or said cell.

2030

FIG. 20

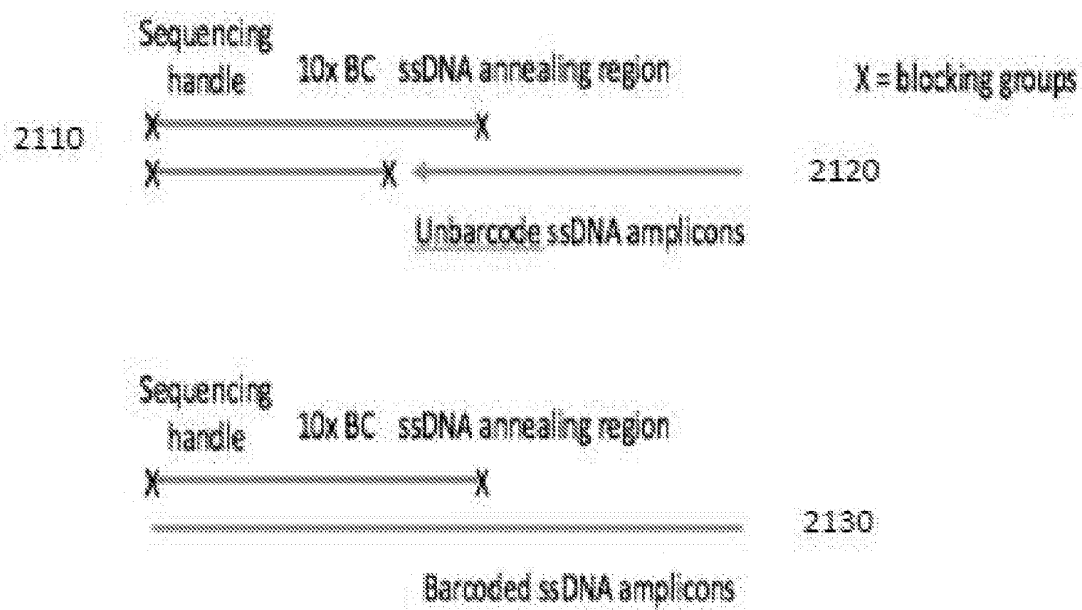


FIG. 21

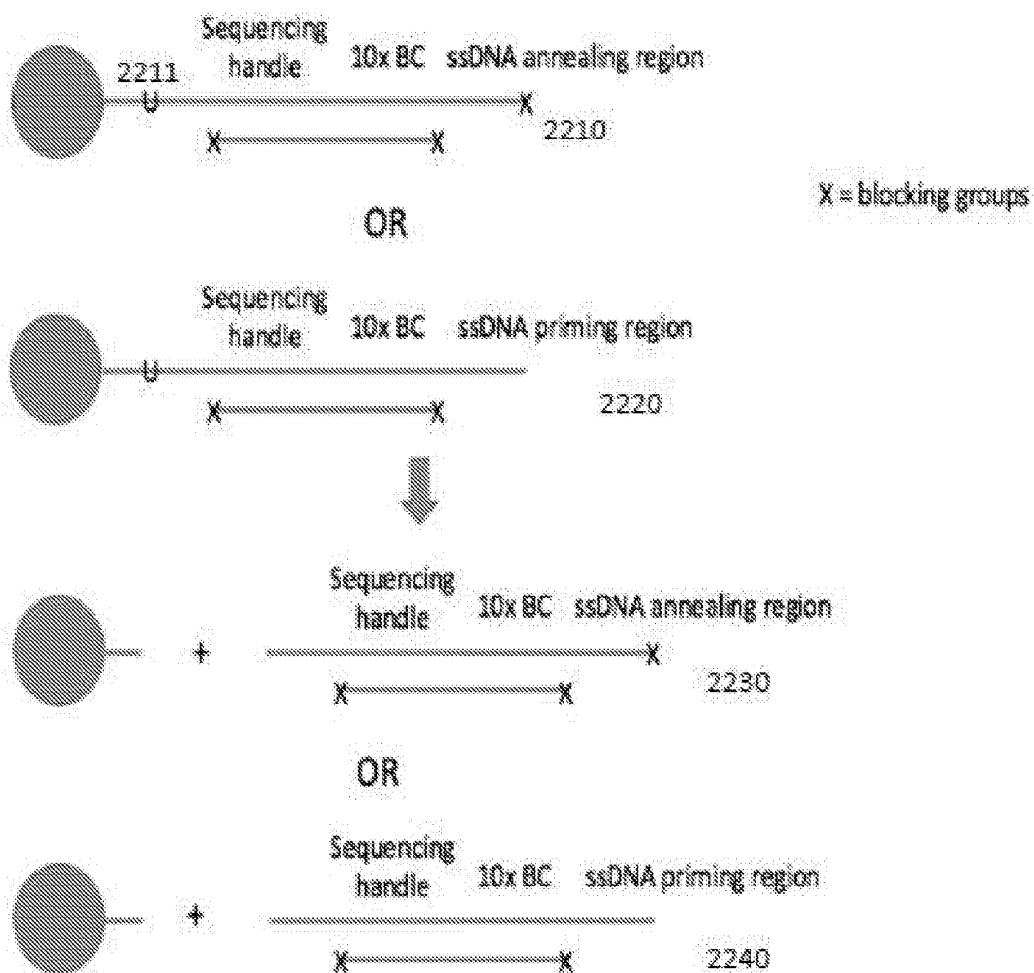


FIG. 22

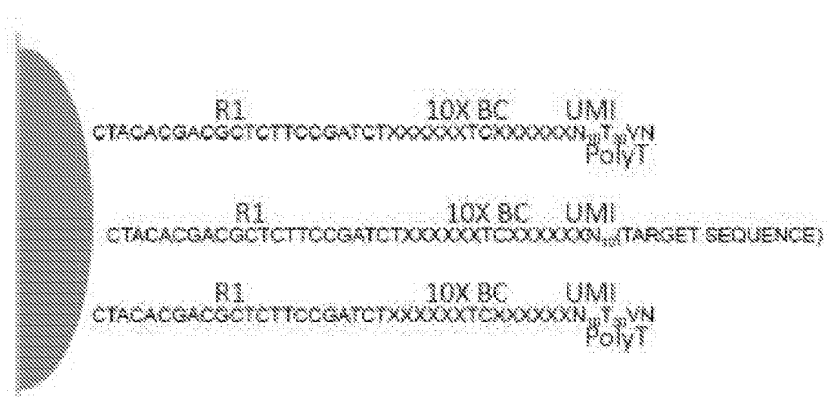


FIG. 23A

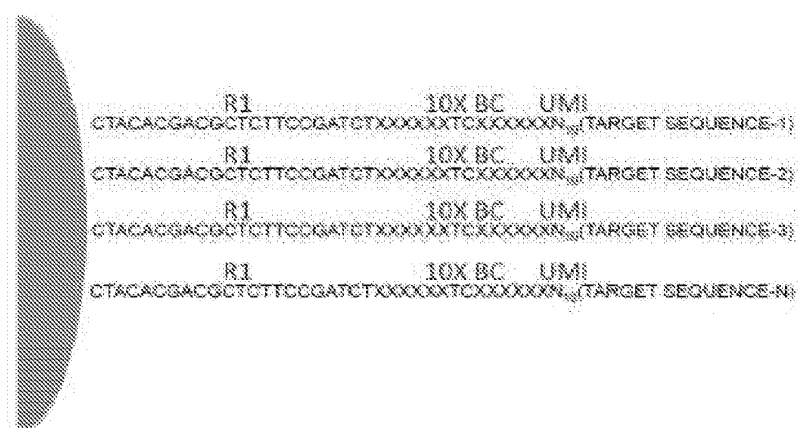


FIG. 23B

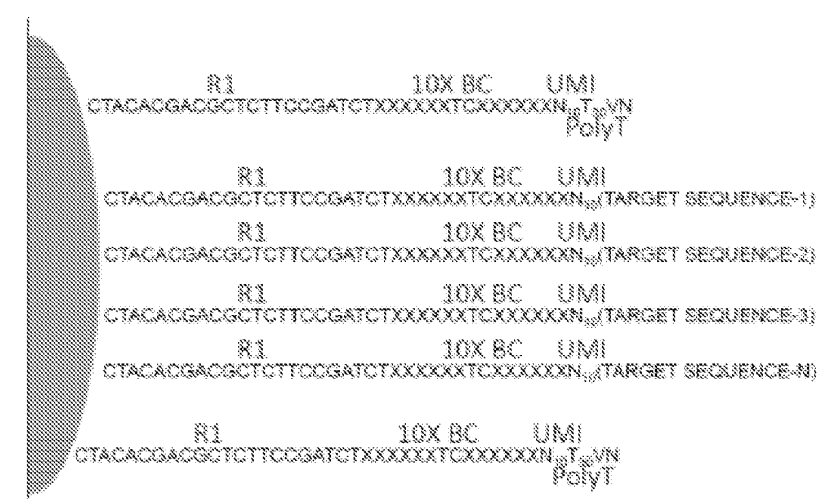


FIG. 23C

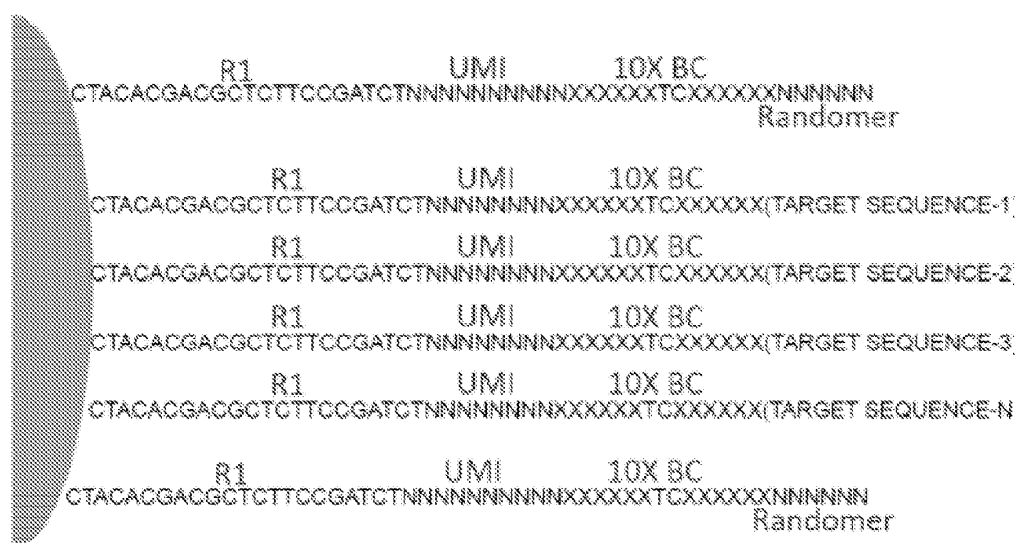


FIG. 24

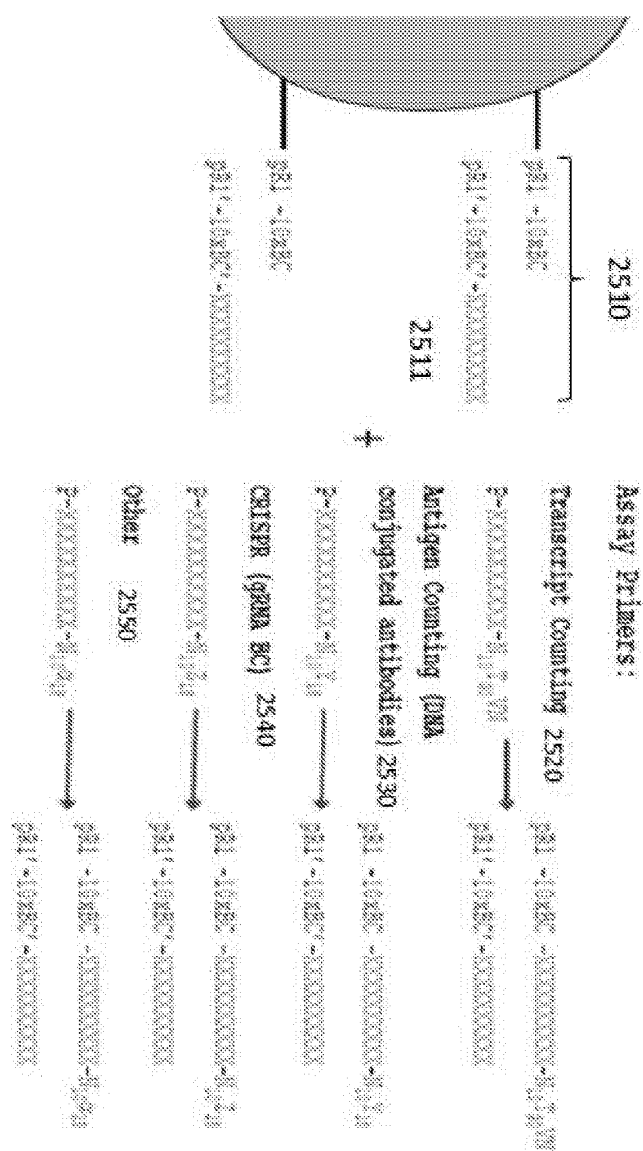


FIG. 25A

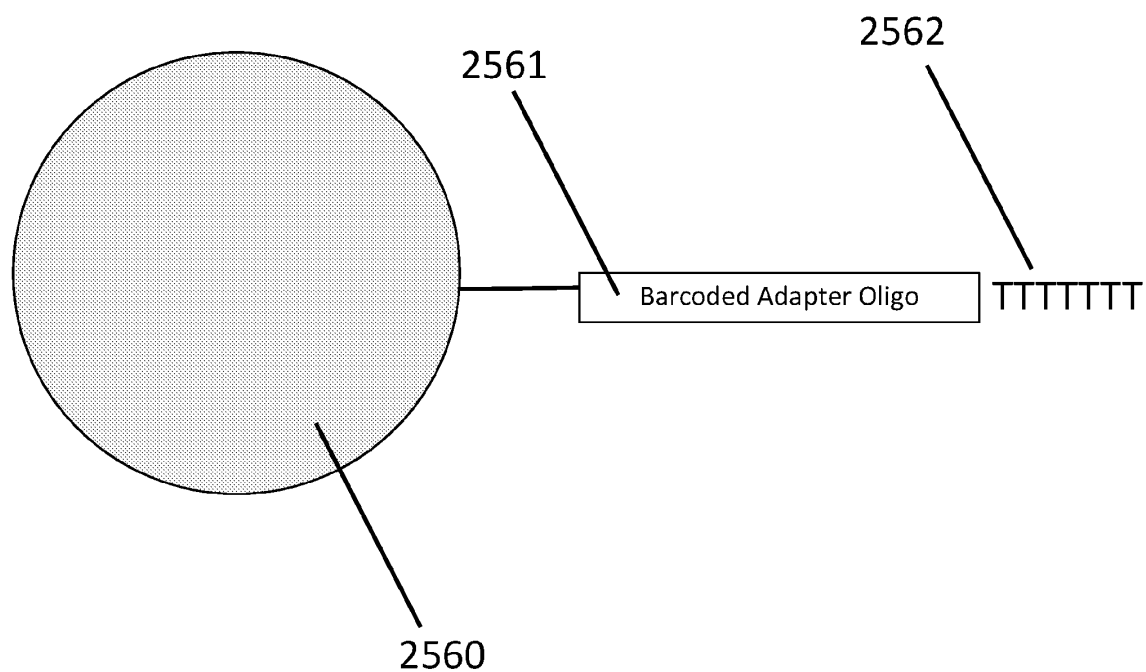


FIG. 25B

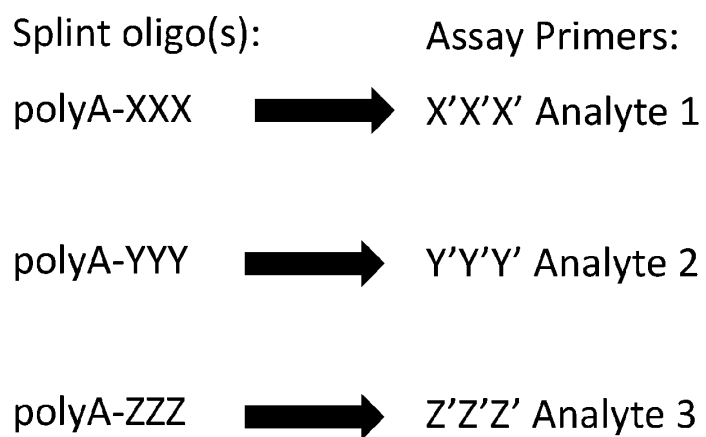


FIG. 25C

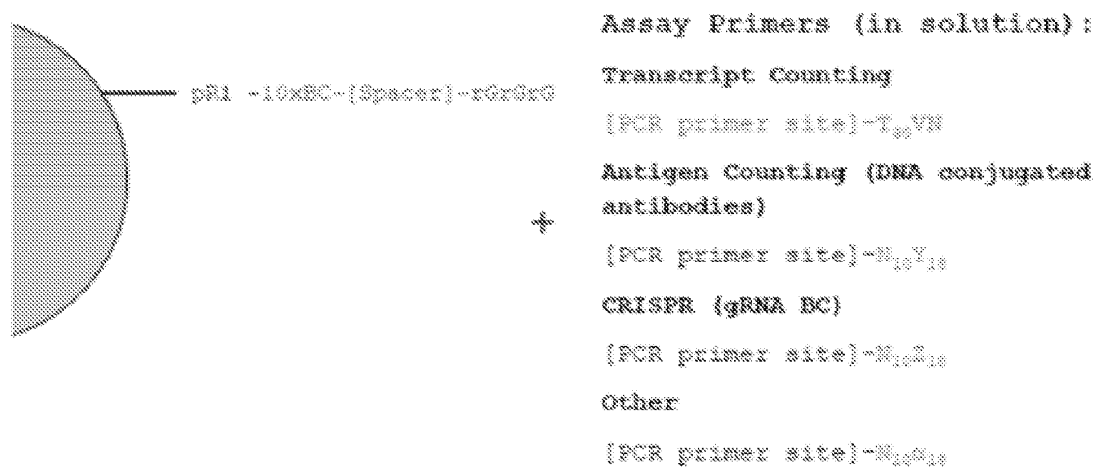


FIG. 26

**Alpha**  
CAAGCAGAAGACGGGCATACGAGATXXXXXXXXGTXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN<sub>10</sub>T<sub>10</sub>VN  
GCCGTATGCTCTAXXXXXXXXCAXXXXXXXXCACTGACCTCAAGTCTGCACACGAGAAGGCTAGA

**Beta**  
CAAGCAGAAGACGGGCATACGAGATXXXXXXXXCAXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN<sub>10</sub>T<sub>10</sub>VN  
GCCGTATGCTCTAXXXXXXXXGTXXXXXXXXCACTGACCTCAAGTCTGCACACGAGAAGGCTAGA

**Gamma**  
CAAGCAGAAGACGGGCATACGAGATXXXXXXXXAGXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN<sub>10</sub>T<sub>10</sub>VN  
GCCGTATGCTCTAXXXXXXXXTCXXXXXXXXCACTGACCTCAAGTCTGCACACGAGAAGGCTAGA

**Delta**  
CAAGCAGAAGACGGGCATACGAGATXXXXXXXXTCXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN<sub>10</sub>T<sub>10</sub>VN  
GCCGTATGCTCTAXXXXXXXXAGXXXXXXXXCACTGACCTCAAGTCTGCACACGAGAAGGCTAGA



FIG. 27A

## Alpha

CTACACGACGCTCTTCCGATCTXXXXXXXXGTXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXCAXXXXXX

## Beta

CTACACGACGCTCTTCCGATCTXXXXXXXXCAXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXGTXXXXXX

## Gamma

CTACACGACGCTCTTCCGATCTXXXXXXXXAGXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXTCXXXXXX

## Delta

CTACACGACGCTCTTCCGATCTXXXXXXXXTCXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXAGXXXXXX

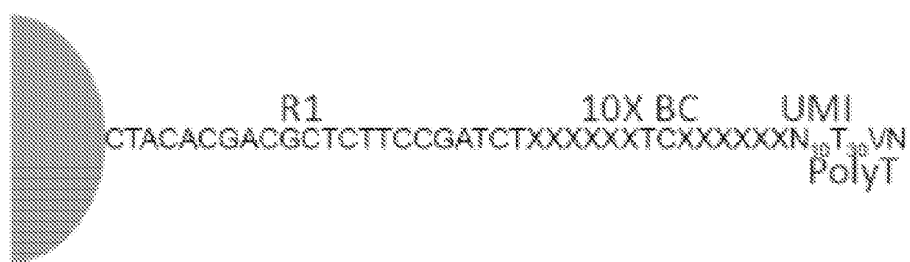


FIG. 27B

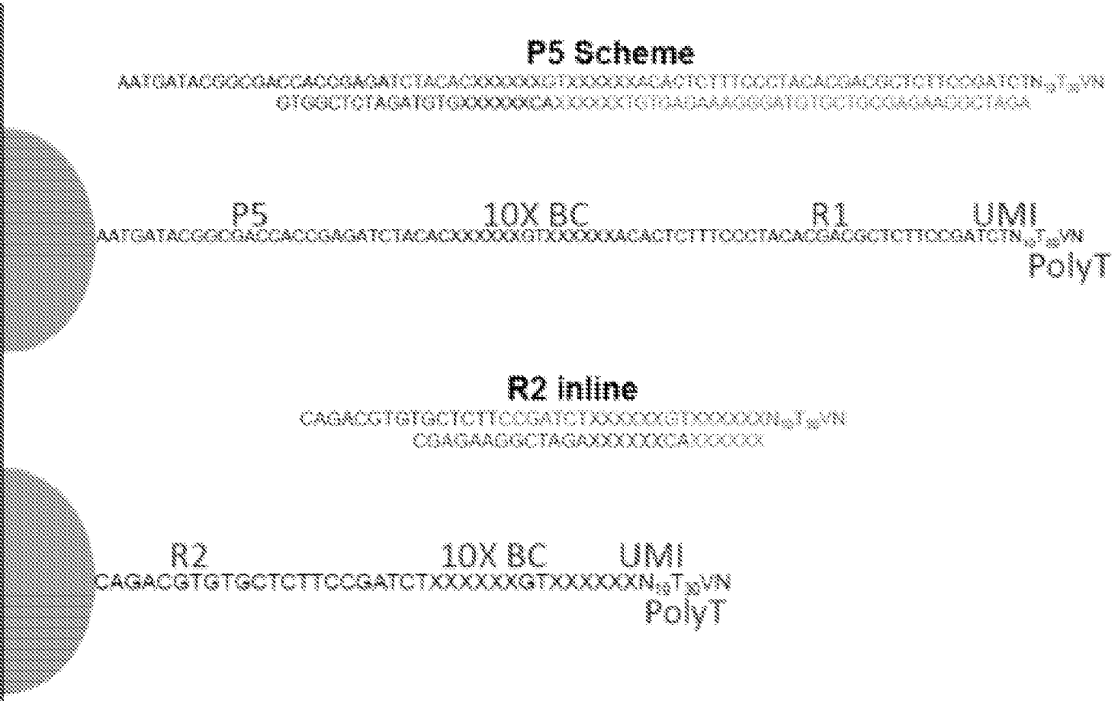


FIG. 27C

CTACACGACGCTCTTCCGATCTNNNNNNNNNNNXXXXXXXXXXSTXXXXXGGGGGGNN  
GCGAGAAGGCTAGA CAXXXX

CTACACGACGCTCTTCCGATCTNNNNNNNNNNNNXXXXXXCAXXXXXXNNNNNN  
GCGAGAAGGCTAGA GTXXXXXX

CTACACGACGCTCTTCGATCTNNNNNNNNNNNNXXXXXAGXXXXNNNNNNN  
GCGAGAAAGGCTAGA TXXXXXX

CTACACGACGCTCTTCGATCTNNNNNNNNNNNNXXXXXXTCXXXXNNNNNN  
GCGAGAAAGCTAGA AGXXXXXX

CTACACGACGCTCTCCGATCTNNNNNNNNNNNNNNXXXXXXTCCCCXXNNNNNN

Randomer

FIG. 27D

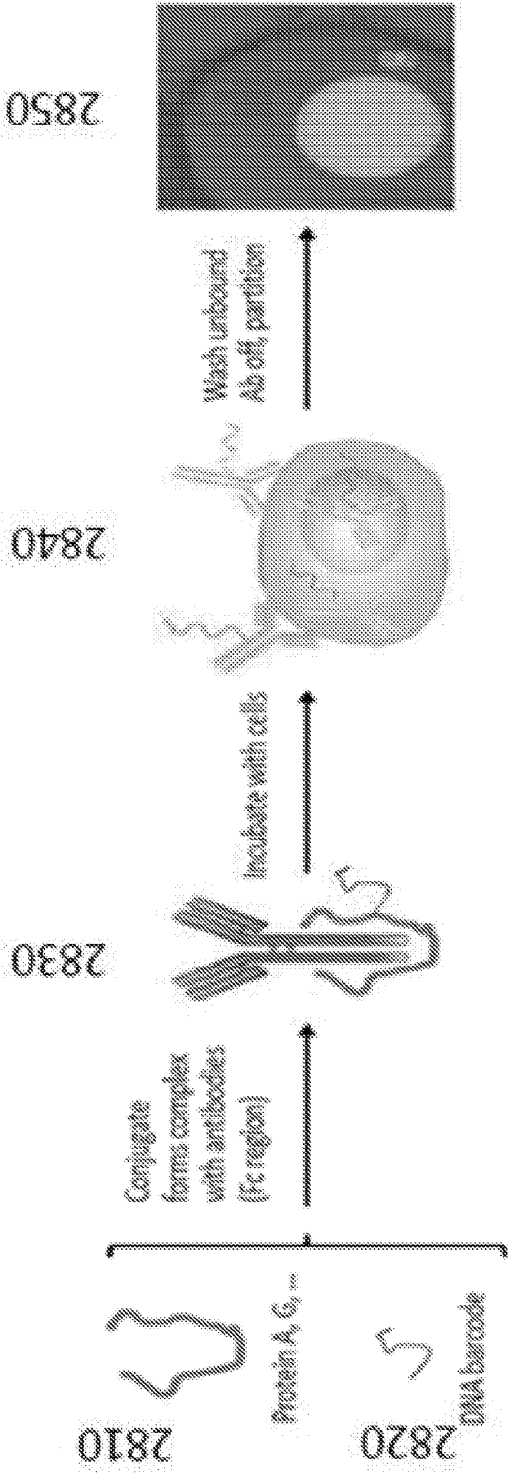


FIG. 28

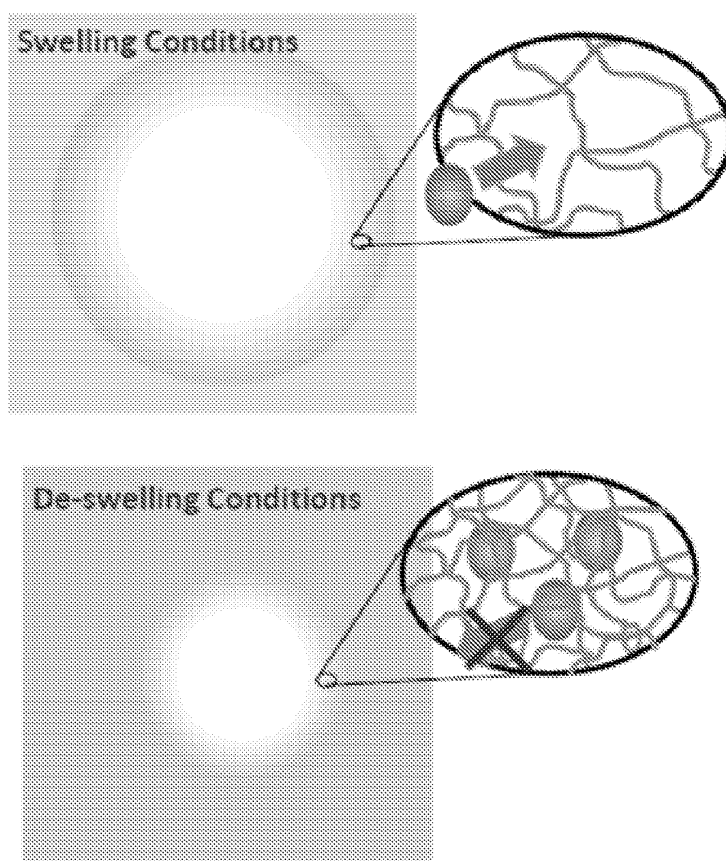


FIG. 29

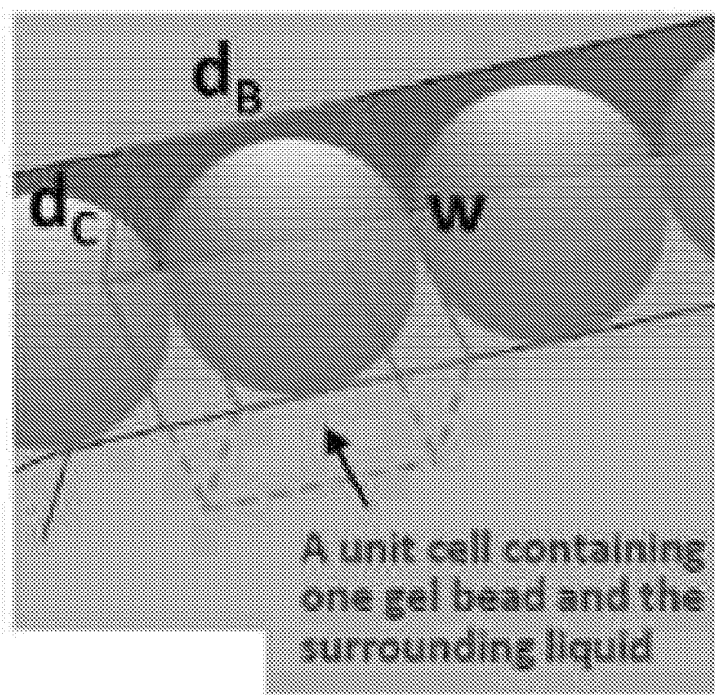


FIG. 30

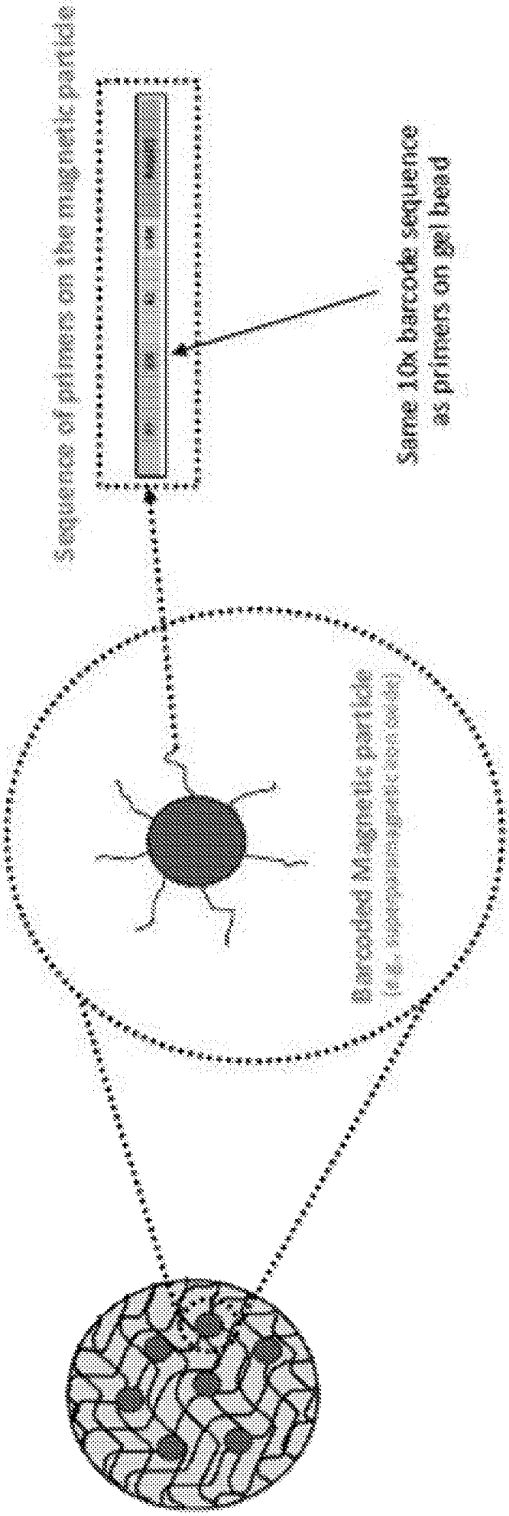


FIG. 31

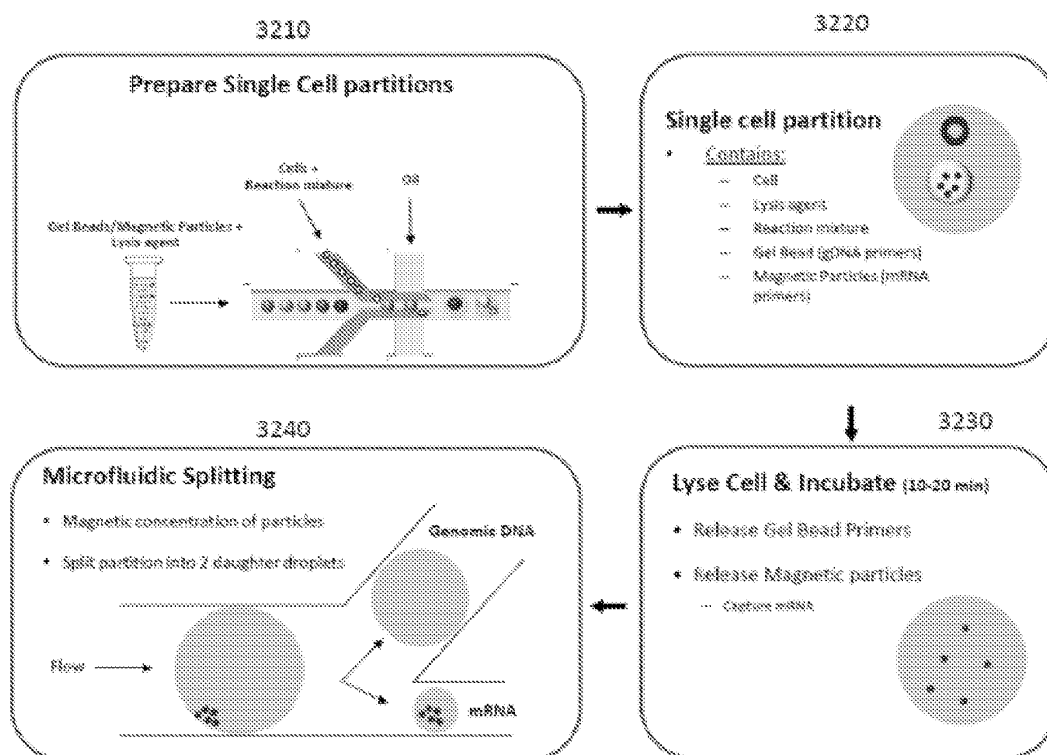


FIG. 32

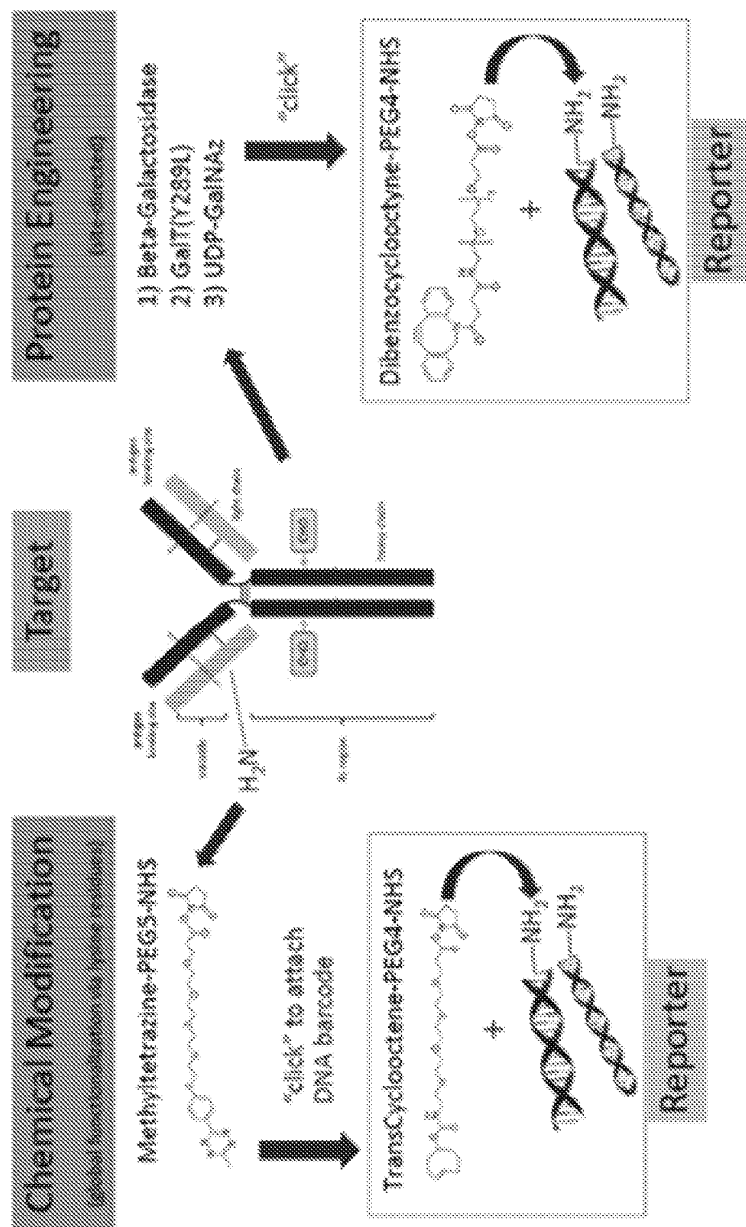
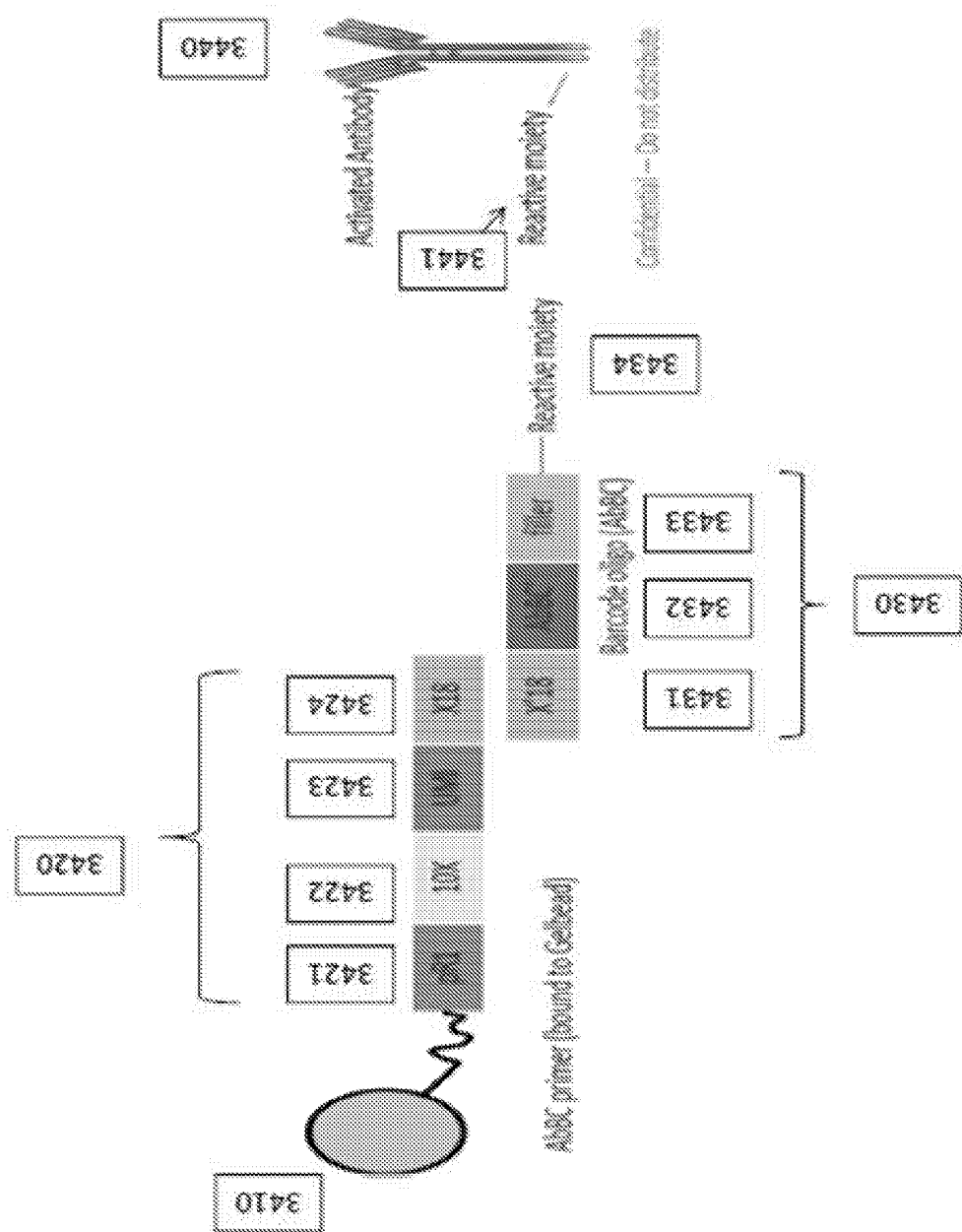


FIG. 33



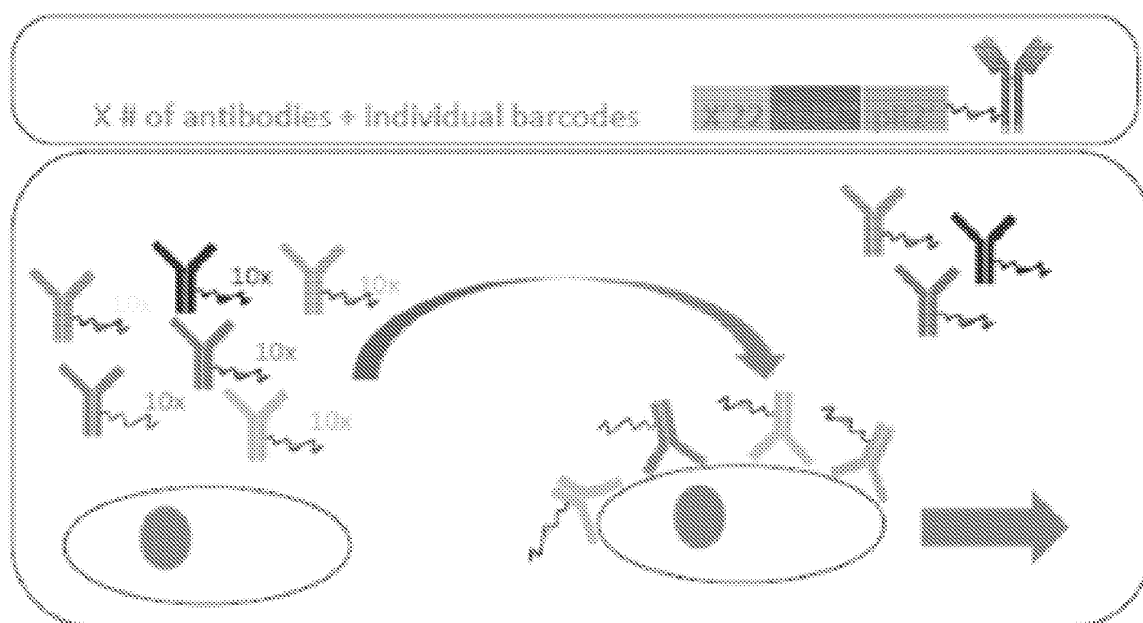


FIG. 35A

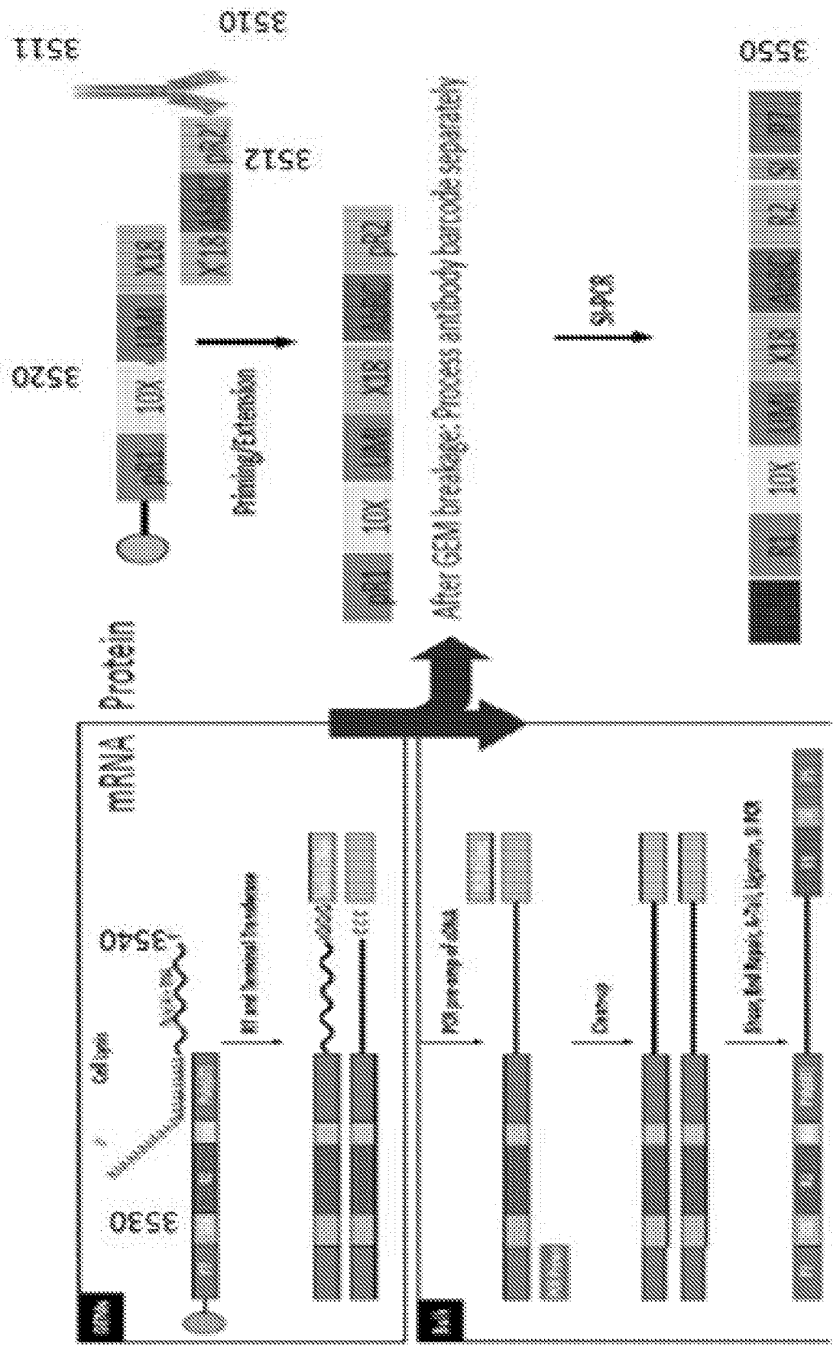


FIG. 35B

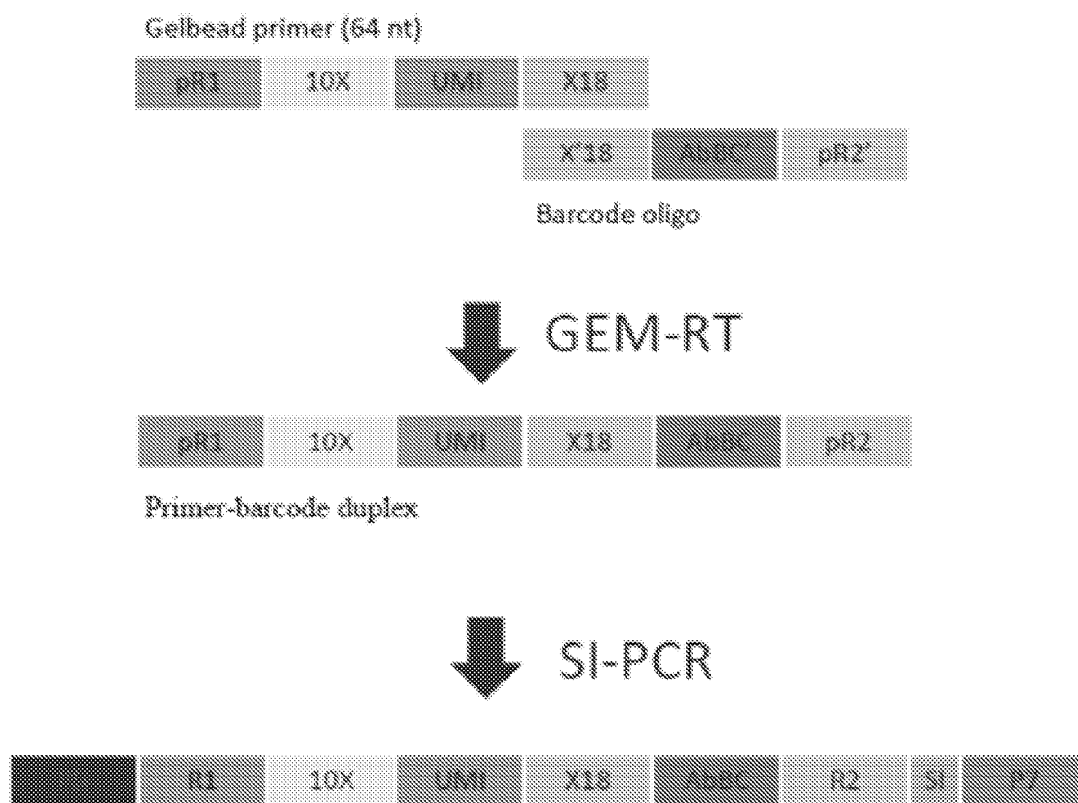


FIG. 35C

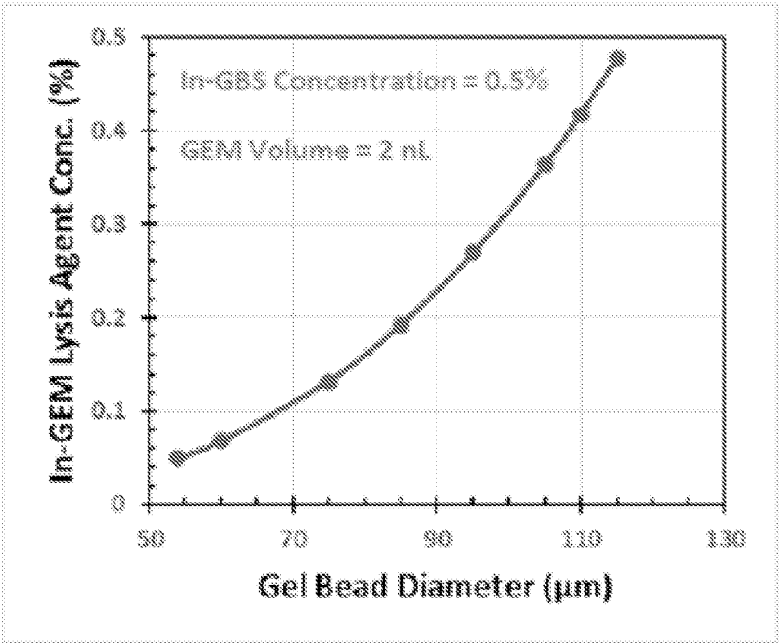


FIG. 36A

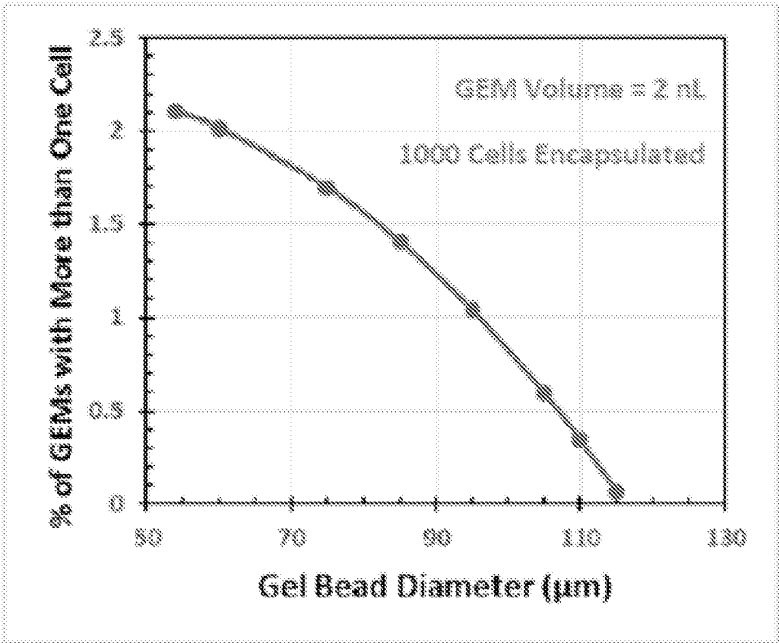


FIG. 36B

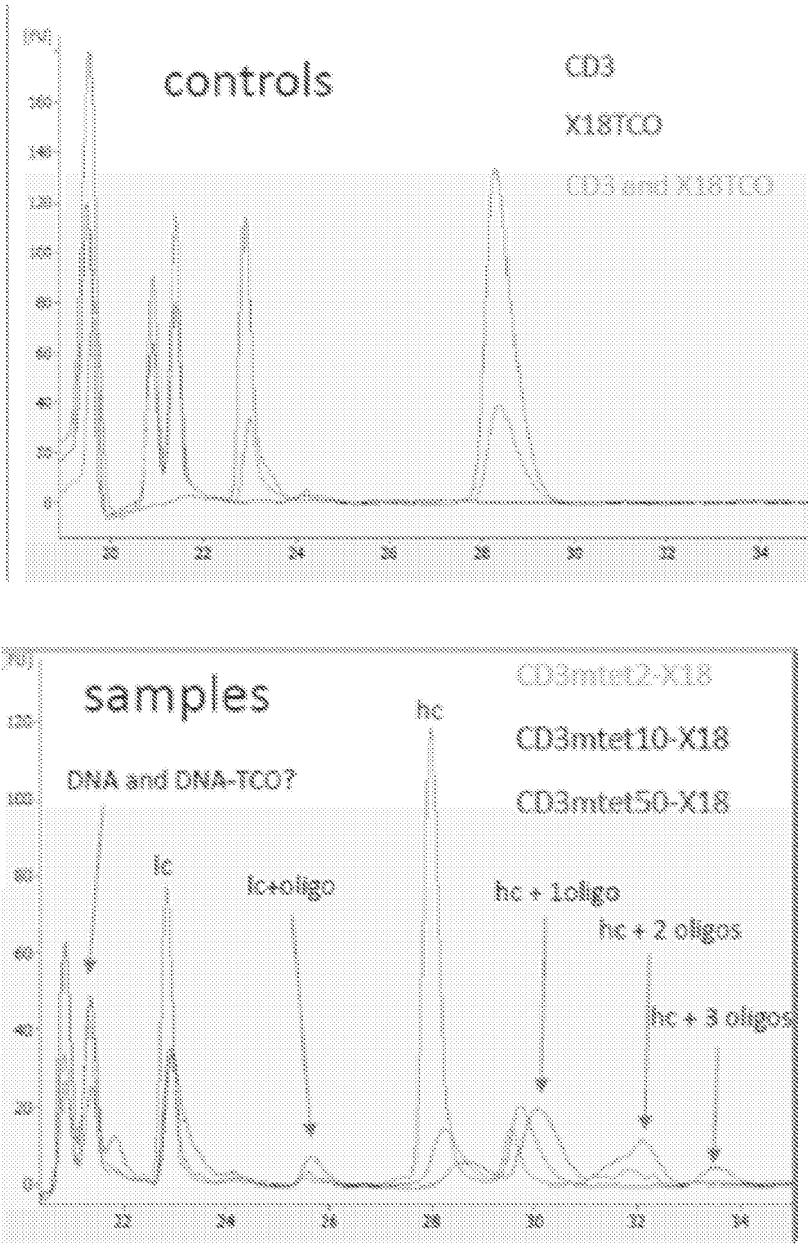


FIG. 37

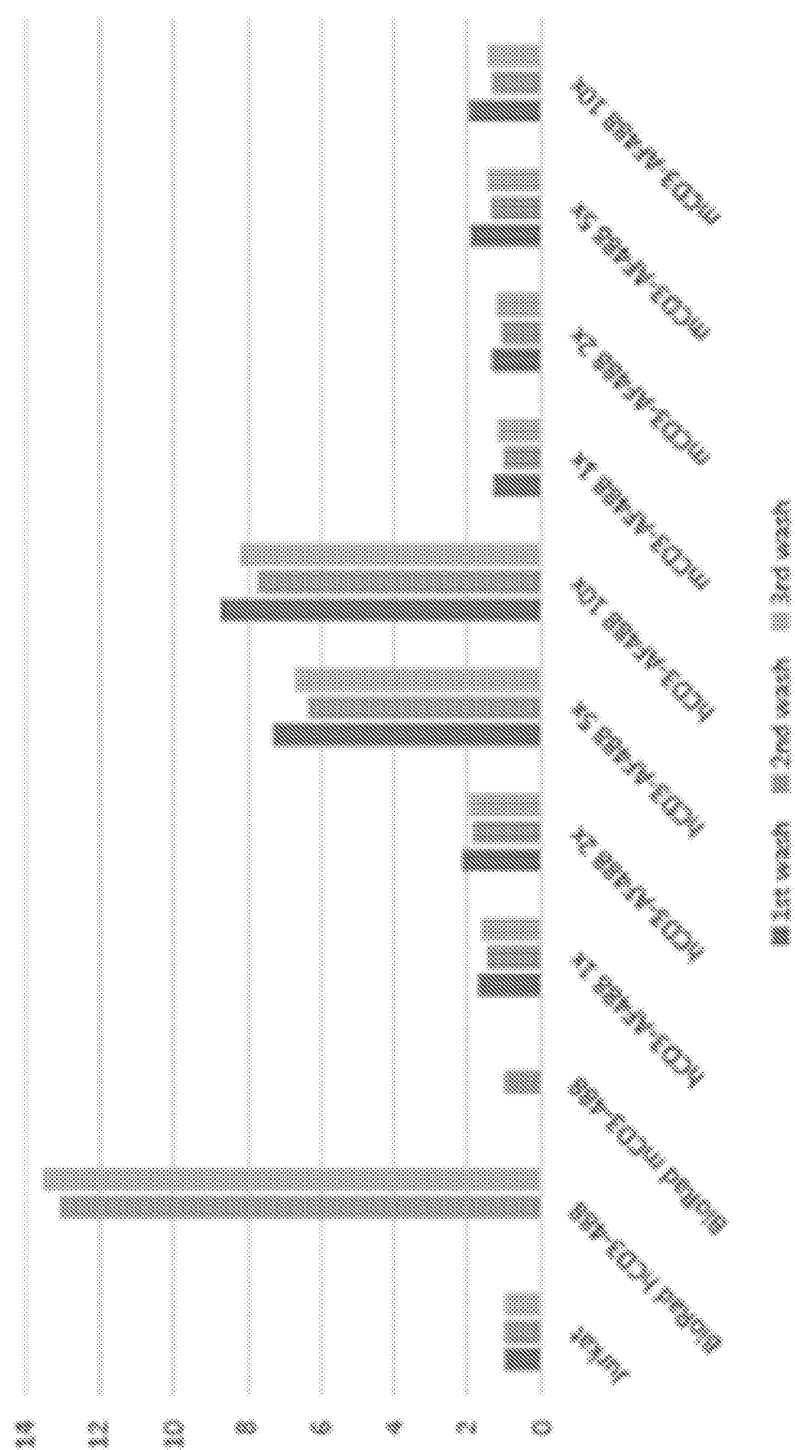


FIG. 38

48/84

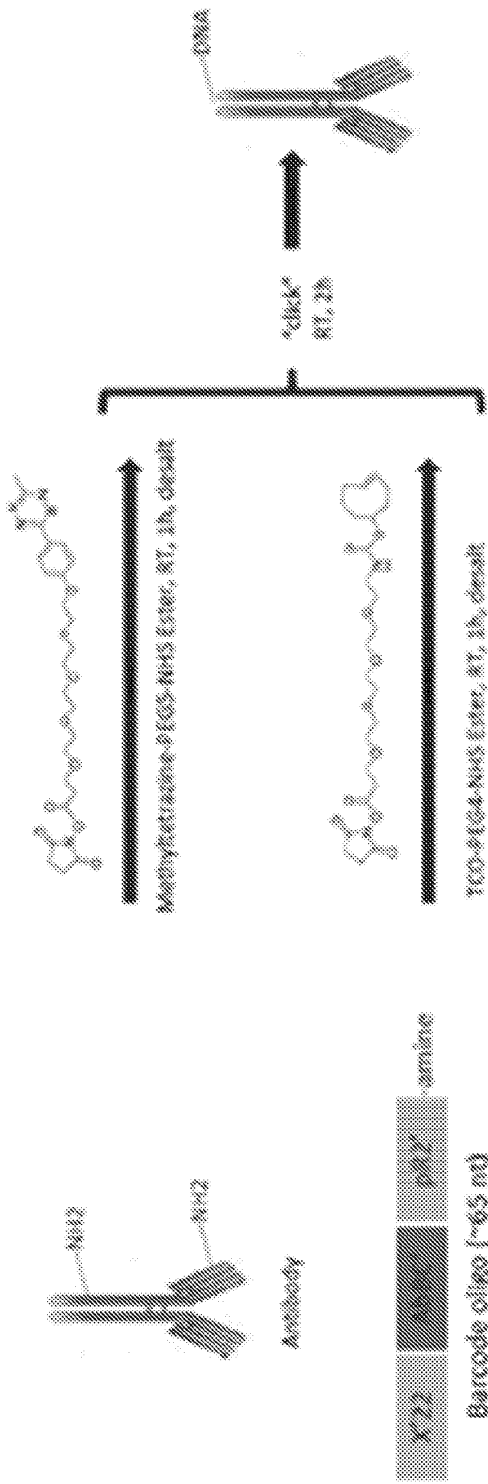


FIG. 39A

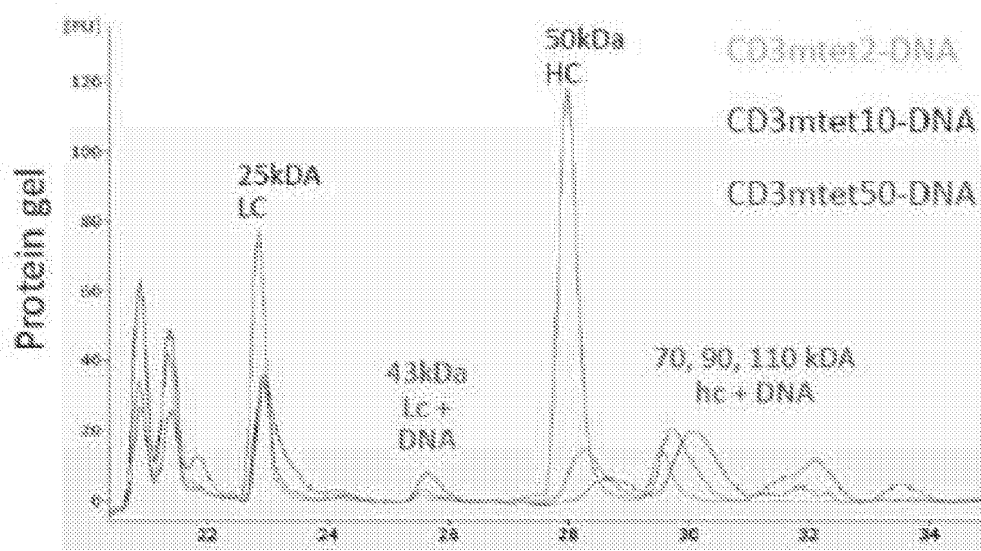


FIG. 39B

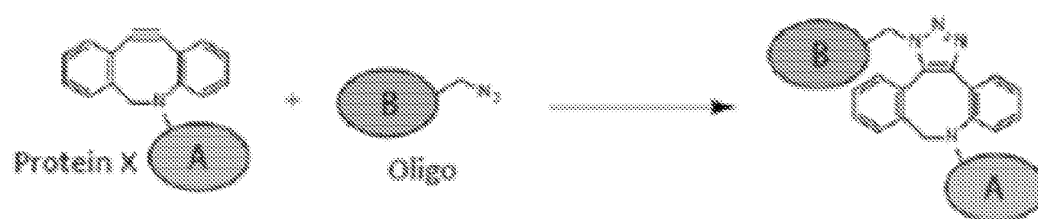


FIG. 40

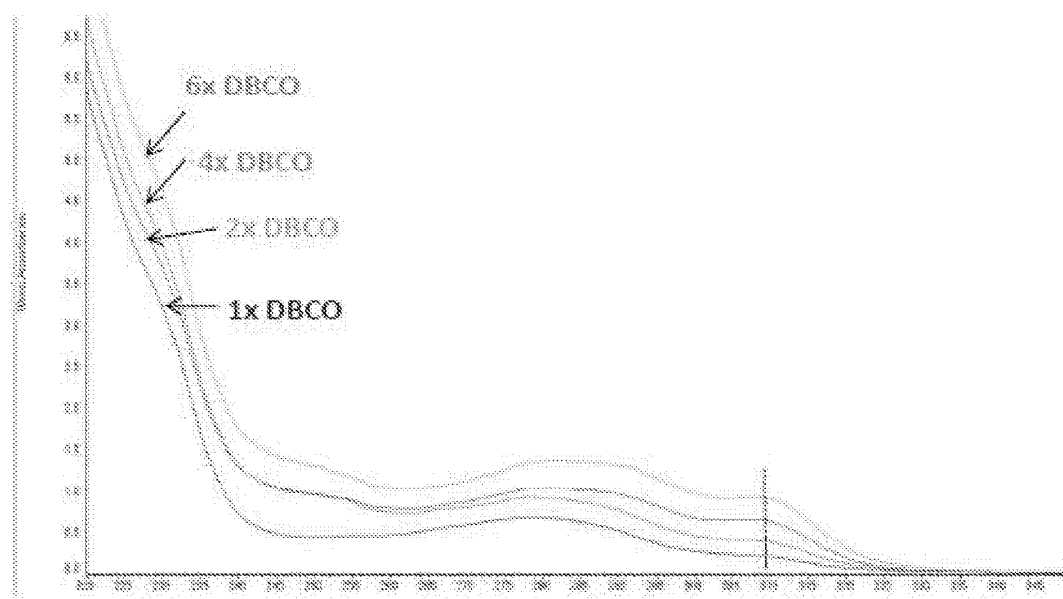


FIG. 41

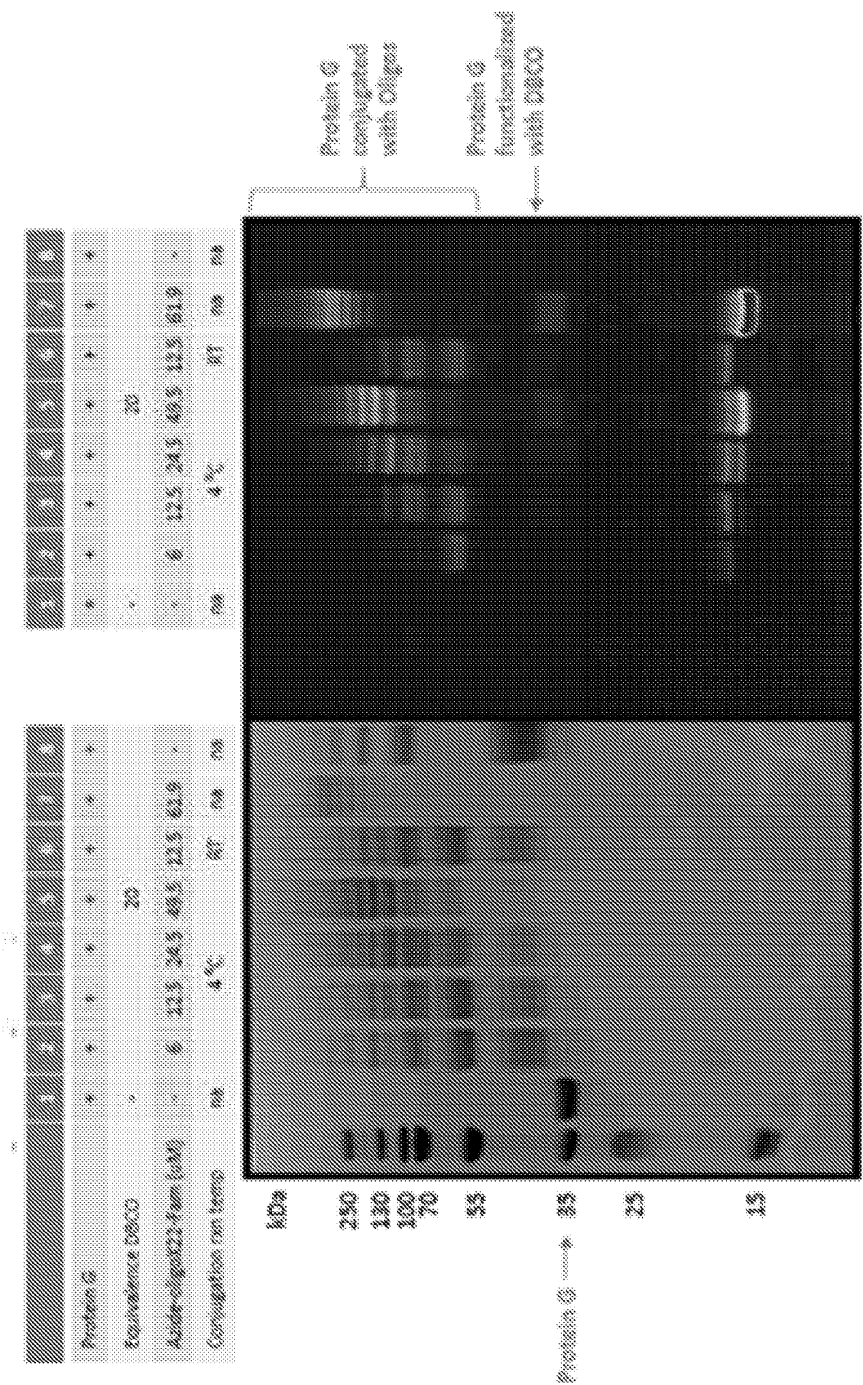


FIG. 42

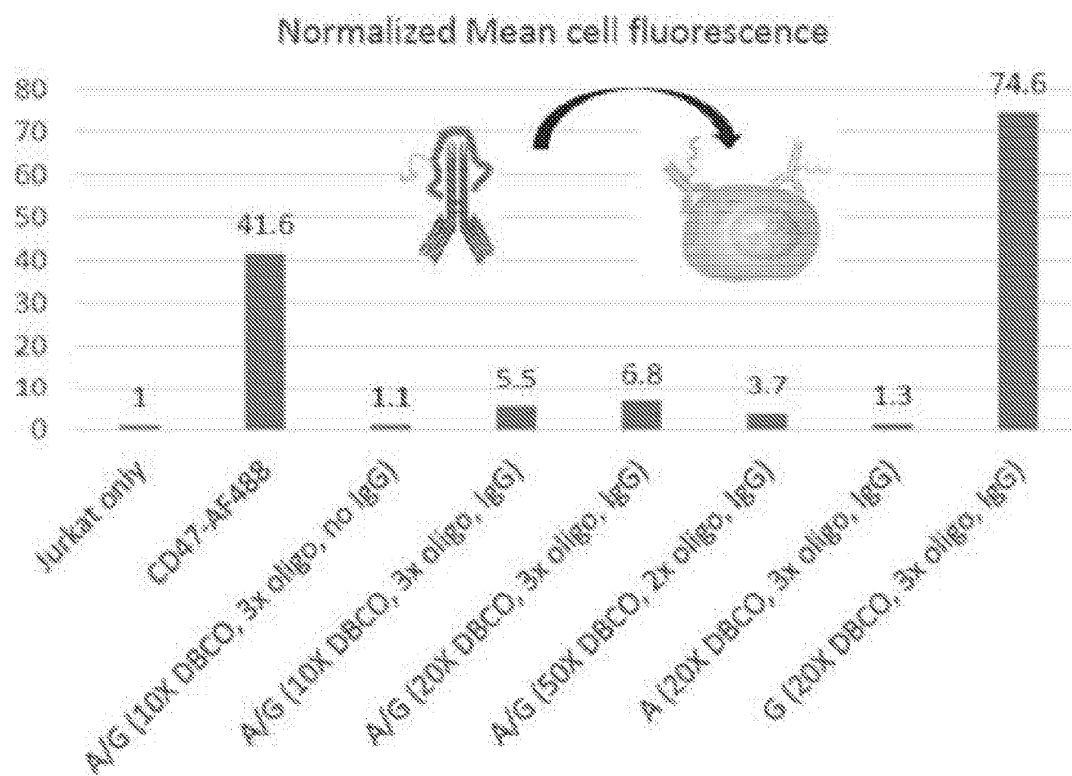


FIG. 43

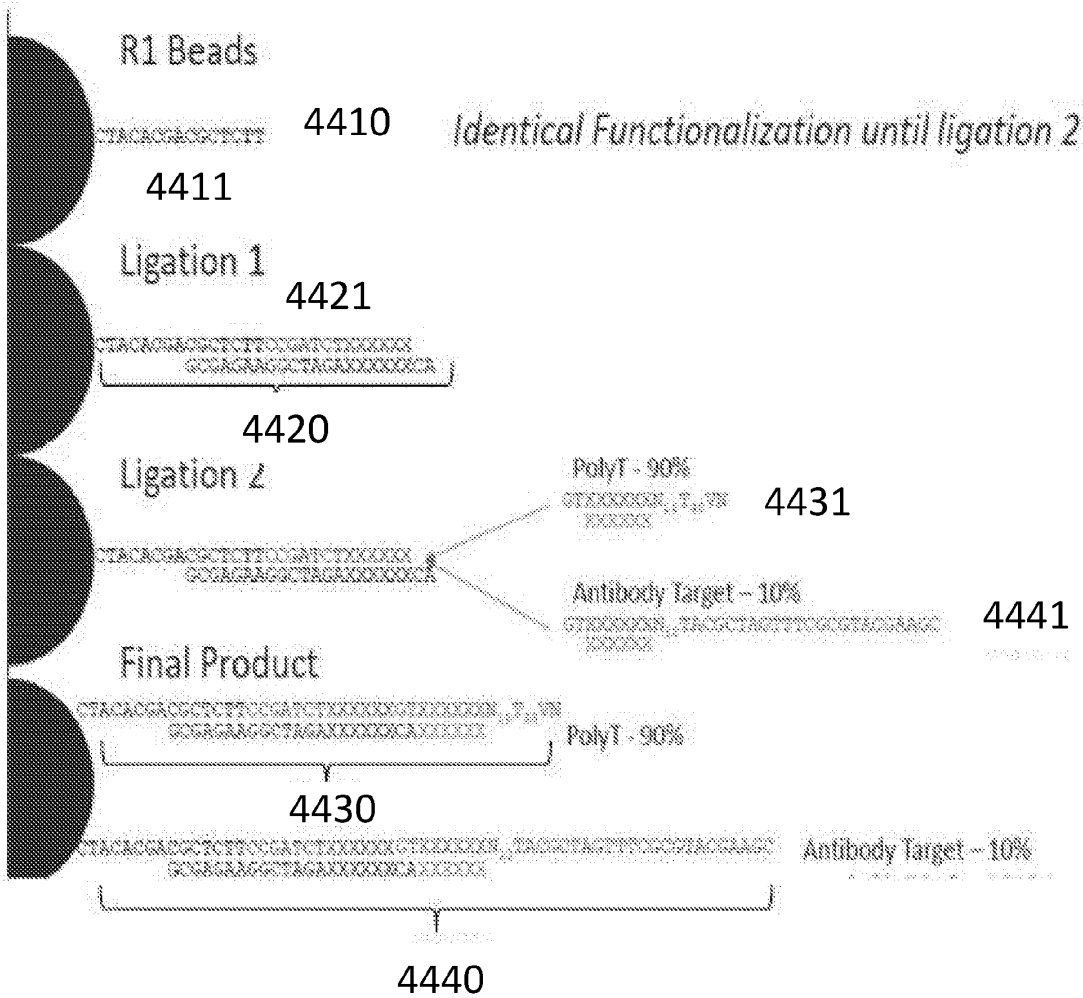


FIG. 44



FIG. 45A

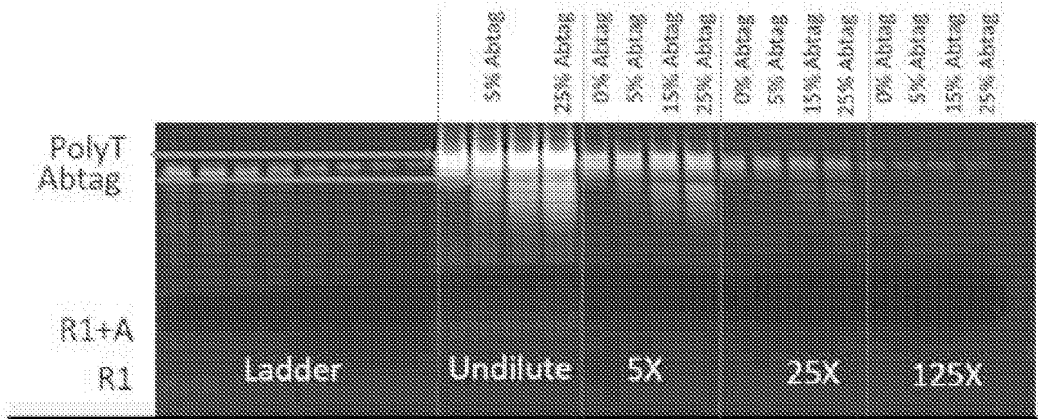


FIG. 45B

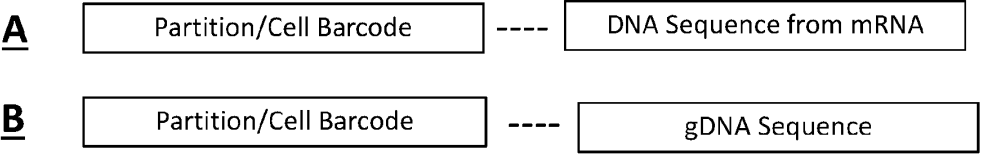
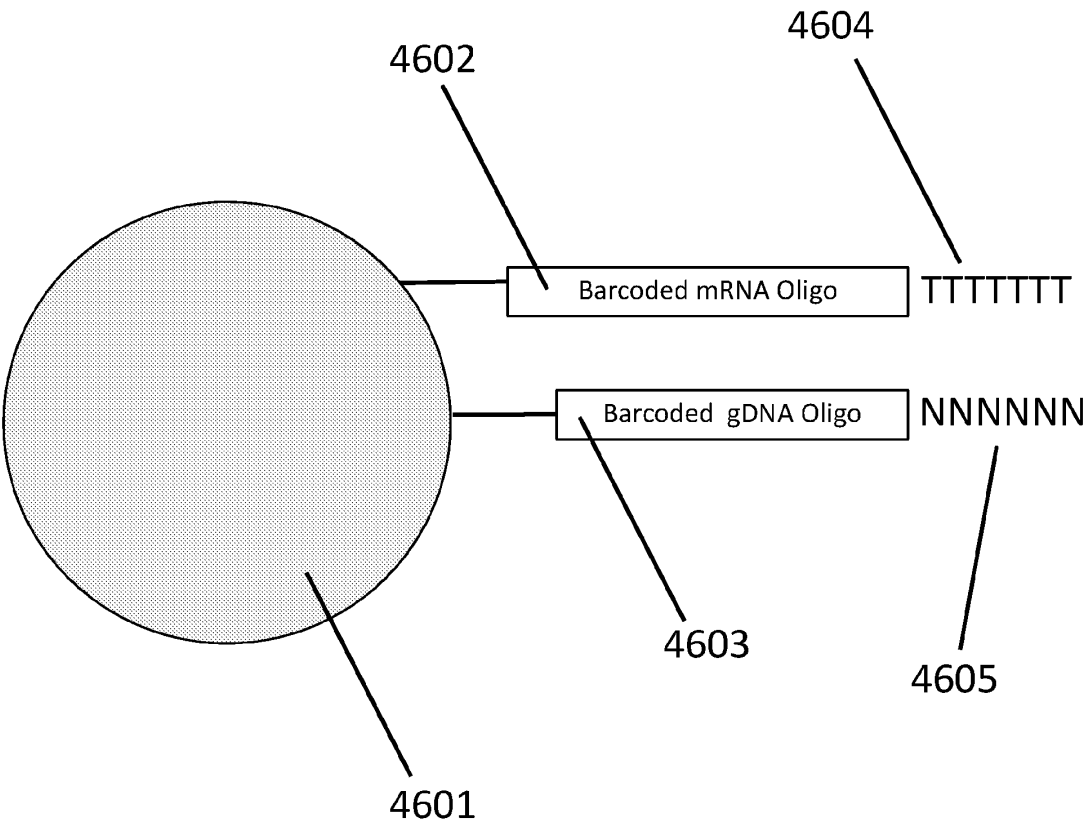


FIG. 46A

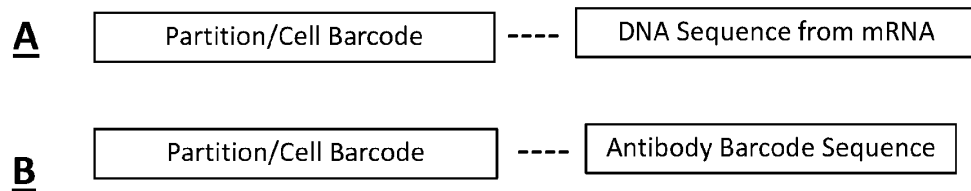
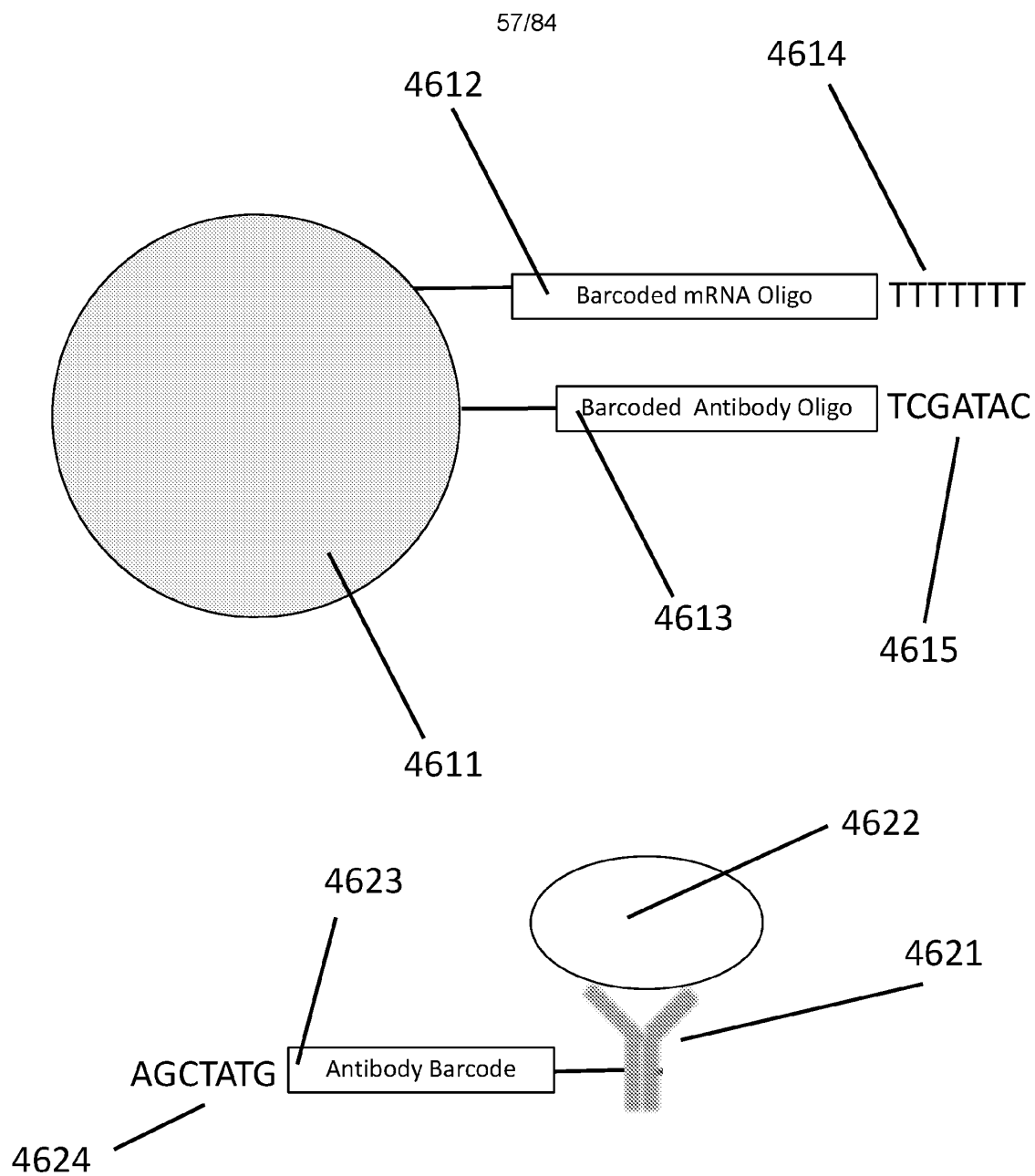
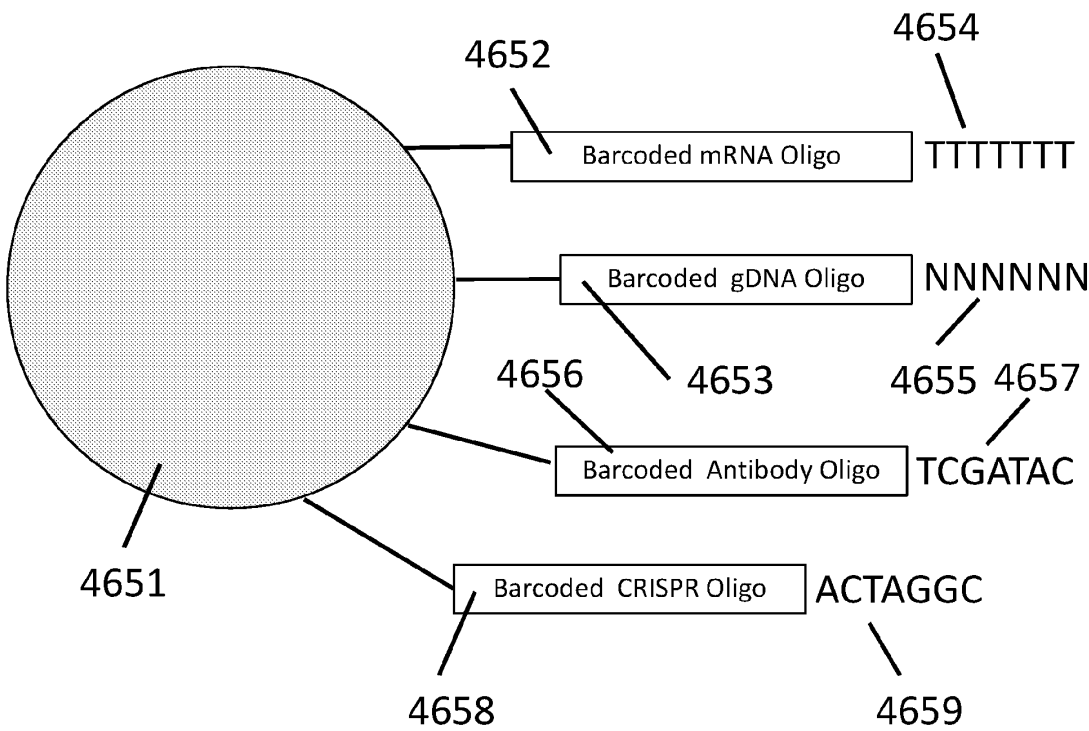


FIG. 46B



|                 |                        |      |                                   |
|-----------------|------------------------|------|-----------------------------------|
| <u><b>A</b></u> | Partition/Cell Barcode | ---- | DNA Sequence from mRNA            |
| <u><b>B</b></u> | Partition/Cell Barcode | ---- | gDNA Sequence                     |
| <u><b>C</b></u> | Partition/Cell Barcode | ---- | Antibody Barcode Sequence         |
| <u><b>D</b></u> | Partition/Cell Barcode | ---- | Sequence from CRISPR nucleic acid |

FIG. 46C

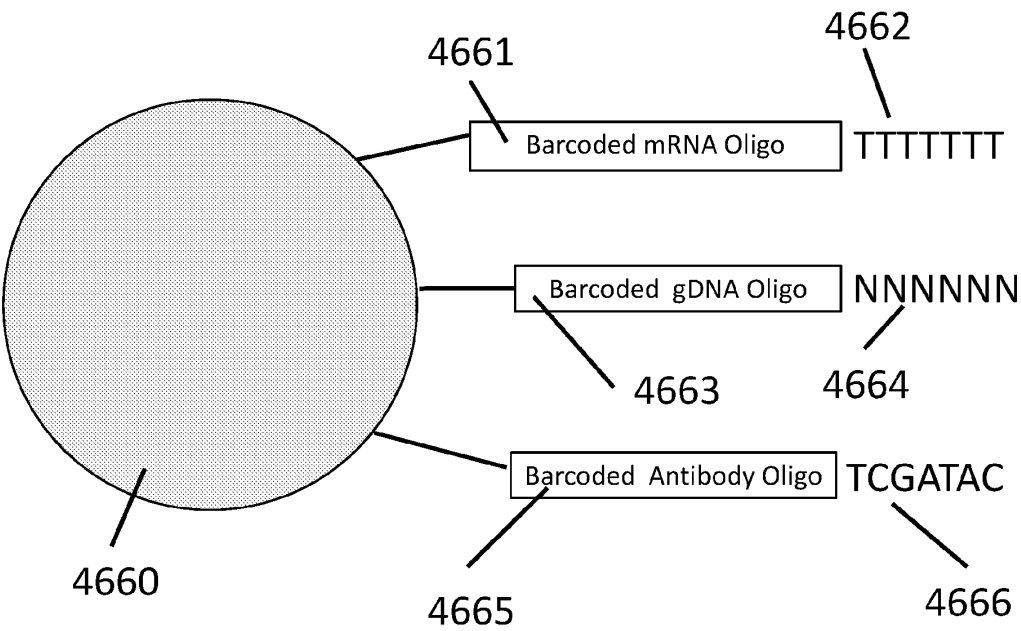


FIG. 46D

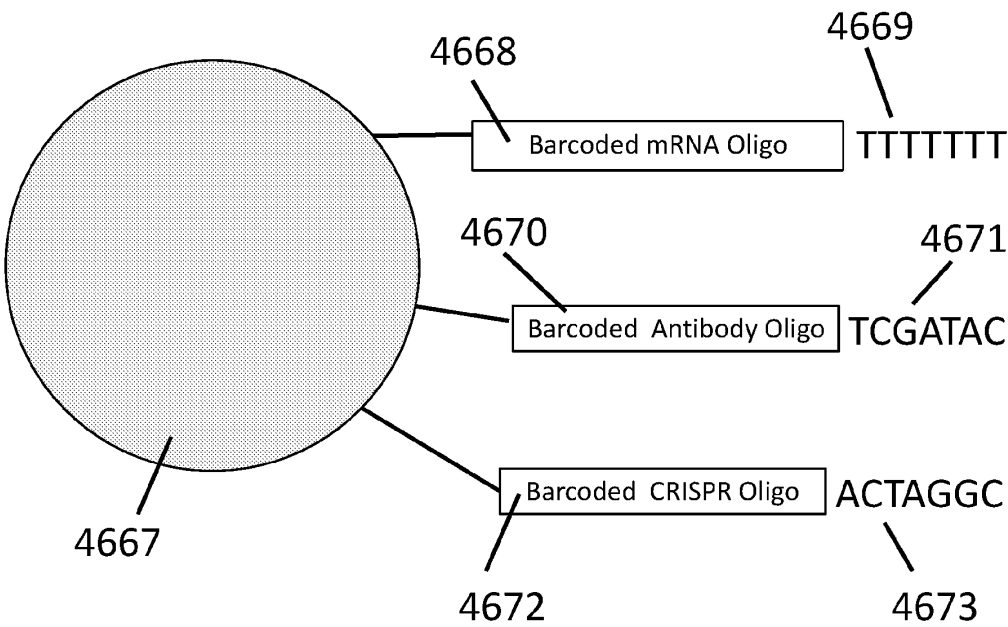


FIG. 46E

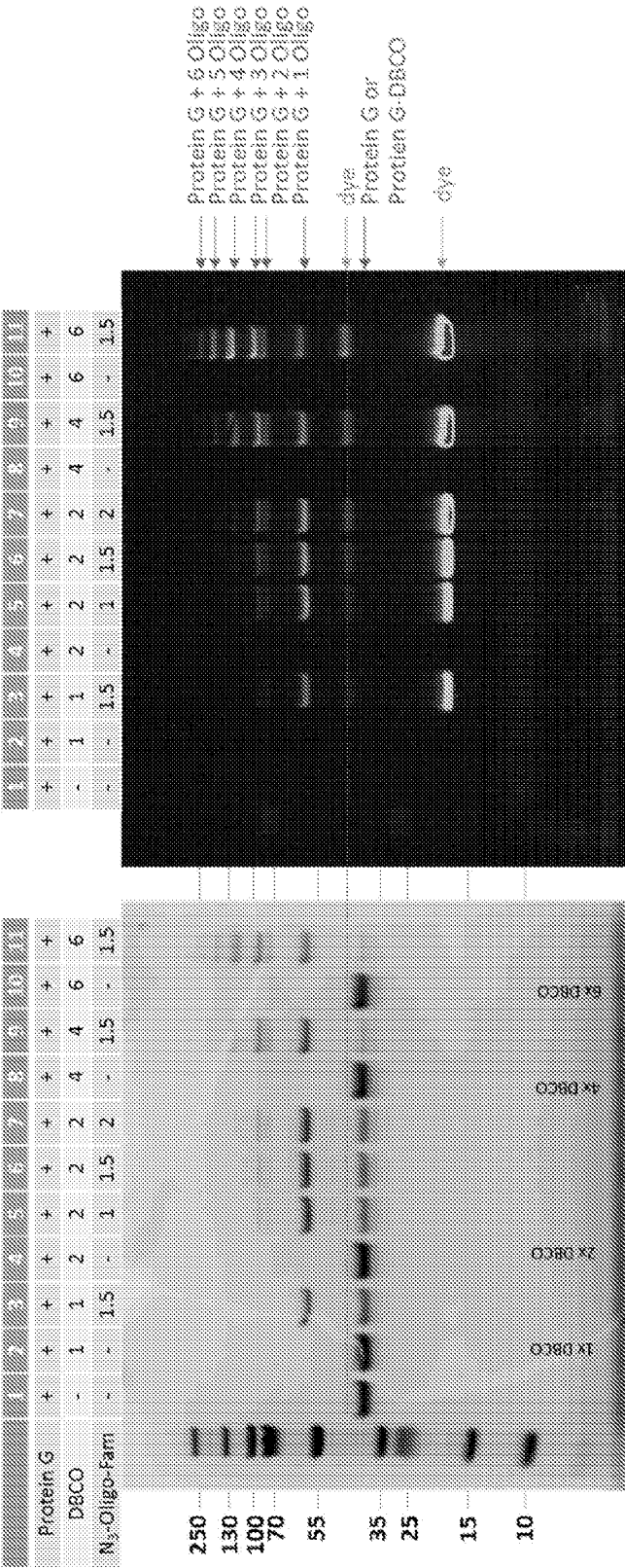


FIG. 47A

|             | Relative Band % (Coomassie gel) |                             |             |               |             |                       |                       |
|-------------|---------------------------------|-----------------------------|-------------|---------------|-------------|-----------------------|-----------------------|
| MW<br>(kDa) | Protein<br>G                    | 1x<br>DBCO<br>1.5x<br>oligo | 2X DBCO     |               |             | 4x DBCO<br>1.5x oligo | 6x DBCO<br>1.5x oligo |
|             |                                 |                             | 1x<br>oligo | 1.5x<br>oligo | 2x<br>oligo |                       |                       |
| 155.6       |                                 |                             |             |               |             |                       | 7.0                   |
| 117.6       |                                 |                             |             |               |             | 4.6                   | 20.1                  |
| 85.0        |                                 |                             | 2.8         | 4.6           | 6.9         | 20.3                  | 21.2                  |
| 70.0        |                                 |                             | 1.6         | 2.9           | 4.0         | 7.7                   | 5.4                   |
| 58.2        |                                 | 32.9                        | 46.6        | 45.8          | 44.4        | 44.4                  | 37.2                  |
| 39.6        | 100                             | 67.1                        | 49.0        | 46.7          | 44.7        | 23.0                  | 9.1                   |

FIG. 47B

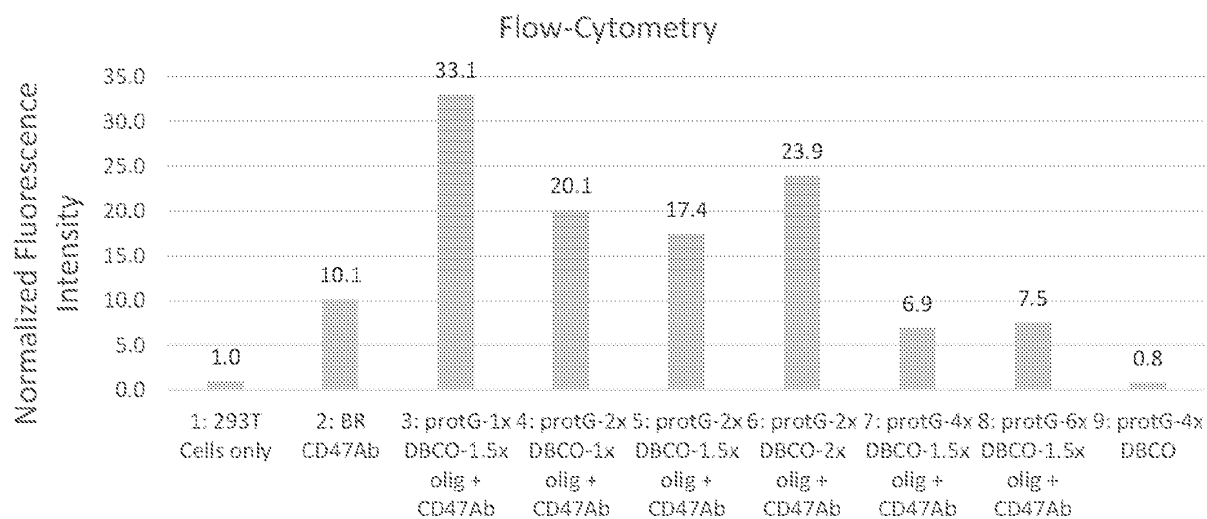
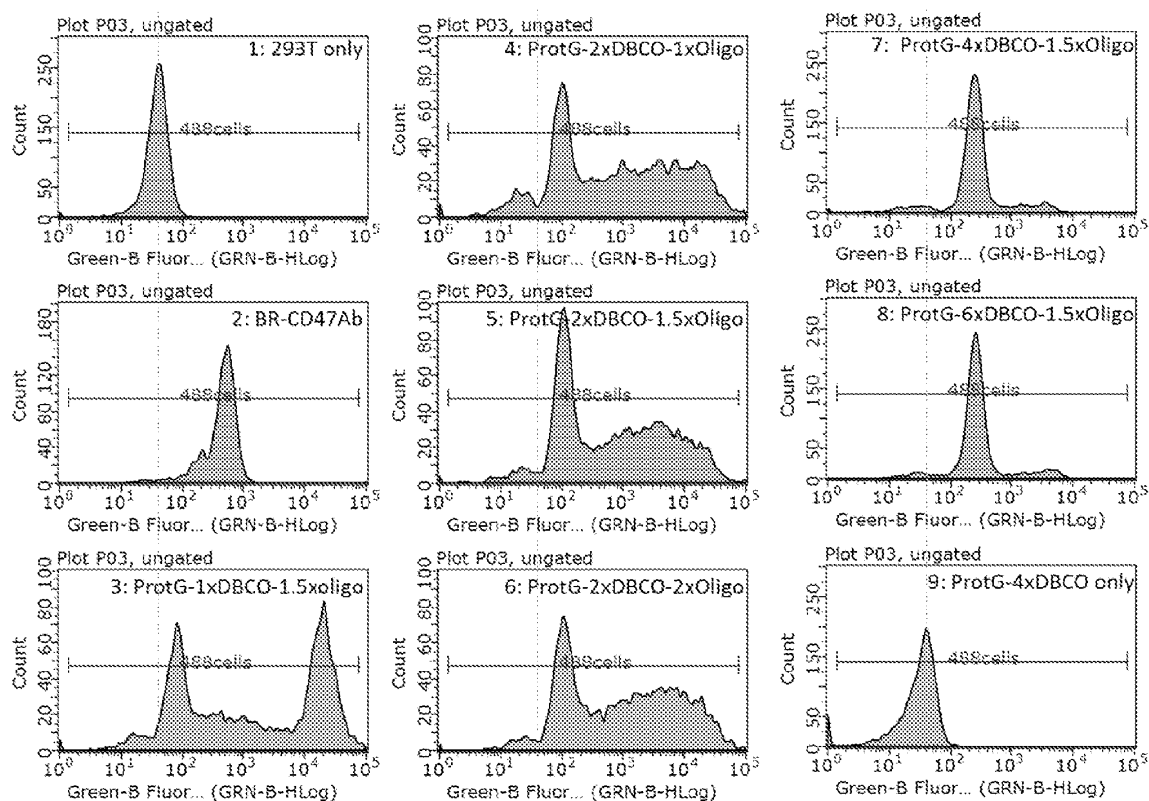
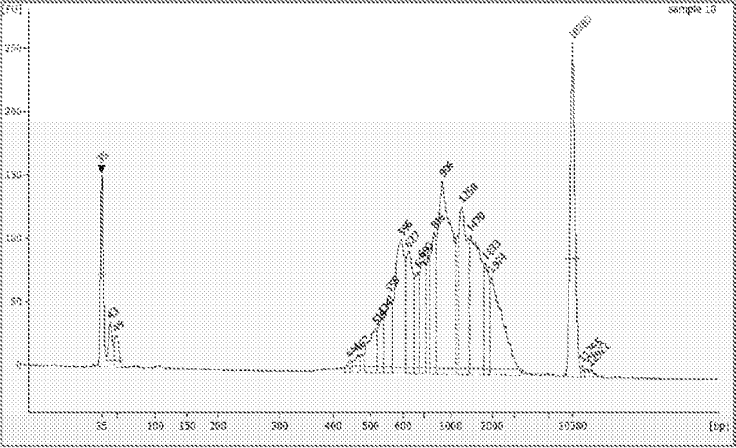


FIG. 48

Typical trace of transcriptome cDNA



Typical trace of transcriptome library

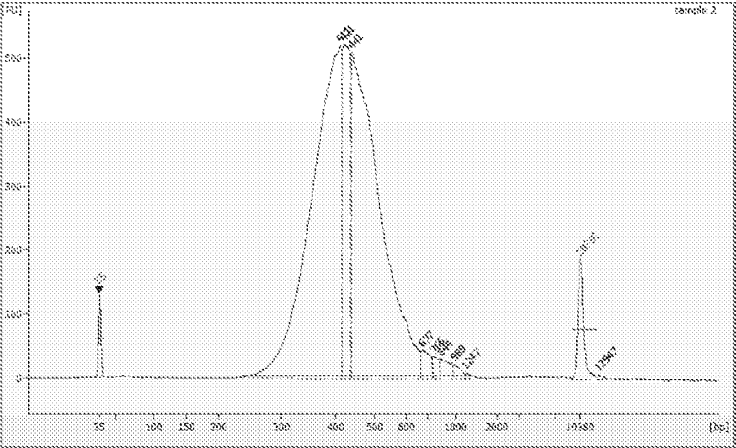
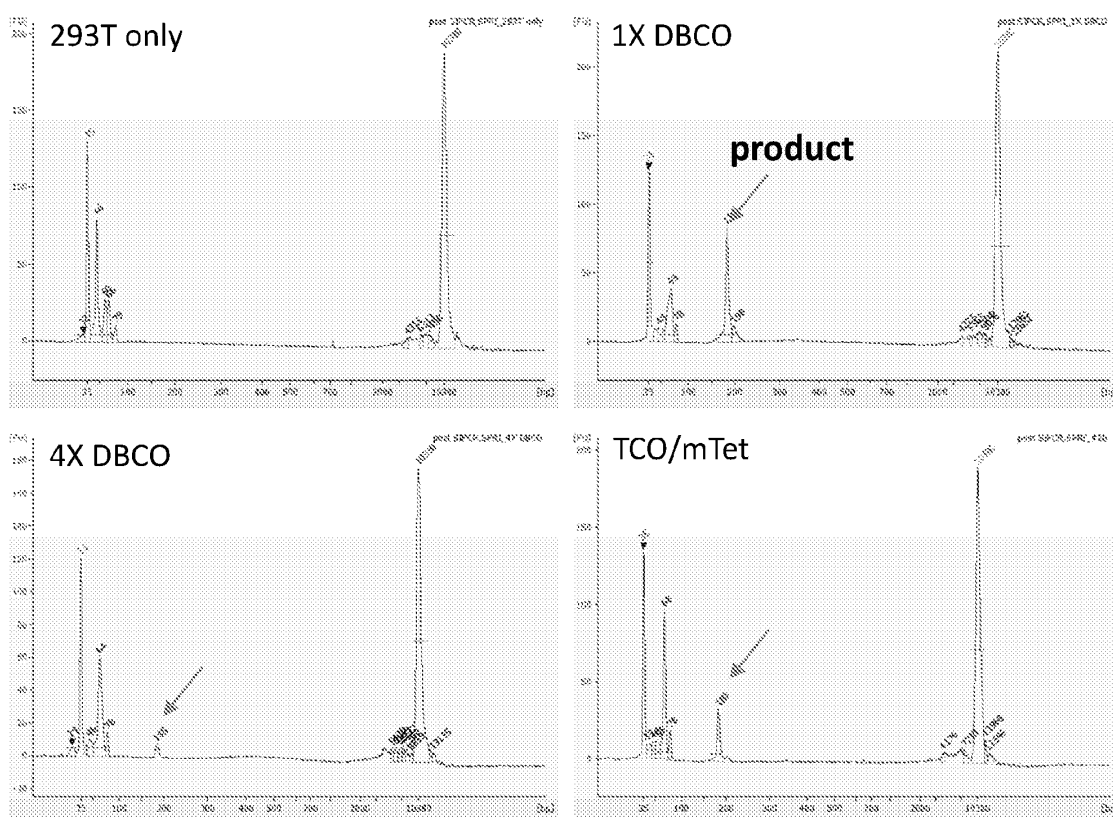


FIG. 49A



| Description                       | Correted Area | Product Peak Size (bp) |
|-----------------------------------|---------------|------------------------|
| 293T Cells only                   | 11.0          | -                      |
| protG-1x DBCO-1.5x oligo + CD47Ab | 178.4         | 184                    |
| protG-2x DBCO-2x oligo + CD47Ab   | 120.5         | 184                    |
| protG-4x DBCO-1.5x oligo + CD47Ab | 17.6          | 185                    |
| protG-6x DBCO-1.5x oligo + CD47Ab | 32.4          | 184                    |
| protG-TCO/mtet-10x oligo + CD47Ab | 45.6          | 183                    |
| protG-oligo                       | 5.0           | -                      |

FIG. 49B

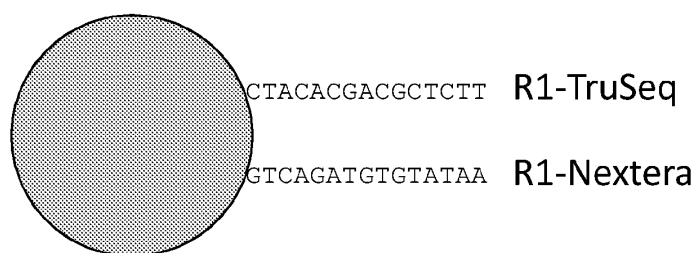


FIG. 50A

**Alpha**  
CTACACGACGCTCTTCCGATCTXXXXXXXXGTXXXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXXXXCAXXXXXXX

**Beta**  
CTACACGACGCTCTTCCGATCTXXXXXXXXCAXXXXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXXXXGTXXXXXX

**Gamma**  
CTACACGACGCTCTTCCGATCTXXXXXXXXAGXXXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXXXXTCXXXXXX

**Delta**  
CTACACGACGCTCTTCCGATCTXXXXXXXXTCXXXXXXXXN<sub>10</sub>T<sub>30</sub>VN  
GCGAGAAGGCTAGAXXXXXXXXXAGXXXXXX

FIG. 50B

**Alpha**  
GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN<sub>10</sub>GCTTCGTACGCGAACTAGCGT  
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

**Beta**  
GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN<sub>10</sub>GCTTCGTACGCGAACTAGCGT  
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

**Gamma**  
GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN<sub>10</sub>GCTTCGTACGCGAACTAGCGT  
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

**Delta**  
GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN<sub>10</sub>GCTTCGTACGCGAACTAGCGT  
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

FIG. 50C

5' CTACAGACGCTCTTCGGATCTNNNNNNNNNNNNNNNNNNNNTTTCTTATATrGrG  
3' AAAGAATATA C CTAGACTGACGTGGAACCTGCCGATTTC AAC-**FAM**

5102

FIG. 51A

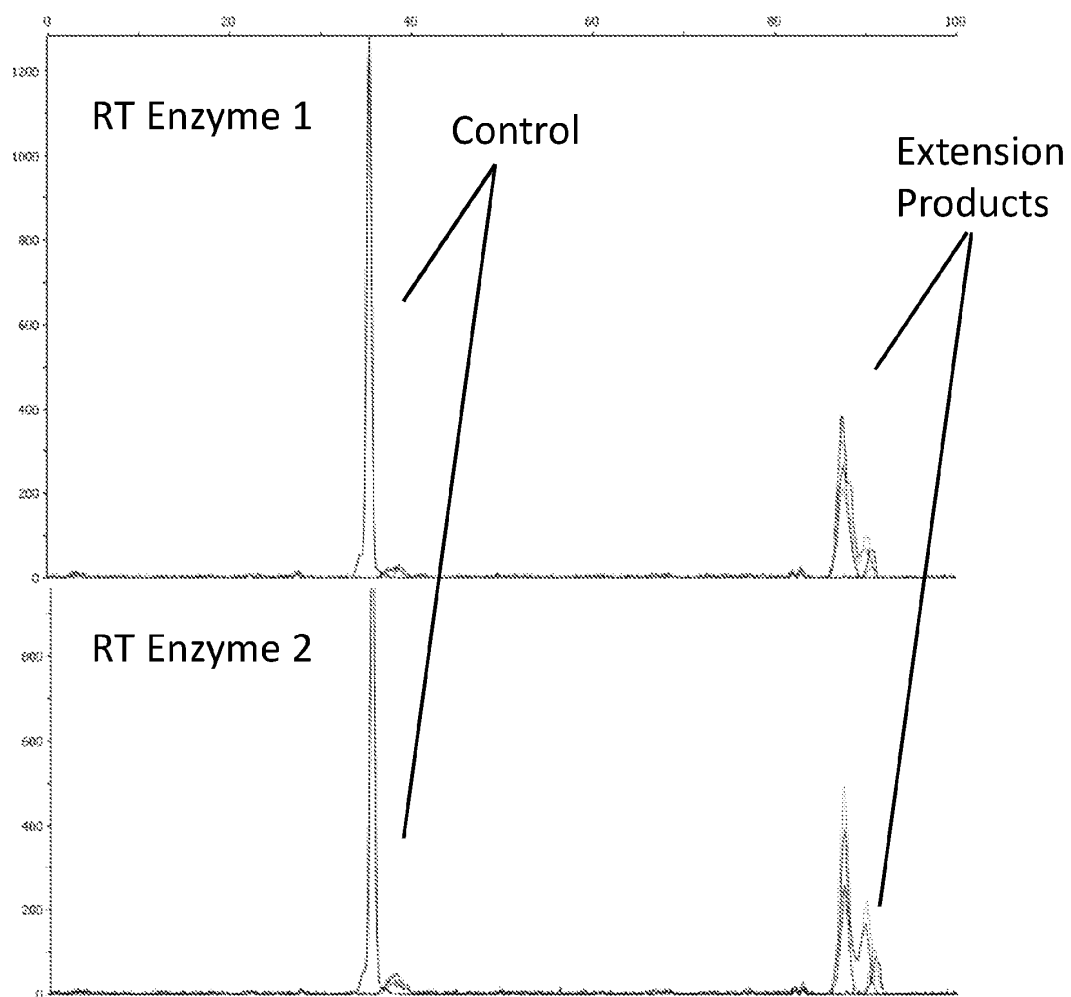


FIG. 51B

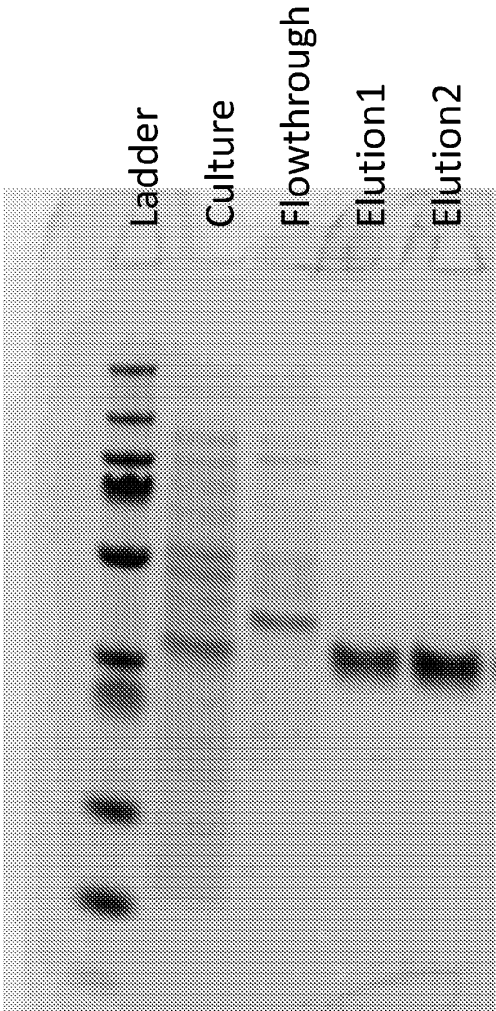


FIG. 52A

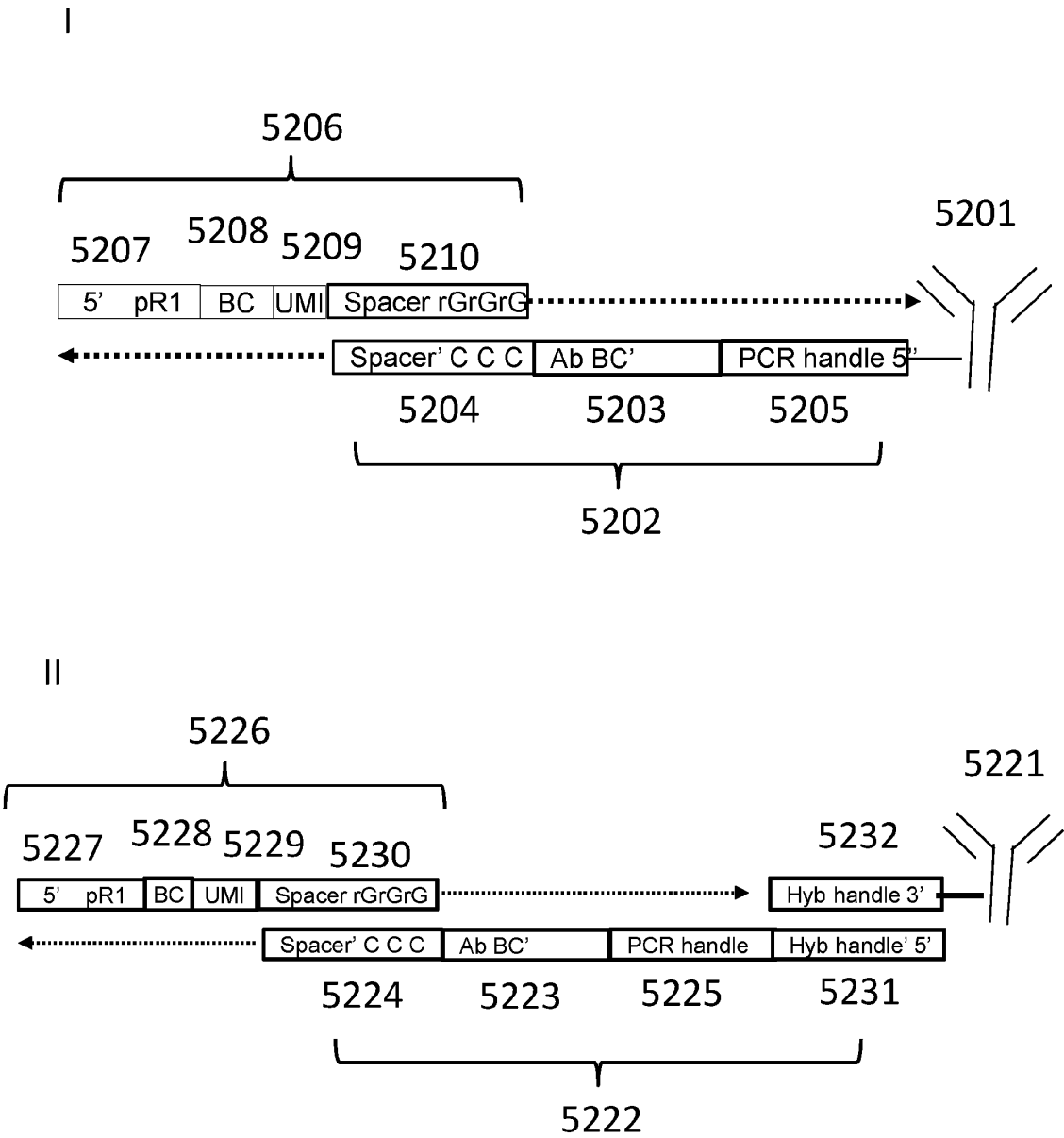
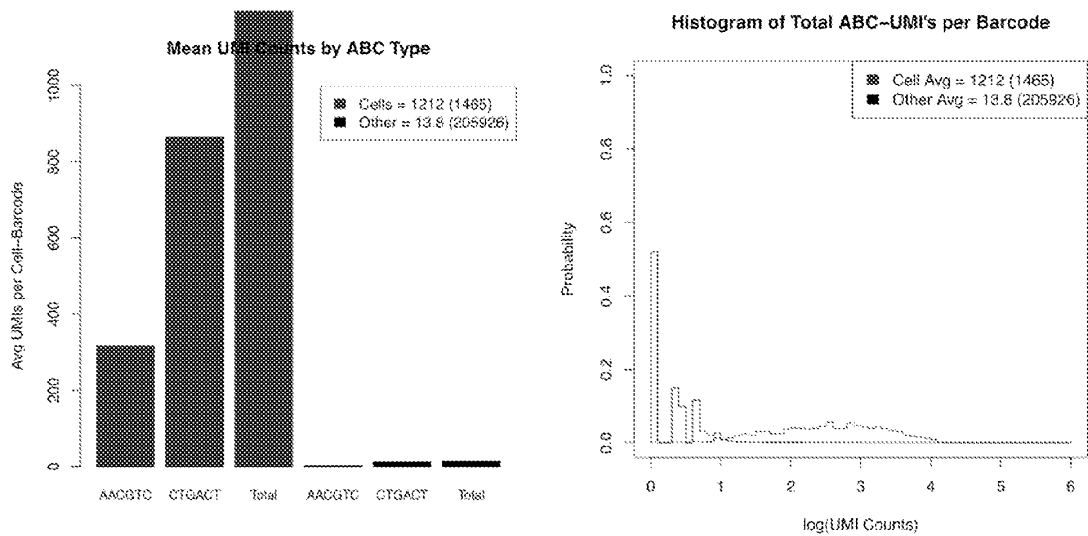


FIG. 52B

I Jurkat + CD47/CD99



II Jurkat + CD47

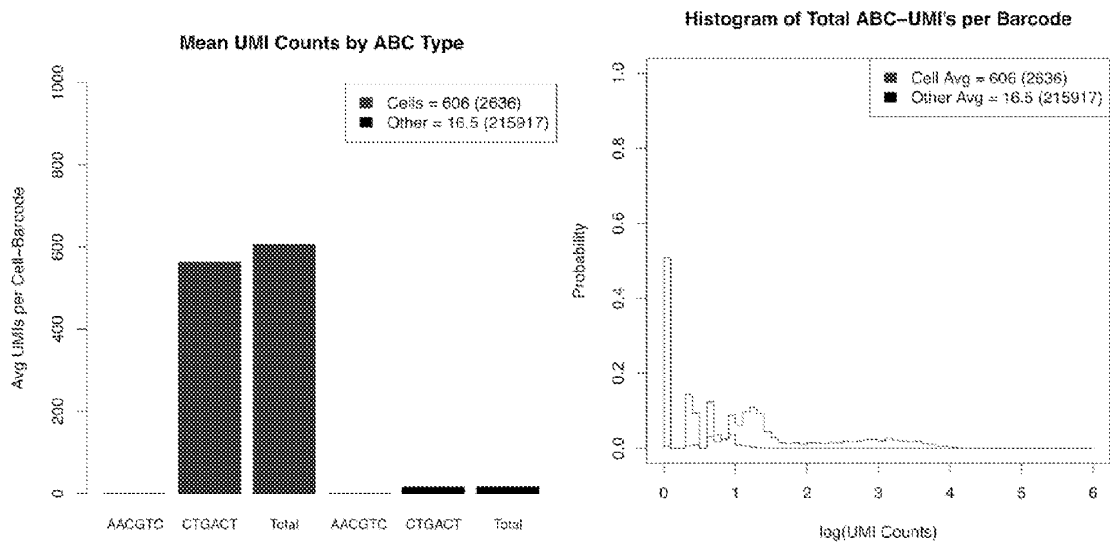


FIG. 53A

| Sample                      | Sample ID | Avg UMIs<br>Per Cell | Avg UMIs Per<br>Other | BC3 per cell | BC4 per cell | Total # of<br>cell BCs<br>detected in<br>AbBC expt | # cells, SCS | # cells,<br>AbBC topN<br>(#cells,<br>SCS) | AbBC topN<br>cells n SCS<br>cells | AbBC called<br>n SCS cells | SCS cells n<br>AbBC topN<br>/ SCS cells | BCAb cells<br>n SCS' cells<br>/ AbBC cells |
|-----------------------------|-----------|----------------------|-----------------------|--------------|--------------|----------------------------------------------------|--------------|-------------------------------------------|-----------------------------------|----------------------------|-----------------------------------------|--------------------------------------------|
| Unbiased Jurkat + BC4       | 33603     | 498                  | 13.9                  | 64647        | 635942       | 128483                                             | 1419         | 1428                                      | 878                               | 1362                       | 370                                     | 0.27                                       |
| Unbiased Jurkat + BC3/4     | 33601     | 577                  | 17.1                  | 247587       | 404815       | 126514                                             | 1141         | 1141                                      | 368                               | 992                        | 516                                     | 0.32                                       |
| Unbiased Jurkat + BC4       | 33602     | 946                  | 9.24                  | 1474578      | 6119         | 144263                                             | 1505         | 1504                                      | 861                               | 1193                       | 762                                     | 0.64                                       |
| Unbiased Jurkat spike BC3/4 | 33603     | 38.8                 | 14.1                  | 1163         | 71316        | 206337                                             | 1898         | 1980                                      | 103                               | 62631                      | 1570                                    | 0.05                                       |

FIG. 53B

| Sample | description                                  | Mean Reads per Cell | Valid Barcodes | Reads Mapped Confidently to Transcriptome | Fraction Reads in Cells | Fraction reads usable | Reads Mapped Confidently to Exonic Regions | Reads Mapped Confidently to Intronic Regions | Reads Mapped Confidently to Intergenic Regions | Reads Mapped to Gene | Fraction reads unmapped | rDNA PCR Duplication (10x raw reads per cell) | Median genes per cell (20x raw reads per cell) | Median UMIs counts per cell (20x raw reads per cell) |
|--------|----------------------------------------------|---------------------|----------------|-------------------------------------------|-------------------------|-----------------------|--------------------------------------------|----------------------------------------------|------------------------------------------------|----------------------|-------------------------|-----------------------------------------------|------------------------------------------------|------------------------------------------------------|
| 37158  | cDNA control                                 | 217,543             | 83.60%         | 56.00%                                    | 95.70%                  | 26.30%                | 64.50%                                     | 12.70%                                       | 8.90%                                          | 9.00%                | 3.30%                   | 46.90%                                        | 1.103                                          | 2,764                                                |
| 37772  | Unbleed 5: CG-CD3 GEM 53/85C D <sub>5</sub>  | 31,899              | 70.30%         | 32.90%                                    | 95.10%                  | 15.30%                | 41.80%                                     | 9.00%                                        | 16.60%                                         | 12.80%               | 4.70%                   | 43.30%                                        | 750                                            | 1,690                                                |
| 37773  | Unbleed 6: CG-CD3 GEM 53/85C D <sub>5</sub>  | 29,602              | 69.30%         | 29.90%                                    | 94.40%                  | 13.70%                | 38.90%                                     | 9.36%                                        | 16.80%                                         | 14.00%               | 4.70%                   | 42.80%                                        | 664                                            | 1,562                                                |
| 37776  | Unbleed 21: SC-CD3 GEM 53/85C D <sub>5</sub> | 36,545              | 76.00%         | 37.10%                                    | 95.40%                  | 17.20%                | 47.40%                                     | 13.20%                                       | 13.50%                                         | 13.90%               | 5.10%                   | 44.60%                                        | 812                                            | 1,935                                                |
| 37777  | Unbleed 22: SC-CD3 GEM 53/85C D <sub>5</sub> | 44,883              | 78.40%         | 39.20%                                    | 96.10%                  | 18.36%                | 48.96%                                     | 12.60%                                       | 13.10%                                         | 13.00%               | 5.16%                   | 43.20%                                        | 855                                            | 2,077                                                |
| 37780  | Unbleed 23: SC-CD3 GEM 53/85C D <sub>5</sub> | 33,828              | 76.20%         | 36.30%                                    | 94.40%                  | 17.60%                | 47.80%                                     | 13.00%                                       | 14.30%                                         | 17.80%               | 4.50%                   | 46.30%                                        | 781                                            | 1,798                                                |
| 37781  | Unbleed 24: SC-CD3 GEM 53/85C D <sub>5</sub> | 33,085              | 71.90%         | 33.90%                                    | 94.80%                  | 15.60%                | 43.96%                                     | 11.30%                                       | 15.30%                                         | 14.30%               | 4.60%                   | 46.00%                                        | 750                                            | 1,666                                                |
| 37784  | Unbleed 25: SC-CD3 GEM 53/85C D <sub>5</sub> | 40,117              | 77.70%         | 40.20%                                    | 95.30%                  | 18.60%                | 50.40%                                     | 14.90%                                       | 12.90%                                         | 12.90%               | 4.60%                   | 49.60%                                        | 803                                            | 1,880                                                |
| 37785  | Unbleed 26: SC-CD3 GEM 53/85C D <sub>5</sub> | 40,931              | 80.30%         | 39.10%                                    | 95.00%                  | 18.10%                | 50.30%                                     | 16.20%                                       | 13.40%                                         | 14.00%               | 4.90%                   | 52.20%                                        | 747                                            | 1,714                                                |
| 37770  | Unbleed 1: CG-CD3 GEM 53C Dyna               | 29,116              | 91.40%         | 64.50%                                    | 94.90%                  | 29.80%                | 71.1%                                      | 12.00%                                       | 7.90%                                          | 6.20%                | 6.50%                   | 58.70%                                        | 673                                            | 1,824                                                |
| 37771  | Unbleed 2: CG-CD3 GEM 53C Dyna               | 26,533              | 91.30%         | 65.40%                                    | 95.30%                  | 30.30%                | 71.6%                                      | 11.90%                                       | 7.40%                                          | 5.80%                | 6.40%                   | 64.80%                                        | 751                                            | 2,057                                                |
| 37774  | Unbleed 17: SC-CD3 GEM 53C Dyna              | 42,069              | 94.90%         | 62.40%                                    | 95.10%                  | 28.80%                | 69.4%                                      | 15.30%                                       | 7.32%                                          | 6.20%                | 6.70%                   | 64.20%                                        | 752                                            | 3,009                                                |
| 37775  | Unbleed 18: SC-CD3 GEM 53C Dyna              | 38,254              | 94.50%         | 63.60%                                    | 95.30%                  | 29.10%                | 69.9%                                      | 15.30%                                       | 7.10%                                          | 6.60%                | 6.60%                   | 65.30%                                        | 751                                            | 2,000                                                |
| 37778  | Unbleed 19: SC-CD3 GEM 53C Dyna              | 32,775              | 93.60%         | 67.70%                                    | 94.90%                  | 31.30%                | 73.6%                                      | 11.70%                                       | 6.90%                                          | 5.70%                | 5.90%                   | 64.60%                                        | 848                                            | 2,113                                                |
| 37779  | Unbleed 4: CG-CD3 GEM 53C Strept             | 50,369              | 92.80%         | 67.40%                                    | 94.40%                  | 30.90%                | 72.40%                                     | 12.30%                                       | 6.70%                                          | 5.90%                | 6.10%                   | 63.90%                                        | 855                                            | 2,147                                                |
| 37782  | Unbleed 19: SC-CD3 GEM 53C Strept            | 45,118              | 92.00%         | 61.40%                                    | 95.30%                  | 28.90%                | 68.4%                                      | 16.60%                                       | 6.70%                                          | 6.70%                | 6.30%                   | 68.00%                                        | 757                                            | 1,744                                                |
| 37783  | Unbleed 20: SC-CD3 GEM 53C Strept            | 37,671              | 92.00%         | 61.60%                                    | 94.50%                  | 28.20%                | 68.6%                                      | 18.20%                                       | 6.50%                                          | 6.80%                | 6.80%                   | 67.90%                                        | 741                                            | 1,702                                                |

FIG. 54

74/84

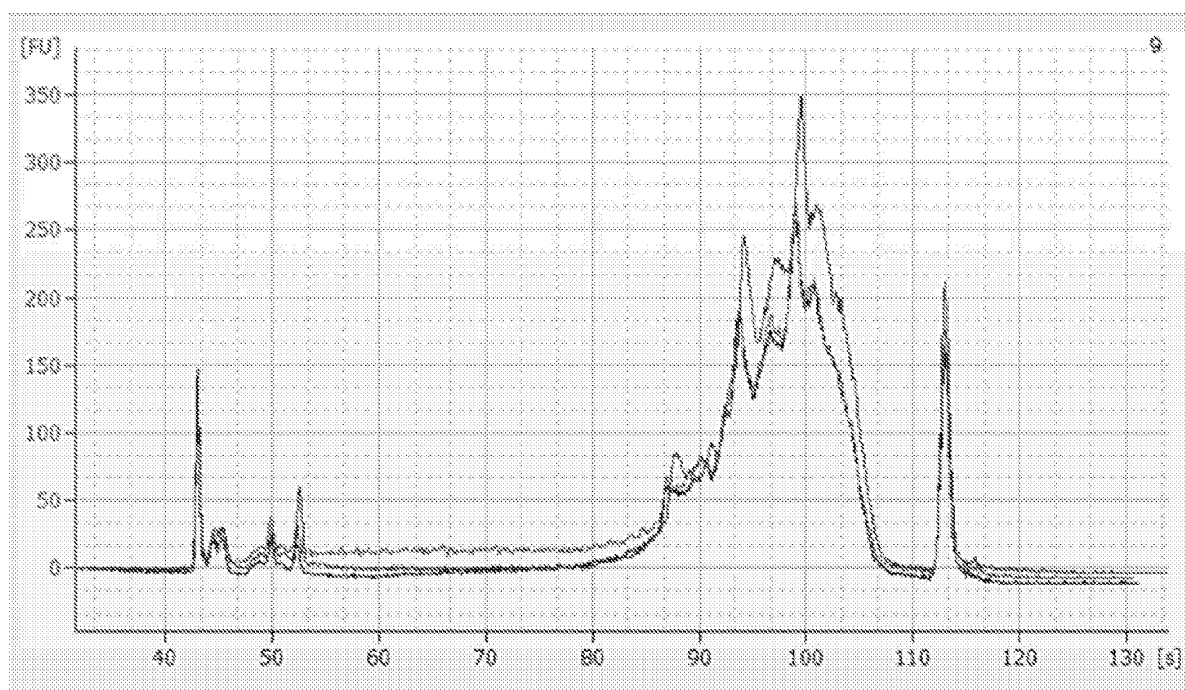


FIG. 55

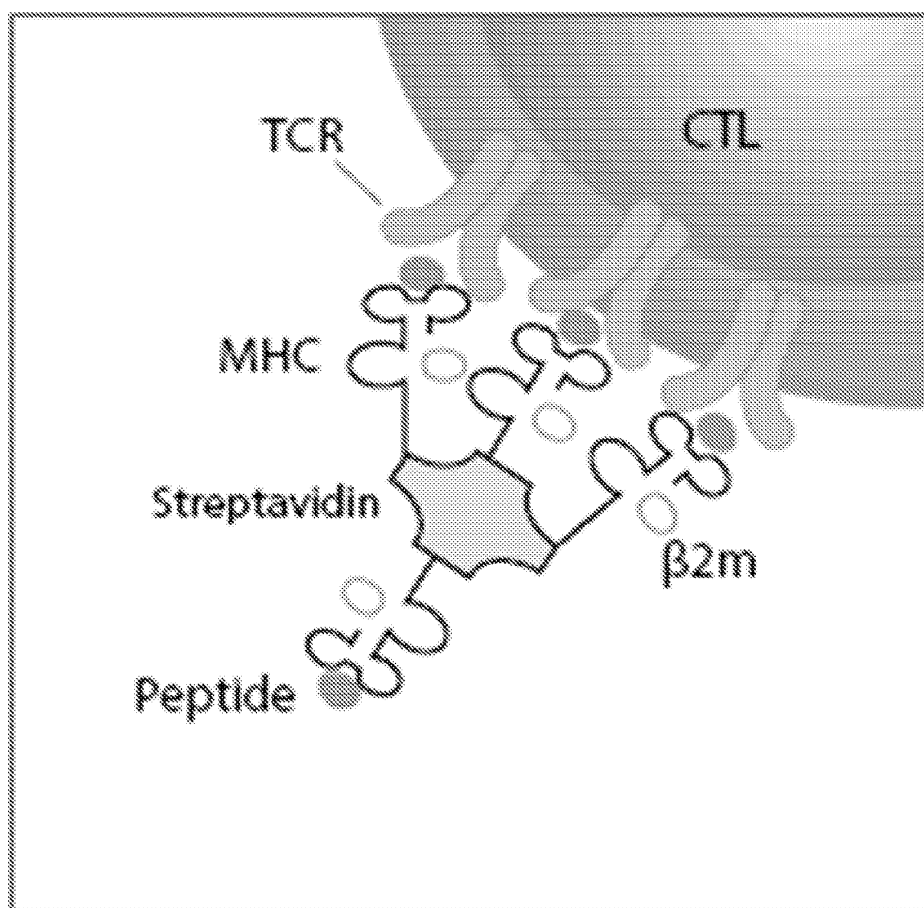


FIG. 56A

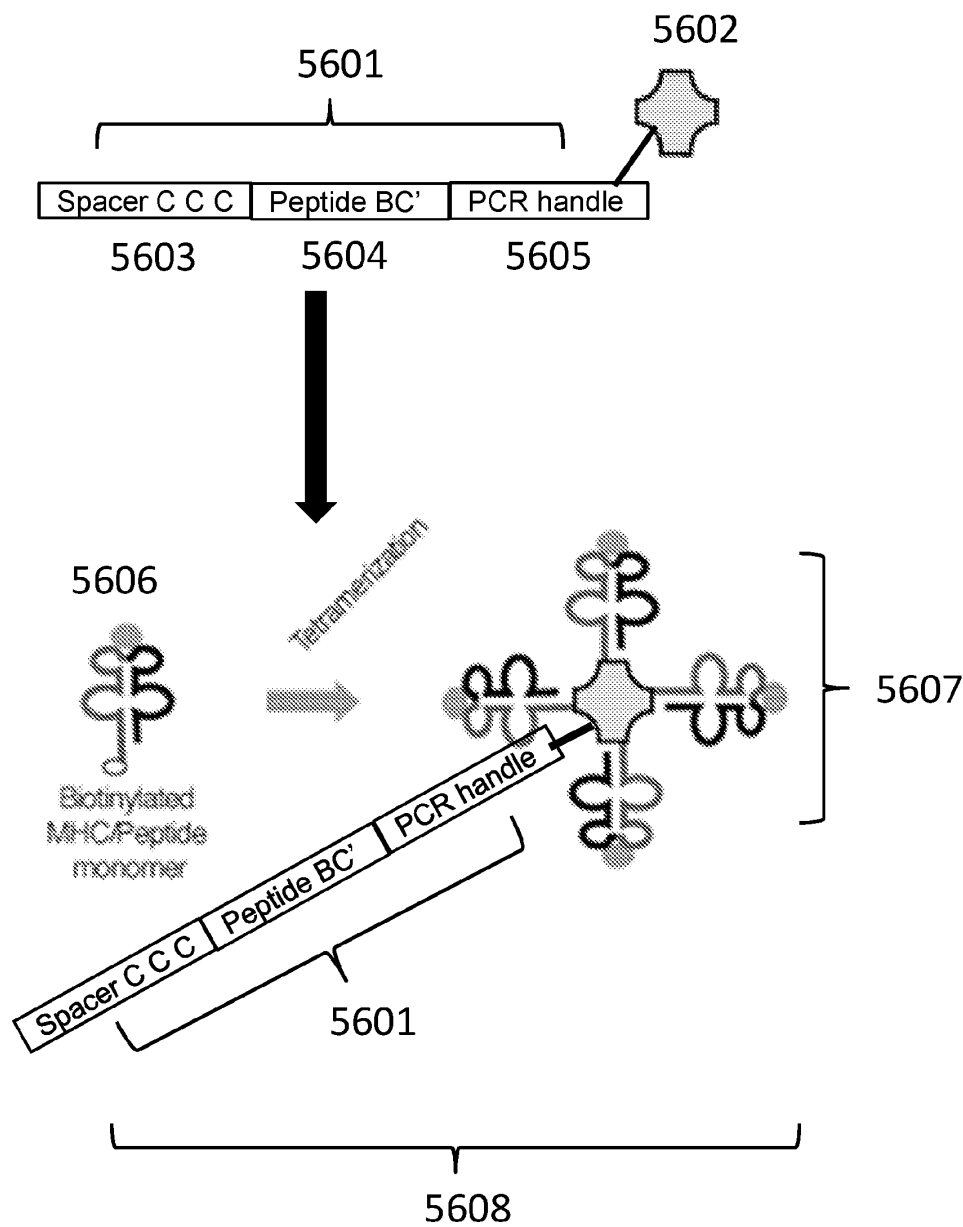


FIG. 56B

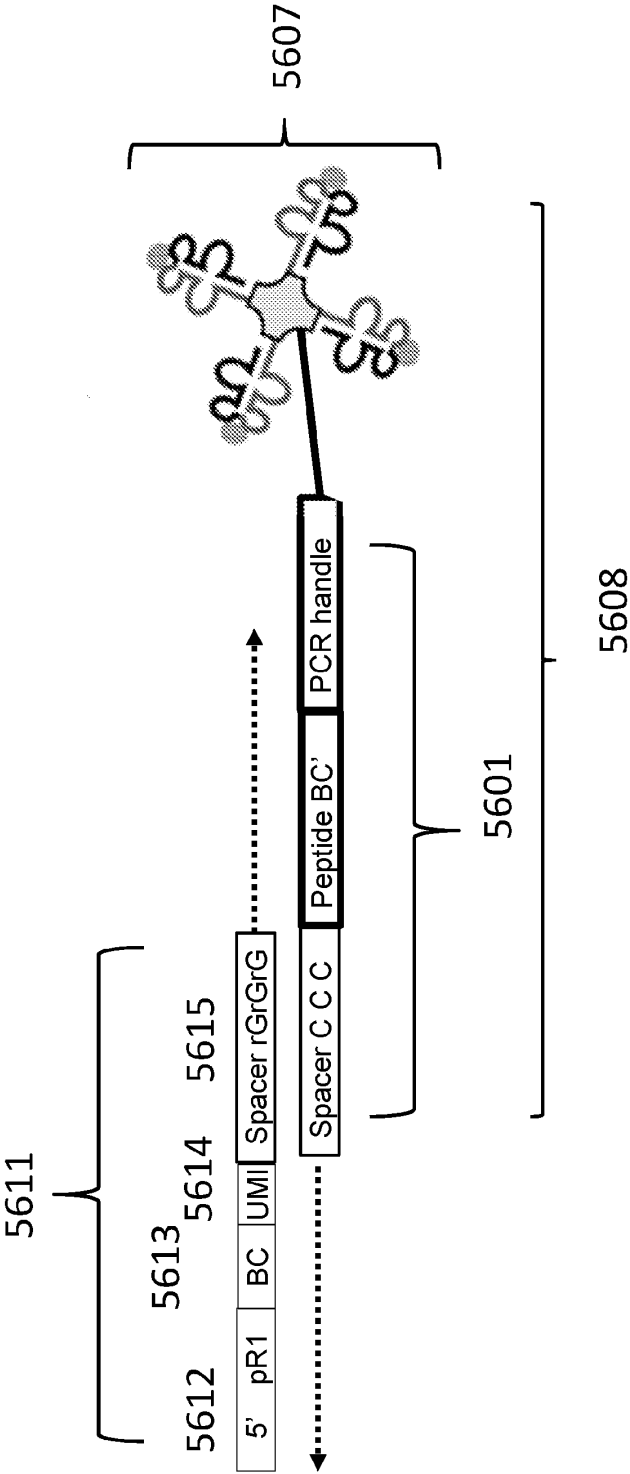


FIG. 56C

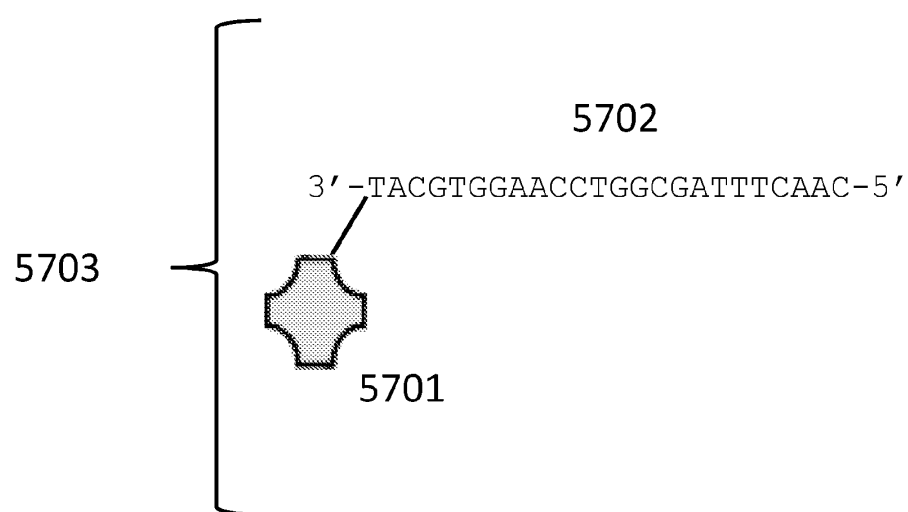


FIG. 57A

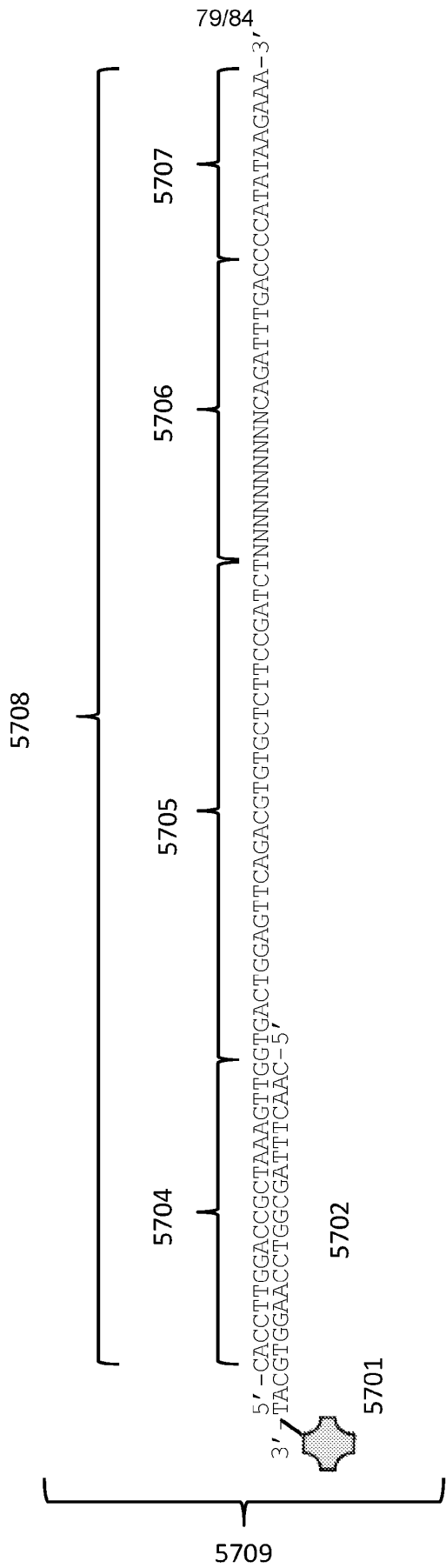


FIG. 57B



FIG. 58A

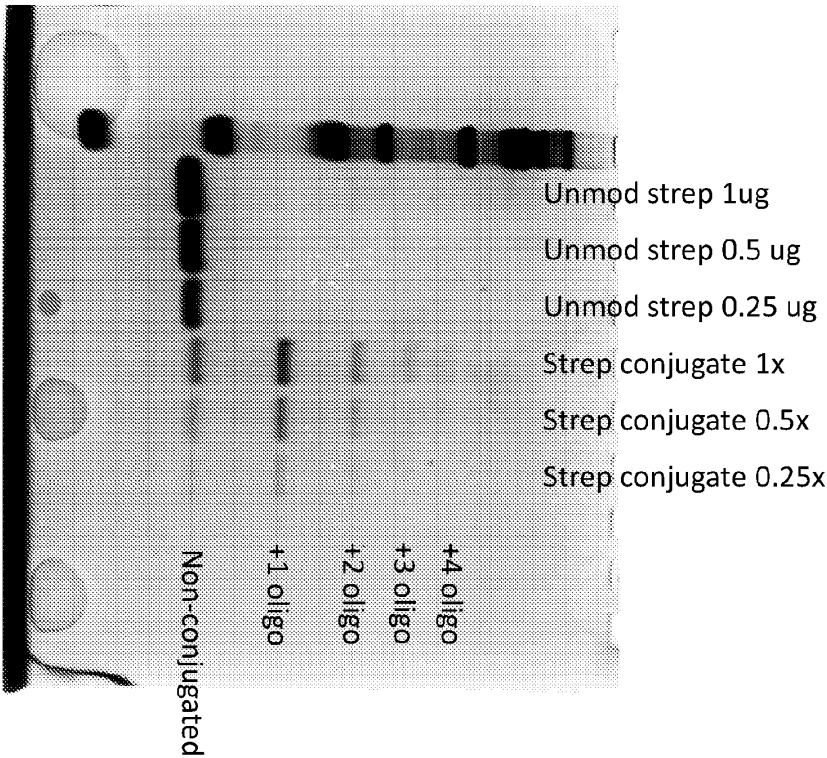


FIG. 58B

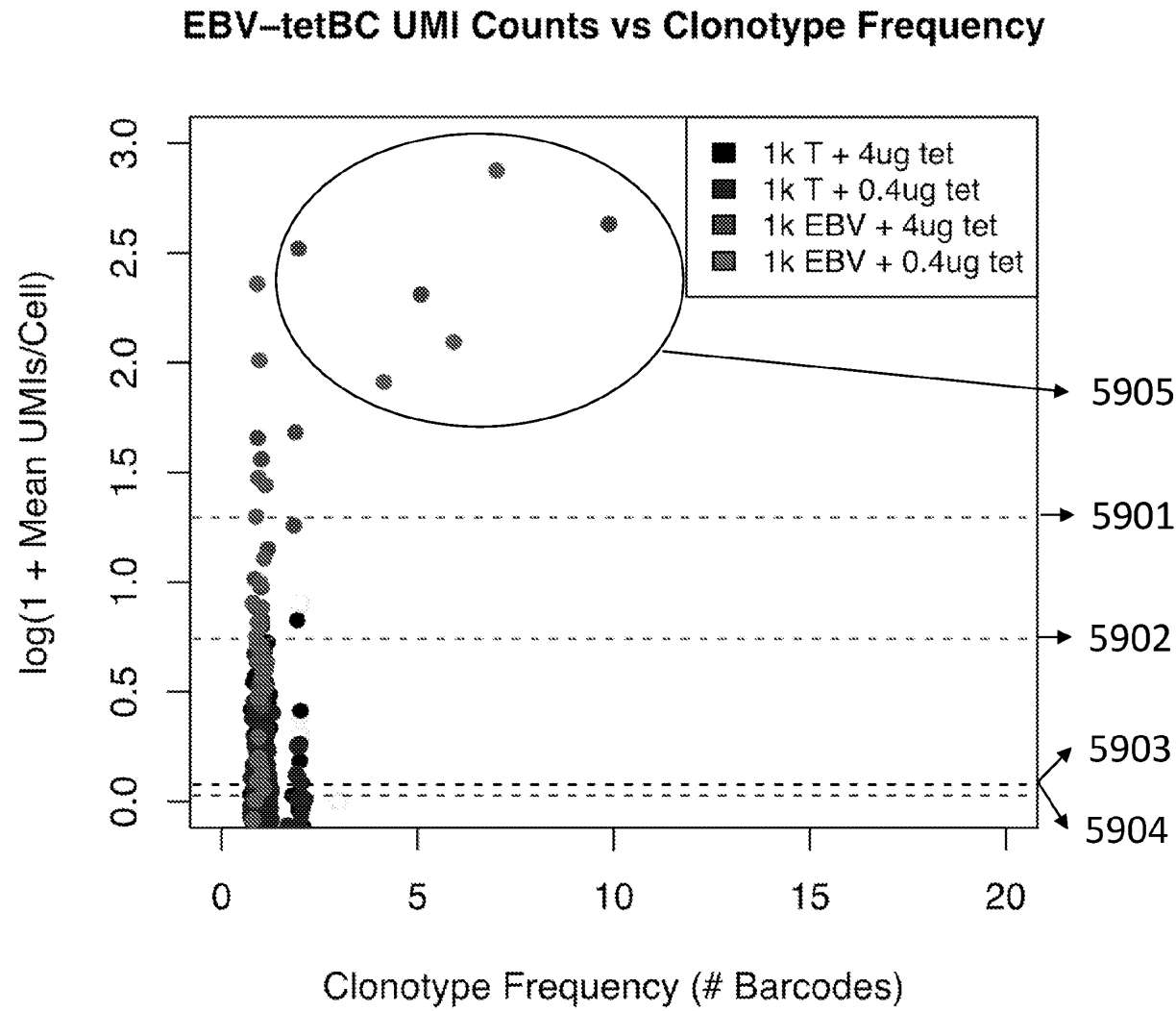


FIG. 59

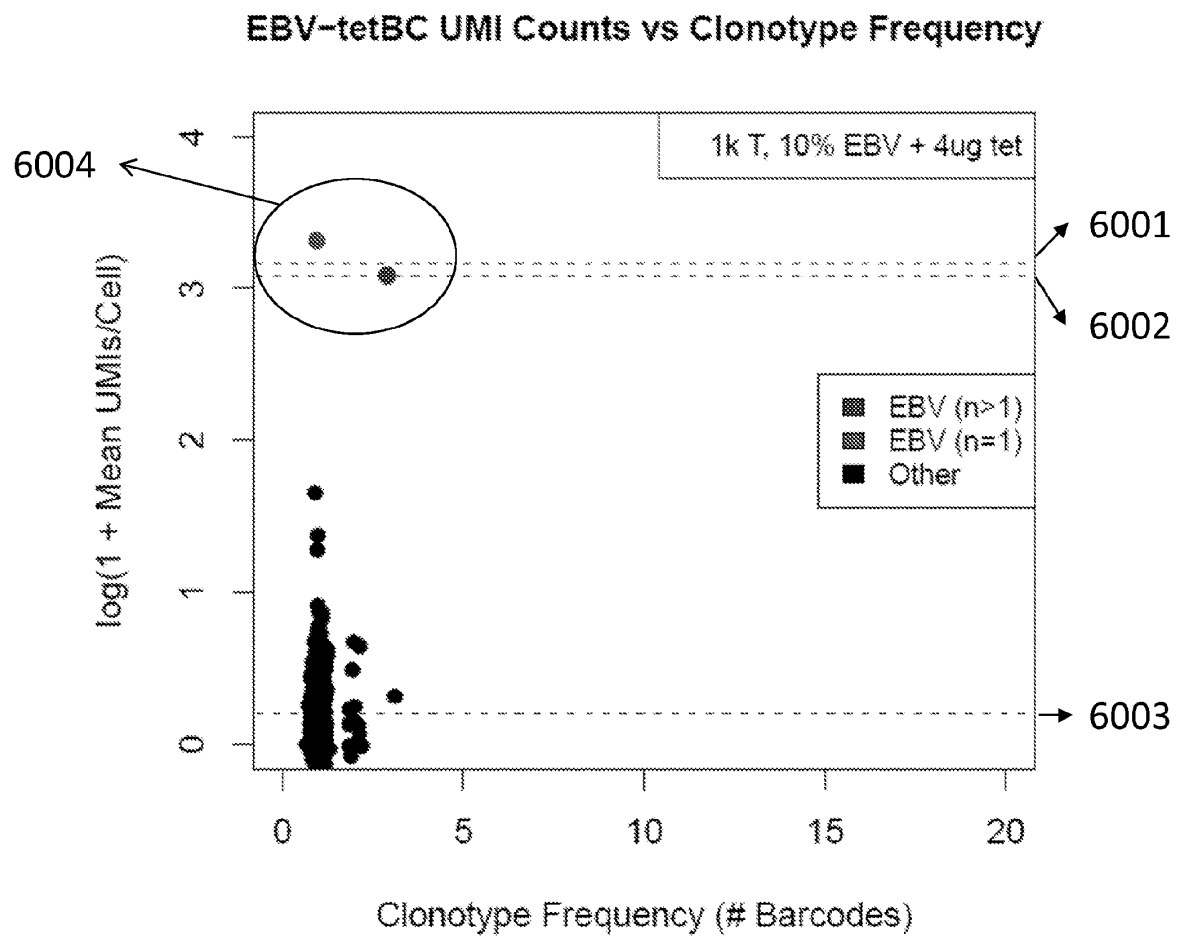


FIG. 60

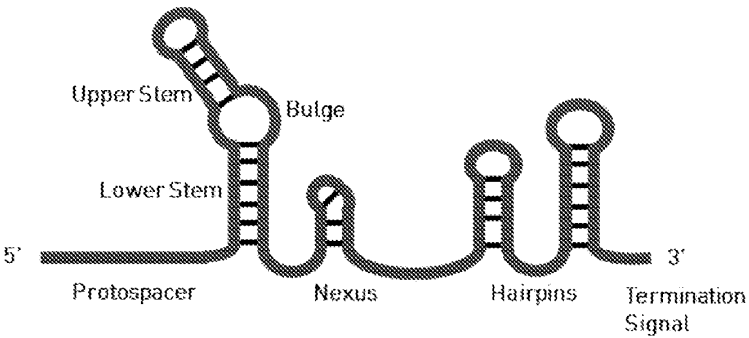


FIG. 61A

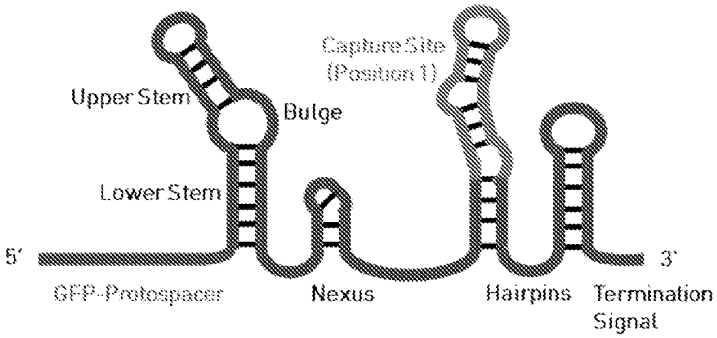


FIG. 61B

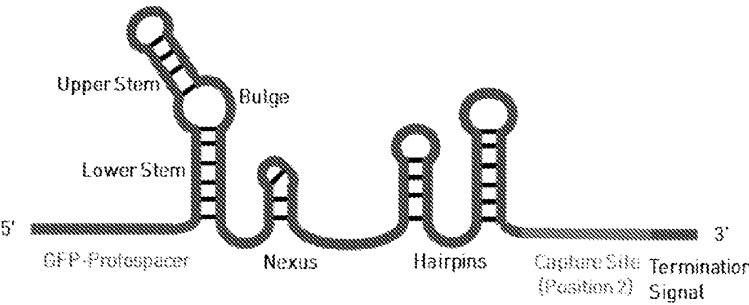


FIG. 61C

84/84

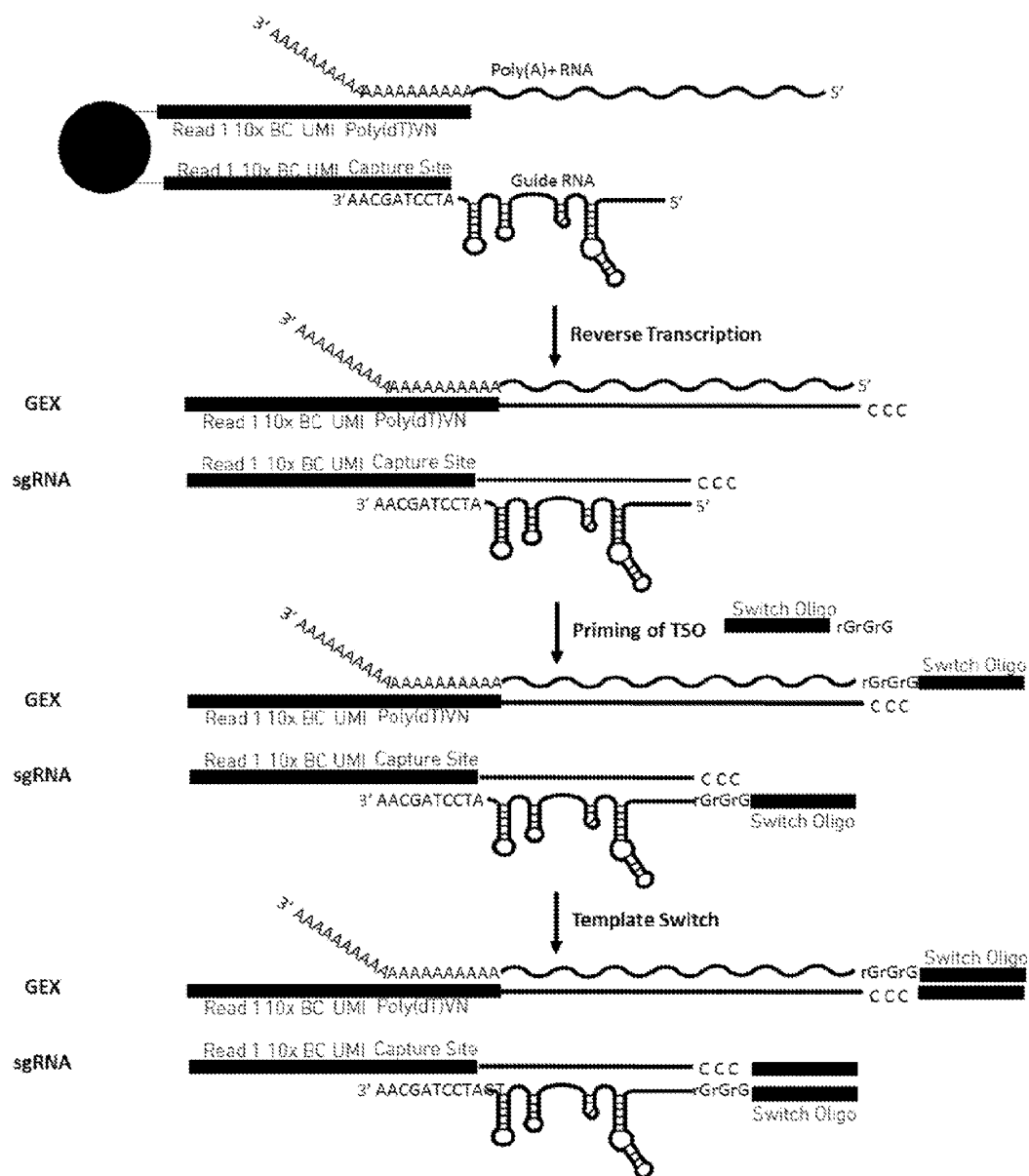


FIG. 61D