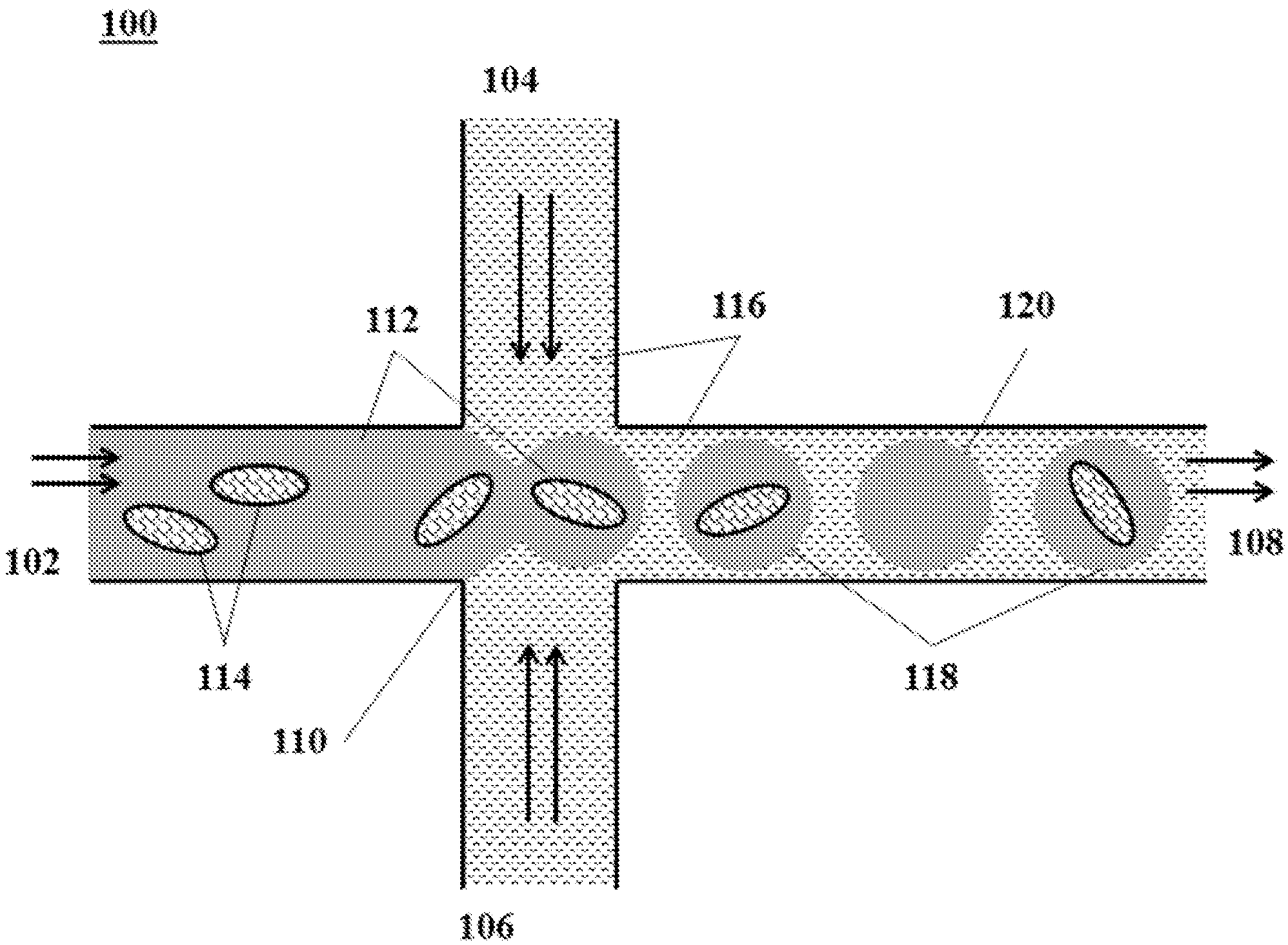


FIG. 1

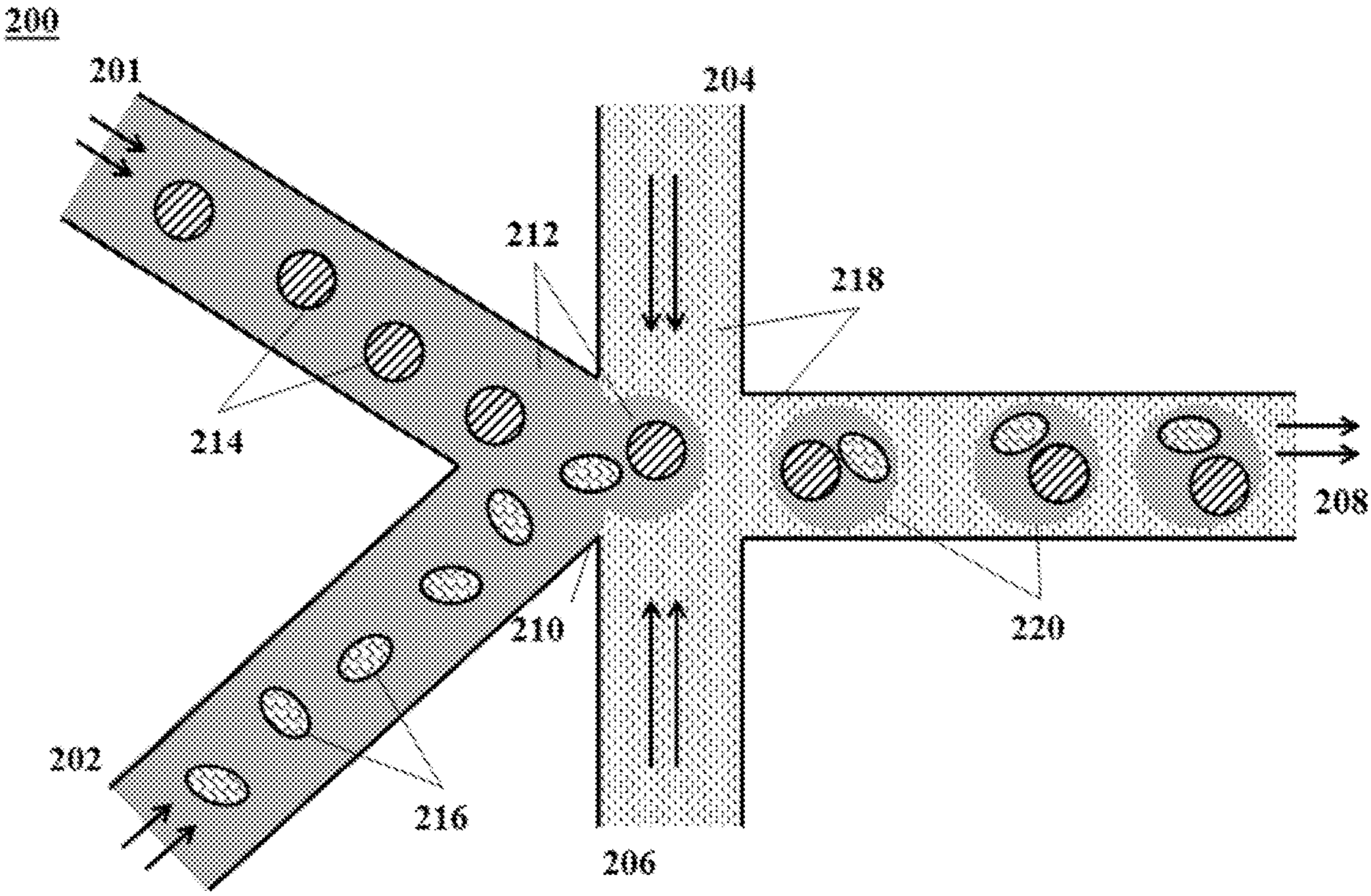


FIG. 2

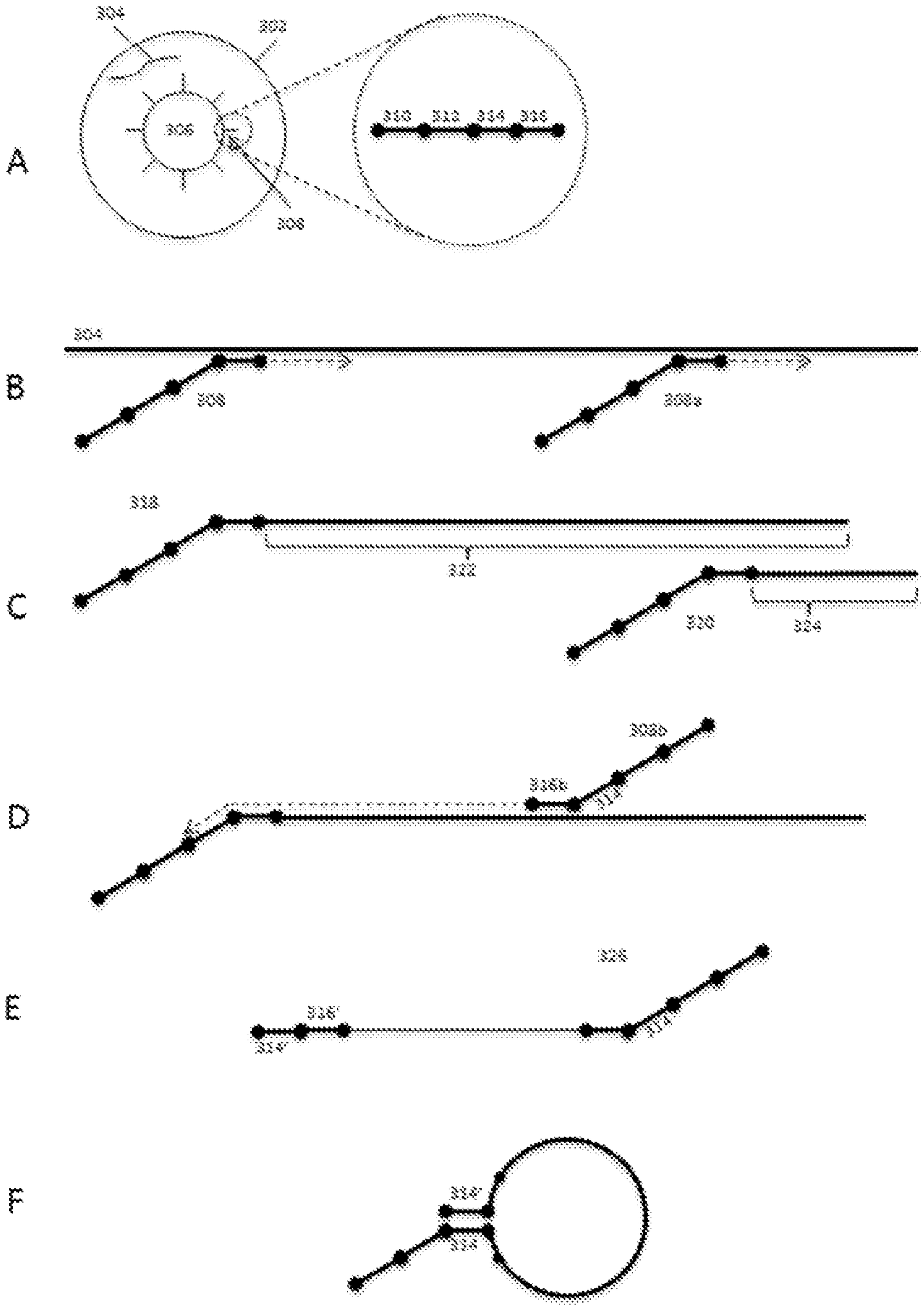

A
304
302
306
308
310
312
314
316
B
304
320
320a
C
318
322
320
324
D
320b
316b
E
326
316'
314'
F
314'
312'

FIG. 3

FIG. 4

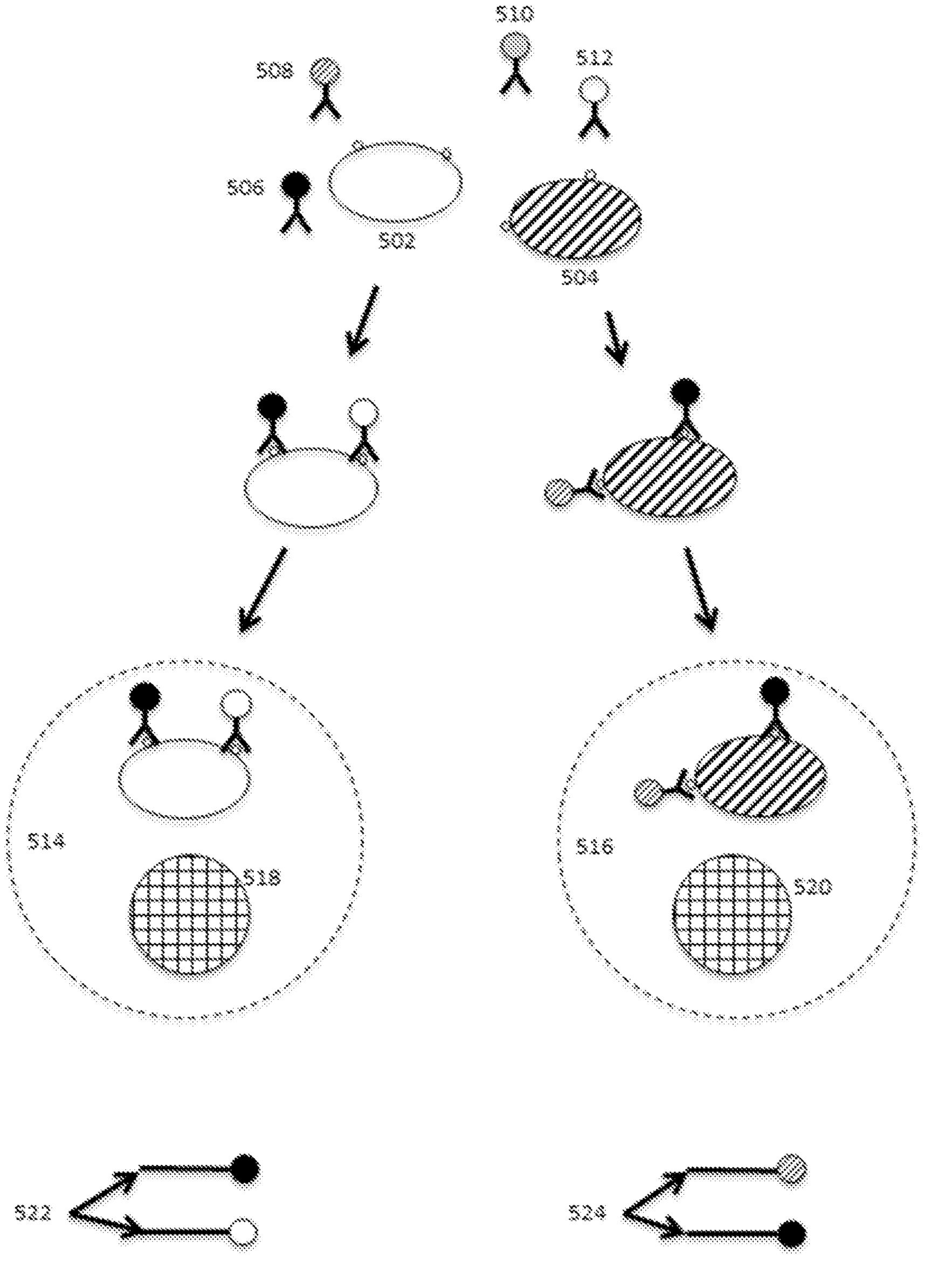


FIG. 5

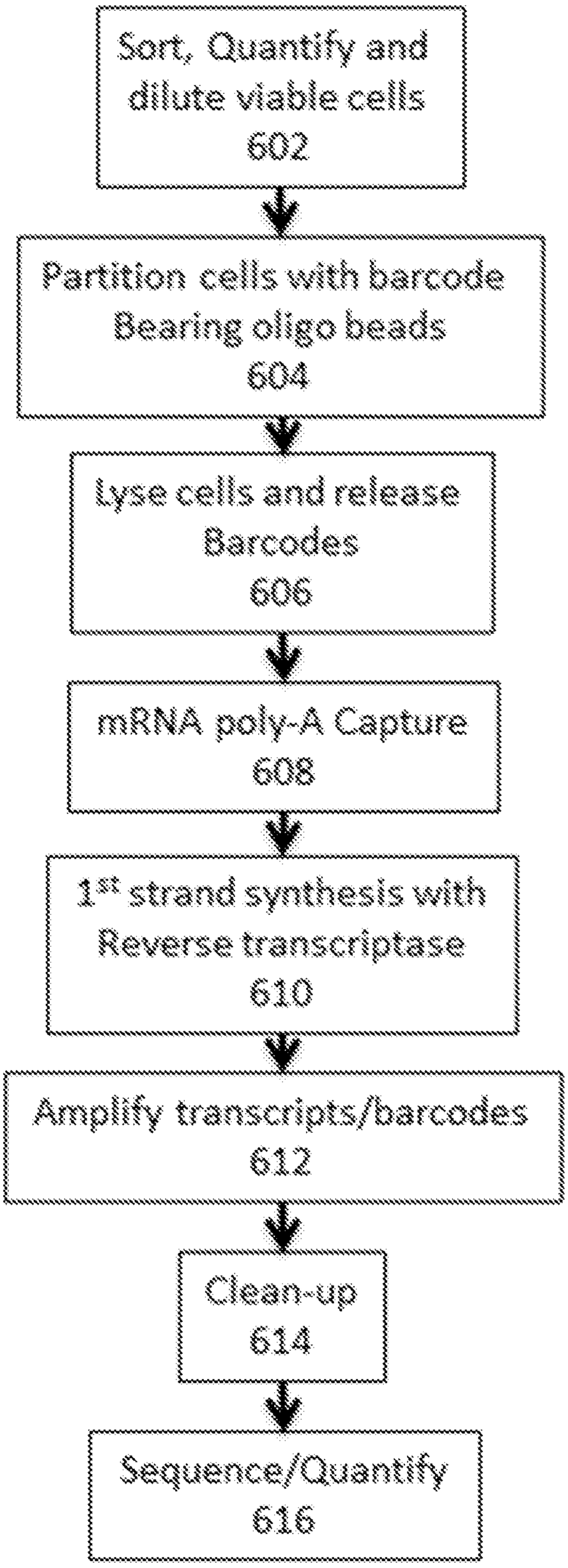

Sort, Quantify and dilute viable cells 602
Partition cells with barcode Bearing oligo beads 604
Lyse cells and release Barcodes 606
mRNA poly-A Capture 608
1st strand synthesis with Reverse transcriptase 610
Amplify transcripts/barcodes 612
Clean-up 614
Sequence/Quantify 616

FIG. 6

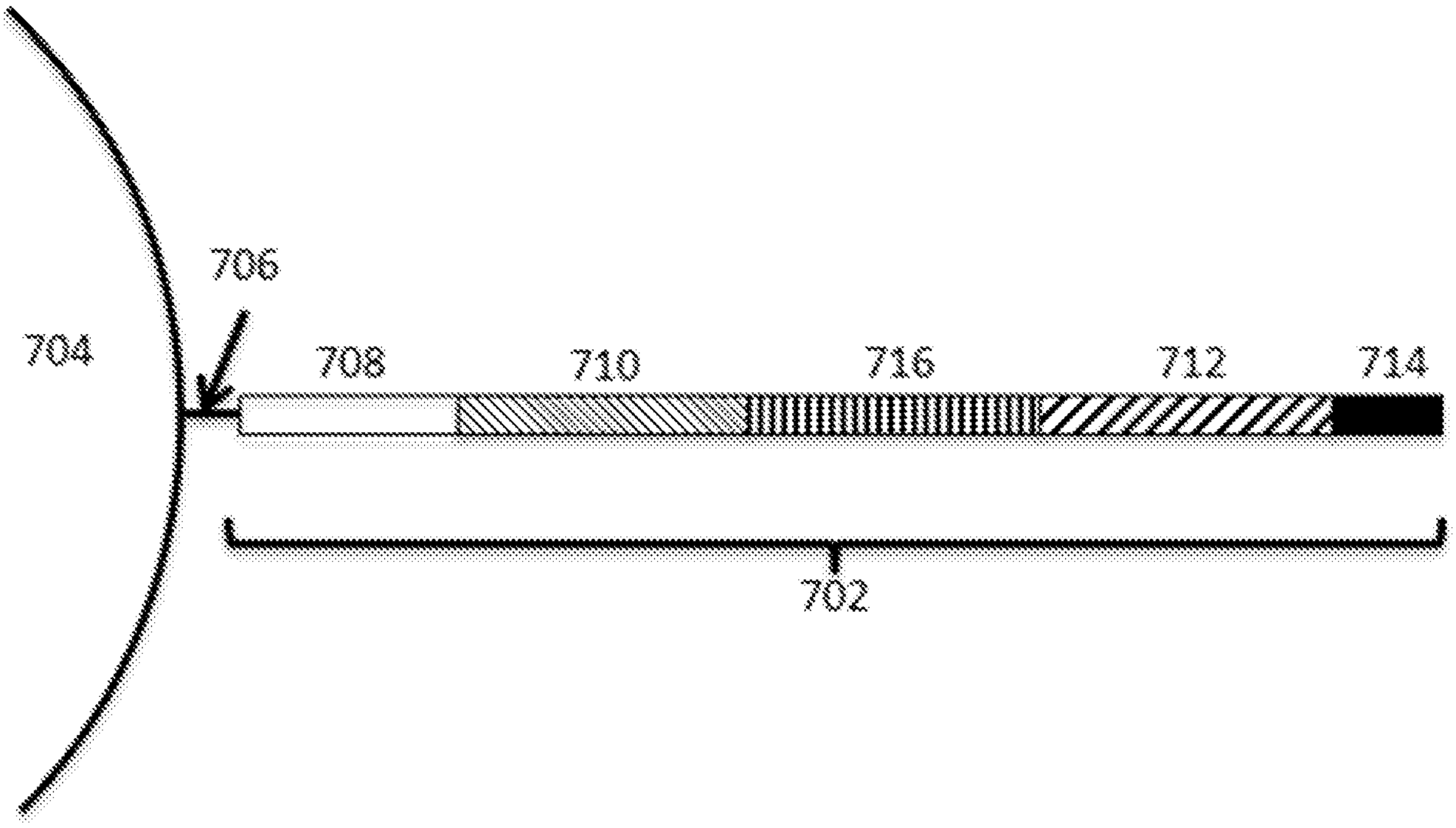
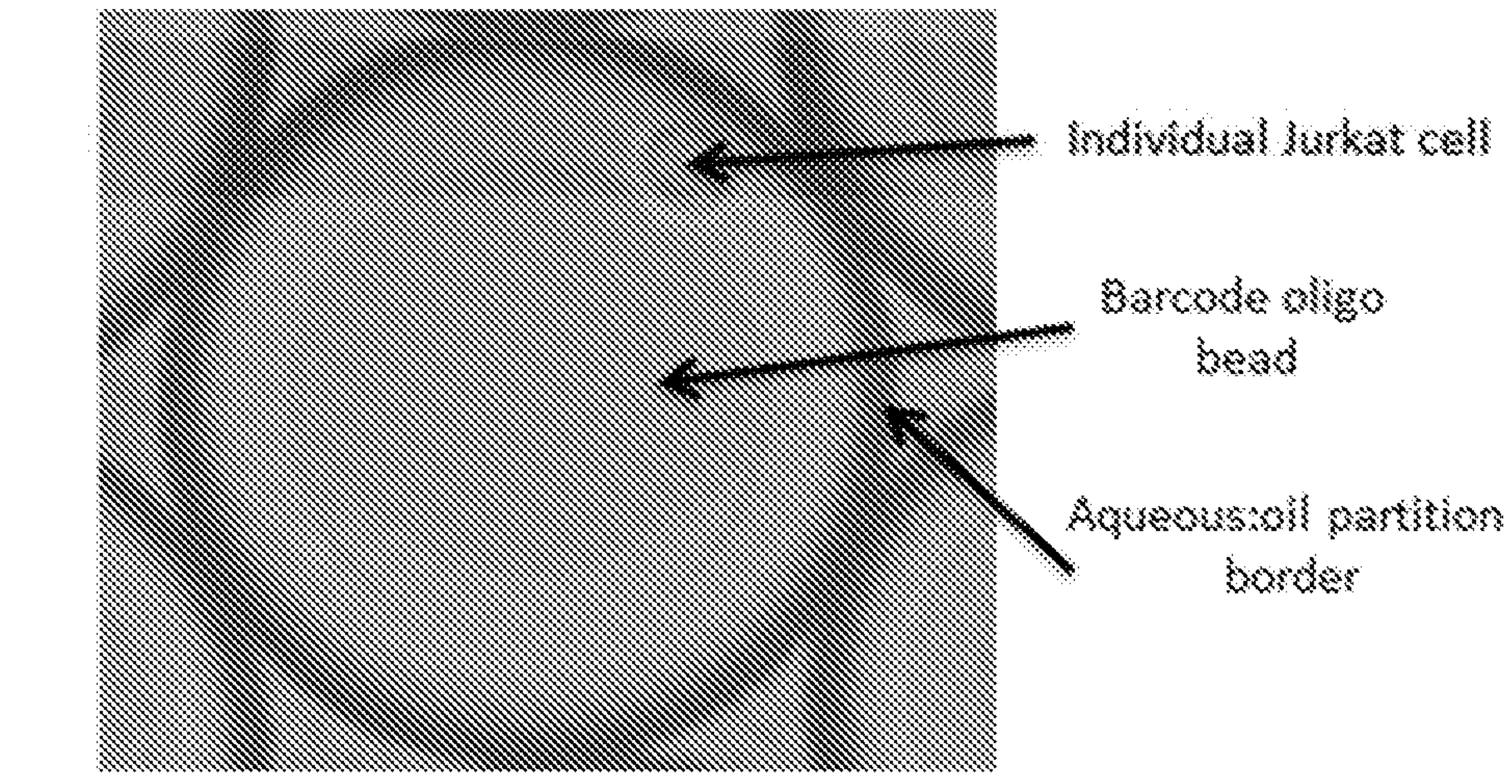


FIG. 7


Individual Jurkat cell
Barcode oligo bead
Aqueous:oil partition border

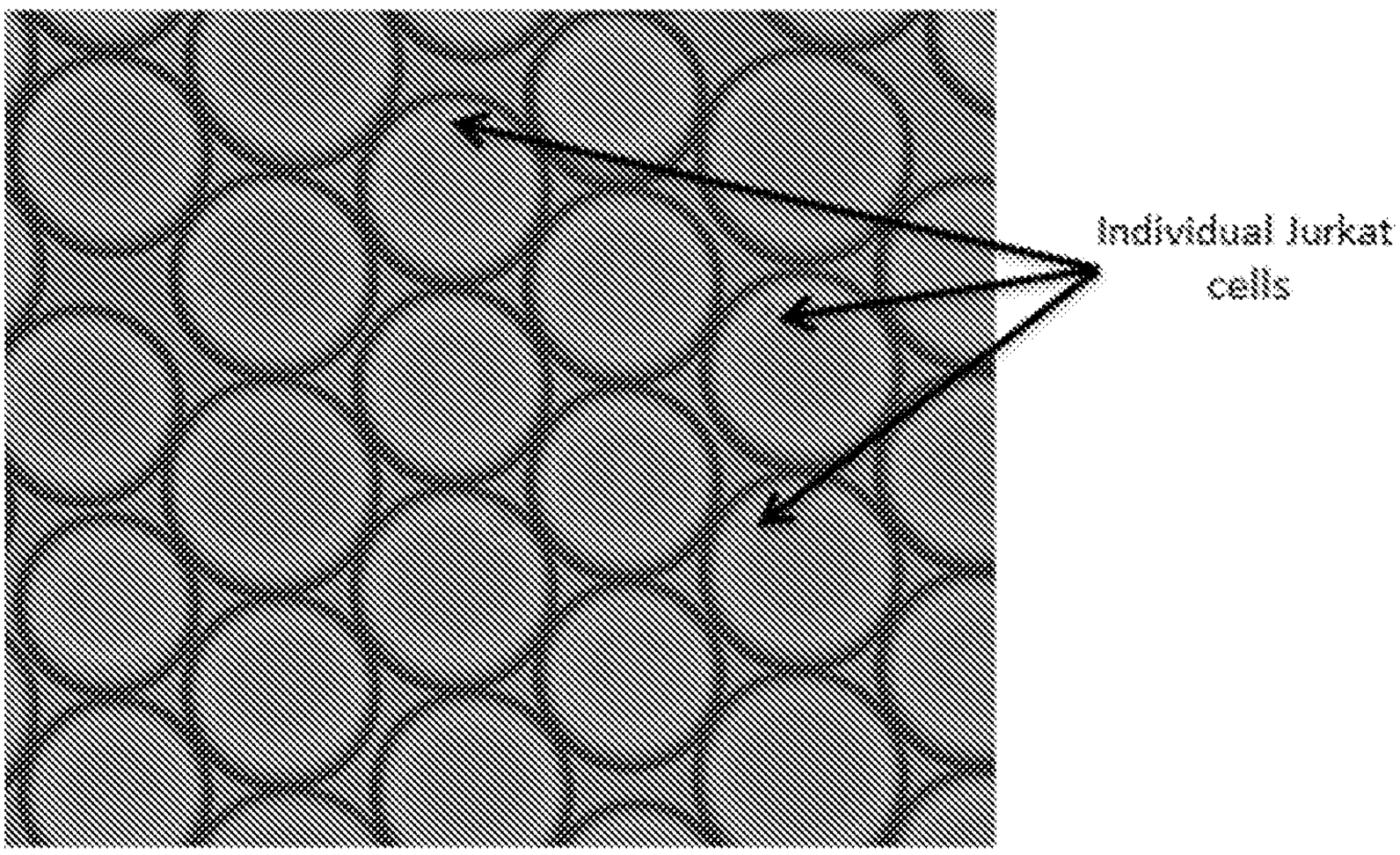

Individual Jurkat cells

FIG. 8

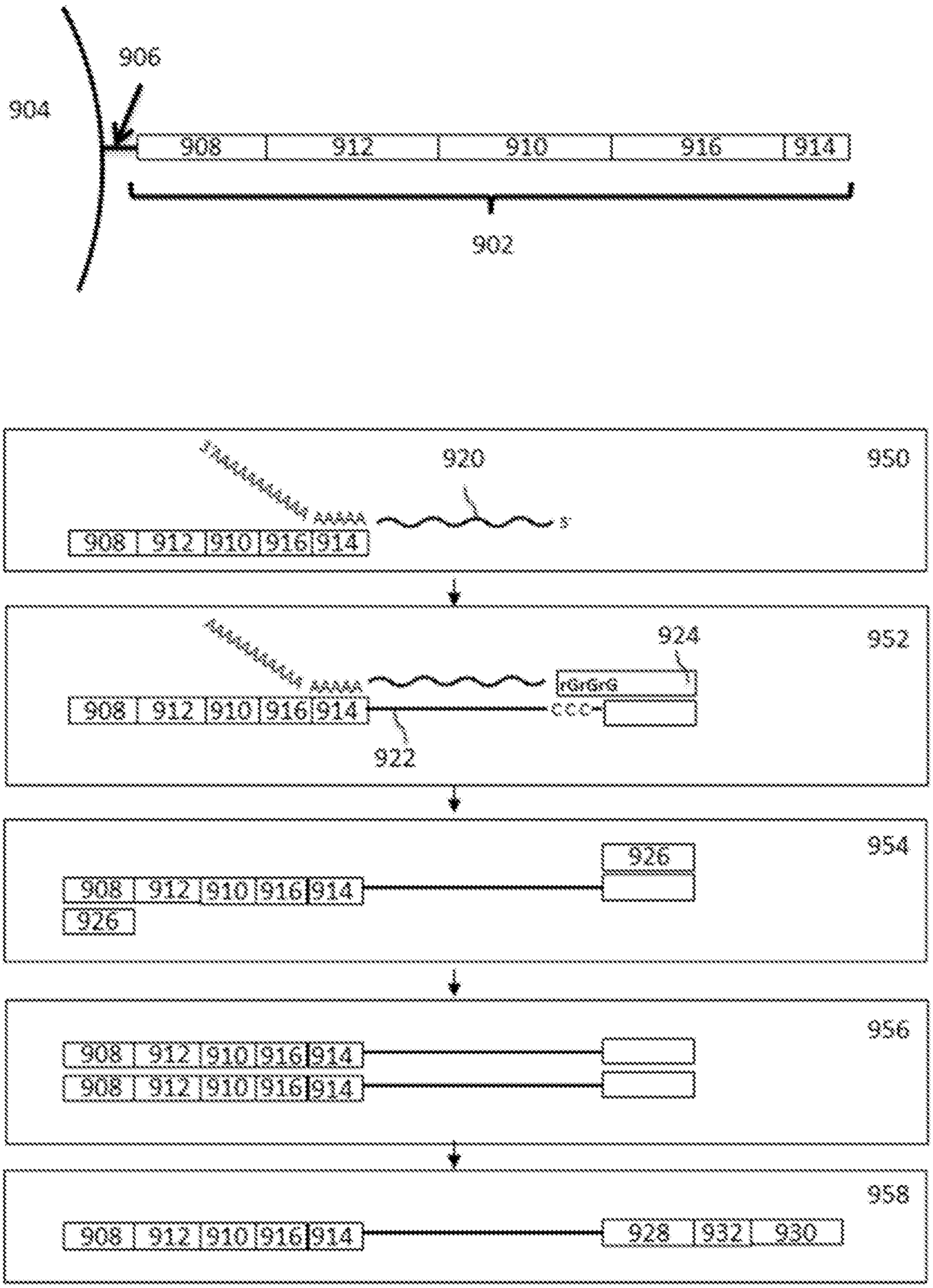

906
904
908
912
910
916
914
902
920
950
AAAAA
908 912 910 916 914
924
952
rGrGrG
CCC
922
954
926
926
956
908 912 910 916 914
908 912 910 916 914
958
908 912 910 916 914
928
932
930

FIG. 9A

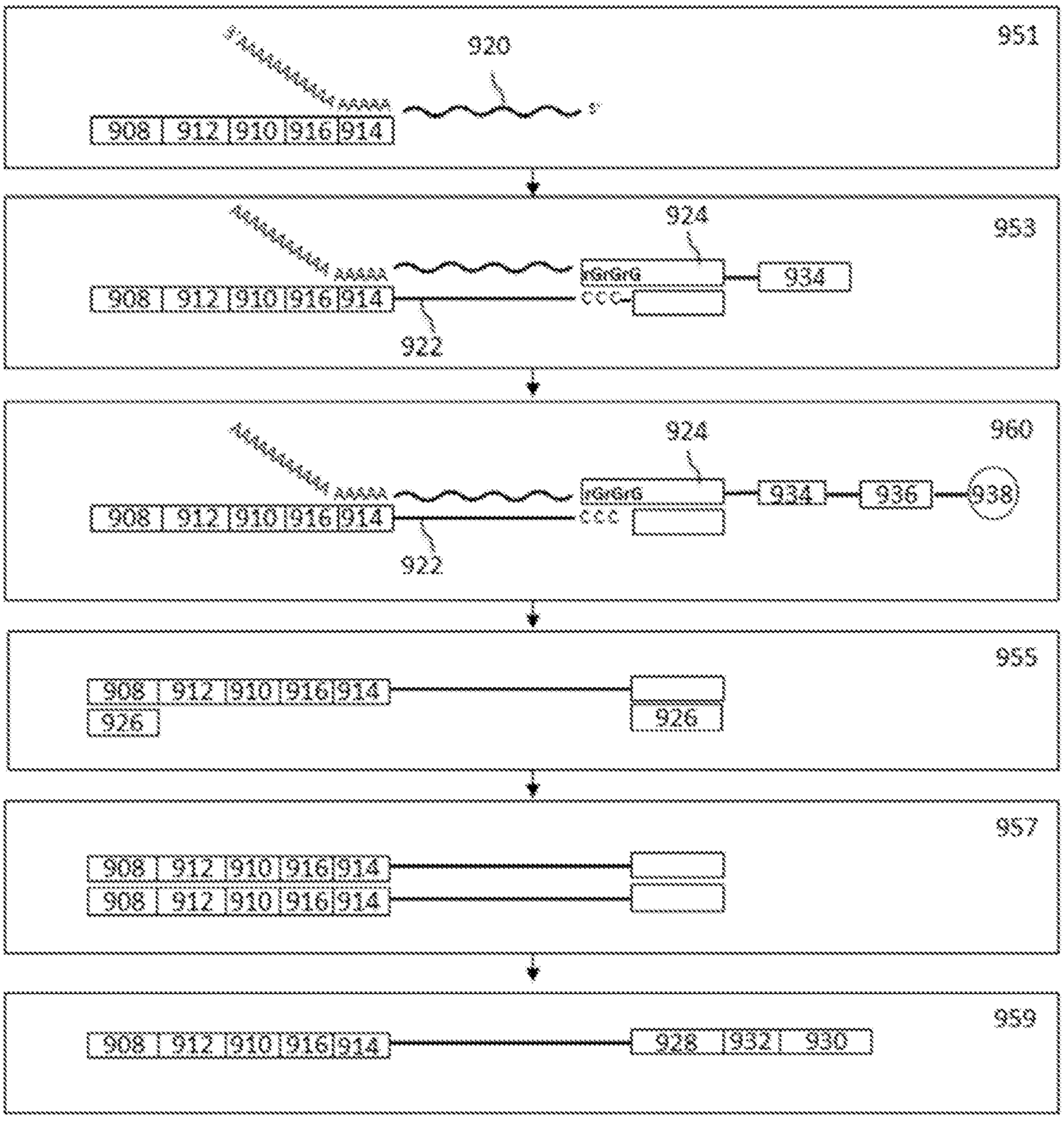

951
920
908
912
910
916
914
953
924
934
922
960
936
938
955
926
957
959
928
932
930

FIG. 9B

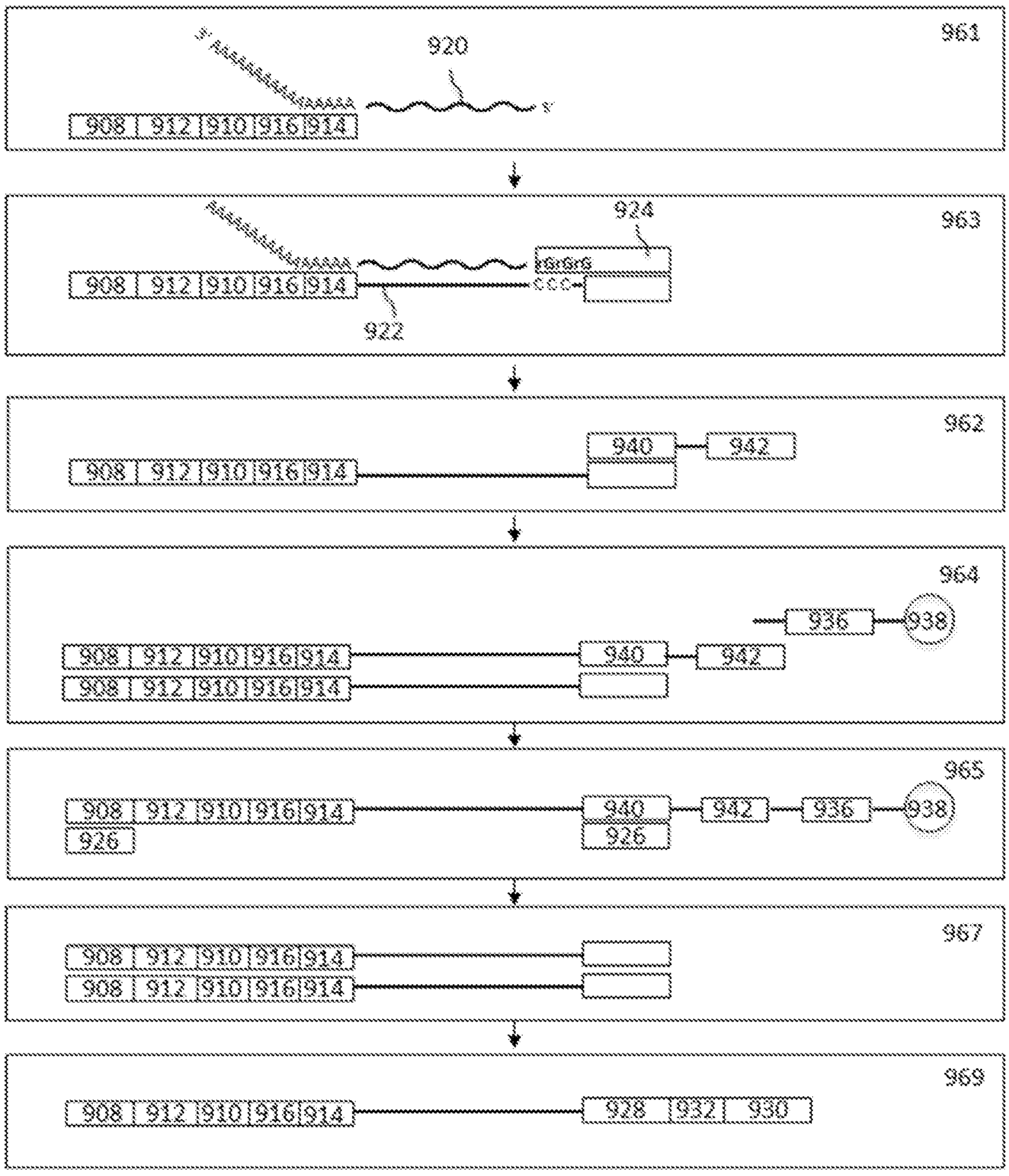

961
920
908 912 910 916 914
963
924
908 912 910 916 914
922
962
940
942
908 912 910 916 914
964
936
938
940
942
908 912 910 916 914
908 912 910 916 914
965
908 912 910 916 914
926
940
926
942
936
938
967
908 912 910 916 914
908 912 910 916 914
969
908 912 910 916 914
928 932 930

FIG. 9C

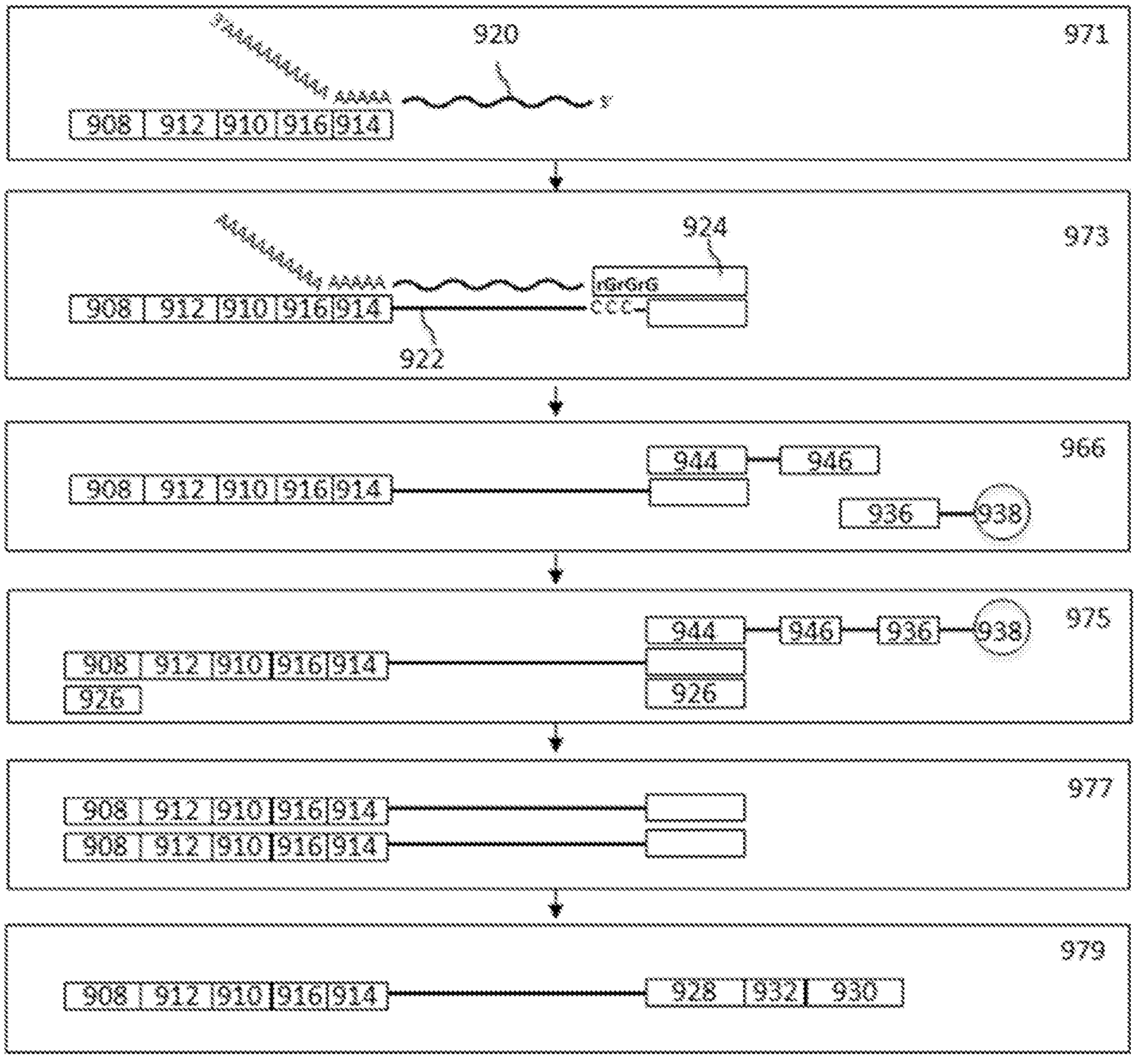

971
920
908
912
910
916
914
973
924
922
966
944
946
936
938
975
926
977
979
928
932
930

FIG. 9D

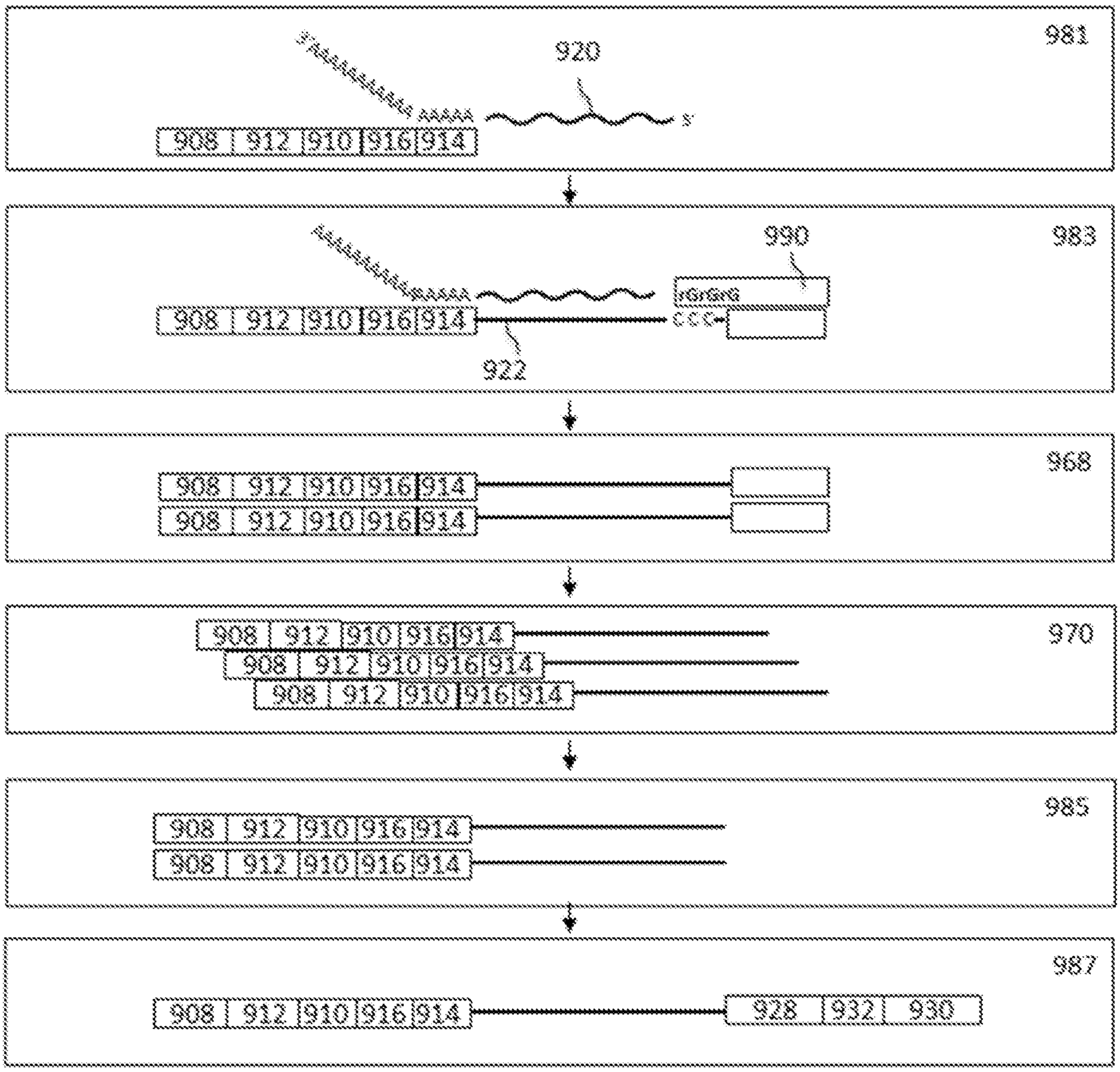

981
920
908
912
910
916
914
983
990
922
968
970
985
987
928
932
930

FIG. 9E

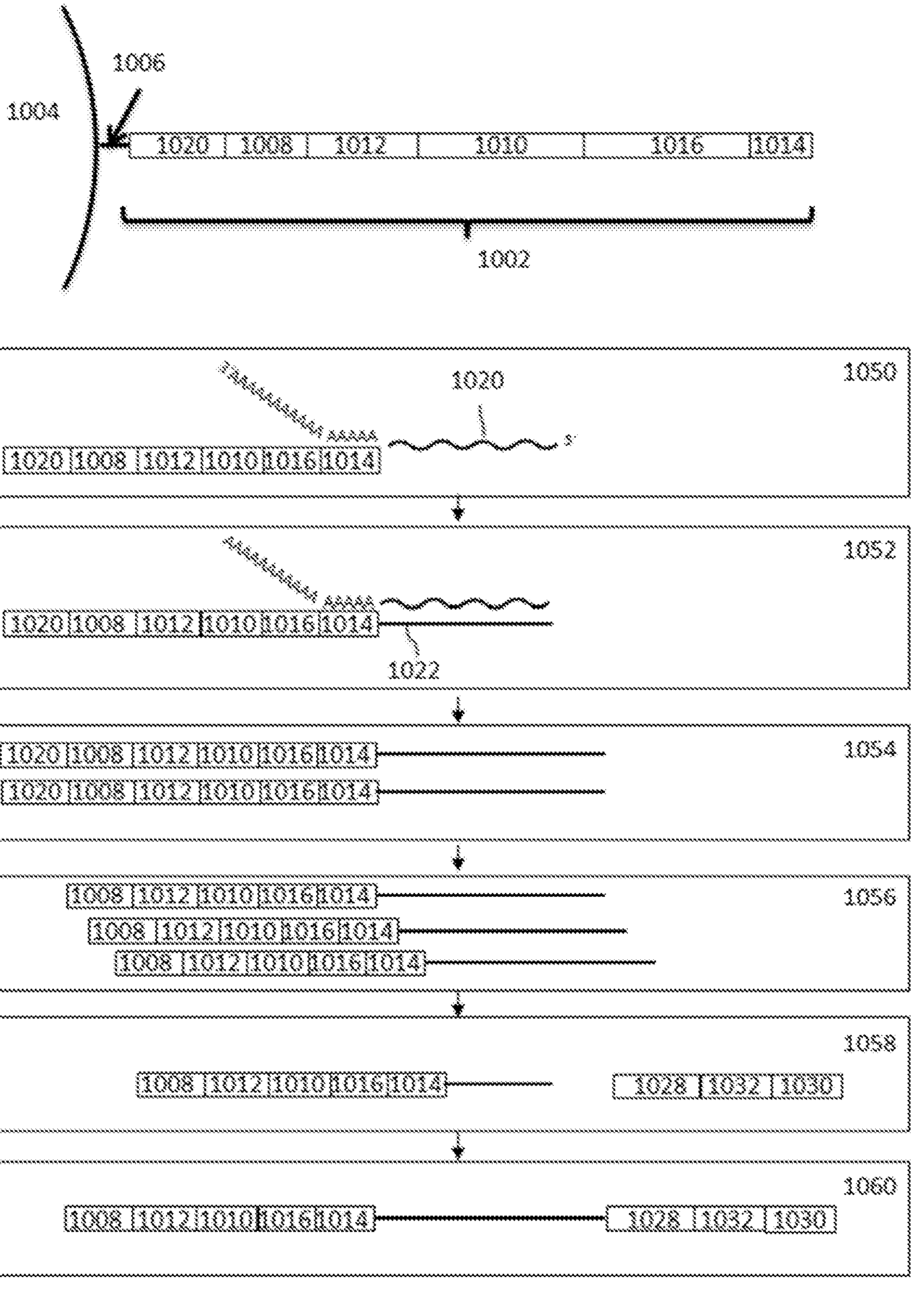

1006
1004
1020
1008
1012
1010
1016
1014
1002
1050
1020
1020 1008 1012 1010 1016 1014
1052
1020 1008 1012 1010 1016 1014
1022
1054
1020 1008 1012 1010 1016 1014
1020 1008 1012 1010 1016 1014
1056
1008 1012 1010 1016 1014
1008 1012 1010 1016 1014
1008 1012 1010 1016 1014
1058
1008 1012 1010 1016 1014
1028 1032 1030
1060
1008 1012 1010 1016 1014
1028 1032 1030

FIG. 10

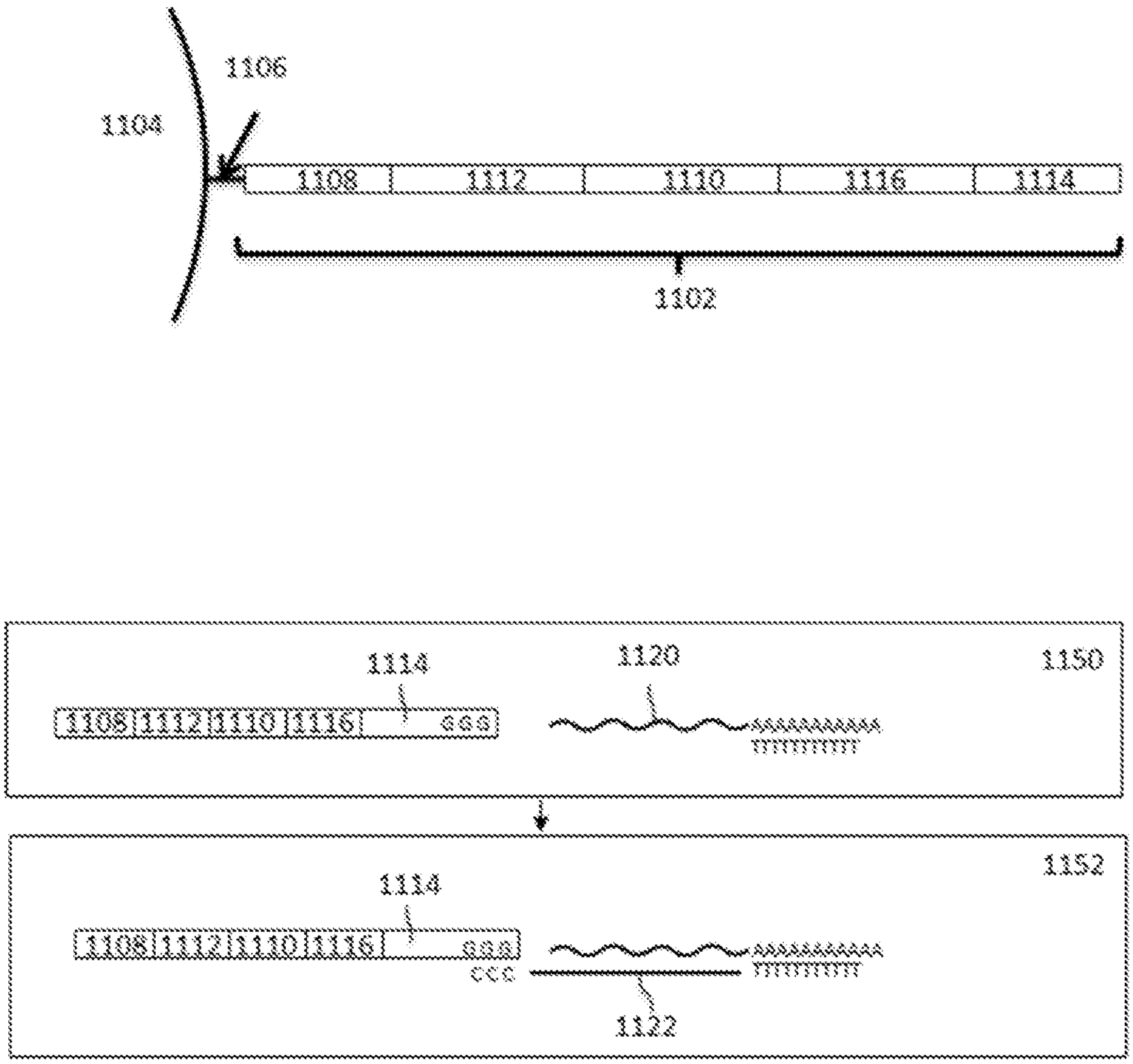

1106
1104
1108
1112
1110
1116
1114
1102
1114
1120
1150
1108 1112 1110 1116
1152
1114
1108 1112 1110 1116
1122

FIG. 11

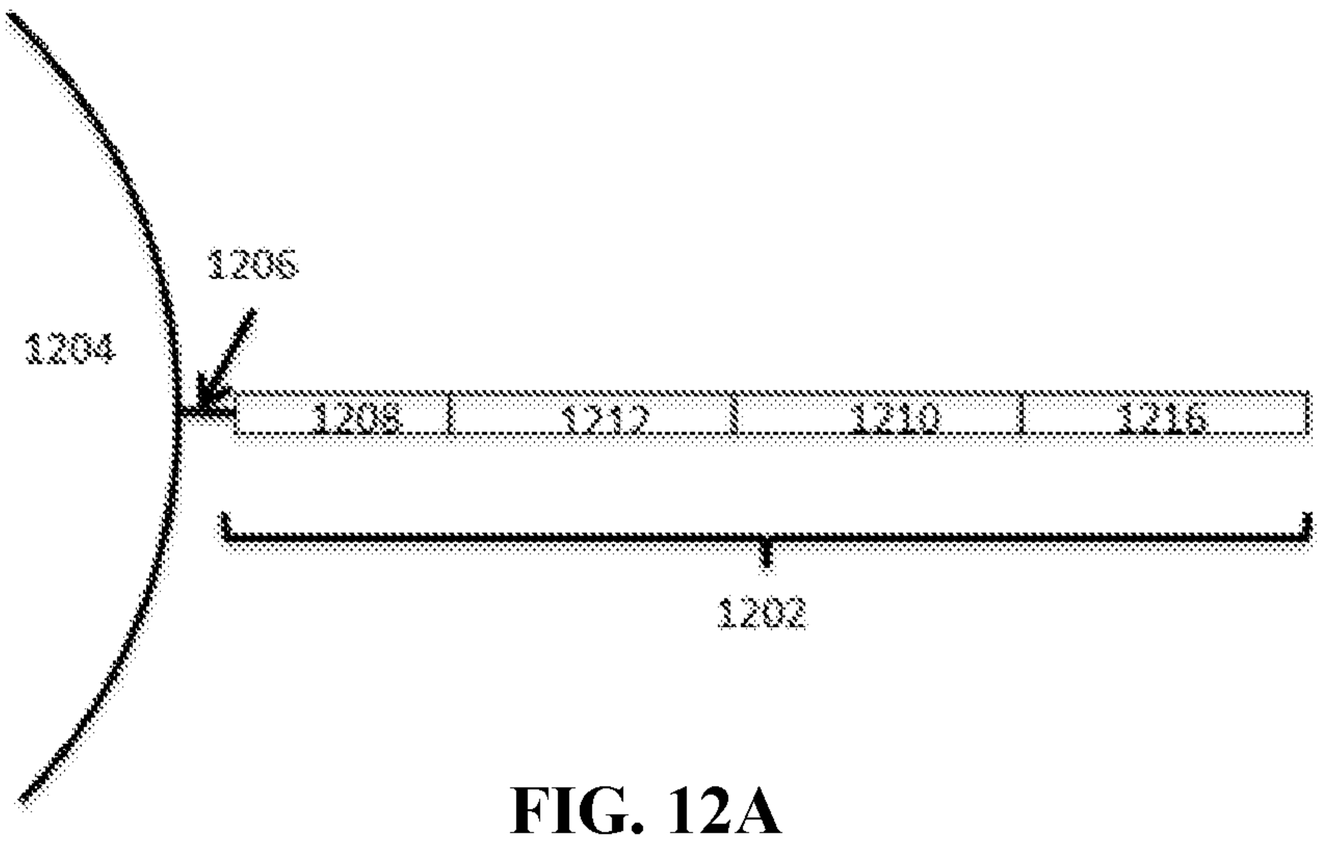


FIG. 12A

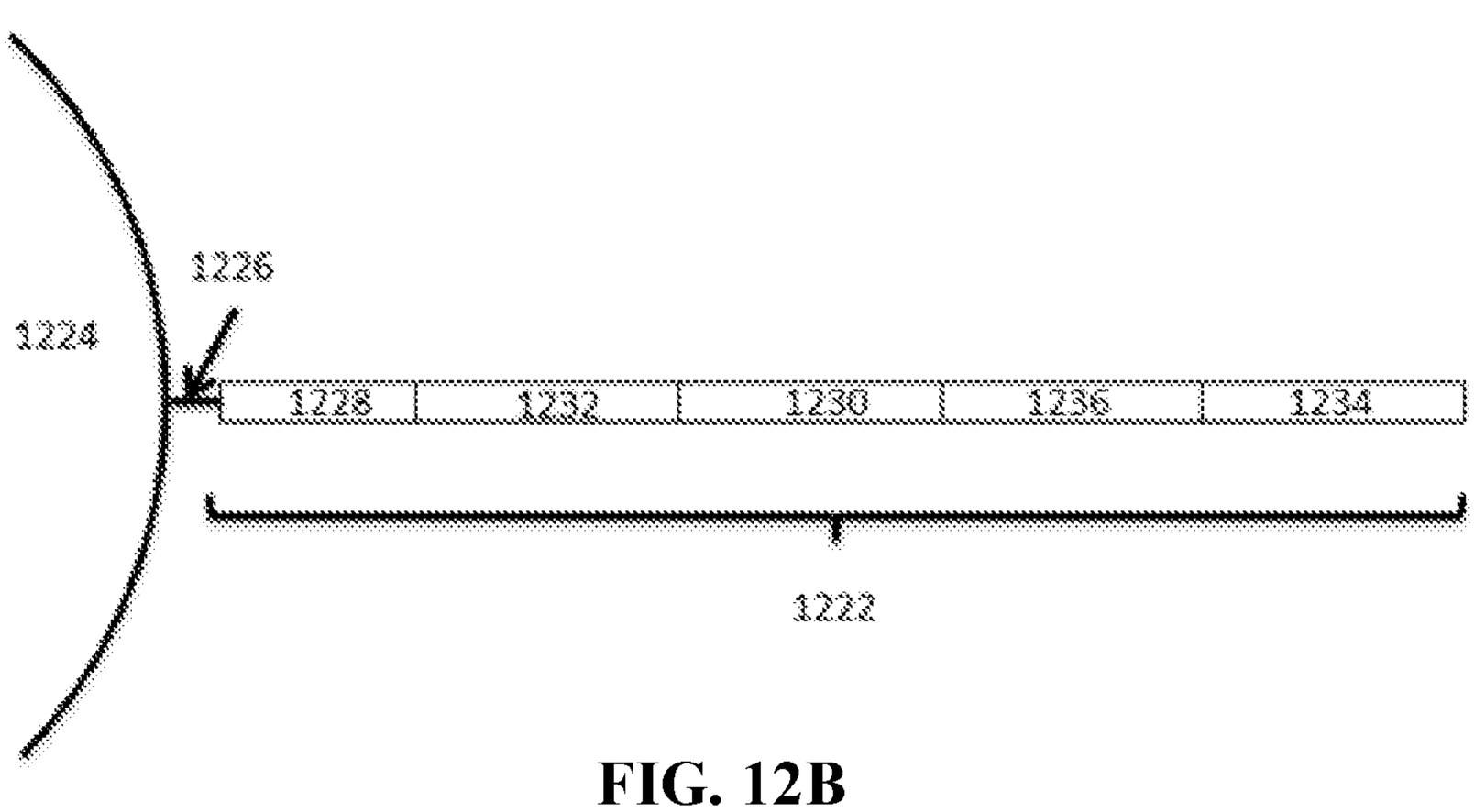


FIG. 12B

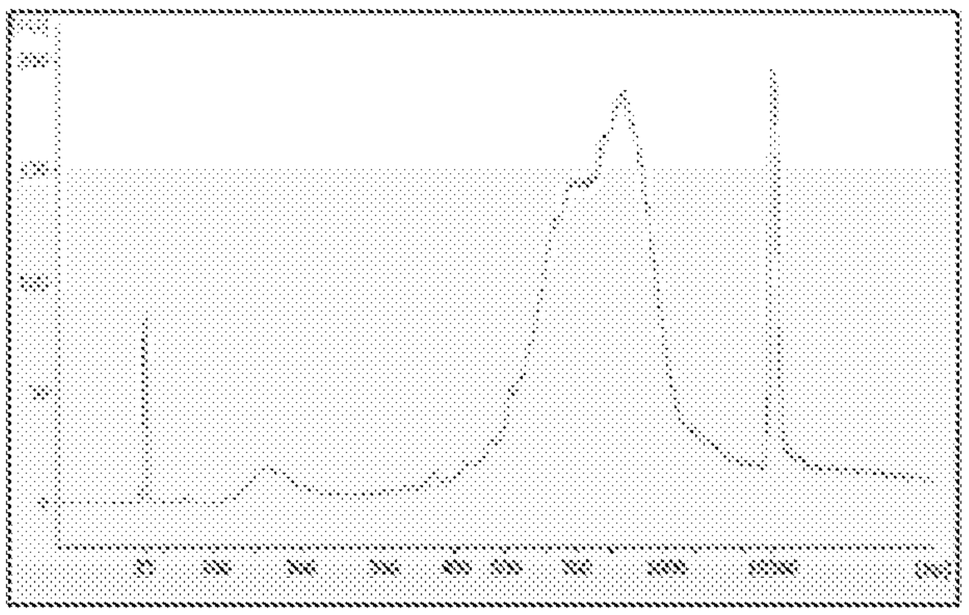


FIG. 13A

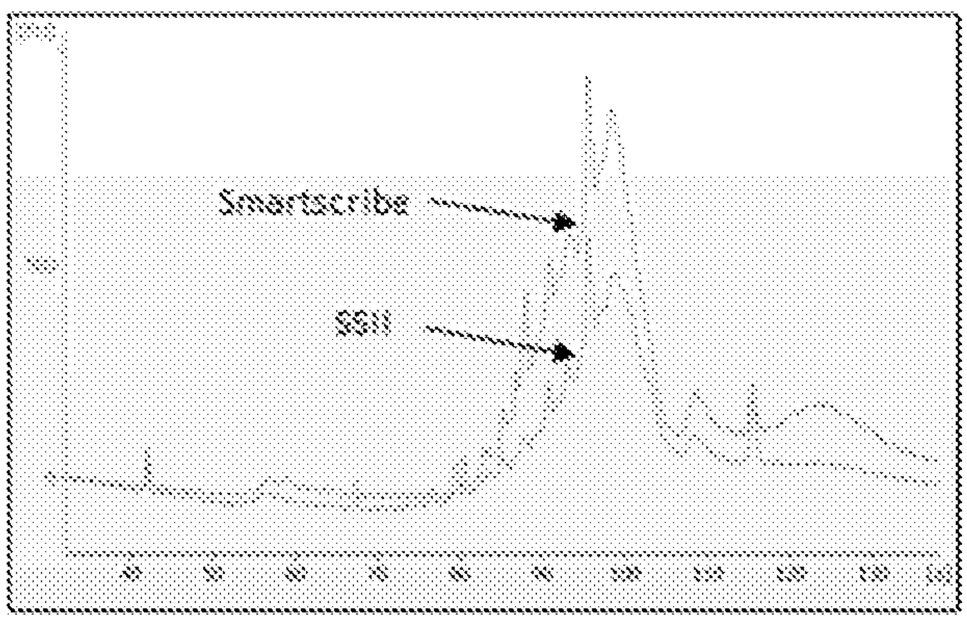


FIG. 13B

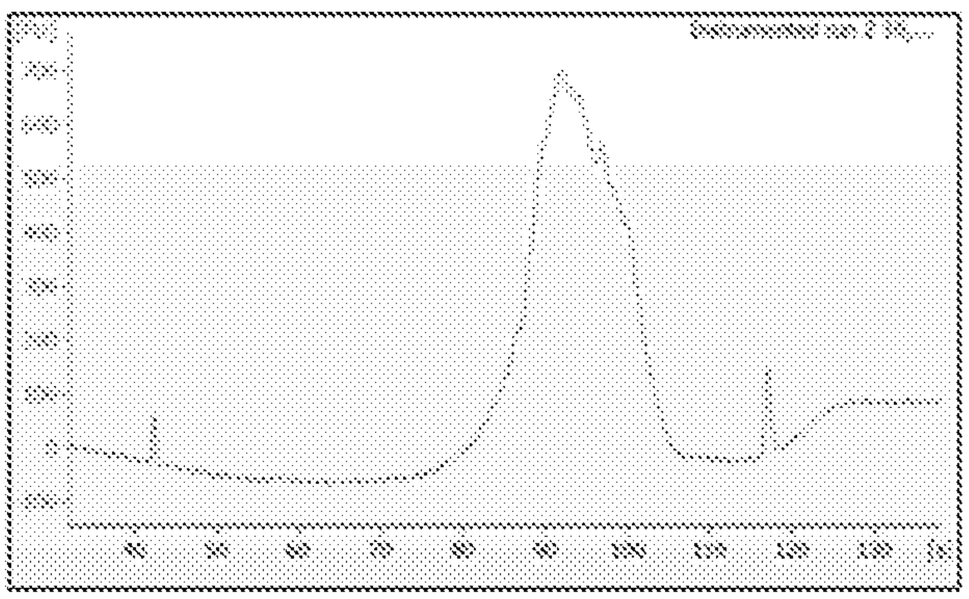


FIG. 13C

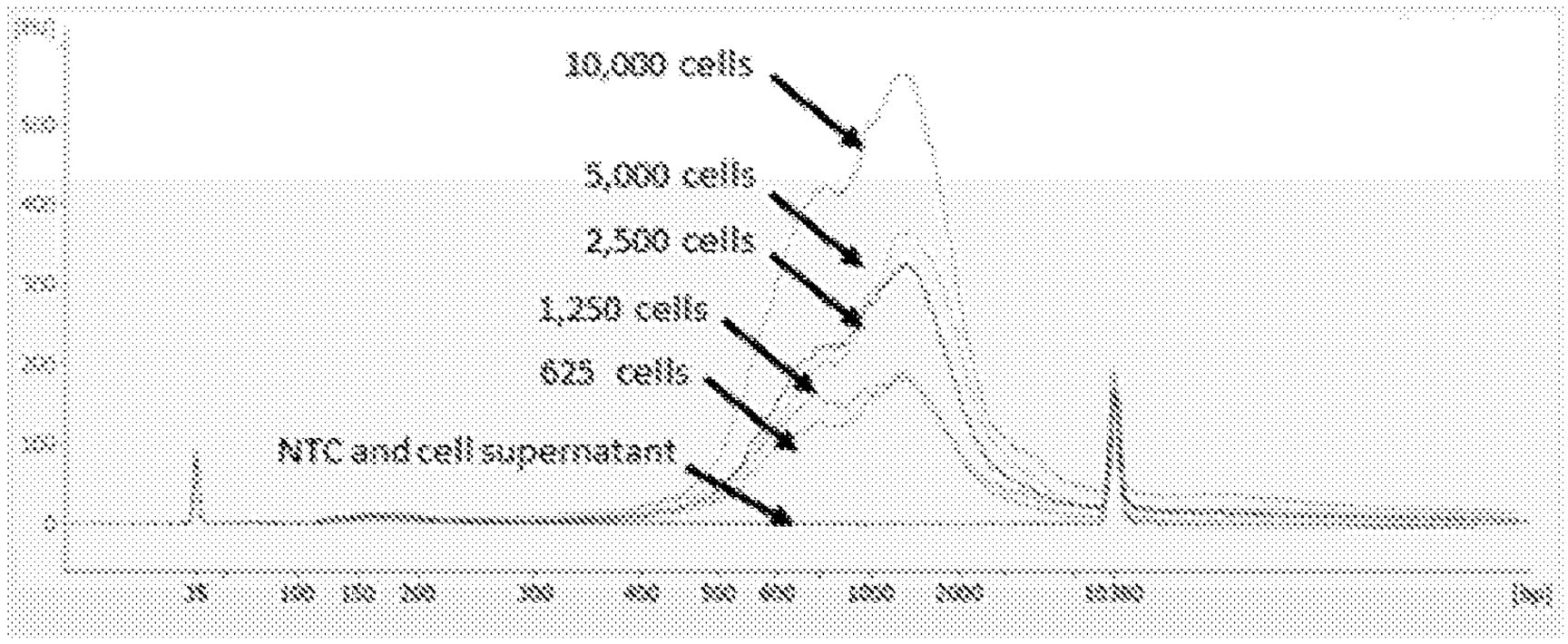


FIG. 14A

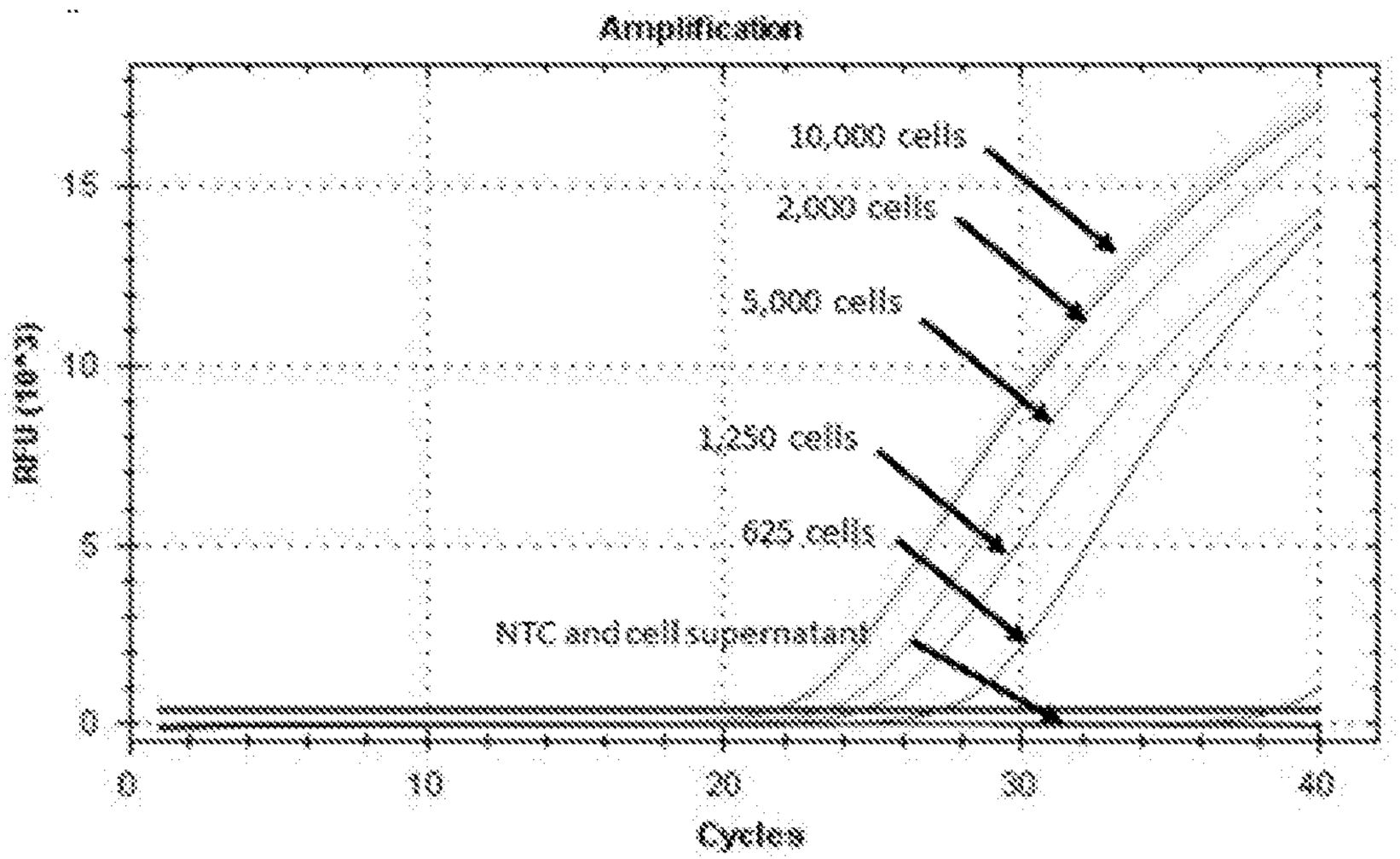


FIG. 14B

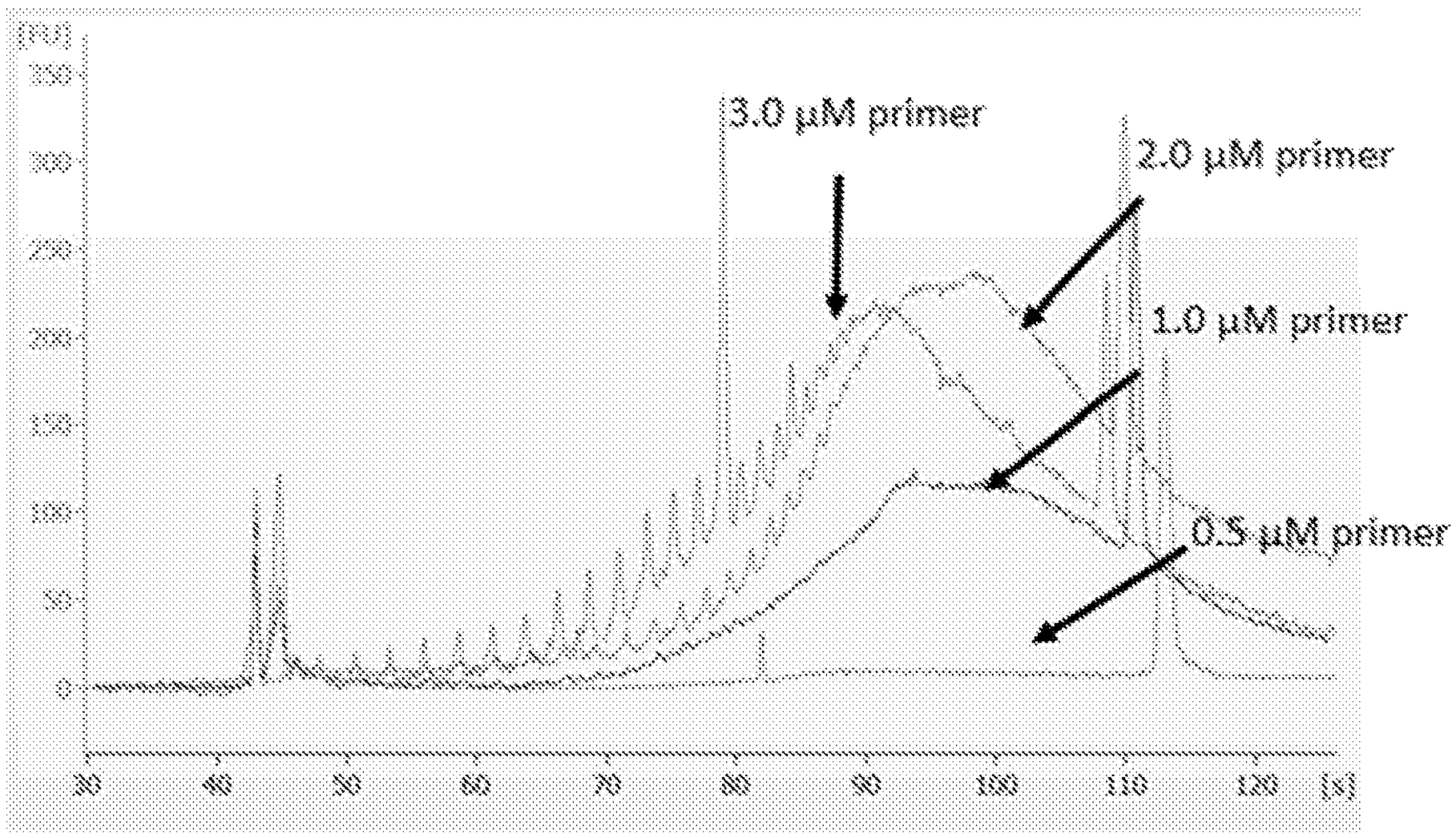

[RU]
350
300
250
200
150
100
50
0
3.0 µM primer
2.0 µM primer
1.0 µM primer
0.5 µM primer
30
40
50
60
70
80
90
100
110
120
[s]

FIG. 15

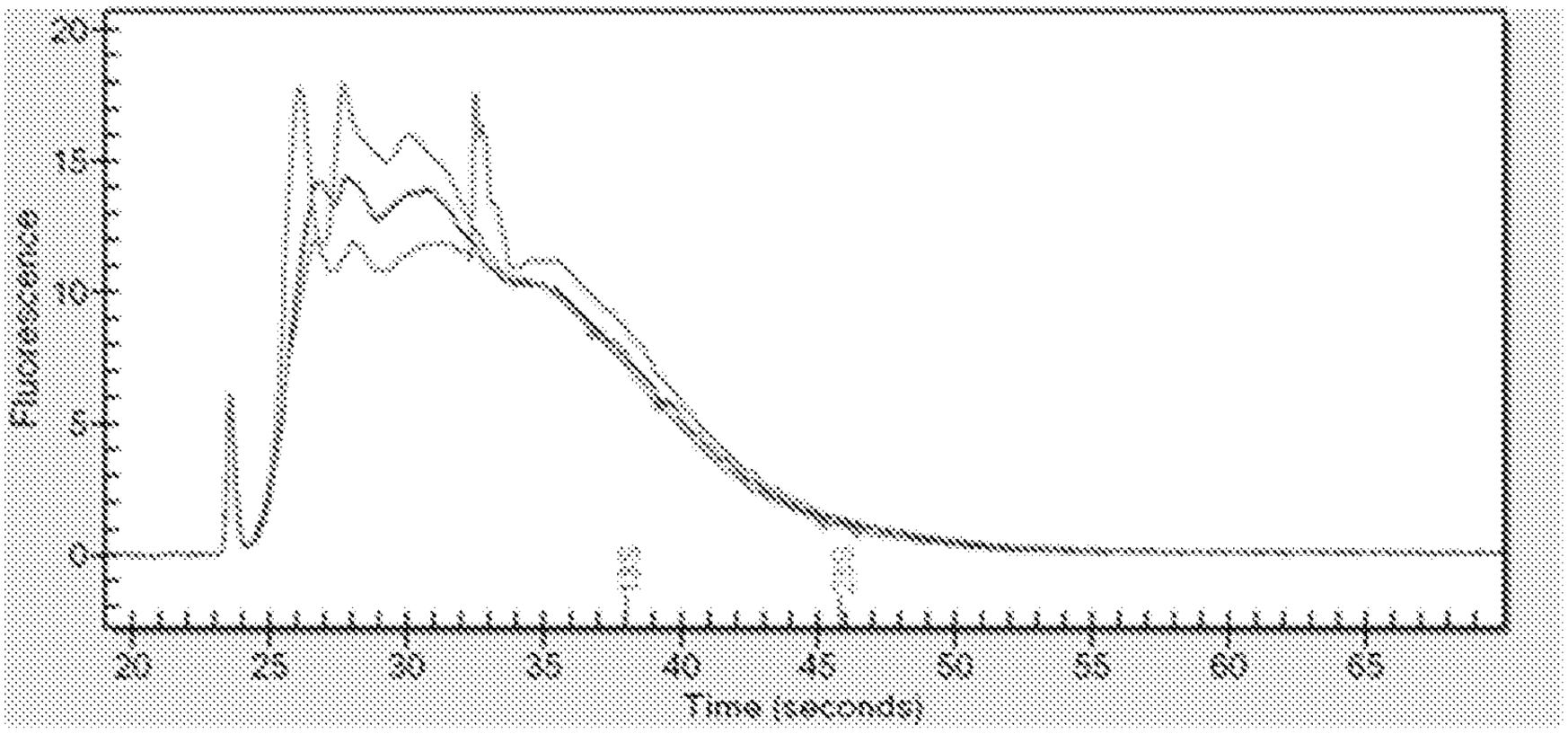

20
15
10
5
0
Fluorescence
20
25
30
35
40
45
50
55
60
65
Time (seconds)

FIG. 16

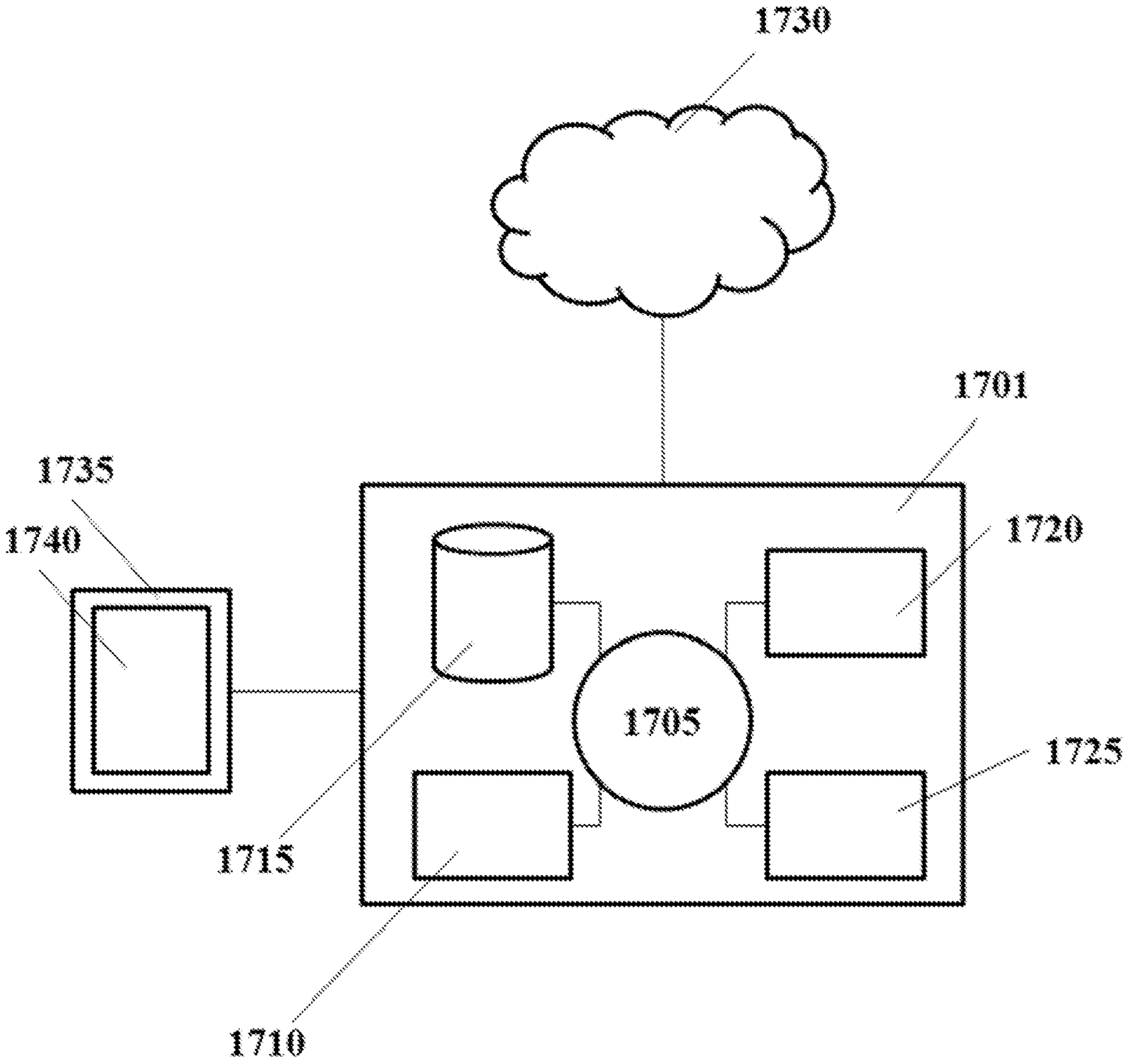


FIG. 17

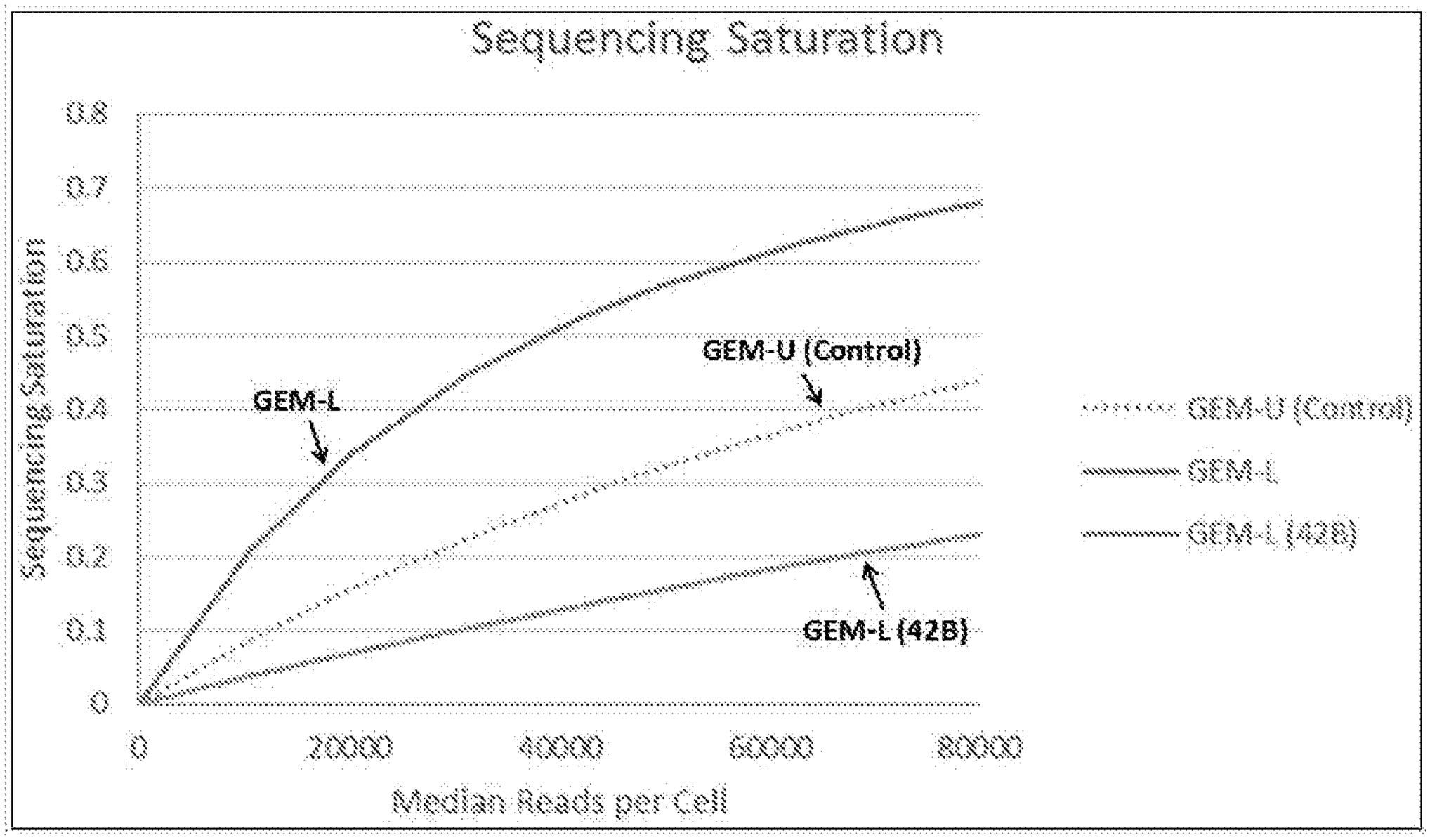

Sequencing Saturation
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Sequencing Saturation
GEM-U (Control)
GEM-L
GEM-L (42B)
0
20000
40000
60000
80000
Median Reads per Cell
GEM-U (Control)
GEM-L
GEM-L (42B)

FIG. 18

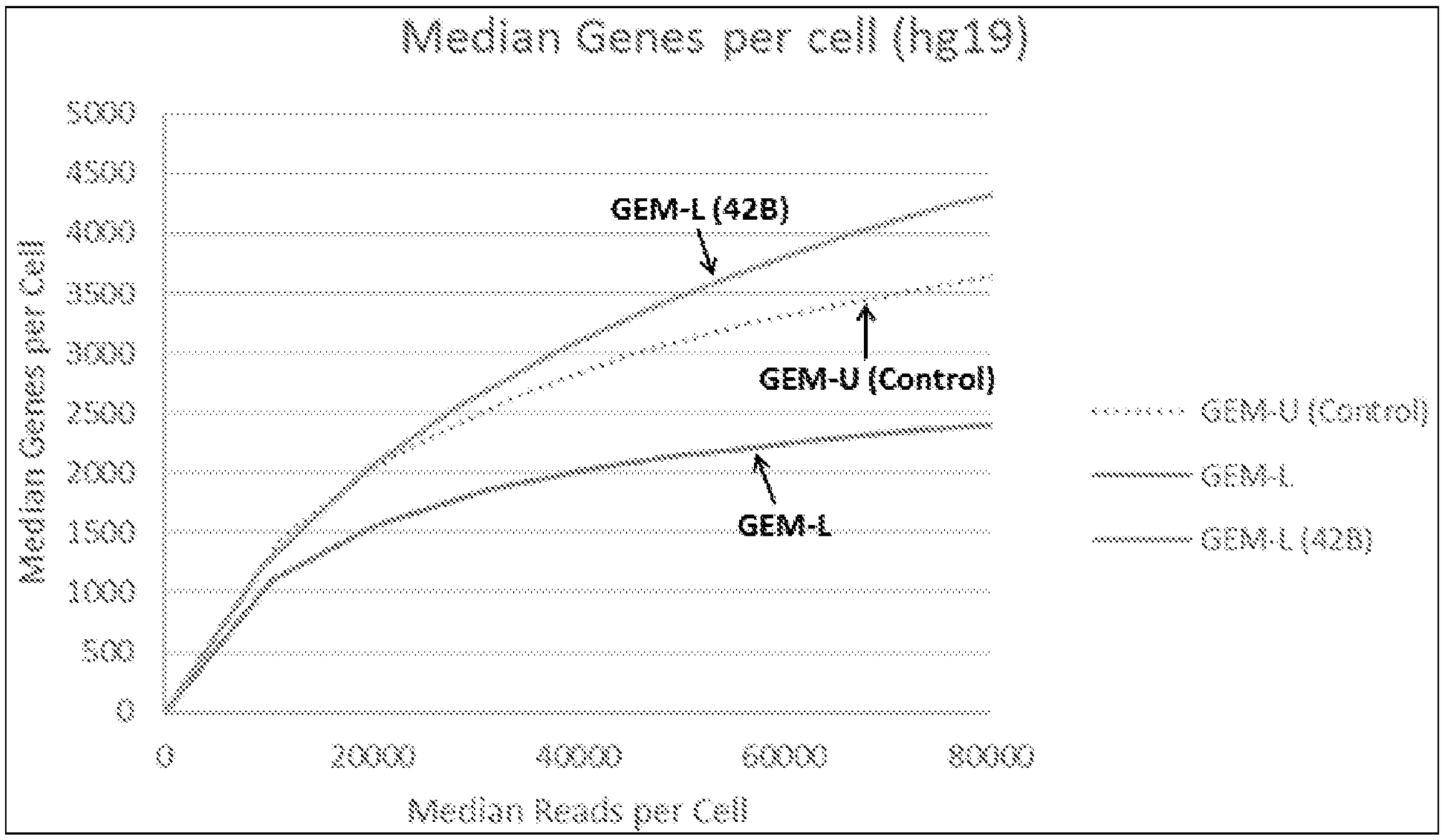

Median Genes per cell (hg19)
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
Median Genes per Cell
GEM-L (42B)
GEM-U (Control)
GEM-L
0
20000
40000
60000
80000
Median Reads per Cell
GEM-U (Control)
GEM-L
GEM-L (42B)

FIG. 19

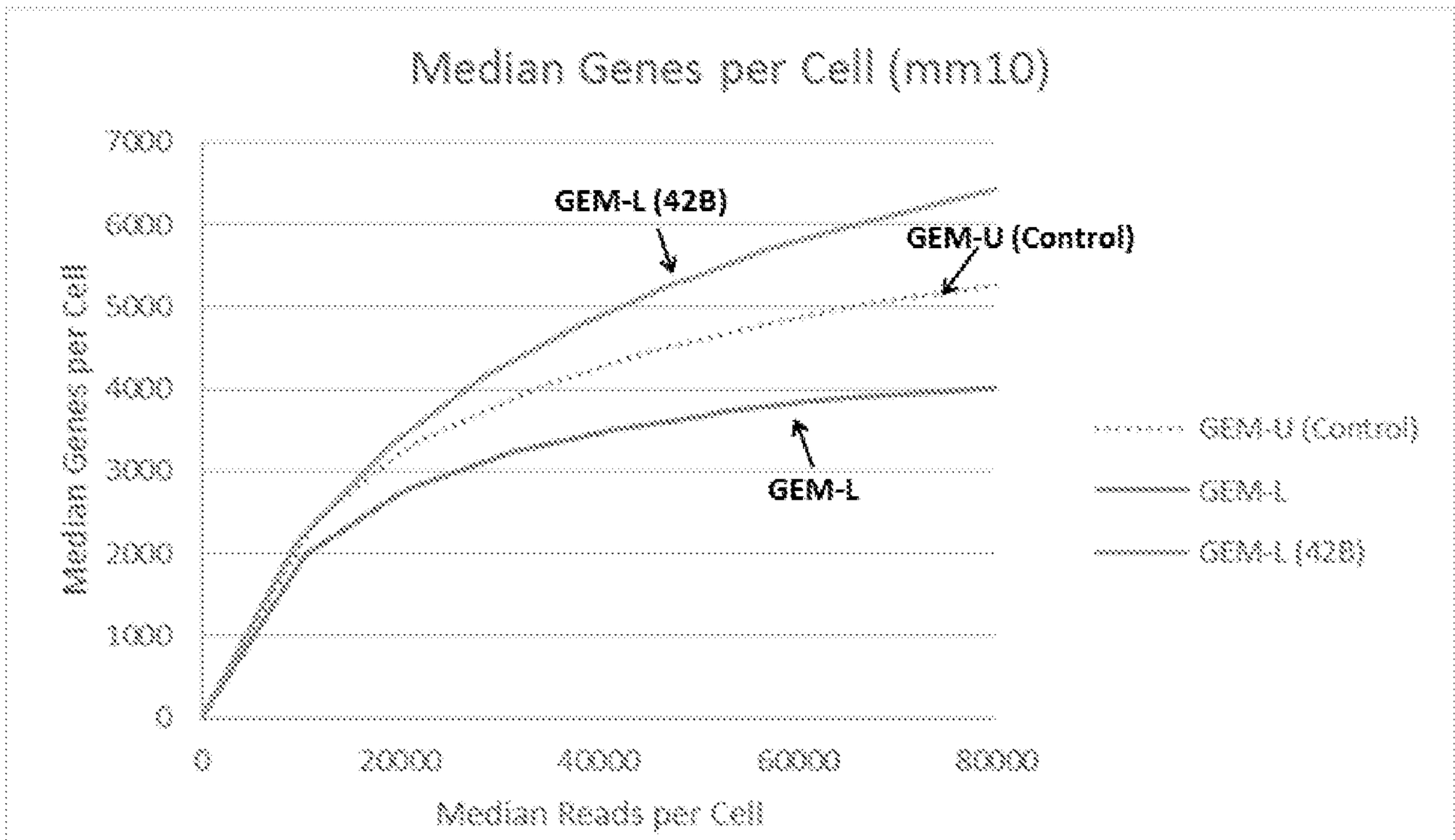

Median Genes per Cell (mm10)
GEM-L (42B)
GEM-U (Control)
GEM-L
Median Genes per Cell
Median Reads per Cell
0
1000
2000
3000
4000
5000
6000
7000
0
20000
40000
60000
80000
GEM-U (Control)
GEM-L
GEM-L (42B)

FIG. 20

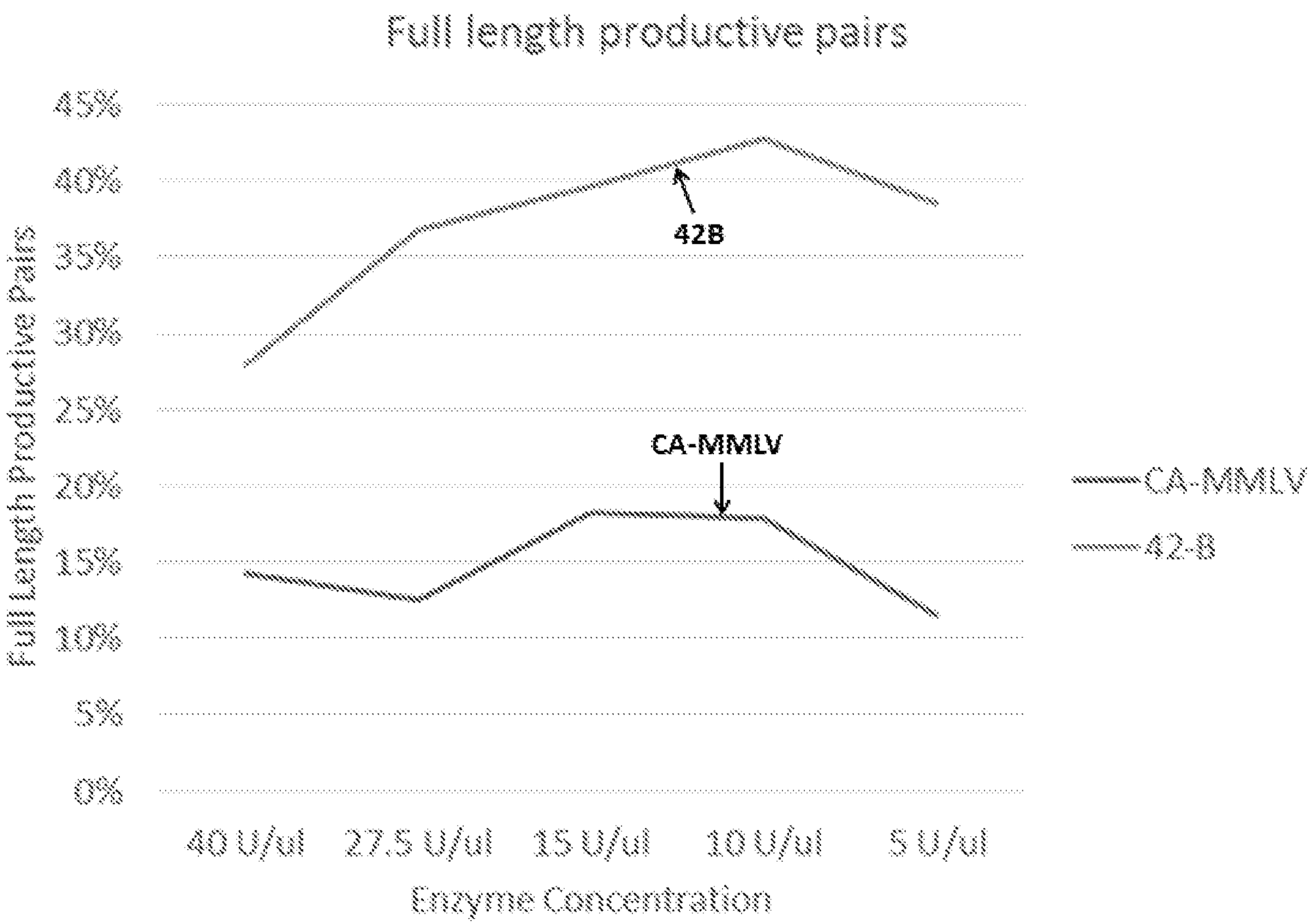

Full length productive pairs
45%
40%
35%
30%
25%
20%
15%
10%
5%
0%
Full Length Productive Pairs
42B
CA-MMLV
CA-MMLV
42-B
40 U/ul
27.5 U/ul
15 U/ul
10 U/ul
5 U/ul
Enzyme Concentration

FIG. 21

description	775pL GEMs CA-MMLV	1.1nL GEMs CA-MMLV	775pL GEMs 428	1.1nL GEMs 428
Estimated Number of cells	5119	4911	5325	5922
Relative difference of detected cells from expected cells	-0.15	-0.18	-0.11	-0.01
Mean assembled reads per cell	4804	6148	4251	3559
Adjusted TRA TRB Fraction cells with full-length productive pair	0.28	0.22	0.42	0.46
Fraction reads mapped to recombinome	0.86	0.86	0.71	0.74
Valid Barcodes	0.91	0.89	0.81	0.84
Low-support UMI read fraction	0.05	0.05	0.06	0.05
Q30 Bases in RNA Read	0.97	0.97	0.98	0.98
VDJ Fraction corrected barcodes	0.06	0.06	0.05	0.05
Fraction rRNA reads	0.010	0.006	0.096	0.082
Fraction mtRNA reads	0.001	0.001	0.033	0.025
Fraction reads with any R1 sequence	0.013	0.024	0.006	0.008
Adjusted TRA Fraction of CDR3+ cells with >1 CDR3	0.09	0.07	0.14	0.13
Adjusted TRB Fraction of CDR3+ cells with >1 CDR3	0.12	0.09	0.17	0.16
Median contig length	562	565	562	562
Fraction unannotated contigs	0.04	0.03	0.04	0.05
Adjusted TRA TRB Fraction cells in a productive, full-length, and paired clonotype (INFERRED)	0.35	0.29	0.50	0.54
TRA TRB number of clonotypes (INFERRED)	4183	3898	4357	4928

FIG. 22