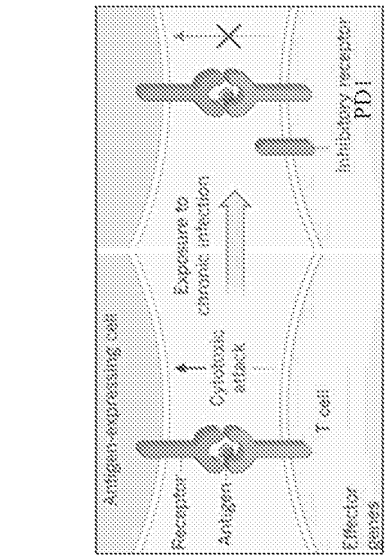


FIG. 1C

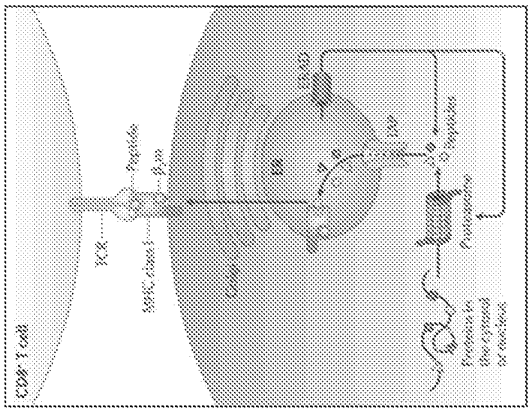


FIG. 1B

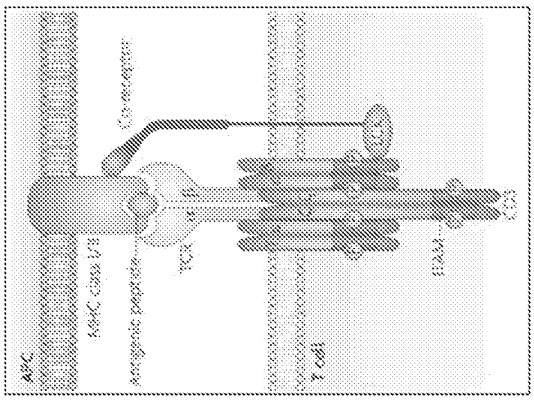


FIG. 1A

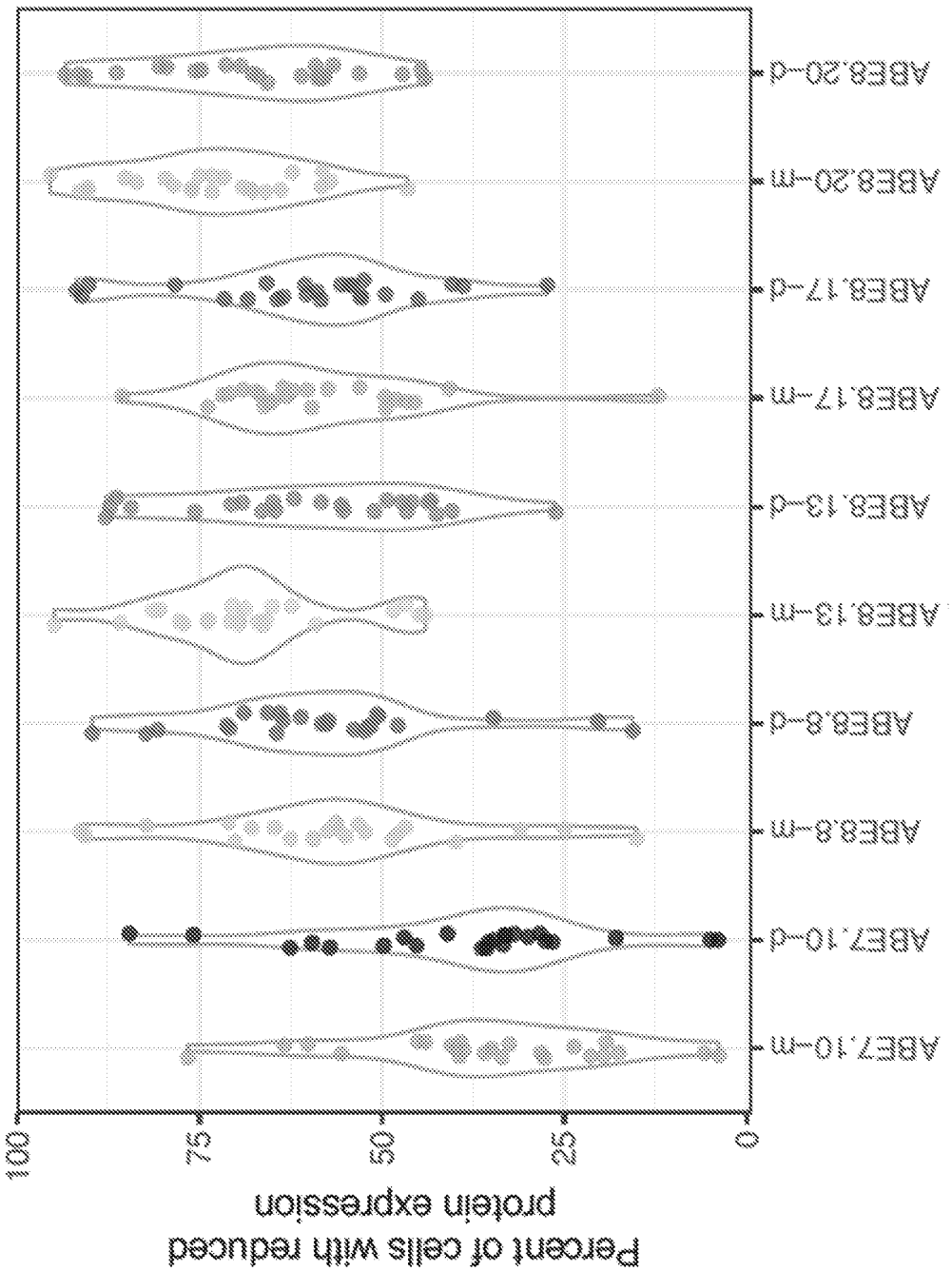

Percent of cells with reduced protein expression
100
75
50
25
0
ABE7.10-m
ABE7.10-d
ABE8.8-m
ABE8.8-d
ABE8.13-m
ABE8.13-d
ABE8.17-m
ABE8.17-d
ABE8.20-m
ABE8.20-d

FIG. 2A

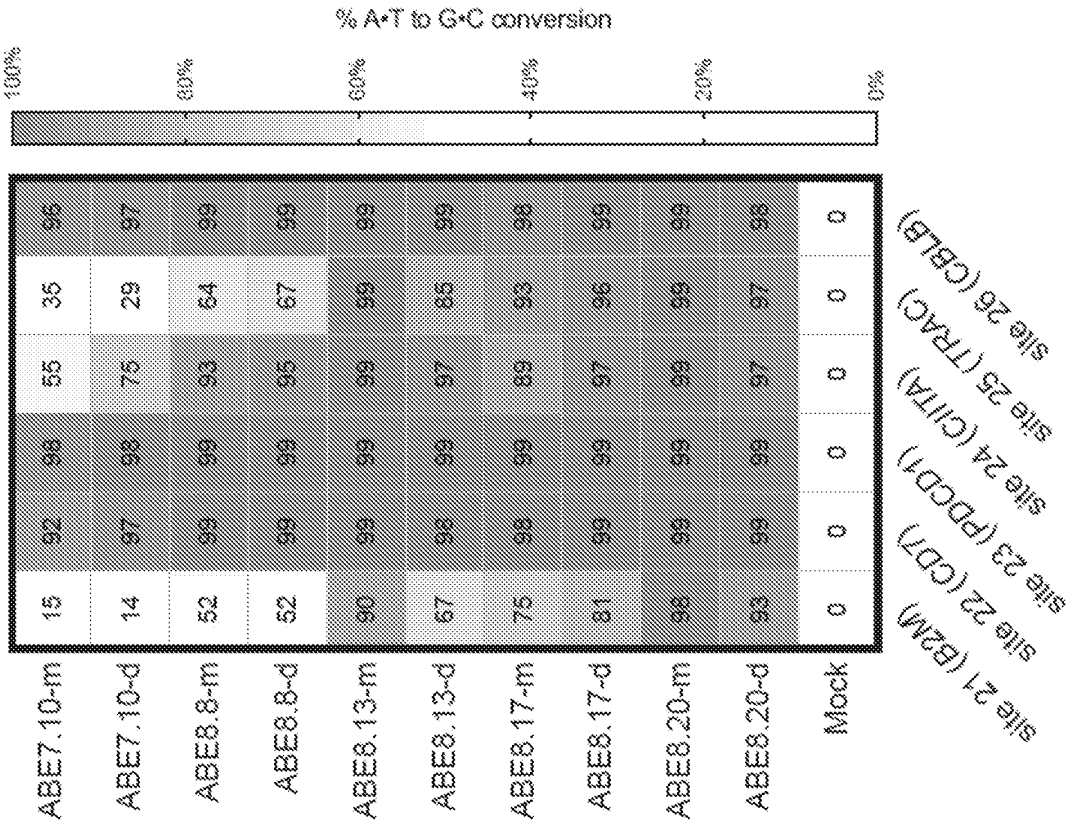

% A•T to G•C conversion
100%
80%
60%
40%
20%
0%
ABE7.10-m
ABE7.10-d
ABE8.8-m
ABE8.8-d
ABE8.13-m
ABE8.13-d
ABE8.17-m
ABE8.17-d
ABE8.20-m
ABE8.20-d
Mock
site 21 (B2M)
site 22 (CD7)
site 23 (PDCD1)
site 24 (CIITA)
site 25 (TRAC)
site 26 (CBLB)
15 92 98 55 35 96
14 97 98 75 29 97
52 98 99 93 64 99
52 99 99 95 67 99
90 99 99 99 99 99
67 99 99 97 85 99
75 99 99 99 93 98
81 99 99 97 96 99
98 99 99 99 99 99
93 99 99 97 97 98
0 0 0 0 0 0

FIG. 2B

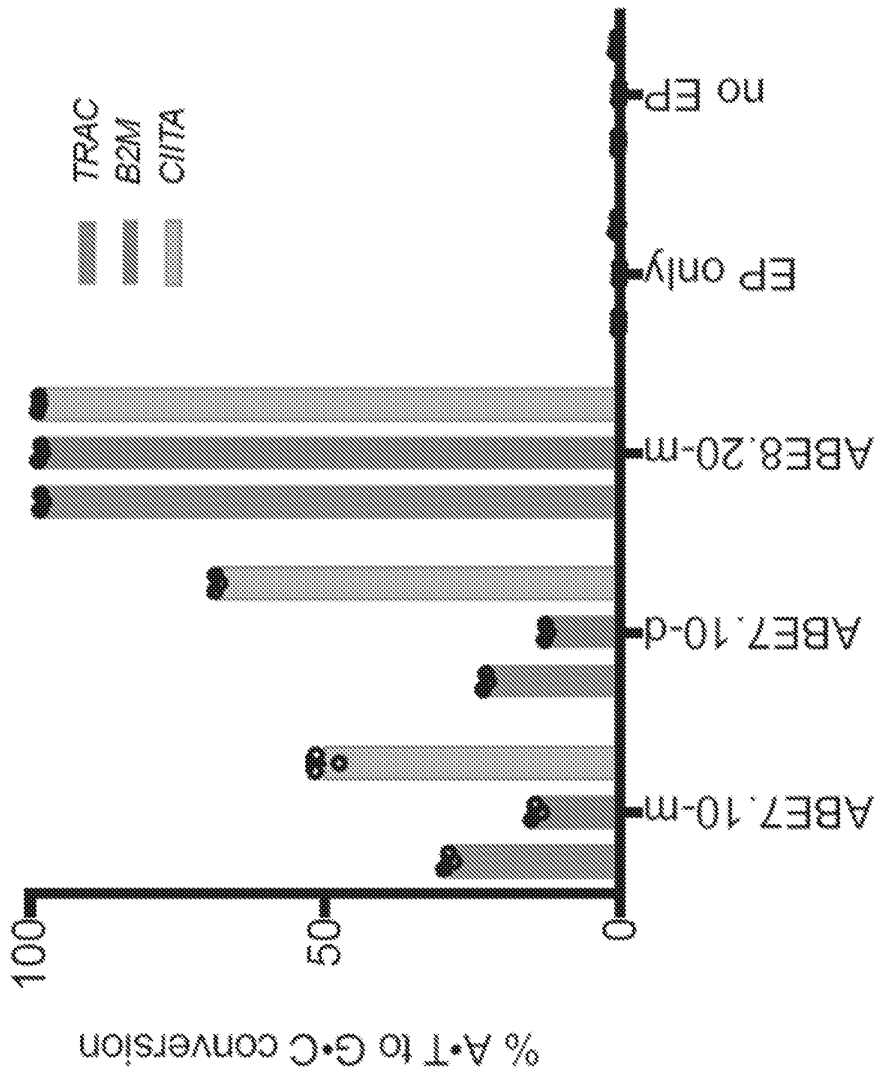
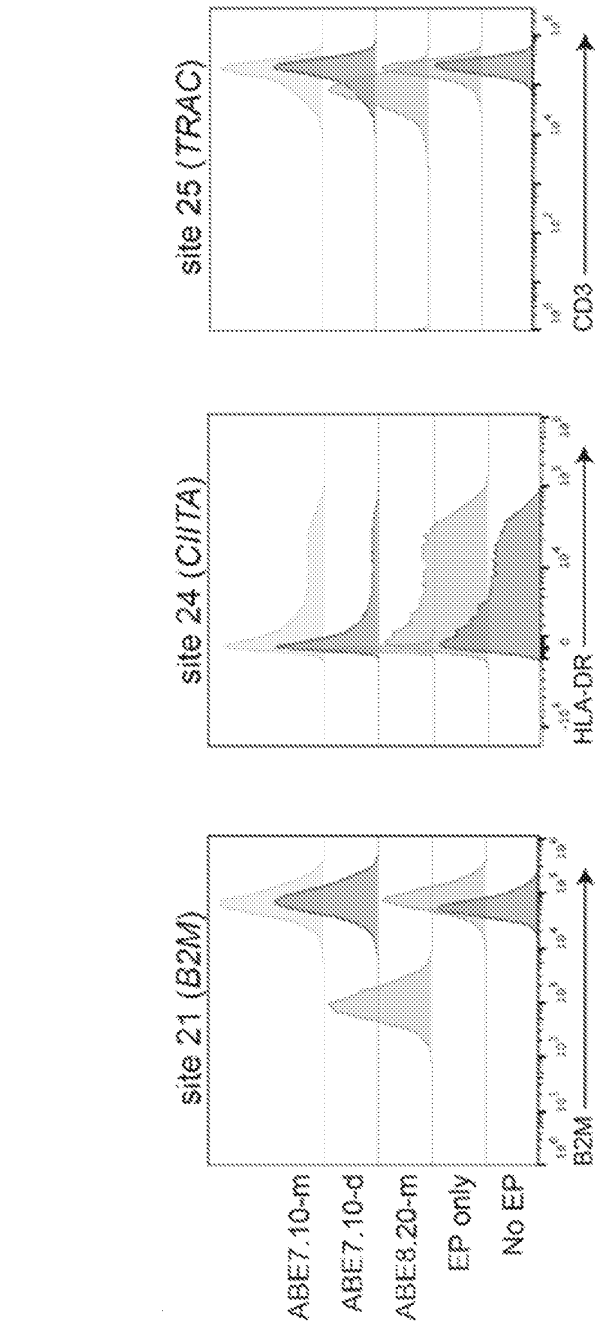

% A•T to G•C conversion
100
50
0
ABE7.10-m
ABE7.10-d
ABE8.20-m
EP only
no EP
TRAC
B2M
CIITA

FIG. 2C



Percentage of cells B2M- HLA-DR- CD3- as measured by flow cytometry

Sample	Donor 2	Donor 4	Donor 5
ABE7.10-m	0.14	0.14	0.067
ABE7.10-d	0.1	0.13	0.037
ABE8.20-m	30.9	33.9	39.6

FIG. 2D

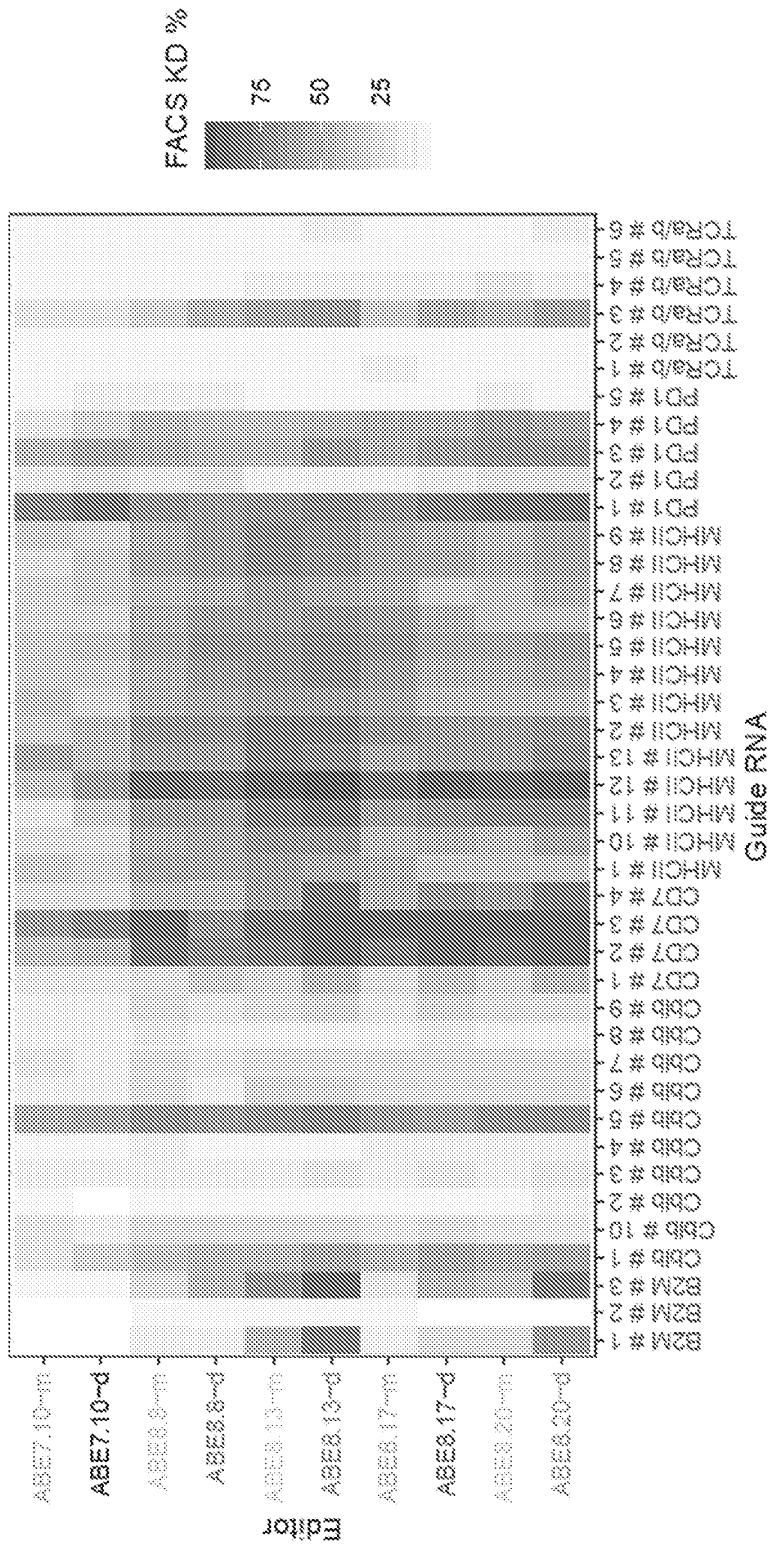

FACS KD %
75
50
25
Guide RNA
B2M # 1
B2M # 2
B2M # 3
CIITA # 1
CIITA # 10
CIITA # 2
CIITA # 3
CIITA # 4
CIITA # 5
CIITA # 6
CIITA # 7
CIITA # 8
CIITA # 9
CD7 # 1
CD7 # 2
CD7 # 3
CD7 # 4
MHCII # 1
MHCII # 10
MHCII # 11
MHCII # 12
MHCII # 13
MHCII # 2
MHCII # 3
MHCII # 4
MHCII # 5
MHCII # 6
MHCII # 7
MHCII # 8
MHCII # 9
PD1 # 1
PD1 # 2
PD1 # 3
PD1 # 4
PD1 # 5
TCRa/b # 1
TCRa/b # 2
TCRa/b # 3
TCRa/b # 4
TCRa/b # 5
TCRa/b # 6
Editor
ABE7.10-m
ABE7.10-d
ABE8.8-m
ABE8.8-d
ABE8.13-m
ABE8.13-d
ABE8.17-m
ABE8.17-d
ABE8.20-m
ABE8.20-d

FIG. 3

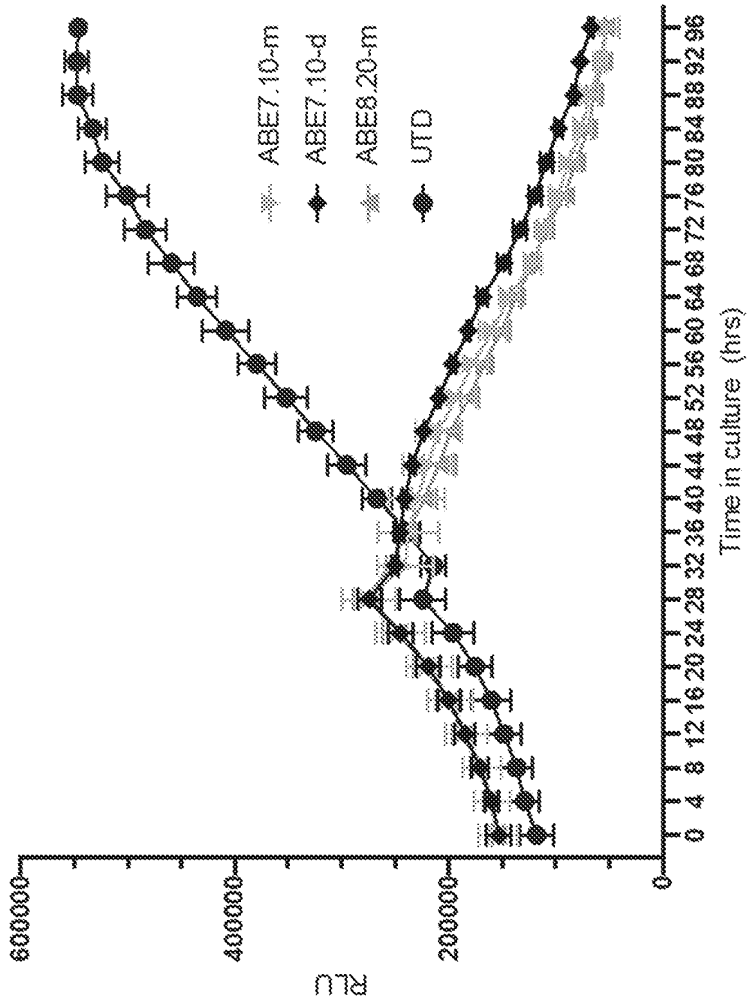

ABE7.10-m
ABE7.10-d
ABE8.20-m
UTD
RLU
600000
400000
200000
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60 64 68 72 76 80 84 88 92 96
Time in culture (hrs)

FIG. 4

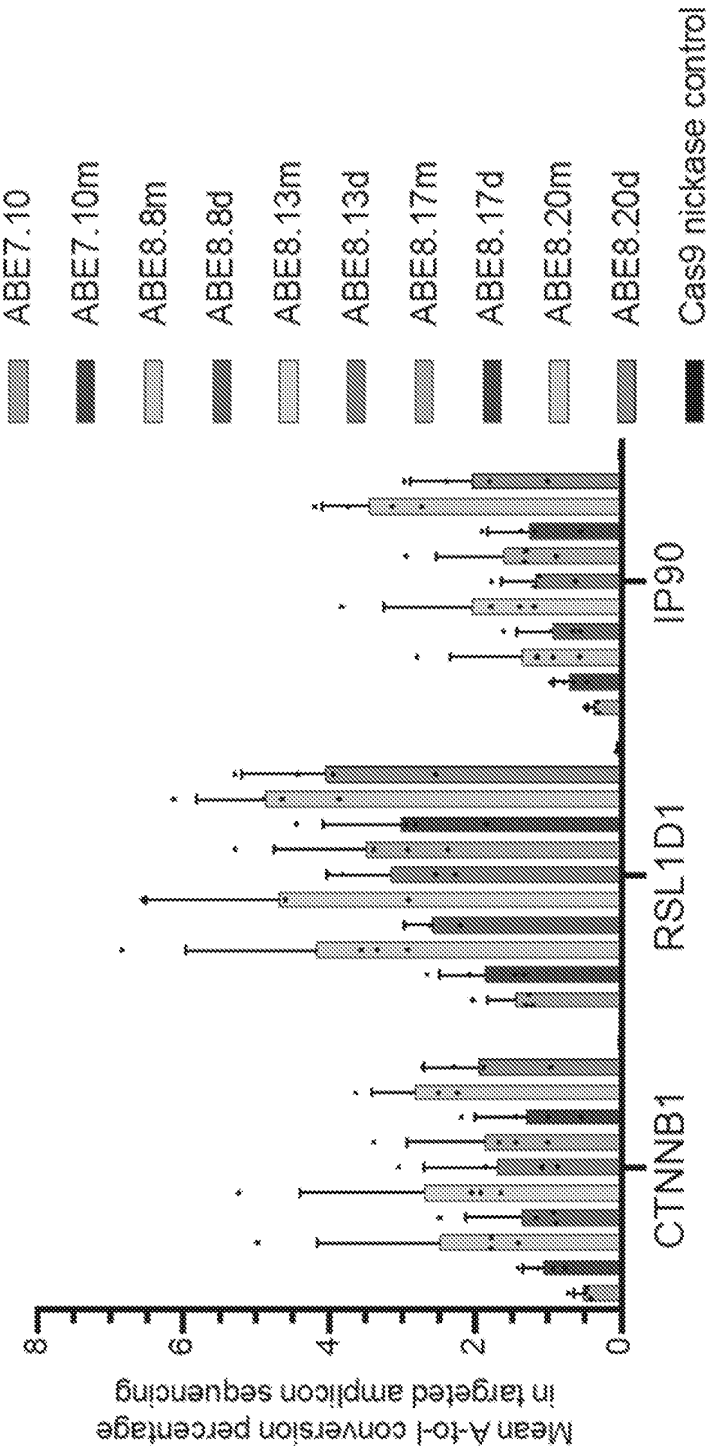

ABE7.10
ABE7.10m
ABE8.8m
ABE8.8d
ABE8.13m
ABE8.13d
ABE8.17m
ABE8.17d
ABE8.20m
ABE8.20d
Cas9 nickase control
Mean A-to-I conversion percentage in targeted amplicon sequencing
0
2
4
6
8
CTNNB1
RSL1D1
IP90

FIG. 5A

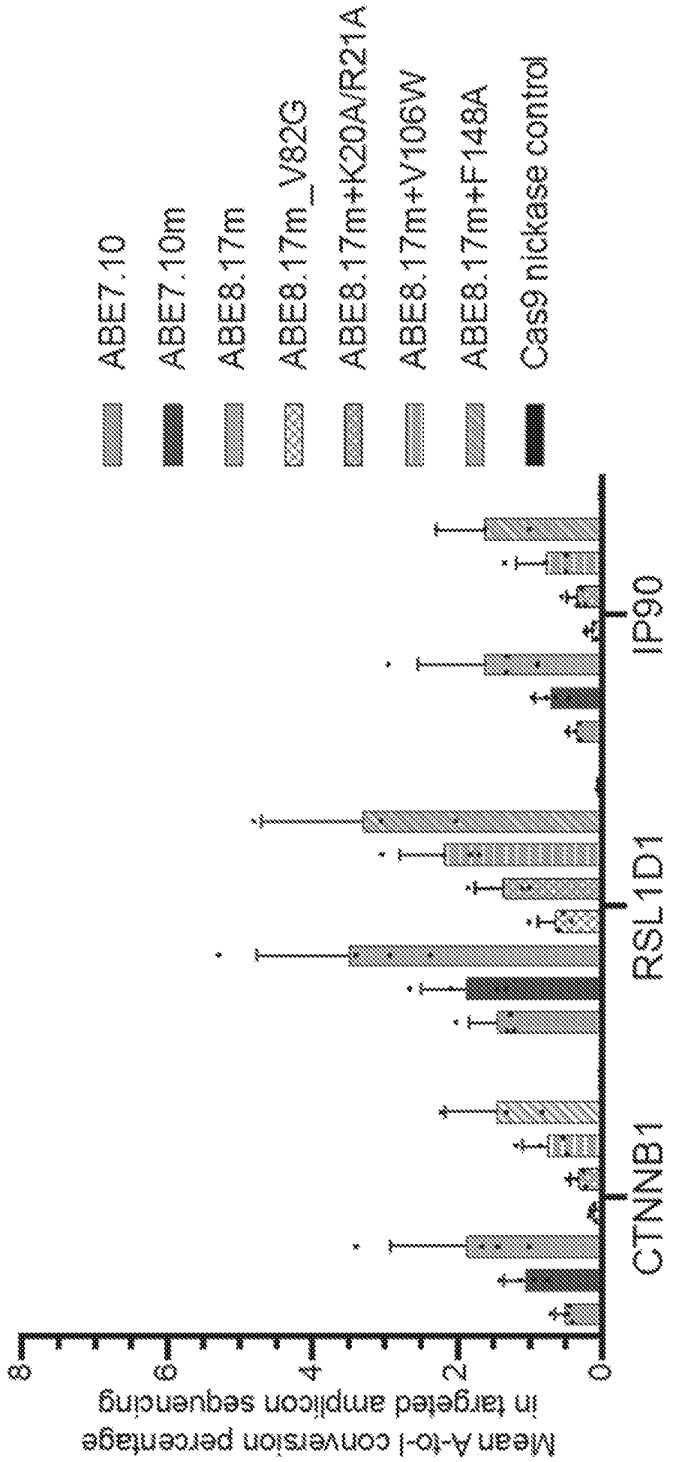

ABE7.10
ABE7.10m
ABE8.17m
ABE8.17m_V82G
ABE8.17m+K20A/R21A
ABE8.17m+V106W
ABE8.17m+F148A
Cas9 nickase control
Mean A-to-I conversion percentage in targeted amplicon sequencing
0
2
4
6
8
CTNNB1
RSL1D1
IP90

FIG. 5B

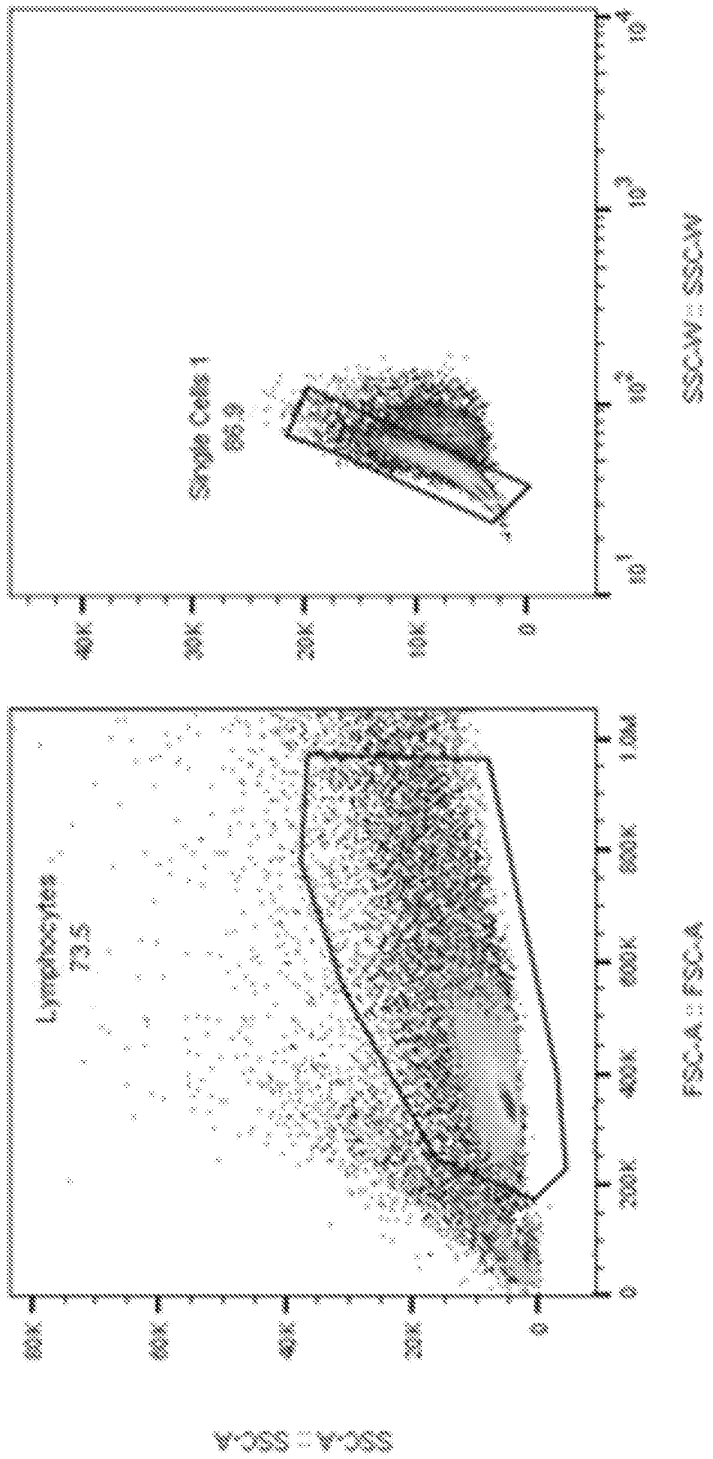

Lymphocytes
73.5
Single Cells 1
88.9
SSC-A :: SSC-A
FSC-A :: FSC-A
SSC-W :: SSC-W

FIG. 6A

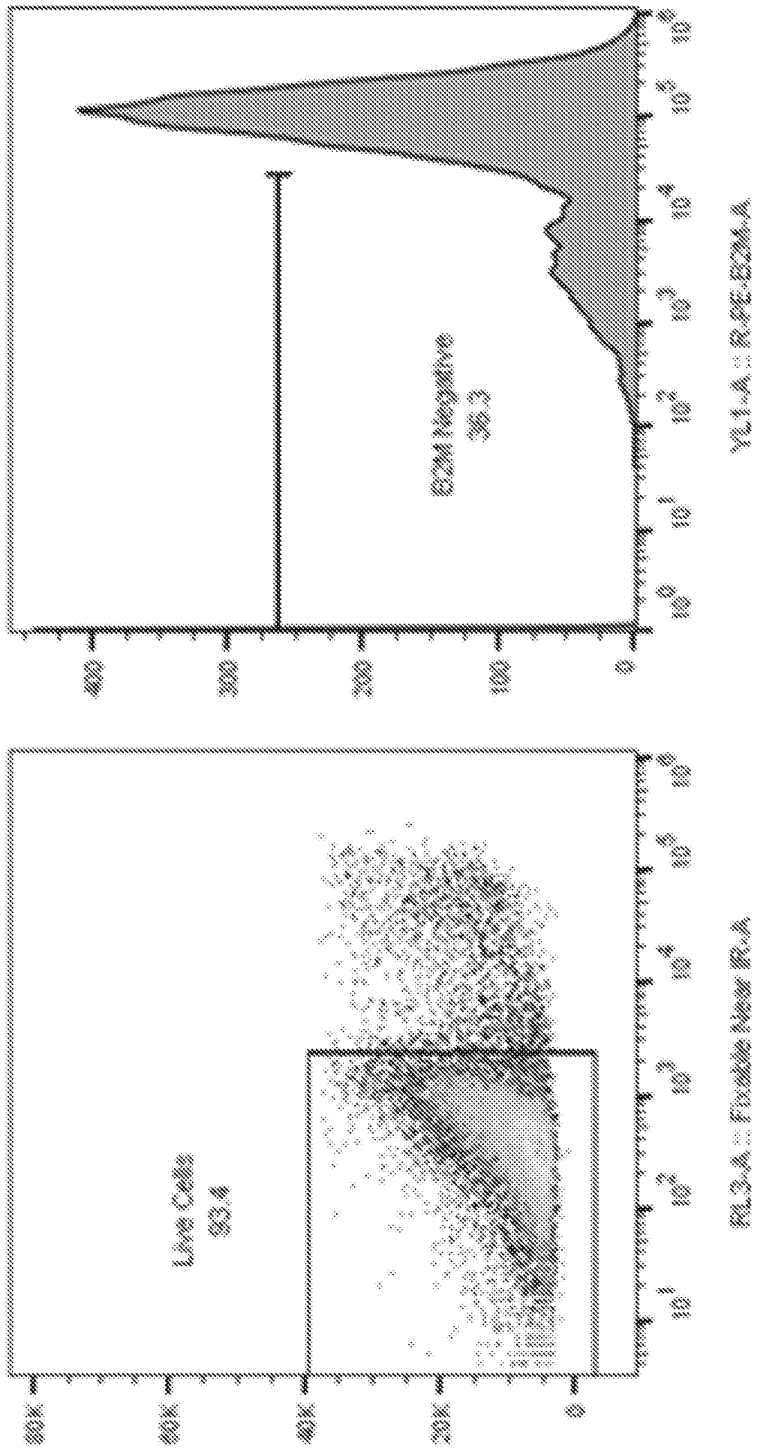

Live Cells
83.4
FL3-A :: Fixable Near IR-A
E2M Negative
96.3
Y-1-A :: R-PE-E2M-A

FIG. 6B

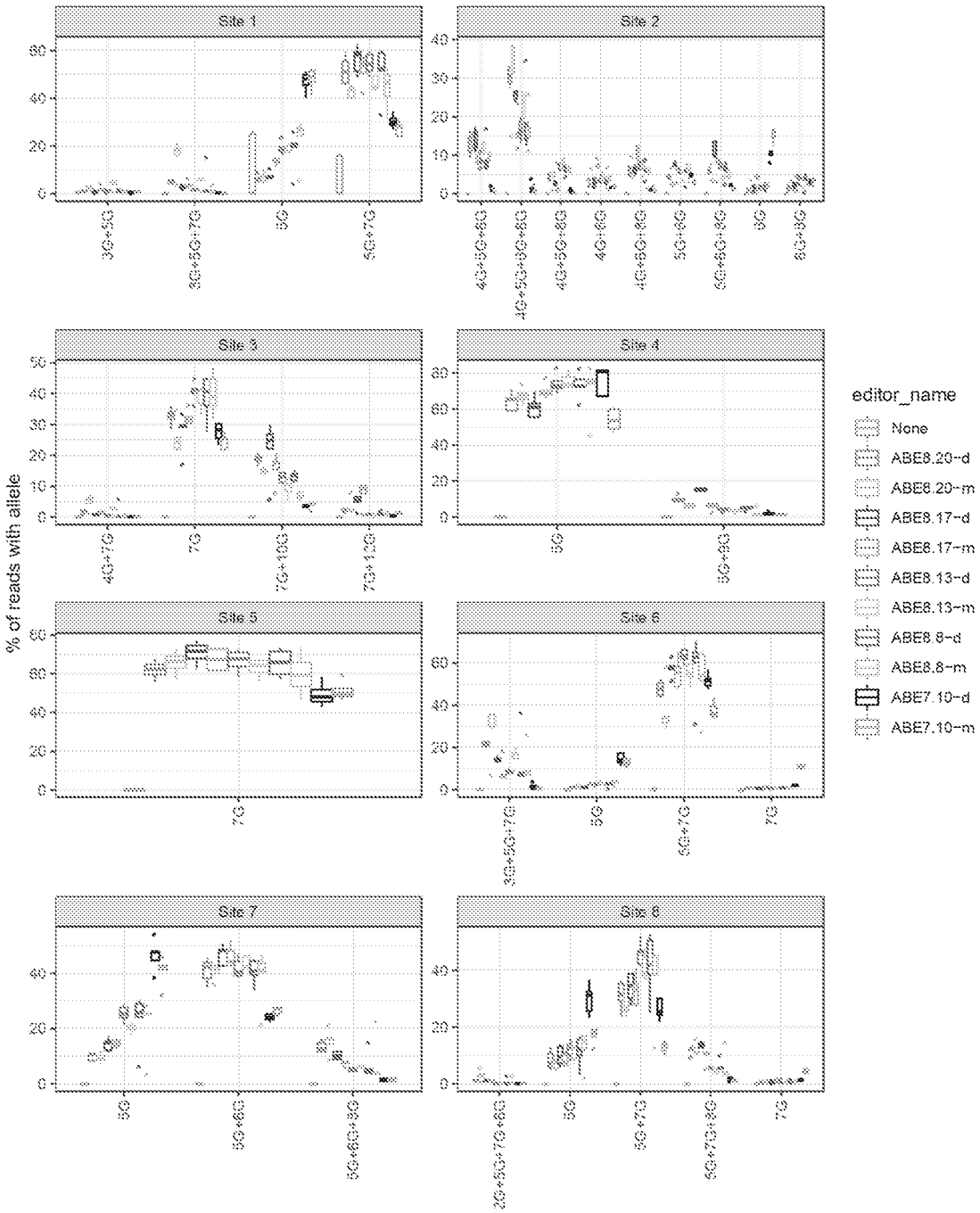

Site 1
Site 2
Site 3
Site 4
Site 5
Site 6
Site 7
Site 8
% of reads with allele
editor_name
None
ABE8.20-d
ABE8.20-m
ABE8.17-d
ABE8.17-m
ABE8.13-d
ABE8.13-m
ABE8.8-d
ABE8.8-m
ABE7.10-d
ABE7.10-m

FIG. 7

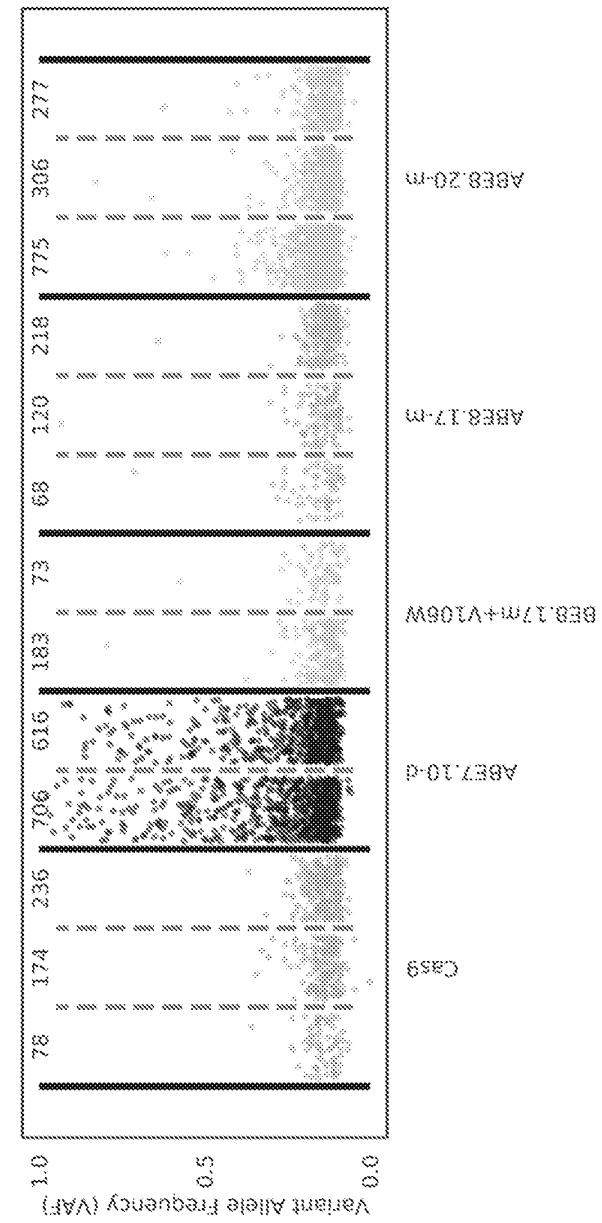

Variant Allele Frequency (VAF)
1.0
0.5
0.0
78
174
236
706
616
183
73
68
120
218
775
306
277
Cas9
ABE7.10-d
BE8.17m+V106W
ABE8.17-m
ABE8.20-m

FIG. 8A

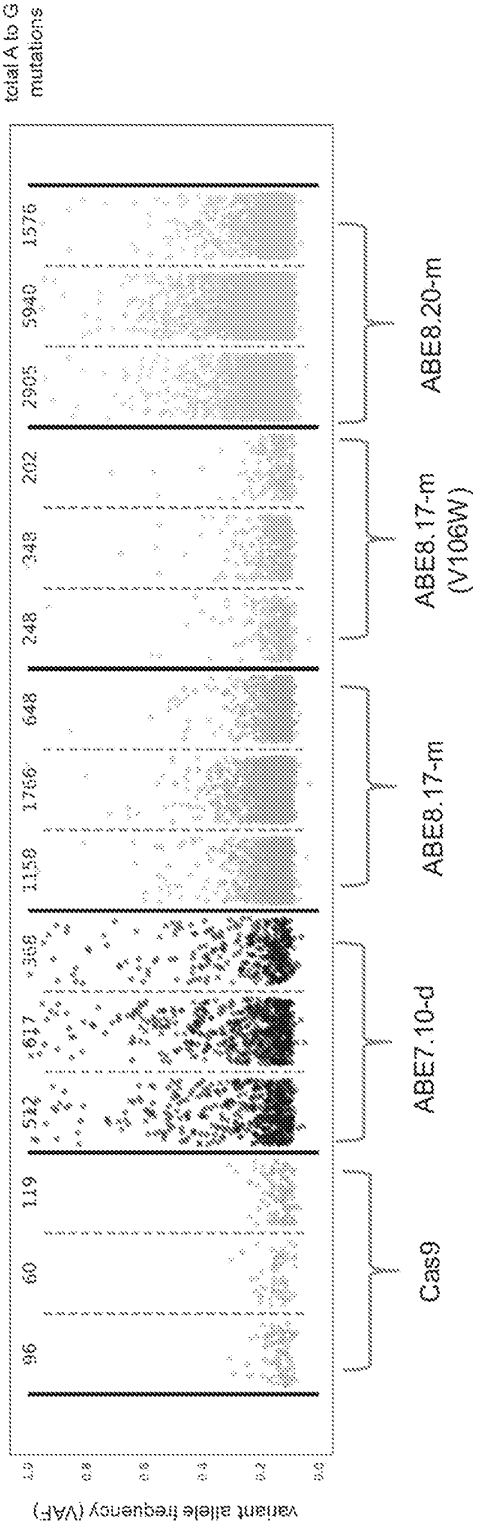

total A to G mutations
variant allele frequency (VAF)
96
60
119
542
617
369
1159
1766
648
248
348
202
2905
5940
1576
Cas9
ABE7.10-d
ABE8.17-m
ABE8.17-m (V106W)
ABE8.20-m

FIG. 8B

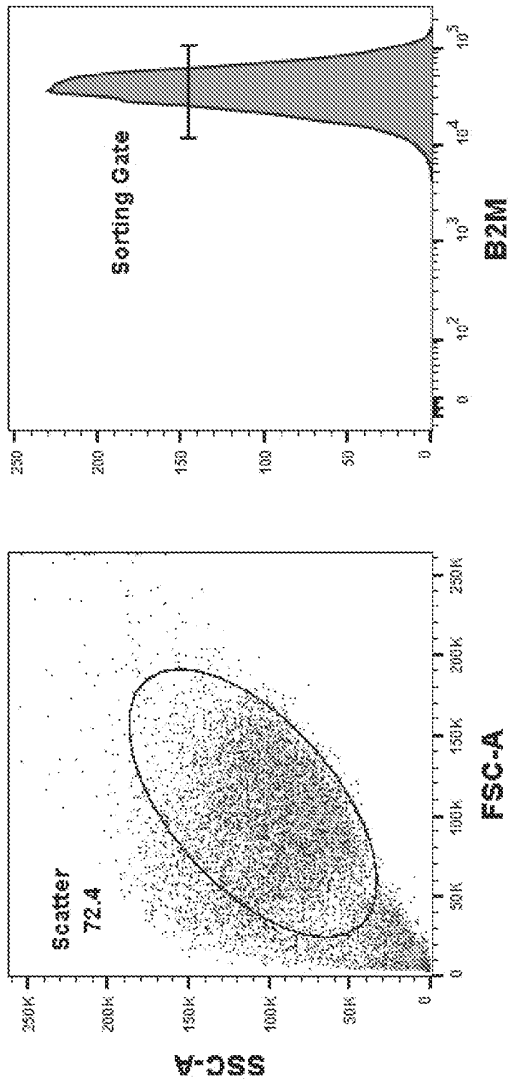

Sorting Gate
B2M
Scatter
72.4
SSC-A
FSC-A

FIG. 9A

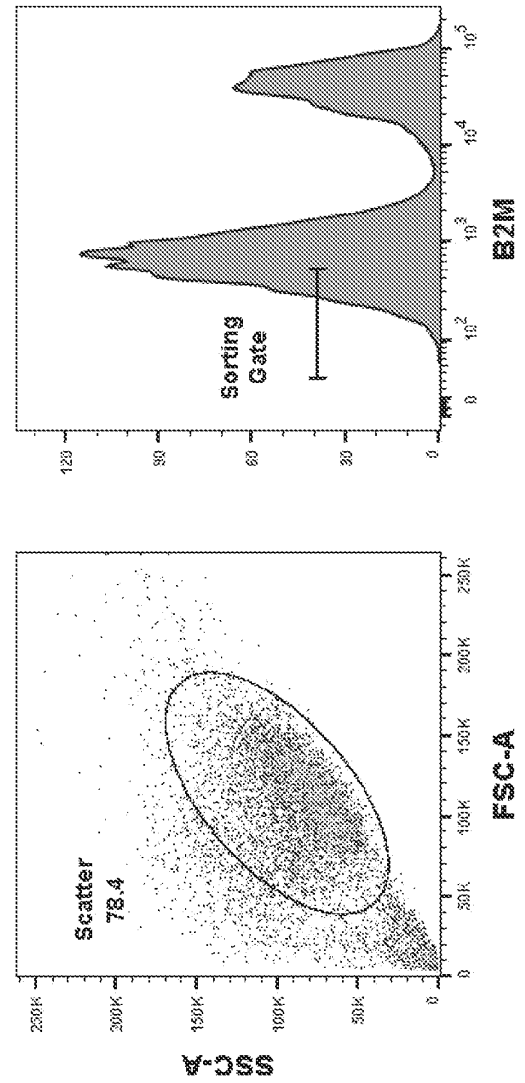

Sorting
Gate
B2M
Scatter
78.4
SSC-A
FSC-A

FIG. 9B

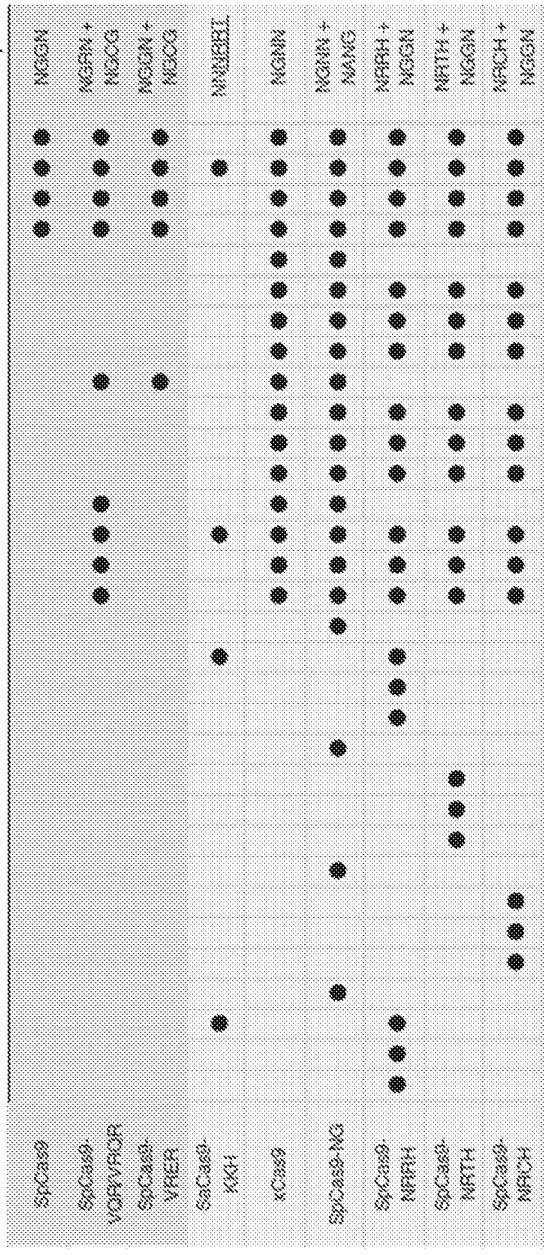

PAM
scope
NGGN
NGRN + NGCG
NGGN + NGCG
NNNRRT
NGNN
NGNN + NAAG
NRRH + NGGN
NRTH + NGGN
NRCH + NGGN
SpCas9
SpCas9-VQRVRQR
SpCas9-VRER
SaCas9-KKH
xCas9
SpCas9-NG
SpCas9-NRRH
SpCas9-NRTH
SpCas9-NRCH
NAAA
NAAC
NAAT
NAAG
NACA
NACC
NACT
NACG
NATA
NATC
NATT
NATG
NAGA
NAGC
NAGT
NAGG
NAAA
NAAC
NAAT
NAAG
NACA
NACC
NACT
NACG
NATA
NATC
NATT
NATG
NAGA
NAGC
NAGT
NAGG

FIG. 10