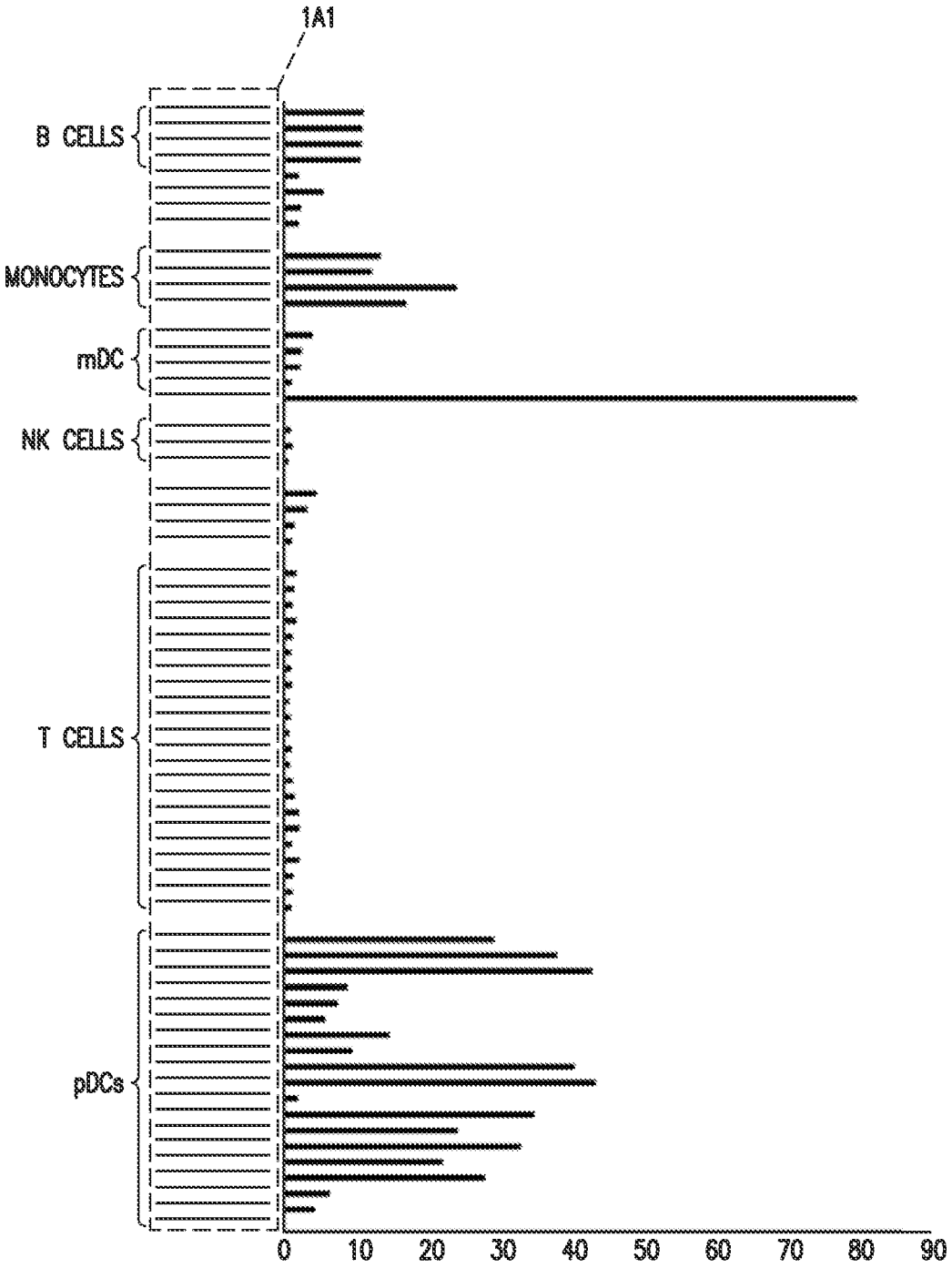

1A1
B CELLS
MONOCYTES
mDC
NK CELLS
T CELLS
pDCs
0
10
20
30
40
50
60
70
80
90

FIG. 1A

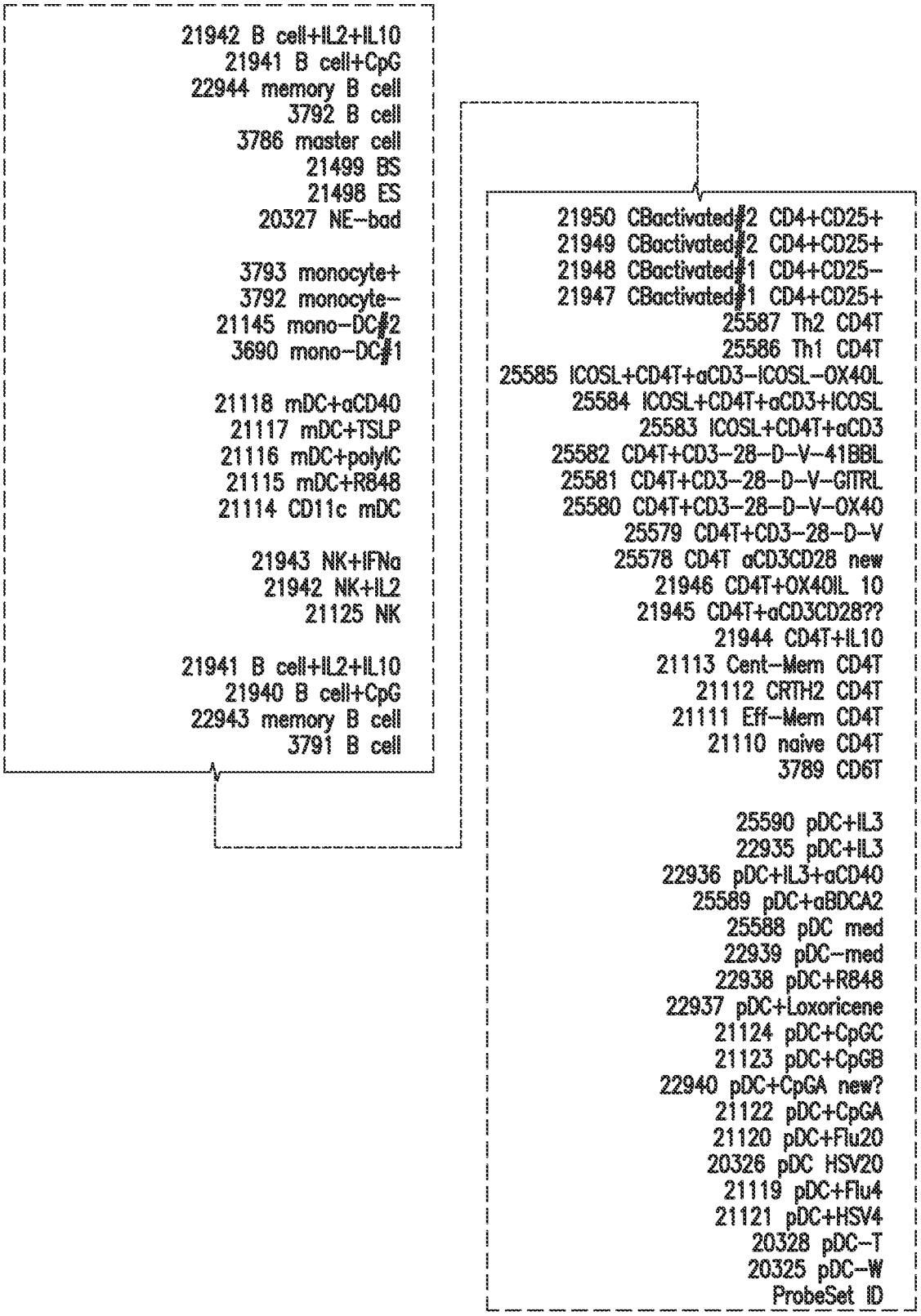

21942 B cell+IL2+IL10
21941 B cell+CpG
22944 memory B cell
3792 B cell
3786 master cell
21499 BS
21498 ES
20327 NE-bad
3793 monocyte+
3792 monocyte-
21145 mono-DC#2
3690 mono-DC#1
21118 mDC+aCD40
21117 mDC+TSLP
21116 mDC+polyIC
21115 mDC+R848
21114 CD11c mDC
21943 NK+IFNa
21942 NK+IL2
21125 NK
21941 B cell+IL2+IL10
21940 B cell+CpG
22943 memory B cell
3791 B cell
21950 CBactivated#2 CD4+CD25+
21949 CBactivated#2 CD4+CD25+
21948 CBactivated#1 CD4+CD25-
21947 CBactivated#1 CD4+CD25+
25587 Th2 CD4T
25586 Th1 CD4T
25585 ICOSL+CD4T+aCD3-ICOSL-OX40L
25584 ICOSL+CD4T+aCD3+ICOSL
25583 ICOSL+CD4T+aCD3
25582 CD4T+CD3-28-D-V-41BBL
25581 CD4T+CD3-28-D-V-GITRL
25580 CD4T+CD3-28-D-V-OX40
25579 CD4T+CD3-28-D-V
25578 CD4T aCD3CD28 new
21946 CD4T+OX40IL 10
21945 CD4T+aCD3CD28??
21944 CD4T+IL10
21113 Cent-Mem CD4T
21112 CRTH2 CD4T
21111 Eff-Mem CD4T
21110 naive CD4T
3789 CD6T
25590 pDC+IL3
22935 pDC+IL3
22936 pDC+IL3+aCD40
25589 pDC+aBDCA2
25588 pDC med
22939 pDC-med
22938 pDC+R848
22937 pDC+Loxoricene
21124 pDC+CpGC
21123 pDC+CpGB
22940 pDC+CpGA new?
21122 pDC+CpGA
21120 pDC+Flu20
20326 pDC HSV20
21119 pDC+Flu4
21121 pDC+HSV4
20328 pDC-T
20325 pDC-W
ProbeSet ID

FIG. 1A1

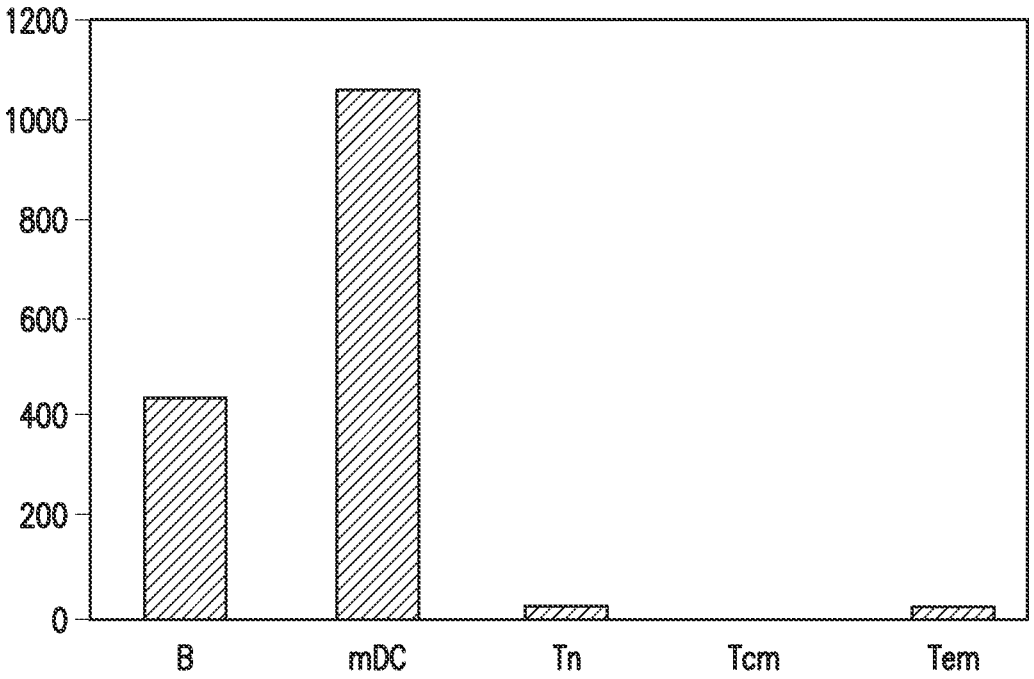

1200
1000
800
600
400
200
0
B
mDC
Tn
Tcm
Tem

FIG. 1B

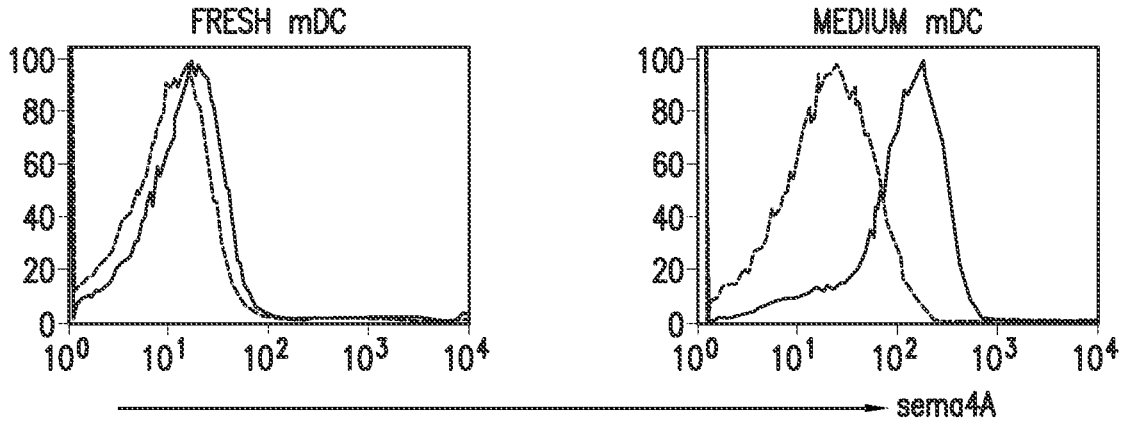

FRESH mDC
MEDIUM mDC
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
sema4A

FIG. 1C

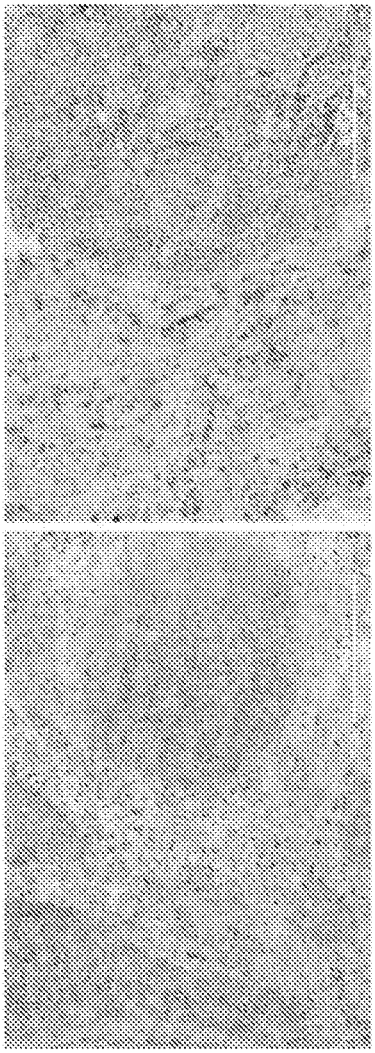


FIG. 2A

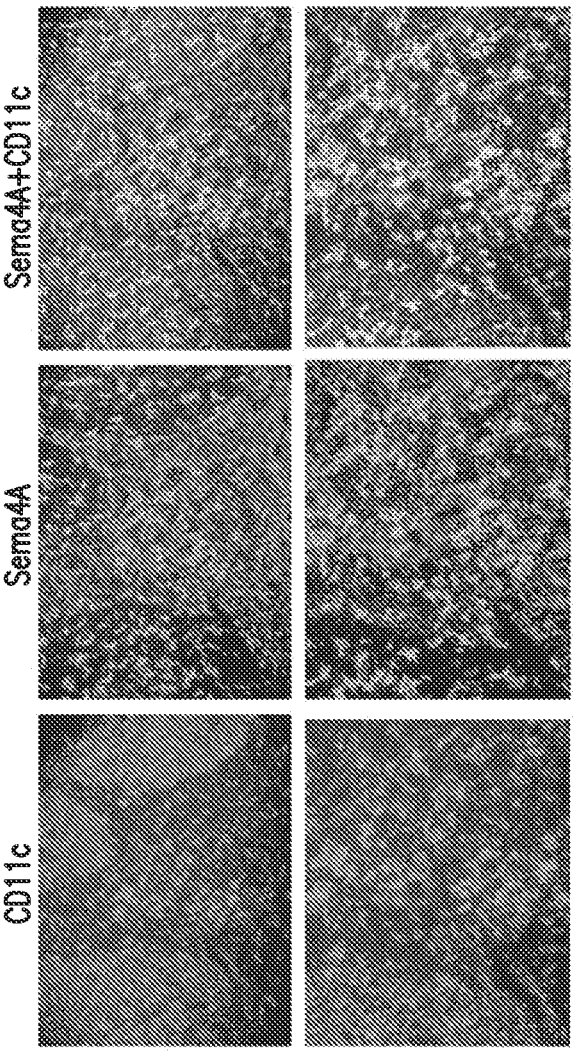


FIG. 2B

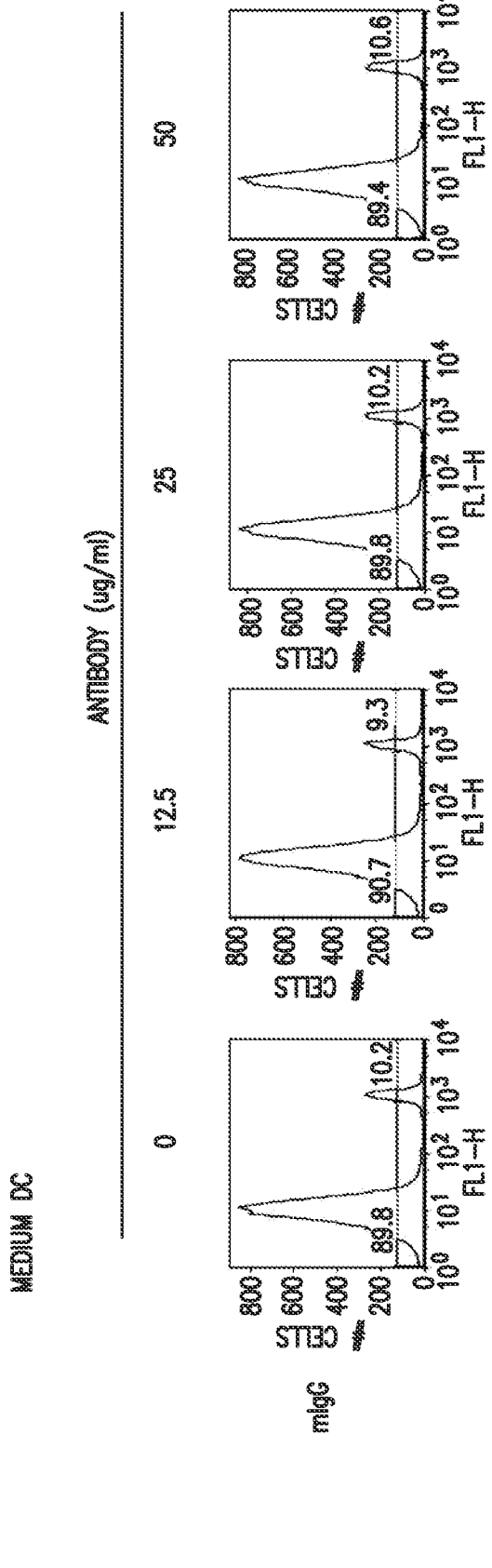

MEDIUM DC
ANTIBODY (ug/ml)
0
12.5
25
50
mIgG
CELLS
FL1-H
89.8
90.7
89.8
89.4
10.2
9.3
10.2
10.6

FIG. 3A

anti-sema4A mAb
CELLS
FL1-H
87.9
81.2
6.65
7.75
12.1
18.8
93.4
92.2

FIG. 3B

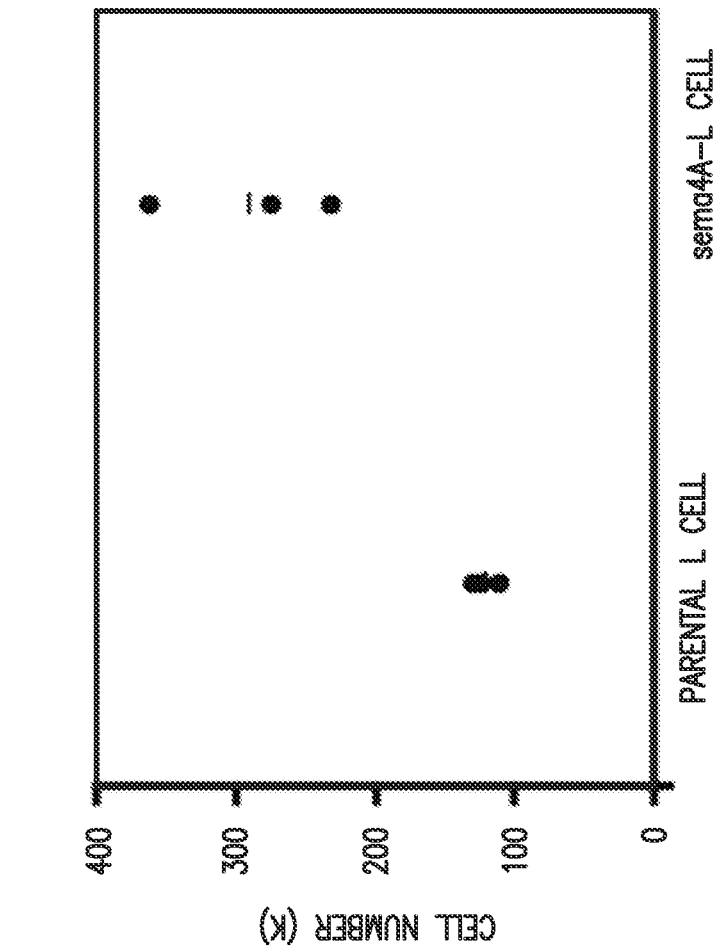

CELL NUMBER (K)
400
300
200
100
0
PARENTAL L CELL
sema4A-L CELL

FIG. 4B

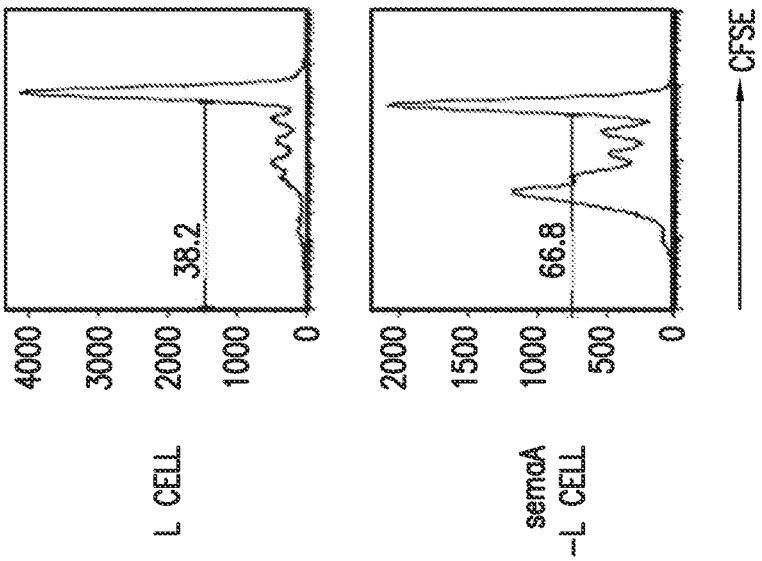

L CELL
4000
3000
2000
1000
0
38.2
semaA -L CELL
2000
1500
1000
500
0
66.8
CFSE

FIG. 4A

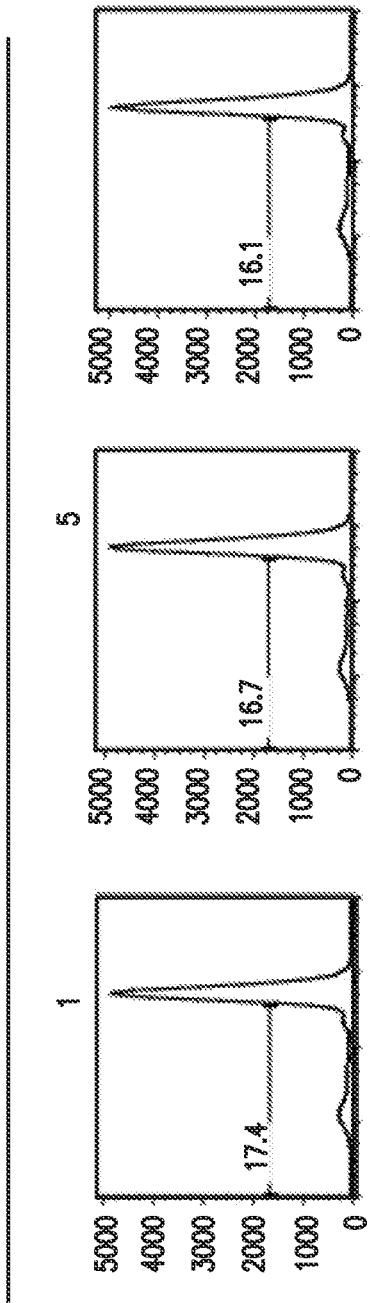

anti-CD3+hIgG (ug/ml)
0
1
5
25
10.3
17.4
16.7
16.1
5000
4000
3000
2000
1000
0

FIG. 4C

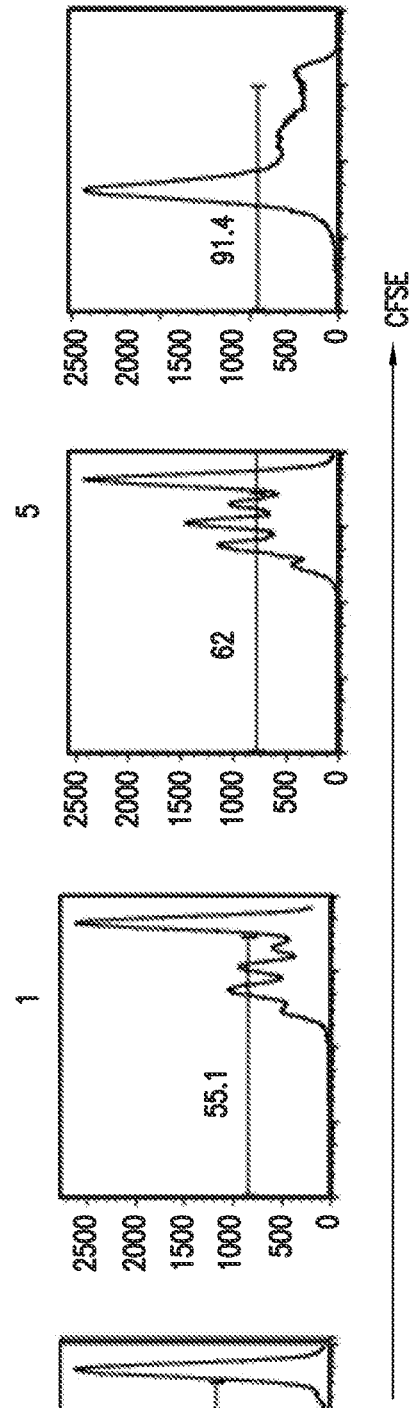

anti-CD3+sema4A Fc FUSION PROTEIN (ug/ml)
0
1
5
25
8.64
55.1
62
91.4
4000
3000
2000
1000
2500
1500
500
0
CFSE

FIG. 4D

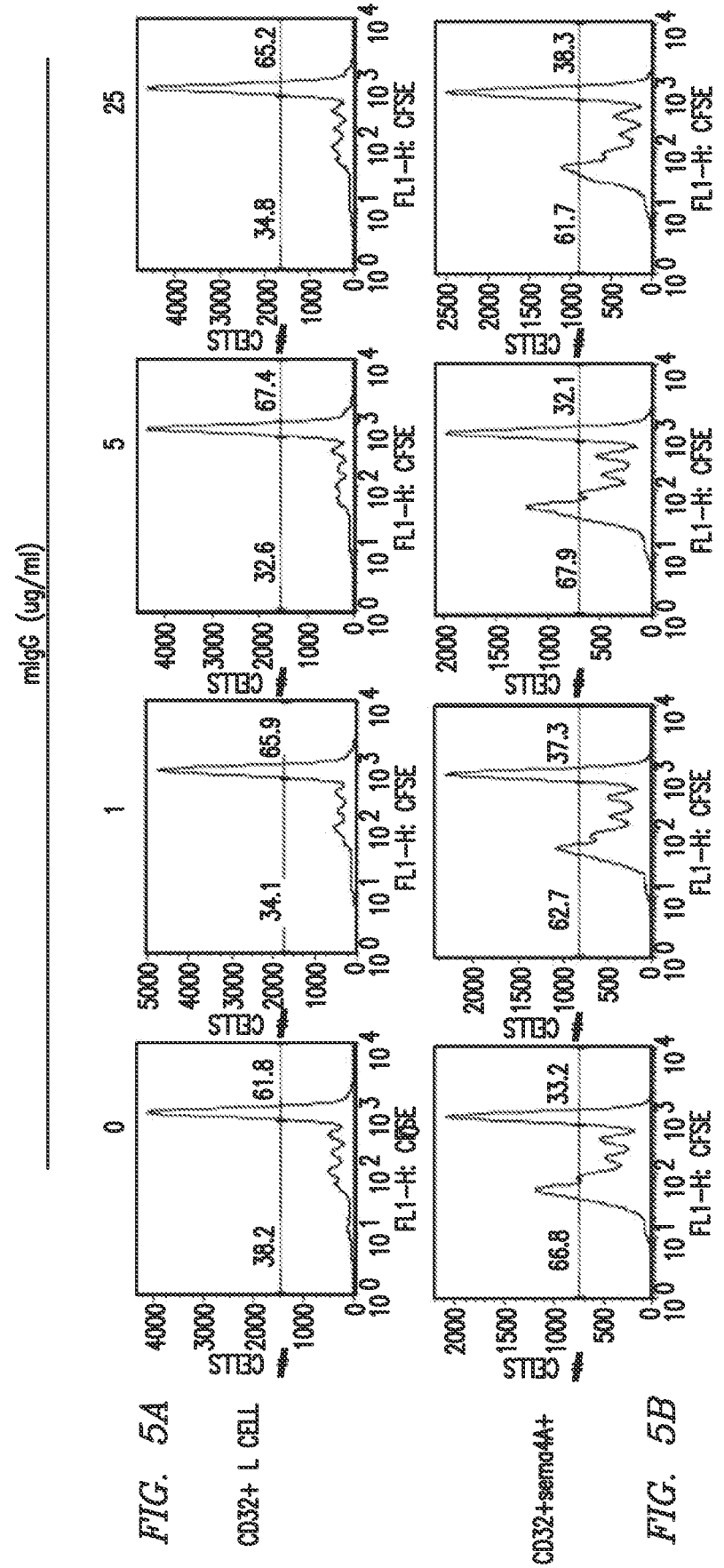

mIgG (ug/ml)
0
1
5
25
CD32+ L CELL
CD32+sema4A+
FL1-H: CFSE
61.8
38.2
34.1
65.9
32.6
67.4
34.8
65.2
66.8
33.2
62.7
37.3
67.9
32.1
61.7
38.3

FIG. 5A

FIG. 5B

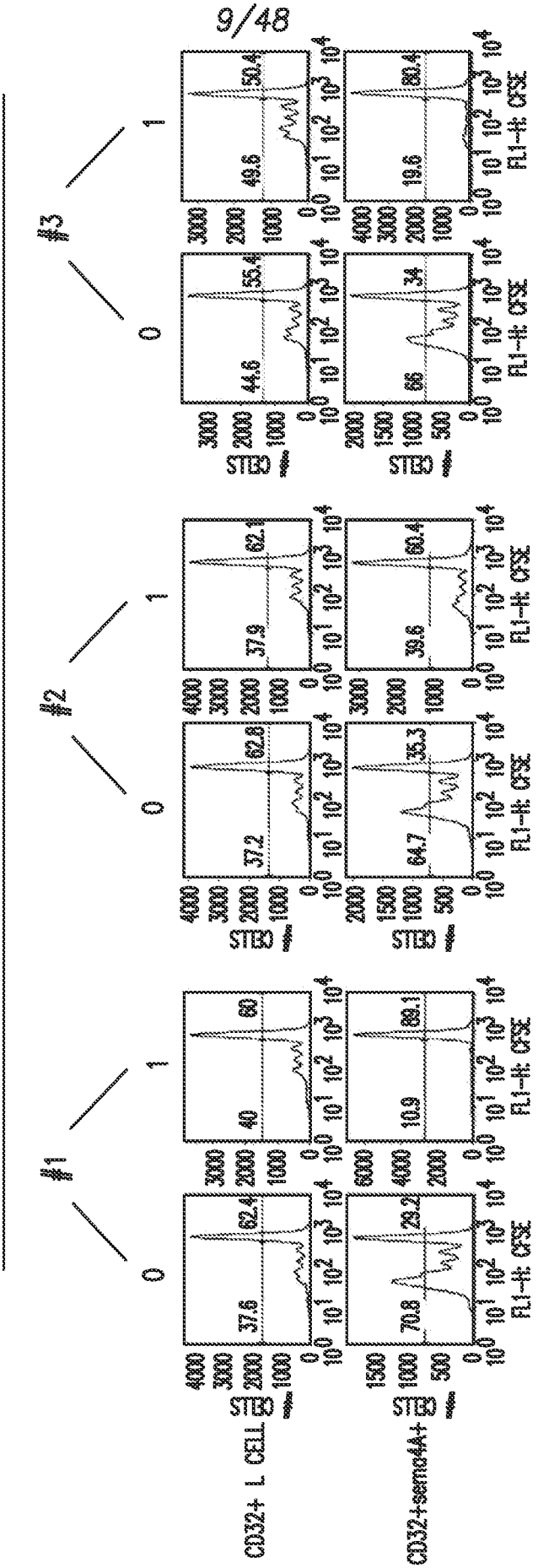


FIG. 5C

FIG. 5D

FIG. 5E

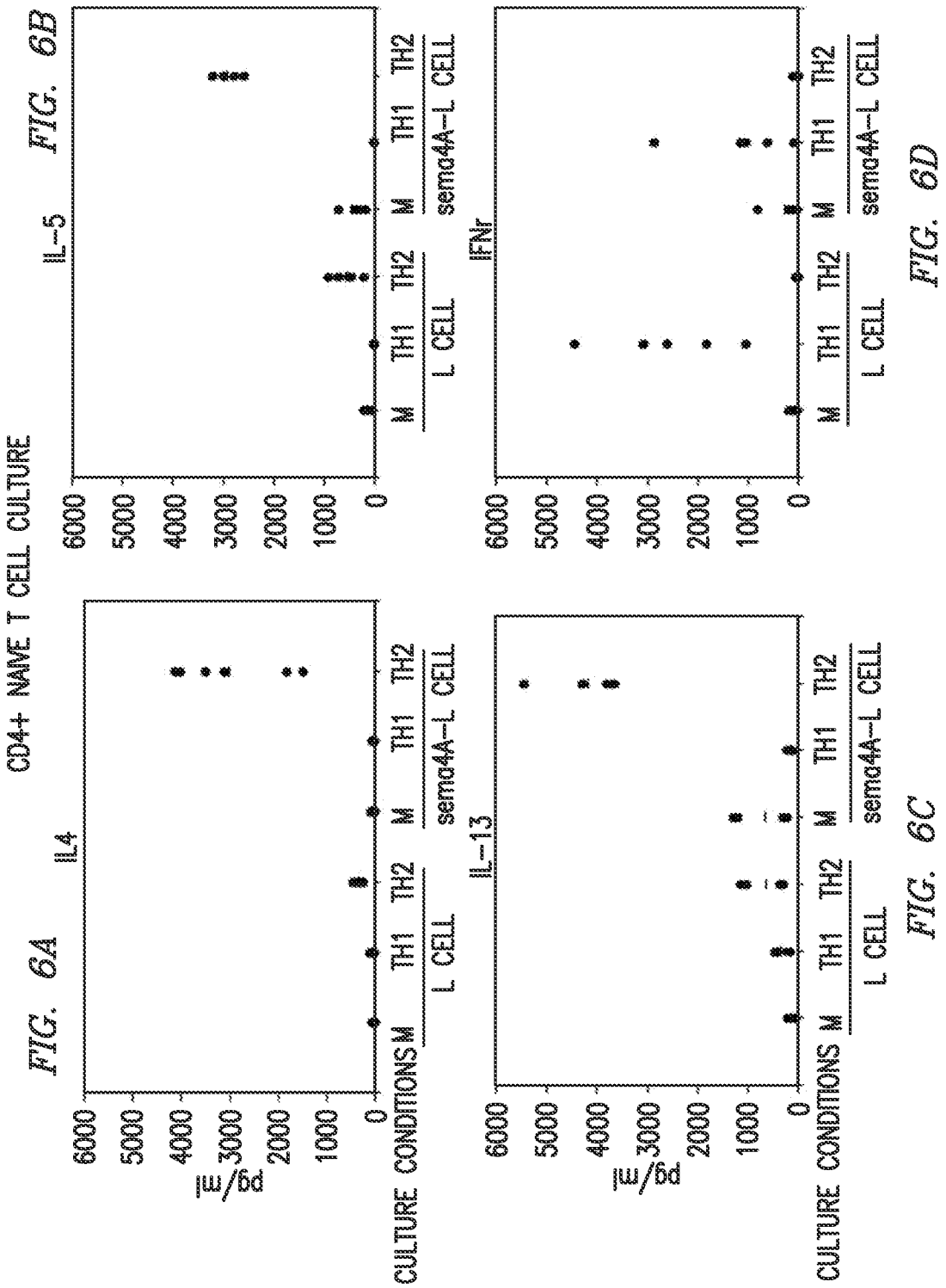


FIG. 6A

FIG. 6B

FIG. 6C

FIG. 6D

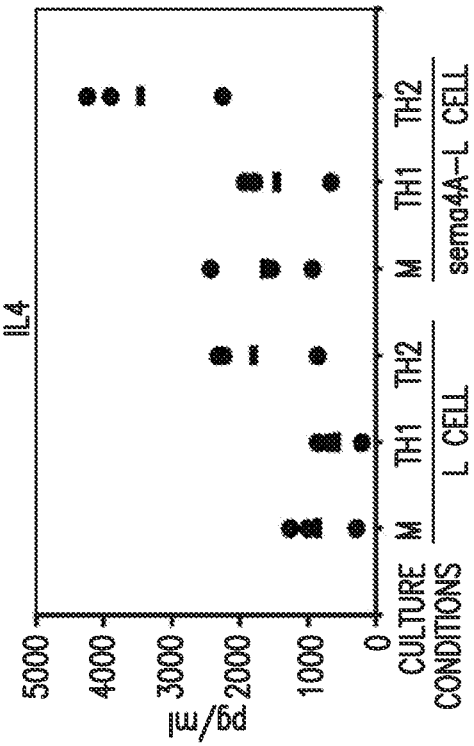


FIG. 7A

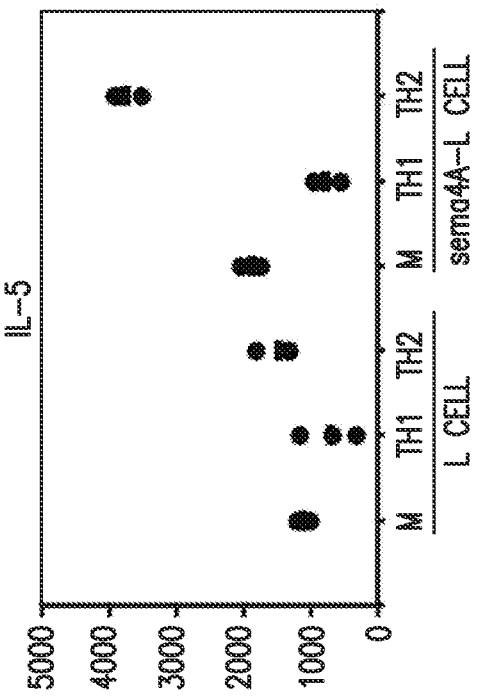


FIG. 7B

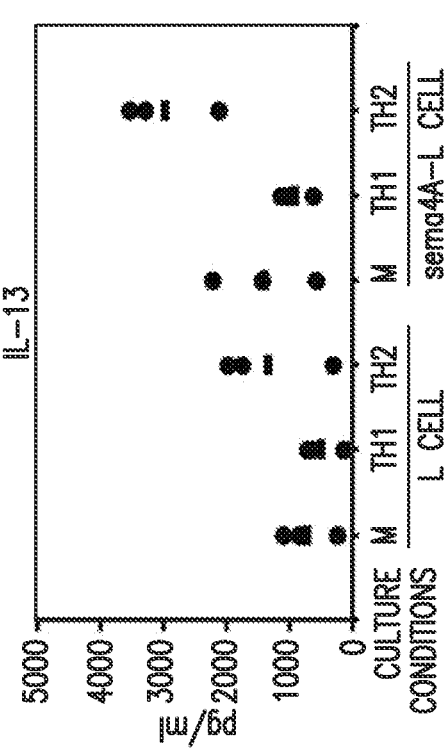


FIG. 7C

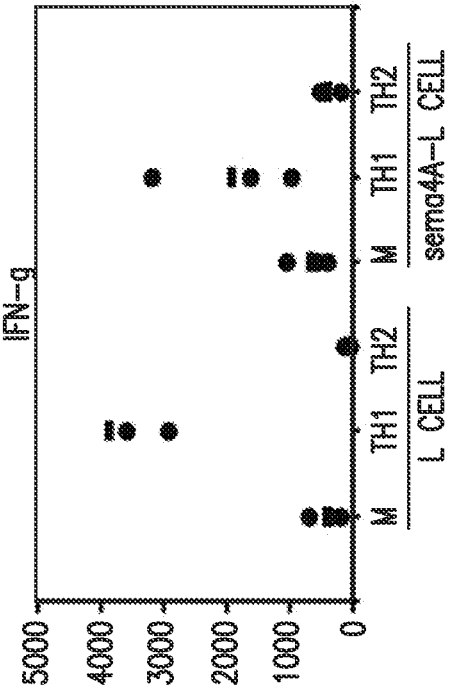


FIG. 7D

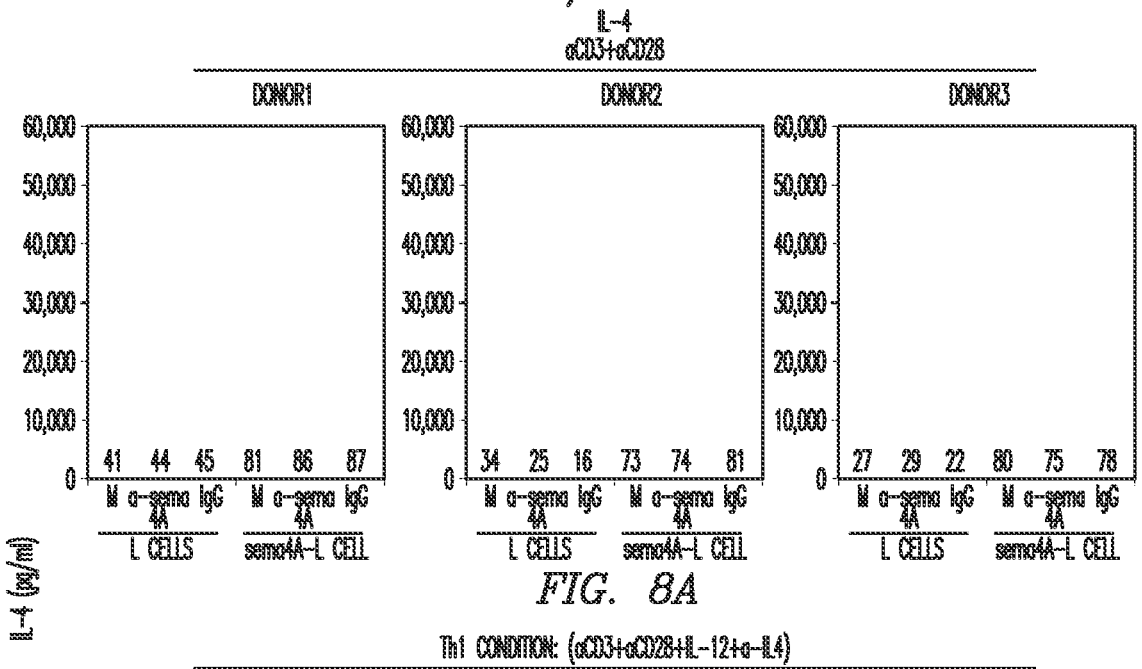


FIG. 8A

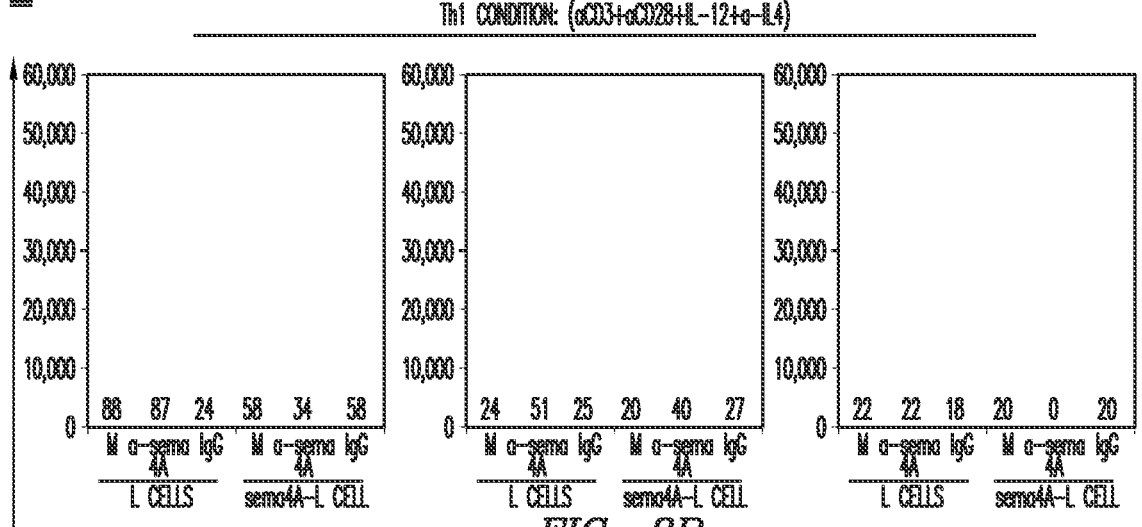


FIG. 8B

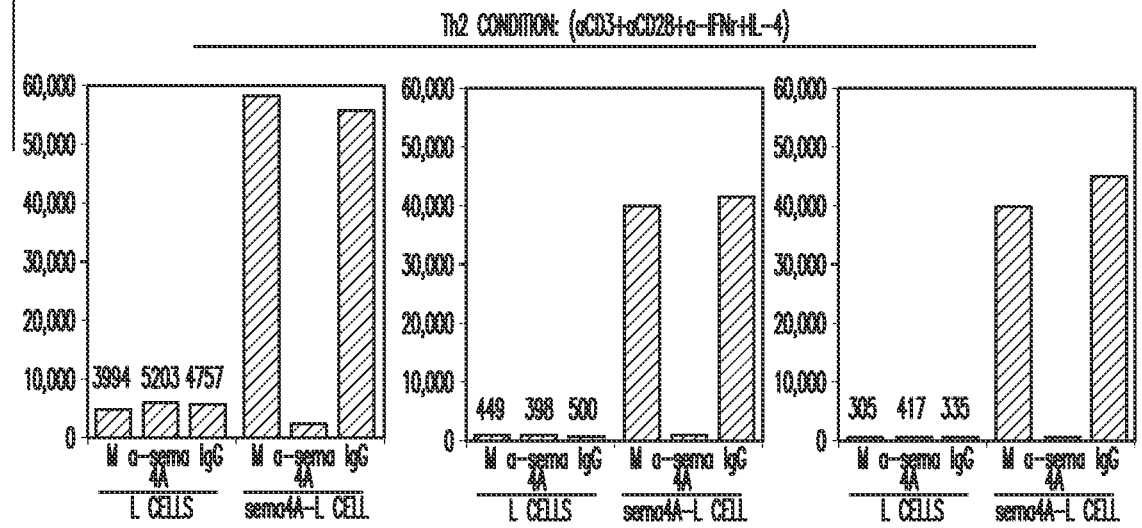


FIG. 8C

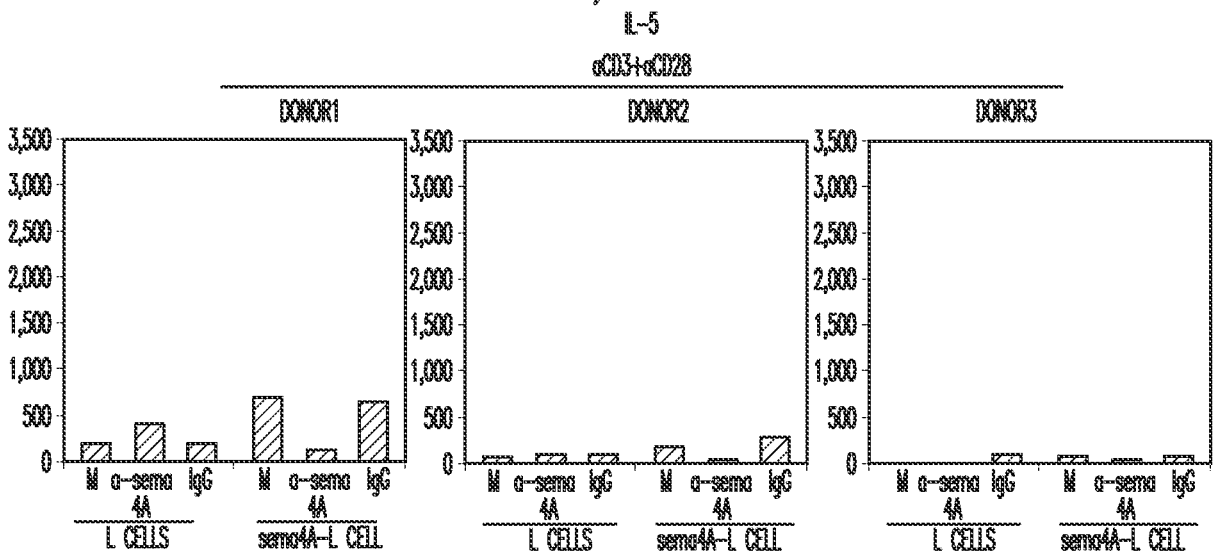


FIG. 8D

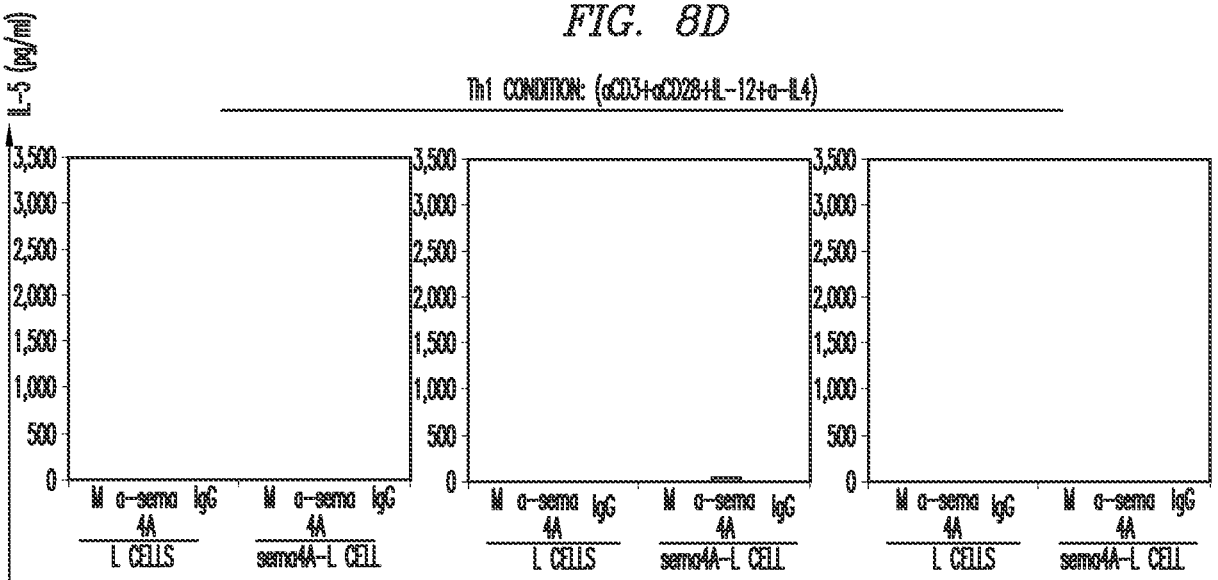


FIG. 8E

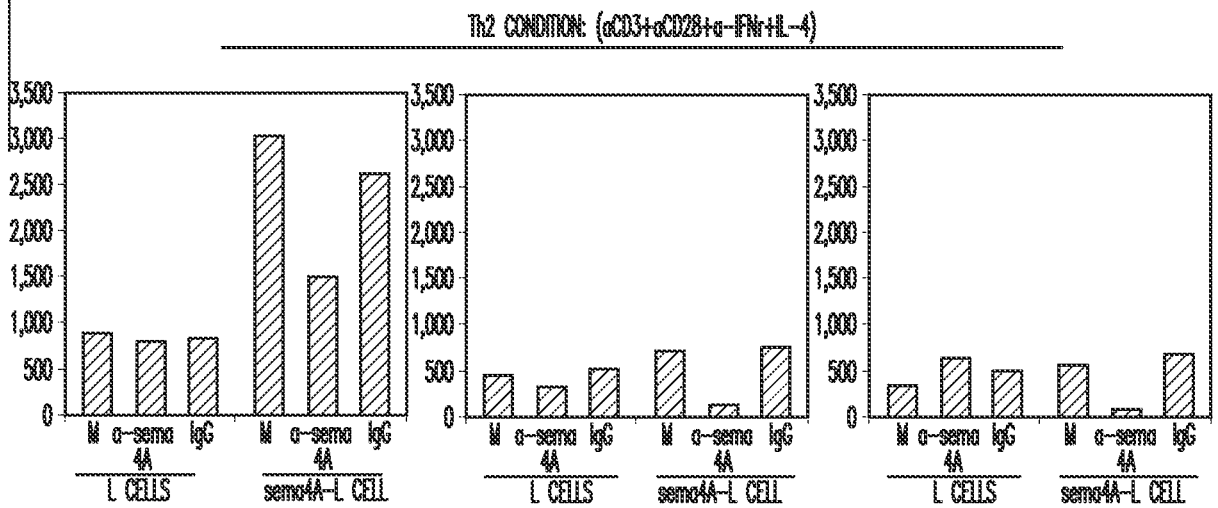


FIG. 8F

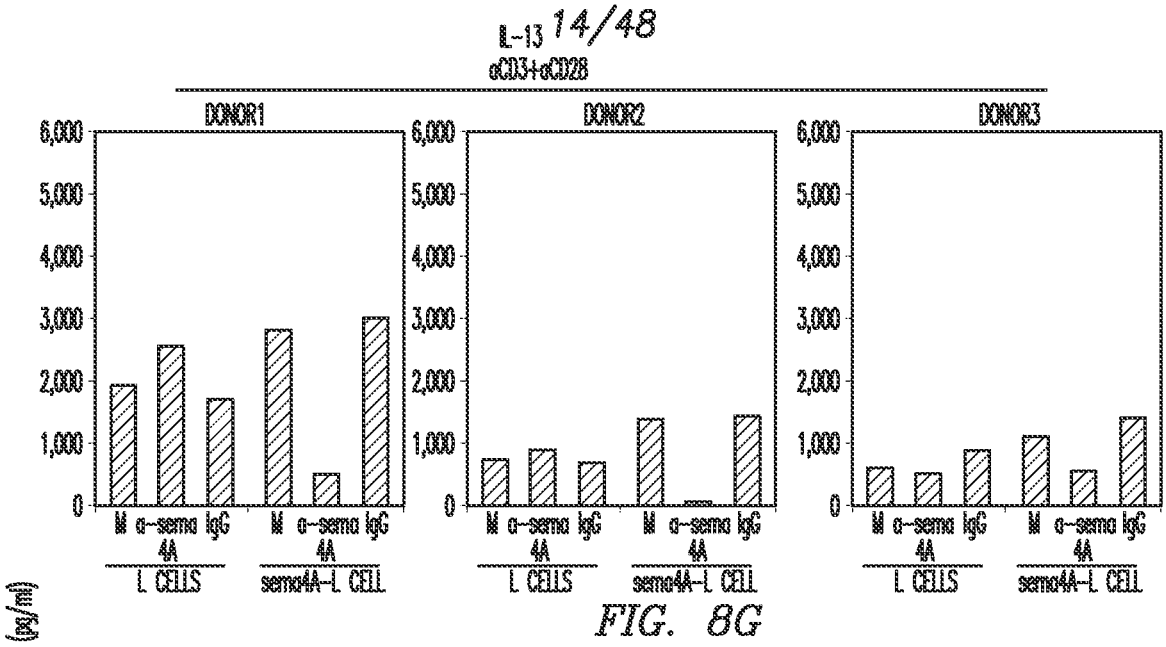


FIG. 8G

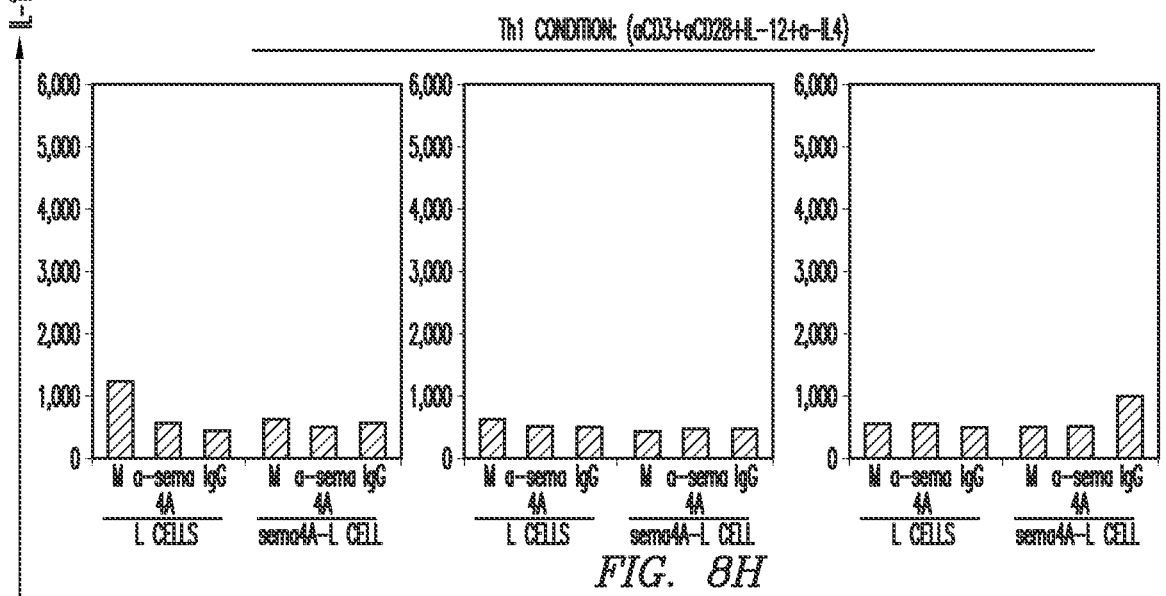


FIG. 8H

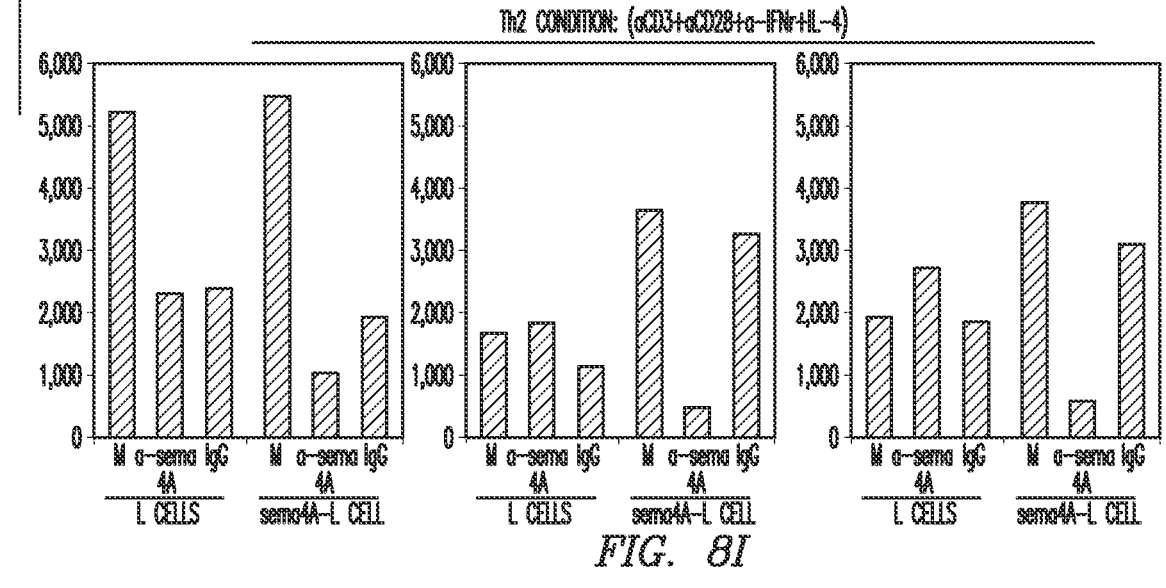


FIG. 8I

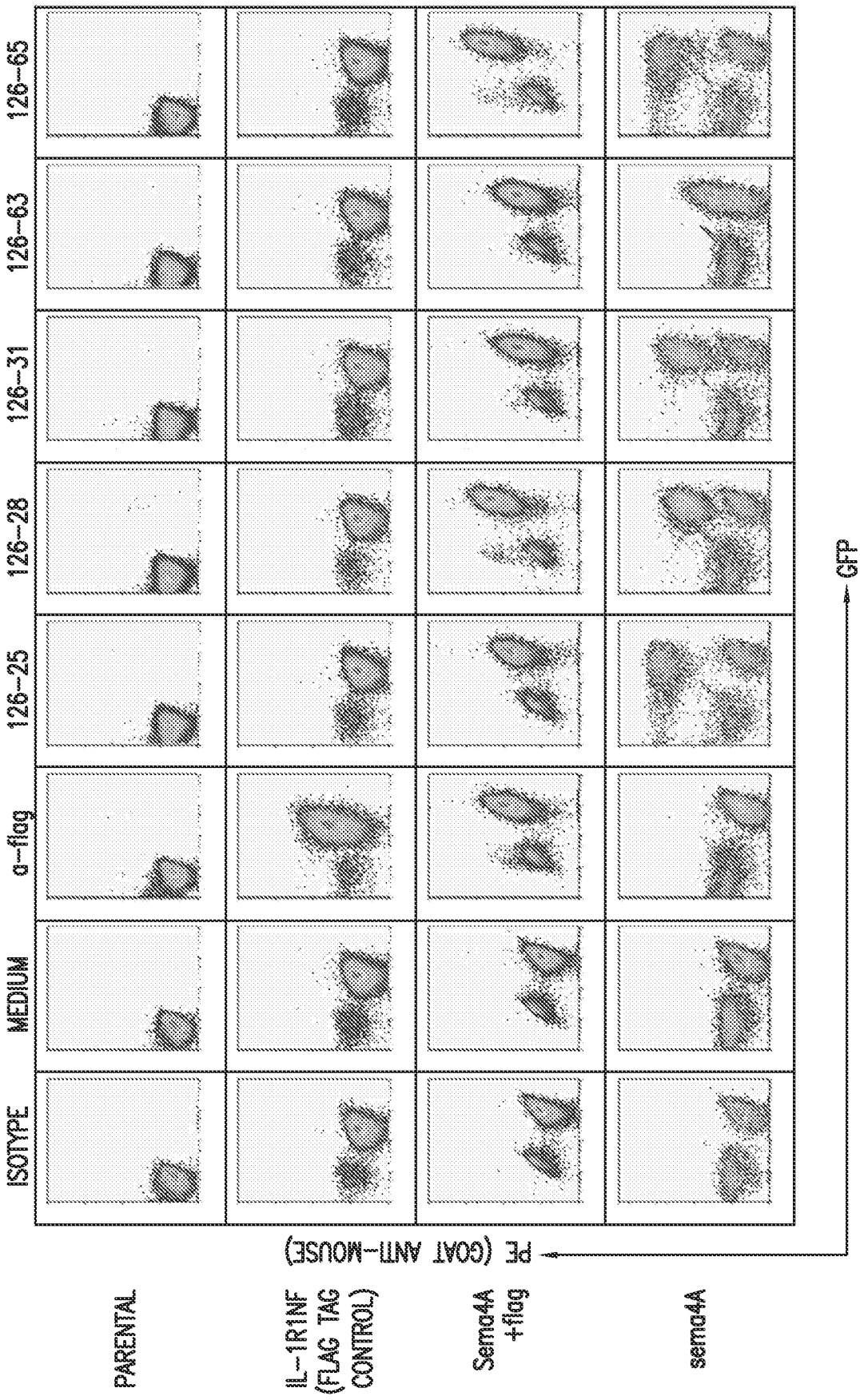

ISOTYPE
MEDIUM
α-flag
126-25
126-28
126-31
126-63
126-65
PARENTAL
IL-1R1NF (FLAG TAG CONTROL)
Sema4A +flag
sema4A
PE (GOAT ANTI-MOUSE)
GFP

FIG. 9

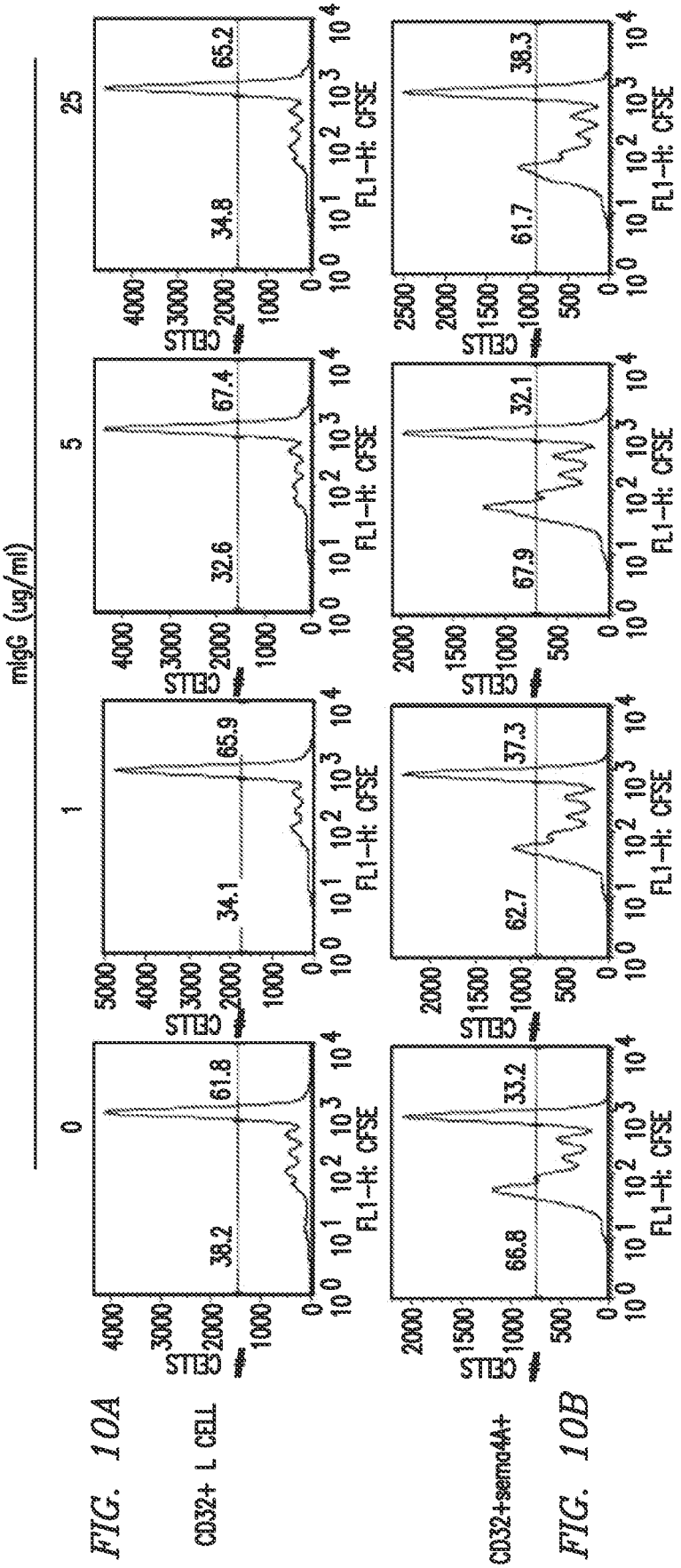


FIG. 10A

FIG. 10B

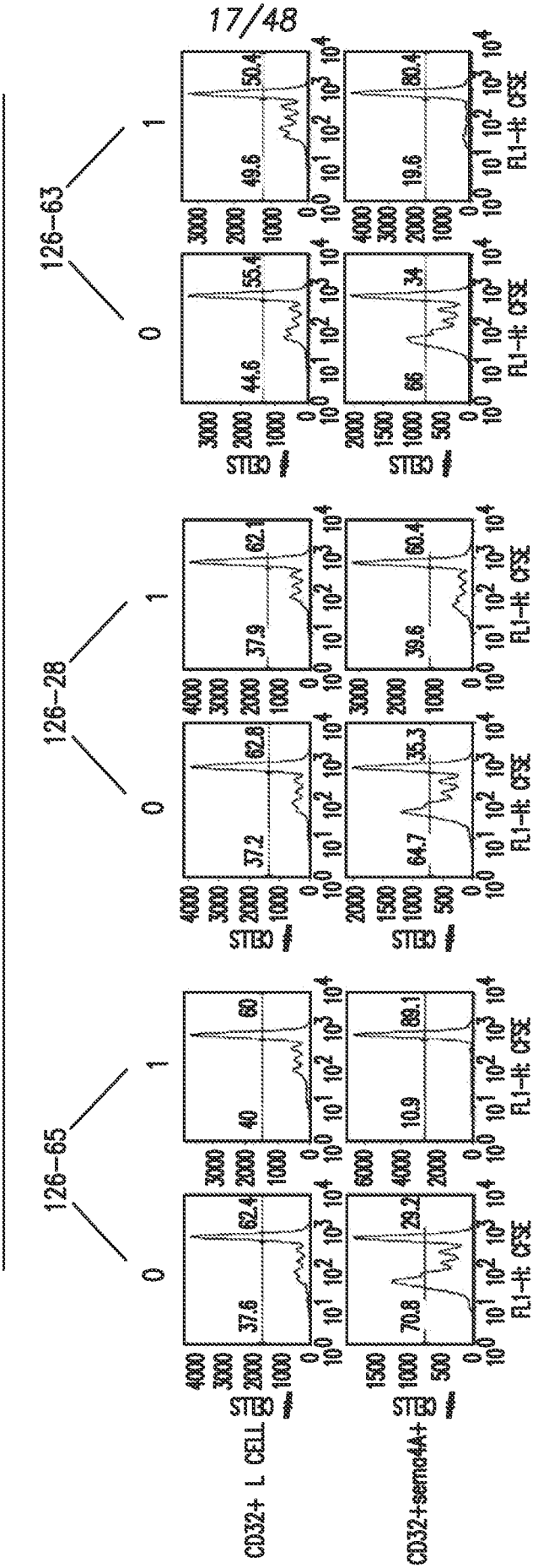


FIG. 10C

FIG. 10D

FIG. 10E

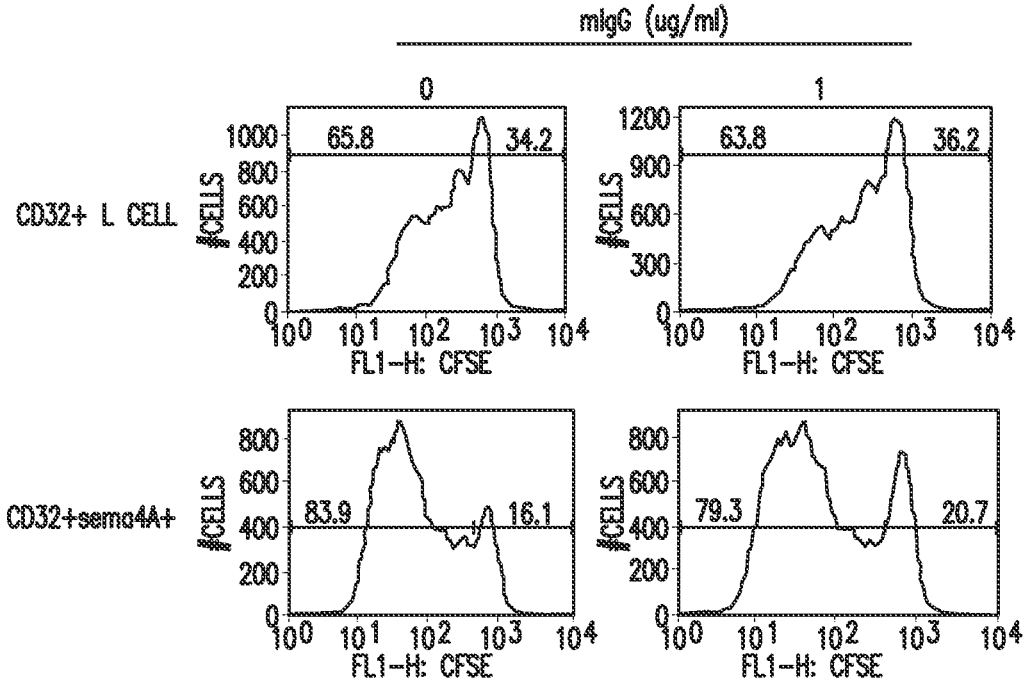


FIG. 11A

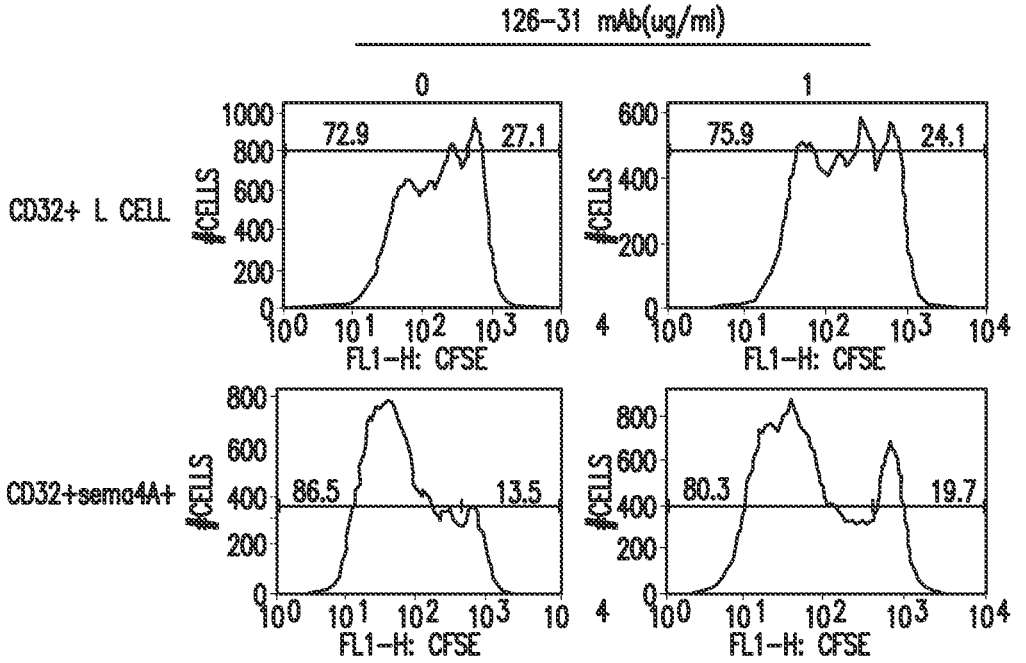


FIG. 11B

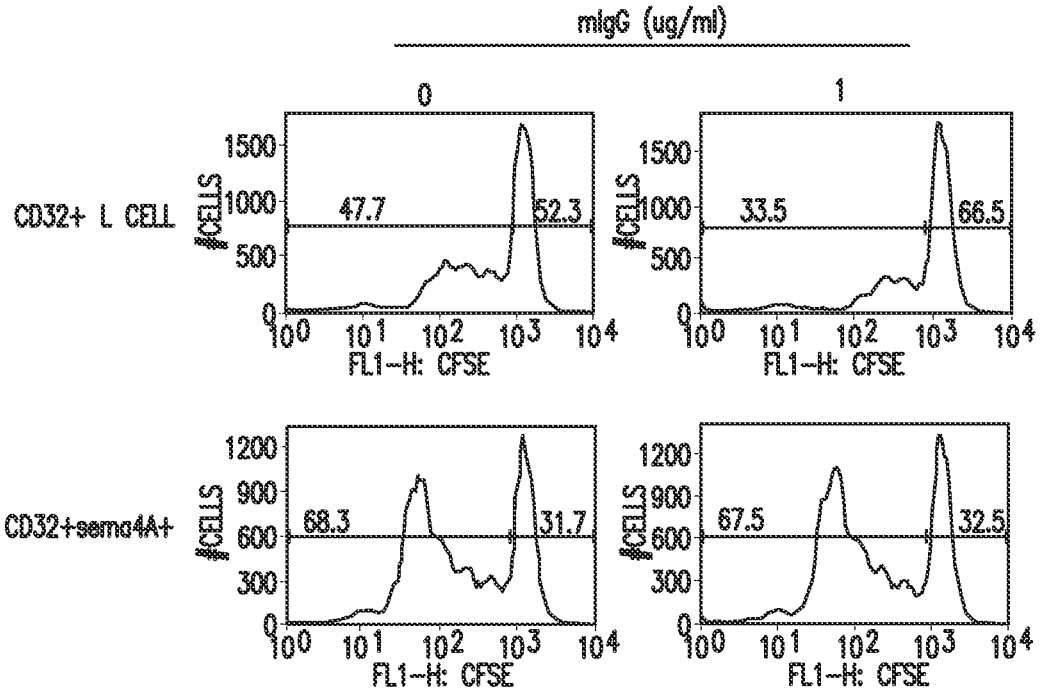


FIG. 11C

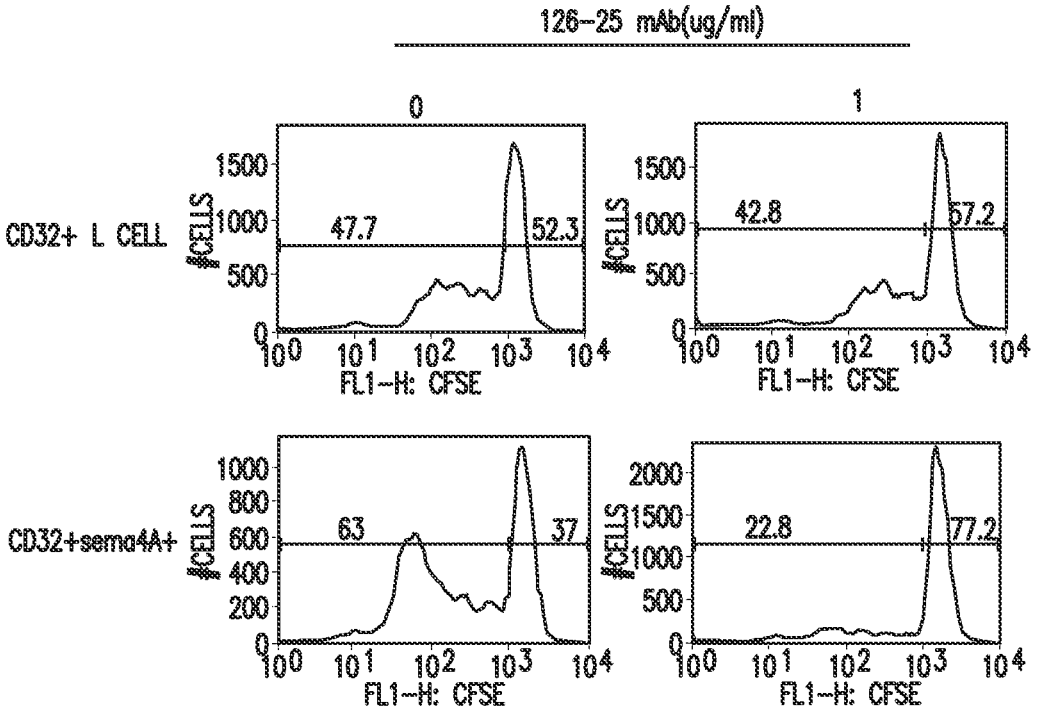


FIG. 11D

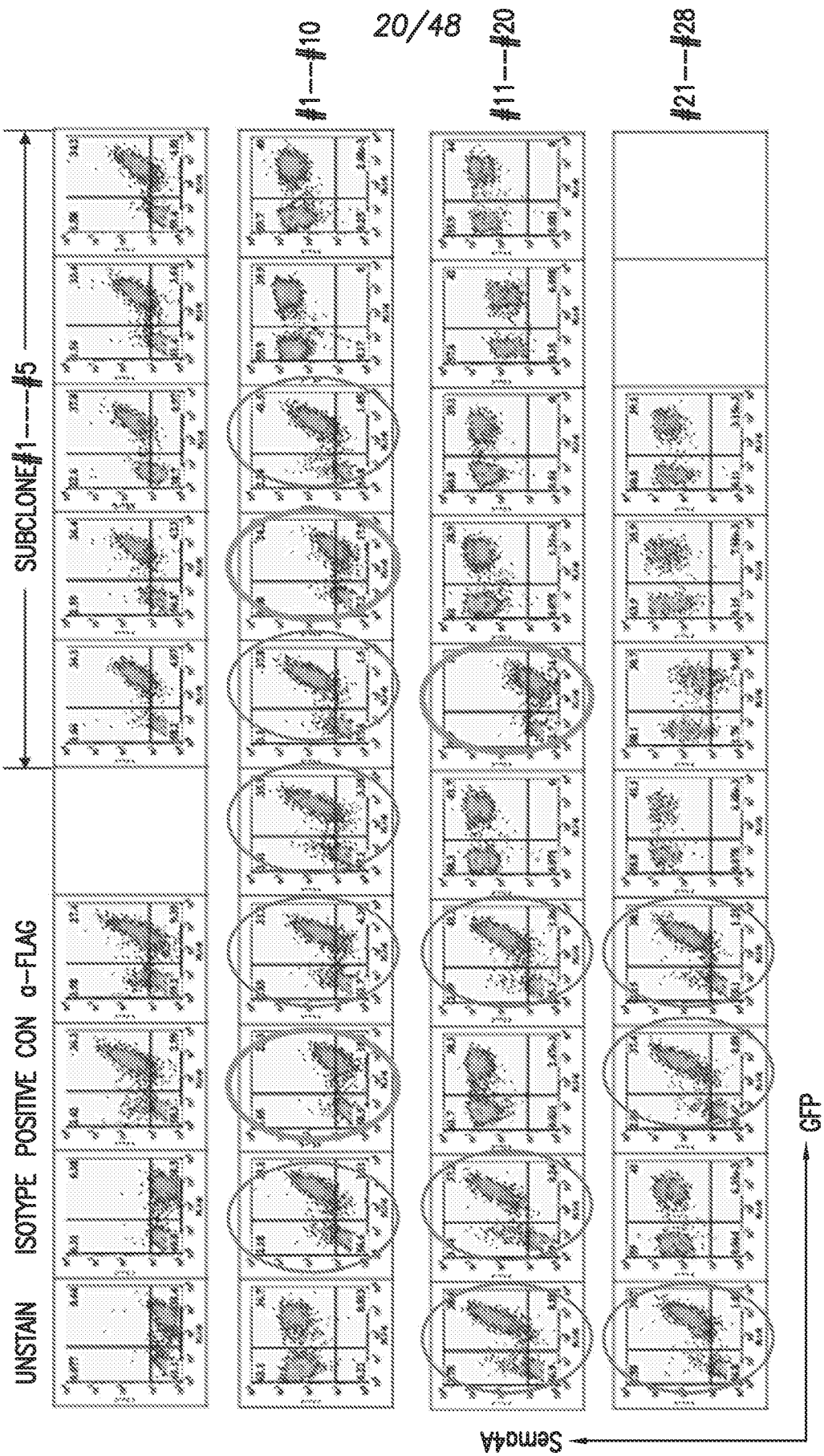

UNSTAIN
ISOTYPE
POSITIVE CON α-FLAG
SUBCLONE #1—#5
#1—#10
#11—#20
#21—#28
Sema4A
GFP

FIG. 12

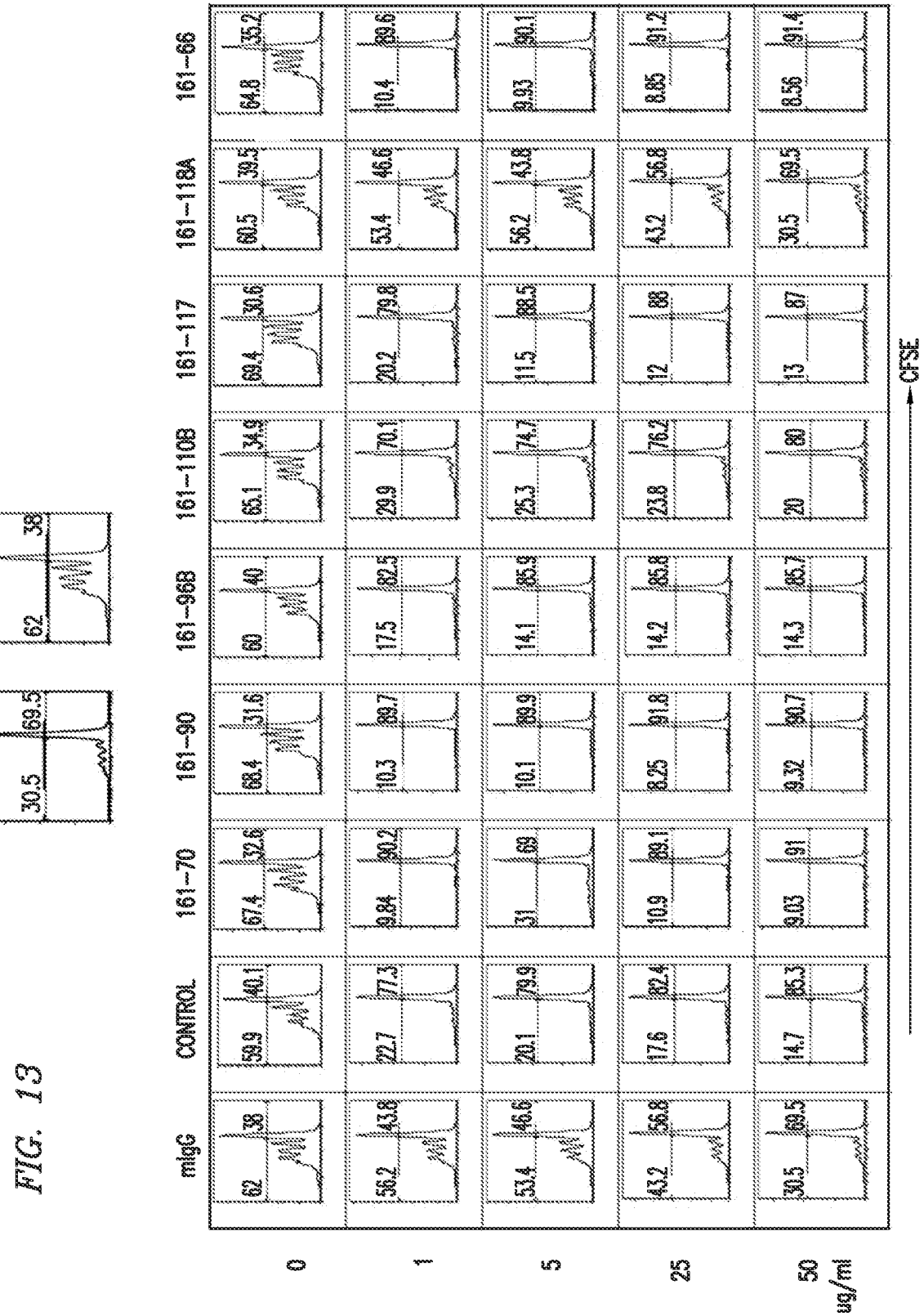
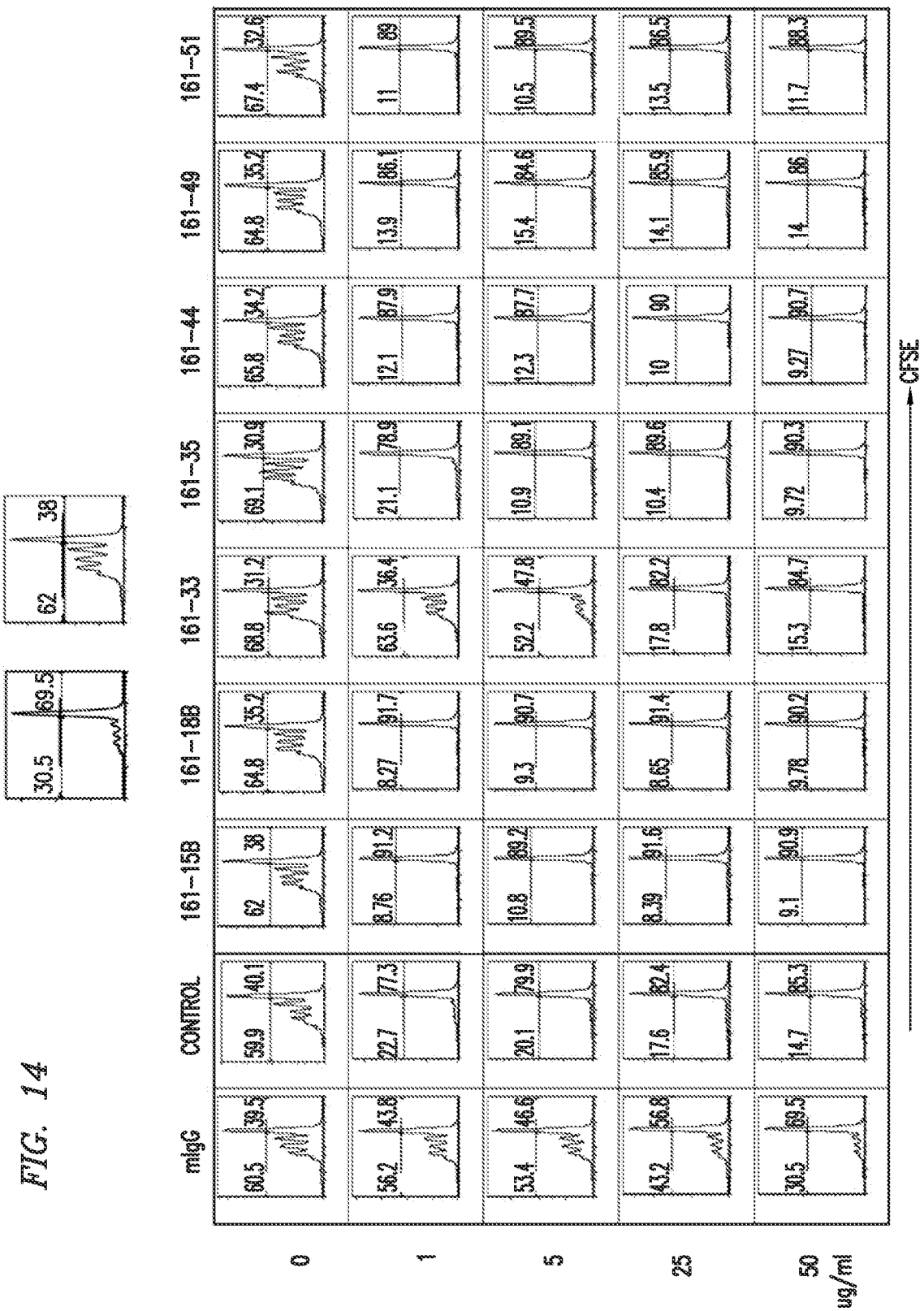

L CELL
30.5
69.5
sema4L CELL
62
38
migG
CONTROL
161-70
161-90
161-96B
161-110B
161-117
161-118A
161-66
0
1
5
25
50
ug/ml
CFSE

FIG. 13

FIG. 14


L CELL
30.5
69.5
semi+L CELL
62
38
migC
CONTROL
161--15B
161--18B
161--33
161--35
161--44
161--49
161--51
0
1
5
25
50
ug/ml
CFSE

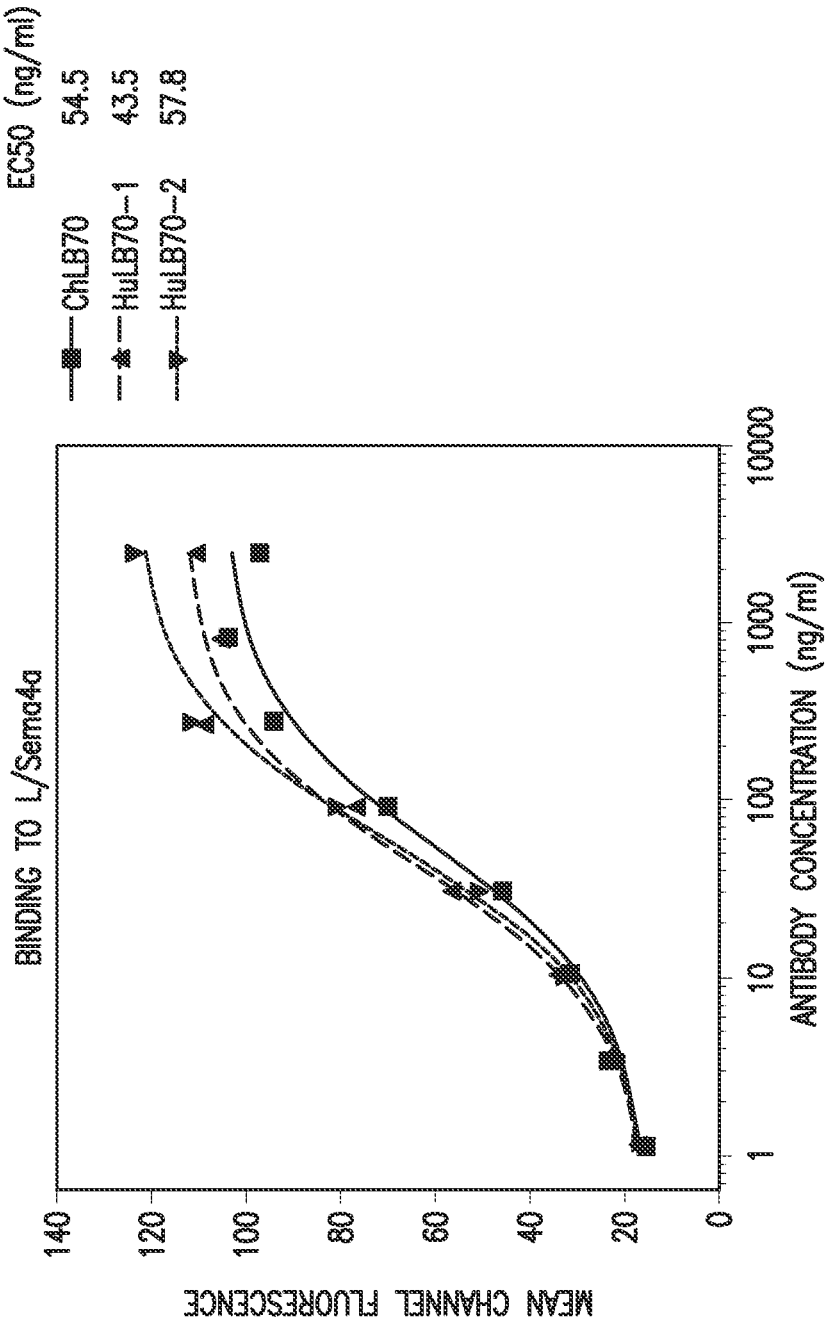

EC50 (ng/ml)
ChLB70 54.5
HuLB70-1 43.5
HuLB70-2 57.8
BINDING TO L/Sema4a
MEAN CHANNEL FLUORESCENCE
0
20
40
60
80
100
120
140
1
10
100
1000
10000
ANTIBODY CONCENTRATION (ng/ml)

FIG. 15

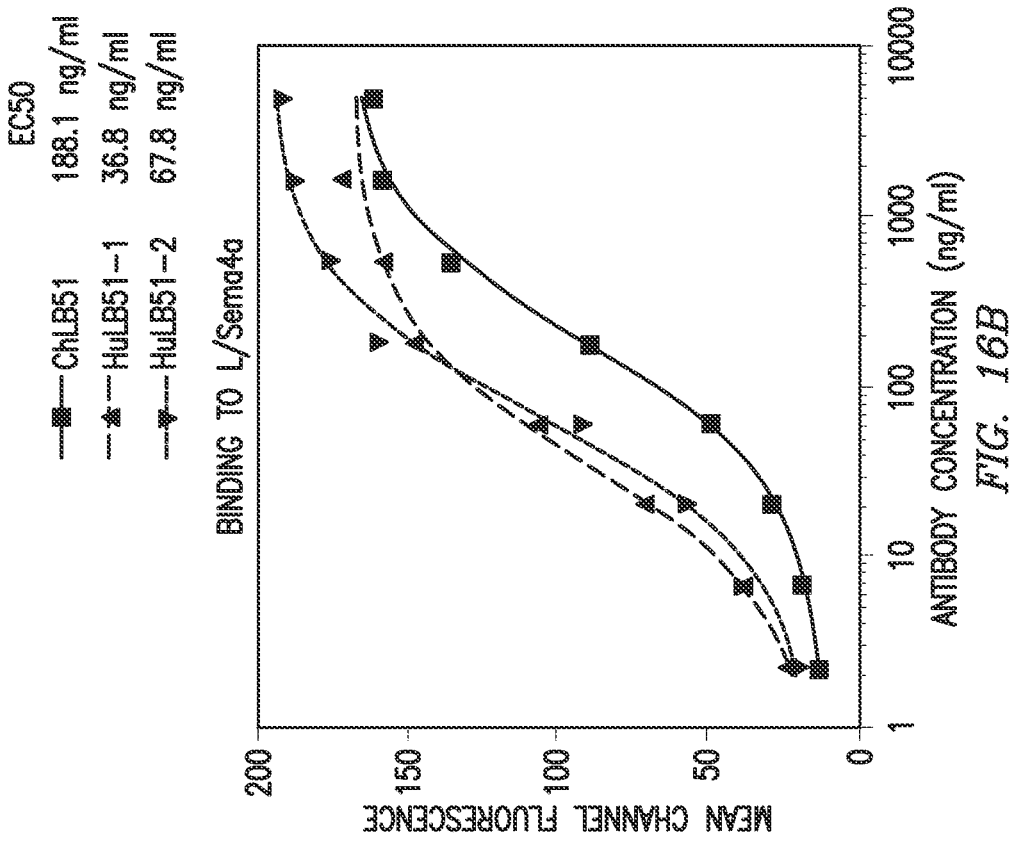


FIG. 16B

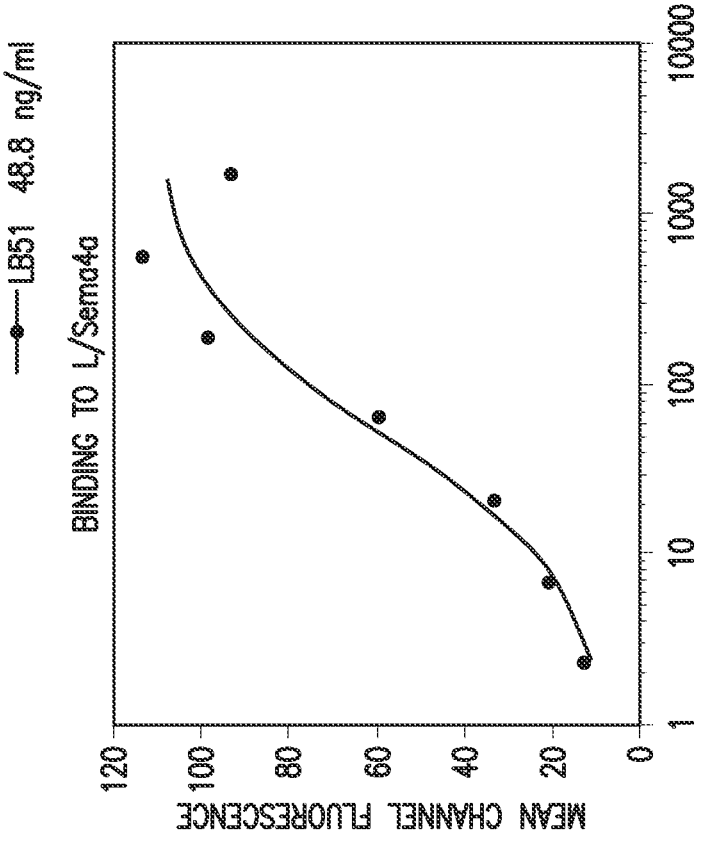


FIG. 16A

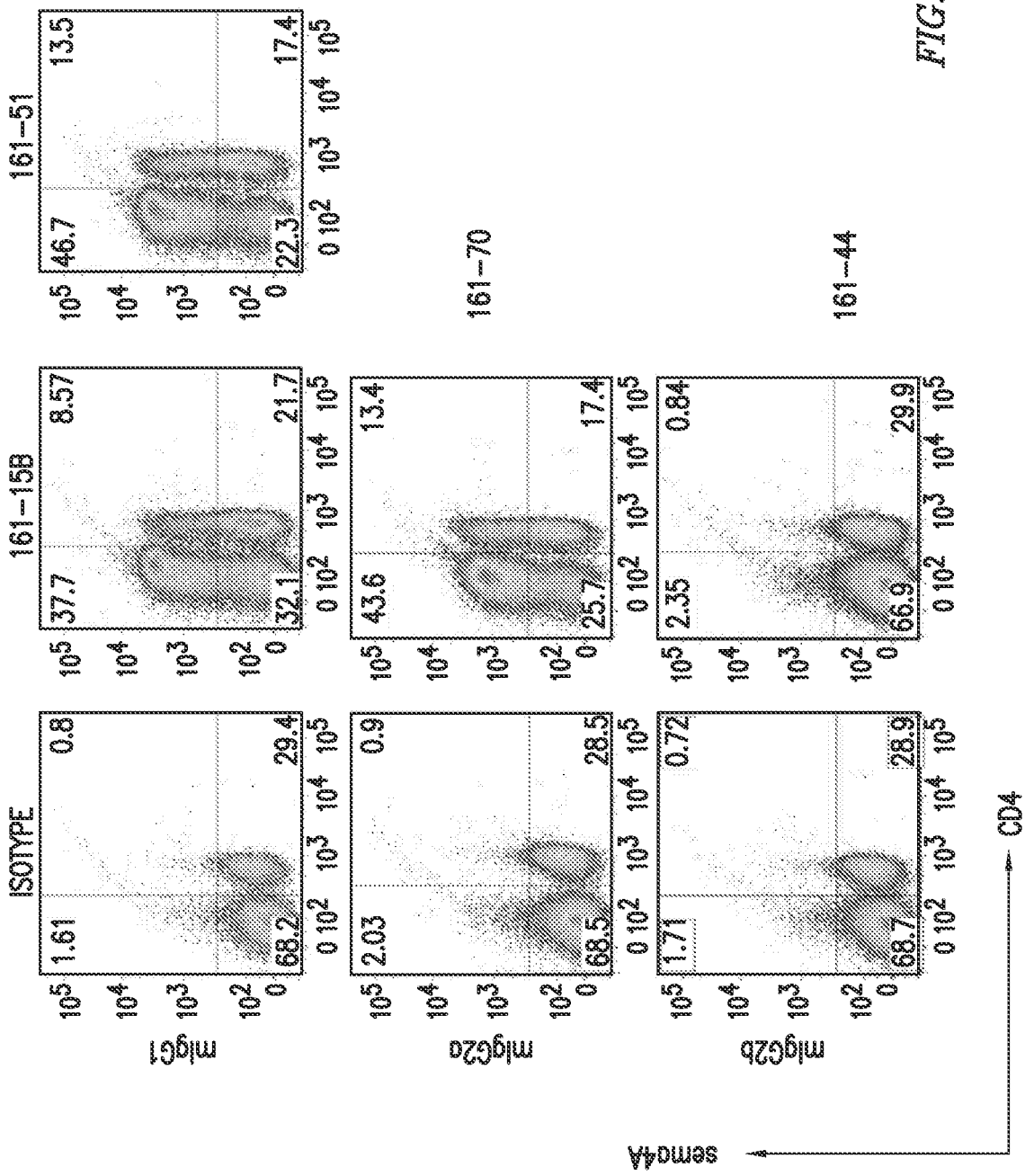

ISOTYPE
161-15B
161-70
161-44
161-51
mIgG1
mIgG2a
mIgG2b
sema4A
CD4
1.61
0.8
29.4
68.2
37.7
8.57
21.7
32.1
43.6
13.4
17.4
25.7
2.35
0.84
29.9
66.9
46.7
13.5
17.4
22.3
2.03
0.9
28.5
68.5
1.71
0.72
28.9
68.7

FIG. 17A

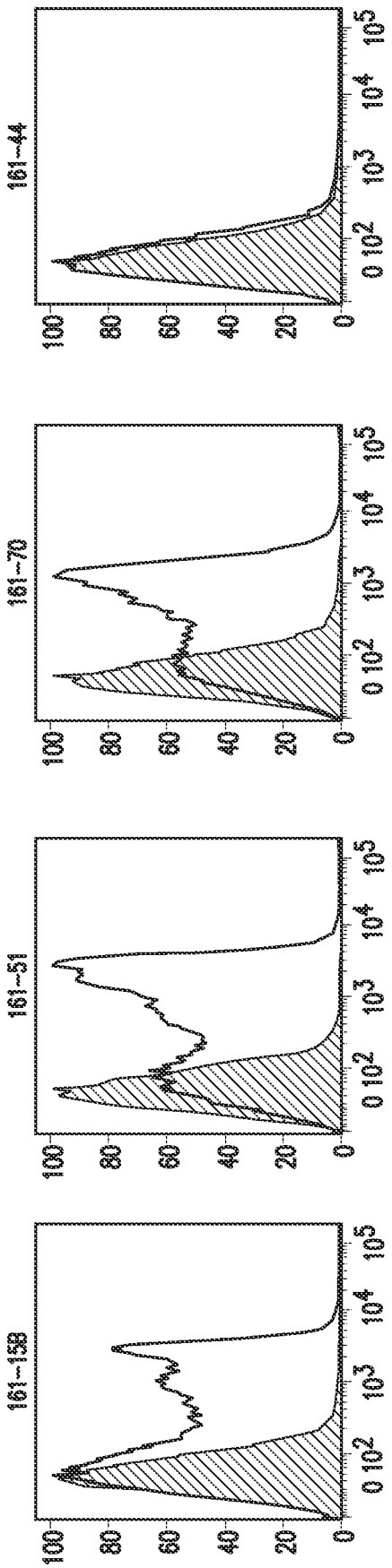

161-158
161-51
161-70
161-44
sema4A
0
20
40
60
80
100
0 10^2 10^3 10^4 10^5

FIG. 17B

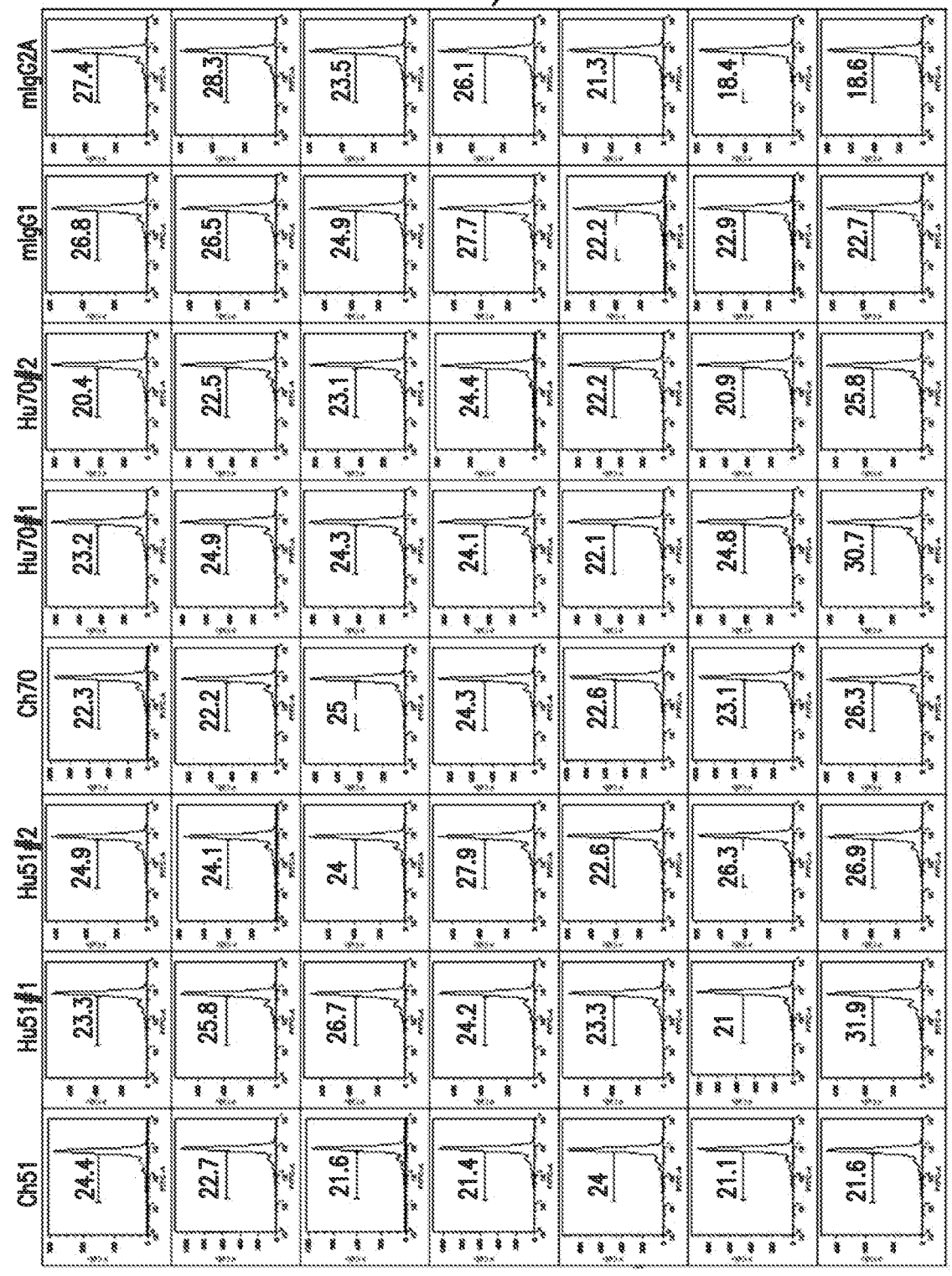

L CELL CULTURE
0
10ng/ml
25ng/ml
50ng/ml
200ng/ml
1ug/ml
5ug/ml
Ch51
Hu51#1
Hu51#2
Ch70
Hu70#1
Hu70#2
mIg61
mIg62A
24.4
23.3
24.9
22.3
23.2
20.4
26.8
27.4
22.7
25.8
24.1
22.2
24.9
22.5
26.5
28.3
21.6
26.7
24
25
24.3
23.1
24.9
23.5
21.4
24.2
27.9
24.3
24.1
24.4
27.7
26.1
24
23.3
22.6
22.6
22.1
22.2
22.2
21.3
21.1
21
26.3
23.1
24.8
20.9
22.9
18.4
21.6
31.9
26.9
26.3
30.7
25.8
22.7
18.6
CFSE

FIG. 18A

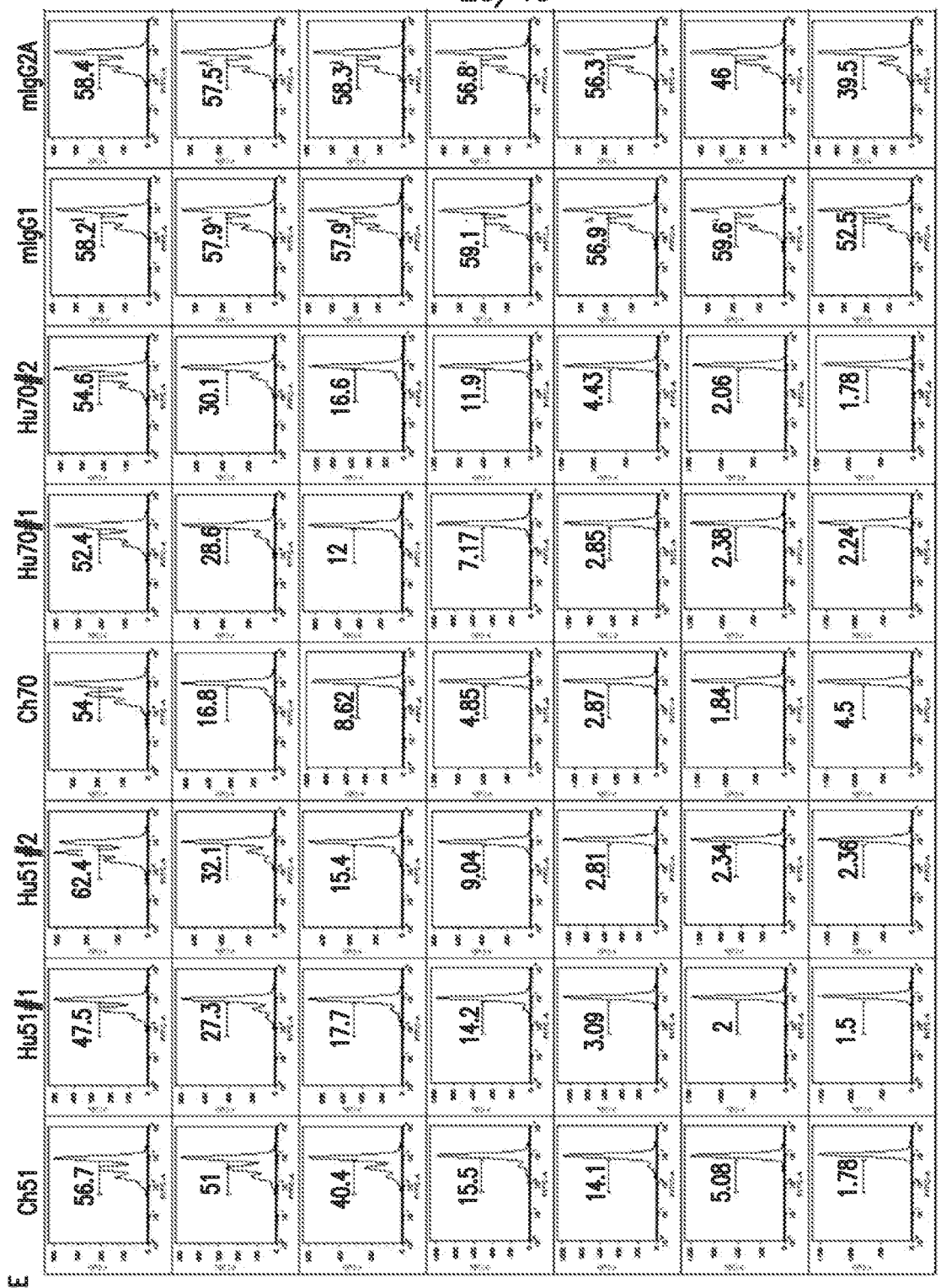

Sema4L CELL CULTURE
Ch51
Hu51#1
Hu51#2
Ch70
Hu70#1
Hu70#2
mIgG1
mIgG2A
0
10ng/ml
25ng/ml
50ng/ml
200ng/ml
1ug/ml
5ug/ml
CFSE

FIG. 18B

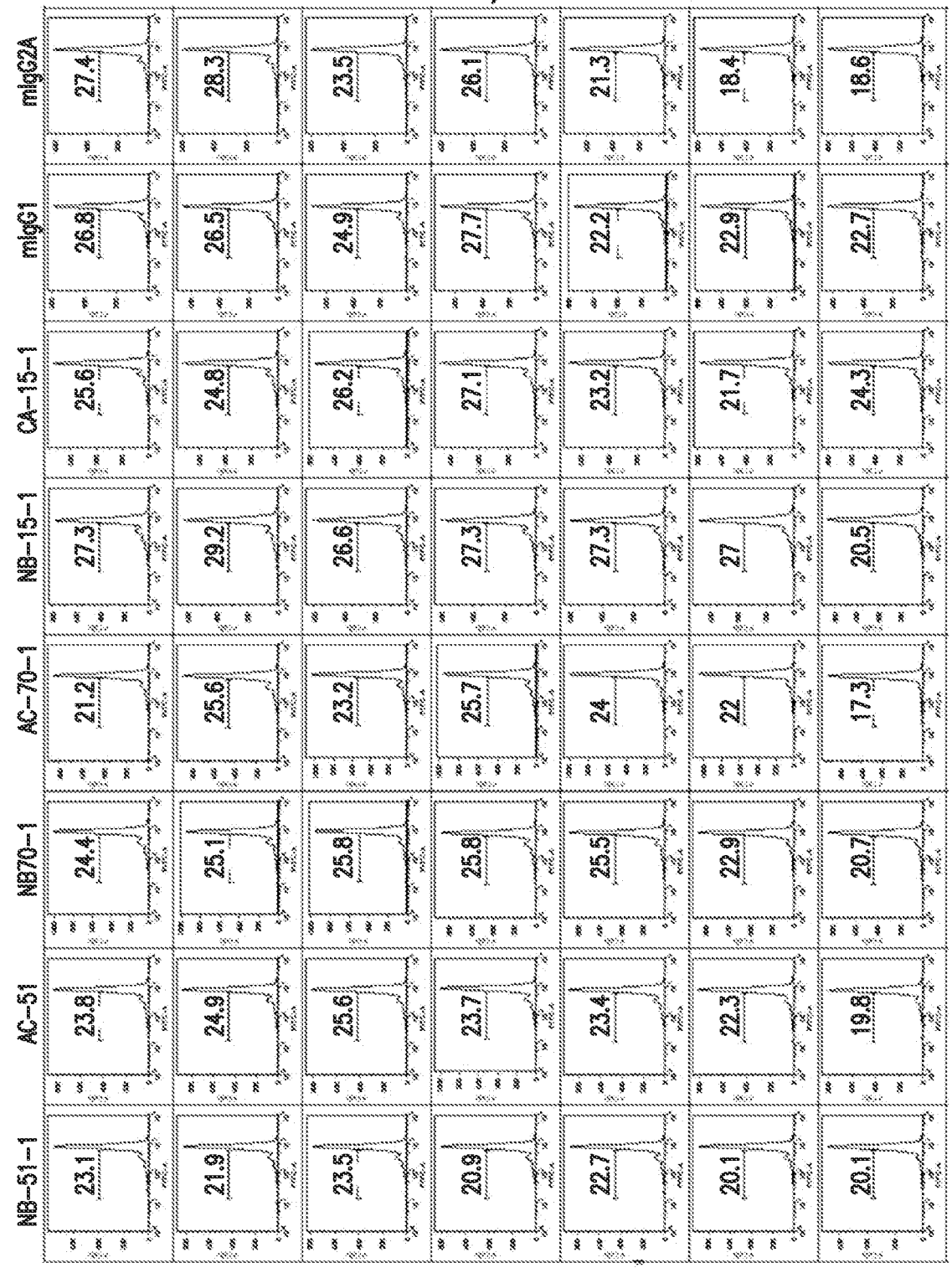

L CELL CULTURE
NB-51-1
AC-51
NB70-1
AC-70-1
NB-15-1
CA-15-1
mIgG1
mIgG2A
0
10ng/ml
25ng/ml
50ng/ml
200ng/ml
1ug/ml
5ug/ml
23.1
23.8
24.4
21.2
27.3
25.6
26.8
27.4
21.9
24.9
25.1
25.6
29.2
24.8
26.5
28.3
23.5
25.6
25.8
23.2
26.6
26.2
24.9
23.5
20.9
23.7
25.8
25.7
27.3
27.1
27.7
26.1
22.7
23.4
25.5
24
27.3
23.2
22.2
21.3
20.1
22.3
22.9
22
27
21.7
22.9
18.4
20.1
19.8
20.7
17.3
20.5
24.3
22.7
18.6
CFSE

FIG. 18C

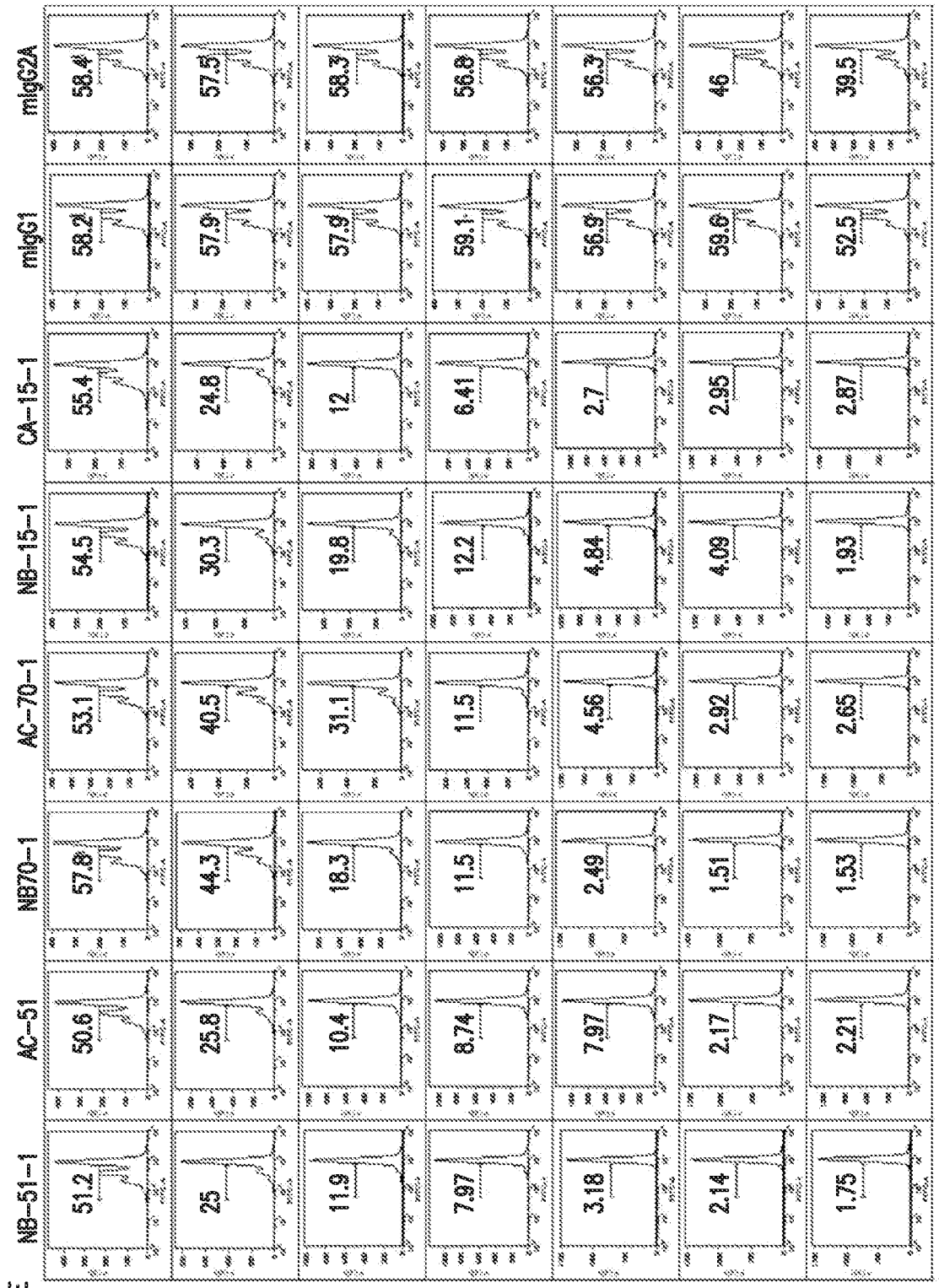

Sema4L CELL CULTURE
NB-51-1
AC-51
NB70-1
AC-70-1
NB-15-1
CA-15-1
mIgG1
mIgG2A
0
10ng/ml
25ng/ml
50ng/ml
200ng/ml
1ug/ml
5ug/ml
51.2
50.6
57.8
53.1
54.5
55.4
58.2
58.4
25
25.8
44.3
40.5
30.3
24.8
57.9
57.5
11.9
10.4
18.3
31.1
19.8
12
57.9
58.3
7.97
8.74
11.5
11.5
12.2
6.41
59.1
56.8
3.18
7.97
2.49
4.56
4.84
2.7
56.9
56.3
2.14
2.17
1.51
2.92
4.09
2.95
59.6
46
1.75
2.21
1.53
2.65
1.93
2.87
52.5
39.5
CFSE

FIG. 18D

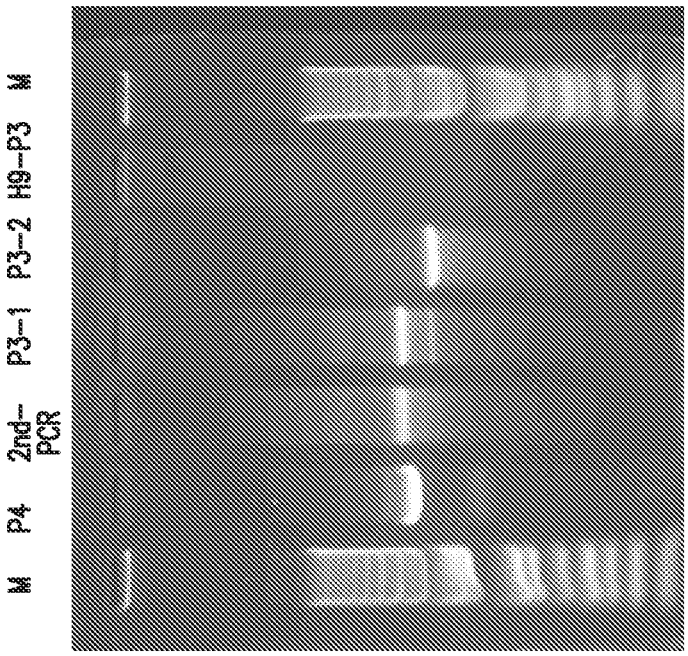


FIG. 19B

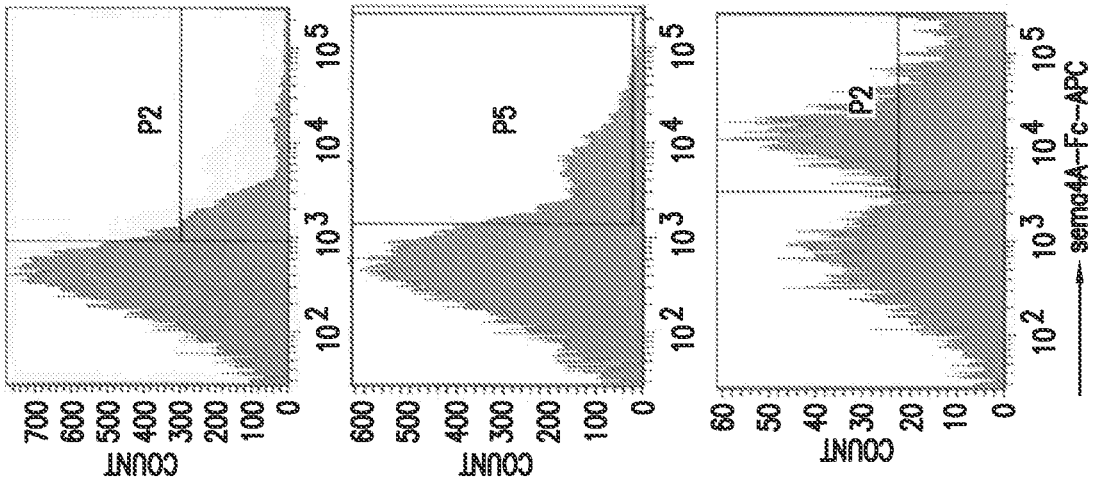


FIG. 19A

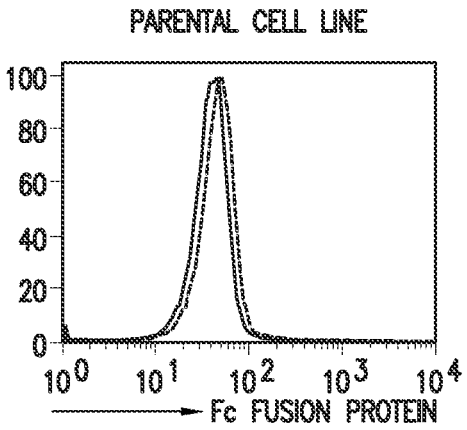


FIG. 20A

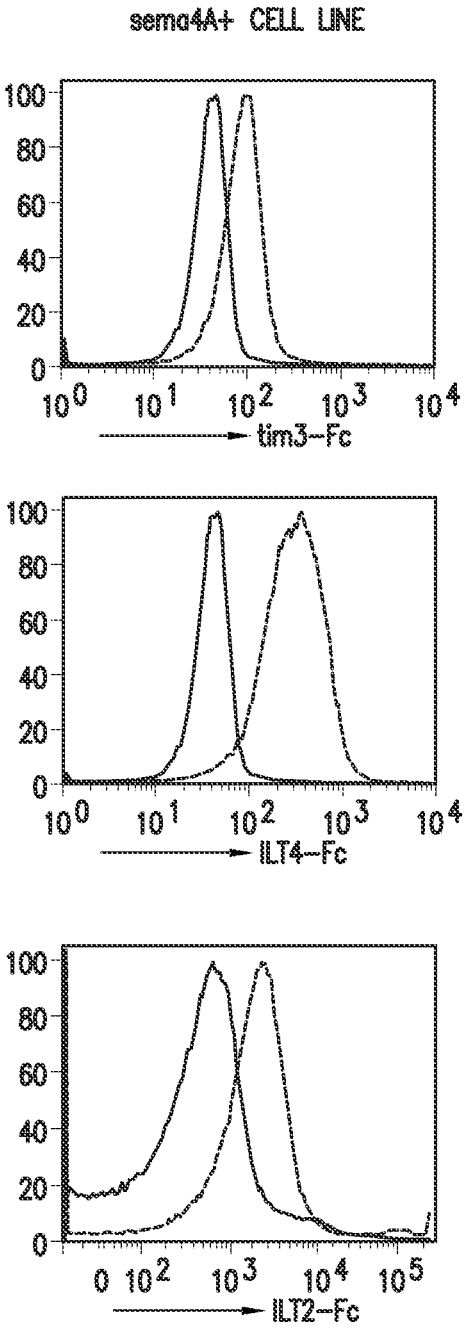


FIG. 20B

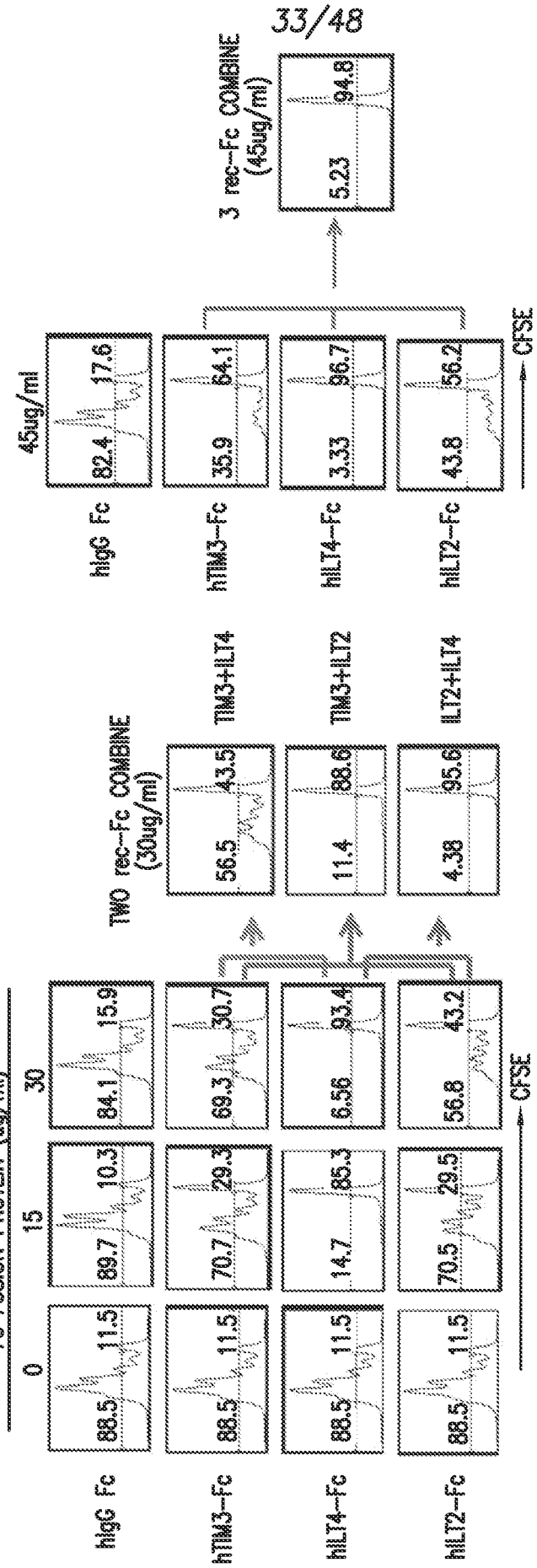

Fc FUSION PROTEIN (ug/ml)
0
15
30
hIgG Fc
hTIM3-Fc
hILT4-Fc
hILT2-Fc
88.5
11.5
89.7
10.3
84.1
15.9
70.7
29.3
69.3
30.7
14.7
85.3
6.56
93.4
70.5
29.5
56.8
43.2
CFSE
TWO rec-Fc COMBINE (30ug/ml)
TIM3+ILT4
TIM3+ILT2
ILT2+ILT4
56.5
43.5
11.4
88.6
4.38
95.6
45ug/ml
82.4
17.6
35.9
64.1
3.33
96.7
43.8
56.2
3 rec-Fc COMBINE (45ug/ml)
5.23
94.8

FIG. 21A

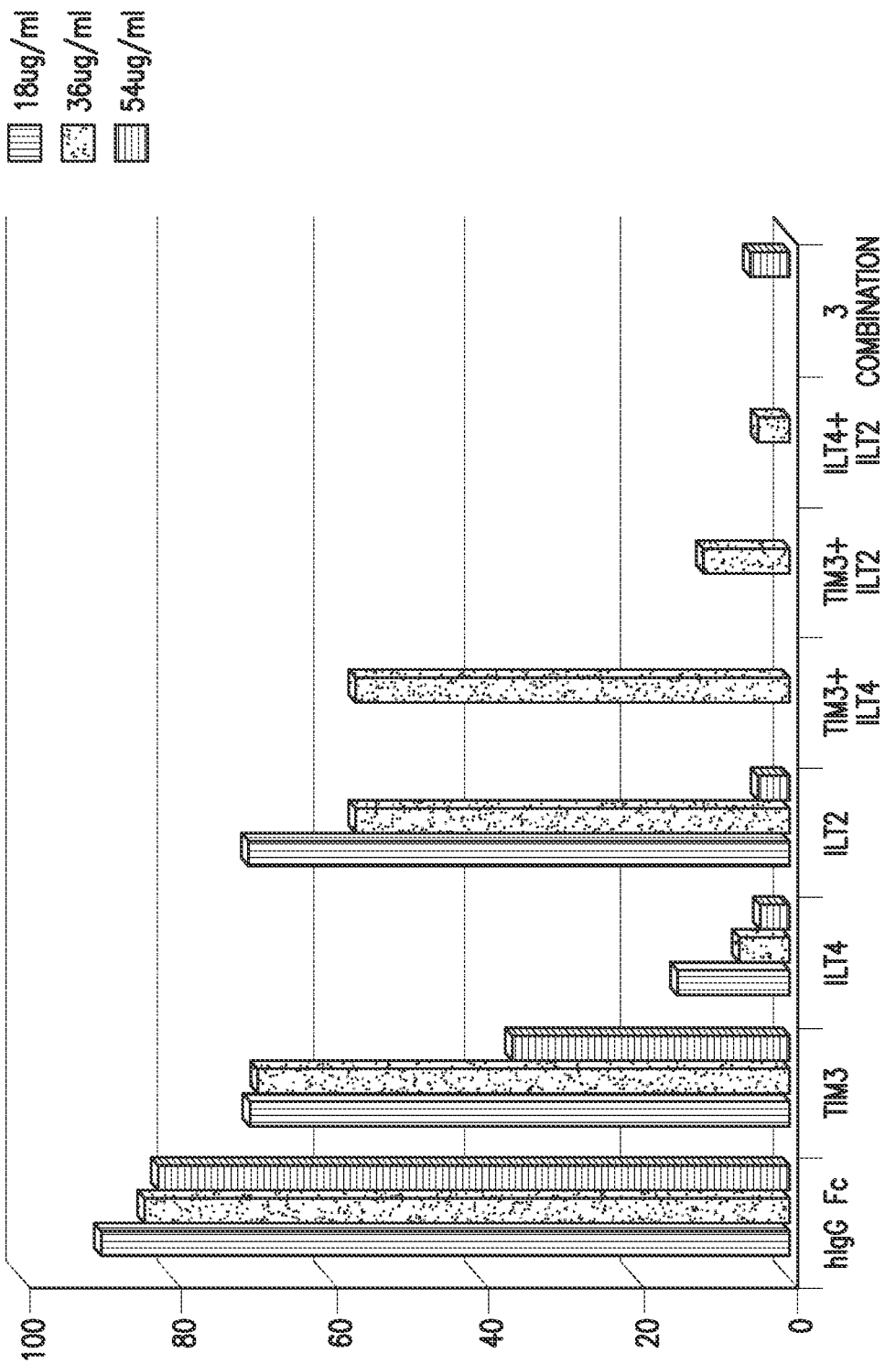

18ug/ml
36ug/ml
54ug/ml
100
80
60
40
20
0
hIgG Fc
TIM3
ILT4
ILT2
TIM3+ ILT4
TIM3+ ILT2
ILT4+ ILT2
3 COMBINATION

FIG. 21B

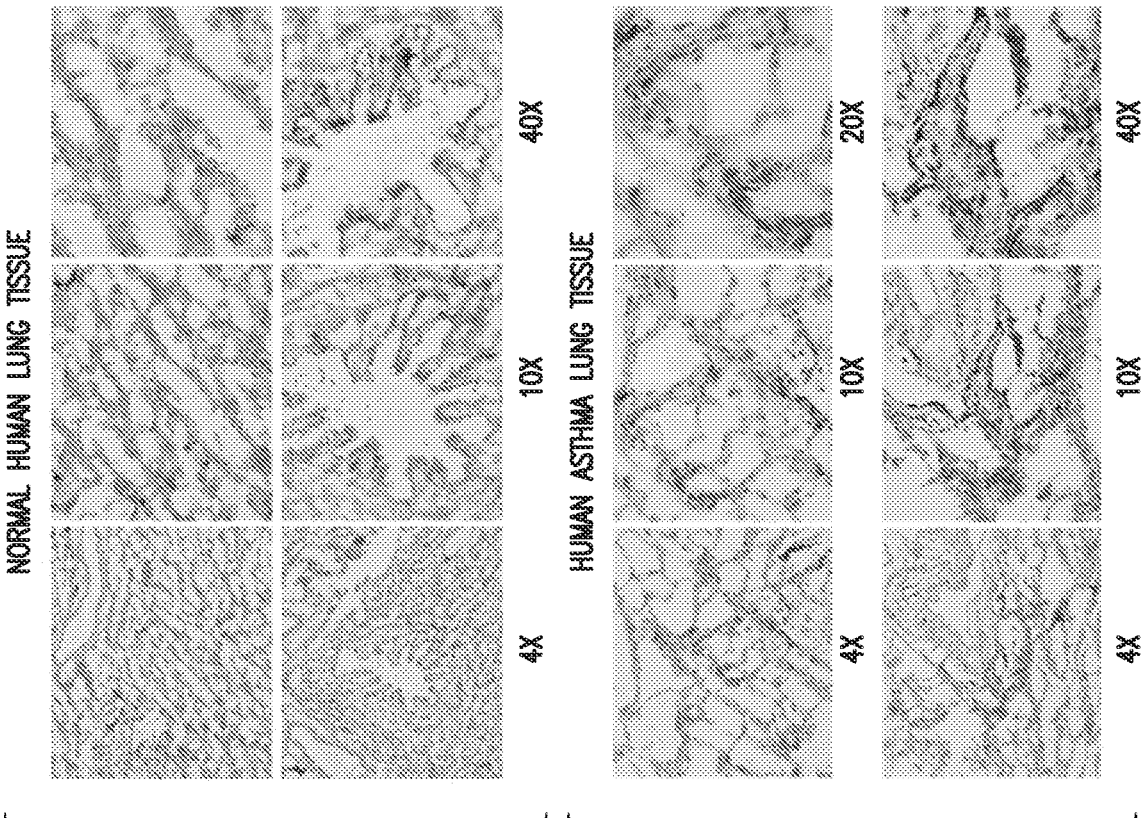


FIG. 22B

FIG. 22C

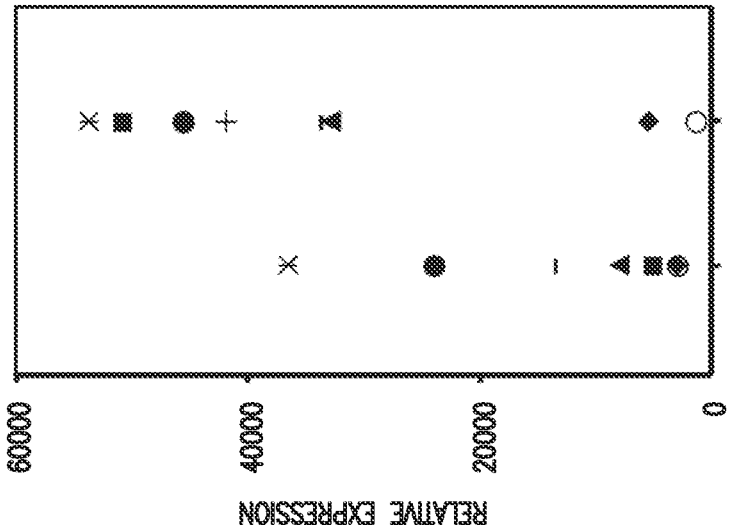


FIG. 22A

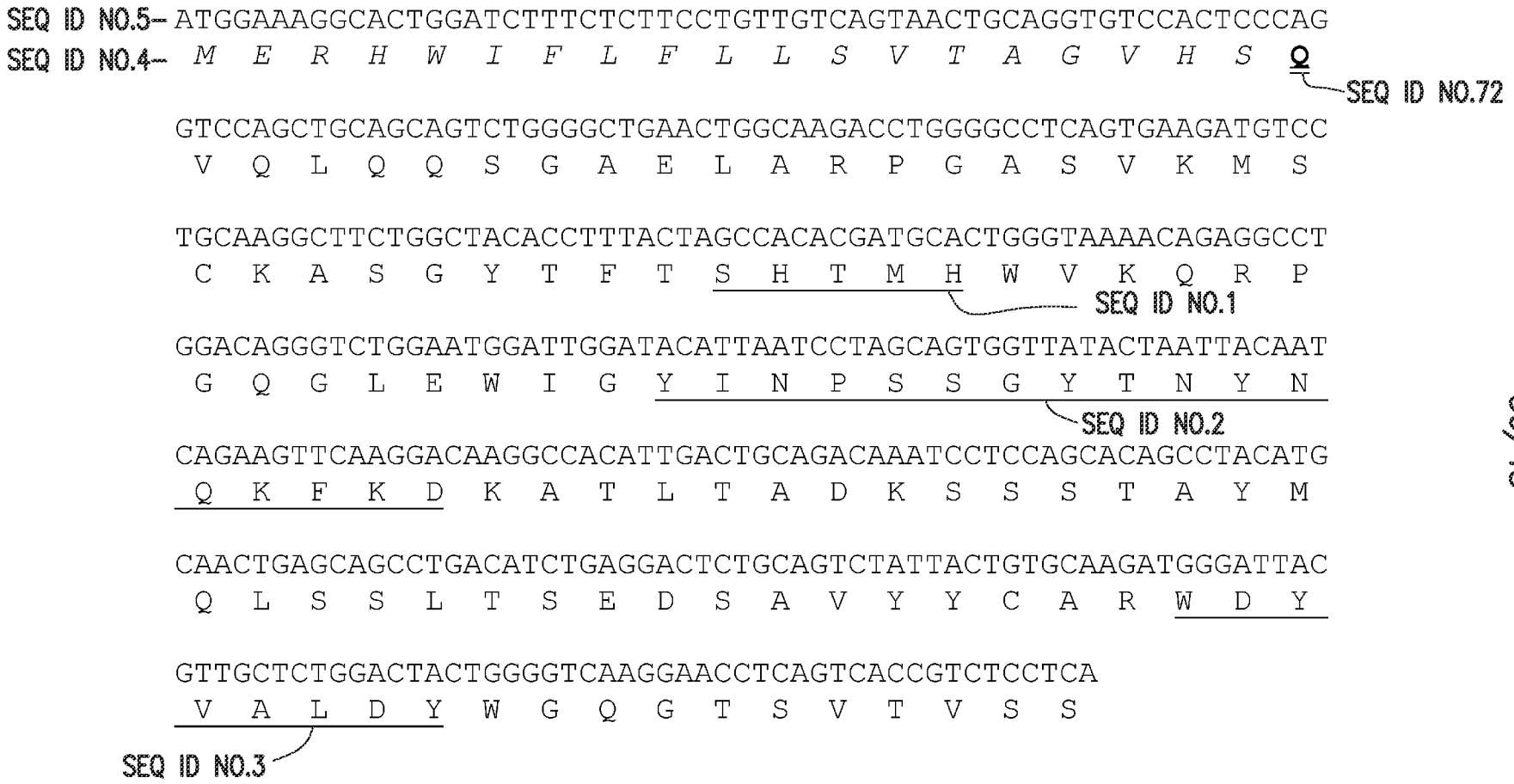

SEQ ID NO.5-- ATGGAAAGGCACTGGATCTTTCTCTTCCTGTTGTCAGTAACTGCAGGTGTCCACTCCCAG
SEQ ID NO.4-- M E R H W I F L F L L S V T A G V H S Q
SEQ ID NO.72
GTCCAGCTGCAGCAGTCTGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCC
V Q L Q Q S G A E L A R P G A S V K M S
TGCAAGGCTTCTGGCTACACCTTTACTAGCCACACGATGCACTGGGTAAAACAGAGGCCT
C K A S G Y T F T S H T M H W V K Q R P
SEQ ID NO.1
GGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCAGTGGTTATACTAATTACAAT
G Q G L E W I G Y I N P S S G Y T N Y N
SEQ ID NO.2
CAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG
Q K F K D K A T L T A D K S S S T A Y M
CAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGATGGGATTAC
Q L S S L T S E D S A V Y Y C A R W D Y
GTTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
V A L D Y W G Q G T S V T V S S
SEQ ID NO.3

FIG. 23

SEQ ID NO.10— ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTTCAAGGTACCAGATGT

SEQ ID NO.9— M M S S A Q F L G L L L L L C F Q G T R C

GAGATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC

E I Q M T Q T T S S L S A S L G D R V T

SEQ ID NO.73

ATCAGTTGCAGTGCAAGTCAGGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA

I S C S A S Q G I S N Y L N W Y Q Q K P

SEQ ID NO.6

GATGGAACTGTTAAACTCCTGATCTATTACATATCAAGTTTACACTCAGGAGTCACATCA

D G T V K L L I Y Y I S S L H S G V T S

SEQ ID NO.7

AGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT

R F S G S G S G T D Y S L T I S N L E P

GAAGATATTGCCACTTACTATTGTCAGCAGTATAGTAAGCTTCCGTACACGTTCGGAGGG

E D I A T Y Y C Q Q Y S K L P Y T F G G

SEQ ID NO.8

GGGACCAAGCTGGAAATAAAA

G T K L E I K

FIG. 24

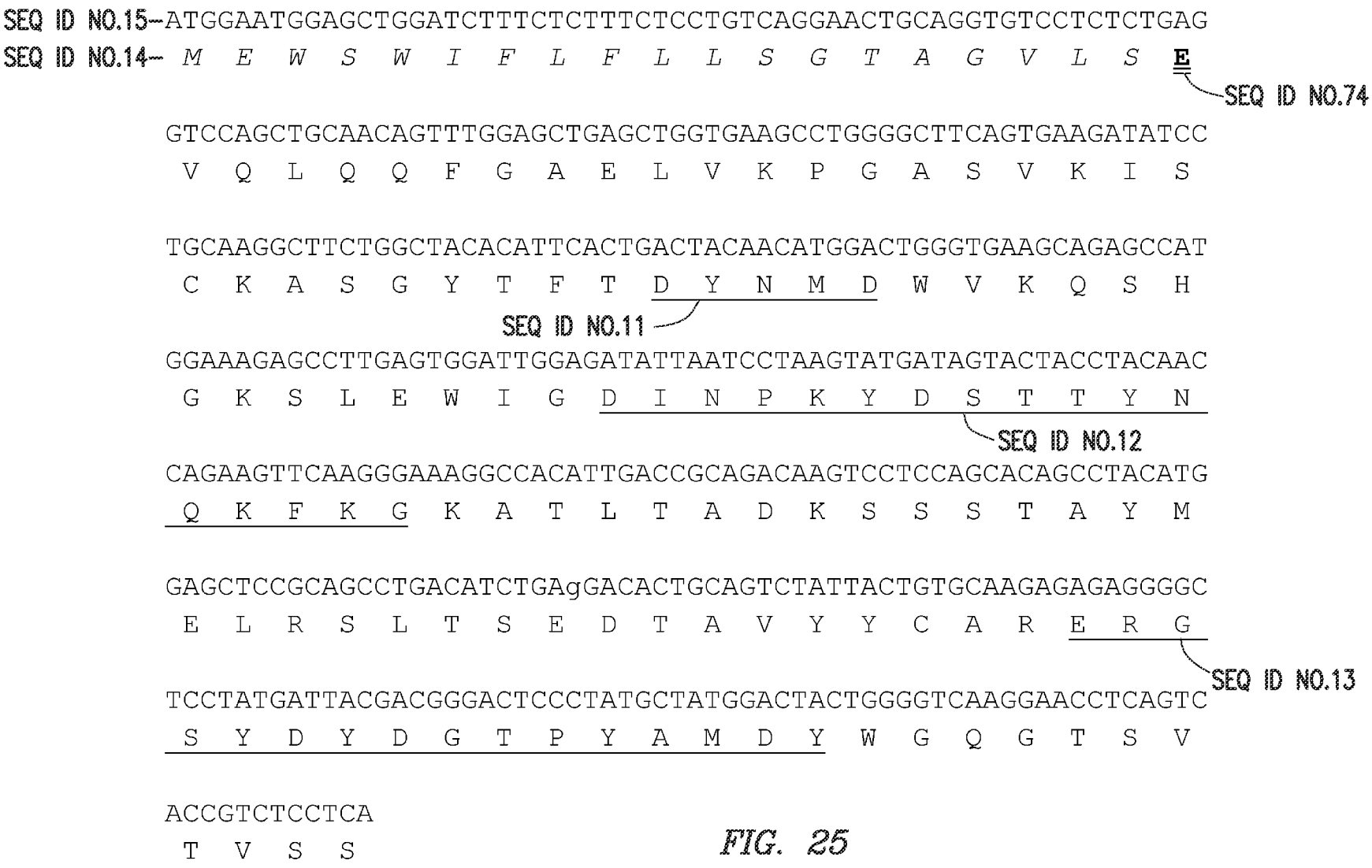

SEQ ID NO.15--ATGGAATGGAGCTGGATCTTTCTCTTTCTCCTGTCAGGAACTGCAGGTGTCCTCTCTGAG
SEQ ID NO.14-- M E W S W I F L F L L S G T A G V L S E
SEQ ID NO.74
GTCCAGCTGCAACAGTTTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCC
V Q L Q Q F G A E L V K P G A S V K I S
TGCAAGGCTTCTGGCTACACATTCACTGACTACAACATGGACTGGGTGAAGCAGAGCCAT
C K A S G Y T F T D Y N M D W V K Q S H
SEQ ID NO.11
GGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTAAGTATGATAGTACTACCTACAAC
G K S L E W I G D I N P K Y D S T T Y N
SEQ ID NO.12
CAGAAGTTCAAGGGAAAGGCCACATTGACCGCAGACAAGTCCTCCAGCACAGCCTACATG
Q K F K G K A T L T A D K S S S T A Y M
GAGCTCCGCAGCCTGACATCTGAgGACACTGCAGTCTATTACTGTGCAAGAGAGAGGGGC
E L R S L T S E D T A V Y Y C A R E R G
SEQ ID NO.13
TCCTATGATTACGACGGGACTCCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTC
S Y D Y D G T P Y A M D Y W G Q G T S V
ACCGTCTCCTCA
T V S S

FIG. 25

SEQ ID NO.20— ATGGATTCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGGTATCTGGTACCTGTGGG

SEQ ID NO.19— *M D S Q A Q V L M L L L L W V S G T C G*

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT

D I V M S Q S P S S L A V S V G E K V T

SEQ ID NO.75

ATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCAATCGAAAGAACTACTTGGCC

M S C K S S Q S L L Y S S N R K N Y L A

SEQ ID NO.16

TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCGTCCACTAGG

W Y Q Q K P G Q S P K L L I Y W A S T R

SEQ ID NO.17

GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC

E S G V P D R F T G S G S G T D F T L T

ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATACCTAT

I S S V K A E D L A V Y Y C Q Q Y Y T Y

SEQ ID NO.18

CCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA

P R T F G G G T K L E I K

FIG. 26


SEQ ID NO.25-
SEQ ID NO.24-
M G W S Y I I L F L V A T A T D V H S Q
SEQ ID NO.76
GTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGCTGTCC
V Q L Q Q P G A E L V K P G A S V K L S
TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGGTGAACTGGGTGAAGCAGAGGCCT
C K A S G Y T F T S Y W V N W V K Q R P
SEQ ID NO.21
GGACAAGGCCTTGAGTGGATTGGAGAGATTAATCCTAGCAACGGTCGTACTGACTACAAT
G Q G L E W I G E I N P S N G R T D Y N
SEQ ID NO.22
GAGAAGTTCAAGAGCAAGGCCATAATGATTGTAGACAAATCTTCTAGCACAGCCTATATG
E K F K S K A I M I V D K S S S T A Y M
CAATTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAGGGGGACTGGAC
Q F S S L T S E D S A V Y Y C A G G L D
SEQ ID NO.23
TACTTTGACTATTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
Y F D Y W G Q G T T L T V S S

FIG. 27

SEQ ID NO.30– ATGGAATCACAGACTCTGGTCTTCATATCCATACTGCTCTGGTTATATGGTGCTGATGGG

SEQ ID NO.29– *M E S Q T L V F I S I L L L W L Y G A D G*

AACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGAGGGTCACC

N I V M T Q S P K S M S M S V G E R V T

SEQ ID NO.77

TTGAGCTGCAAGGCCAGTGAGAATGTGGGTACTTATGTATCCTGGTATCAACAGAAACCA

L S C K A S E N V G T Y V S W Y Q Q K P

SEQ ID NO.26

GACCAGTCTCCTAAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCCGAT

D Q S P K L L I Y G A S N R Y T G V P D

SEQ ID NO.27

CGCTTCACAGGCAGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCT

R F T G S G S A T D F T L T I S S V Q A

GAAGACCTTGCAGATTATCACTGTGGACAGAGTTACAGCTATCCATTCACGTTCGGCTCG

E D L A D Y H C G Q S Y S Y P F T F G S

SEQ ID NO.28

GGGACAAGTTTGGAAATAAAA

G T S L E I K

FIG. 28


SEQ ID NO.35-
ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAGCCAACGGT
SEQ ID NO.34-
M M S P A Q F L F L L V L W I R E A N G
GCTGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC
A V V M T Q T P L T L S V T I G Q P A S
SEQ ID NO.78
ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATCGTGATGGAAAGACATATTTGAATTGG
I S C K S S Q S L L D R D G K T Y L N W
SEQ ID NO.31
TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC
L L Q R P G Q S P K R L I Y L V S K L D
SEQ ID NO.32
TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATC
S G V P D R F T G S G S G T D F T L K I
AGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGTCAAGGTACACATTTTCCA
S R V E A E D L G V Y Y C C Q G T H F P
SEQ ID NO.33
TTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA
F T F G S G T K L E I K

FIG. 29

SpeI

SEQ ID NO.40– ACTAGTACCACCATGGAAAGGCACTGGATCTTTCTCTTCCTGTTGTCAGTGACTGCAGGT

SEQ ID NO.41– *M E R H W I F L F L L S V T A G*

GTCCACTCCCAGGTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA

V H S Q V Q L V Q S G A E V K K P G A S

SEQ ID NO.39

GTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACTAGCCACACCATGCACTGGGTG

V K V S C K A S G Y T F T S H T M H W V

SEQ ID NO.36

CGCCAGGCCCCCGGACAAAGGCTTGAGTGGATTGGATACATTAATCCTAGCAGTGGTTAT

R Q A P G Q R L E W I G Y I N P S S G Y

SEQ ID NO.37

ACTAATTACAATCAGAAGTTCAAGGACAAGGCCACACCCTTACCGCCGACACATCCGCCAGC

T N Y N Q K F K D K A T L T A D T S A S

ACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACCGCTGTGTATTACTGTGCC

T A Y M E L S S L R S E D T A V Y Y C A

AGGTGGGATTACGTTGCTCTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

R W D Y V A L D Y W G Q G T L V T V S S

SEQ ID NO.38

HindIII

GGTGAGTCTGTGTACTGAAGCTT

FIG. 30

SpeI

SEQ ID NO.46– ACTAGTACCACCATGGAAAGGCACTGGATCTTTCTCTTCCTGTTGTCAGTGACTGCAGGT

SEQ ID NO.47– *M E R H W I F L F L L S V T A G*

GTCCACTCCCAGGTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA

V H S Q V Q L V Q S G A E V K K P G A S

SEQ ID NO.45

GTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACTAGCCACACCATGCACTGGGTG

V K V S C K A S G Y T F T S H T M H W V

SEQ ID NO.42

CGCCAGGCCCCCGGACAAAGGCTTGAGTGGATTGGATACATTAATCCTAGCAGTGGTTAT

R Q A P G Q G L E W I G Y I N P S S G Y

SEQ ID NO.43

ACTAATTACAATCAGAAGTTCAAGGACAGAGCCACACCCTTACCGCCGACACATCCGCCAGC

T N Y N Q K F K D R A T L T A D T S A S

ACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACCGCTGTGTATTACTGTGCC

T A Y M E L S S L R S E D T A V Y Y C A

AGGTGGGATTACGTTGCTCTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

R W D Y V A L D Y W G Q G T L V T V S S

SEQ ID NO.44

HindIII

GGTGAGTCTGTGTACTGAAGCTT

FIG. 31


NheI
SEQ ID NO.52-GCTAGCACCACCATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGA
SEQ ID NO.53-M S S A Q F L G L L L L C F Q G
ACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGAC
T R C D I Q M T Q S P S S L S A S V G D
SEQ ID NO.51
AGAGTCACCATCACTTGCAGTGCAAGTCAGGGCATTAGCAATTATCTGAACTGGTATCAG
R V T I T C S A S Q G I S N Y L N W Y Q
SEQ ID NO.48
CAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTACATCTCAAGTCTGCACTCAGGG
Q K P G K V P K L L I Y Y I S S L H S G
SEQ ID NO.49
GTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTATACTCTCACCATCAGCAGC
V P S R F S G S G S G T D Y T L T I S S
CTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAACAGTATAGTAAGCTGCCGTACACC
L Q P E D V A T Y Y C Q Q Y S K L P Y T
SEQ ID NO.50
EcoRI
TTCGGCGGAGGGACCAAAGTGGAGATCAAACGTAAGTGCACTTTCCTAAGAATTC
F G G G T K V E I K

FIG. 32

SpeI
SEQ ID NO.58-- ACTAGTACCACCATGGAATGGAGCTGGATCTTTCTCTTTCTCCTGTCAGGAACTGCAGGC
SEQ ID NO.59-- M E W S W I F L F L L S G T A G
GTCCTCTCTCAGGTCCAGCTTGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCCTCA
V L S Q V Q L V Q S G A E V K K P G A S
SEQ ID NO.57
GTGAAAGTTTCCTGCAAGGCTTCTGGATACACCTTCACTGACTACACAACATGGACTGGGTG
V K V S C K A S G Y T F T D Y N M D W V
SEQ ID NO.54
CGCCAGGCCCCCGGACAAGGCTTGAGTGGATTGGAGATATTTAATCCTAAGTATGATAGT
R Q A P G Q R L E W I G D I N P K Y D S
SEQ ID NO.55
ACTACCTACAACCAGAAGTTCAAGGGAAAGGCCACACCCTTACCGCAGACACATCCGCCAGC
T T Y N Q K F K G K A T L T A D T S A S
ACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAAGACACCGCTGTGTATTACTGTGCC
T A Y M E L S S L R S E D T A V Y Y C A
AGGGAGAGGGGCTCCTATGATTACGACGGGACTCCCTATGCTATGGACTACTGGGGCCAG
R E R G S Y D Y D G T P Y A M D Y
SEQ ID NO.56
HindIII
GGAACCCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTACTGAAGCTT
G T L V T V S S

FIG. 33

SpeI
SEQ ID NO.64— ACTAGTACCACCATGGAATGGAGCTGGATCTTTCTCTTTCCTGTCAGGAACTGCAGGC
SEQ ID NO.65— M E W S W I F L F L L S G T A G

GTCCTCTCTCAGGTCCAGCTTGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCCTCA
V L S Q V Q L V Q S G A E V K K P G A S
SEQ ID NO.63

GTGAAAGTTTCCTGCAAGGCTTCTGGATACACCTTCACTGACTACAACATGGACTGGGTG
V K V S C K A S G Y T F T D Y N M D W V
SEQ ID NO.60

CGCCAGGCCCCCGGACAAAGGCTTGAGTGGATTGGAGATATTAATCCTAAGTATGATAGT
R Q A P G Q G L E W I G D I N P K Y D S
SEQ ID NO.61

ACTACCTACAACCAGAAGTTCAAGGGAAGAGCCACACCCTTACCGCAGACACATCCGCCAGC
T T Y N Q K F K G R A T L T A D T S A S

ACAGCCTACATGGAGCTCAGCAGCCTGAGATCTGAAGACACCGCTGTGTATTACTGTGCC
T A Y M E L S S L R S E D T A V Y Y C A

AGGGAGAGGGGCTCCTATGATTACGACGGGACTCCCTATGCTATGGACTACTGGGGCCAG
R E R G S Y D Y D G T P Y A M D Y W G Q
SEQ ID NO.62

HindIII
GGAACCCTGGTCACCGTCTCCTCAGGTGAGTCTGCTGTACTGAAGCTT
G T L V T V S S

FIG. 34

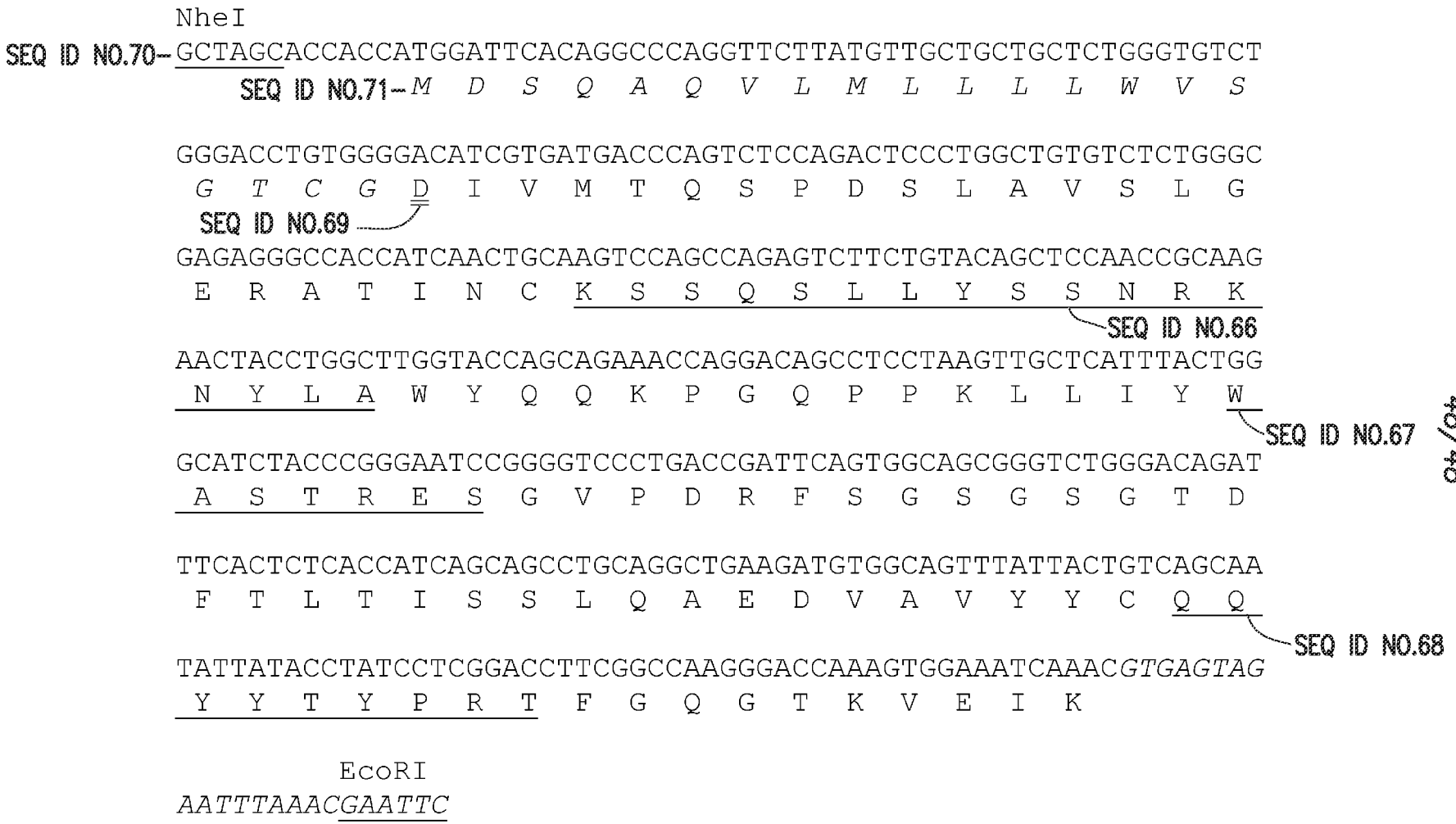

NheI
SEQ ID NO.70- GCTAGCACCACCATGGATTCACAGGCCCAGGTTCTTATGTTGCTGCTGCTCTGGGTGTCT
SEQ ID NO.71- M D S Q A Q V L M L L L L W V S
GGGACCTGTGGGGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGC
G T C G D I V M T Q S P D S L A V S L G
SEQ ID NO.69
GAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTCTTCTGTACAGCTCCAACCGCAAG
E R A T I N C K S S Q S L L Y S S N R K
SEQ ID NO.66
AACTACCTGGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGG
N Y L A W Y Q Q K P G Q P P K L L I Y W
SEQ ID NO.67
GCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGAT
A S T R E S G V P D R F S G S G S G T D
TTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAA
F T L T I S S L Q A E D V A V Y Y C Q Q
SEQ ID NO.68
TATTATACCTATCCTCGGACCTTCGGCCAAGGGACCAAAGTGGAAATCAAACGTGAGTAG
Y Y T Y P R T F G Q G T K V E I K
EcoRI
AATTTAAACGAATTC

FIG. 35