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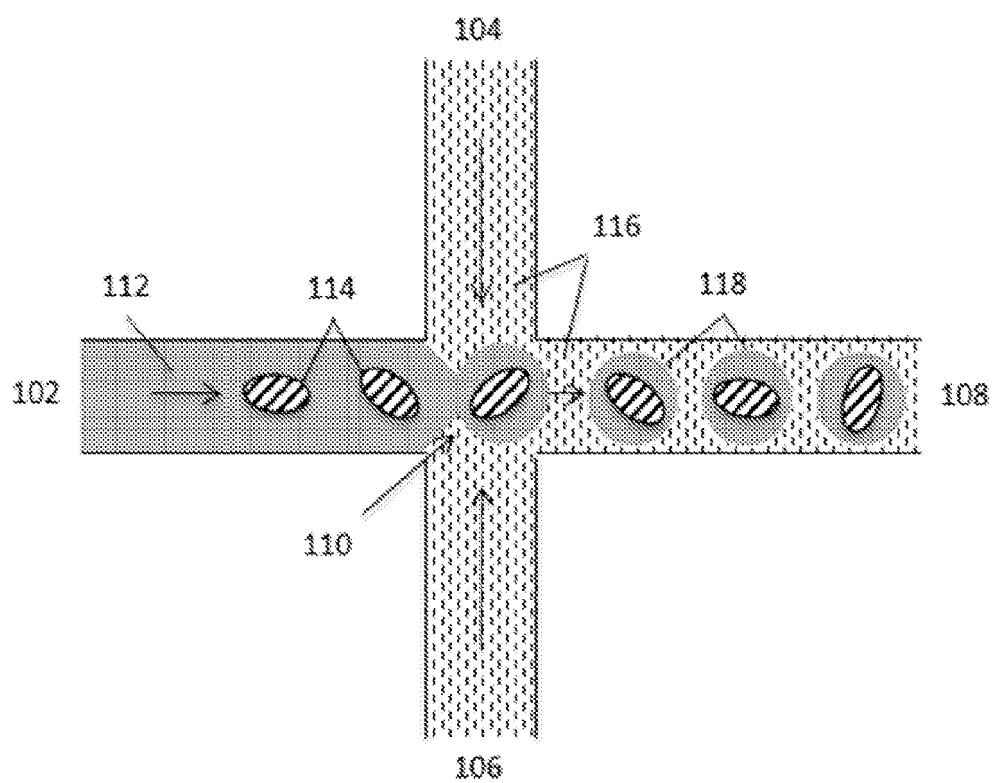


FIG. 1

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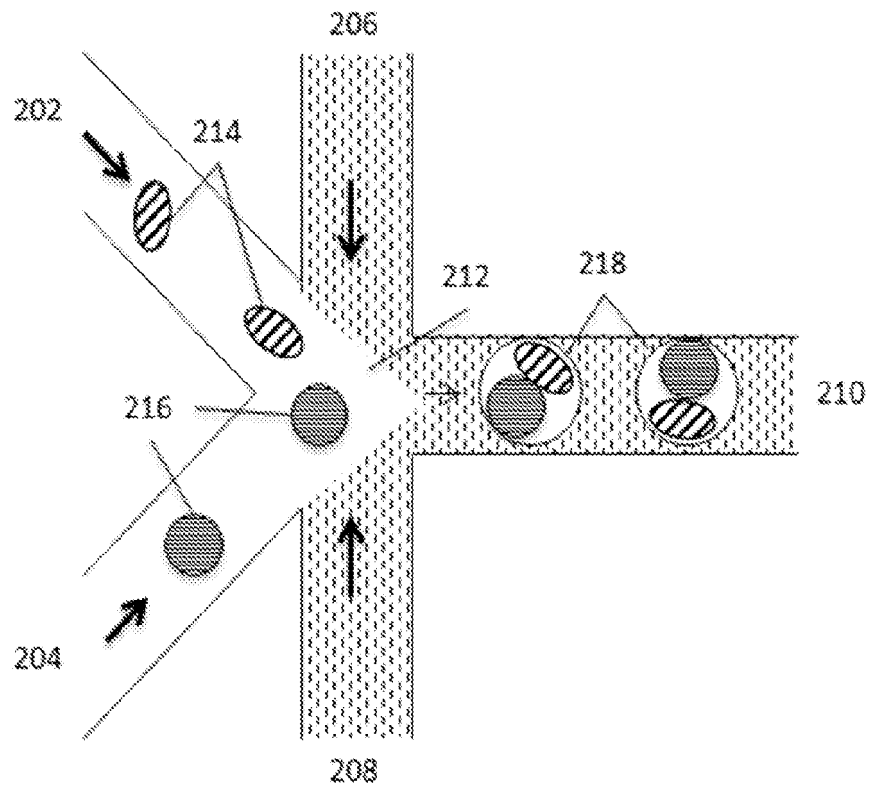
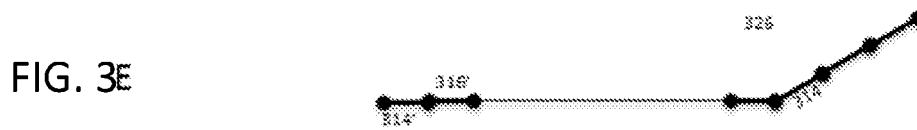
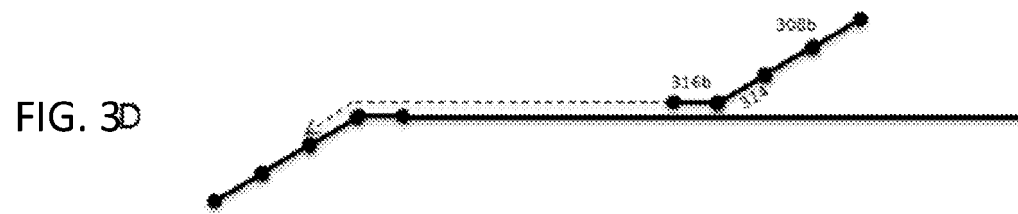
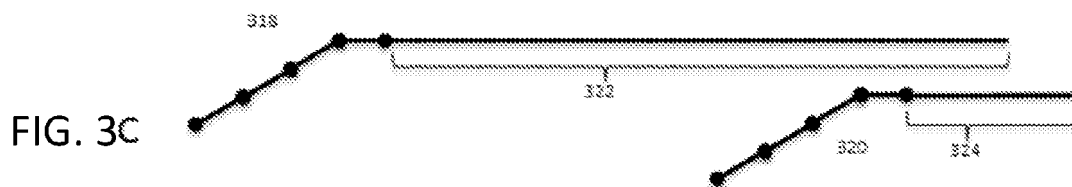
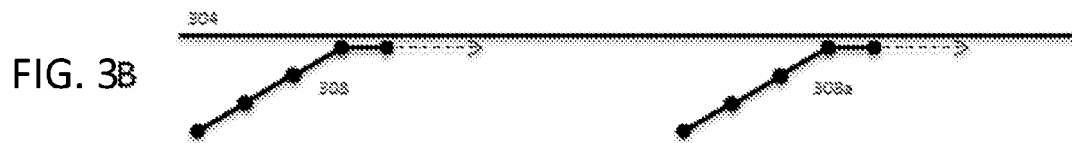
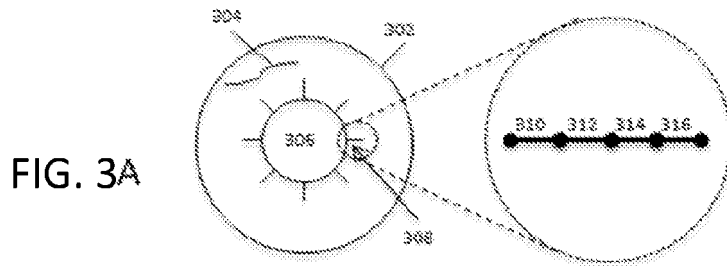


FIG. 2



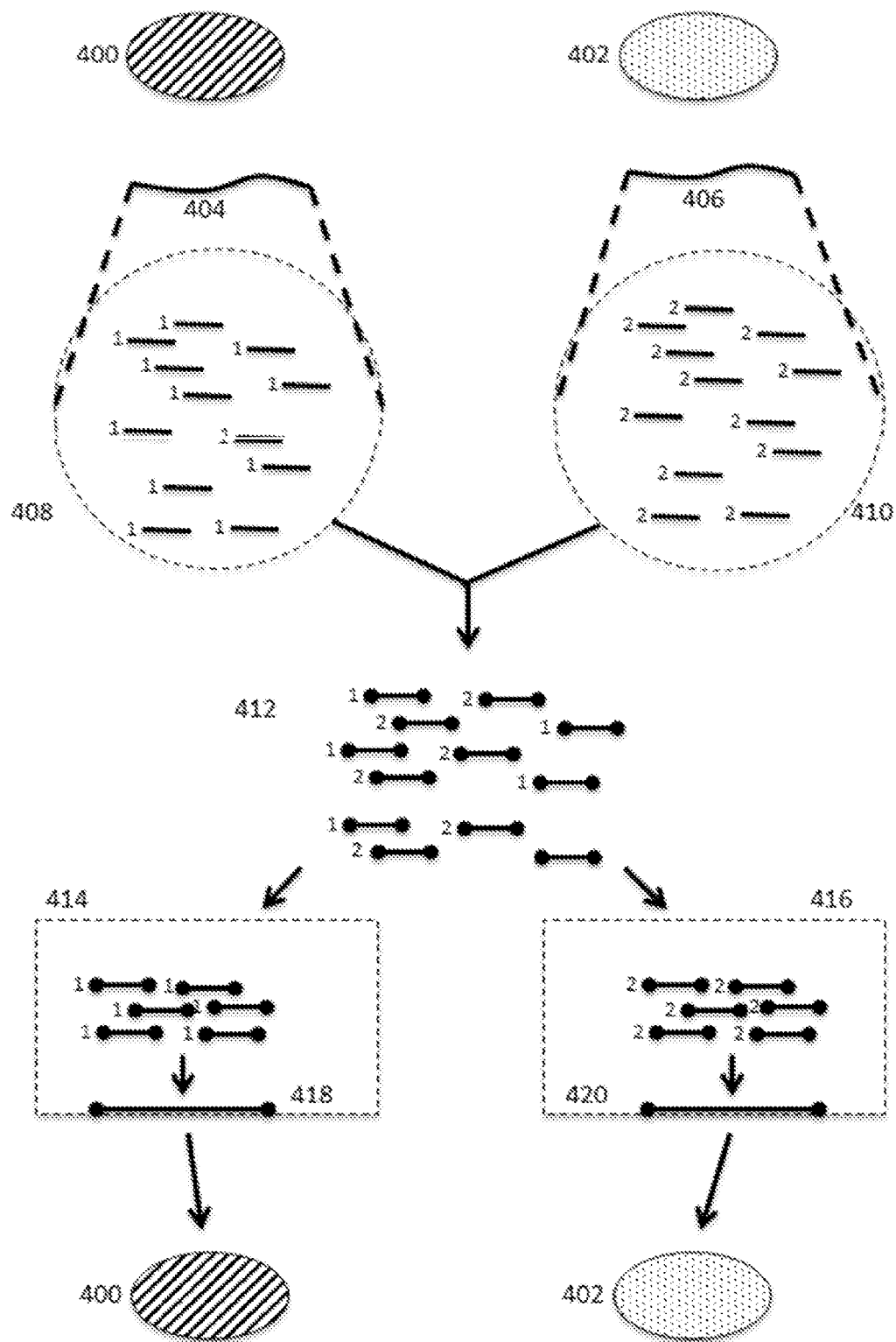


FIG. 4

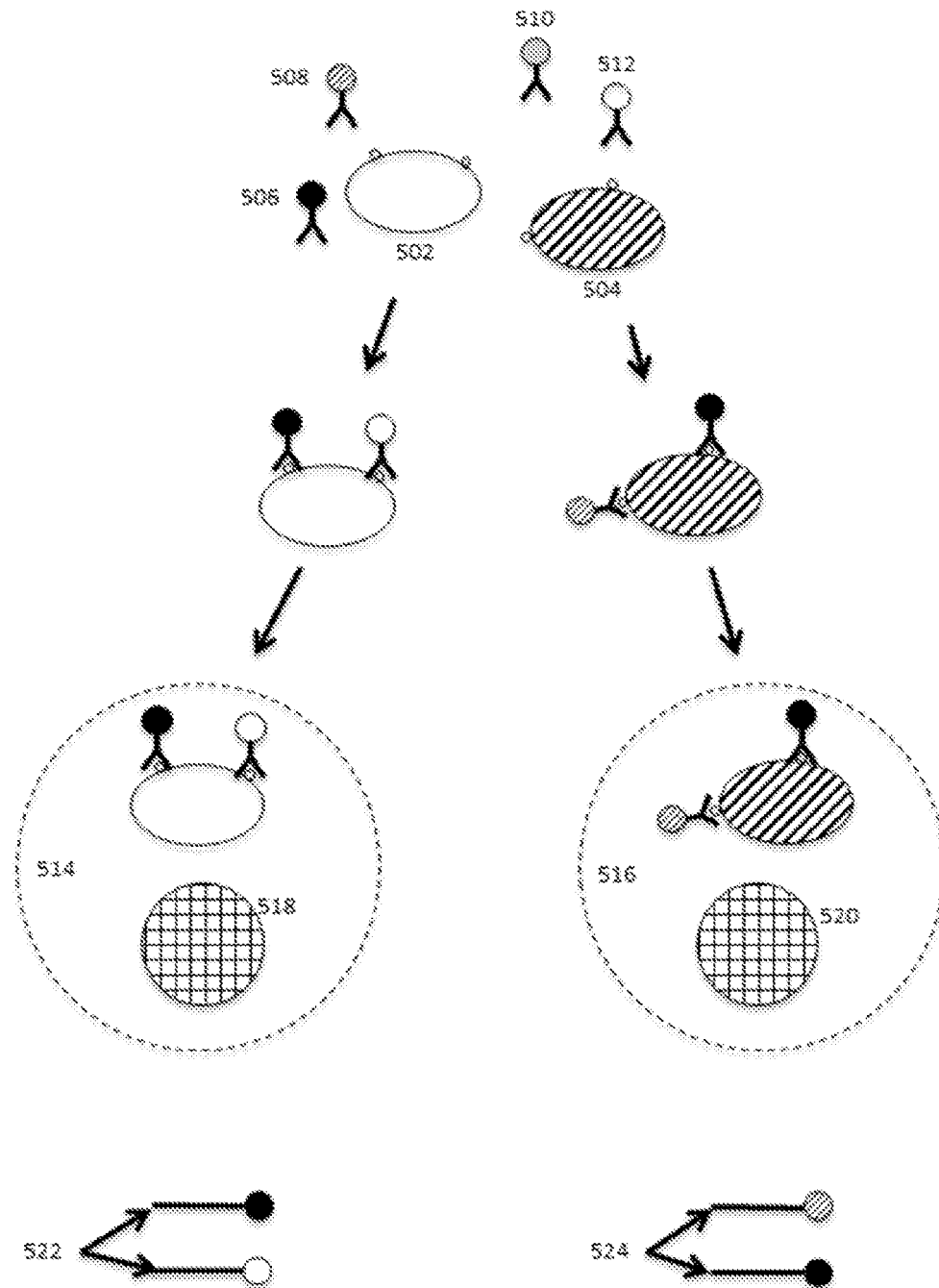


FIG. 5

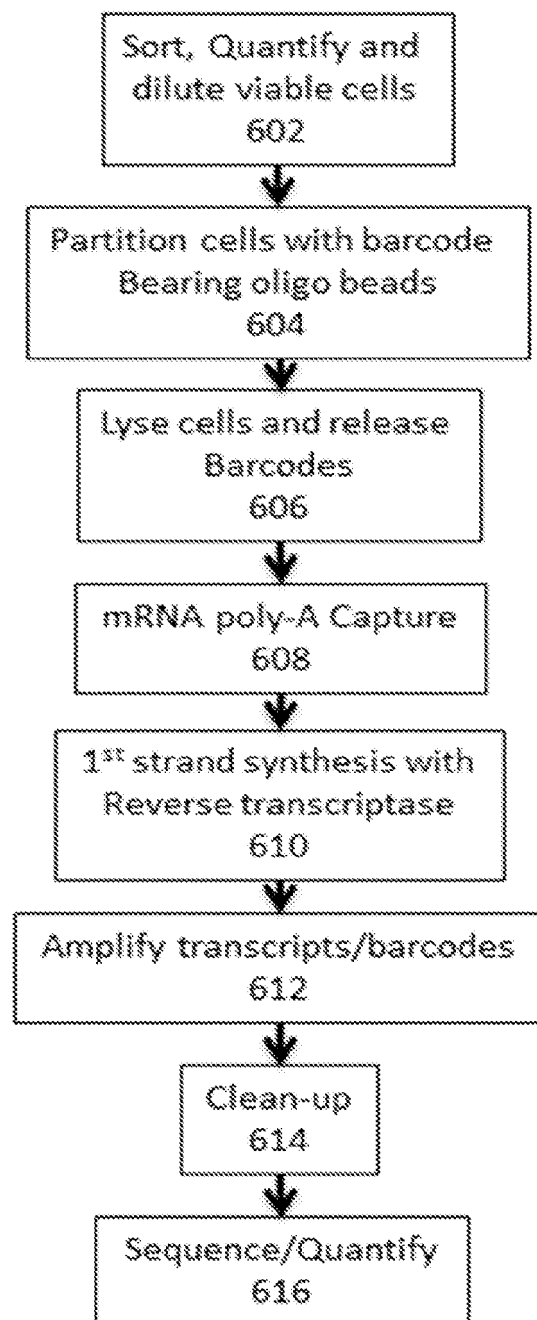


FIG. 6

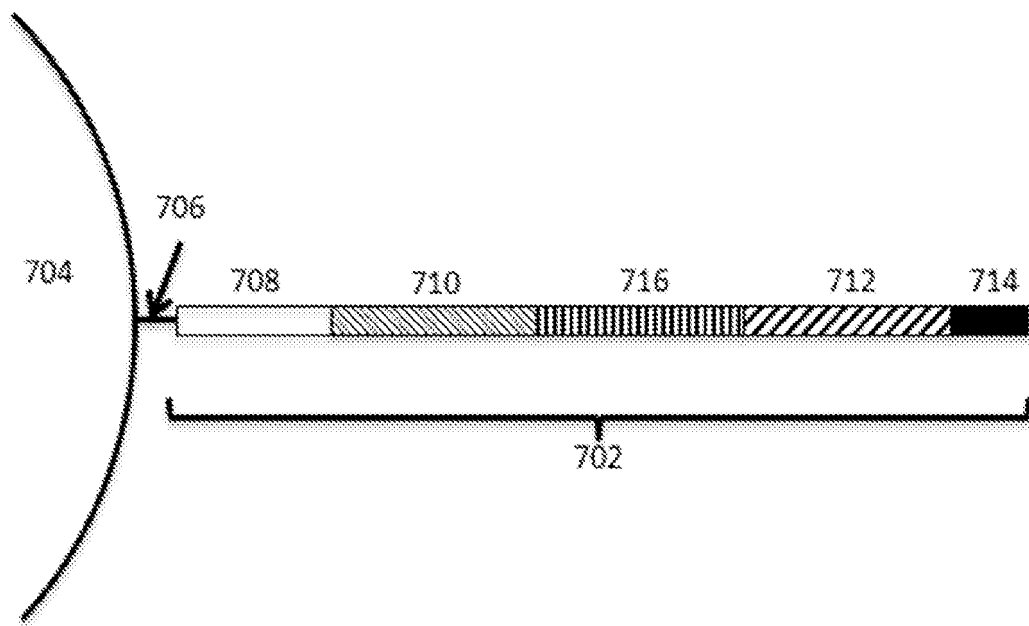


FIG. 7

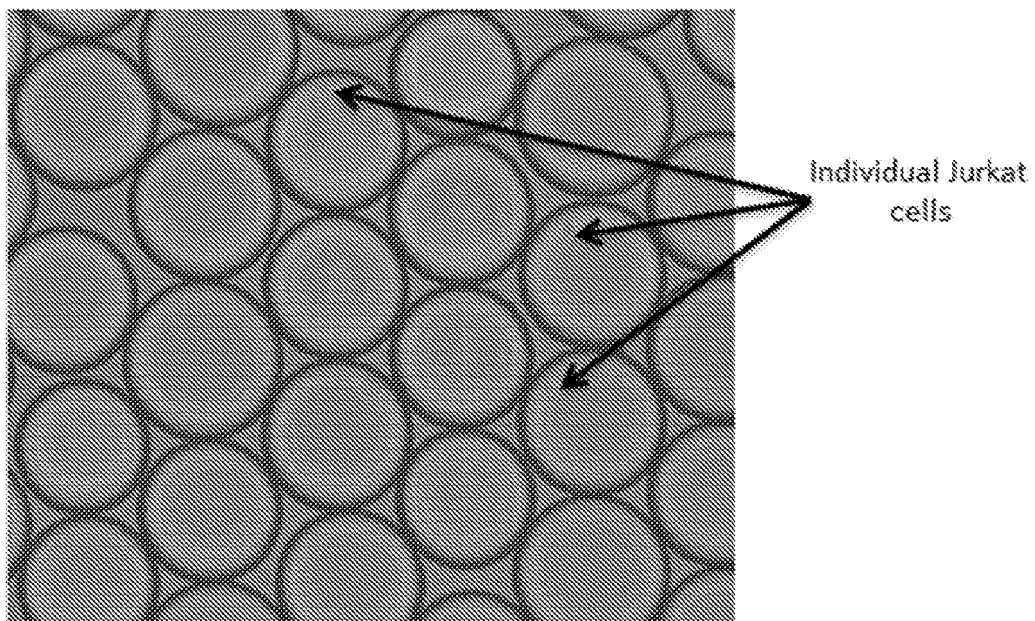
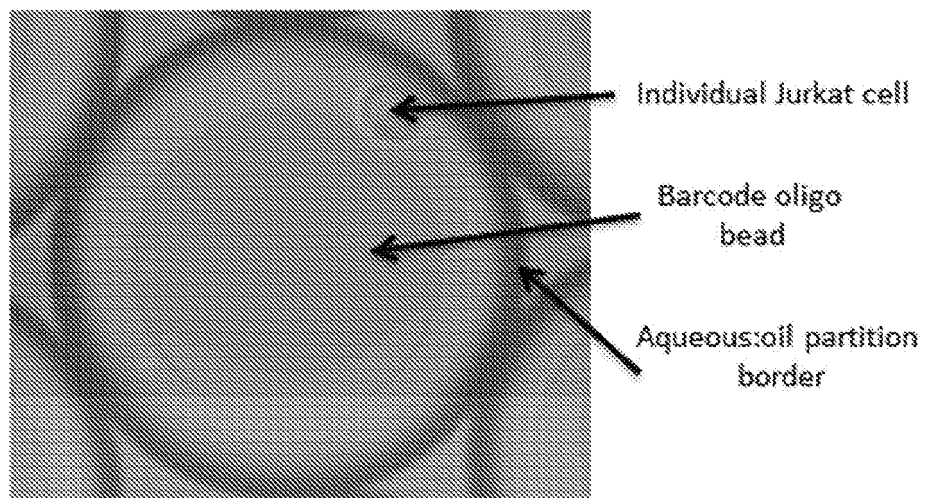


FIG. 8

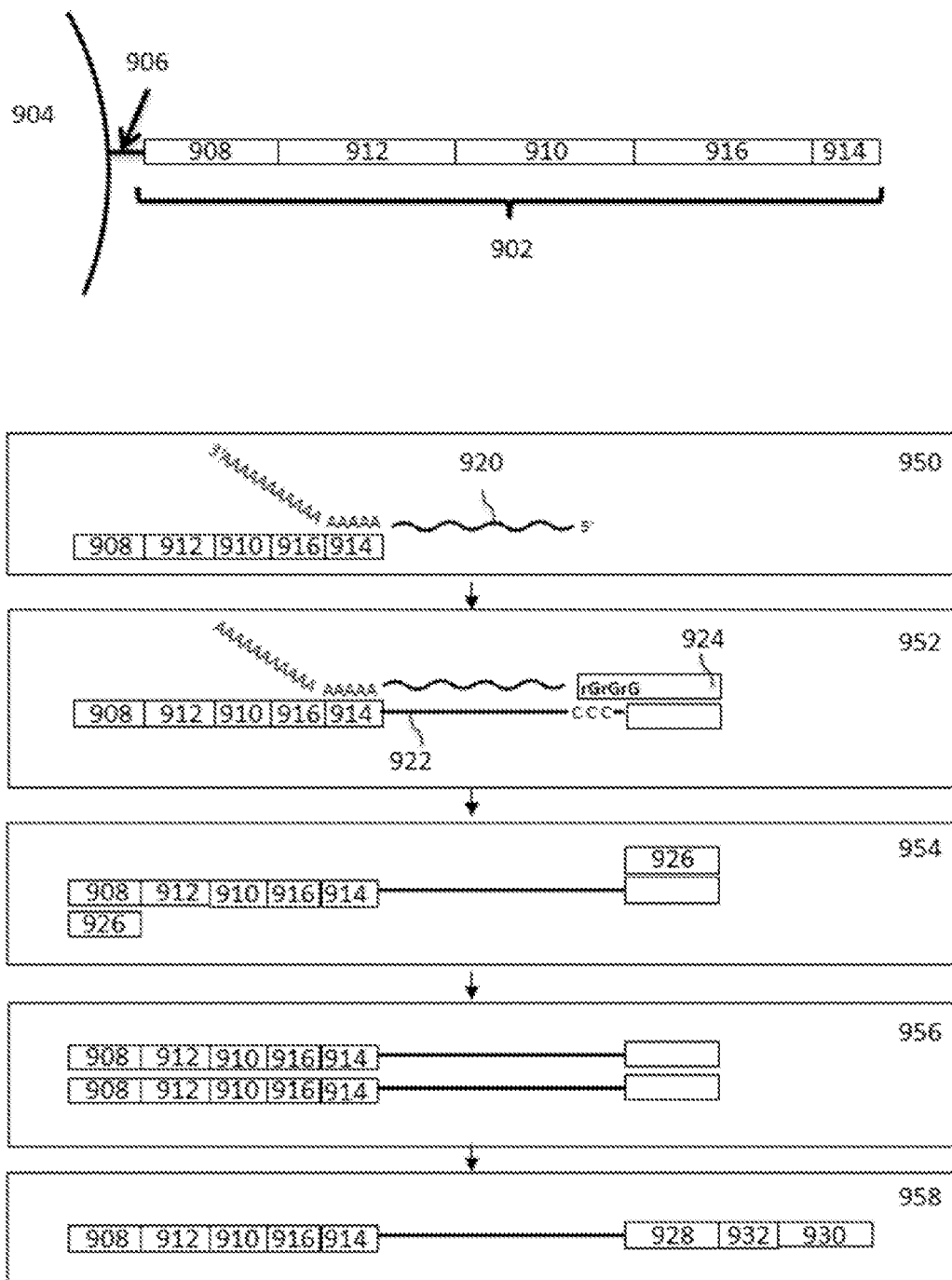


FIG. 9A

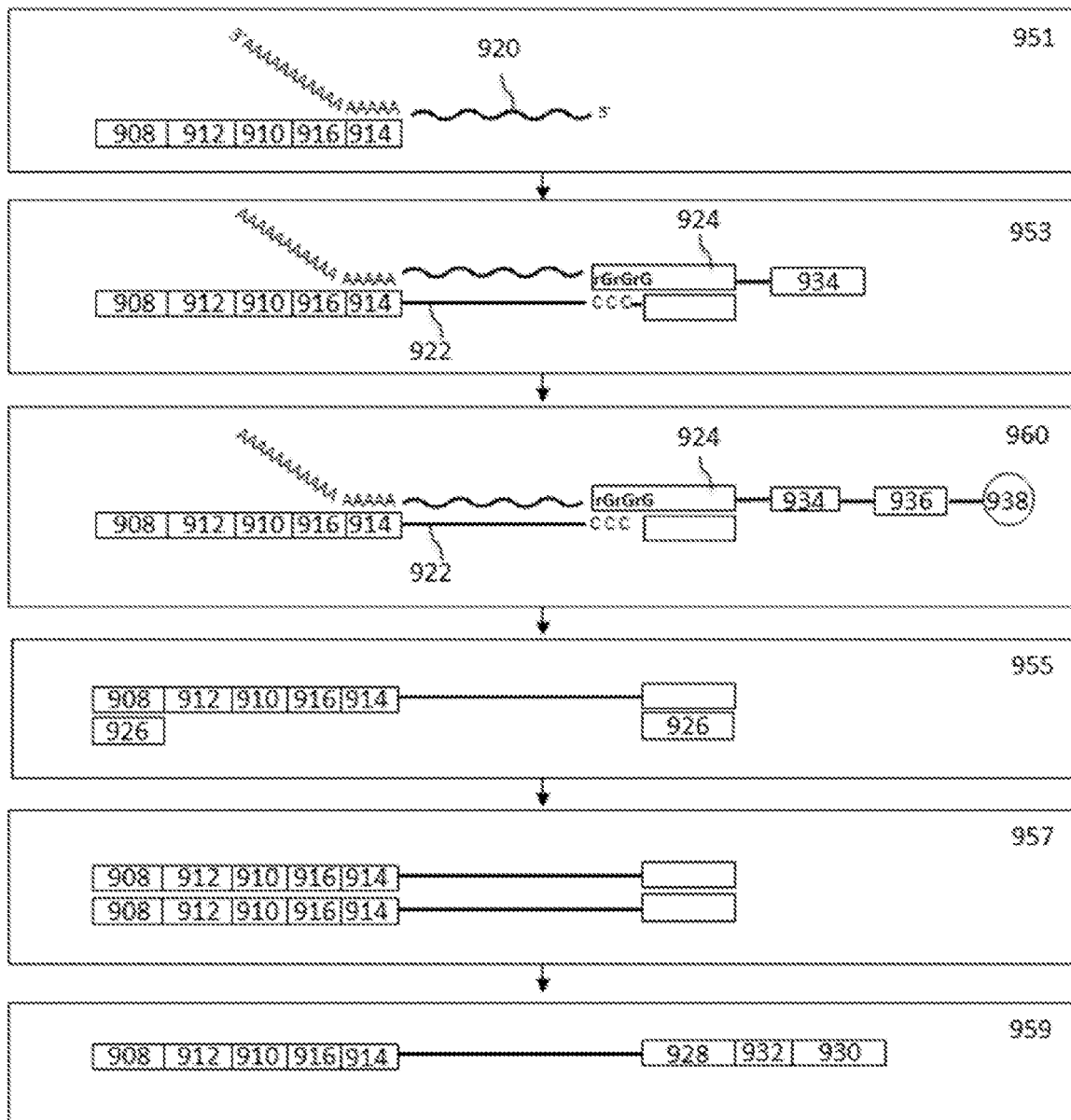


FIG. 9B

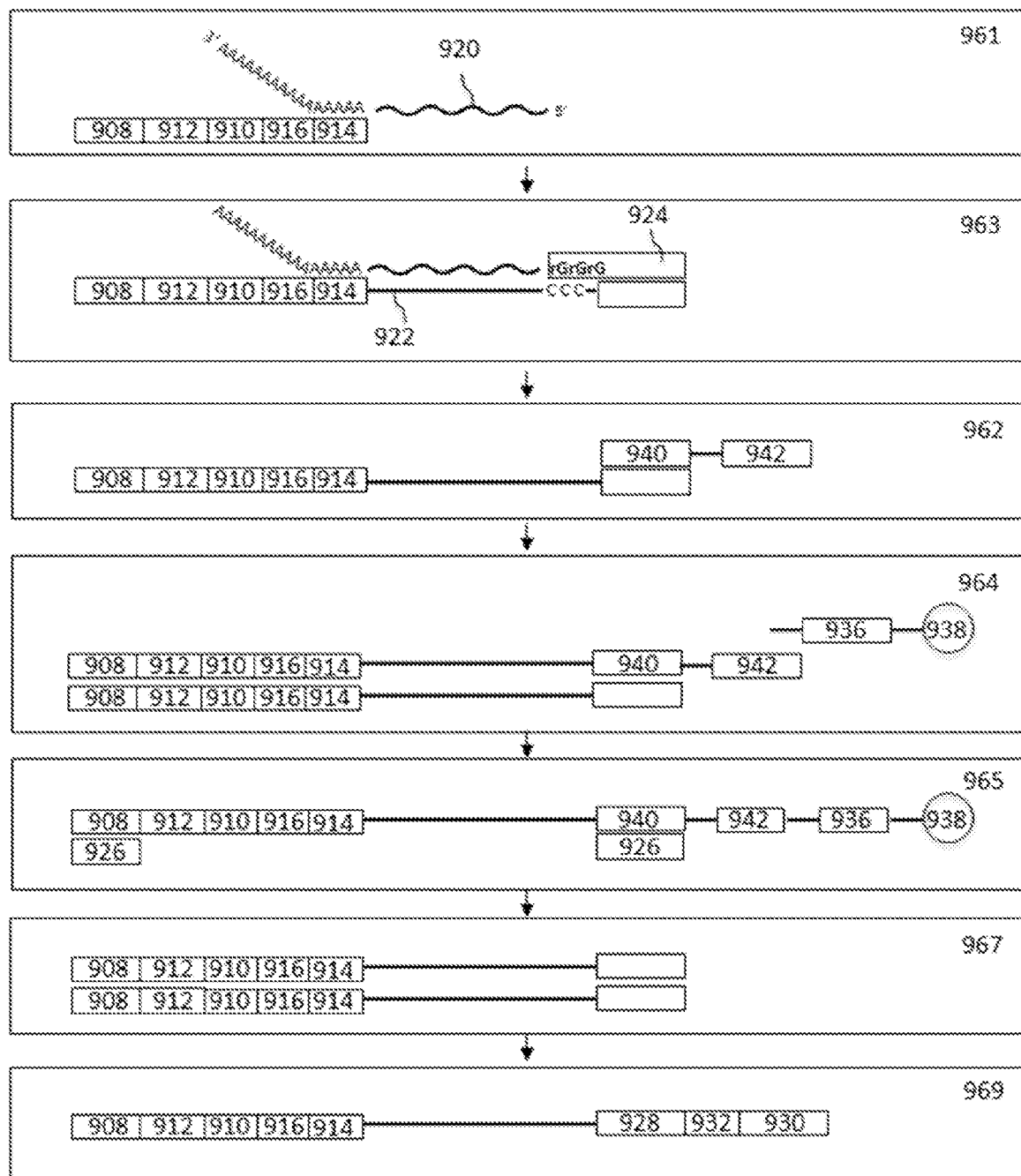


FIG. 9C

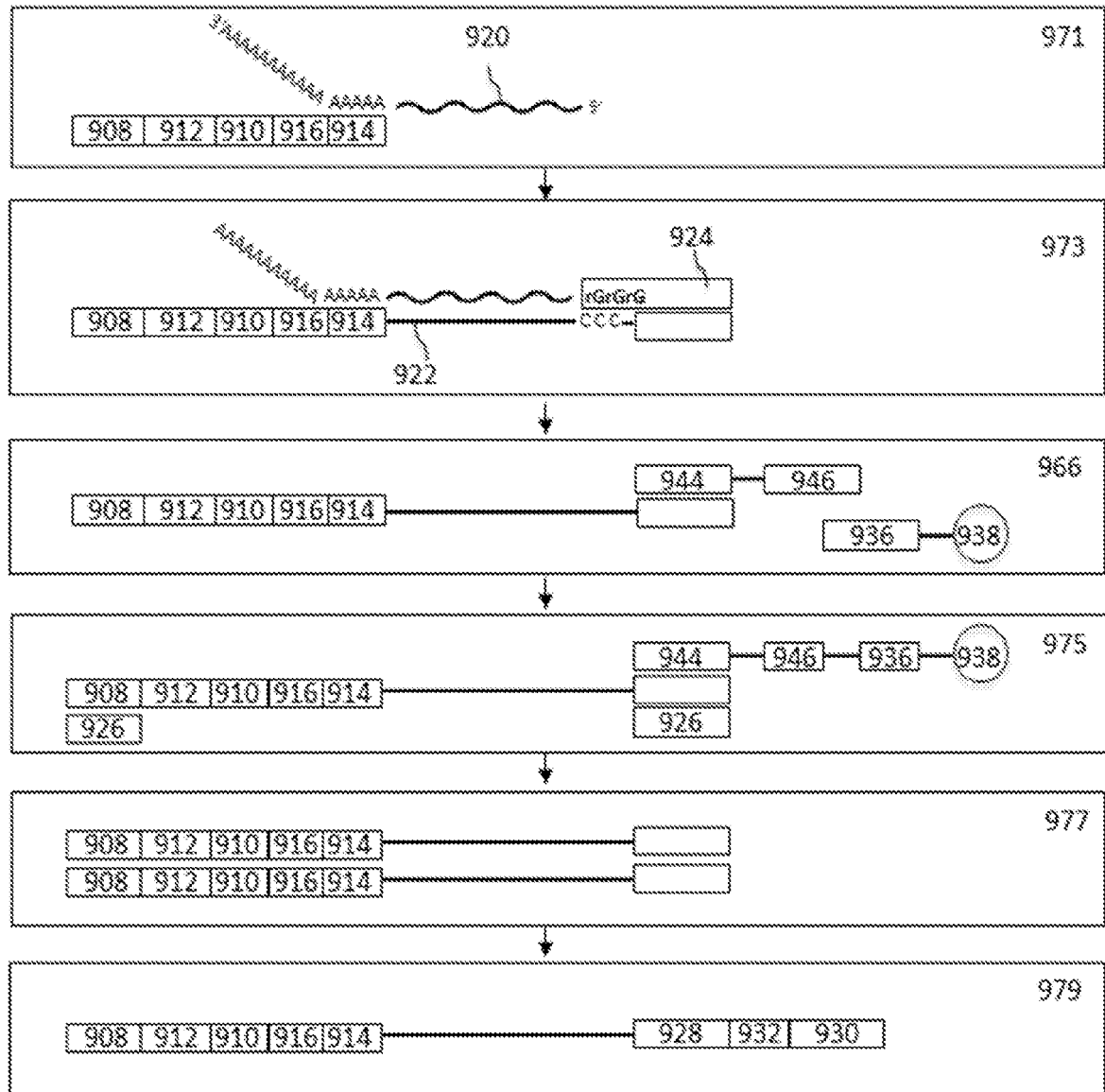


FIG. 9D

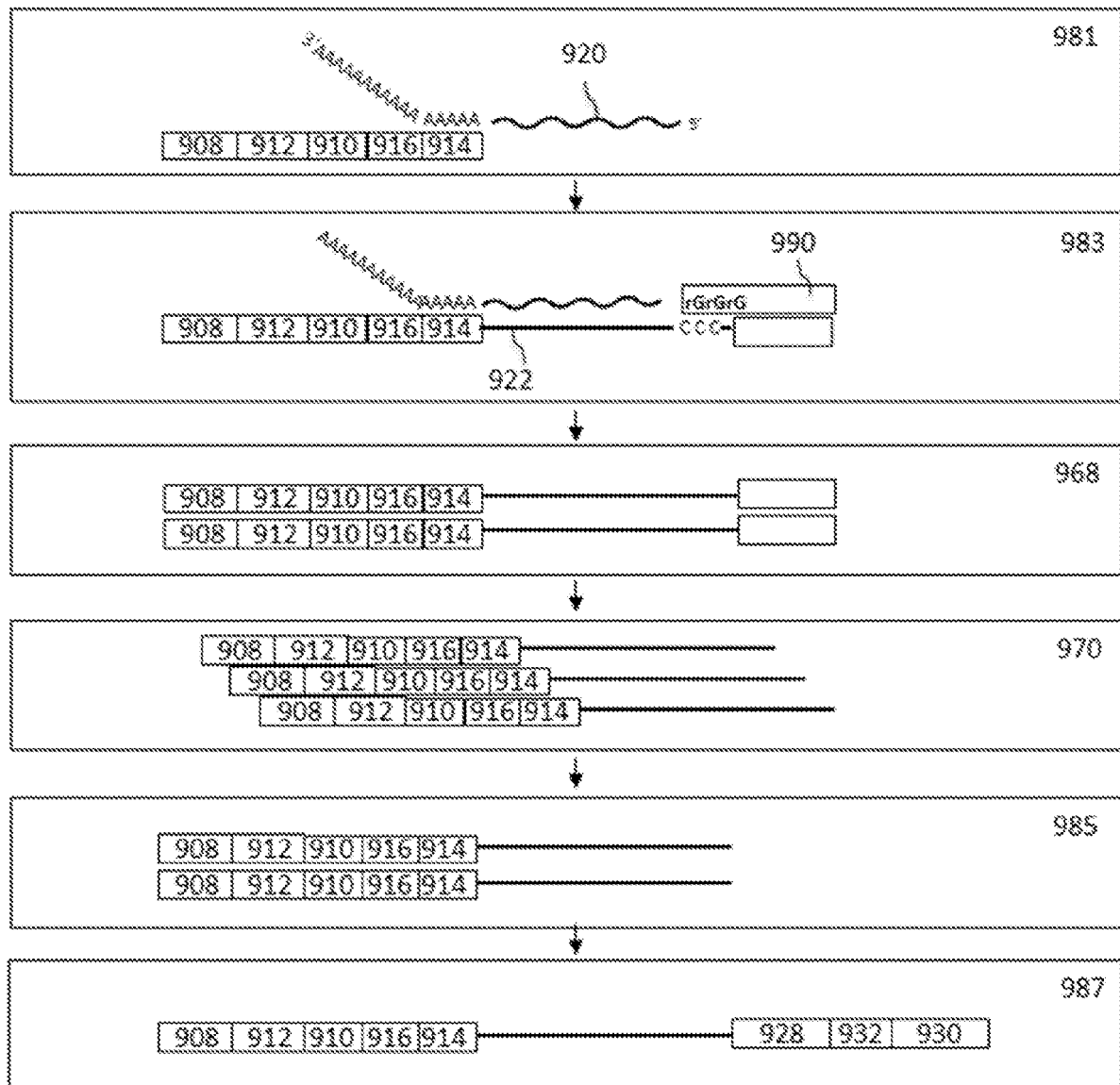


FIG. 9E

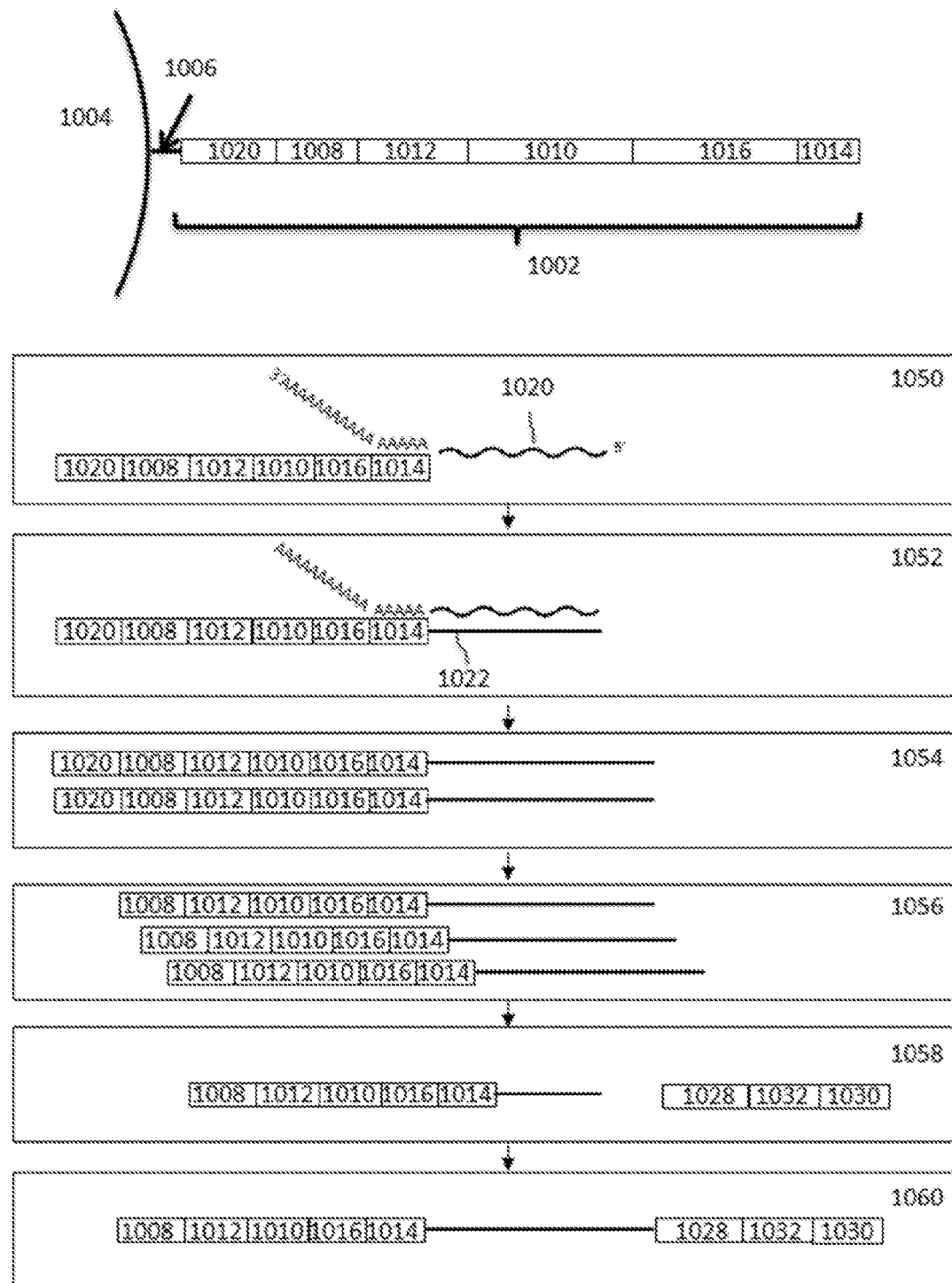


FIG. 10

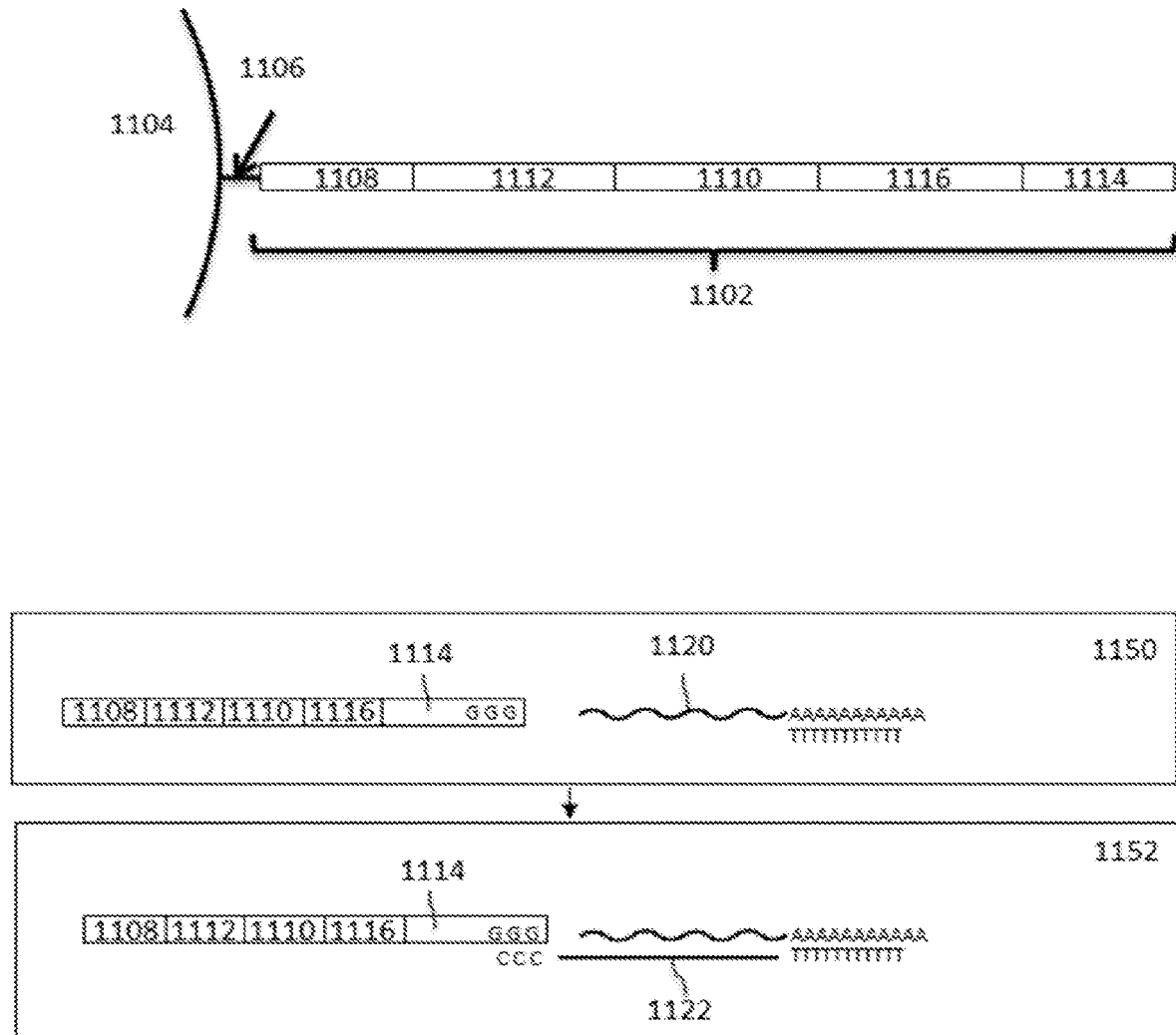


FIG. 11

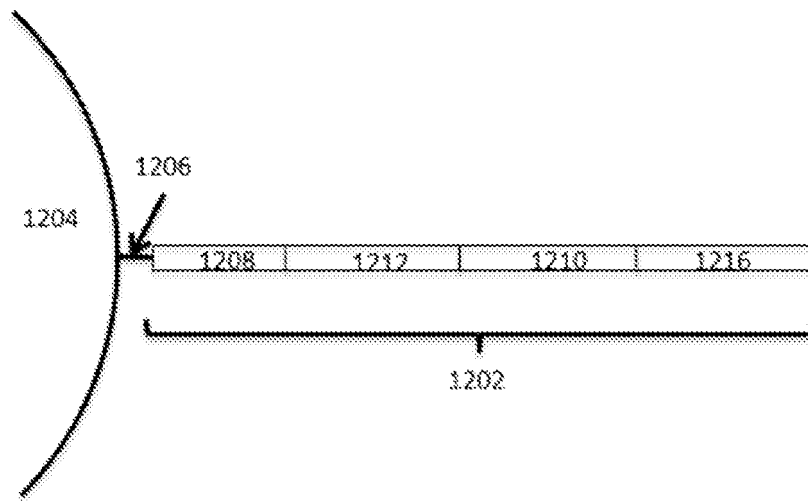


FIG. 12A

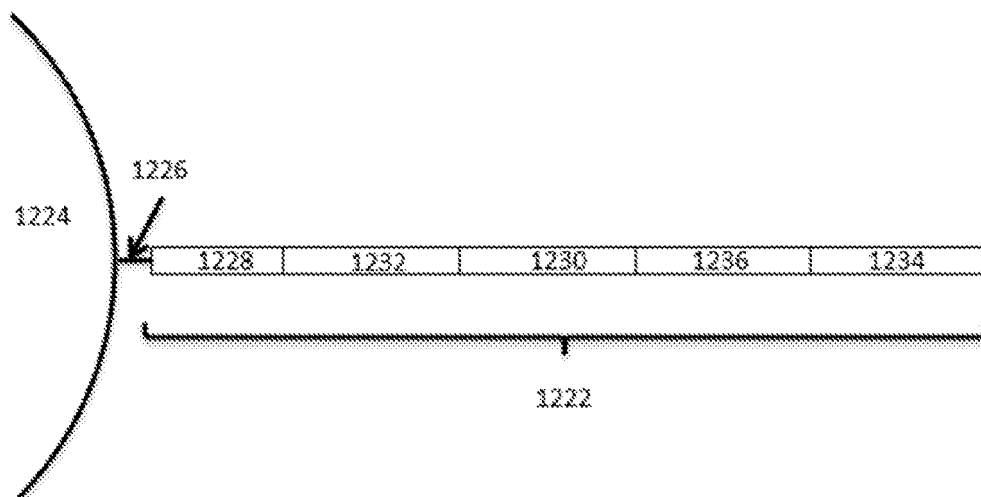


FIG. 12B

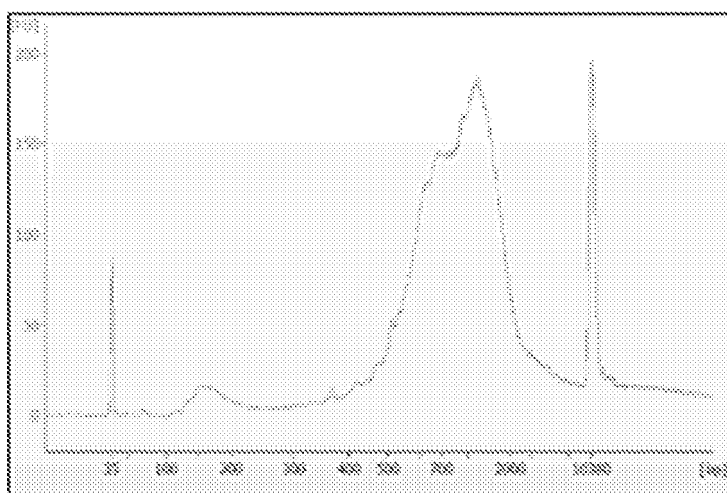


FIG. 13A

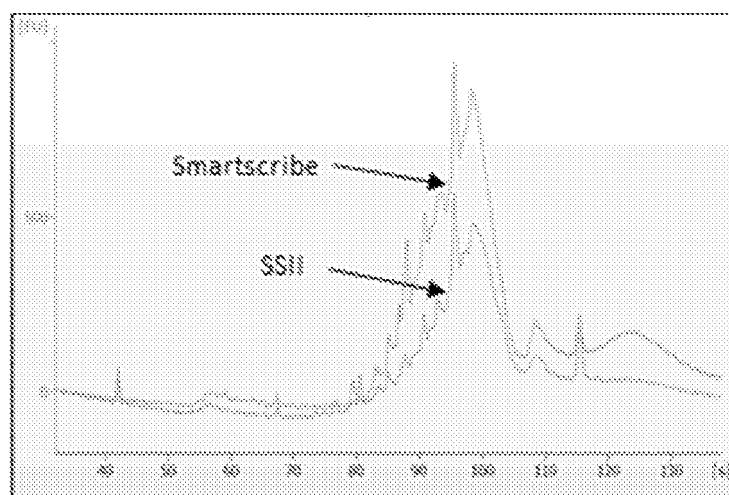


FIG. 13B

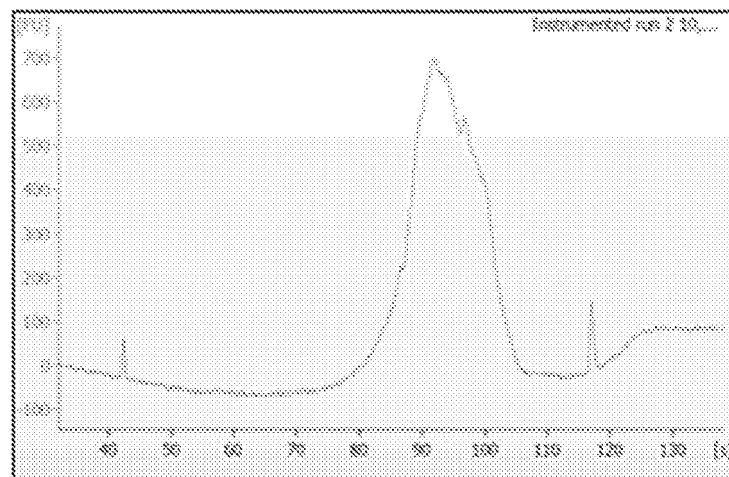


FIG. 13C

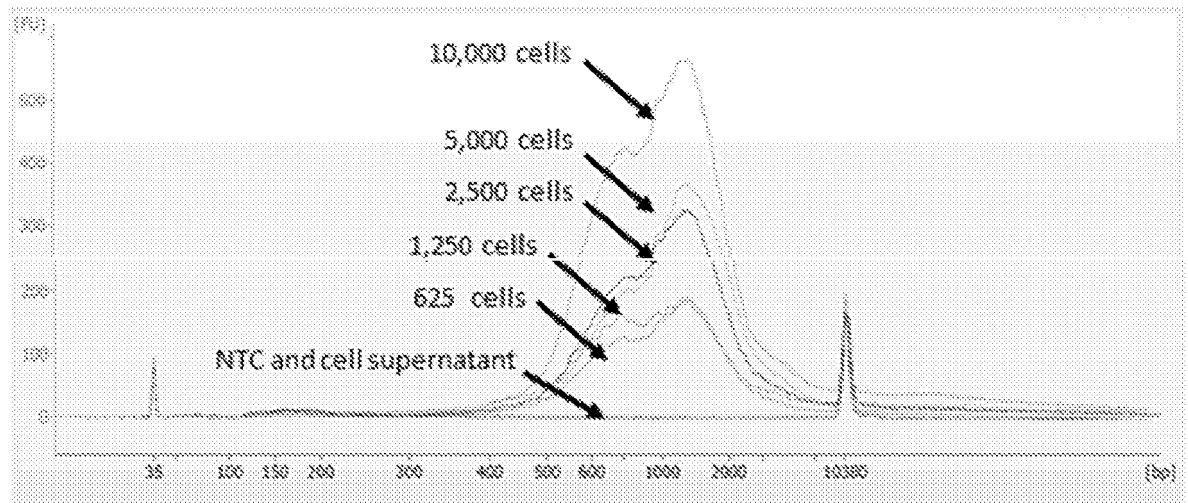


FIG. 14A

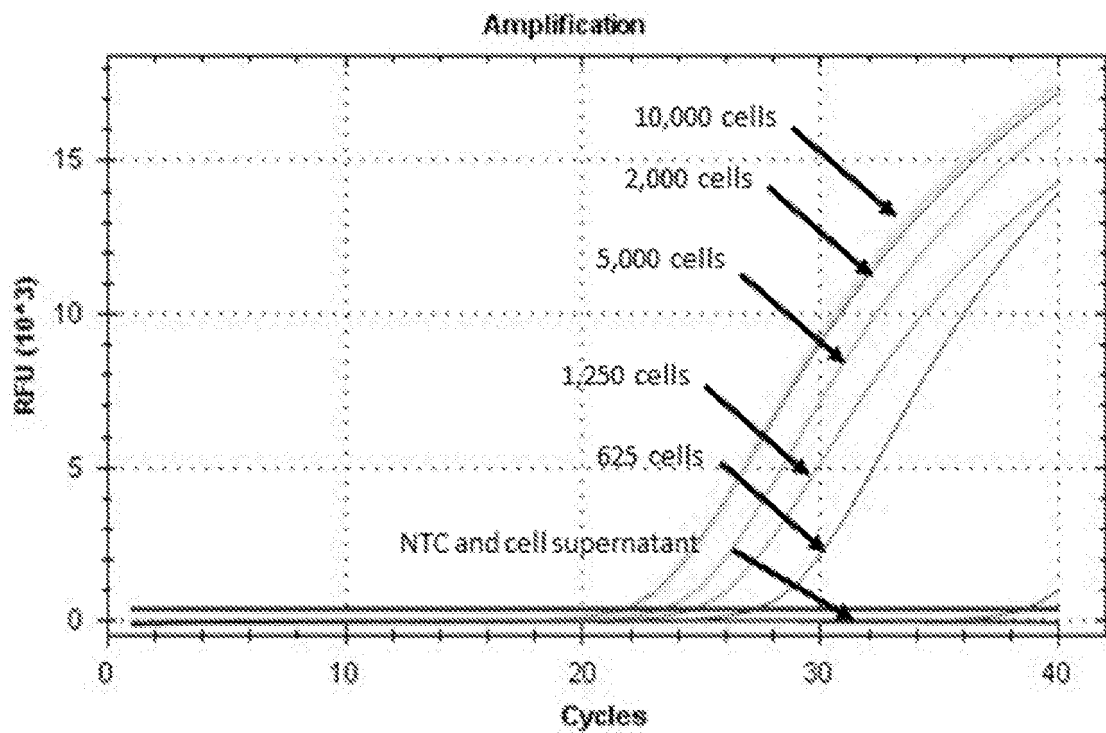


FIG. 14B

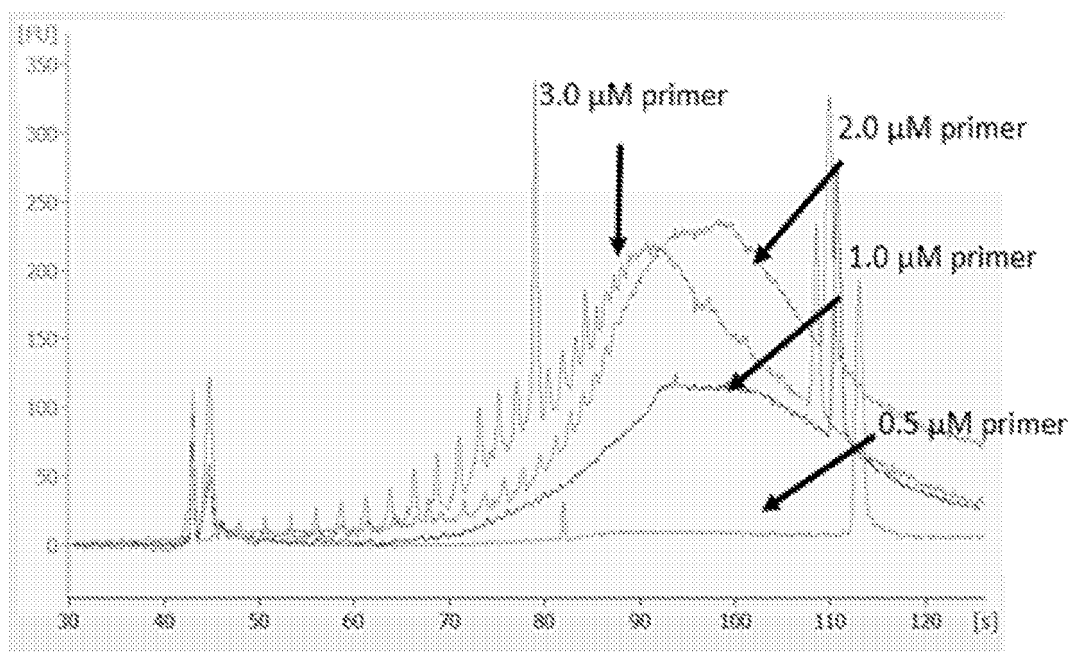


FIG. 15

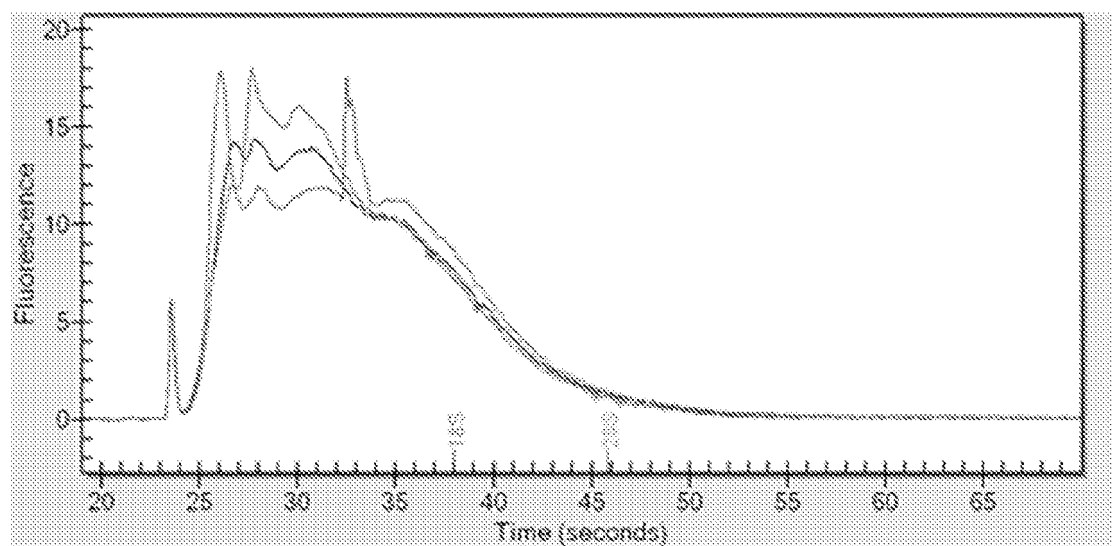


FIG. 16

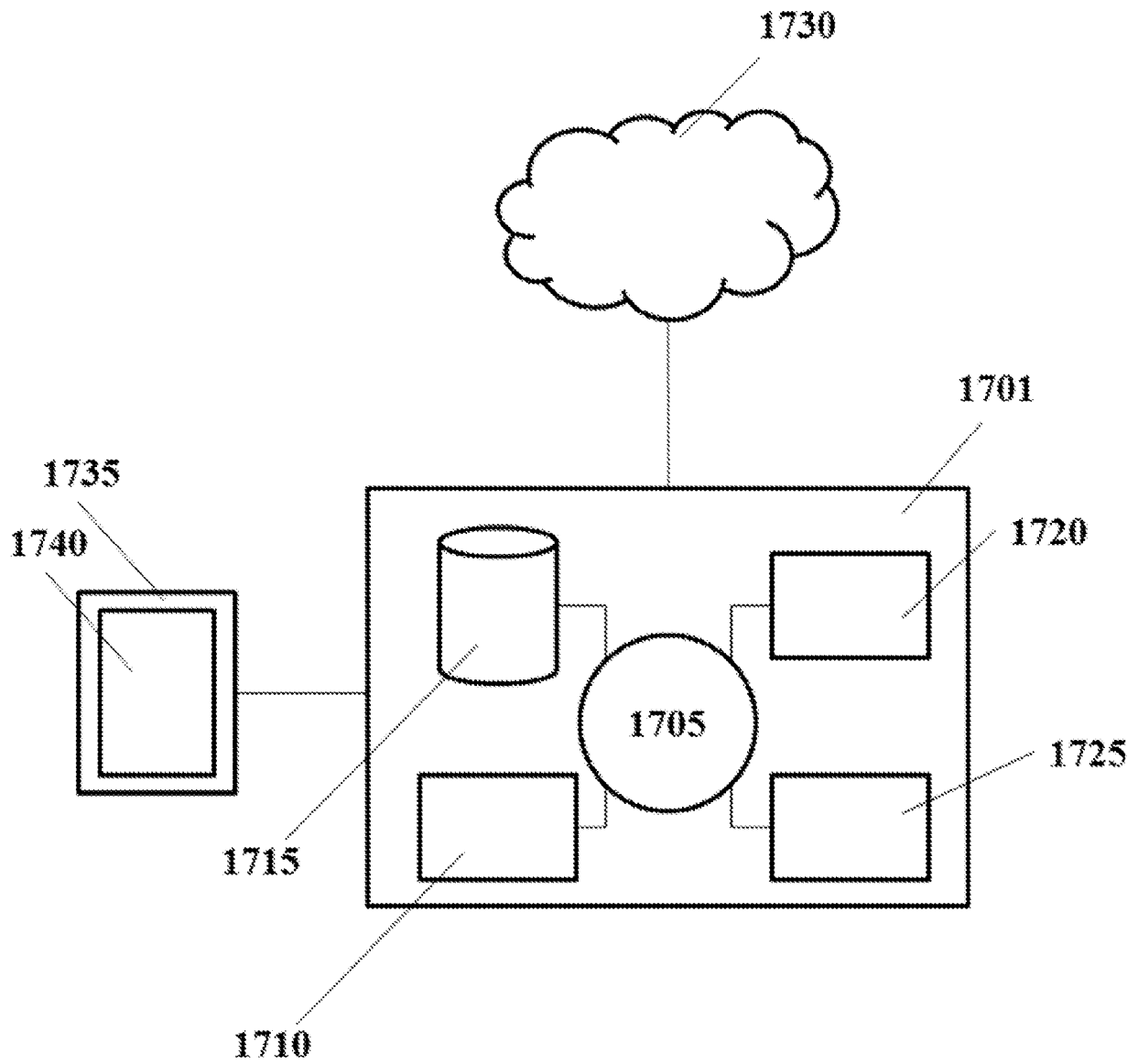


FIG. 17

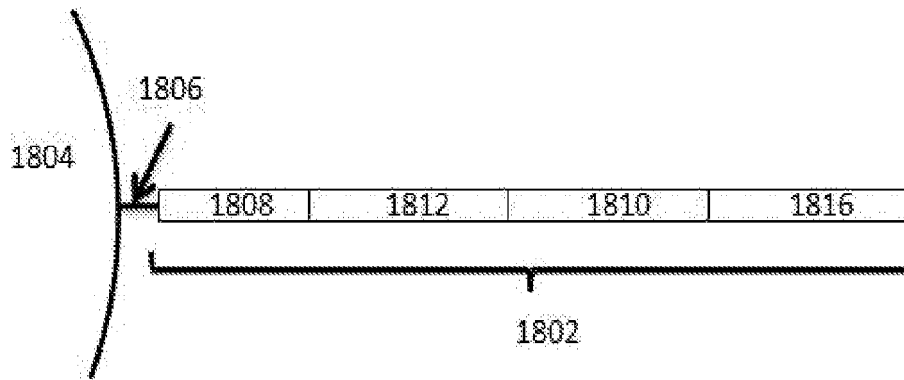


FIG. 18

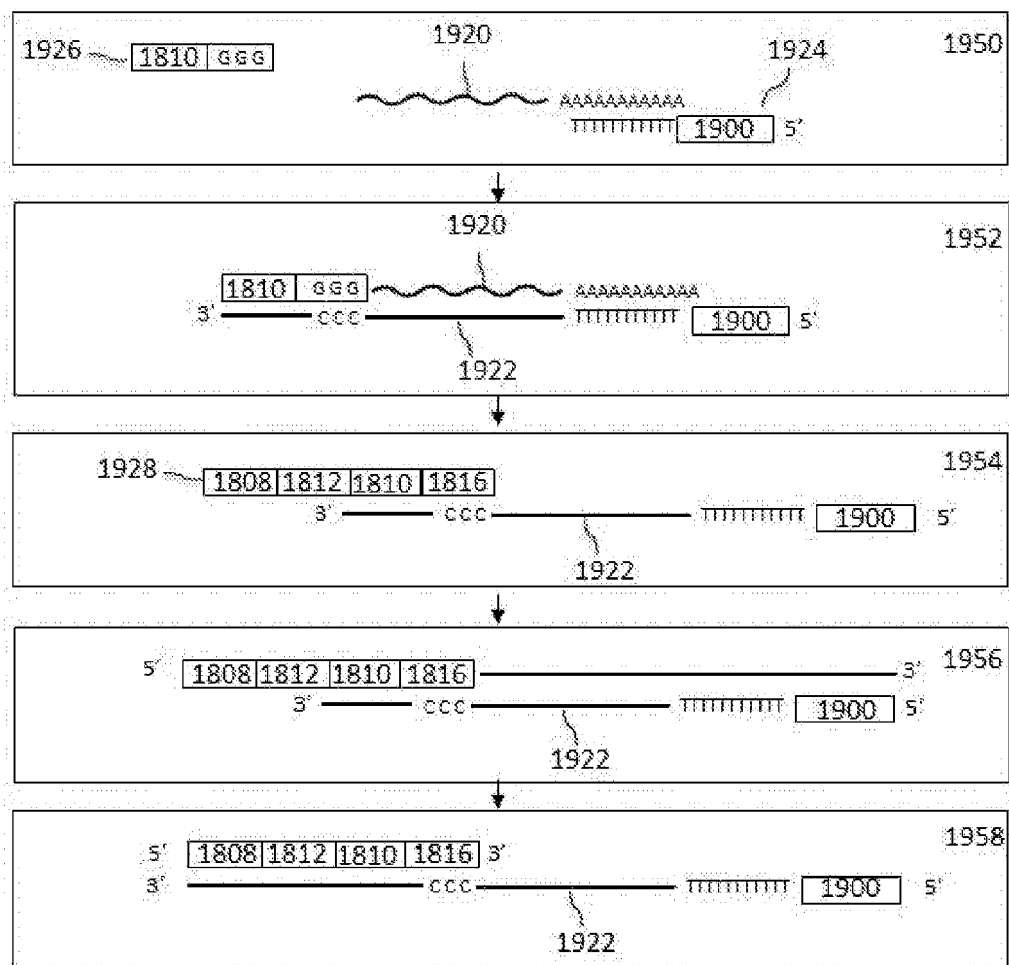


FIG. 19

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

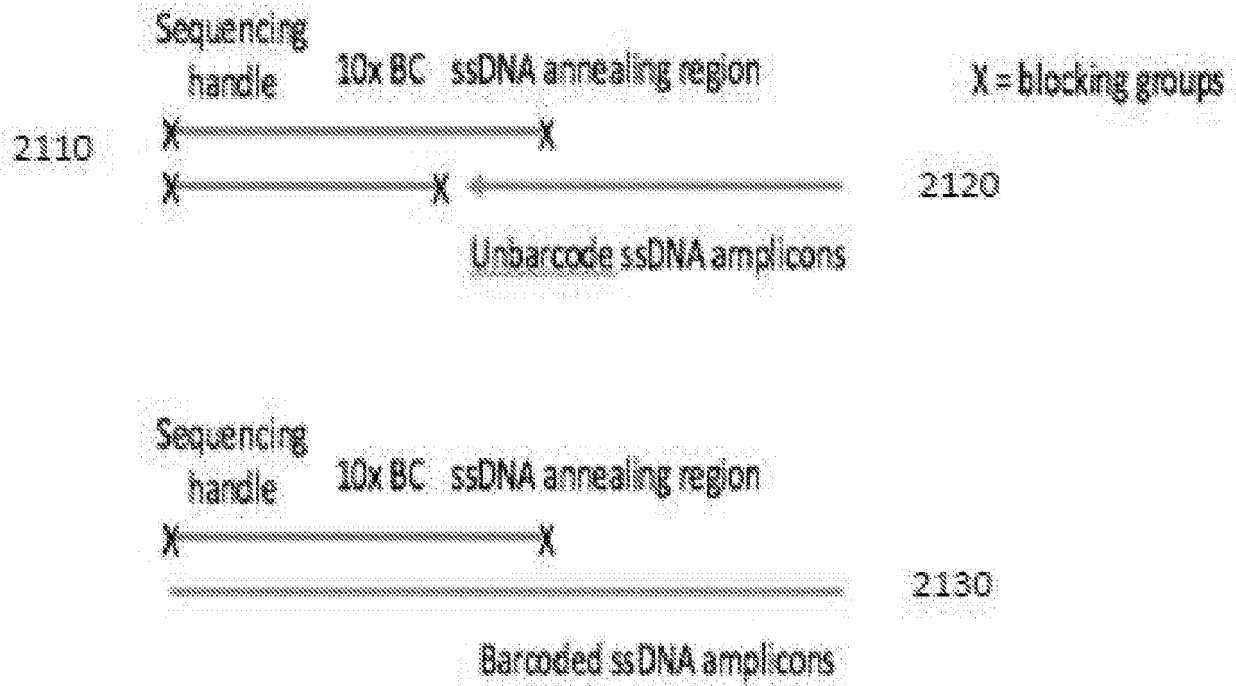


FIG. 21

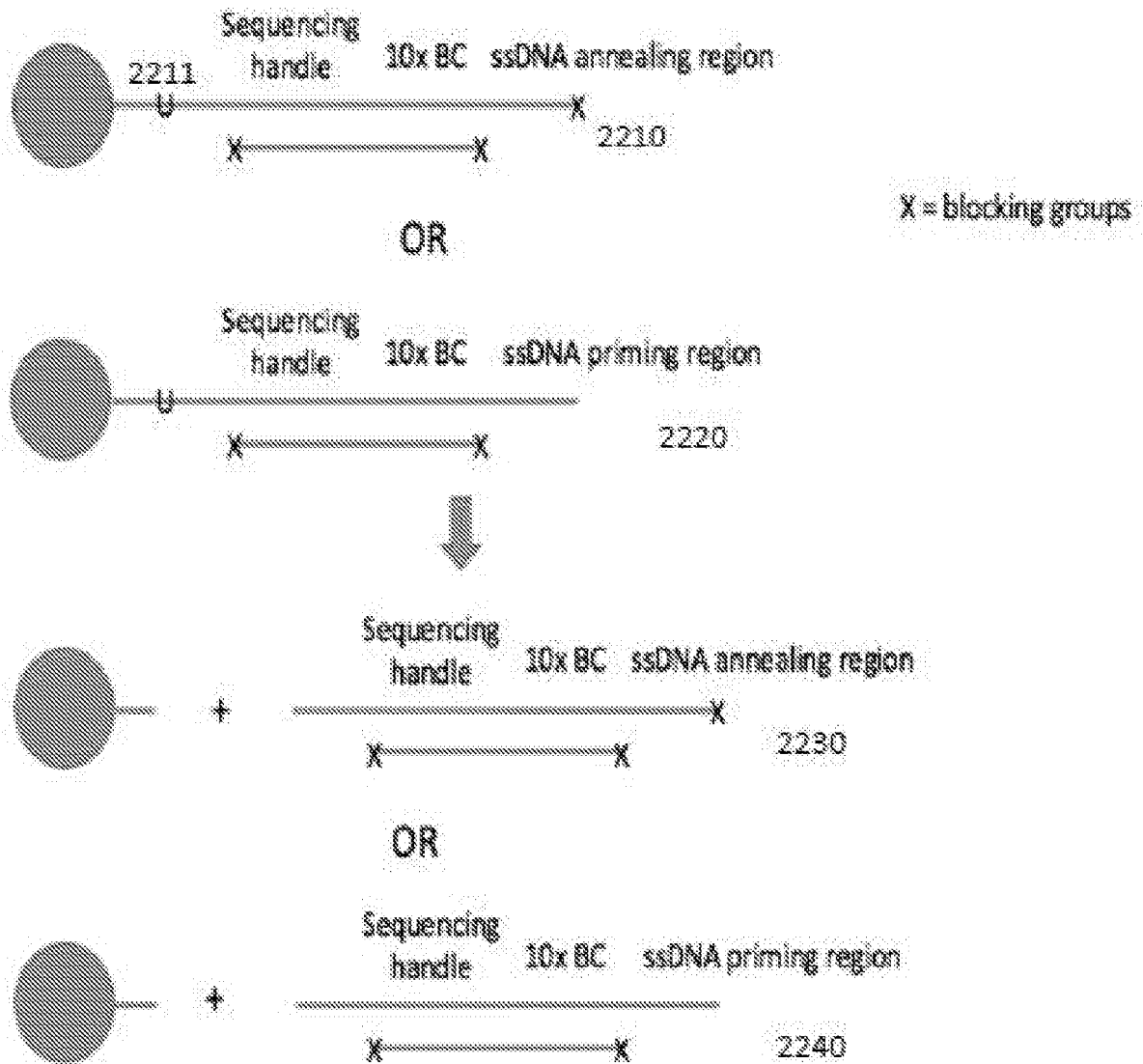


FIG. 22

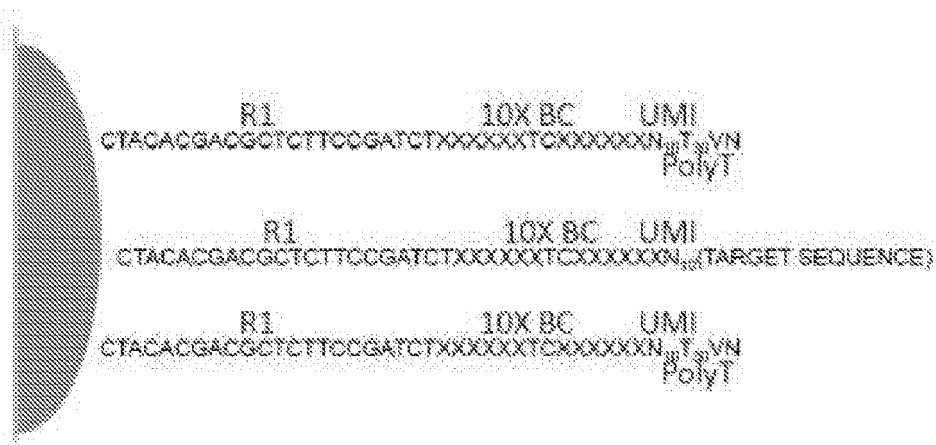


FIG. 23A

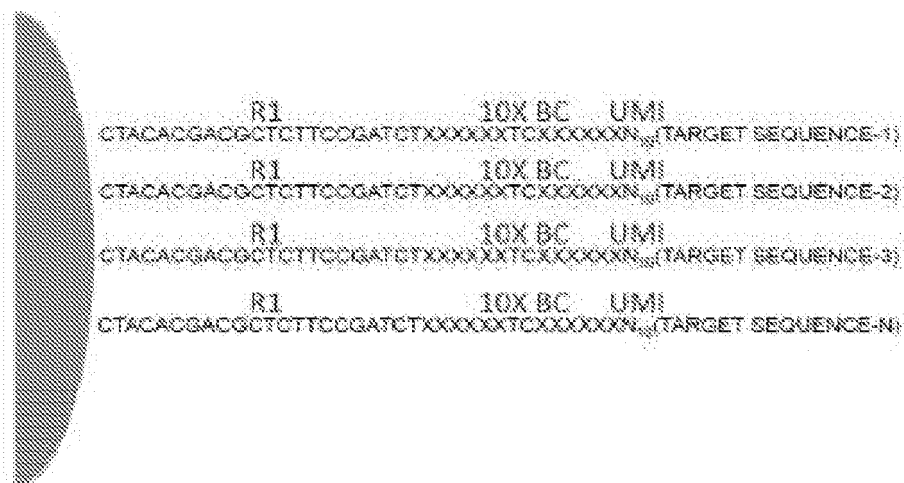


FIG. 23B

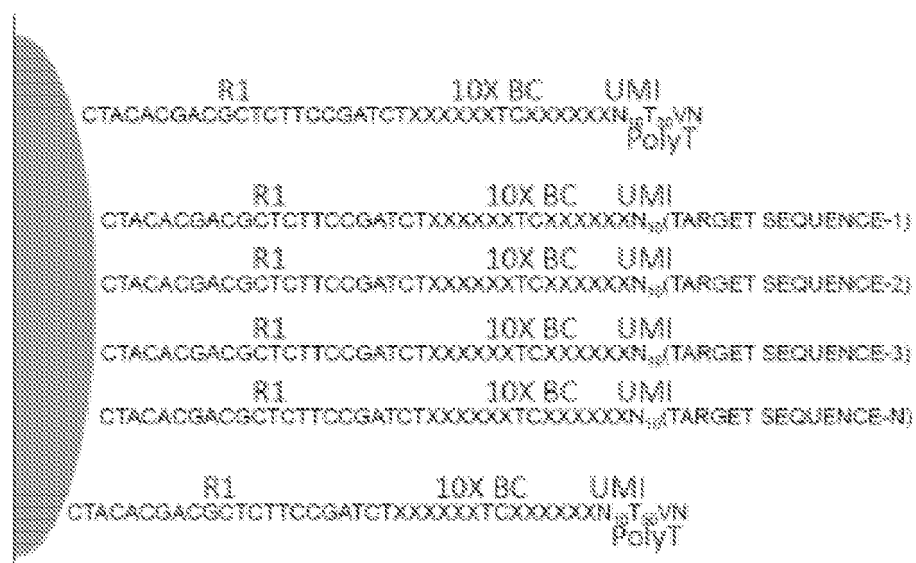


FIG. 23C

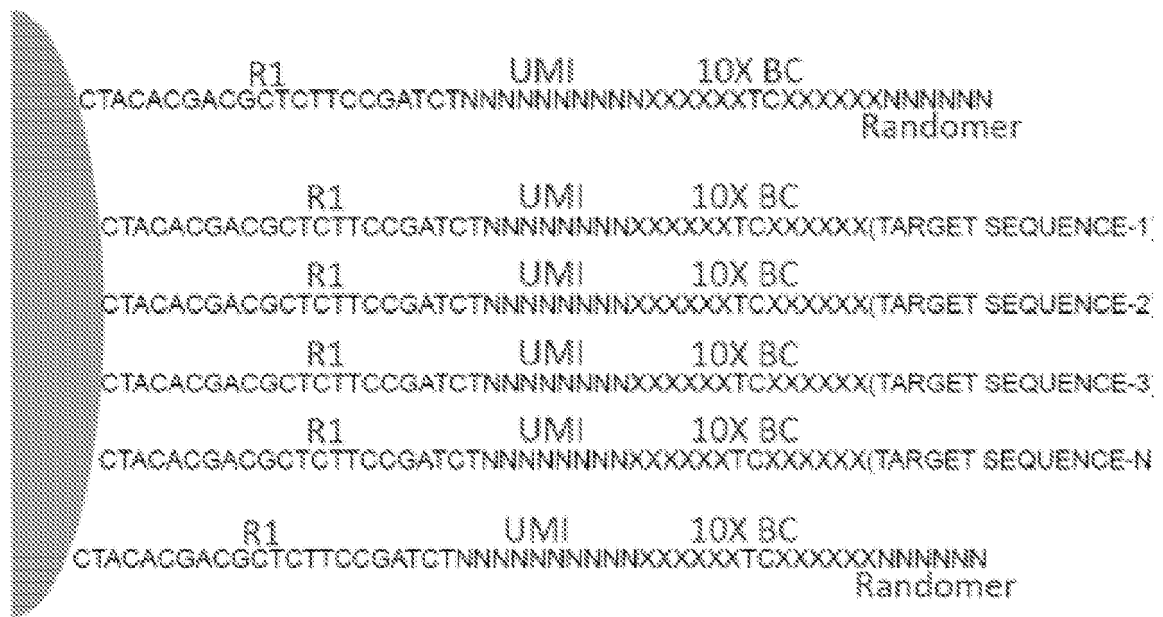


FIG. 24

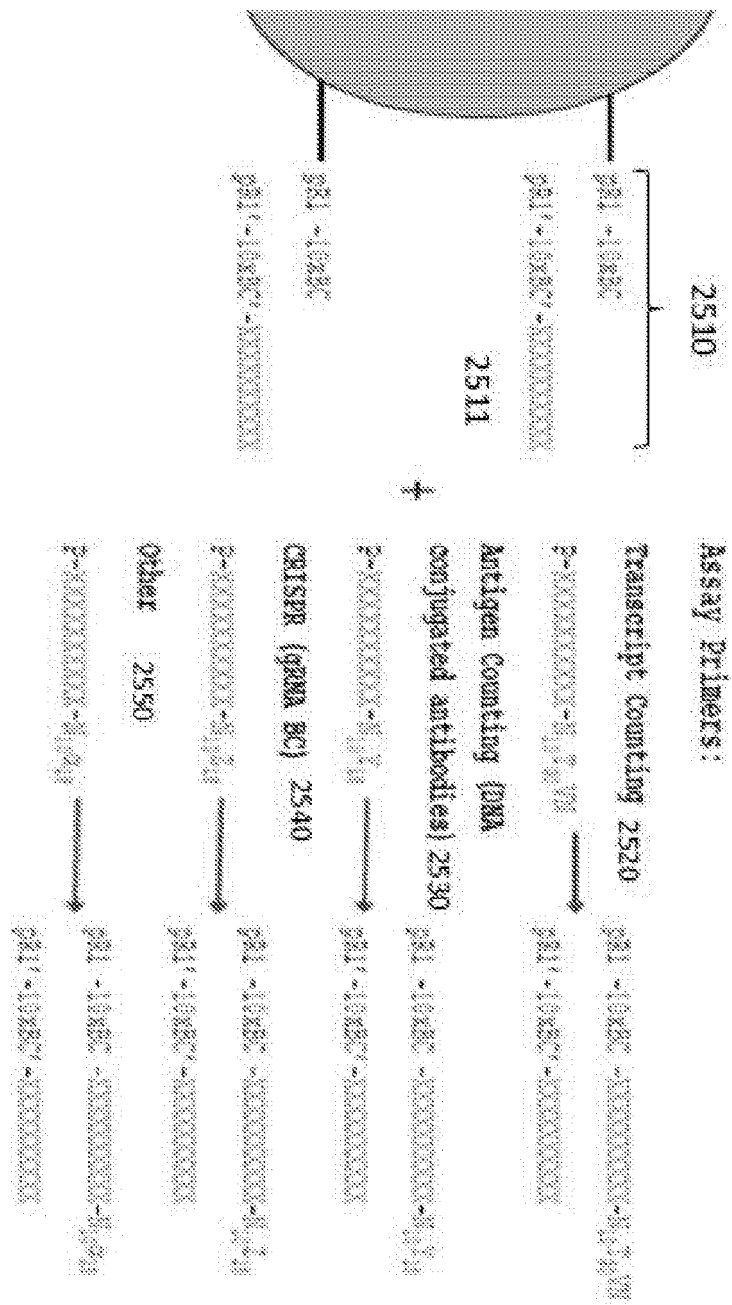


FIG. 25A

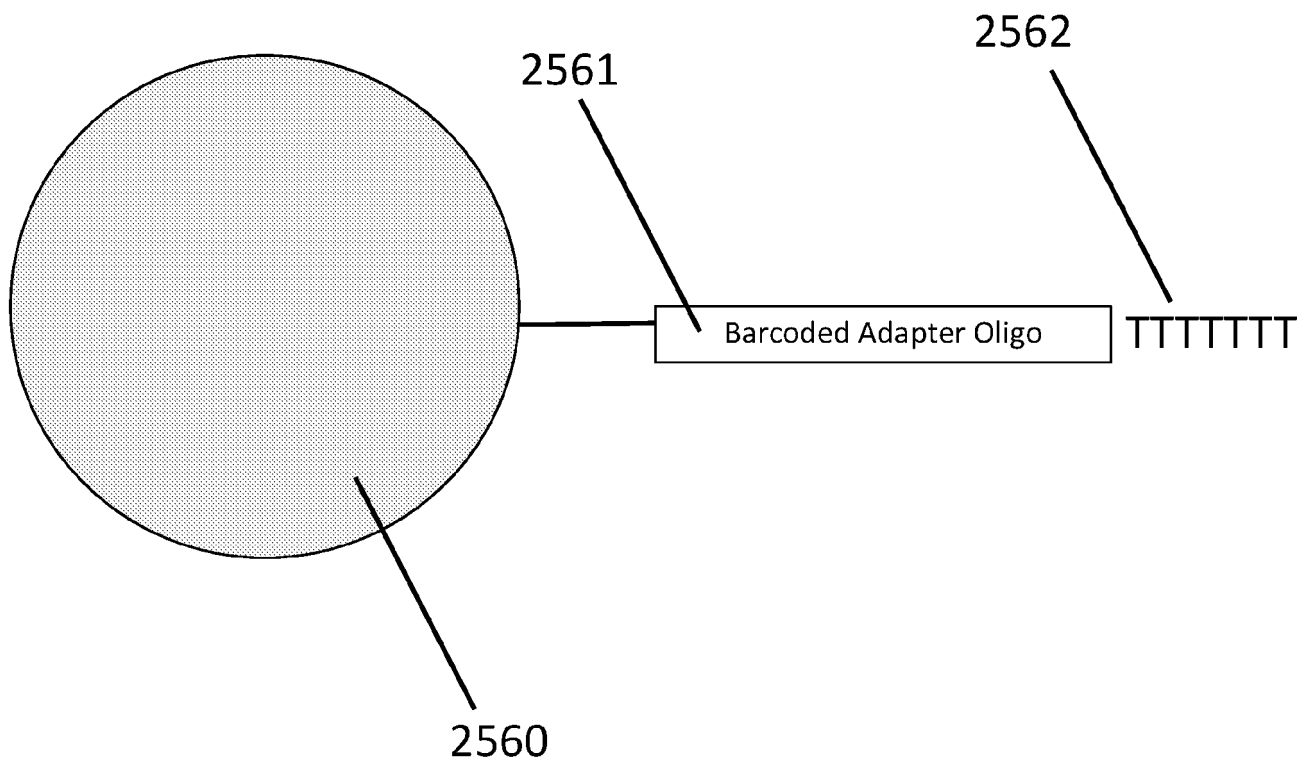


FIG. 25B

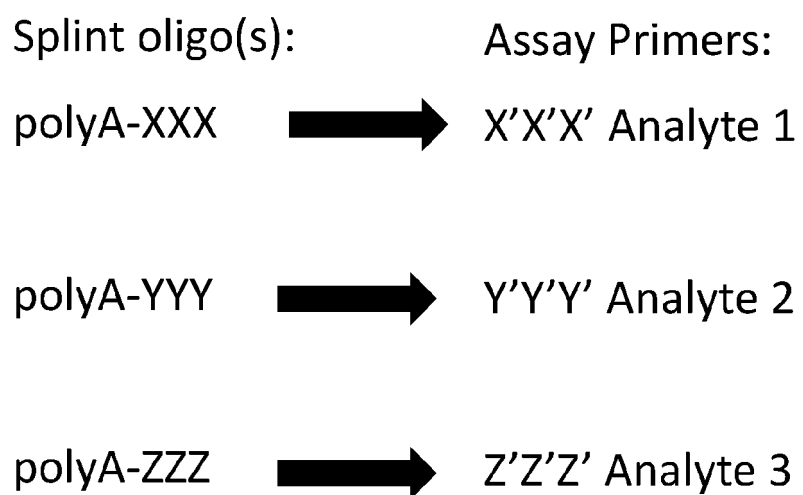


FIG. 25C

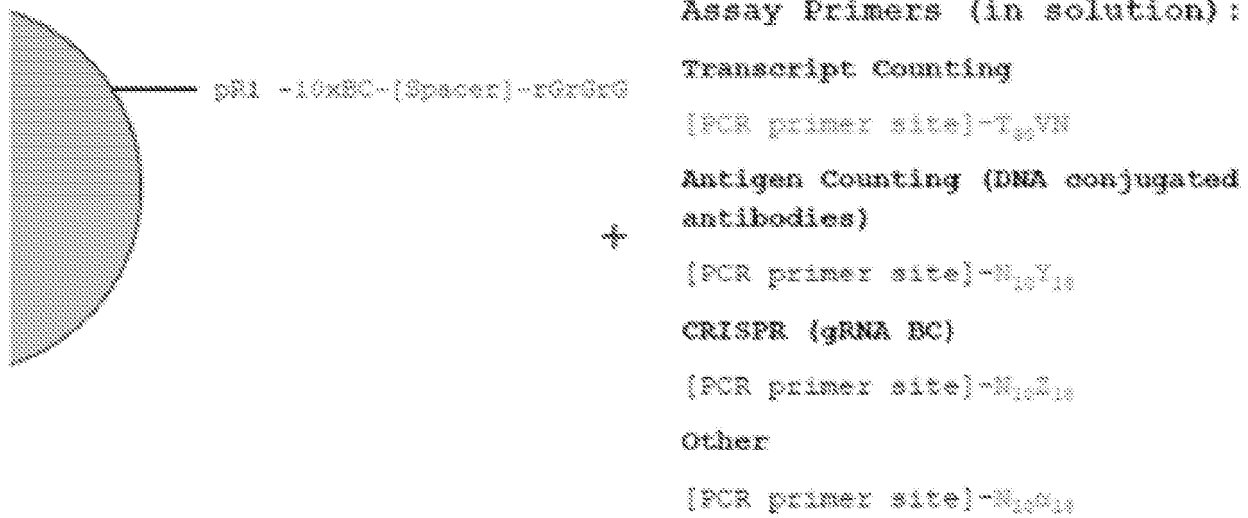


FIG. 26

Alpha

CAAGCAGAAAGACGGCATAACGAGATXXXXXXXXGTXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN₁₀T₂₀VN
GCCGATGCTCTAXXXXXCAXXXXXCACTGACCTCAAGTCTGCACACGAGAAAGGCTAGA

Beta

CAAGCAGAAAGACGGCATAACGAGATXXXXXXXXCAXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN₁₀T₂₀VN
GCCGATGCTCTAXXXXXGTXXXXXXCACTGACCTCAAGTCTGCACACGAGAAAGGCTAGA

Gamma

CAAGCAGAAAGACGGCATAACGAGATXXXXXXXXAGXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN₁₀T₂₀VN
GCCGATGCTCTAXXXXXTCXXXXXXCACTGACCTCAAGTCTGCACACGAGAAAGGCTAGA

Delta

CAAGCAGAAAGACGGCATAACGAGATXXXXXXXXTXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN₁₀T₂₀VN
GCCGATGCTCTAXXXXXAGXXXXXXCACTGACCTCAAGTCTGCACACGAGAAAGGCTAGA

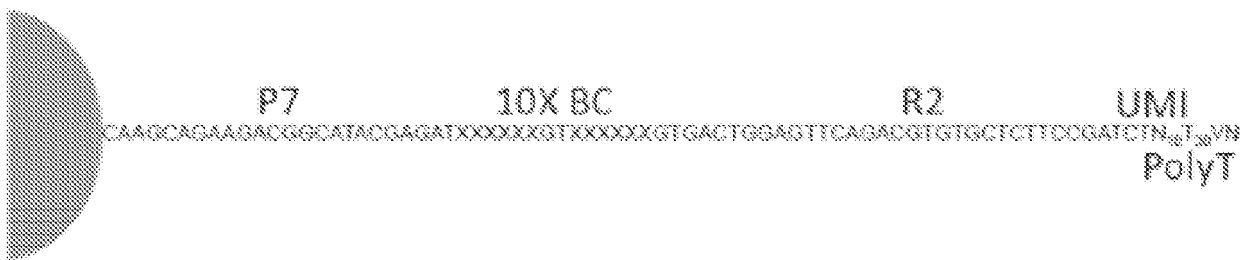


FIG. 27A

CTACACGACGCTCTTCOGATCTXXXXXXGTXXXXXXXN₁₀T₁₀VN
GCGAGAAGCGCTAGAXXXXXXXCAXXXXXX

CTACACGACGCTCTTCGGATCTXXXXXXCAXXXXXXN₉F₉VN
GCGAGAAGGCTAGAXXXXXXGTXXXXXX

CTACACGACGCTCTTCGGATCTXXXXXAGXXXXXXN₂T₂VN
GCGAGAAAGGCTAGAXXXXXTCTXXXXXX

CTACACGACGCTCTTCGGAICTXXXXXTXXXXXXN₁₀T₂₀VN
GCGAGAAGGCTAGAXXXXXXAGXXXXX

CTACACGACGCTCTTCCGATCTXXXXXXXXTCXXXXXXXXN₁₀T₃₀VN
PolyT

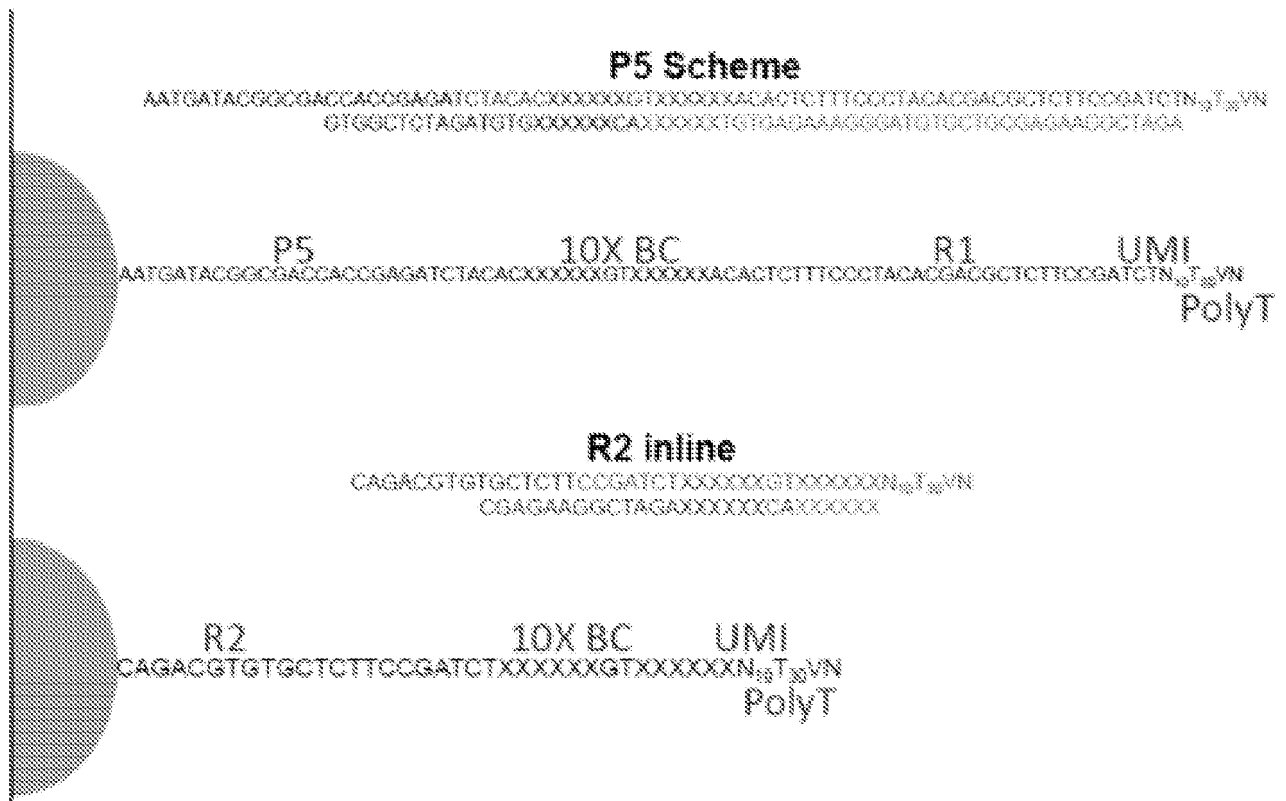


FIG. 27C

CTACACGACGCTCTTCCGATCTNNNNNNNNNNNNXXXCCGTTXXXCCGNNNNNN
GGAGAAGGCTAGA CAXXXXXX

CTACACGAGCGTCTTCGGATCTNNNNNNNNNNNXXXXXXCAXXXXXXNNNNNN
GCGAGAAGGCTAGA GTXXXX

CTACAGACGCTCTTCGGATCTNNNNNNNNNNNNXXXXXAGXXXXNNNNNNN
GCCAGAAGGCTAGA TXXXXX

CTACACGACGCTCTTCGGATCTNNNNNNNNNNXXXXXXXXXXXXXXN
GCGAGAAAGGTAGA AAAAAAAAA

CTACACGACGCTCTTCCGATCTNNNNNNNNNNNNXXXXXXTCXXXXNNNNNNN

FIG. 27D

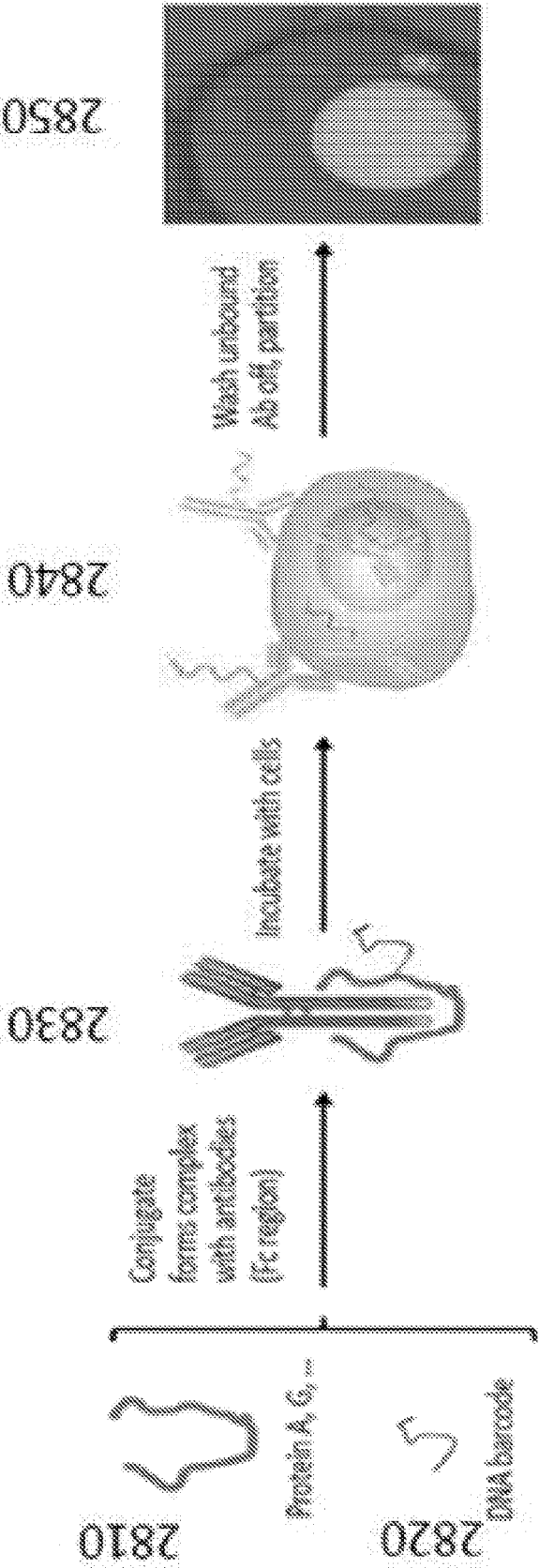


FIG. 28

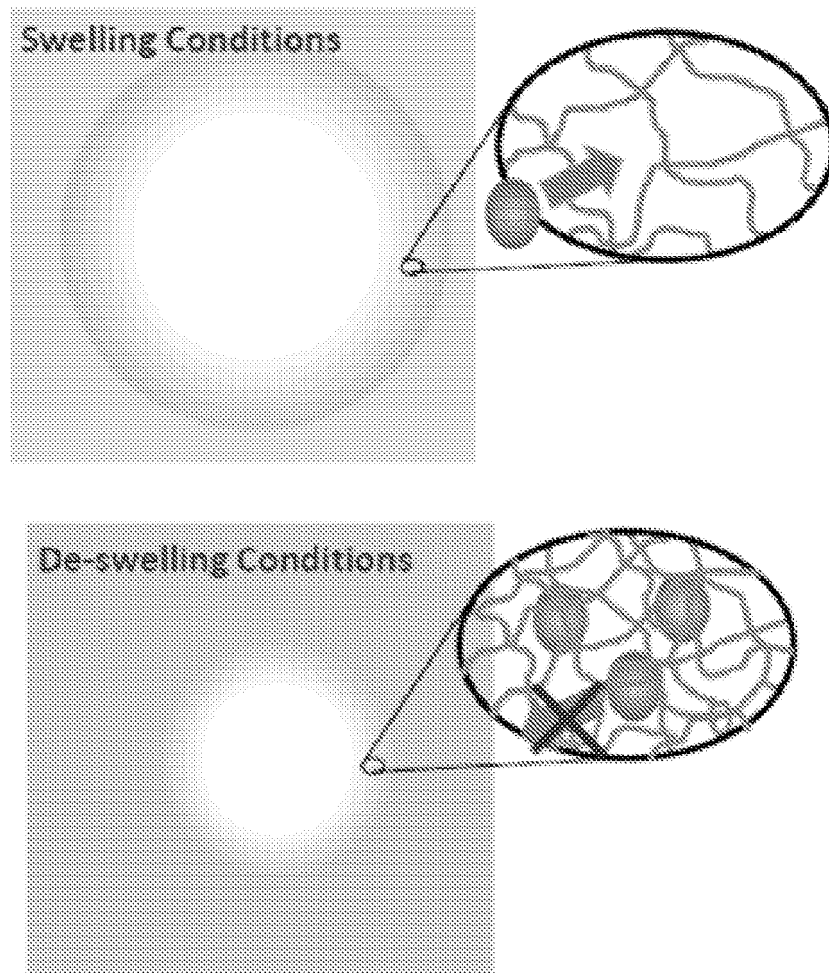


FIG. 29

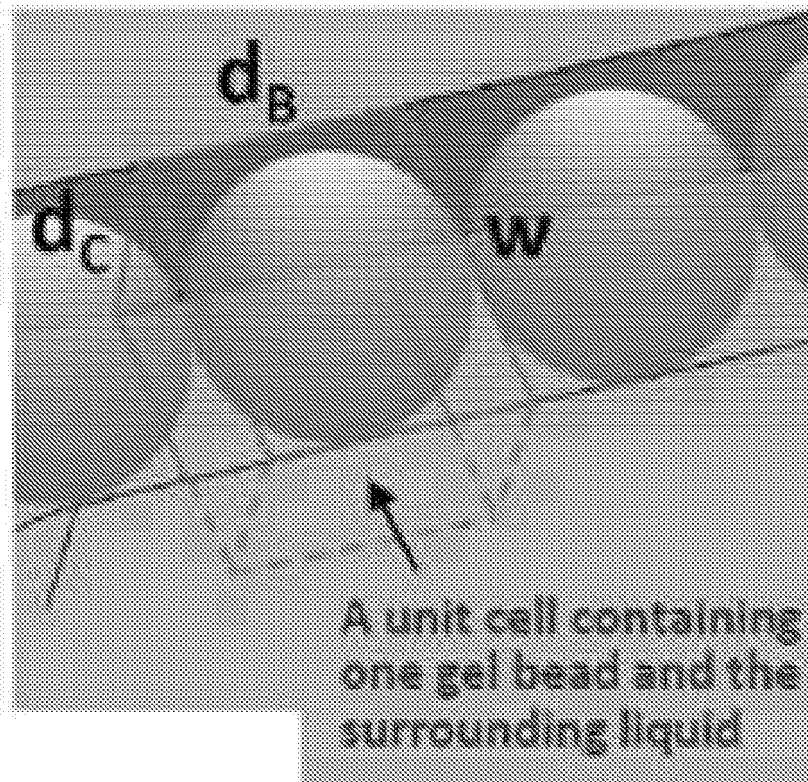


FIG. 30

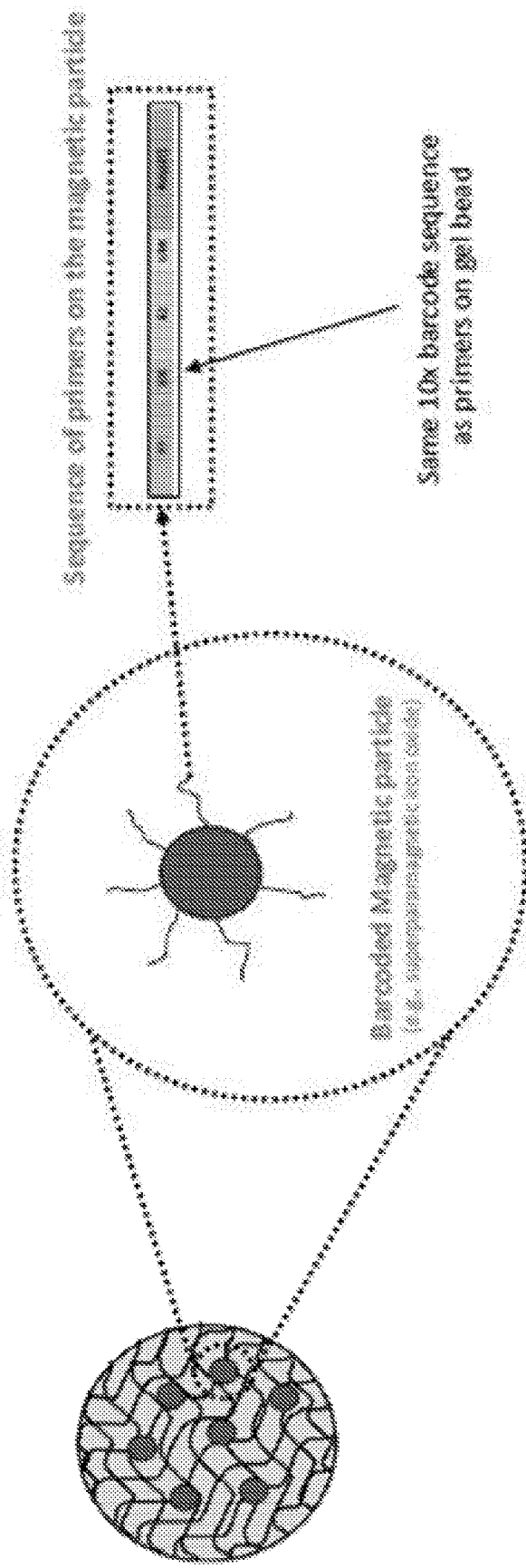


FIG. 31

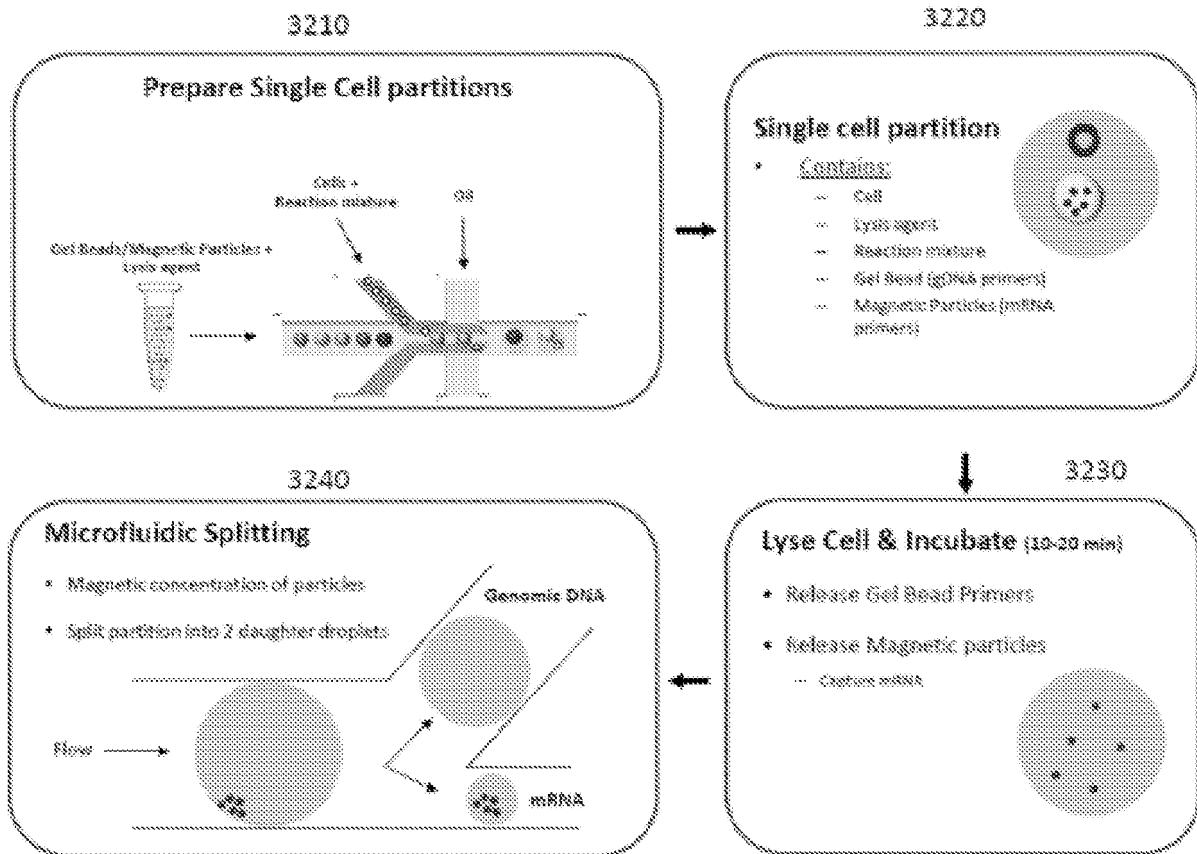


FIG. 32

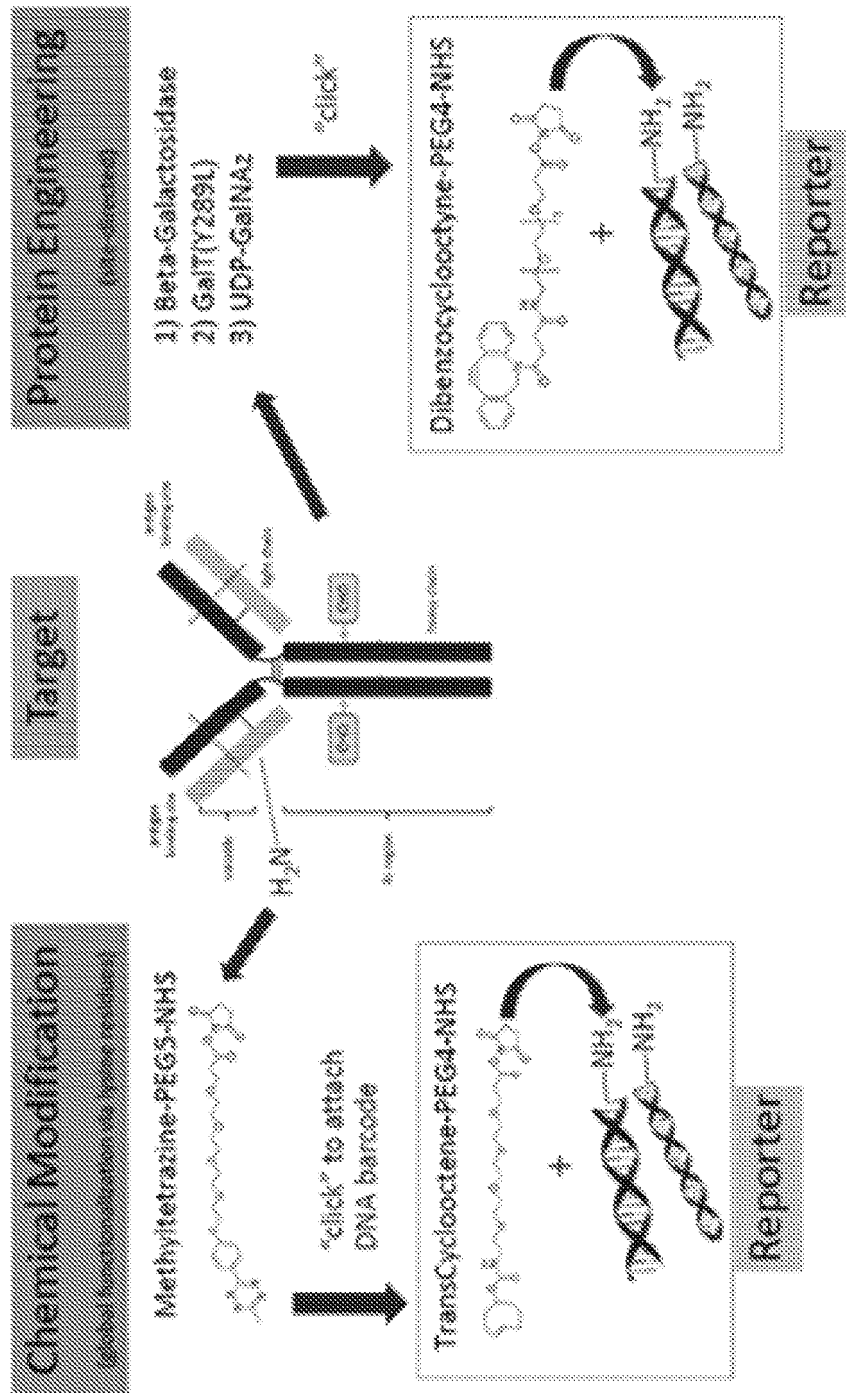


FIG. 33

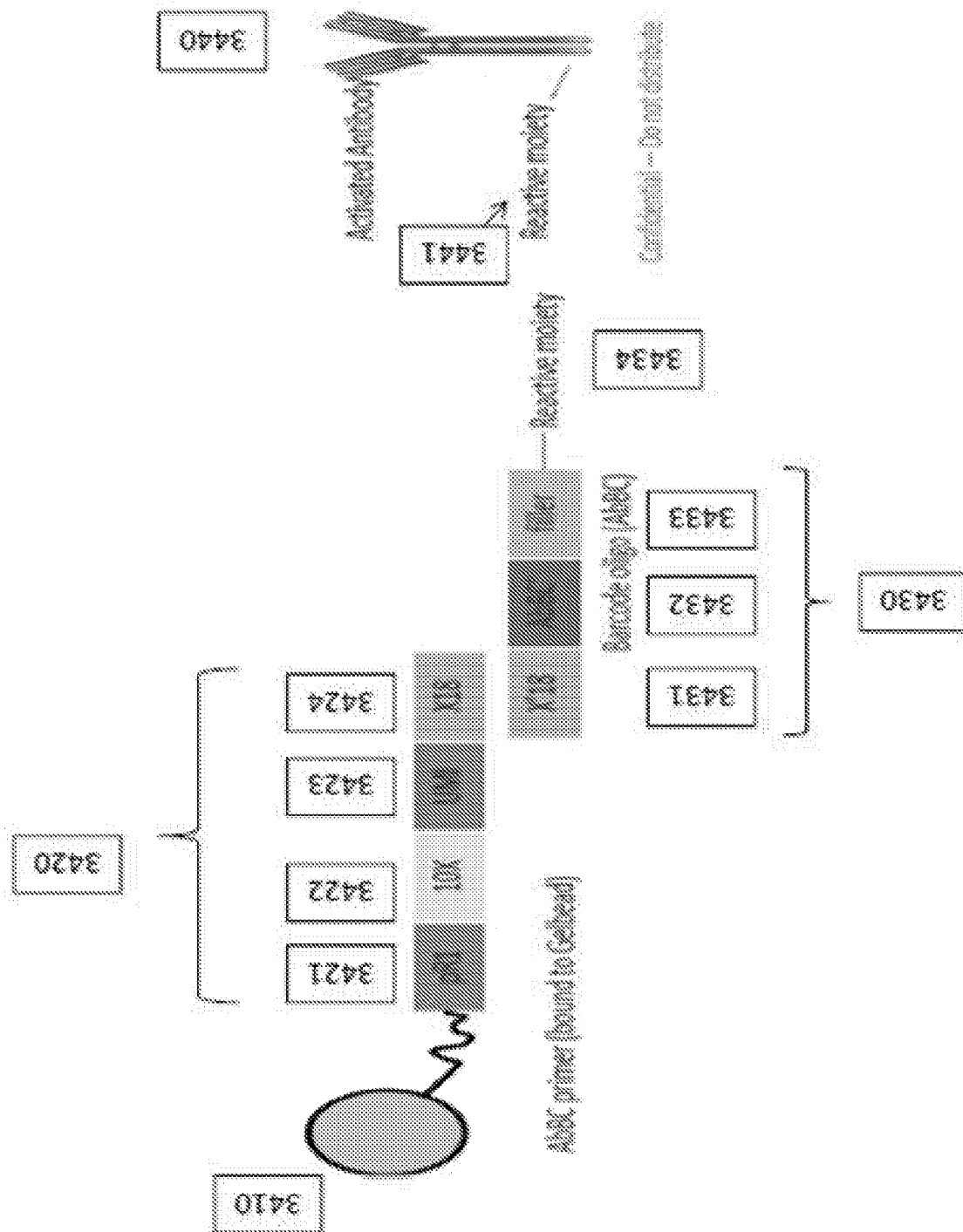


FIG. 34

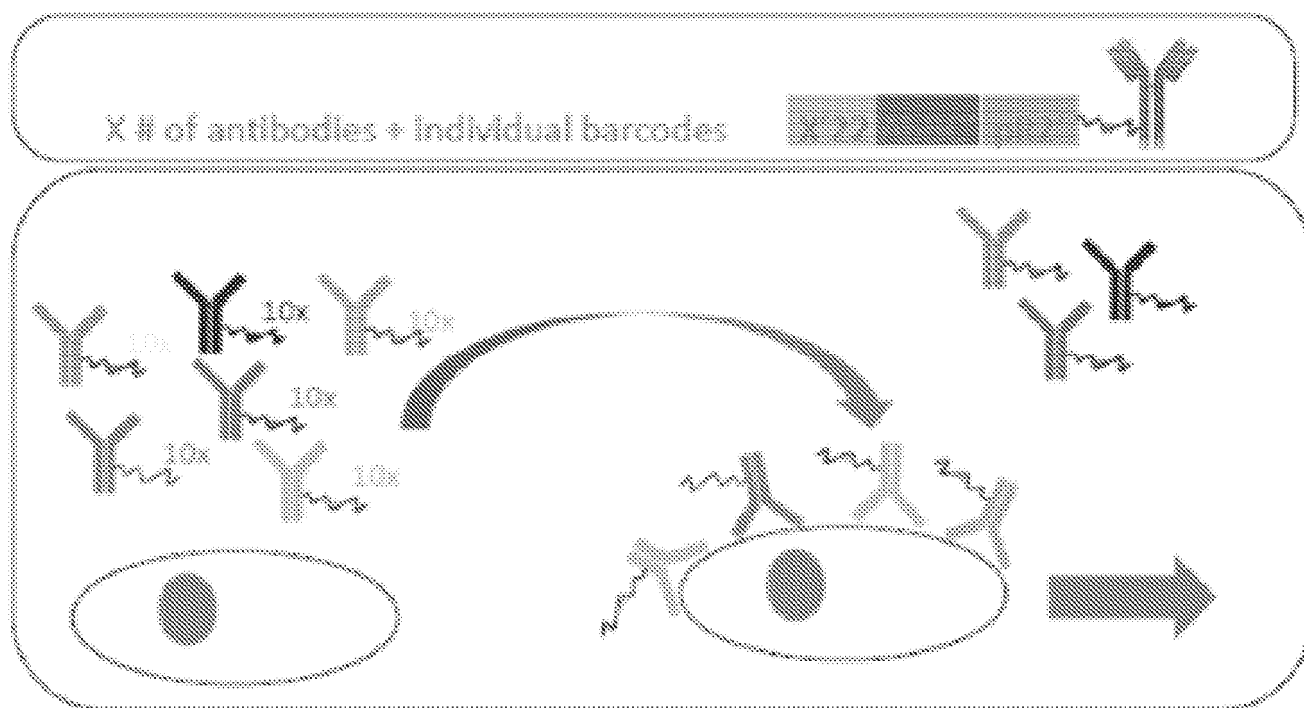


FIG. 35A

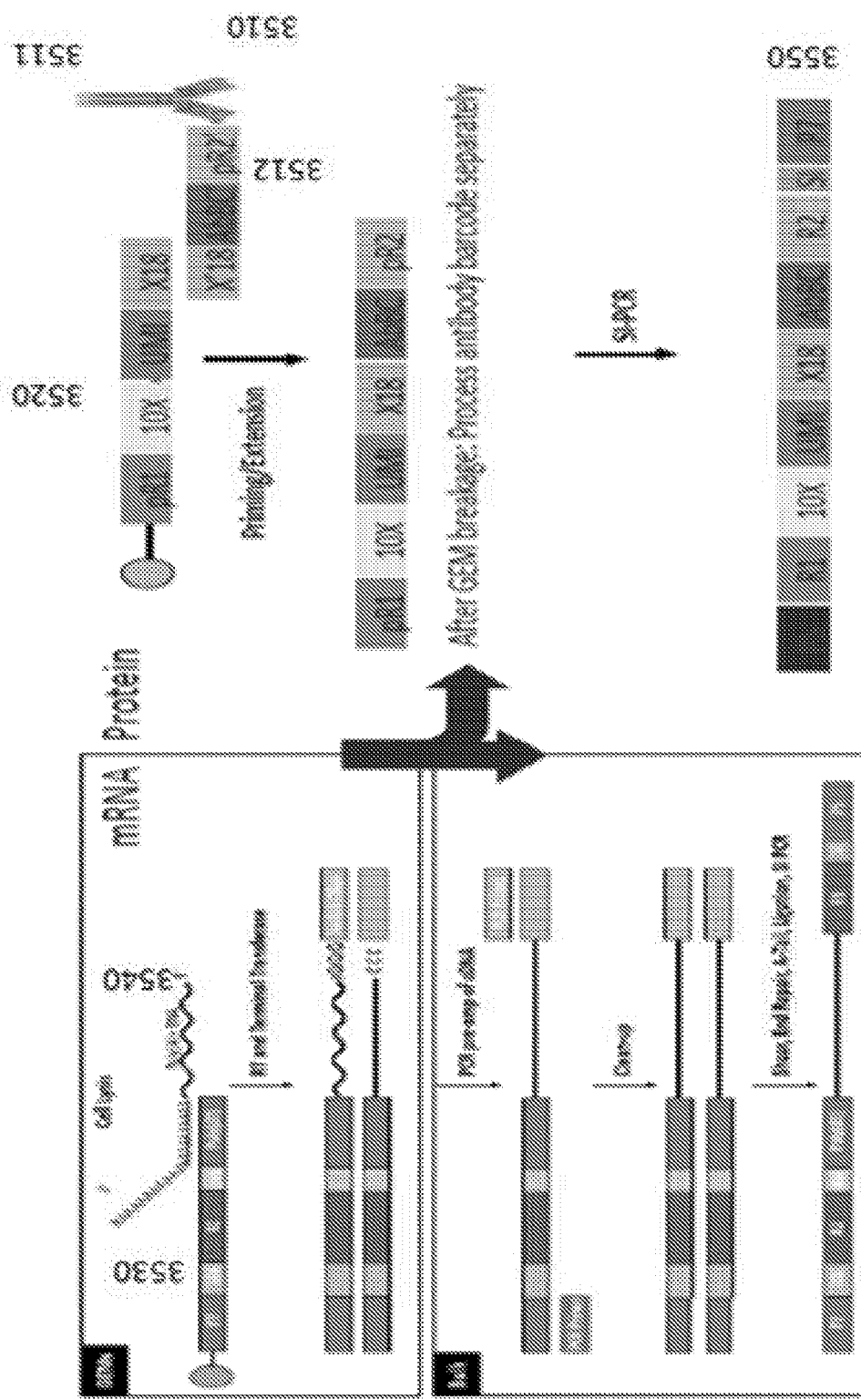


FIG. 35B

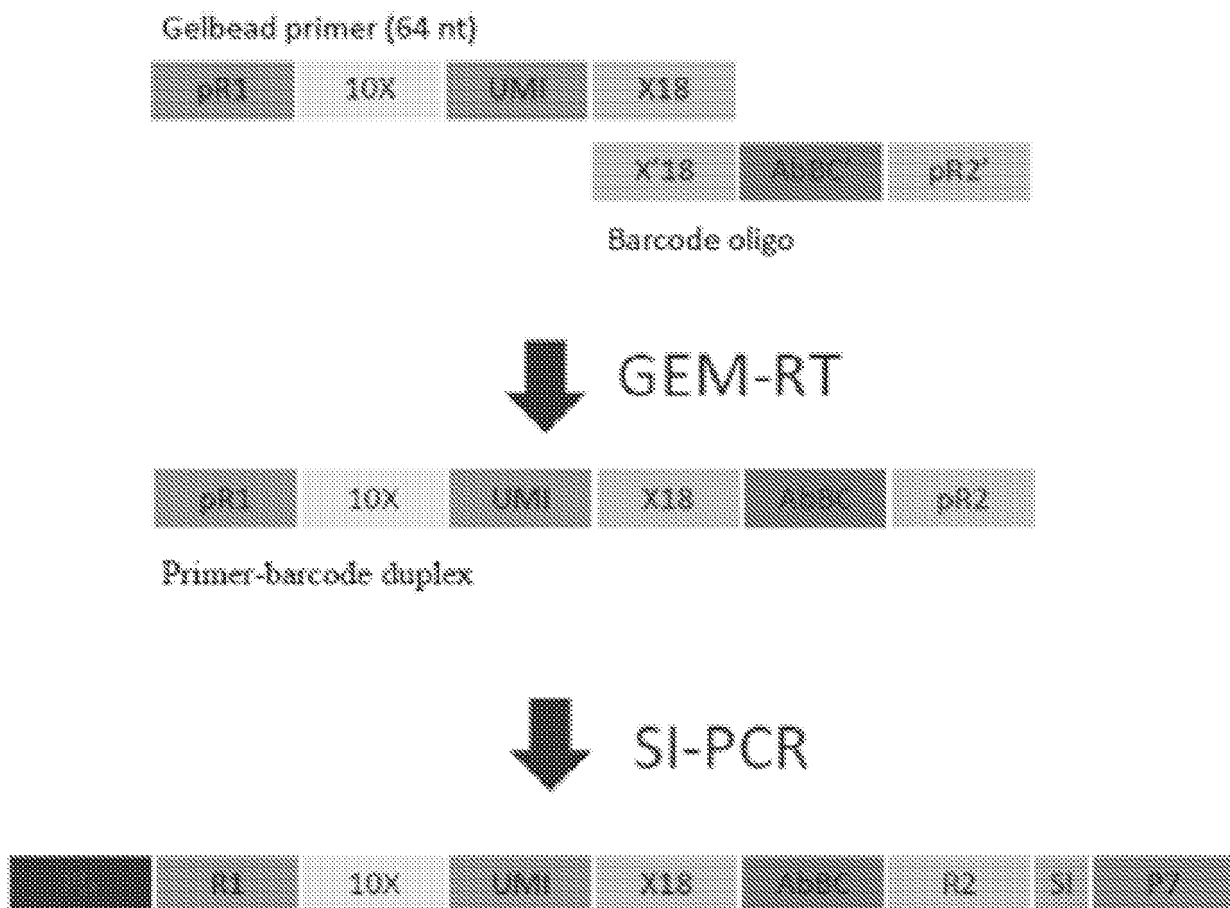


FIG. 35C

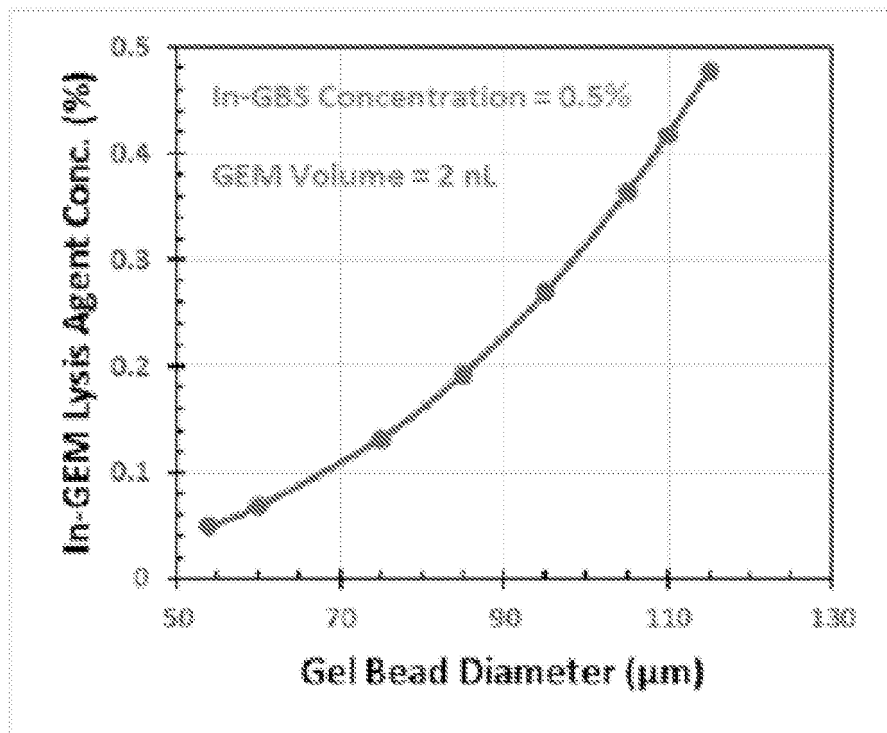


FIG. 36A

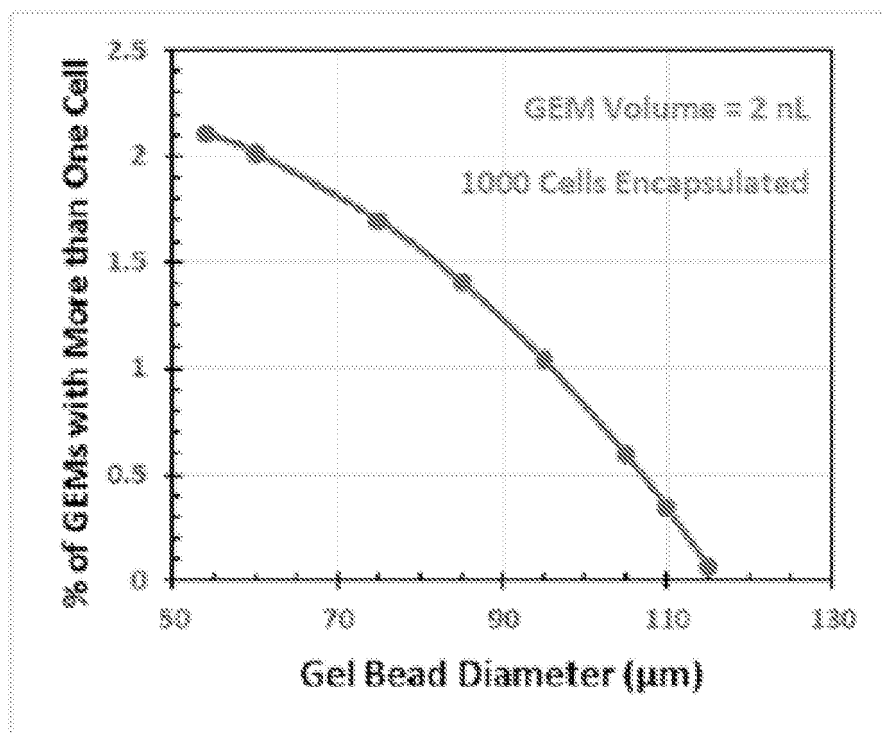


FIG. 36B

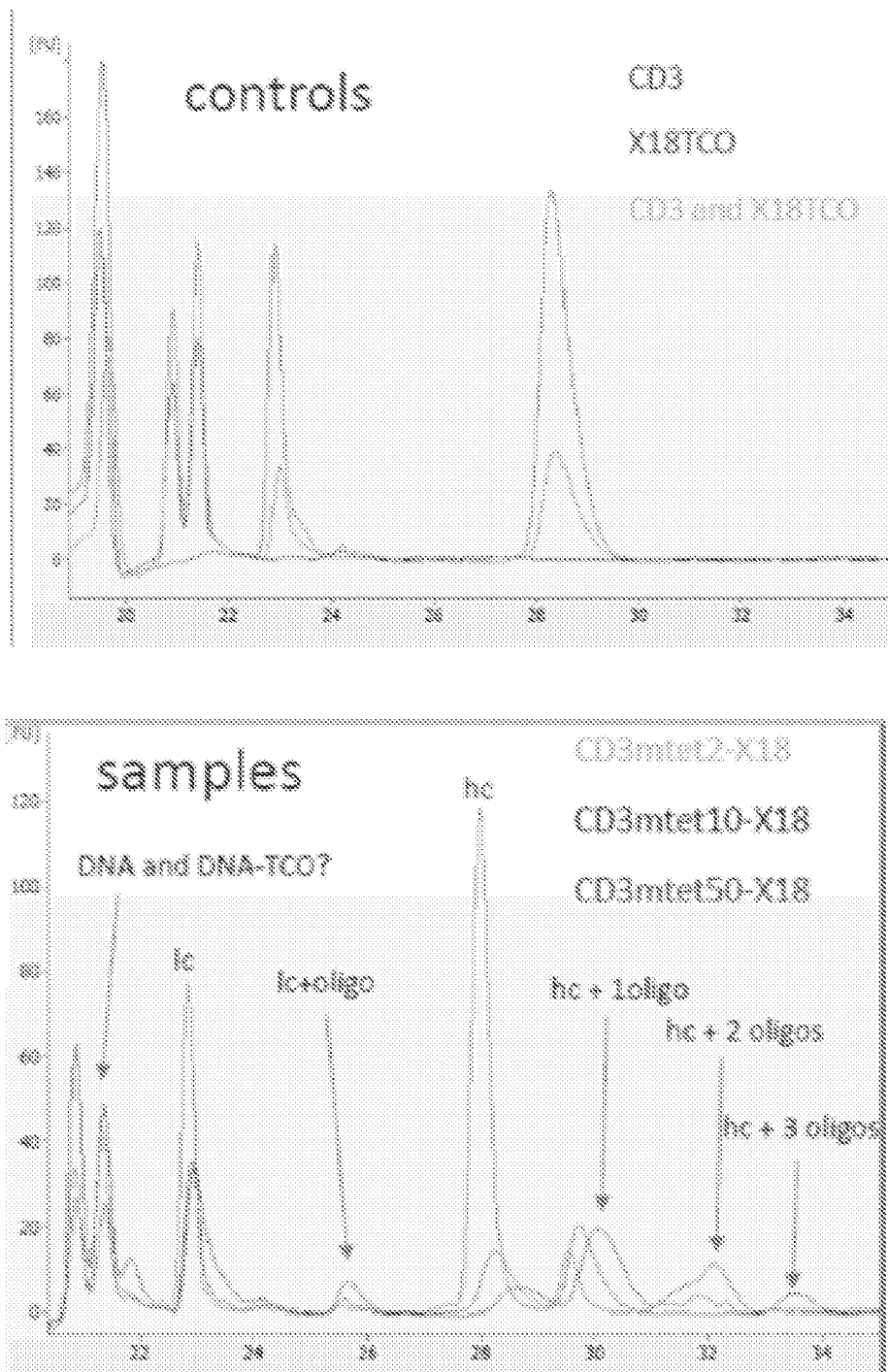


FIG. 37

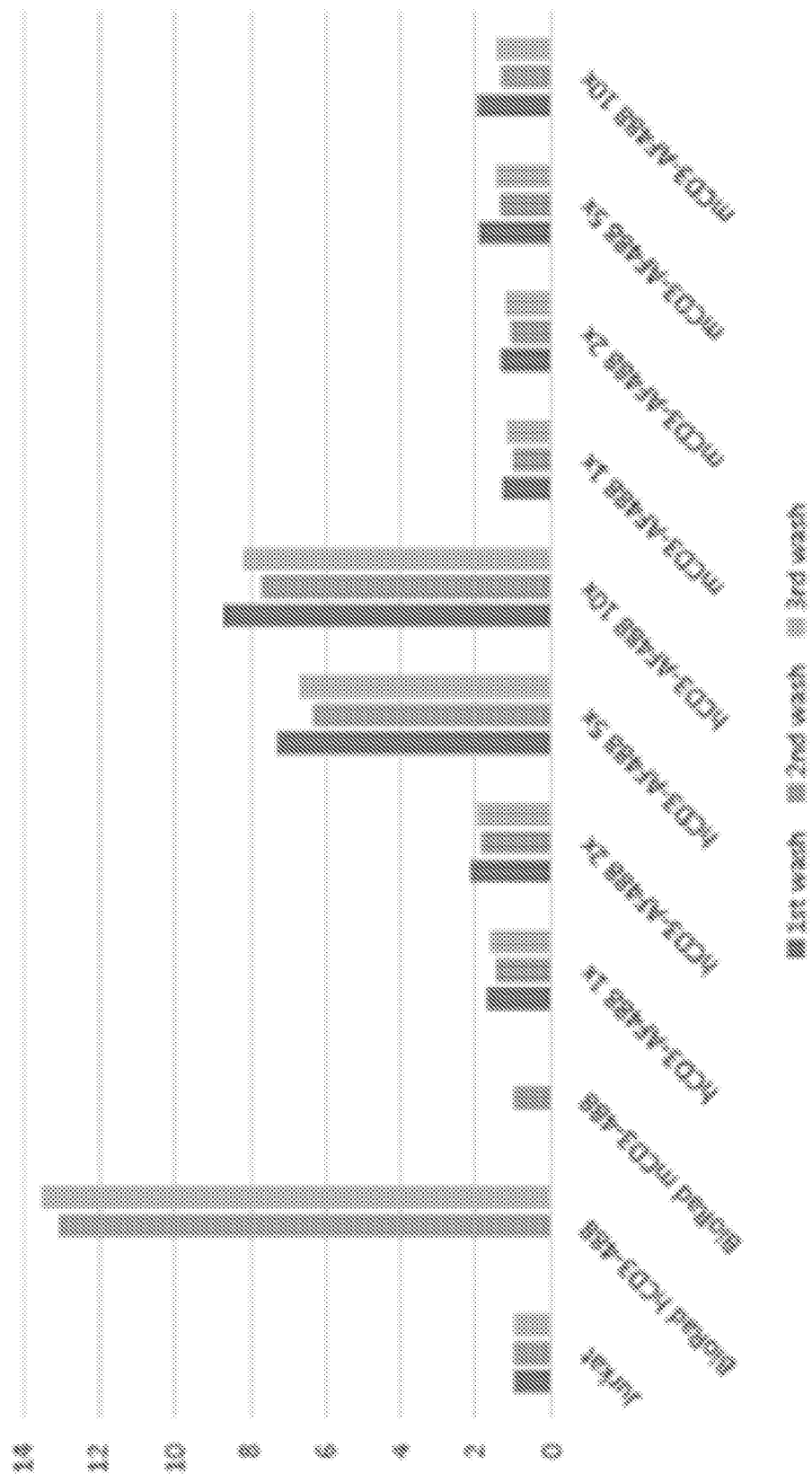


FIG. 38

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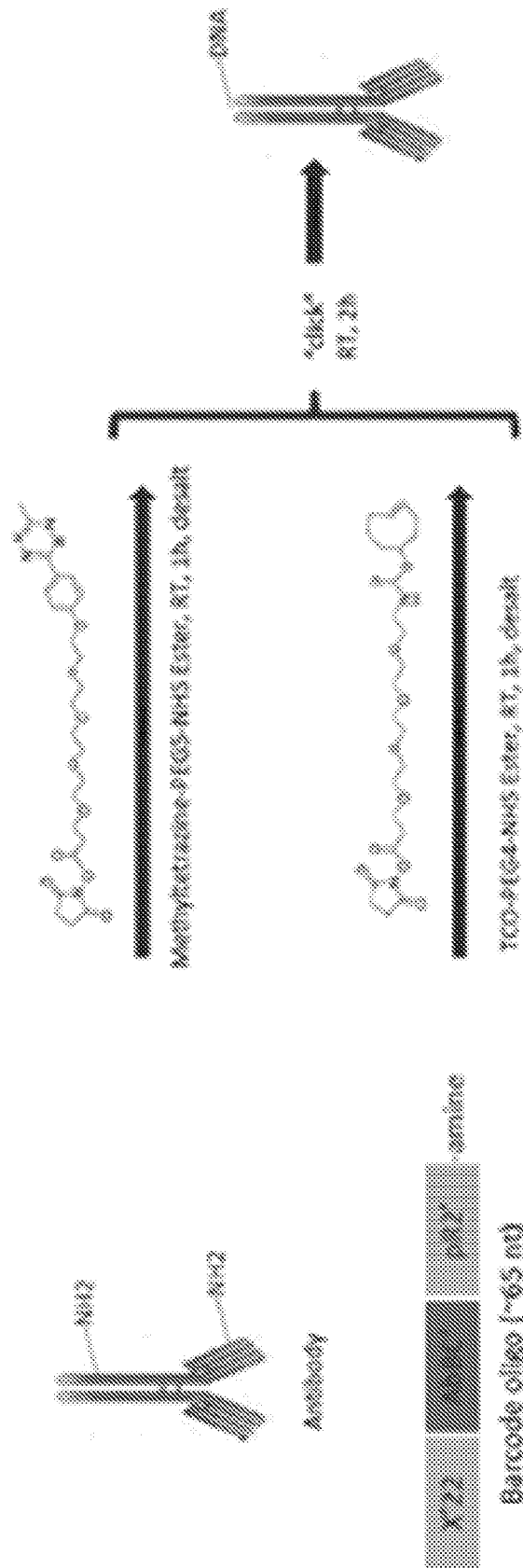


FIG. 39A

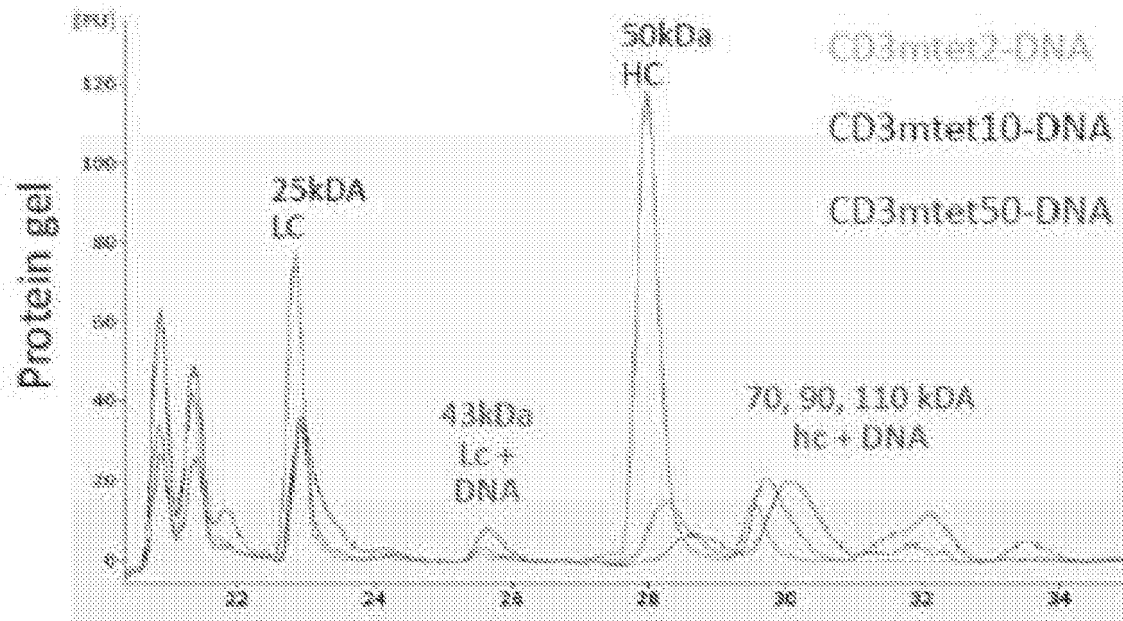


FIG. 39B



FIG. 40

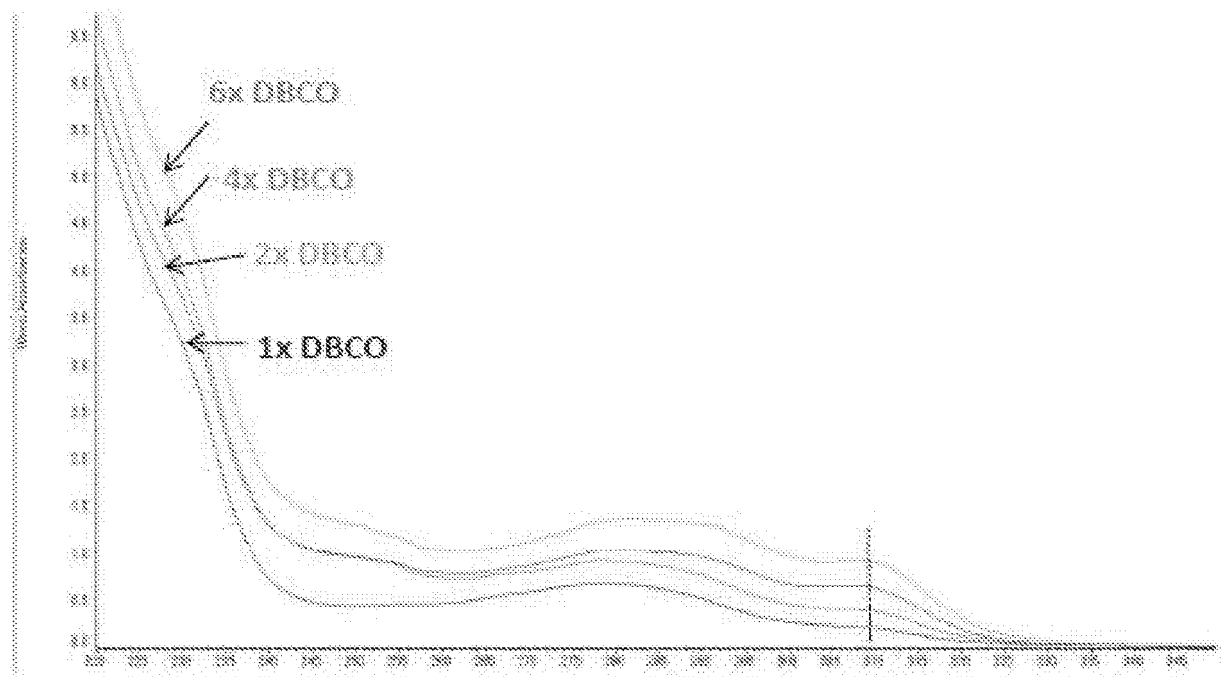


FIG. 41

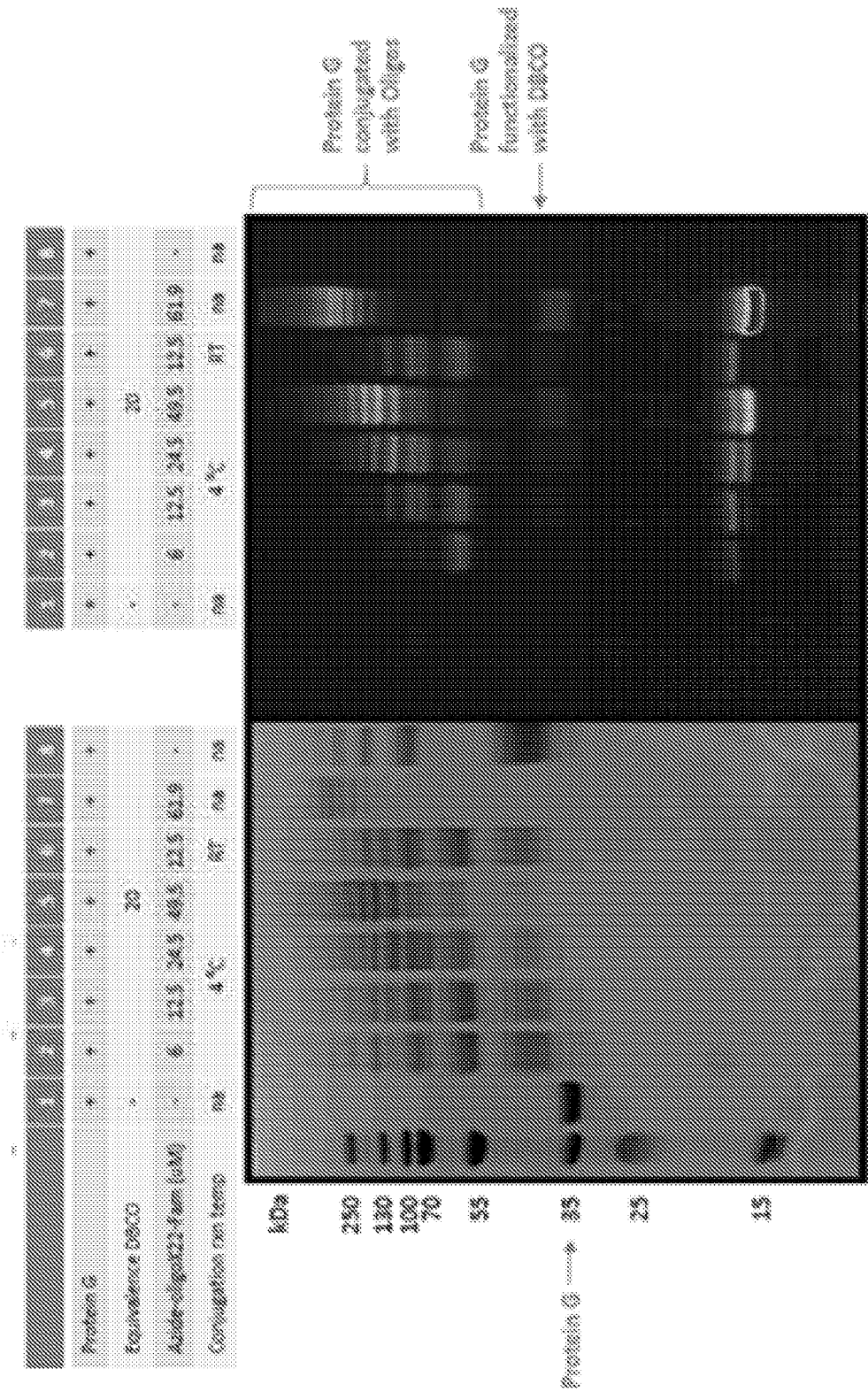


FIG. 42

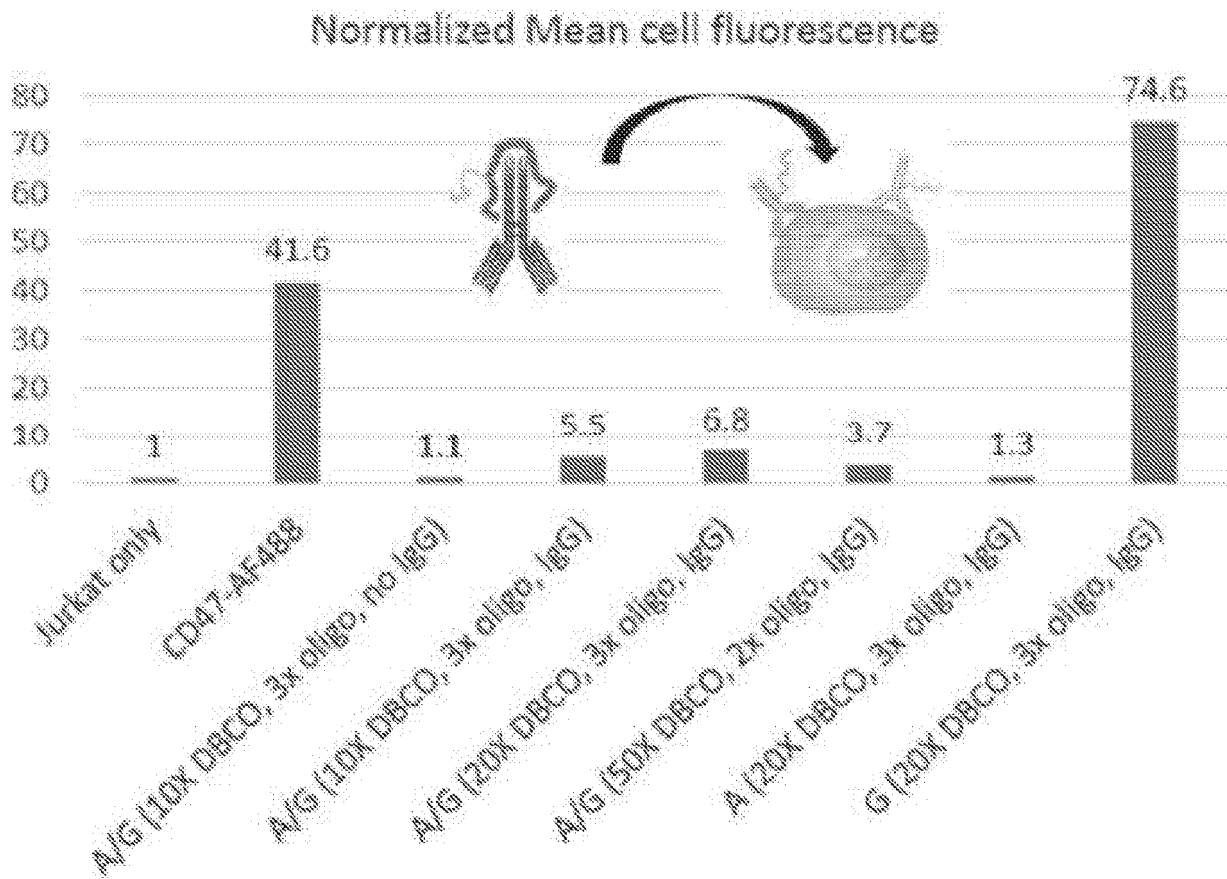


FIG. 43

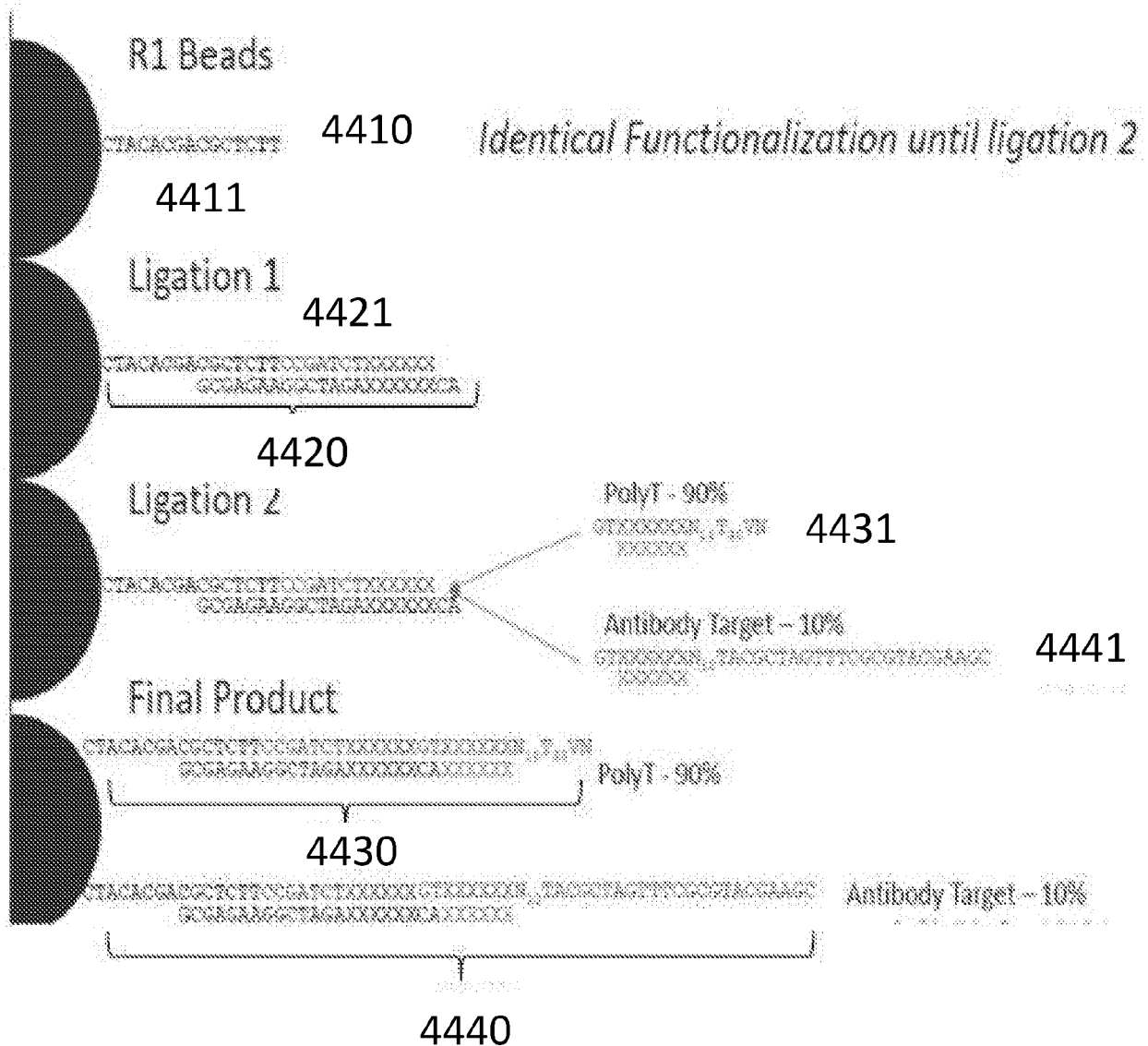


FIG. 44



FIG. 45A

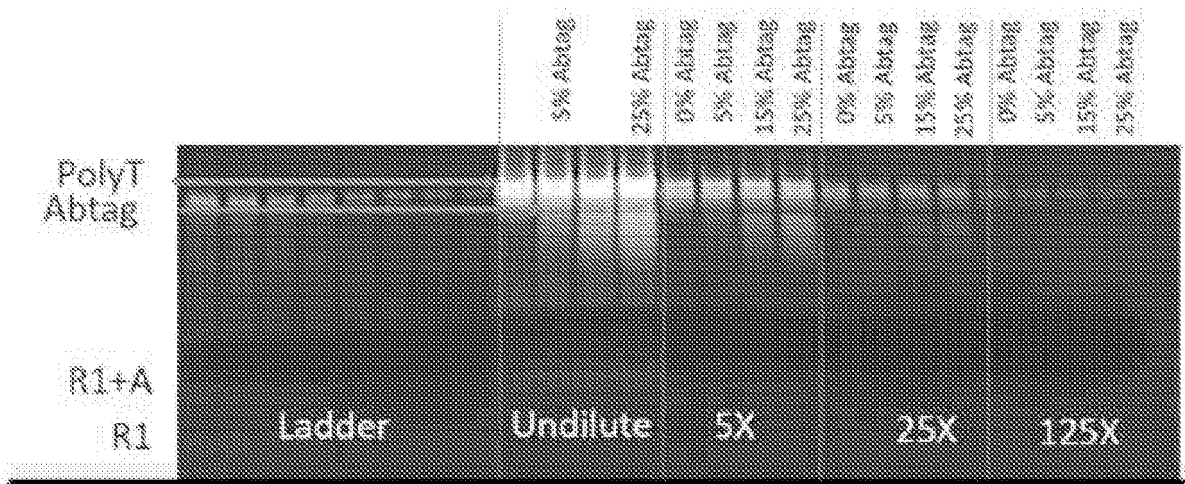


FIG. 45B

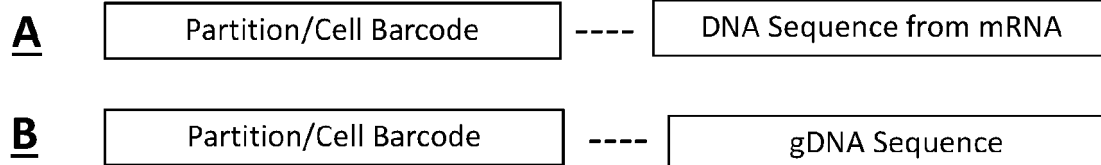
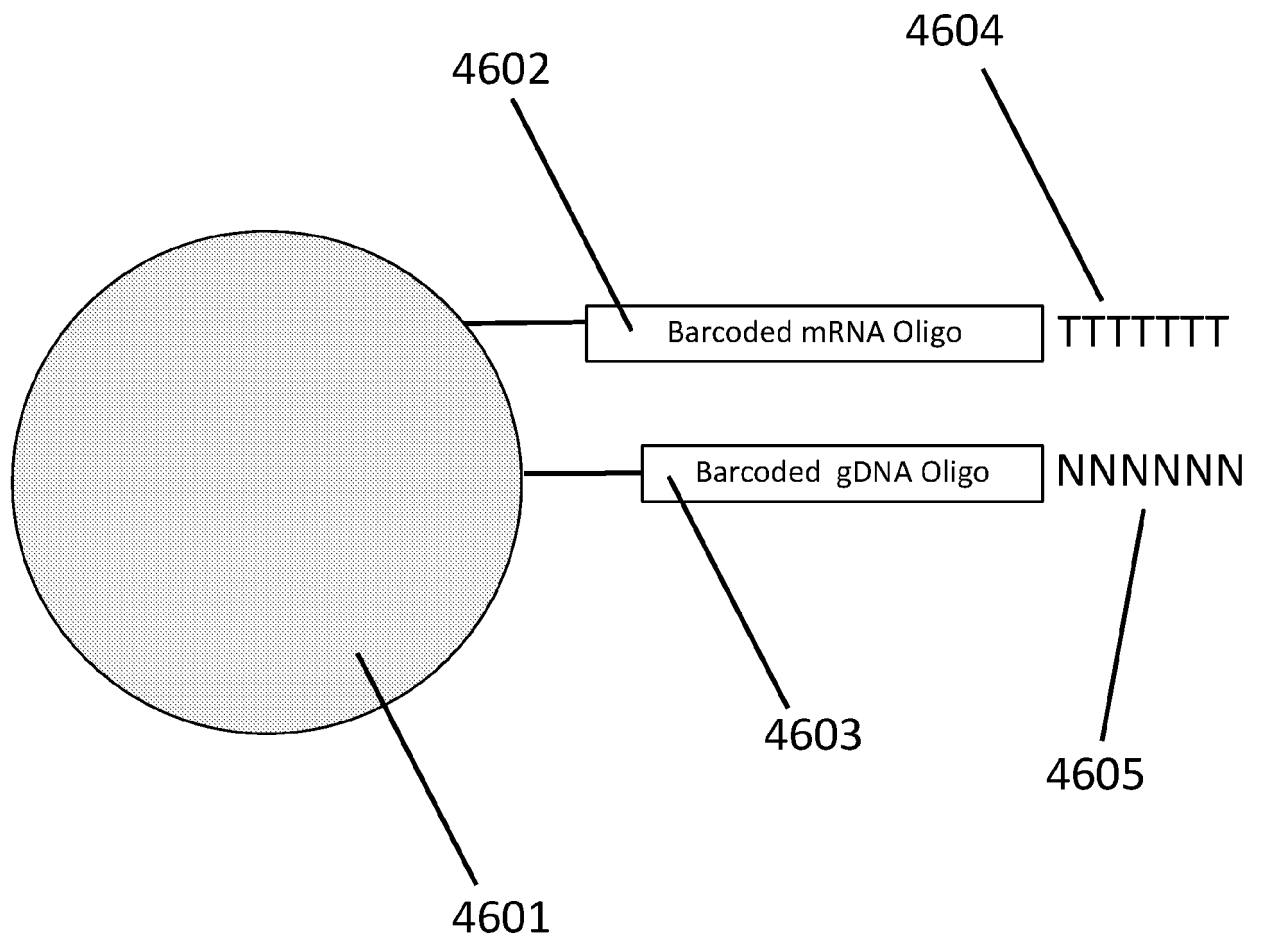
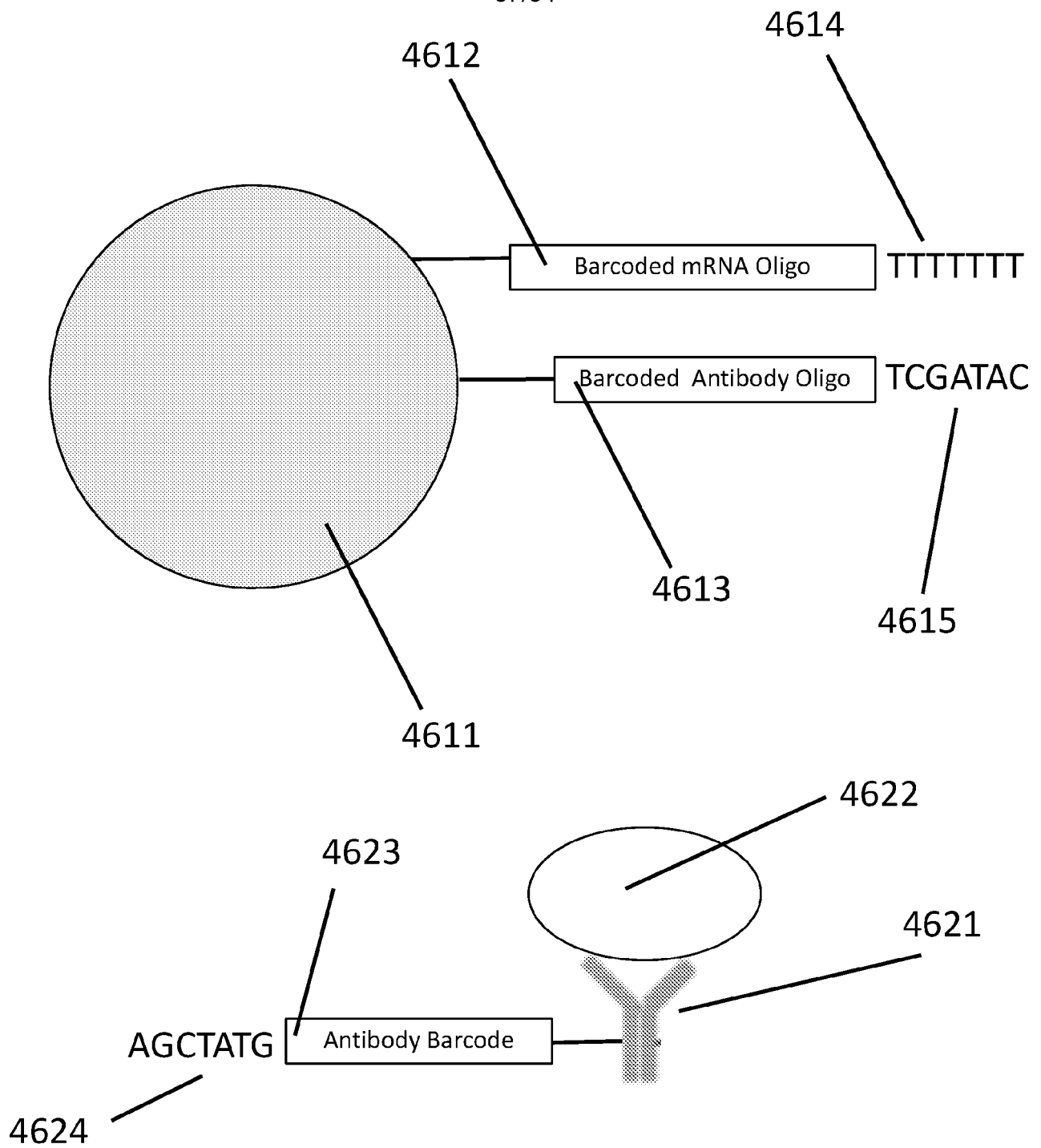
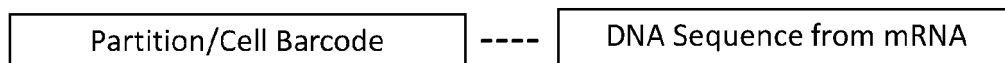


FIG. 46A

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A



B

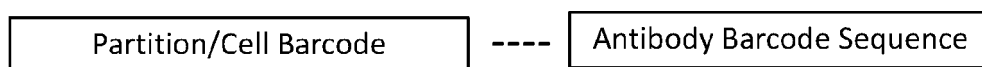


FIG. 46B

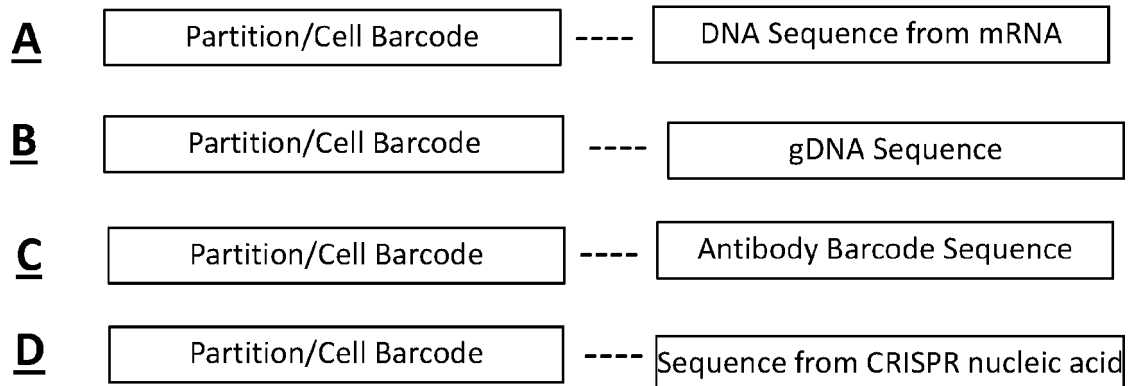
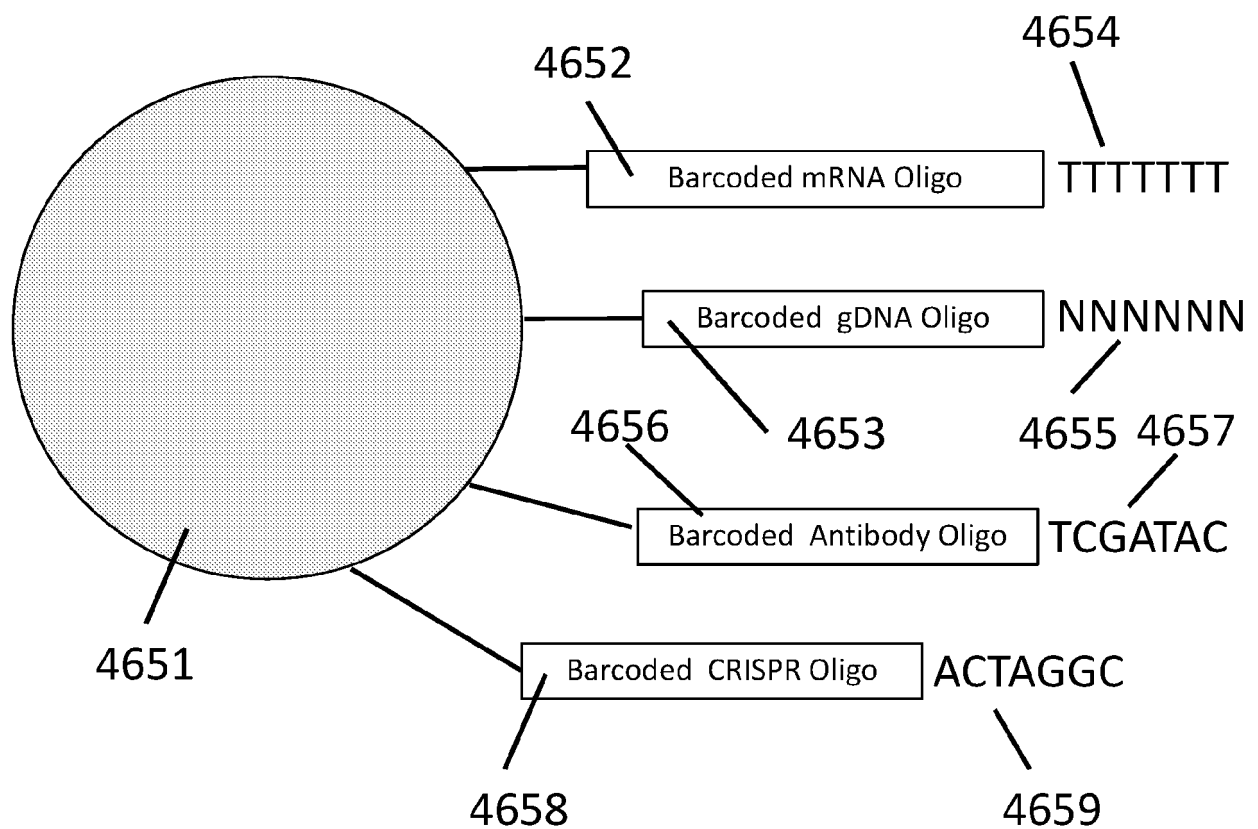


FIG. 46C

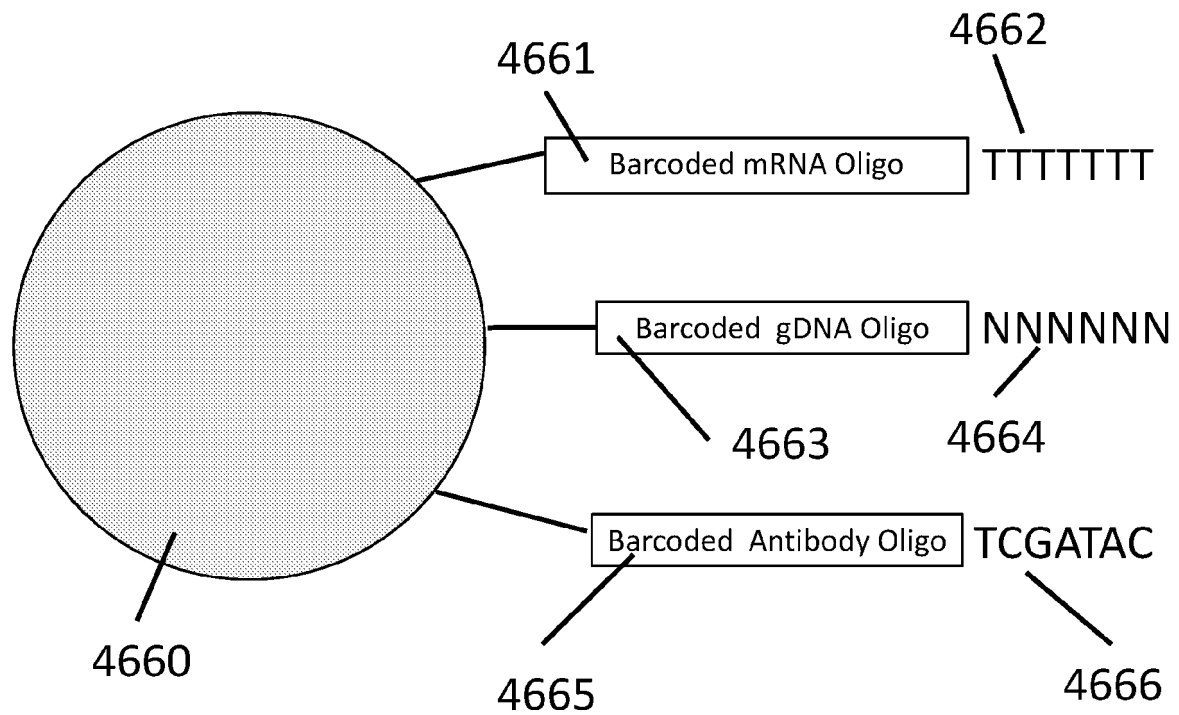


FIG. 46D

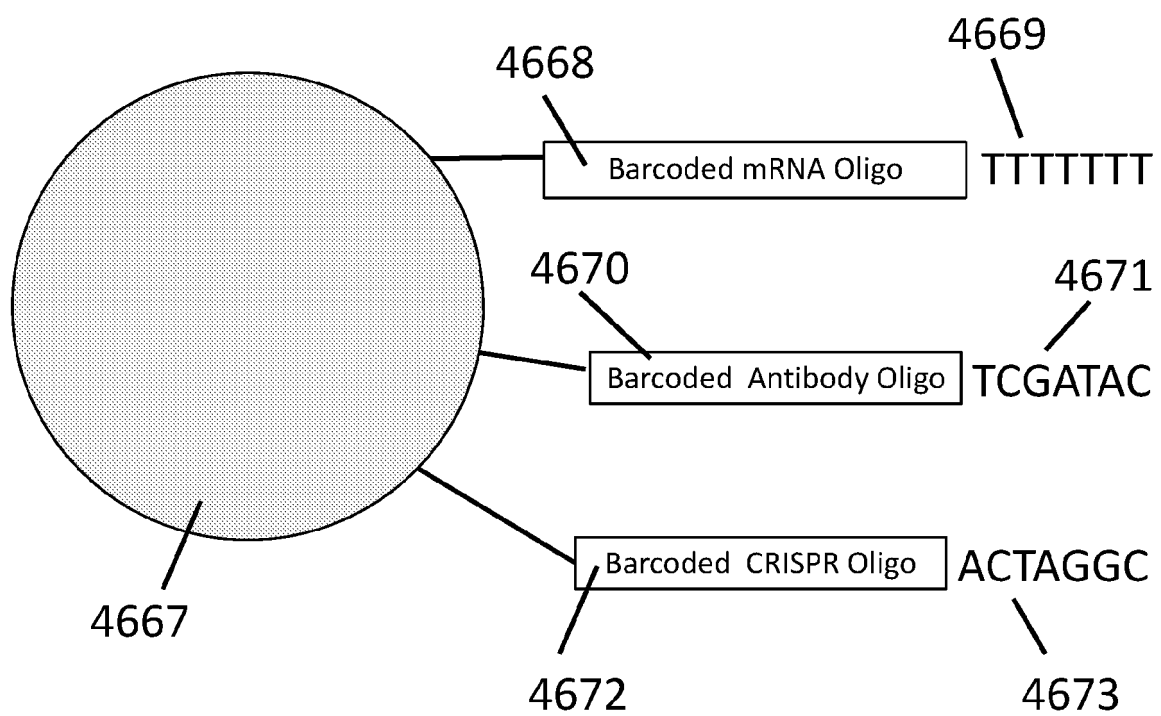


FIG. 46E

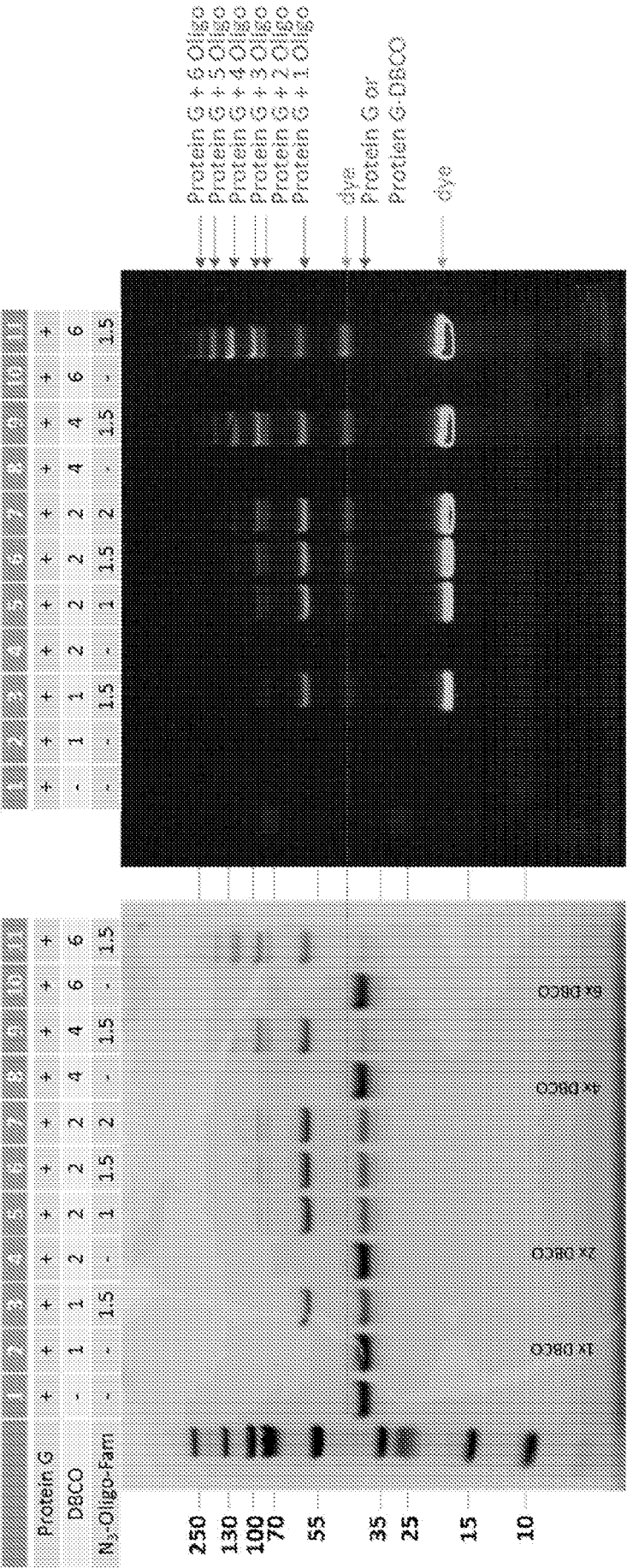


FIG. 47A

	Relative Band % (Coomassie gel)						
MW (kDa)	Protein G	1x DBCO 1.5x oligo	2X DBCO			4x DBCO 1.5x oligo	6x DBCO 1.5x oligo
			1x oligo	1.5x oligo	2x 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

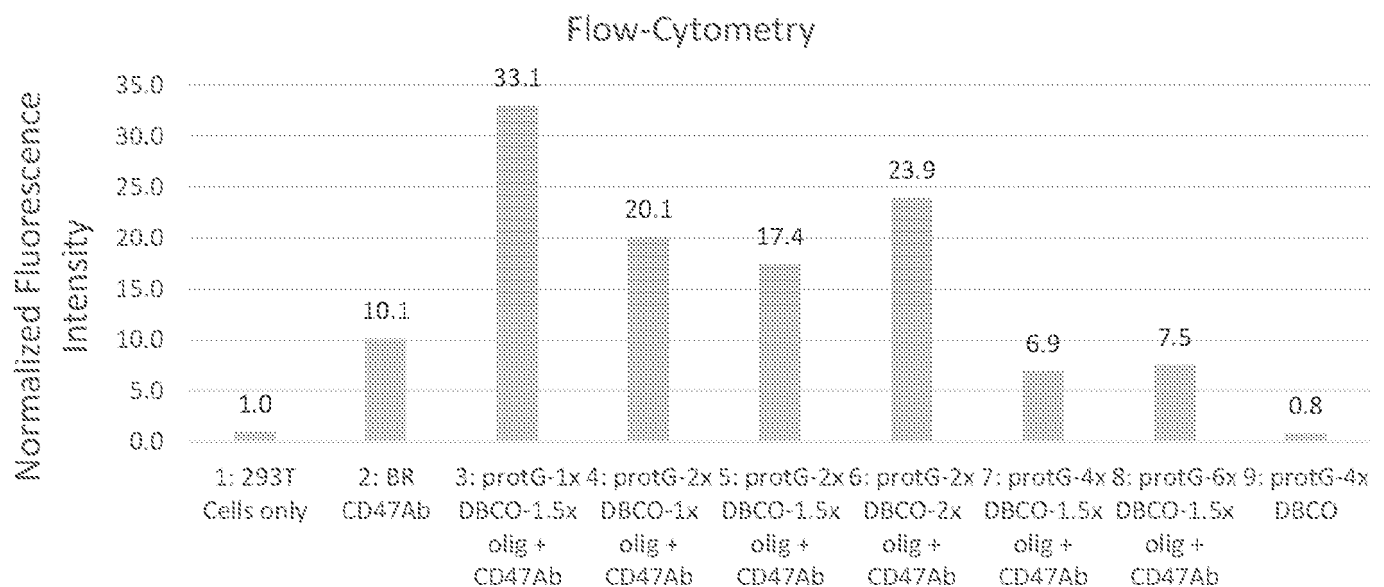
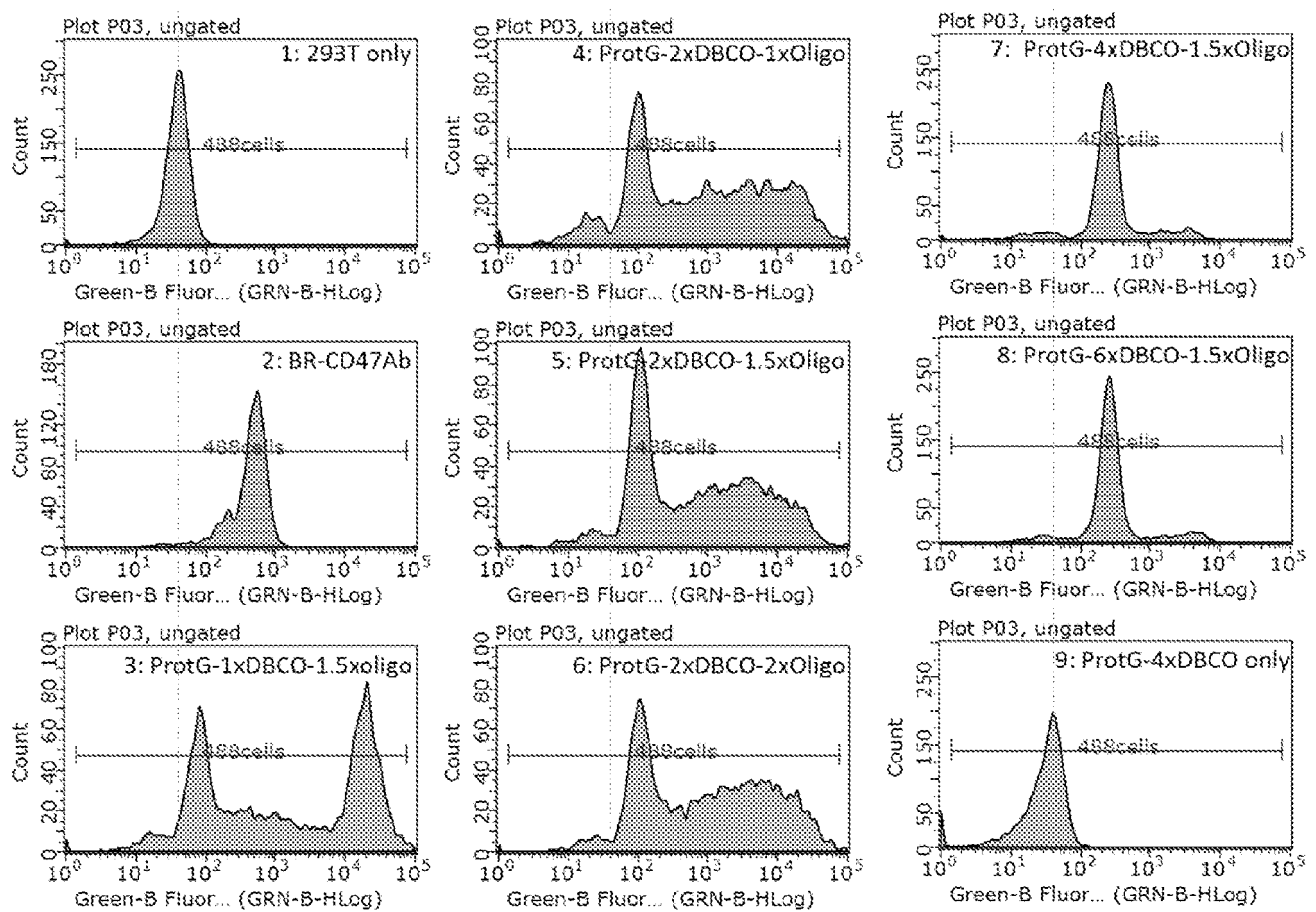
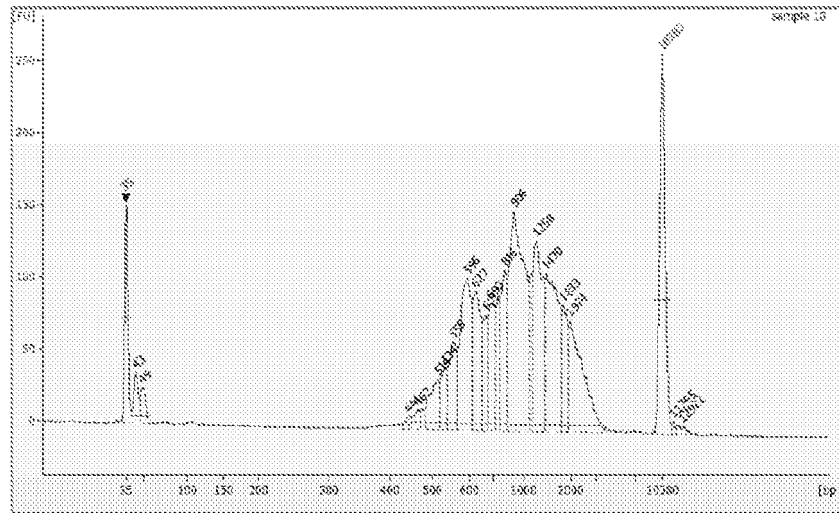


FIG. 48

Typical trace of transcriptome cDNA



Typical trace of transcriptome library

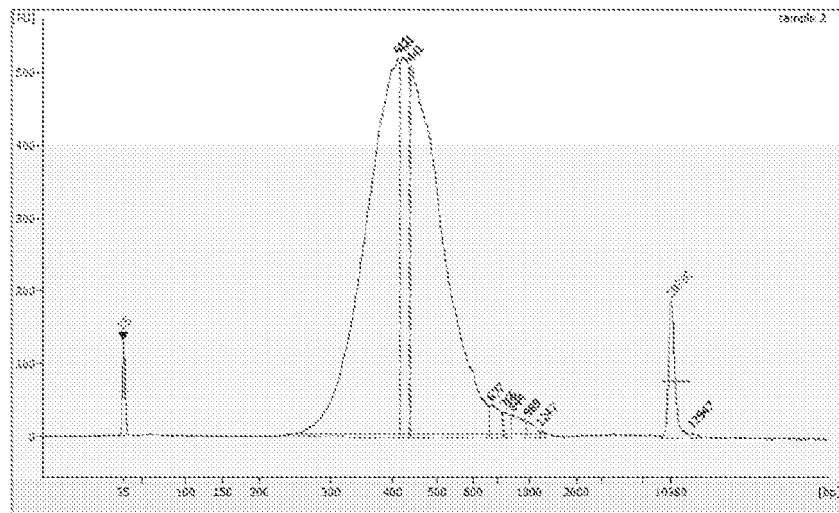
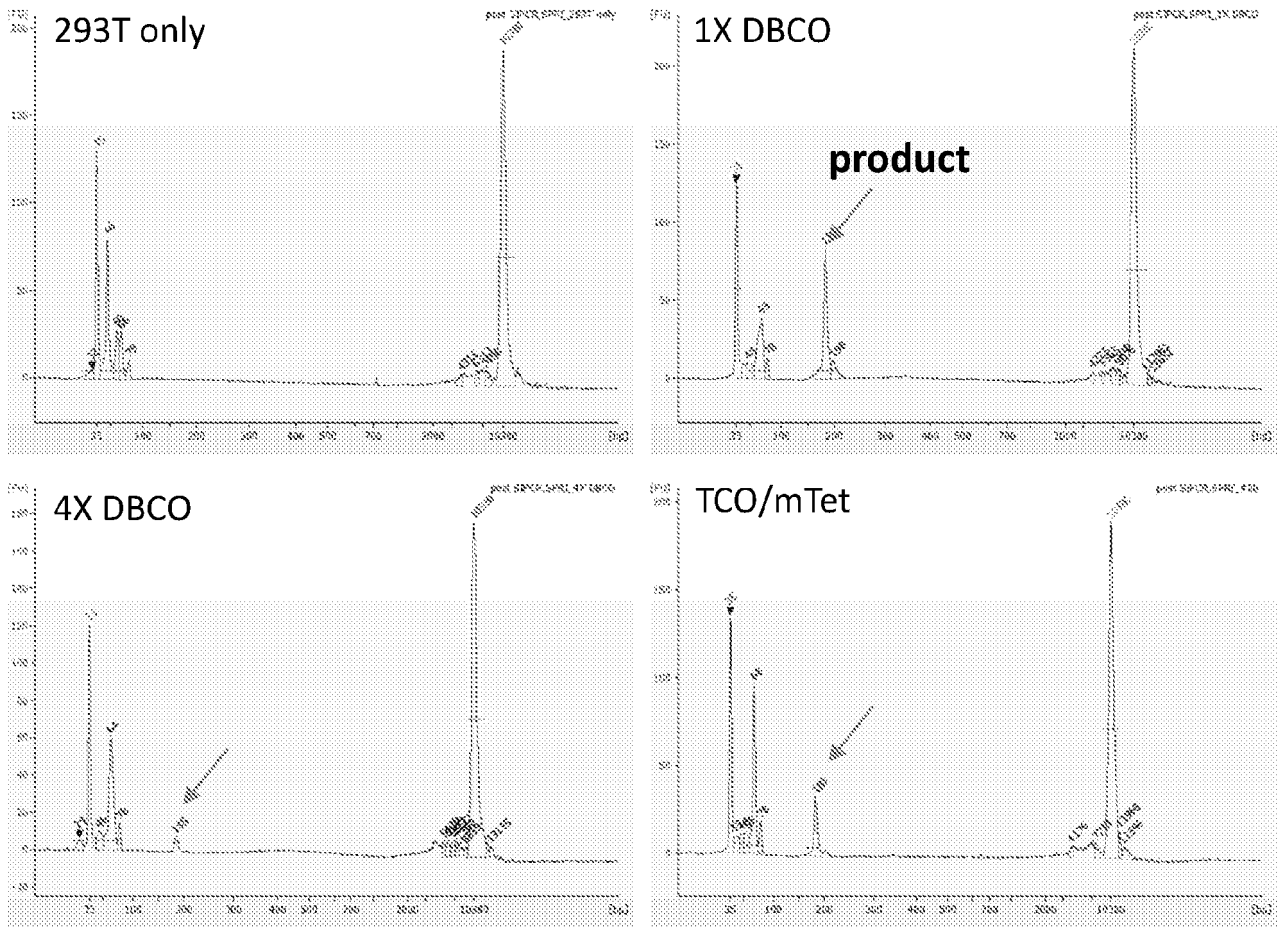


FIG. 49A



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

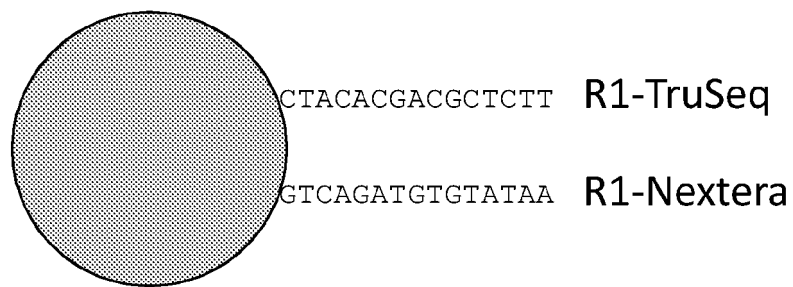


FIG. 50A

Alpha

CTACACGACGCTCTTCCGATCTXXXXXXXXGTXXXXXXXXN₁₀T₃₀VN
GCGAGAAGGCTAGAXXXXXXXXXCAXXXXXXX

Beta

CTACACGACGCTCTTCCGATCTXXXXXXXXCAXXXXXXXXXN₁₀T₃₀VN
GCGAGAAGGCTAGAXXXXXXXXXGTXXXXXXX

Gamma

CTACACGACGCTCTTCCGATCTXXXXXXXXAGXXXXXXXXN₁₀T₃₀VN
GCGAGAAGGCTAGAXXXXXXXXXTCXXXXXXX

Delta

CTACACGACGCTCTTCCGATCTXXXXXXXXTCXXXXXXXXN₁₀T₃₀VN
GCGAGAAGGCTAGAXXXXXXXXXAGXXXXXXX

FIG. 50B

Alpha

GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN₁₀GCTTCGTACGCGAAACTAGCGT
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

Beta

GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN₁₀GCTTCGTACGCGAAACTAGCGT
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

Gamma

GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN₁₀GCTTCGTACGCGAAACTAGCGT
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

Delta

GTCAGATGTGTATAAGAGACAGXXXXXXXXGTXXXXXXXXN₁₀GCTTCGTACGCGAAACTAGCGT
CACATATTCTCTGTCXXXXXXXXCAXXXXXXX

FIG. 50C

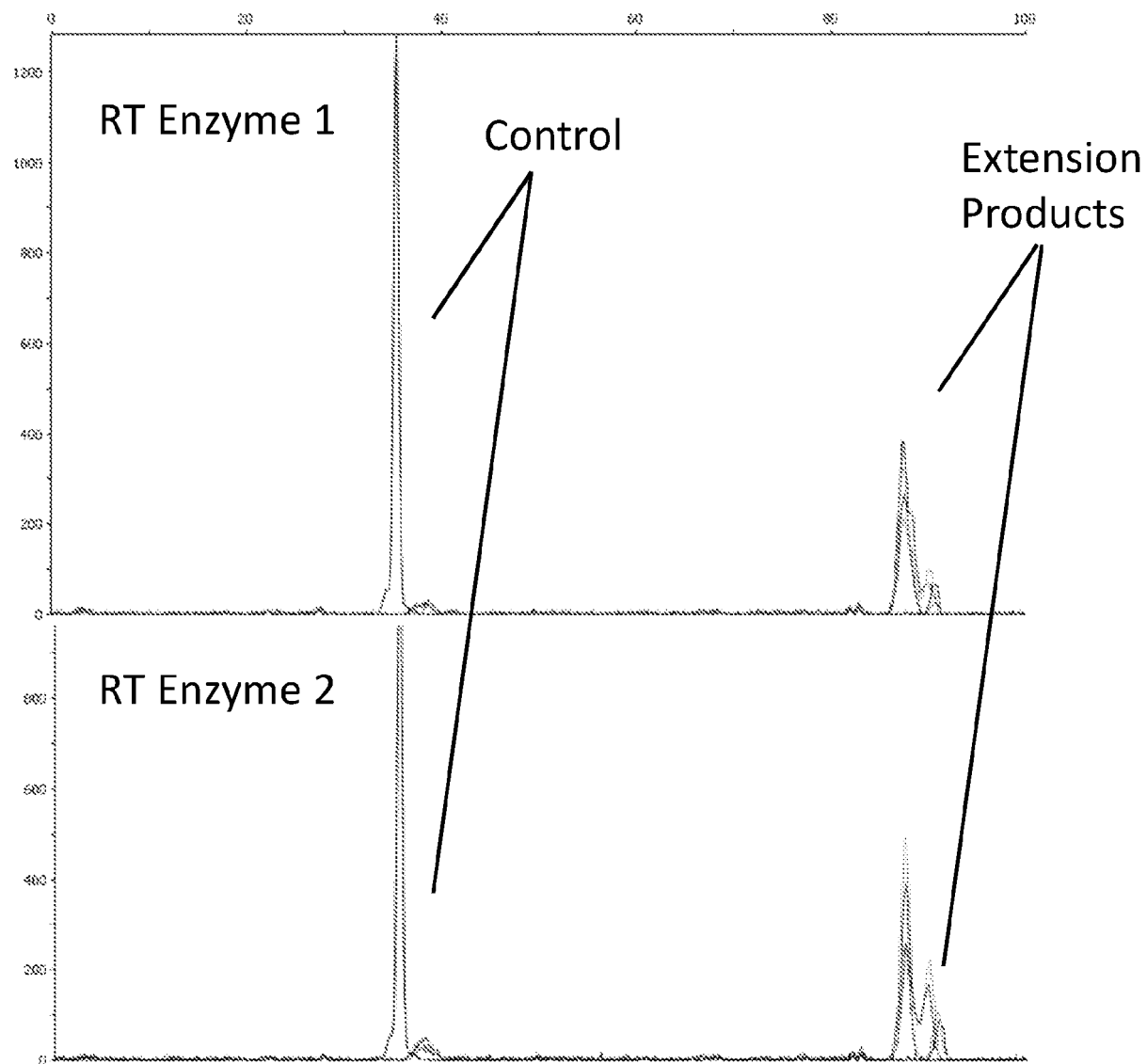


FIG. 51B

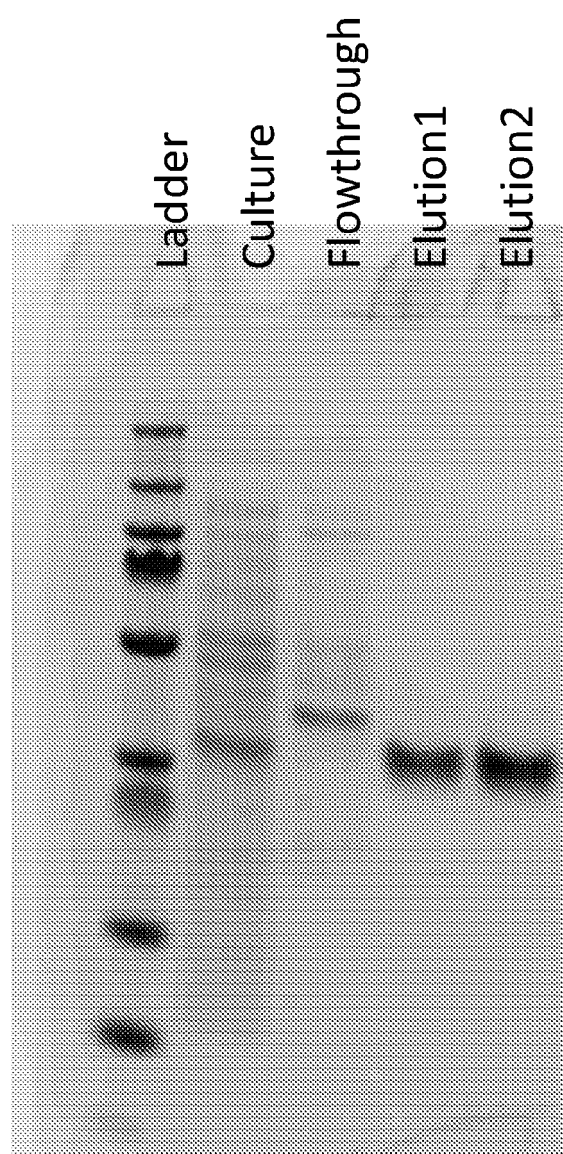
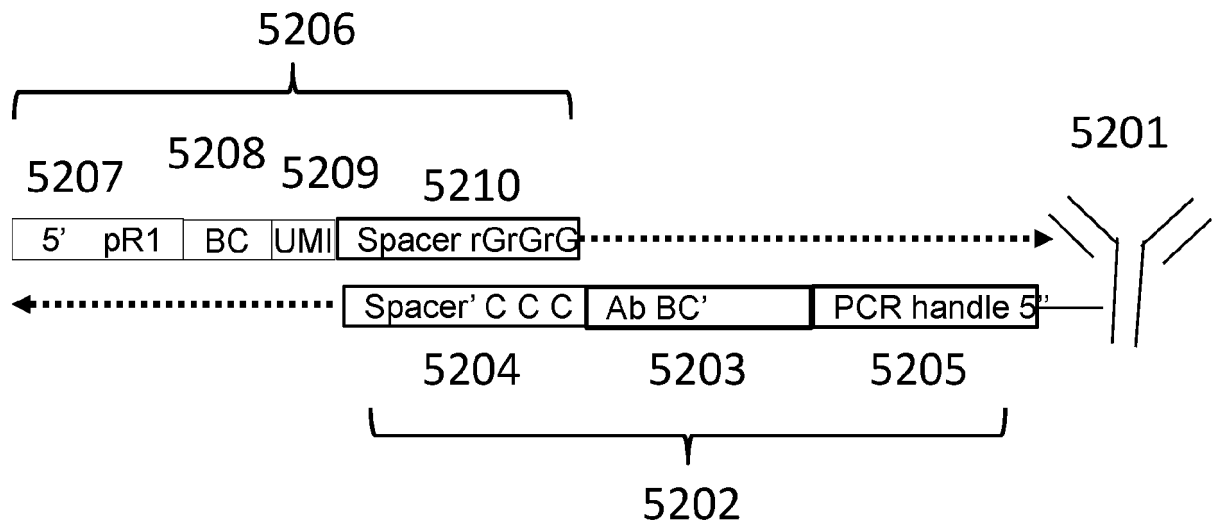


FIG. 52A

I



II

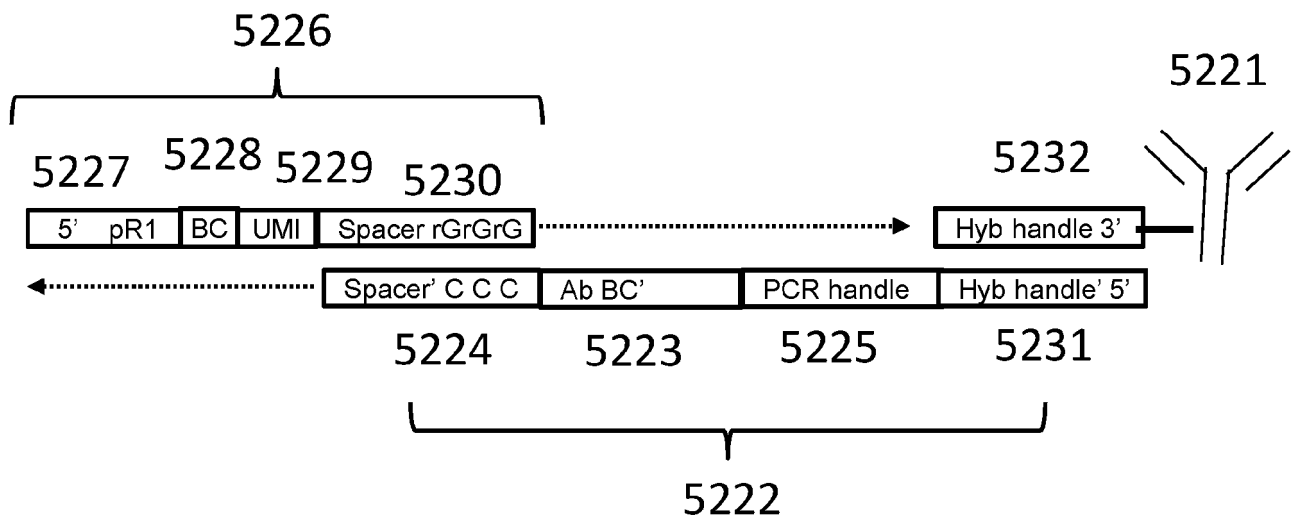
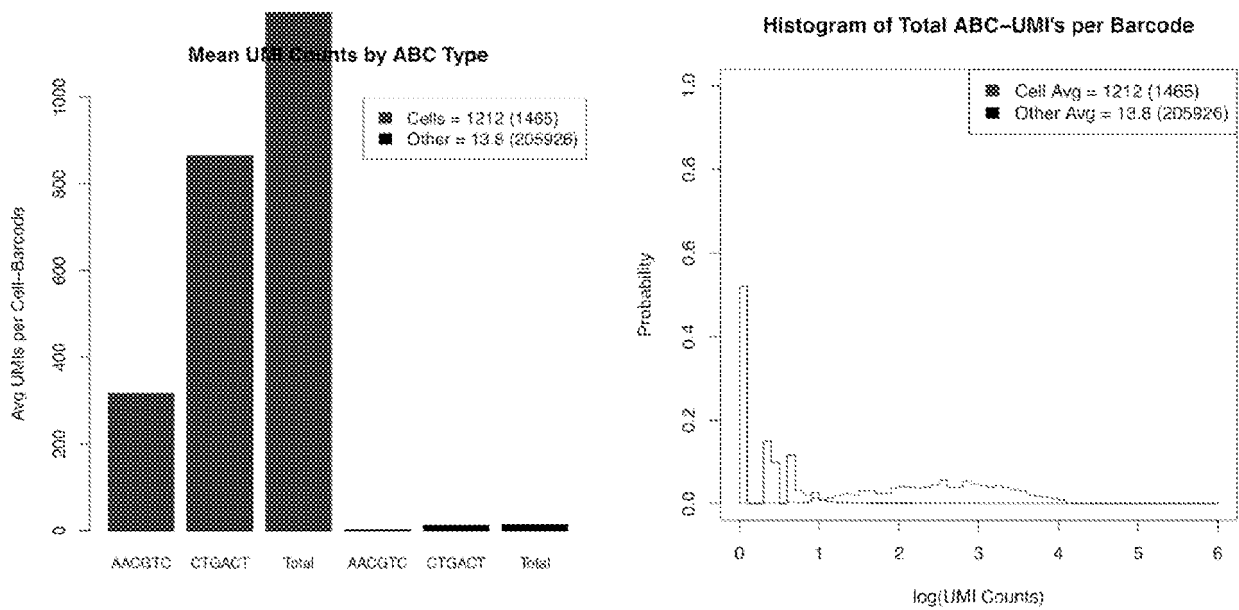


FIG. 52B

Jurkat + CD47/CD99



II

Jurkat + CD47

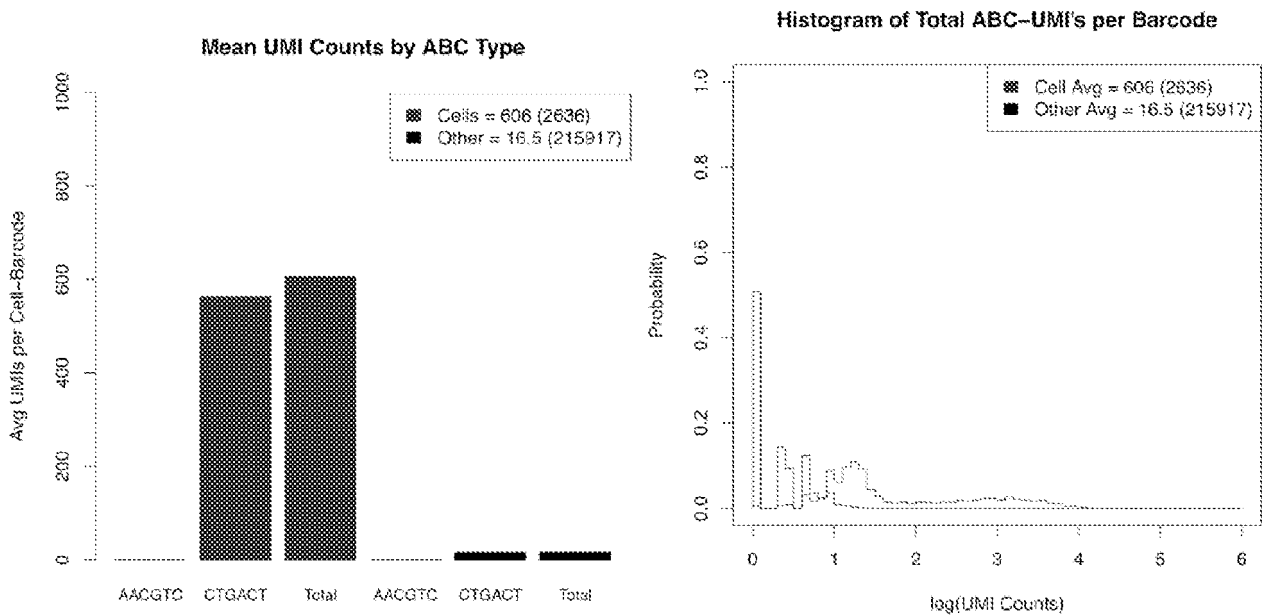


FIG. 53A

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Sample	Sample ID	Avg UMIs Per Cell	Avg UMIs Per Other	BC3 per cell	BC4 per cell	Total # of cell BCs detected in AbBC expt	# cells, SCS	# cells, AbBC topN (%cells, SCS)	AbBC topN cells in SCS cells	AbBC called cells	AbBC cells in SCS cells	SCS cells in AbBC topN / SCS cells	BCAb cells in SCS cells
Unbiased Jurkat + BC4	33603	4.98	15.9	64627	635932	124483	1419	1428	378	1362	370	0.27	0.27
Unbiased Jurkat + BC3/4	33603	5.77	17.1	247587	404815	126514	1141	1141	368	992	316	0.32	0.32
Unbiased Jurkat + BC4	33602	9.96	9.14	2474578	6119	144163	1505	1504	862	1193	762	0.57	0.64
Unbiased Jurkat spike BC3/4	33603	38.8	14.1	1163	71316	206337	1898	1980	103	62631	1570	0.05	0.03

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 Antisense to Genes	Fraction reads unmapped	cDNA PCR Duplication (20k raw reads per cell)	Median genes per cell (20k raw reads per cell)	Median UMIs counts per cell (20k raw reads per cell)
37156	cDNA control	217,543	83.60%	56.00%	95.70%	25.20%	64.50%	12.70%	8.90%	9.00%	3.30%	46.90%	1,103	2,764
37172	Unbiased 5: CG-CD3 GEM 53/85C D	31,699	70.20%	32.90%	95.10%	15.20%	41.80%	9.08%	16.60%	12.60%	4.70%	43.30%	750	1,690
37173	Unbiased 6: CG-CD3 GEM 53/85C D	29,602	69.30%	29.90%	94.40%	13.70%	36.90%	9.30%	16.80%	14.00%	4.70%	42.80%	664	1,562
37176	Unbiased 21: SC-CD3 GEM 53/85C D	36,549	76.00%	37.10%	95.40%	17.20%	47.40%	13.20%	13.50%	13.90%	5.10%	44.60%	812	1,935
37177	Unbiased 23: SC-CD3 GEM 53/85C D	44,884	75.40%	39.20%	96.10%	18.30%	48.90%	12.60%	13.10%	13.00%	5.10%	43.20%	855	2,077
37180	Unbiased 24: SC-CD3 GEM 53/85C S	33,928	76.20%	38.30%	94.40%	17.60%	47.80%	12.00%	14.50%	12.80%	4.50%	48.30%	793	1,796
37183	Unbiased 16: SC-CD3 GEM 53/85C S	33,085	71.90%	33.90%	92.50%	15.60%	33.90%	11.30%	15.30%	14.30%	4.60%	46.00%	750	1,666
37184	Unbiased 23: SC-CD3 GEM 53/85C S	40,137	77.00%	40.20%	96.30%	18.60%	50.40%	14.90%	12.90%	12.90%	4.60%	49.60%	803	1,860
37185	Unbiased 24: SC-CD3 GEM 53/85C S	40,931	90.30%	39.10%	95.00%	16.10%	50.30%	16.20%	13.40%	14.00%	4.90%	52.20%	747	1,734
37170	Unbiased 1: CG-CD3 GEM 53C Dyna	29,136	91.40%	64.50%	94.90%	29.80%	71.10%	12.00%	7.90%	6.20%	6.50%	69.70%	673	1,824
37171	Unbiased 2: CG-CD3 GEM 53C Dyna	28,533	91.30%	65.40%	95.30%	30.30%	71.60%	11.90%	7.40%	5.80%	6.40%	64.80%	751	2,057
37174	Unbiased 17: SC-CD3 GEM 53C Dyna	42,069	91.90%	62.40%	95.10%	28.90%	69.40%	15.30%	7.30%	6.70%	6.70%	64.70%	752	2,009
37175	Unbiased 18: SC-CD3 GEM 53C Dyna	38,254	91.60%	63.60%	95.30%	29.10%	69.90%	15.30%	7.10%	6.60%	6.60%	65.30%	751	2,003
37176	Unbiased 19: SC-CD3 GEM 53C Dyna	32,775	92.60%	67.70%	94.90%	31.30%	73.60%	11.70%	6.90%	5.70%	5.90%	64.60%	848	2,113
37179	Unbiased 4: CG-CD3 GEM 53C Stre	30,309	92.80%	67.40%	94.40%	30.90%	73.40%	12.30%	6.70%	5.90%	6.10%	63.90%	855	2,147
37182	Unbiased 19: SC-CD3 GEM 53C Stre	45,118	92.00%	61.40%	95.30%	28.30%	68.40%	18.60%	6.70%	6.70%	6.30%	68.00%	757	1,744
37183	Unbiased 20: SC-CD3 GEM 53C Stre	37,621	92.60%	61.60%	94.50%	28.20%	68.60%	18.20%	6.50%	6.80%	6.80%	67.90%	741	1,702

FIG. 54

No heat kill

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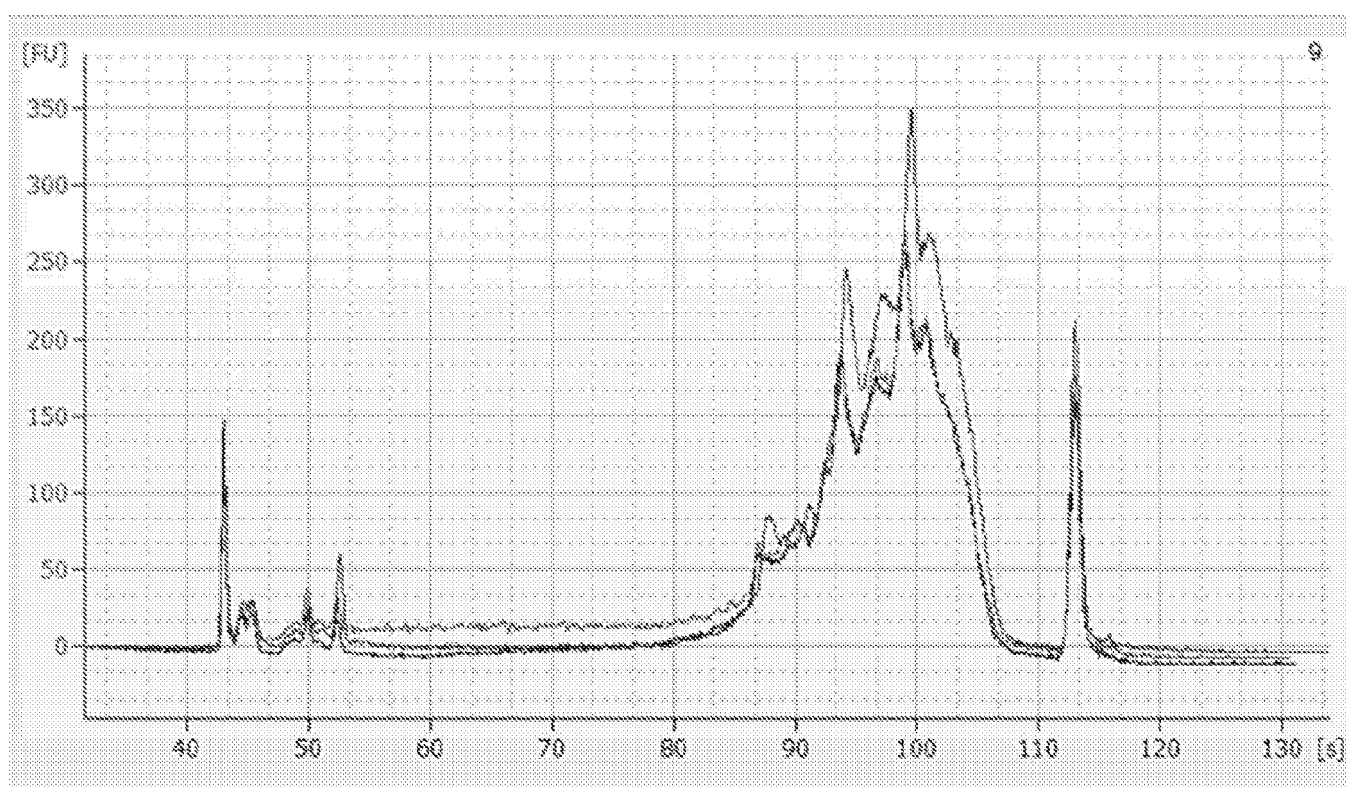


FIG. 55

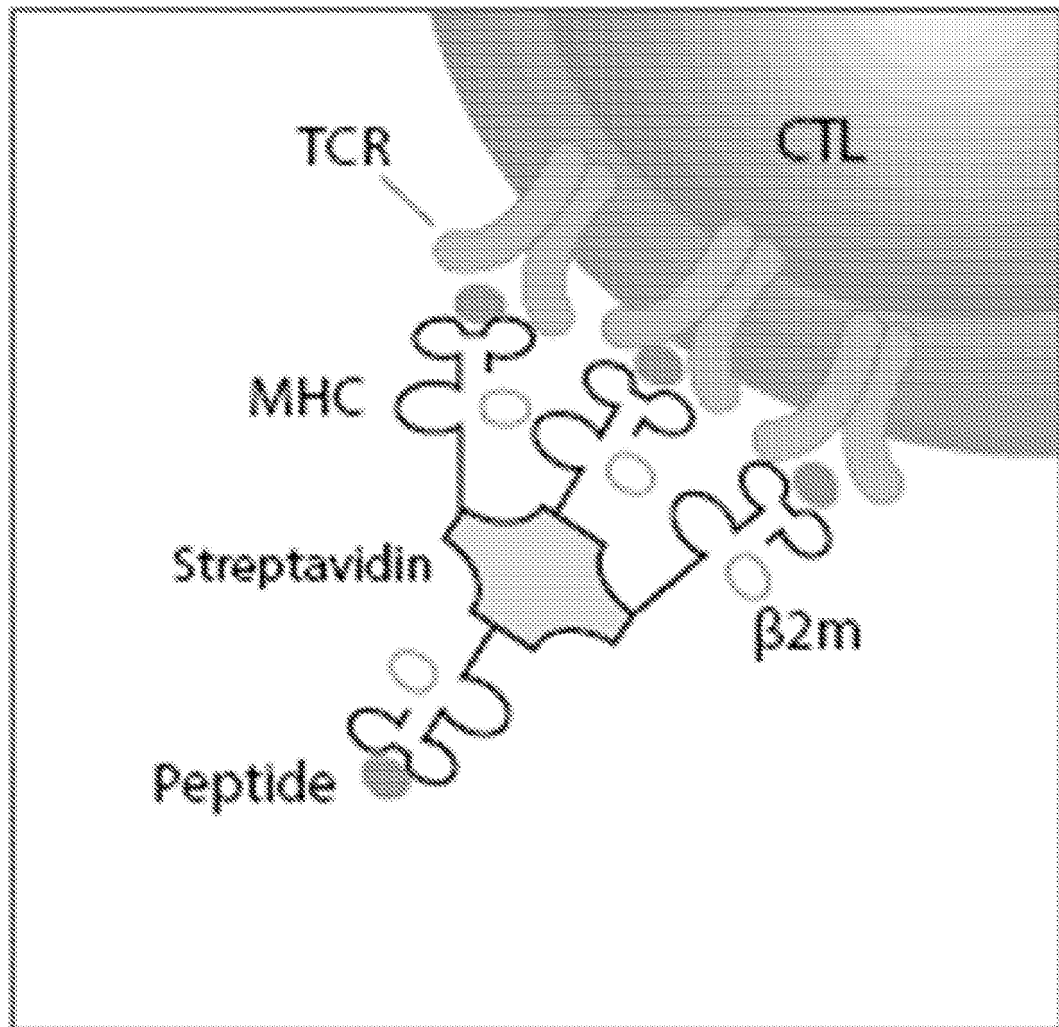


FIG. 56A

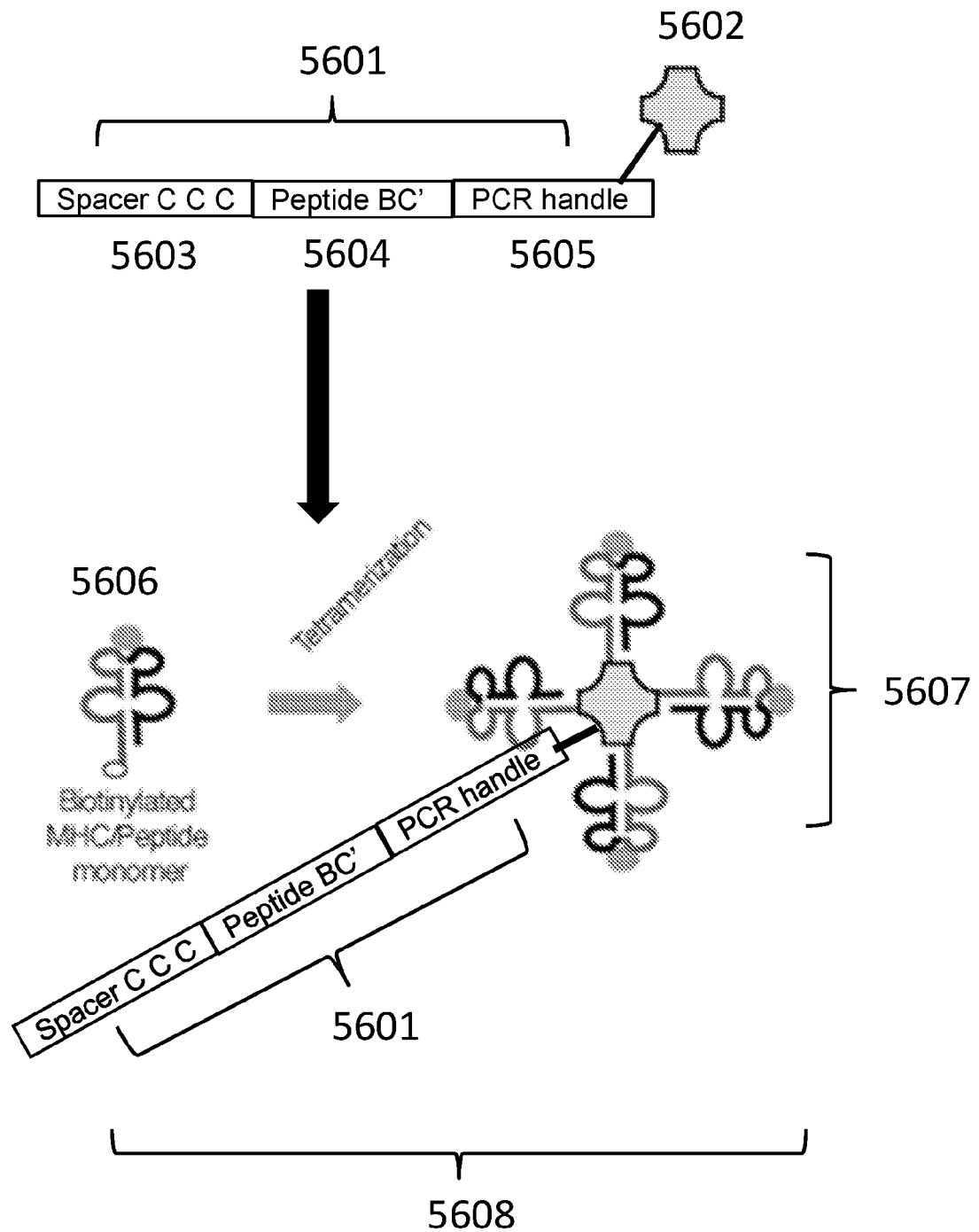


FIG. 56B

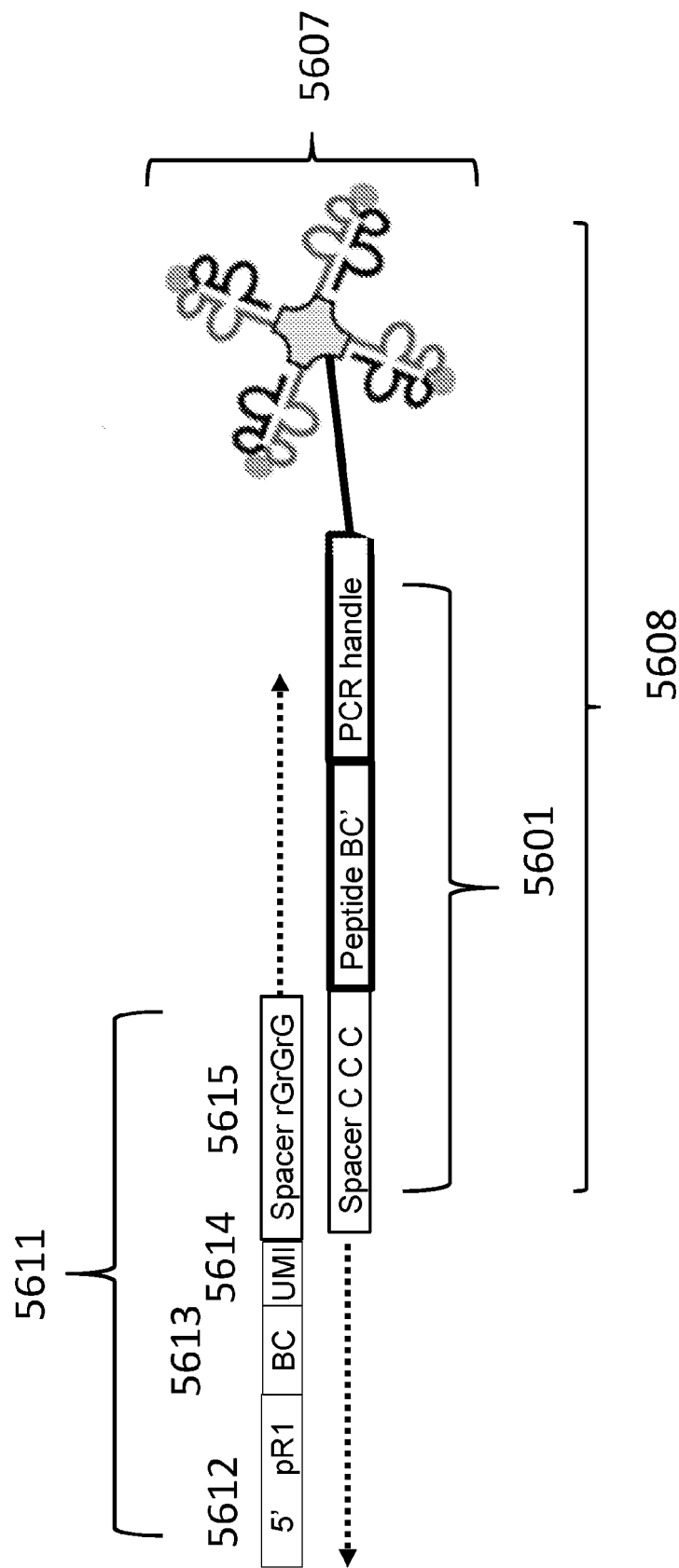


FIG. 56C

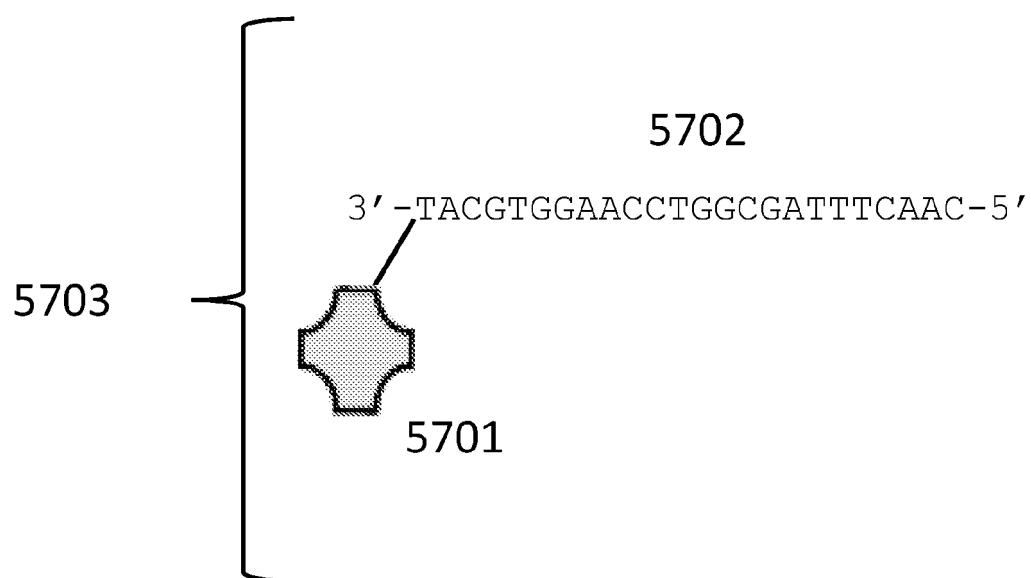


FIG. 57A

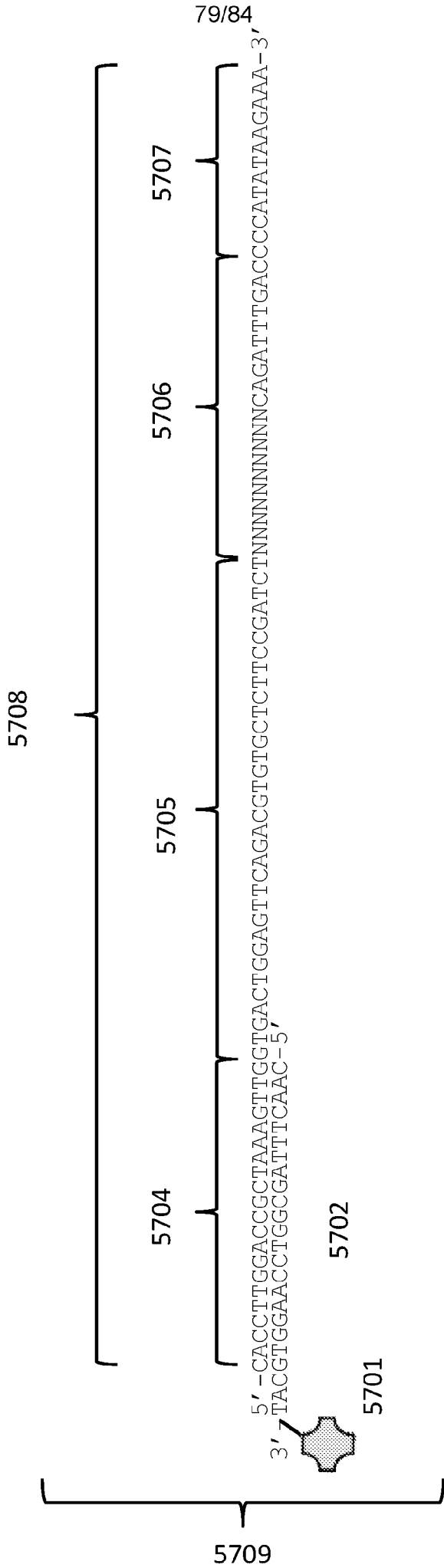


FIG. 57B

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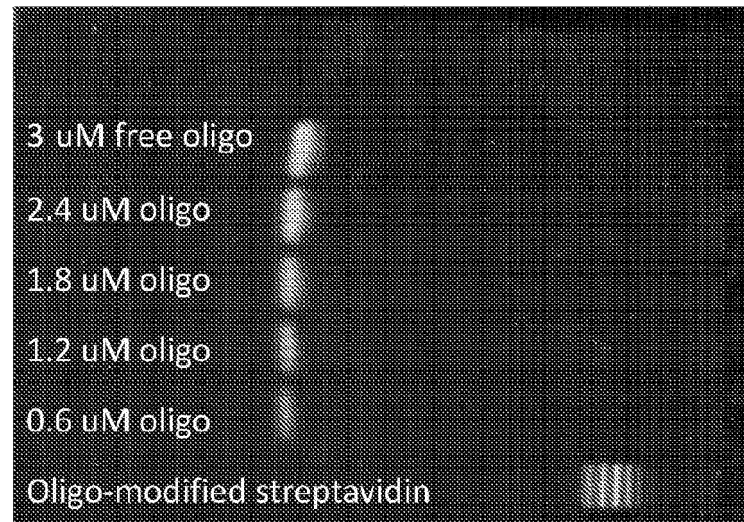


FIG. 58A

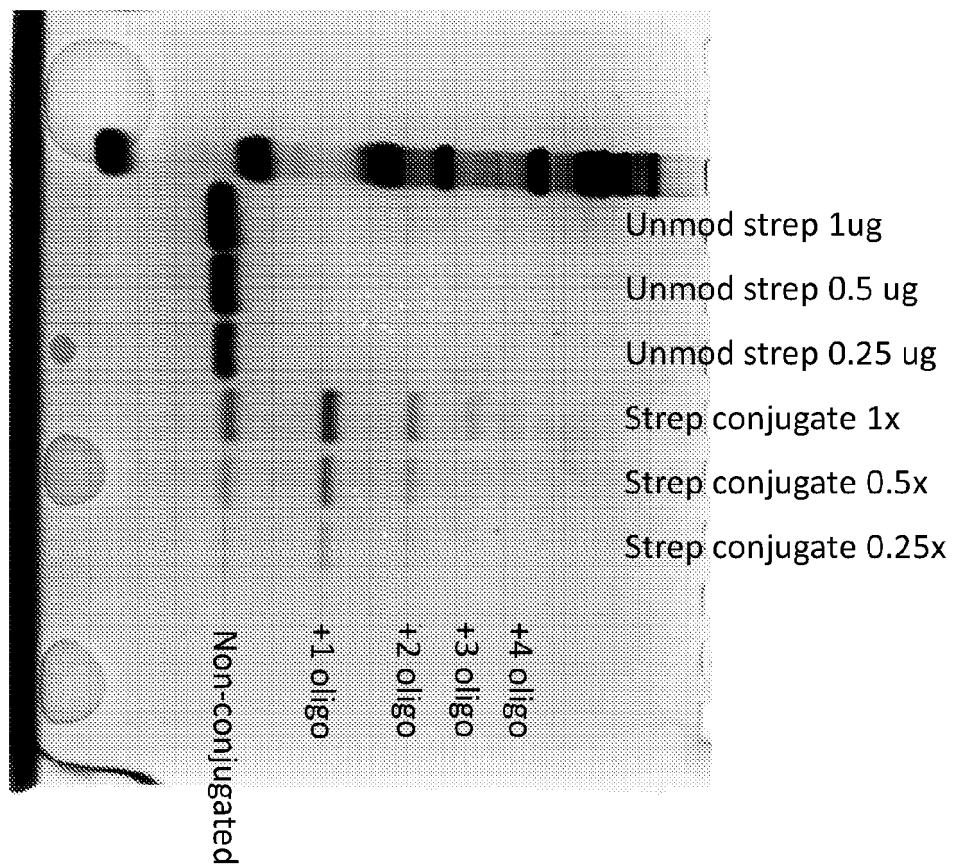


FIG. 58B

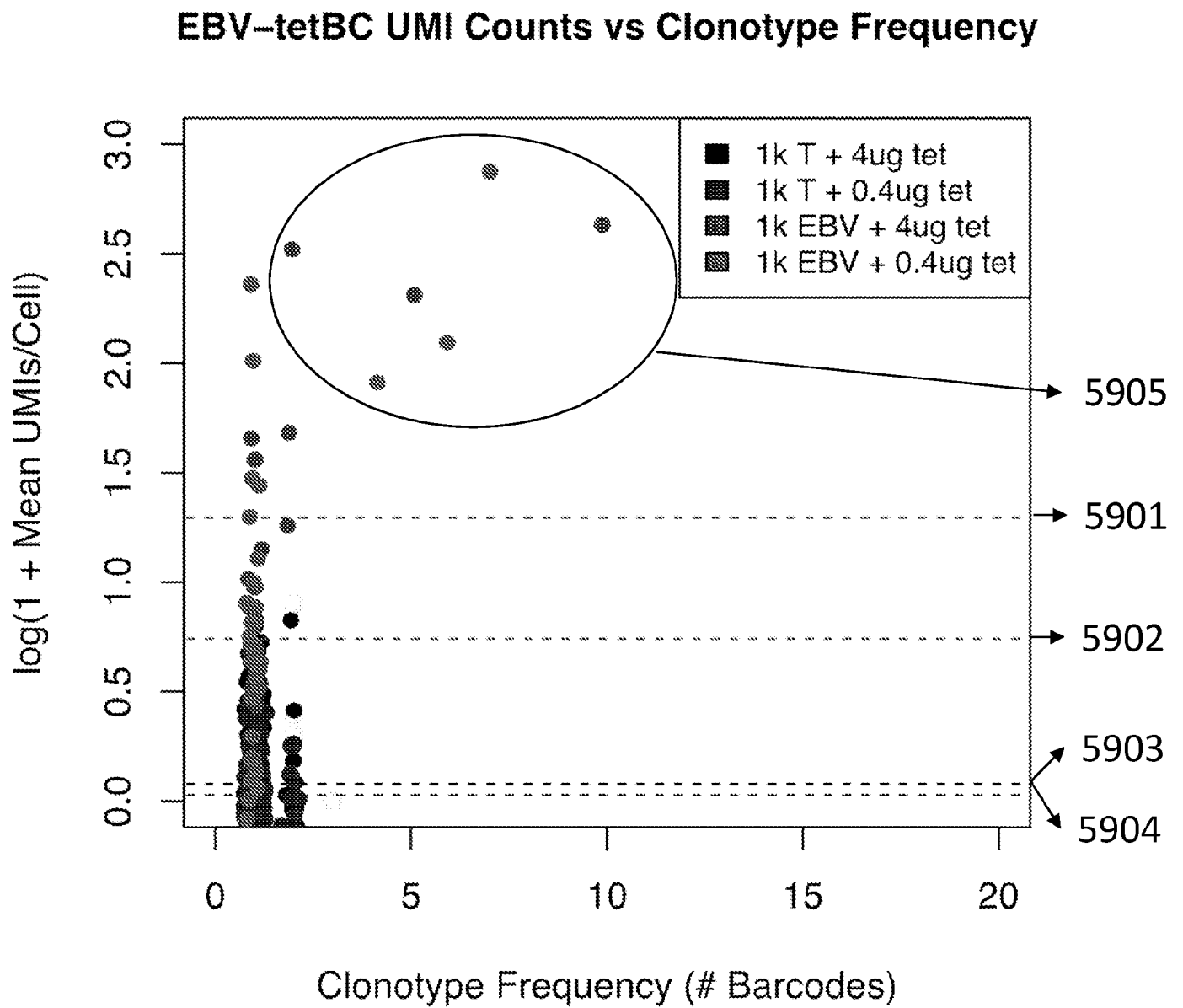


FIG. 59

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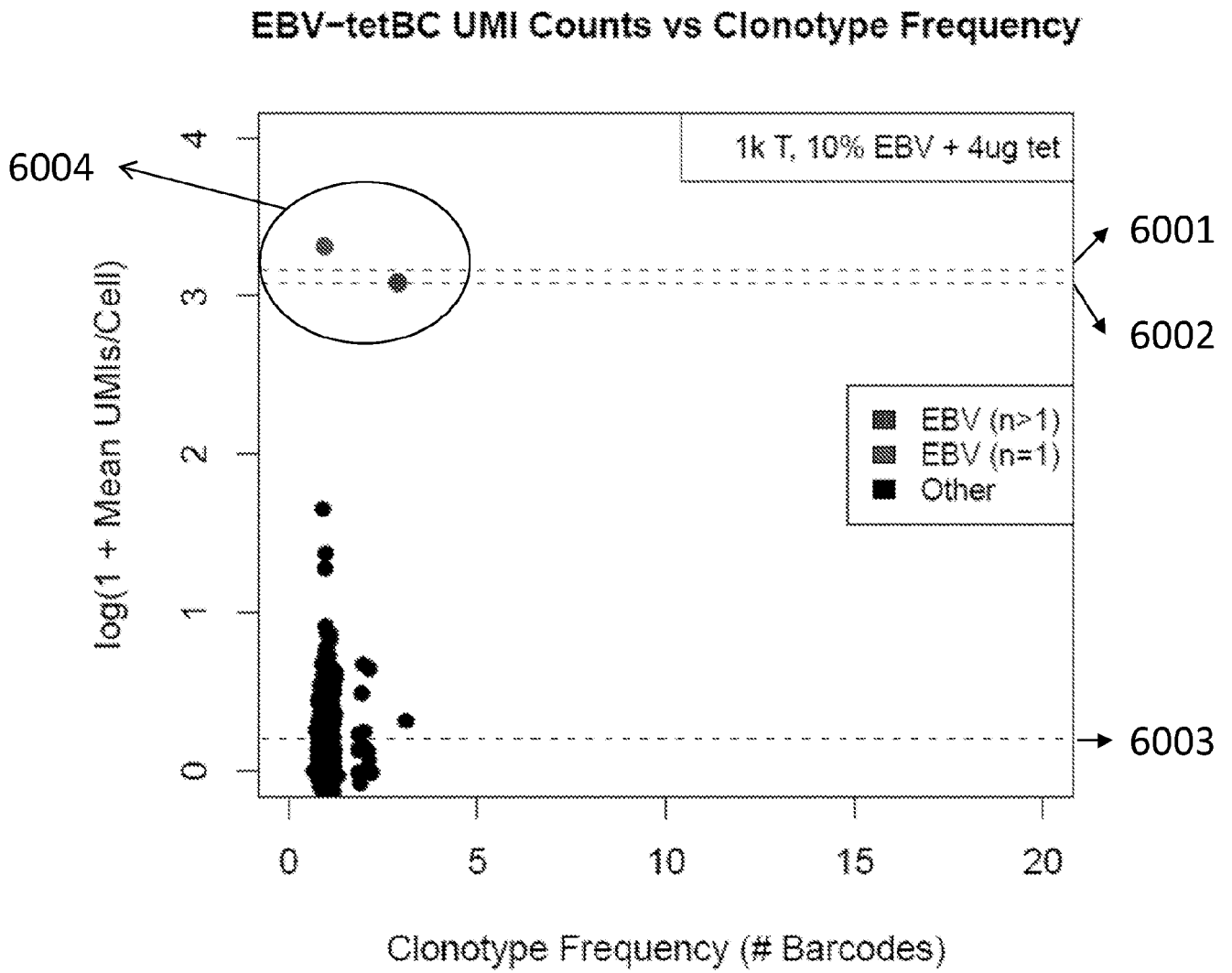


FIG. 60

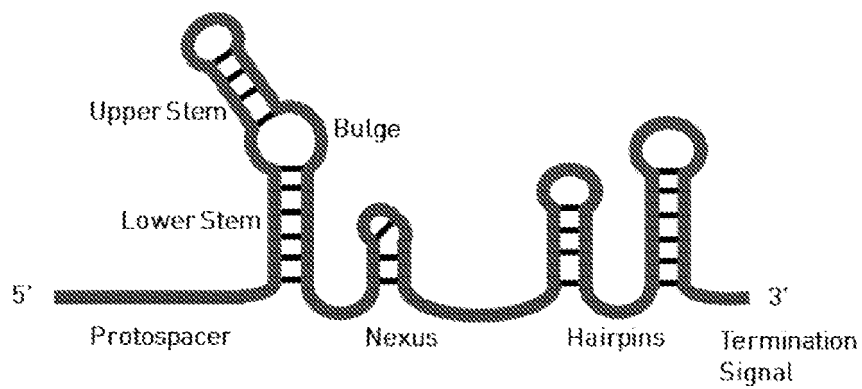


FIG. 61A

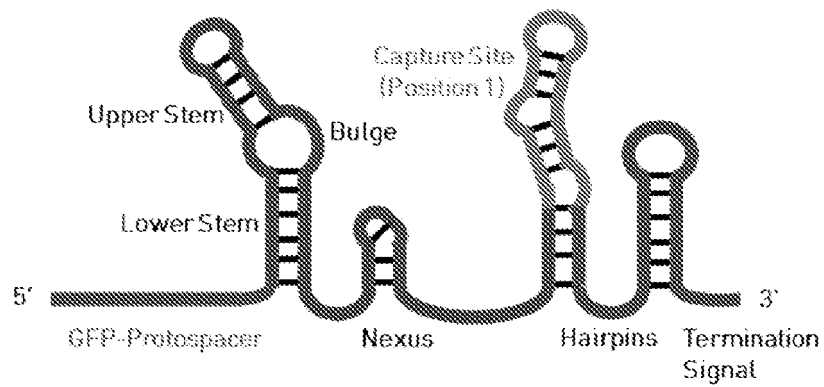


FIG. 61B

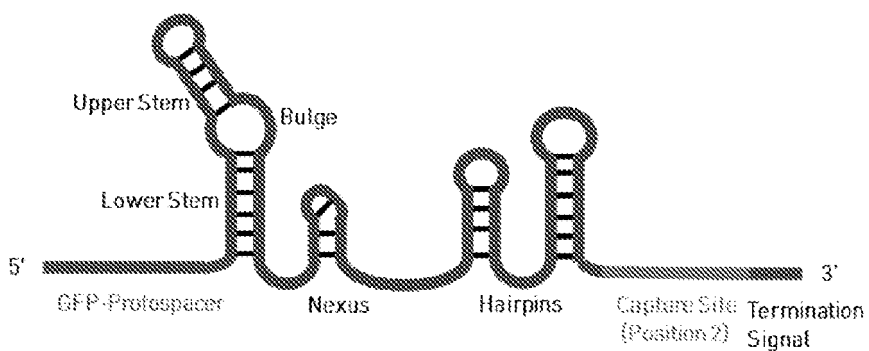


FIG. 61C

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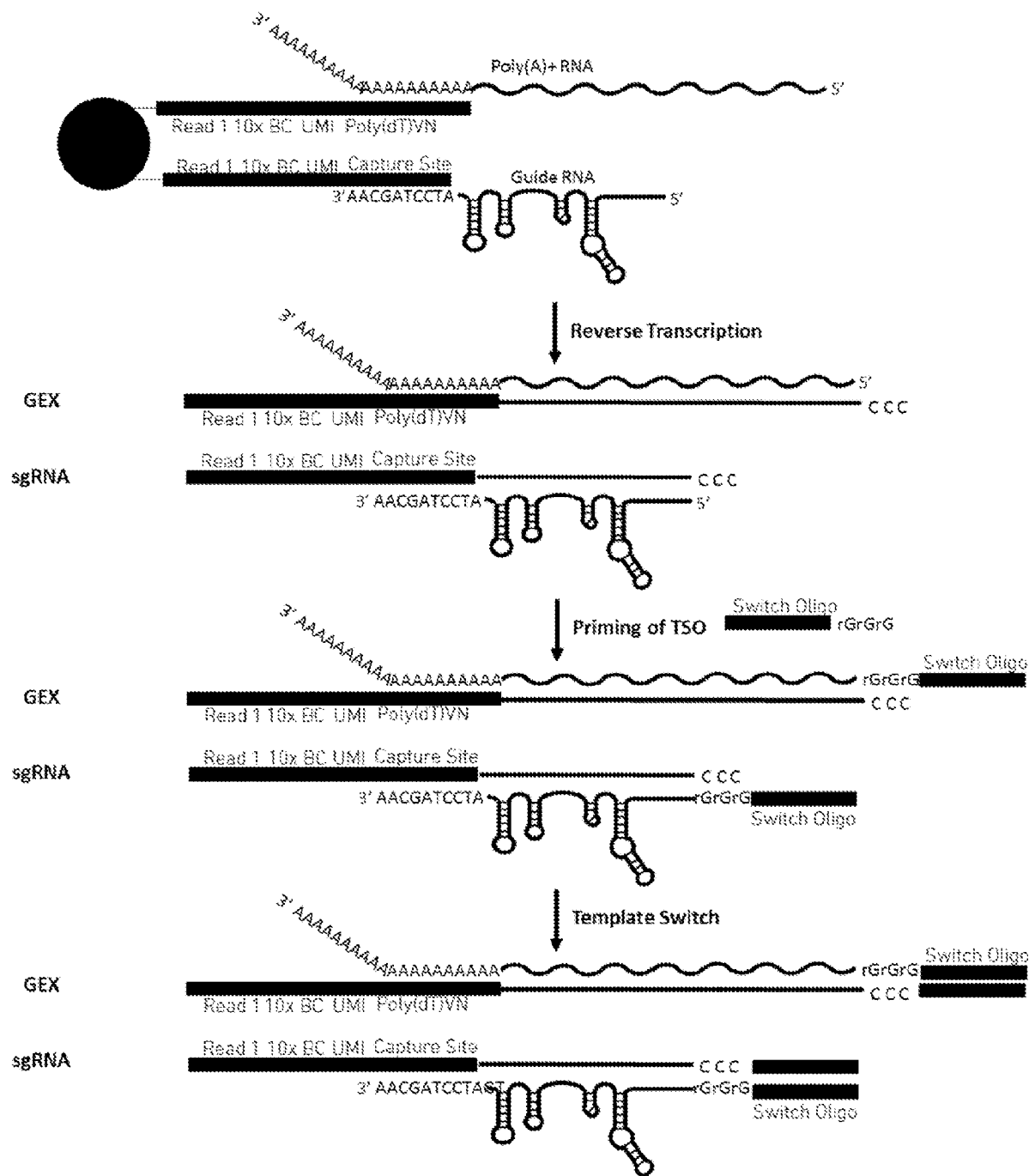


FIG. 61D