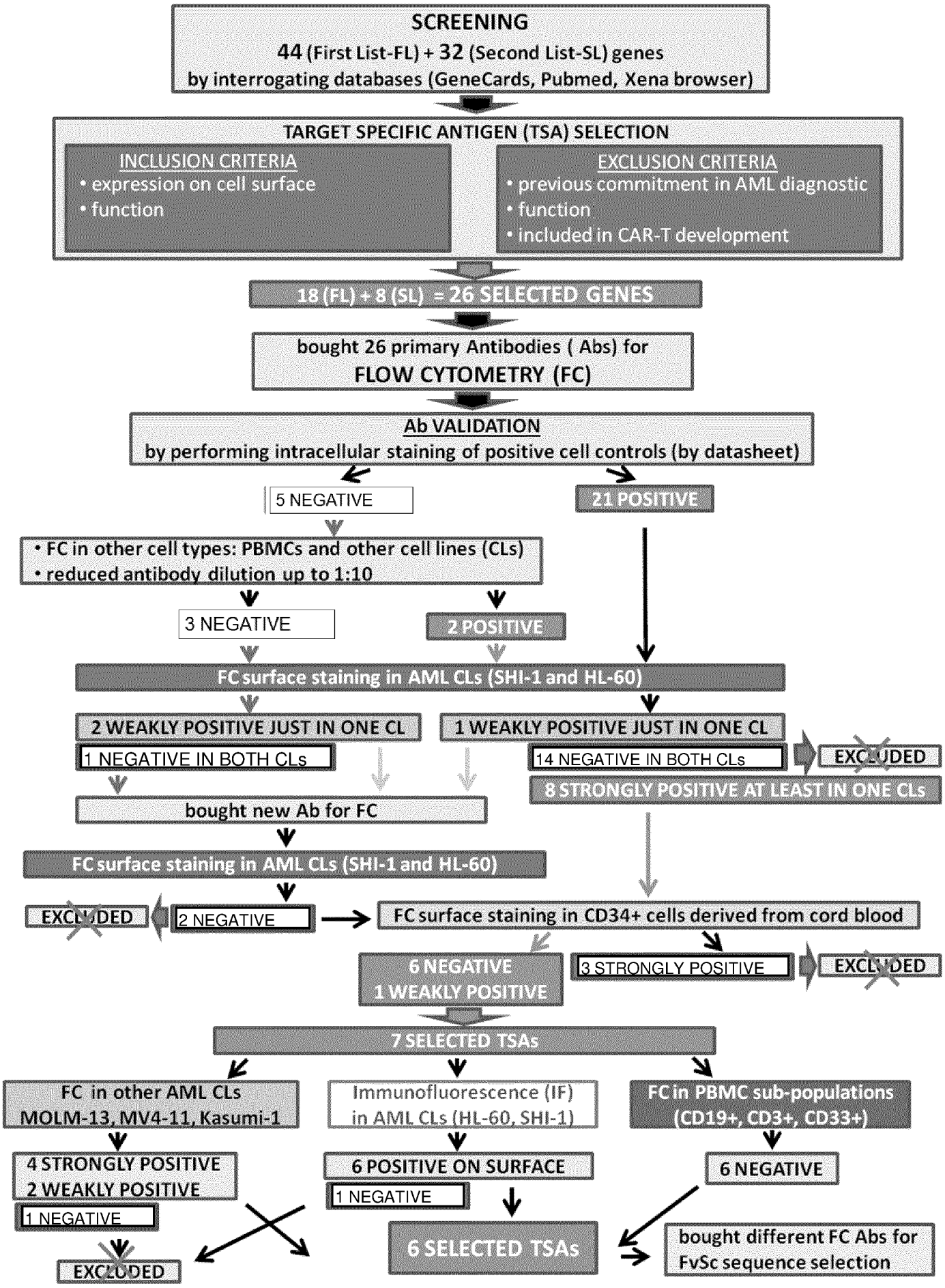

SCREENING
44 (First List-FL) + 32 (Second List-SL) genes
by interrogating databases (GeneCards, Pubmed, Xena browser)
TARGET SPECIFIC ANTIGEN (TSA) SELECTION
INCLUSION CRITERIA
• expression on cell surface
• function
EXCLUSION CRITERIA
• previous commitment in AML diagnostic
• function
• included in CAR-T development
18 (FL) + 8 (SL) = 26 SELECTED GENES
bought 26 primary Antibodies (Abs) for
FLOW CYTOMETRY (FC)
Ab VALIDATION
by performing intracellular staining of positive cell controls (by datasheet)
5 NEGATIVE
21 POSITIVE
• FC in other cell types: PBMCs and other cell lines (CLs)
• reduced antibody dilution up to 1:10
3 NEGATIVE
2 POSITIVE
FC surface staining in AML CLs (SHI-1 and HL-60)
2 WEAKLY POSITIVE JUST IN ONE CL
1 NEGATIVE IN BOTH CLs
1 WEAKLY POSITIVE JUST IN ONE CL
14 NEGATIVE IN BOTH CLs
EXCLUDED
8 STRONGLY POSITIVE AT LEAST IN ONE CLs
bought new Ab for FC
FC surface staining in AML CLs (SHI-1 and HL-60)
EXCLUDED
2 NEGATIVE
FC surface staining in CD34+ cells derived from cord blood
6 NEGATIVE
1 WEAKLY POSITIVE
3 STRONGLY POSITIVE
EXCLUDED
7 SELECTED TSAs
FC in other AML CLs
MOLM-13, MV4-11, Kasumi-1
Immunofluorescence (IF)
in AML CLs (HL-60, SHI-1)
FC in PBMC sub-populations
(CD19+, CD3+, CD33+)
4 STRONGLY POSITIVE
2 WEAKLY POSITIVE
1 NEGATIVE
6 POSITIVE ON SURFACE
1 NEGATIVE
6 NEGATIVE
EXCLUDED
6 SELECTED TSAs
bought different FC Abs for
FvSc sequence selection

FIG. 1

FIG. 2A

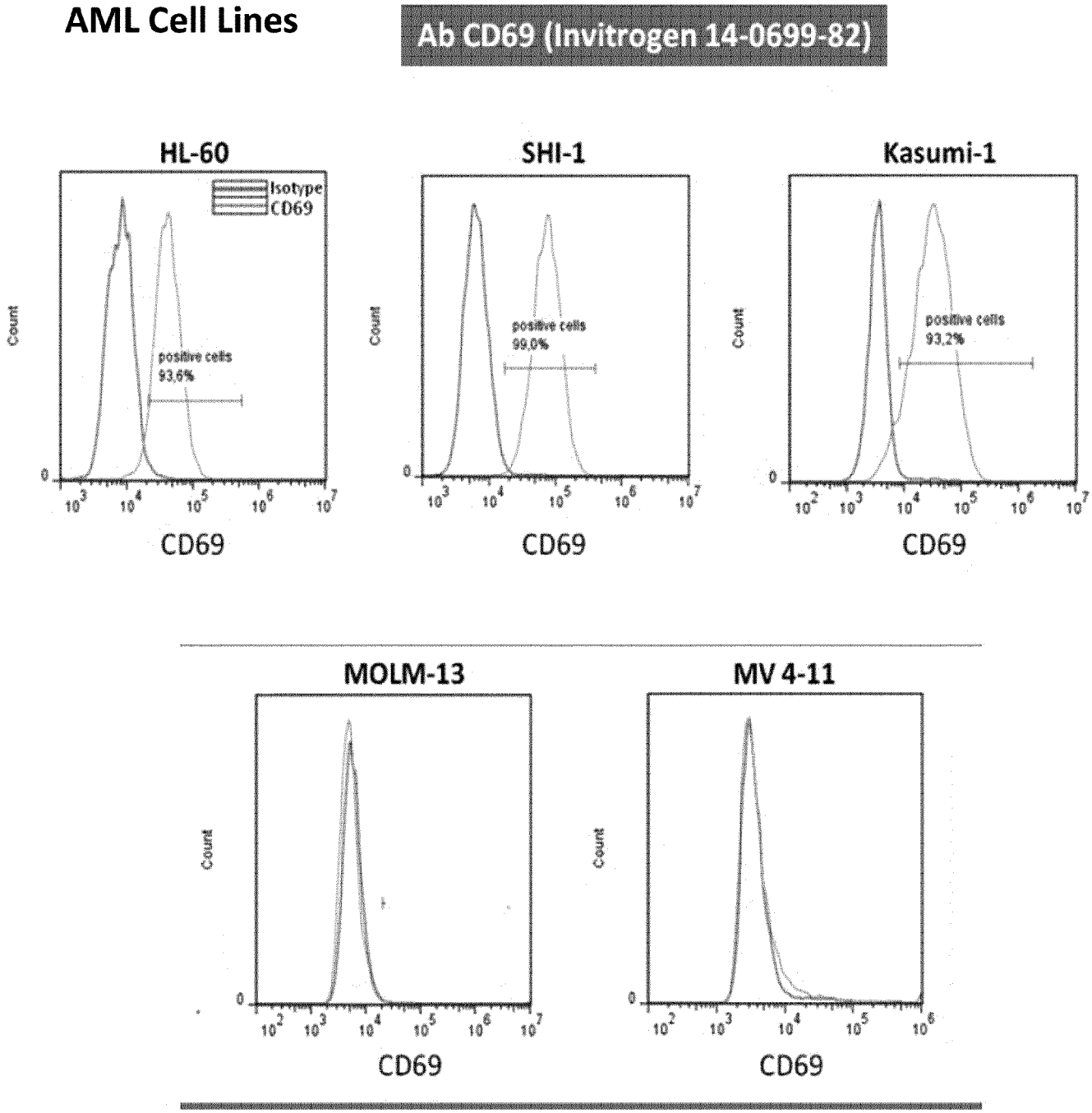

AML Cell Lines
Ab CD69 (Invitrogen 14-0699-82)
HL-60
Isotype
CD69
positive cells
93,6%
Count
CD69
SHI-1
positive cells
99,0%
Count
CD69
Kasumi-1
positive cells
93,2%
Count
CD69
MOLM-13
Count
CD69
MV 4-11
Count
CD69

FIG. 2A (cont'd)

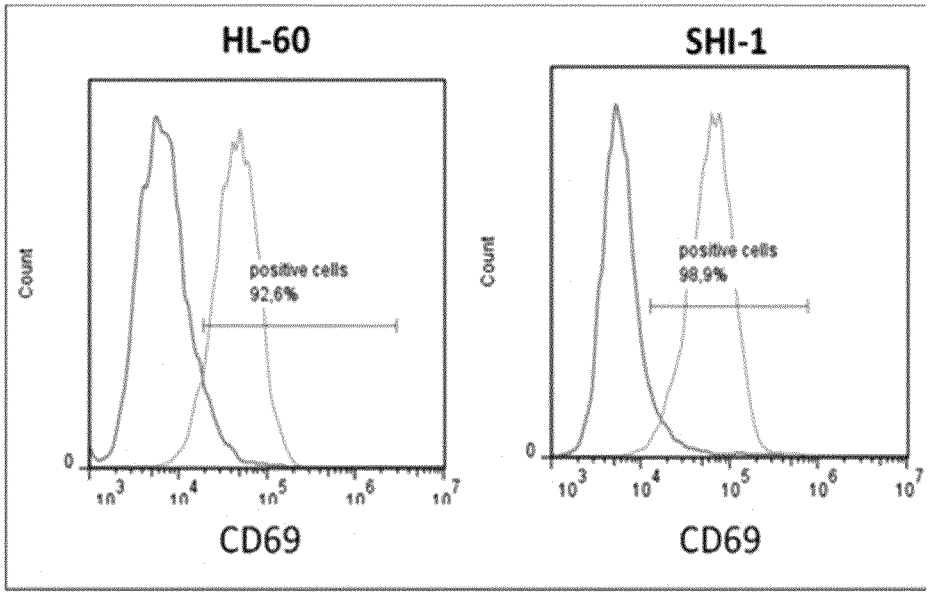


FIG. 2B

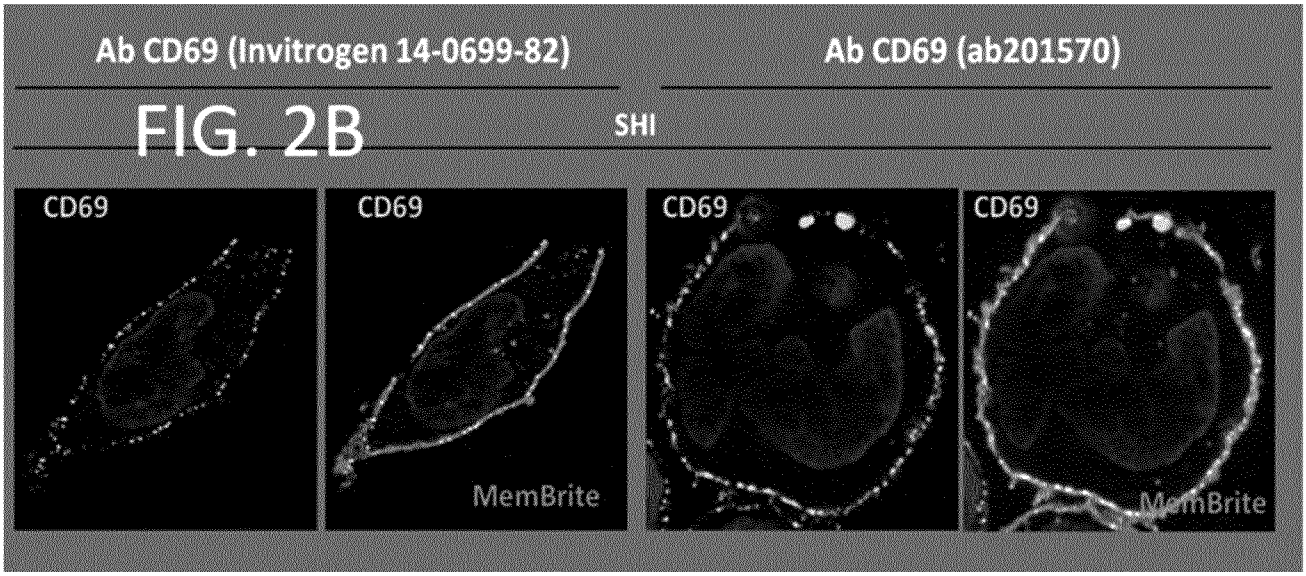


FIG. 2C

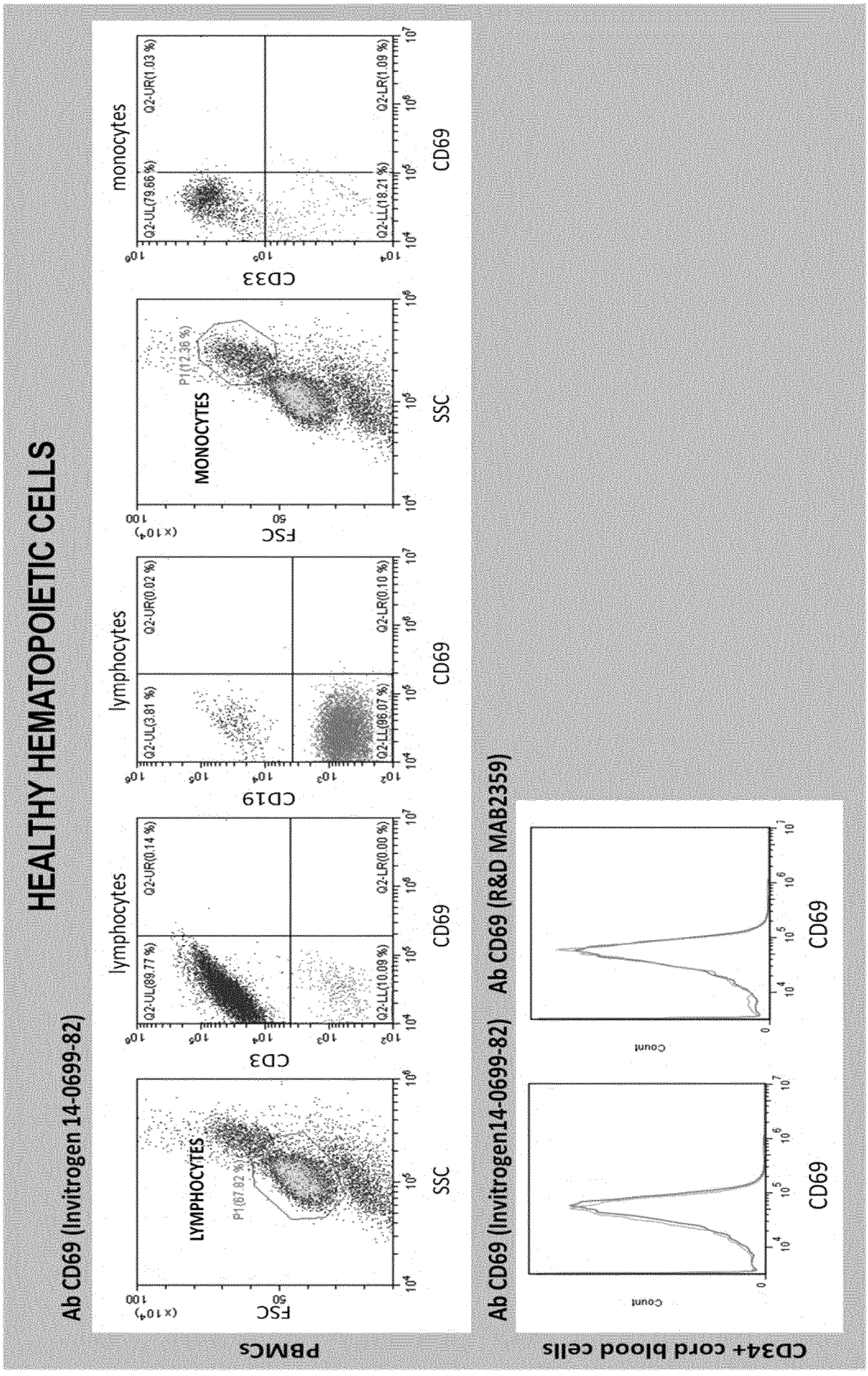

HEALTHY HEMATOPOIETIC CELLS
Ab CD69 (Invitrogen 14-0699-82)
PBMCs
LYMPHOCYTES
P1(67.82 %)
FSC
SSC
CD3
CD69
lymphocytes
Q2-UL(89.77 %)
Q2-UR(0.14 %)
Q2-LL(10.09 %)
Q2-LR(0.00 %)
CD19
Q2-UL(3.81 %)
Q2-UR(0.02 %)
Q2-LL(96.07 %)
Q2-LR(0.10 %)
MONOCYTES
P1(12.36 %)
CD33
monocytes
Q2-UL(79.66 %)
Q2-UR(1.03 %)
Q2-LL(18.21 %)
Q2-LR(1.09 %)
Ab CD69 (Invitrogen14-0699-82)
Ab CD69 (R&D MAB2359)
CD34+ cord blood cells
Count
CD69

FIG. 3A

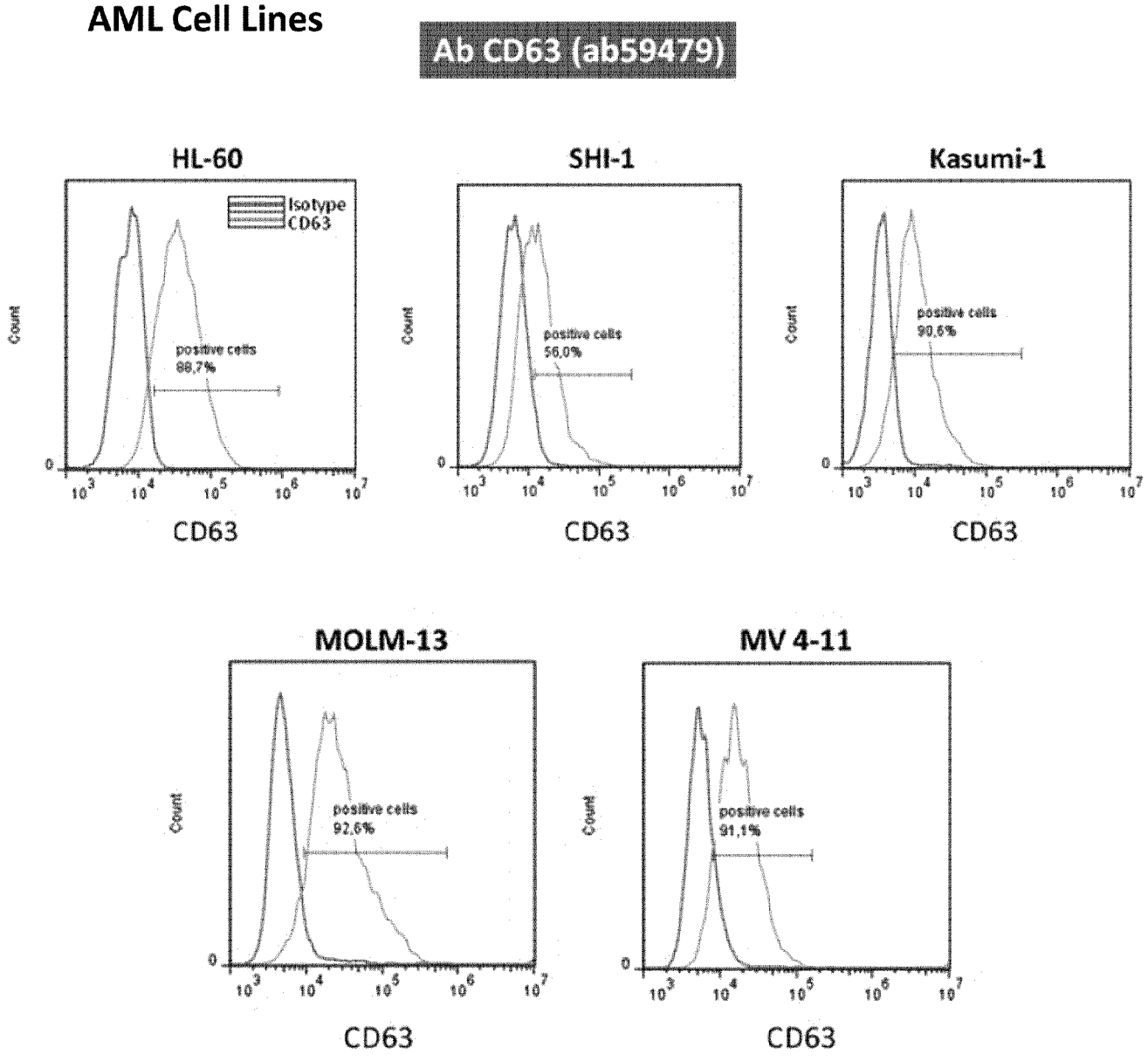

AML Cell Lines
Ab CD63 (ab59479)
HL-60
Isotype
CD63
positive cells
88,7%
Count
CD63
SHI-1
positive cells
56,0%
Count
CD63
Kasumi-1
positive cells
90,6%
Count
CD63
MOLM-13
positive cells
92,6%
Count
CD63
MV 4-11
positive cells
91,1%
Count
CD63

FIG. 3A (cont'd)

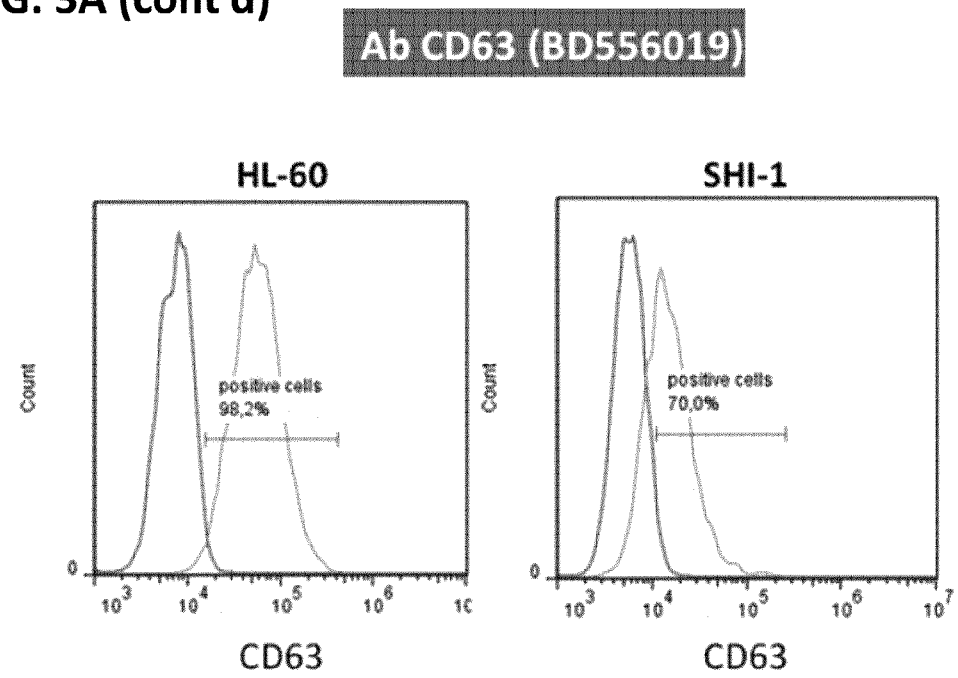


FIG. 3B

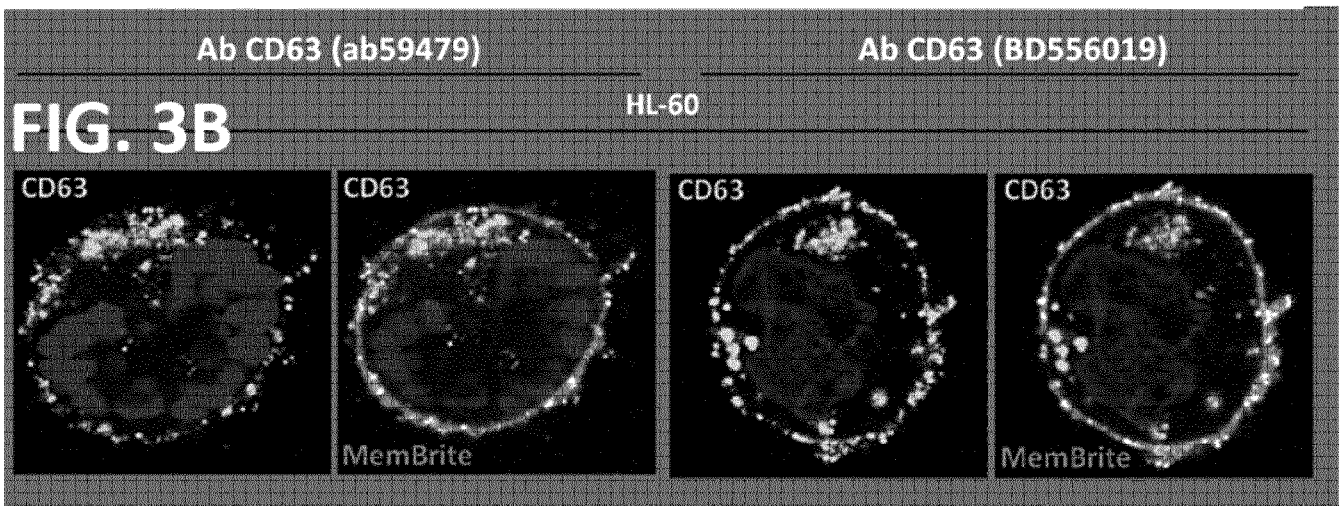


FIG. 3C

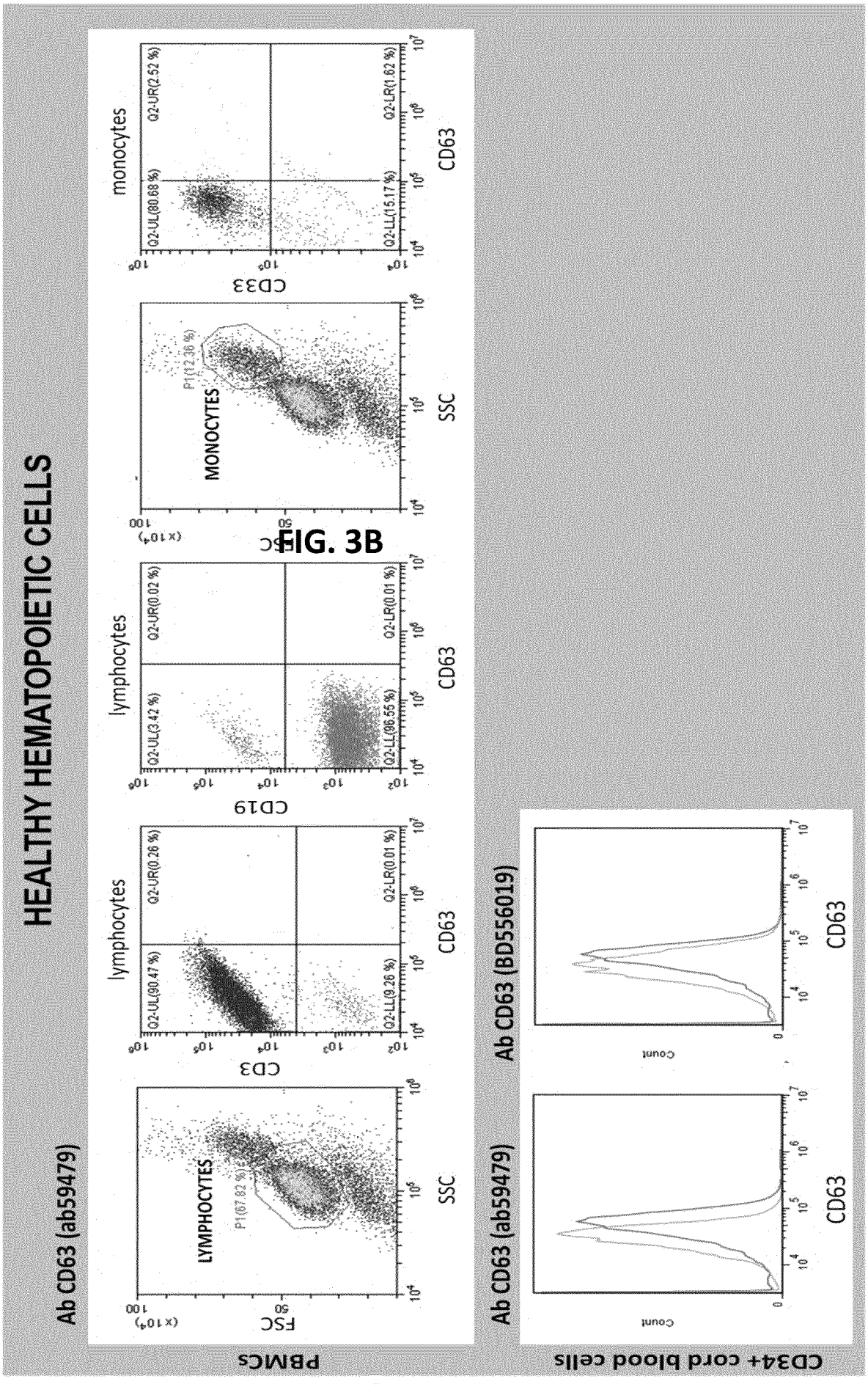

HEALTHY HEMATOPOIETIC CELLS
PBMCs
Ab CD63 (ab59479)
FSC
SSC
LYMPHOCYTES
P1(67.82 %)
CD3
CD63
lymphocytes
Q2-UL(90.47 %)
Q2-UR(0.26 %)
Q2-LL(9.26 %)
Q2-LR(0.01 %)
CD19
Q2-UL(3.42 %)
Q2-UR(0.02 %)
Q2-LL(96.55 %)
Q2-LR(0.01 %)
MONOCYTES
P1(12.36 %)
CD33
monocytes
Q2-UL(80.68 %)
Q2-UR(2.52 %)
Q2-LL(15.17 %)
Q2-LR(1.62 %)
CD34+ cord blood cells
Ab CD63 (ab59479)
Ab CD63 (BD556019)
Count
CD63

FIG. 3B

FIG. 4A

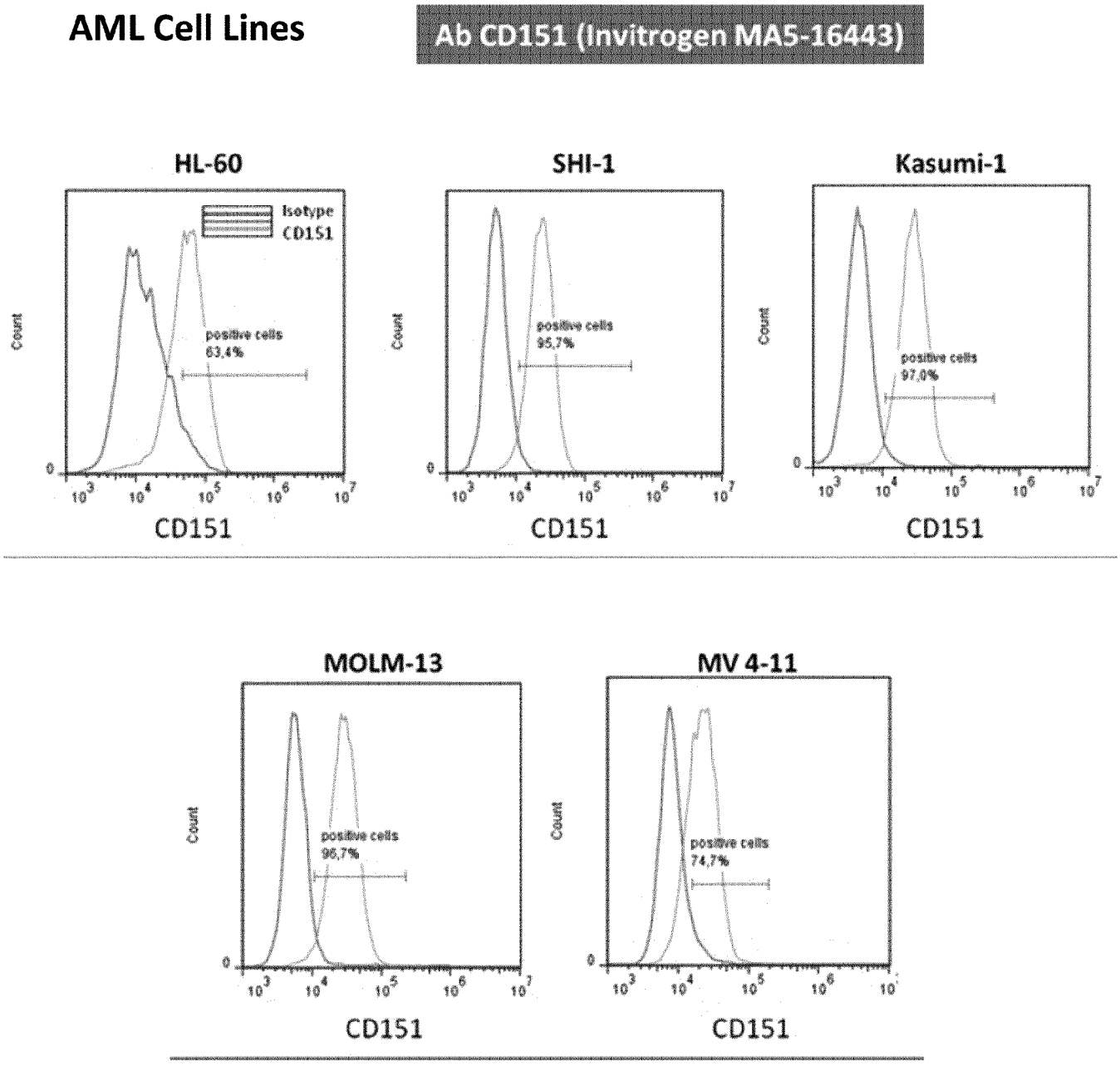

AML Cell Lines
Ab CD151 (Invitrogen MA5-16443)
HL-60
Isotype
CD151
positive cells
63,4%
Count
0
CD151
SHI-1
positive cells
95,7%
Count
0
CD151
Kasumi-1
positive cells
97,0%
Count
0
CD151
MOLM-13
positive cells
96,7%
Count
0
CD151
MV 4-11
positive cells
74,7%
Count
0
CD151

FIG. 4A (cont'd)

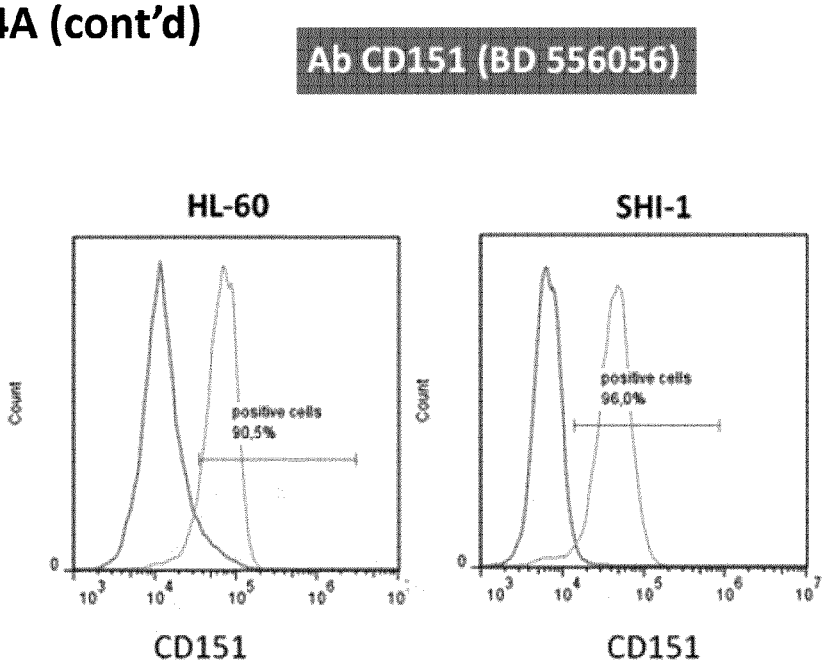


FIG. 4B

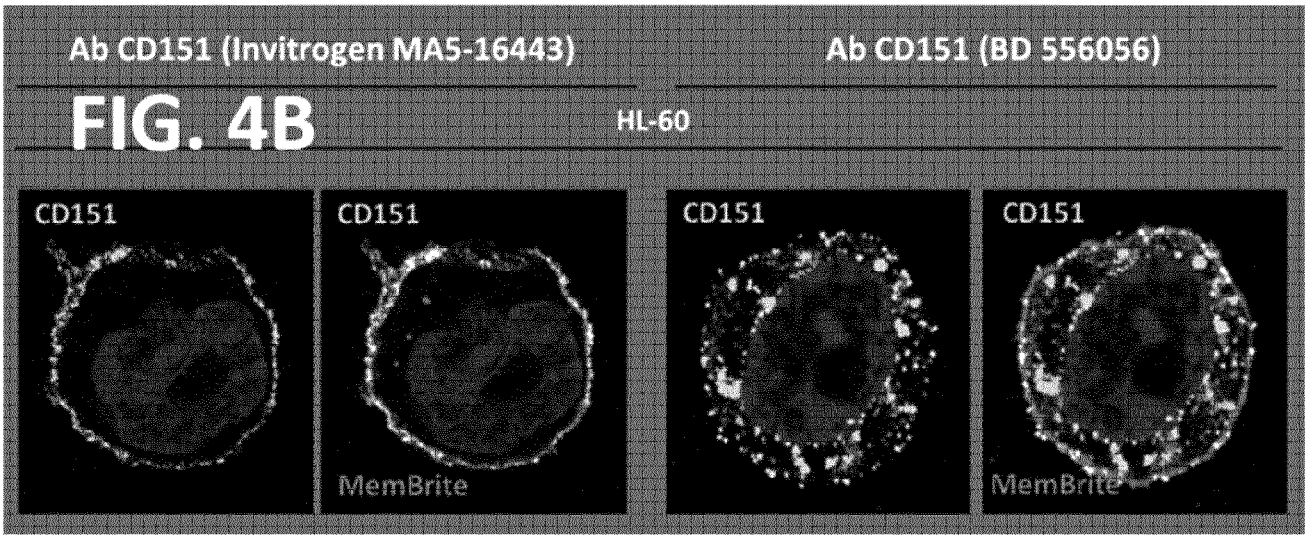


FIG. 4C

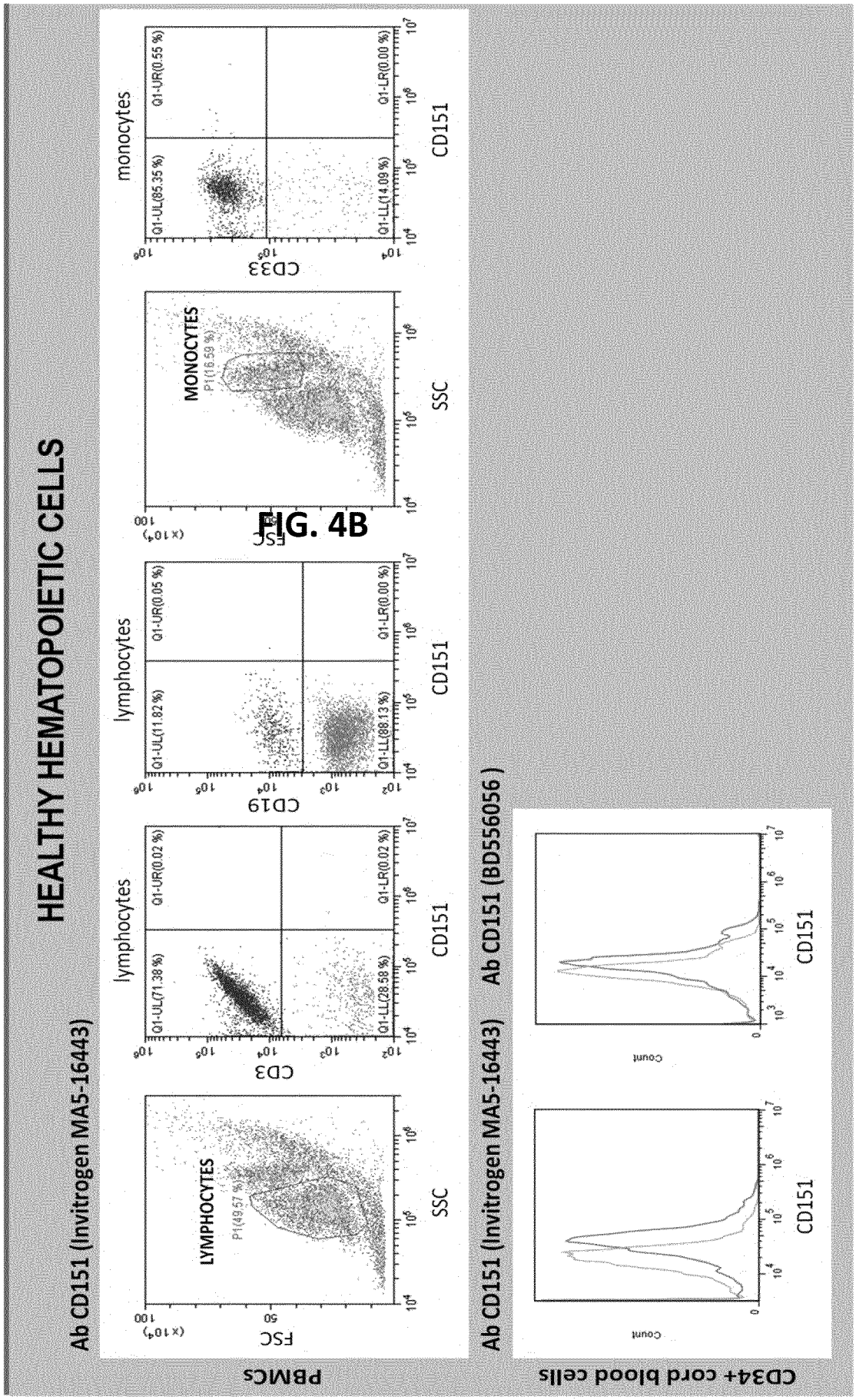

HEALTHY HEMATOPOIETIC CELLS
PBMCs
Ab CD151 (Invitrogen MA5-16443)
LYMPHOCYTES
P1(49.57 %)
FSC
SSC
lymphocytes
CD3
CD151
Q1-UL(71.38 %)
Q1-UR(0.02 %)
Q1-LL(28.58 %)
Q1-LR(0.02 %)
lymphocytes
CD19
CD151
Q1-UL(11.82 %)
Q1-UR(0.05 %)
Q1-LL(88.13 %)
Q1-LR(0.00 %)
MONOCYTES
P1(16.59 %)
FSC
SSC
monocytes
CD33
CD151
Q1-UL(85.35 %)
Q1-UR(0.55 %)
Q1-LL(14.09 %)
Q1-LR(0.00 %)
CD34+ cord blood cells
Ab CD151 (Invitrogen MA5-16443)
Ab CD151 (BD556056)
Count
CD151
Count
CD151

FIG. 4B

FIG. 5A

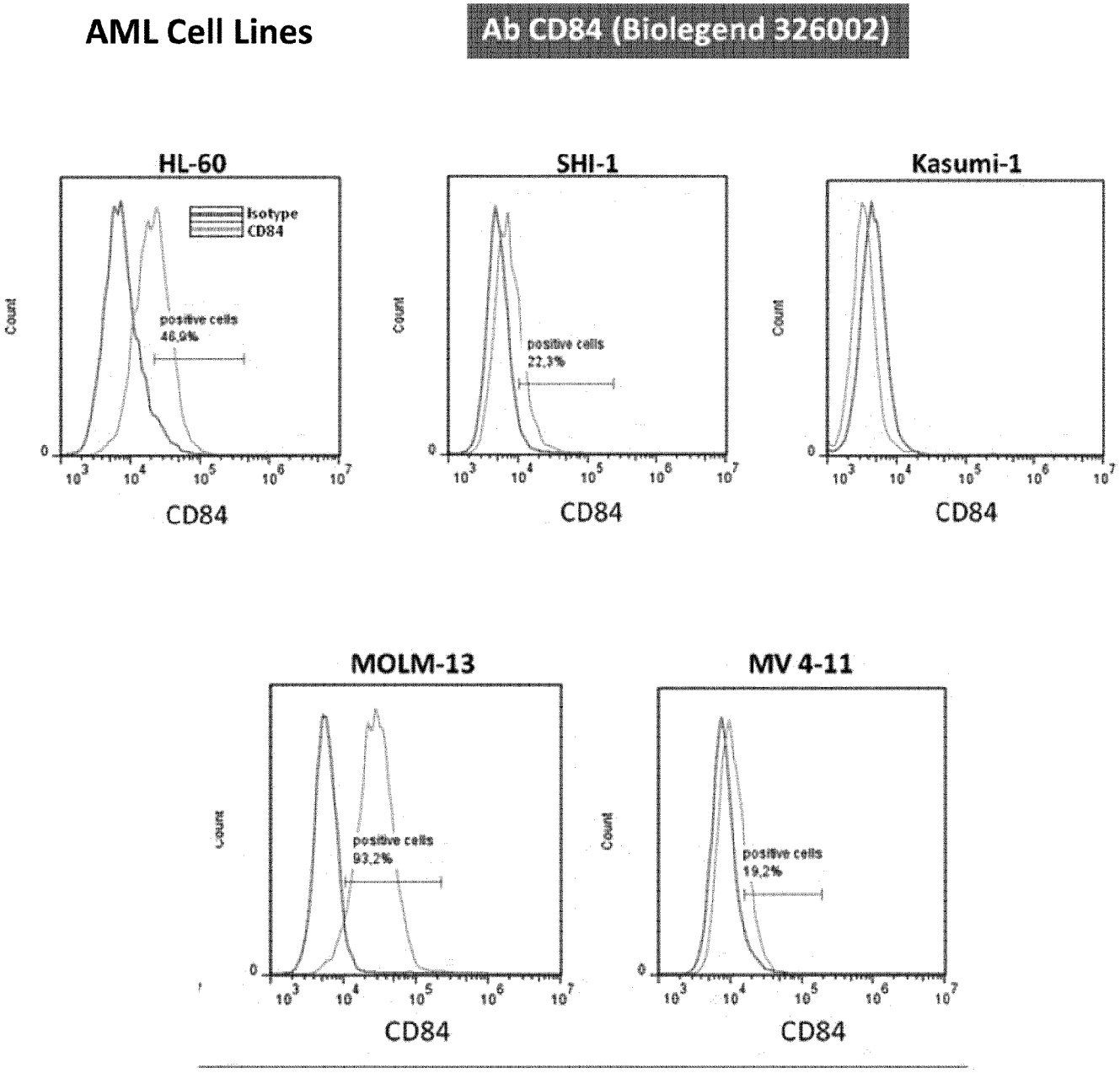

AML Cell Lines
Ab CD84 (Biolegend 326002)
HL-60
Isotype
CD84
positive cells
46,9%
Count
CD84
SHI-1
positive cells
22,3%
Count
CD84
Kasumi-1
Count
CD84
MOLM-13
positive cells
93,2%
Count
CD84
MV 4-11
positive cells
19,2%
Count
CD84

FIG. 5A (cont'd)

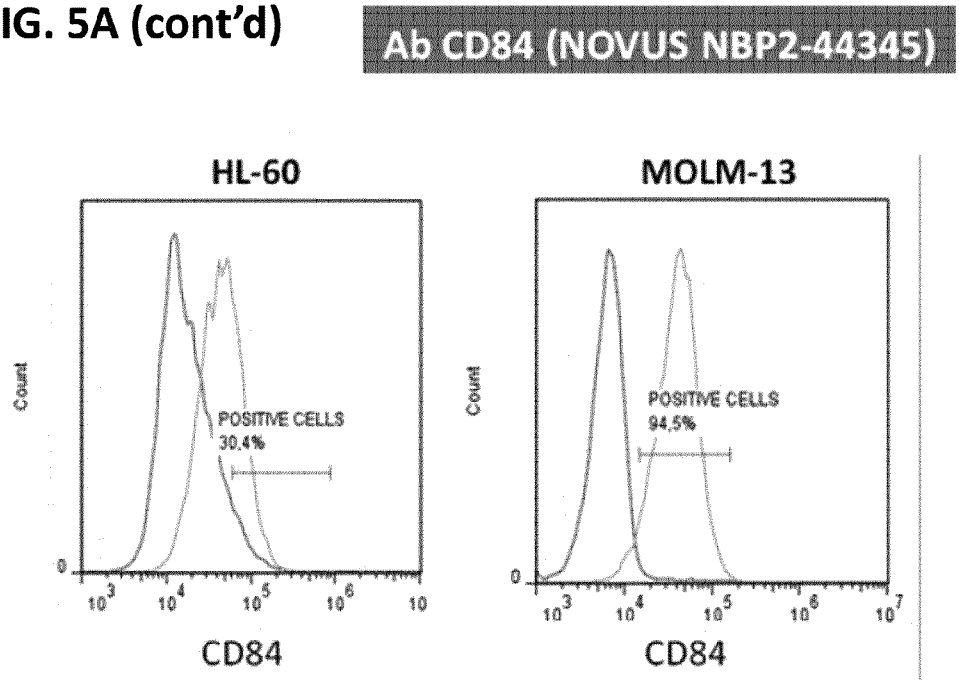


FIG. 5B

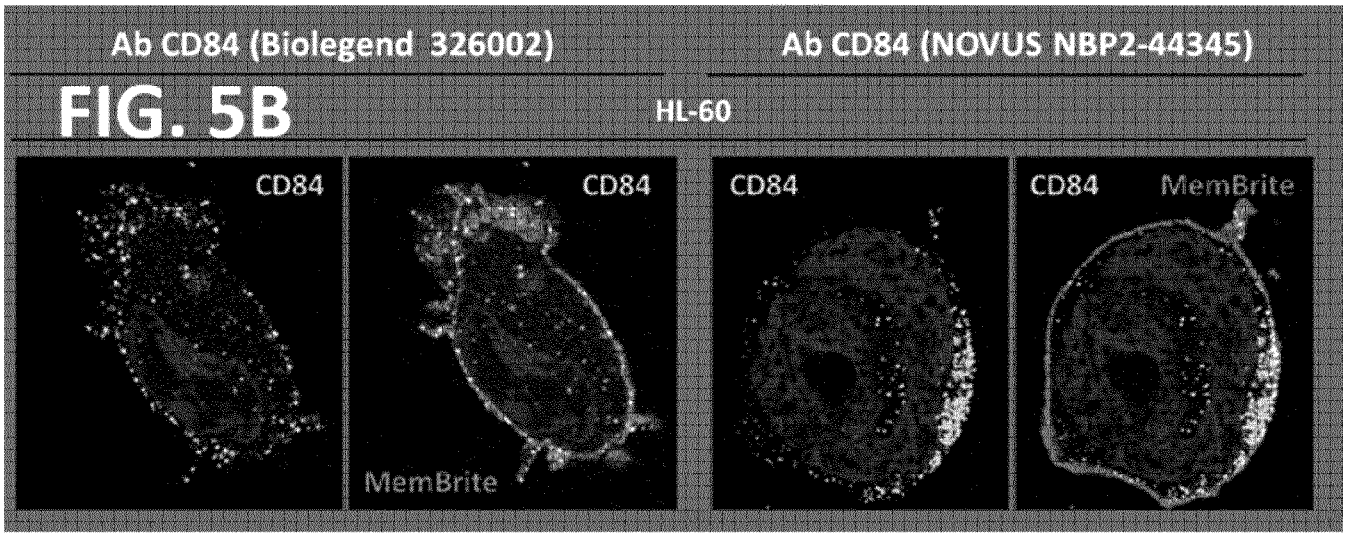


FIG. 5C

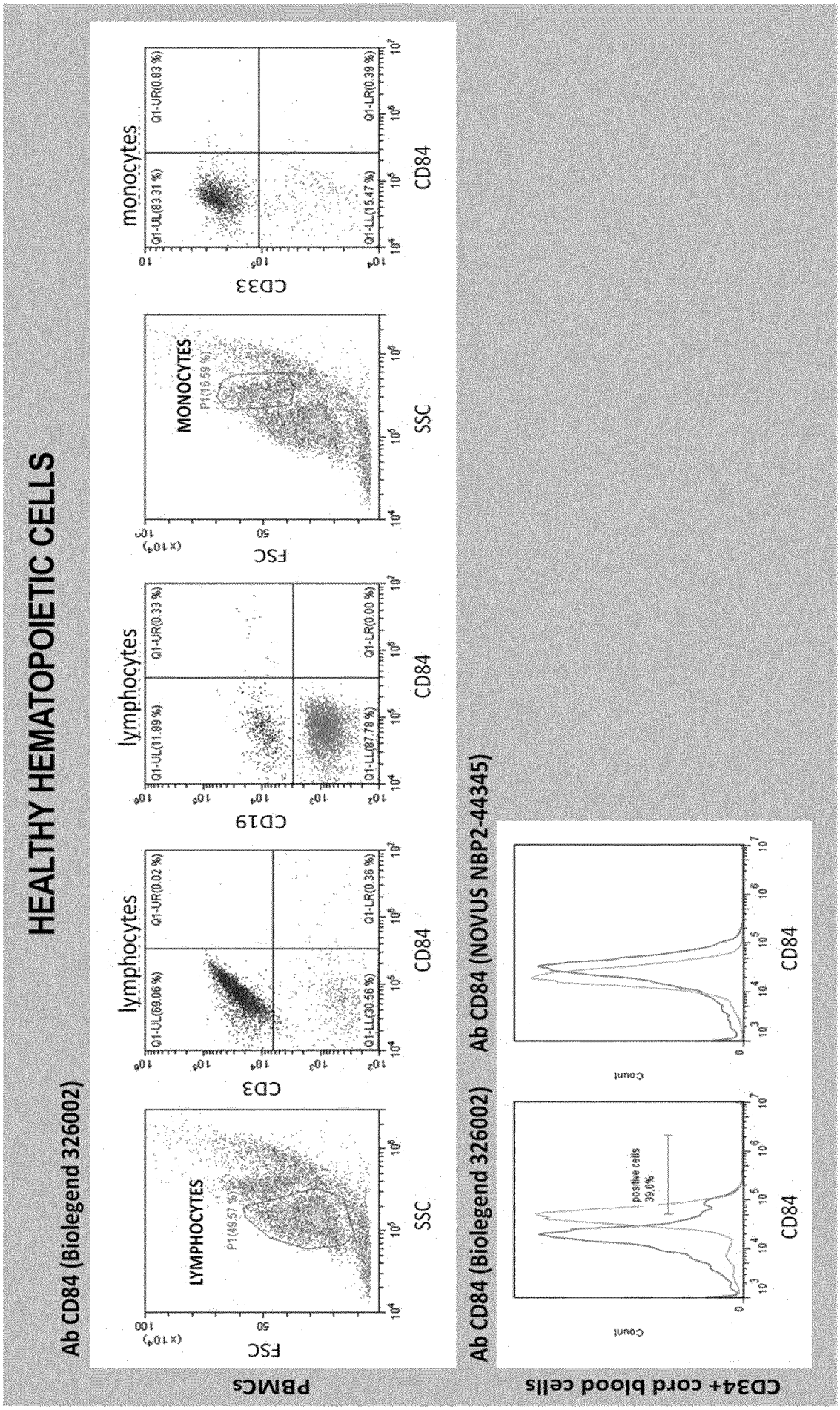

HEALTHY HEMATOPOIETIC CELLS
Ab CD84 (Biolegend 326002)
PBMCs
LYMPHOCYTES
P1(49.57 %)
FSC
SSC
lymphocytes
Q1-UL(69.06 %)
Q1-UR(0.02 %)
Q1-LL(30.56 %)
Q1-LR(0.36 %)
CD3
CD84
lymphocytes
Q1-UL(11.89 %)
Q1-UR(0.33 %)
Q1-LL(87.78 %)
Q1-LR(0.00 %)
CD19
CD84
MONOCYTES
P1(16.59 %)
FSC
SSC
monocytes
Q1-UL(83.31 %)
Q1-UR(0.83 %)
Q1-LL(15.47 %)
Q1-LR(0.39 %)
CD33
CD84
Ab CD84 (Biolegend 326002)
Ab CD84 (NOVUS NBP2-44345)
CD34+ cord blood cells
positive cells
39.0%
Count
CD84
Count
CD84

FIG. 6A

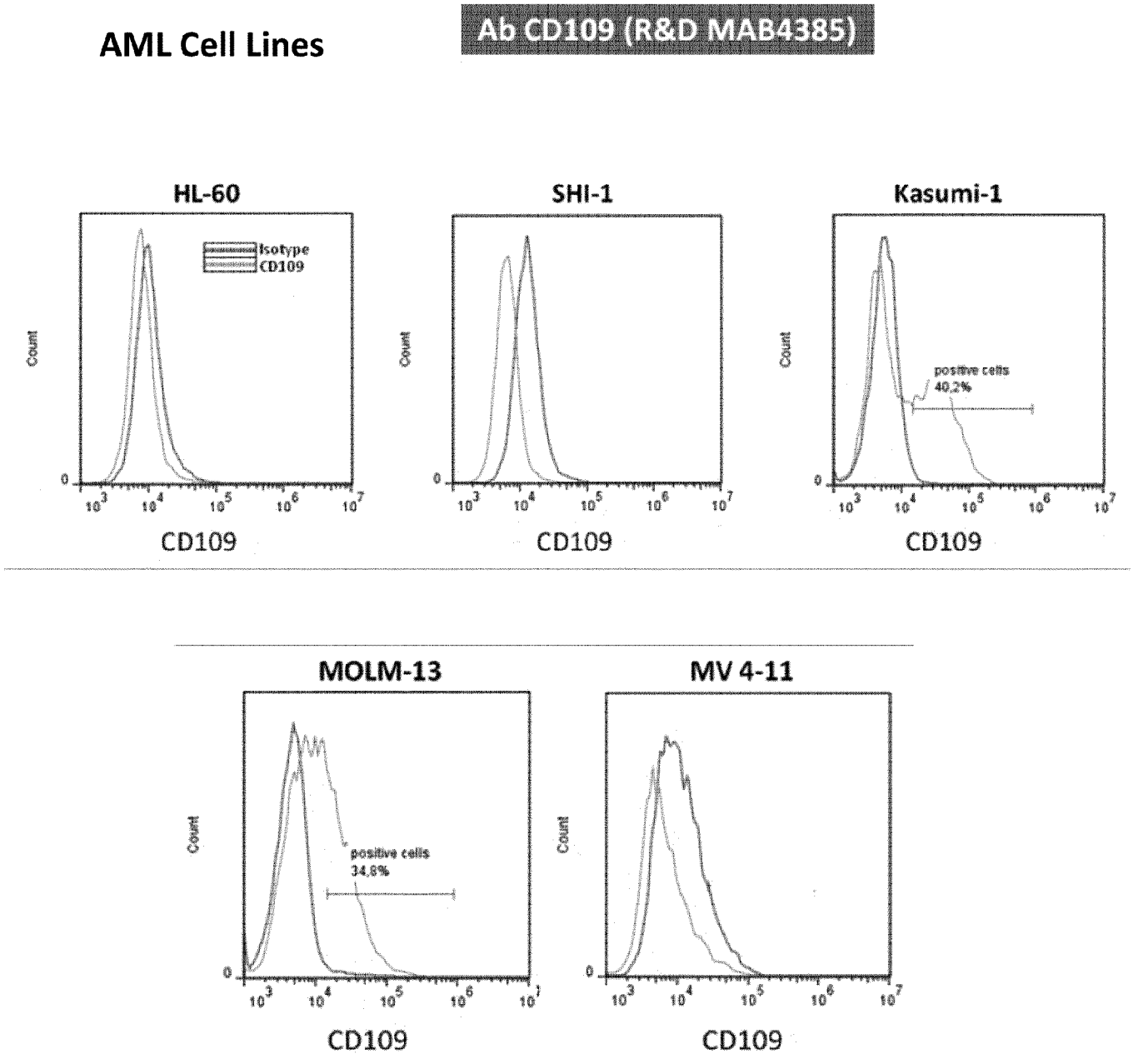

AML Cell Lines
Ab CD109 (R&D MAB4385)
HL-60
SHI-1
Kasumi-1
Isotype
CD109
Count
positive cells
40,2%
MOLM-13
MV 4-11
positive cells
34,8%
CD109

FIG. 6A (cont'd)

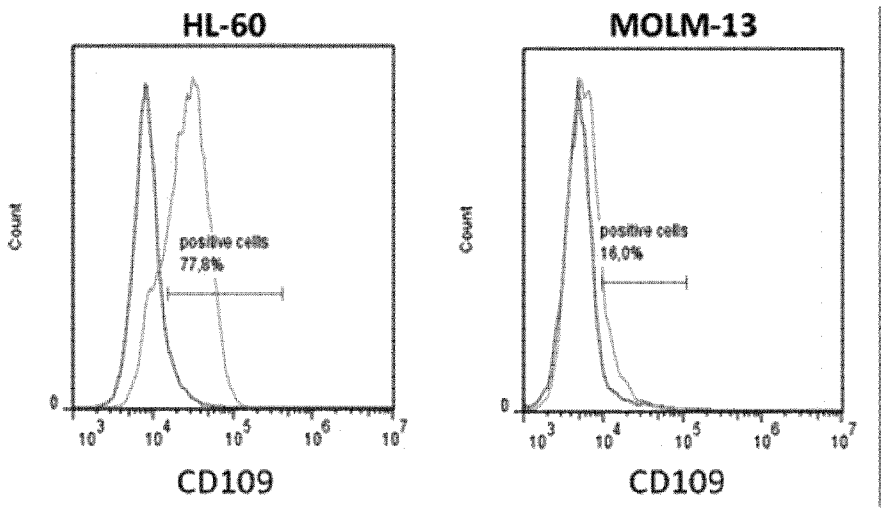


FIG. 6B

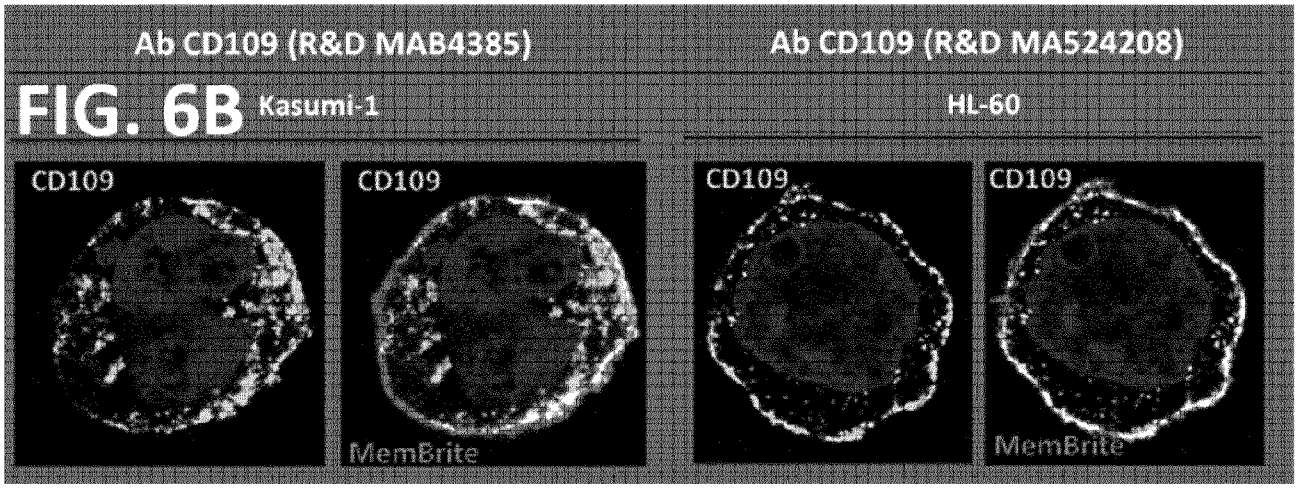


FIG. 6C

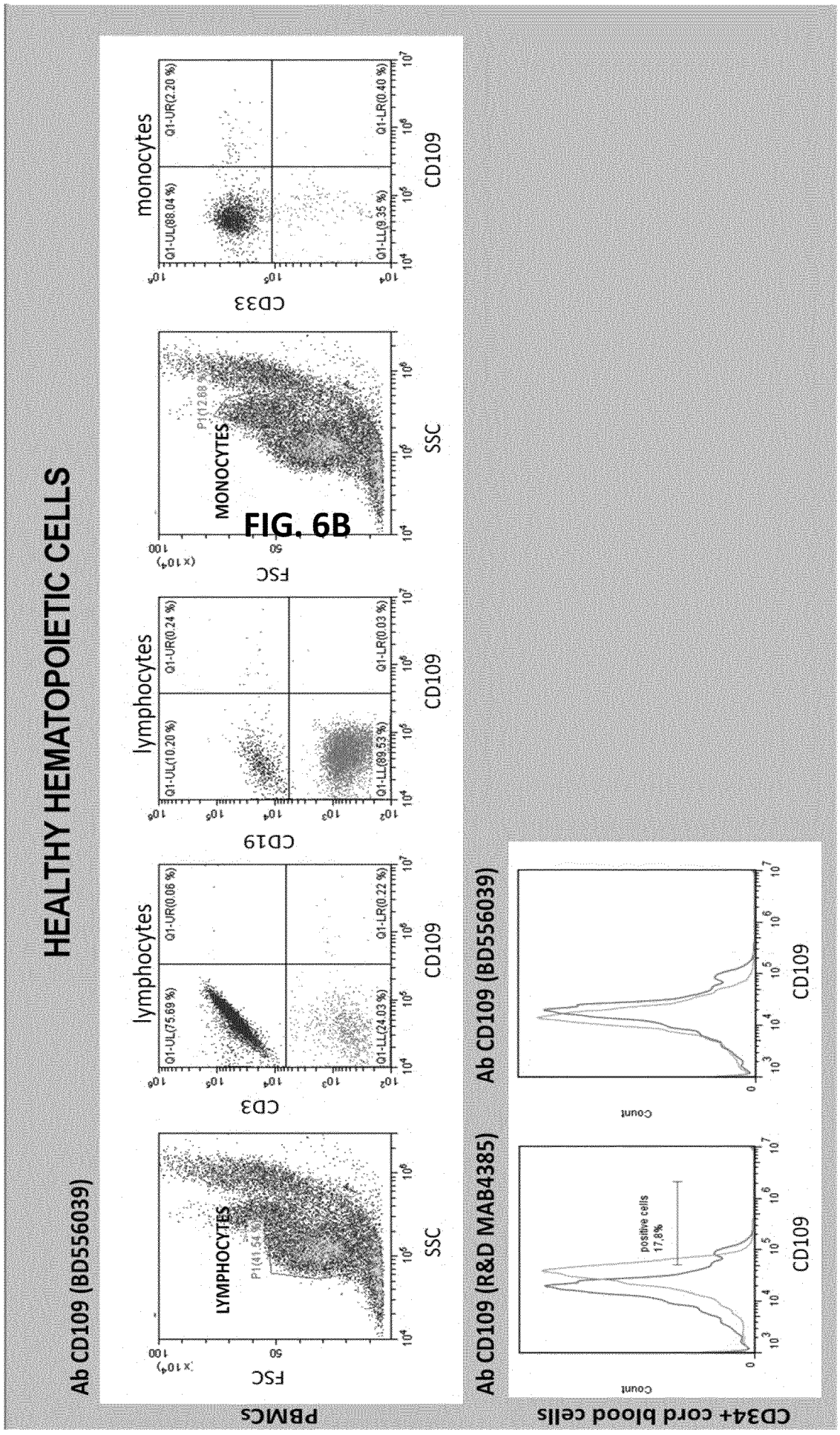

HEALTHY HEMATOPOIETIC CELLS
Ab CD109 (BD556039)
PBMCs
LYMPHOCYTES
FSC
SSC
CD3
CD109
lymphocytes
Q1-UL(75.69 %)
Q1-UR(0.06 %)
Q1-LL(24.03 %)
Q1-LR(0.22 %)
CD19
Q1-UL(10.20 %)
Q1-UR(0.24 %)
Q1-LL(89.53 %)
Q1-LR(0.03 %)
MONOCYTES
monocytes
CD33
Q1-UL(88.04 %)
Q1-UR(2.20 %)
Q1-LL(9.35 %)
Q1-LR(0.40 %)
Ab CD109 (R&D MAB4385)
Ab CD109 (BD556039)
CD34+ cord blood cells
Count
positive cells
17.8%

FIG. 6B

FIG. 7A

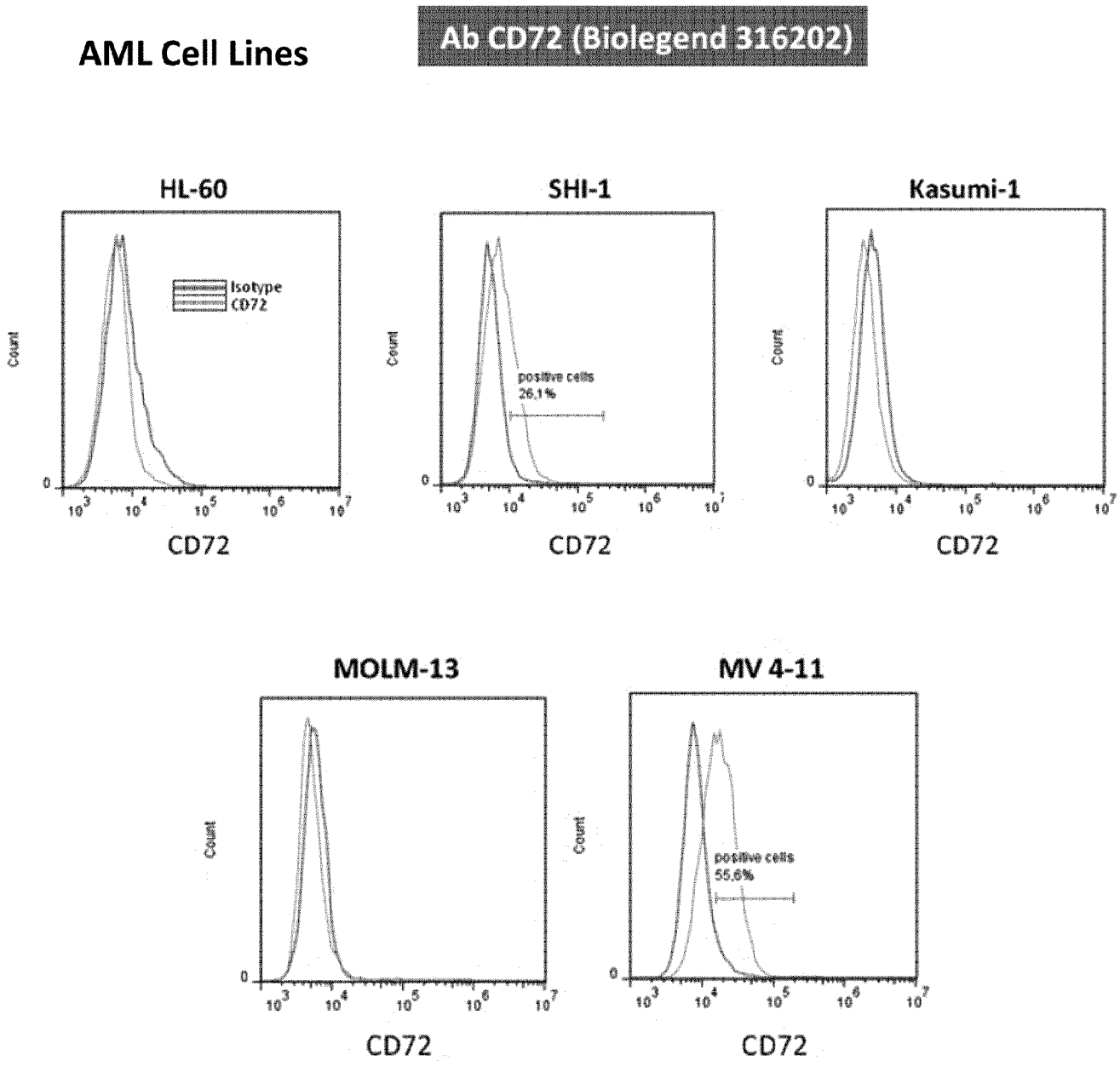

AML Cell Lines
Ab CD72 (Biolegend 316202)
HL-60
Isotype
CD72
Count
CD72
SHI-1
positive cells
26,1%
Count
CD72
Kasumi-1
Count
CD72
MOLM-13
Count
CD72
MV 4-11
positive cells
55,6%
Count
CD72

FIG. 7A (cont'd)

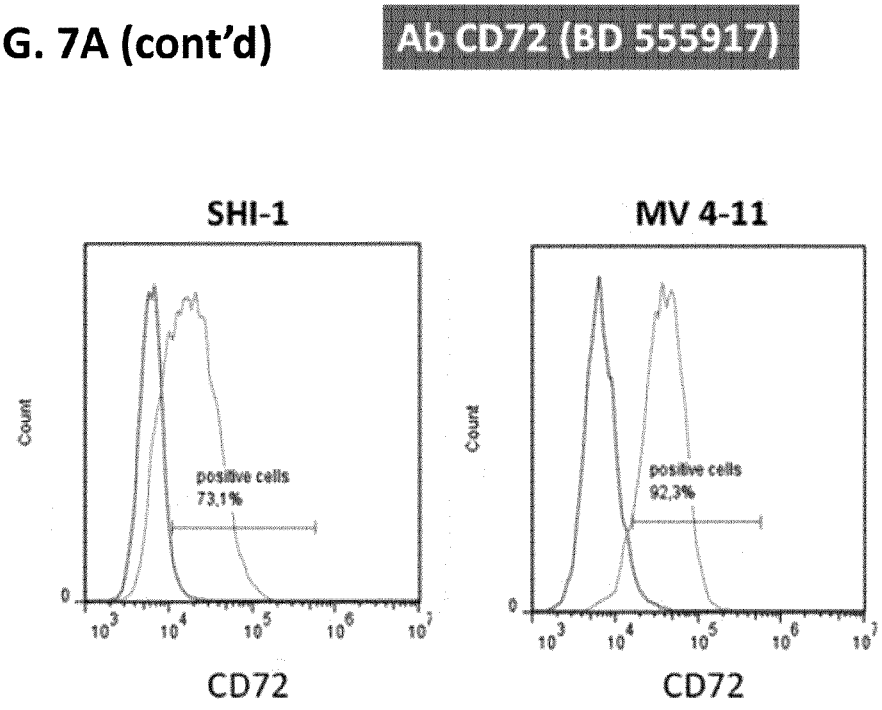


FIG. 7B

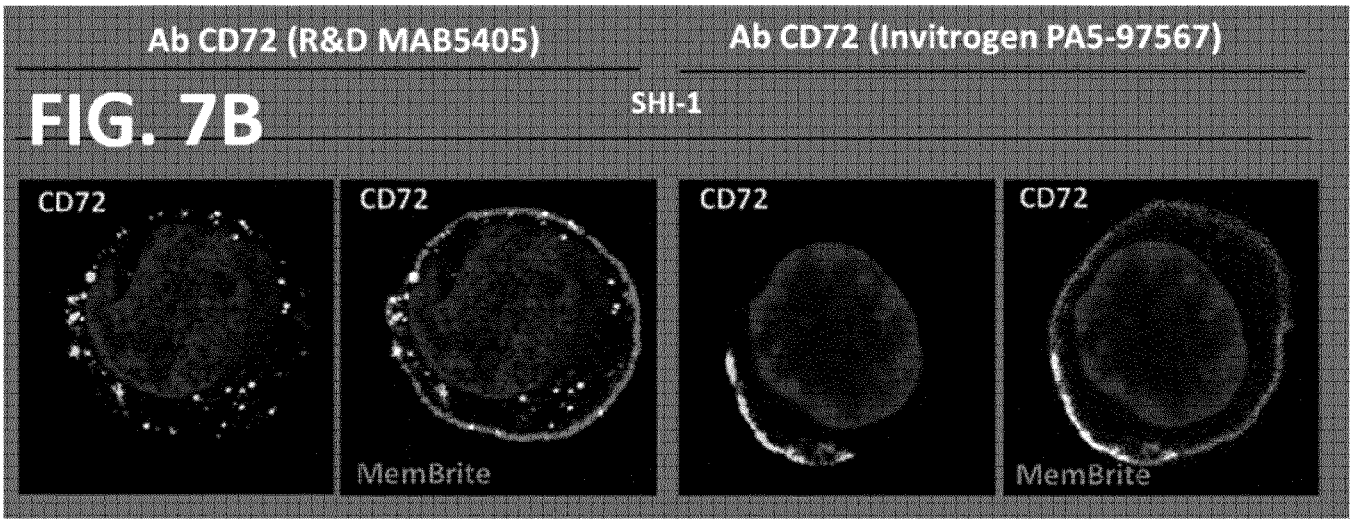


FIG. 7C

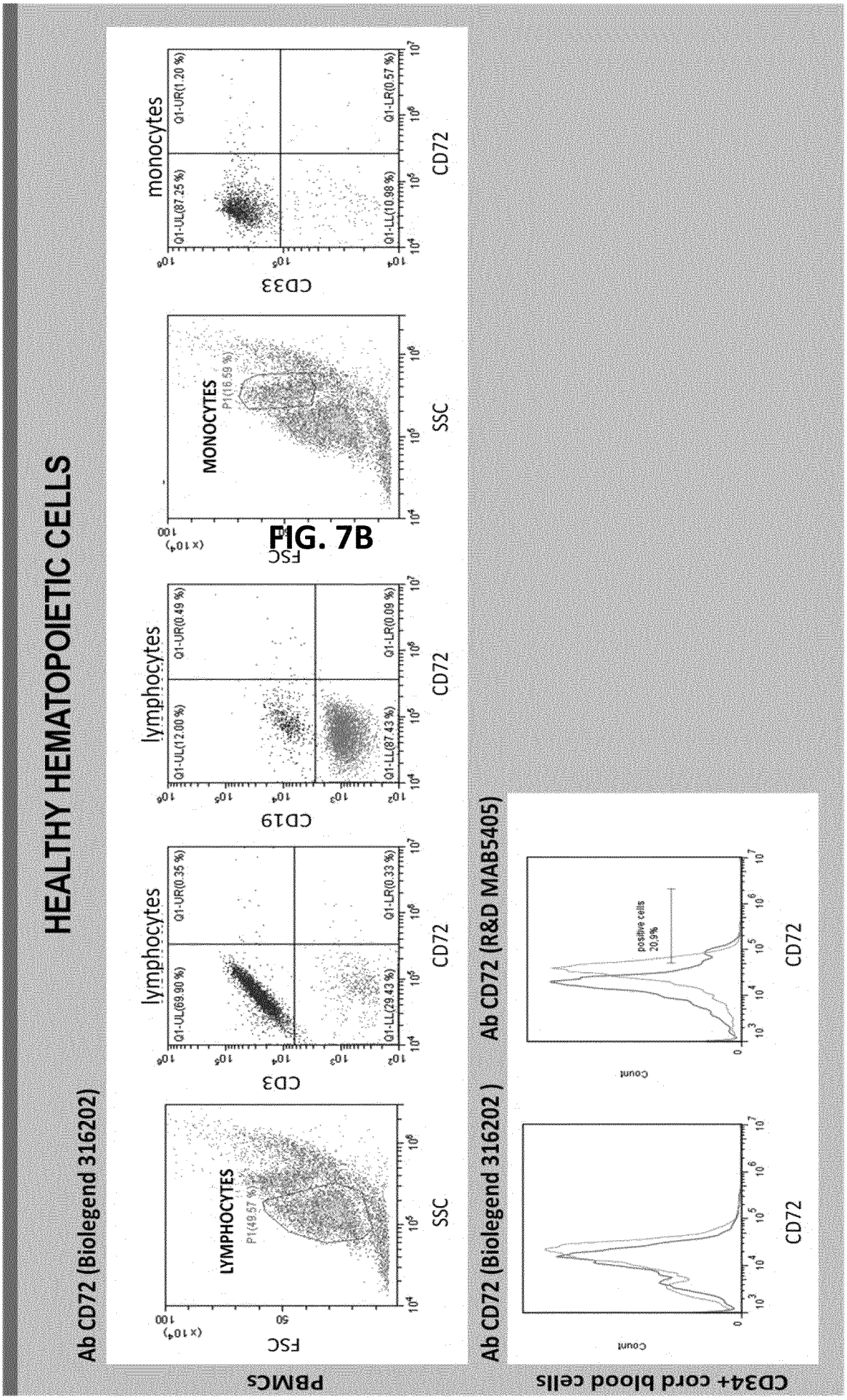

HEALTHY HEMATOPOIETIC CELLS
PBMCs
Ab CD72 (Biolegend 316202)
FSC
SSC
LYMPHOCYTES
P1(49.57 %)
CD3
CD72
lymphocytes
Q1-UL(69.90 %)
Q1-UR(0.35 %)
Q1-LL(29.43 %)
Q1-LR(0.33 %)
CD19
Q1-UL(12.00 %)
Q1-UR(0.49 %)
Q1-LL(87.43 %)
Q1-LR(0.09 %)
MONOCYTES
P1(16.59 %)
CD33
monocytes
Q1-UL(87.25 %)
Q1-UR(1.20 %)
Q1-LL(10.98 %)
Q1-LR(0.57 %)
CD34+ cord blood cells
Ab CD72 (Biolegend 316202)
Ab CD72 (R&D MAB5405)
Count
positive cells
20.9%

FIG. 7B

FIG. 8

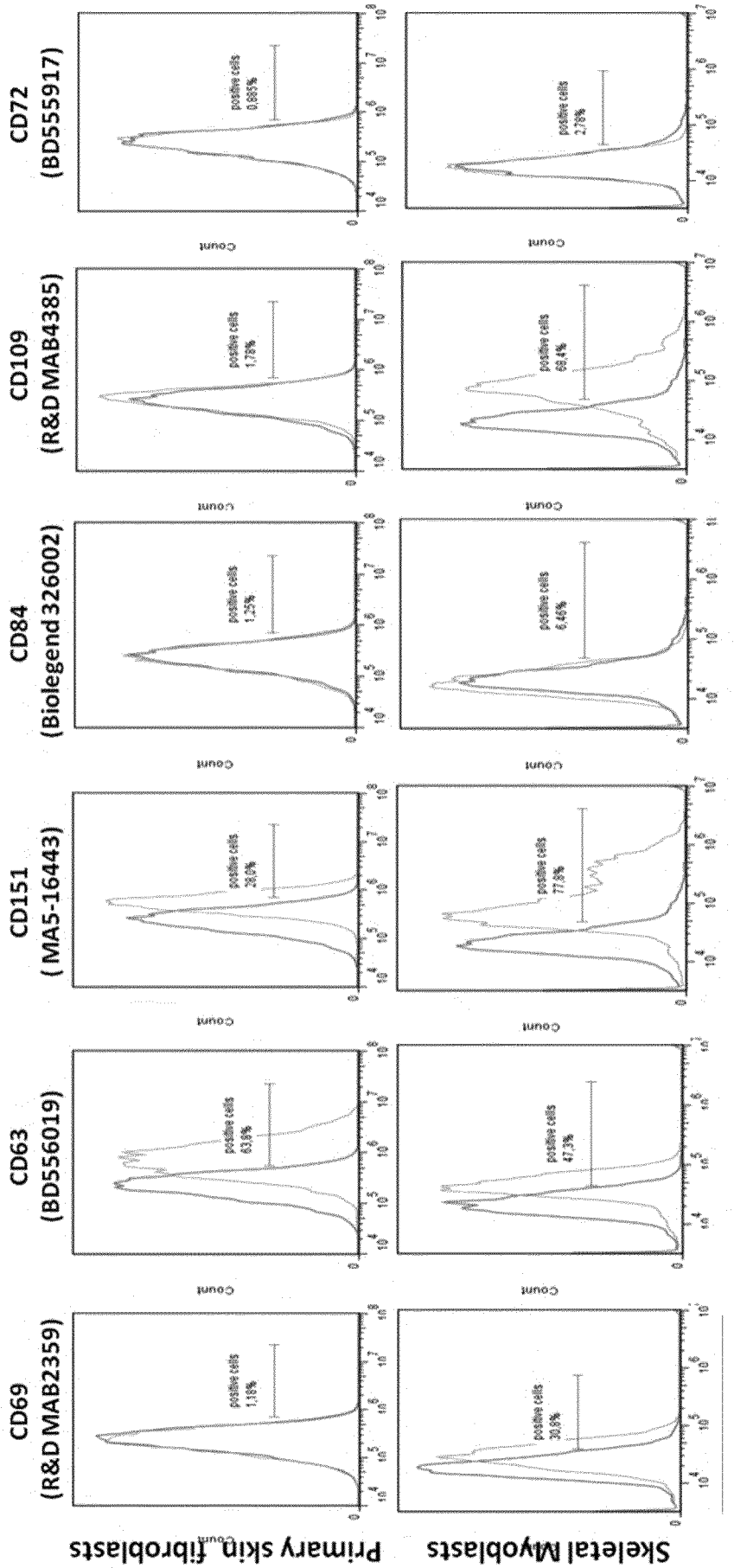

Healthy cells
Skeletal Myoblasts
Primary skin fibroblasts
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
Count
positive cells
1,16%
63,6%
28,0%
1,25%
1,78%
0,685%
30,9%
47,3%
77,8%
6,46%
69,4%
2,78%

FIG. 8 (cont'd)

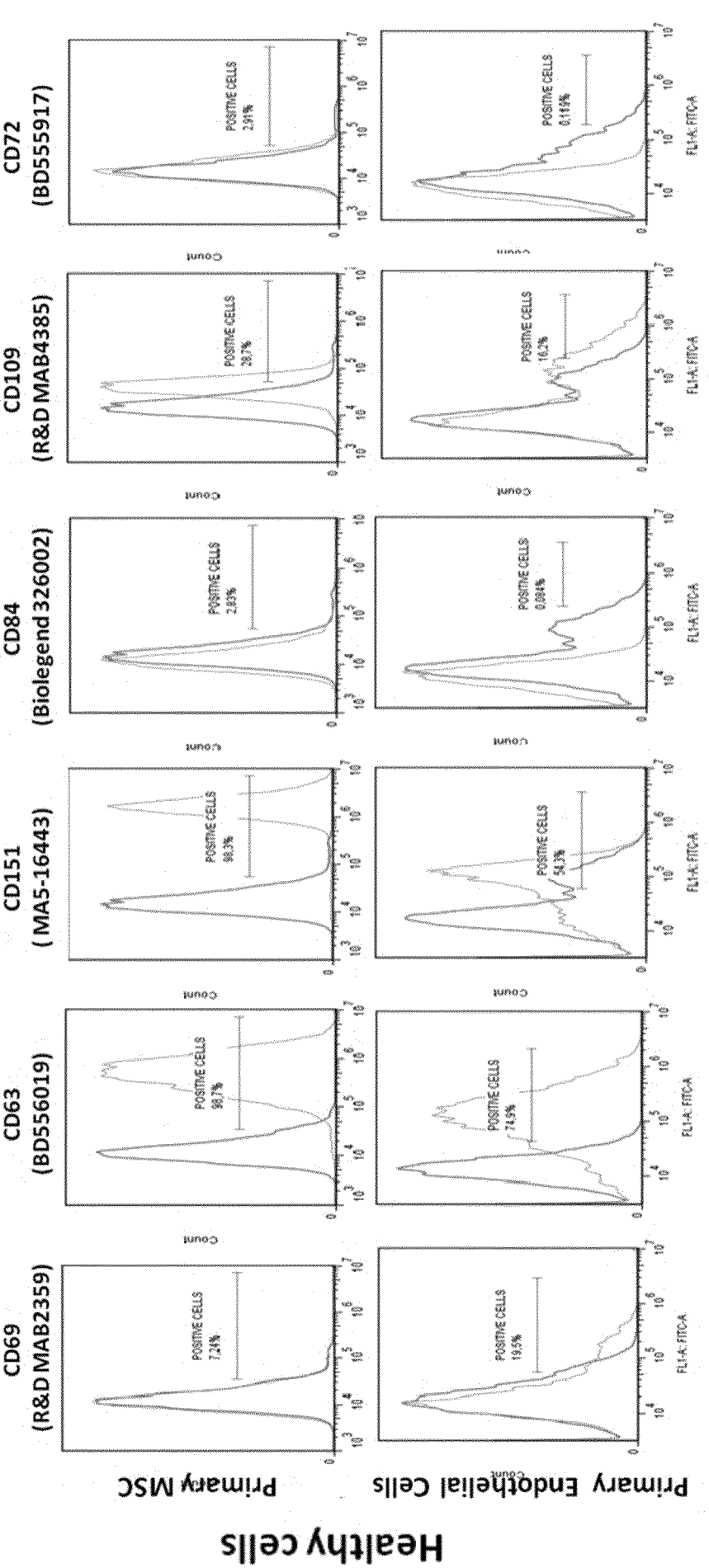

Healthy cells
Primary MSC
Primary Endothelial Cells
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
Count
FL1-A: FITC-A
POSITIVE CELLS
7,24%
98,7%
98,3%
2,83%
38,7%
2,91%
19,5%
74,9%
54,3%
0,894%
16,2%
0,119%

FIG. 9

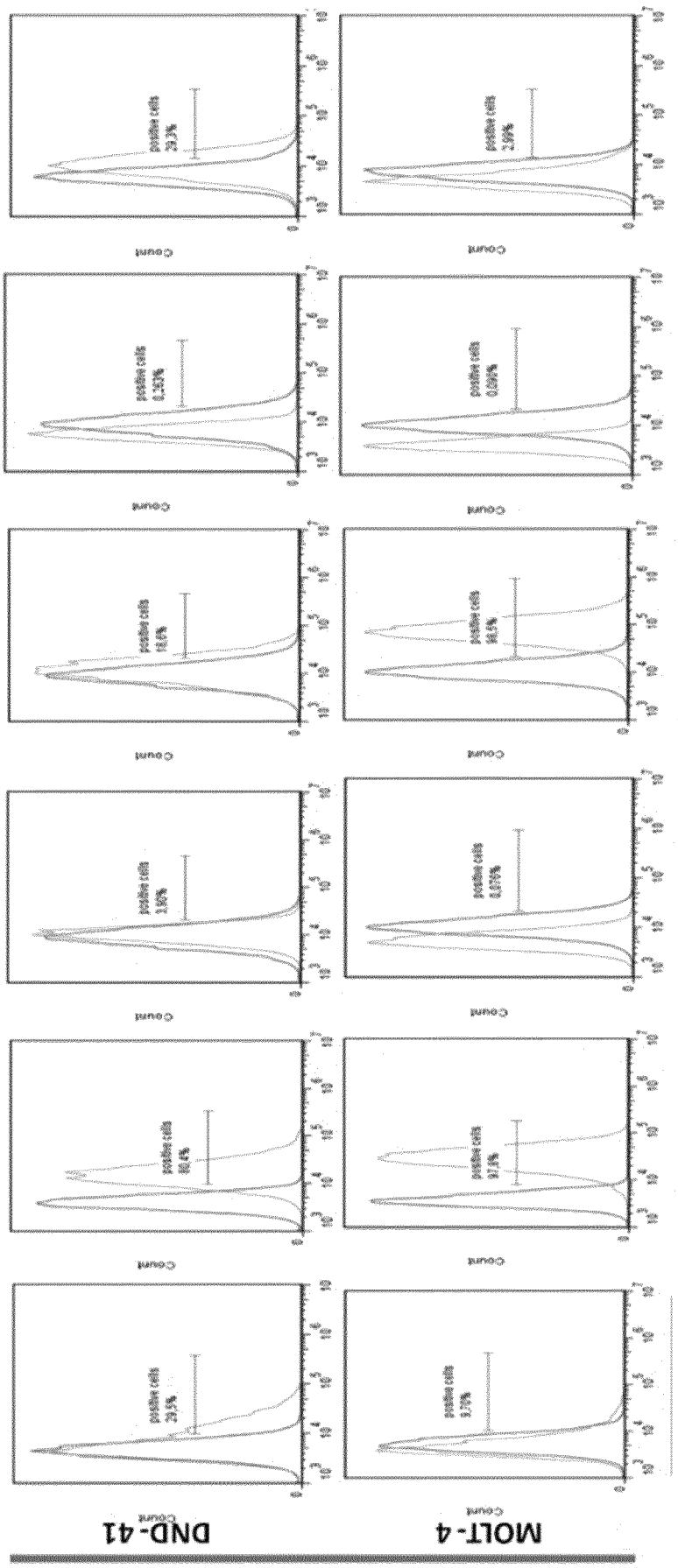

T- ALL
DND-41
MOLT-4
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
Count

FIG. 9 (cont'd)

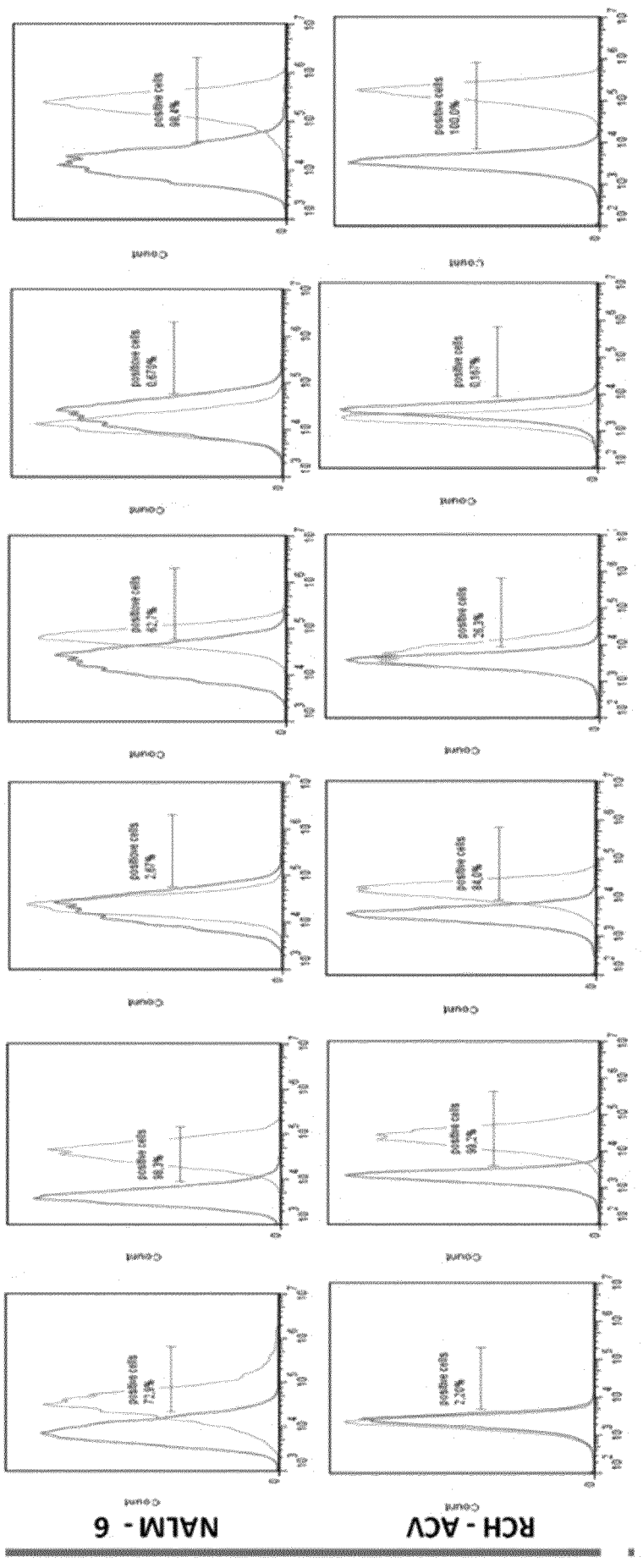

B-ALL
NALM-6
RCH-ACV
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
Count
positive cells

FIG. 9 (cont'd)

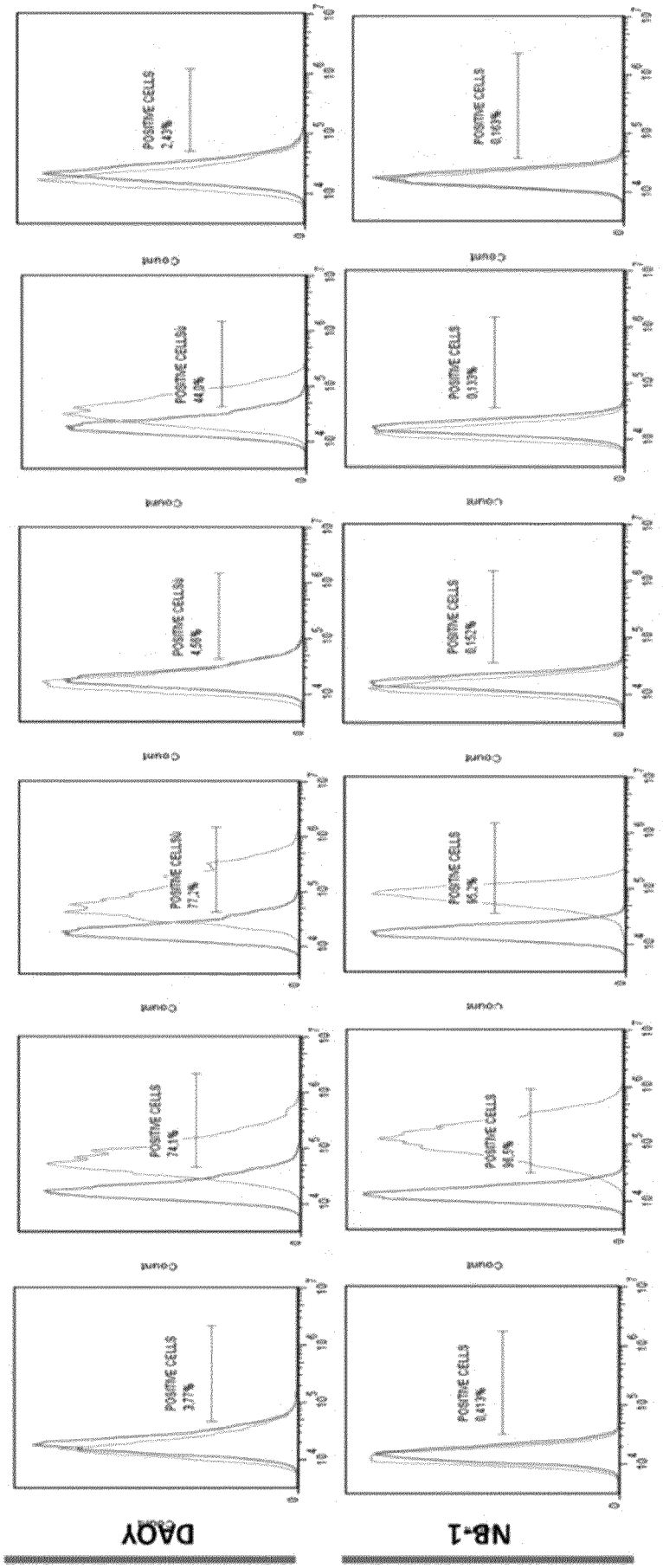

Medulloblastoma
Neuroblastoma
DAOY
NB-1
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
Count
POSITIVE CELLS

FIG. 9 (cont'd)

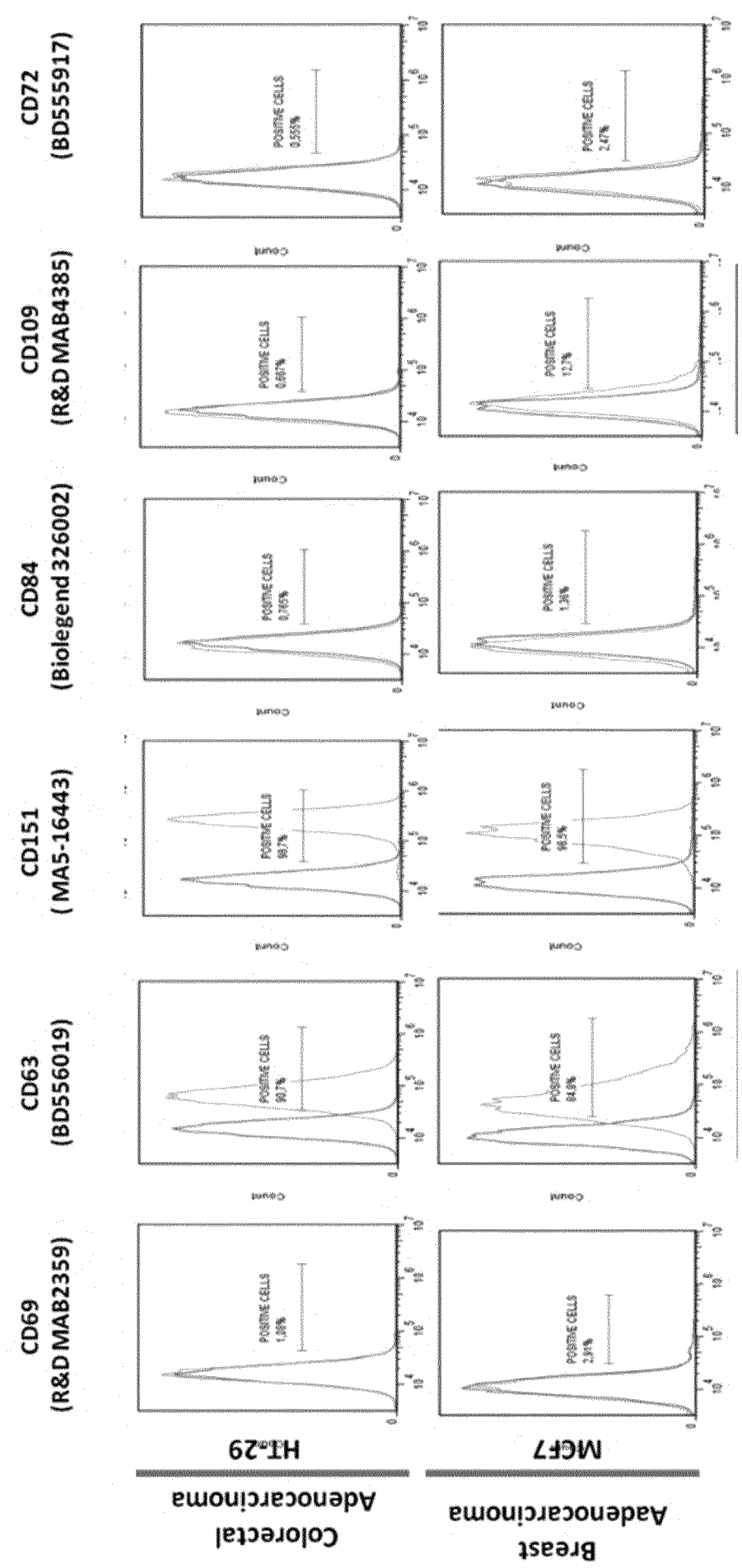

Breast Adenocarcinoma
Colorectal Adenocarcinoma
MCF7
HT-29
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
POSITIVE CELLS
Count

FIG. 9 (cont'd)

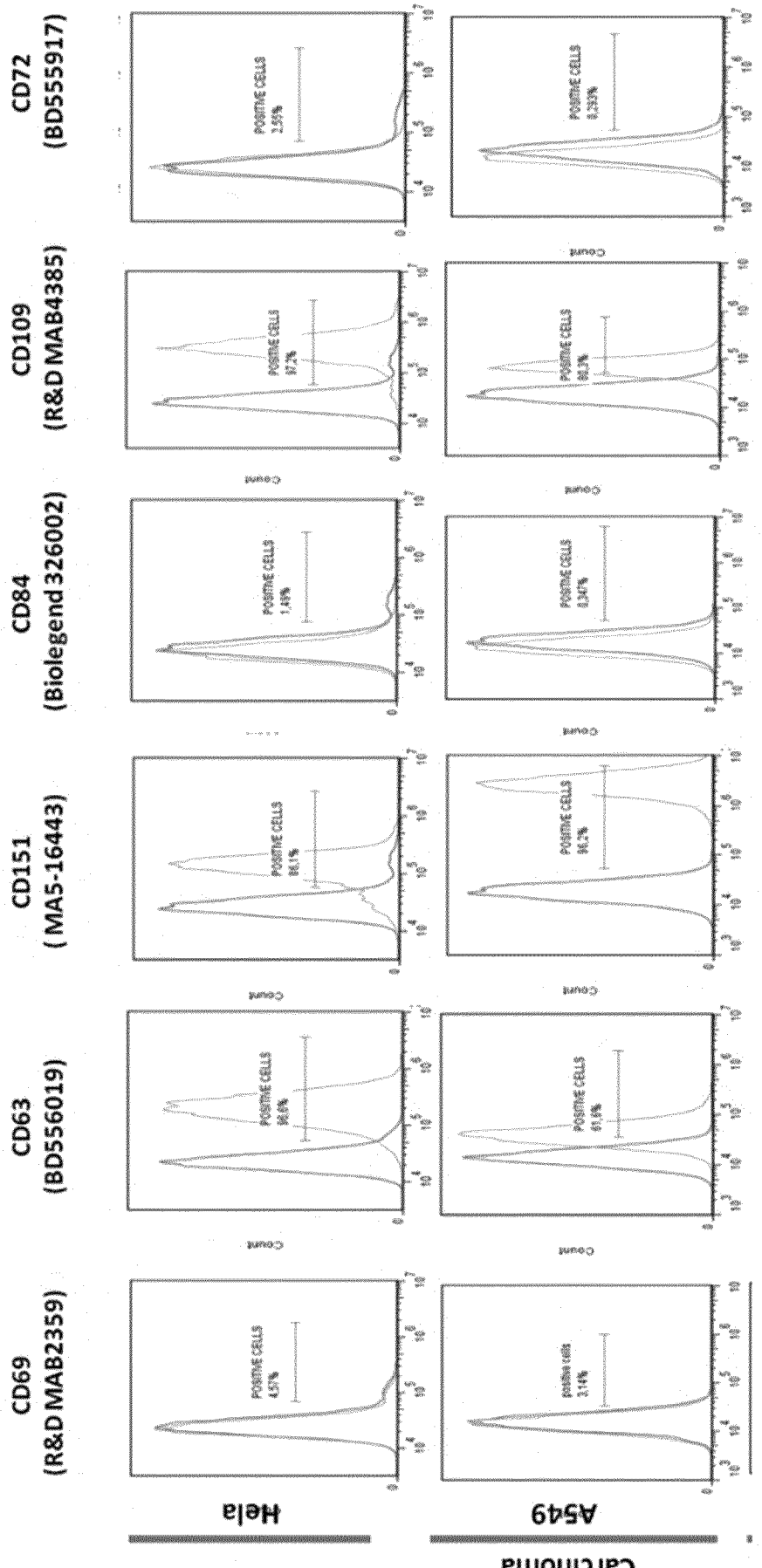

CD69
(R&D MAB2359)
CD63
(BD556019)
CD151
(MA5-16443)
CD84
(Biolegend 326002)
CD109
(R&D MAB4385)
CD72
(BD555917)
Cervix
Adenocarcinoma
HeLa
Lung
Carcinoma
A549
Count
POSITIVE CELLS
4.57%
POSITIVE CELLS
86.8%
POSITIVE CELLS
86.1%
POSITIVE CELLS
1.48%
POSITIVE CELLS
87.2%
POSITIVE CELLS
2.14%
POSITIVE CELLS
61.1%
POSITIVE CELLS
86.2%
POSITIVE CELLS
0.34%
POSITIVE CELLS
80.3%
POSITIVE CELLS
0.33%

FIG. 9 (cont'd)

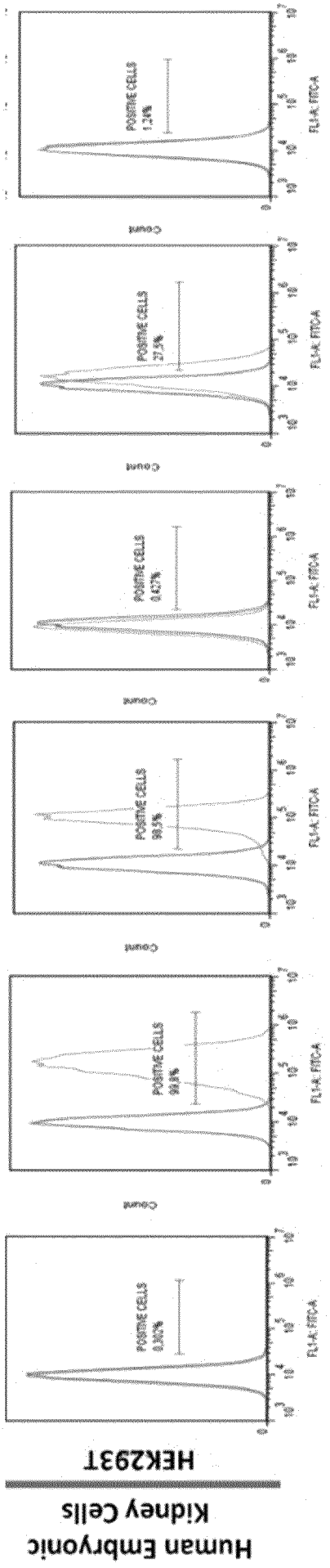

Human Embryonic Kidney Cells
HEK293T
CD69 (R&D MAB2359)
CD63 (BD556019)
CD151 (MA5-16443)
CD84 (Biolegend 326002)
CD109 (R&D MAB4385)
CD72 (BD555917)
POSITIVE CELLS
FL1-A: FITC-A
Count

FIG. 10

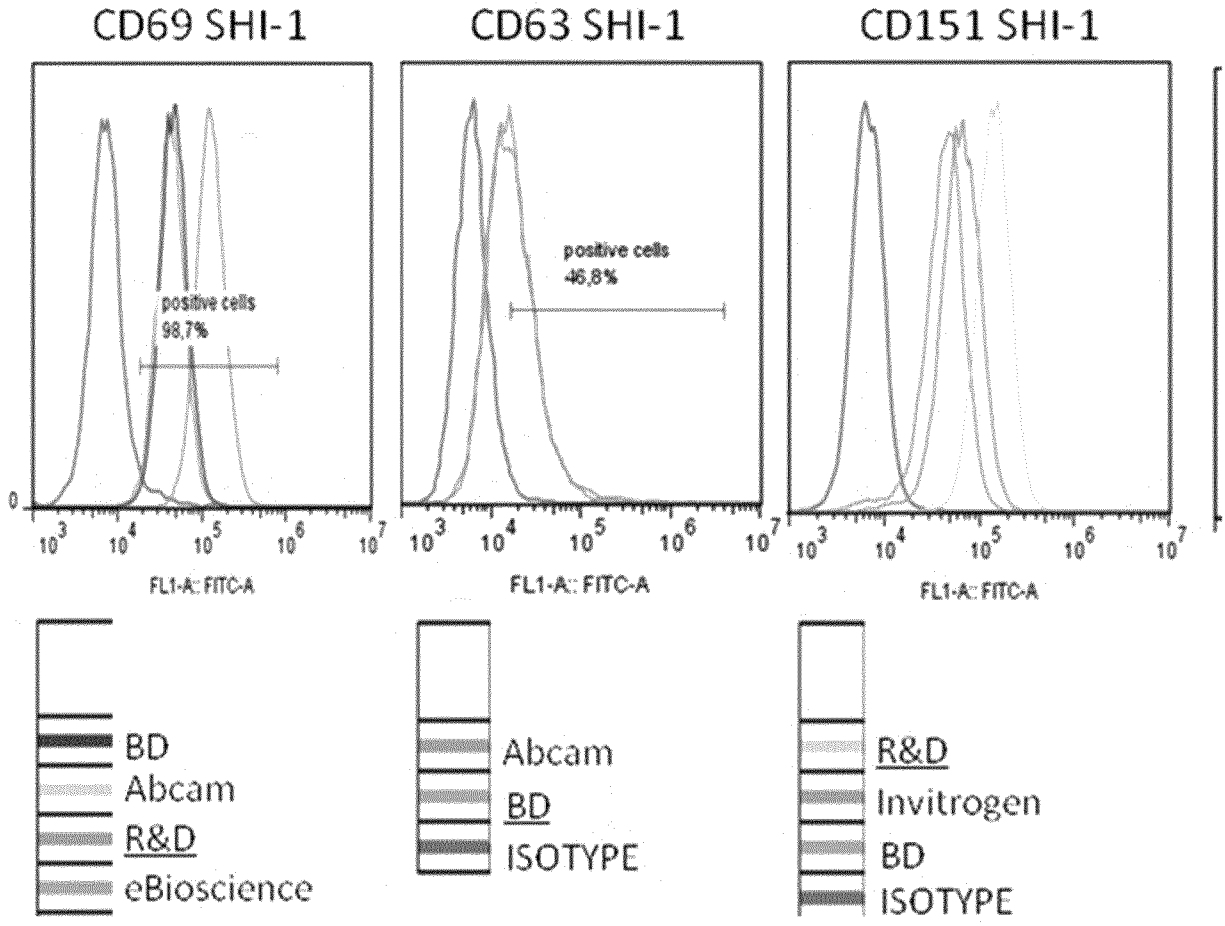

CD69 SHI-1
CD63 SHI-1
CD151 SHI-1
positive cells
98,7%
positive cells
46,8%
0
10^3 10^4 10^5 10^6 10^7
FL1-A:: FITC-A
BD
Abcam
R&D
eBioscience
Abcam
BD
ISOTYPE
R&D
Invitrogen
BD
ISOTYPE

FIG. 10 (Continued)

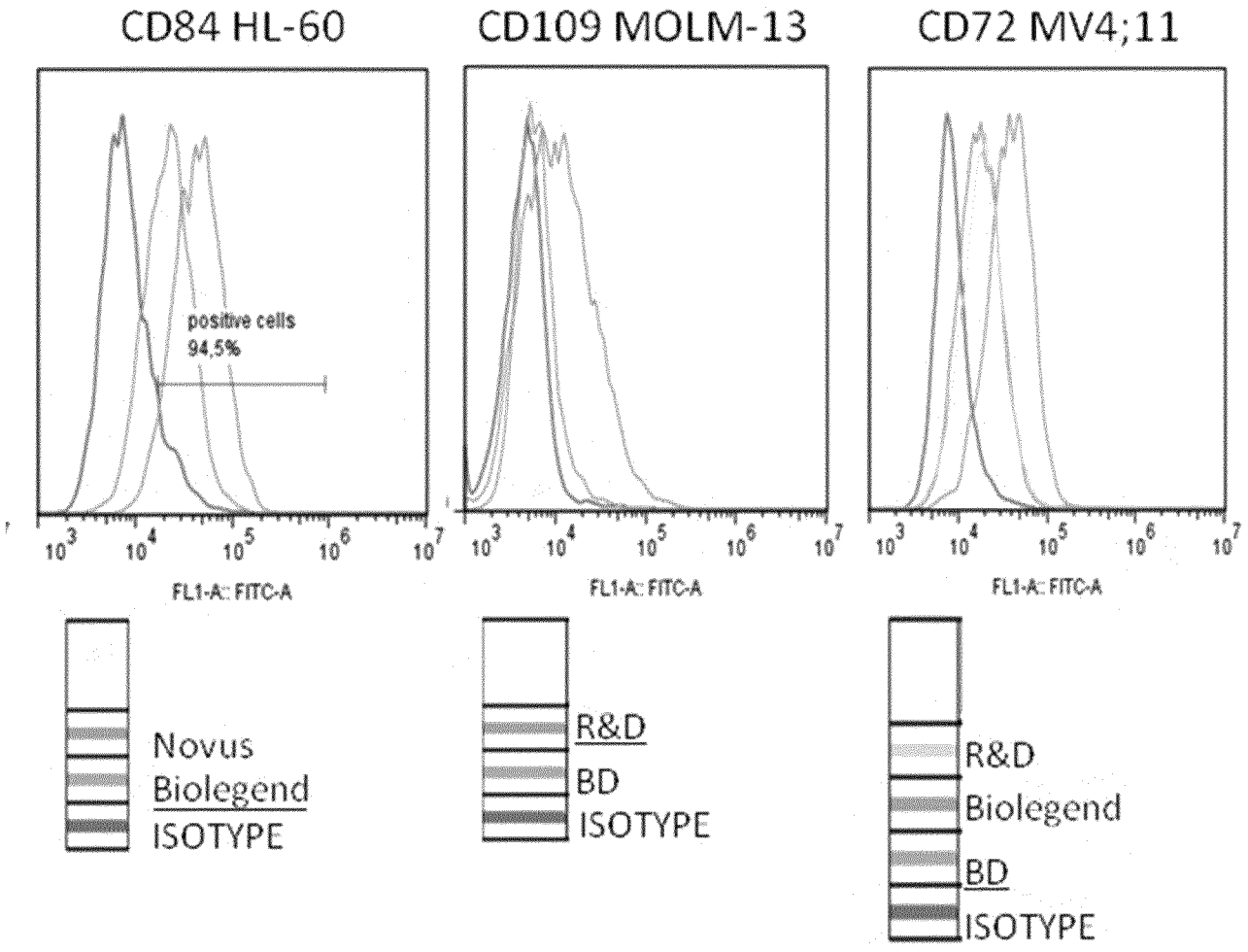


FIG. 11

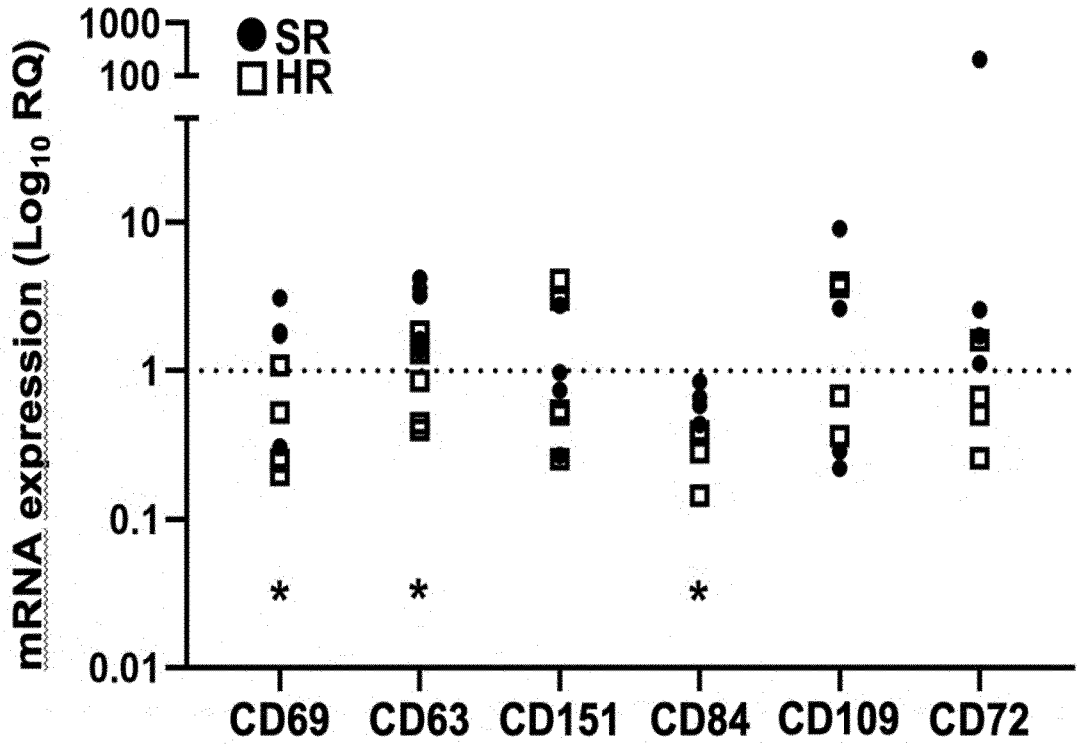

1000
100
10
1
0.1
0.01
SR
HR
mRNA expression (Log10 RQ)
CD69
CD63
CD151
CD84
CD109
CD72

FIG. 12A

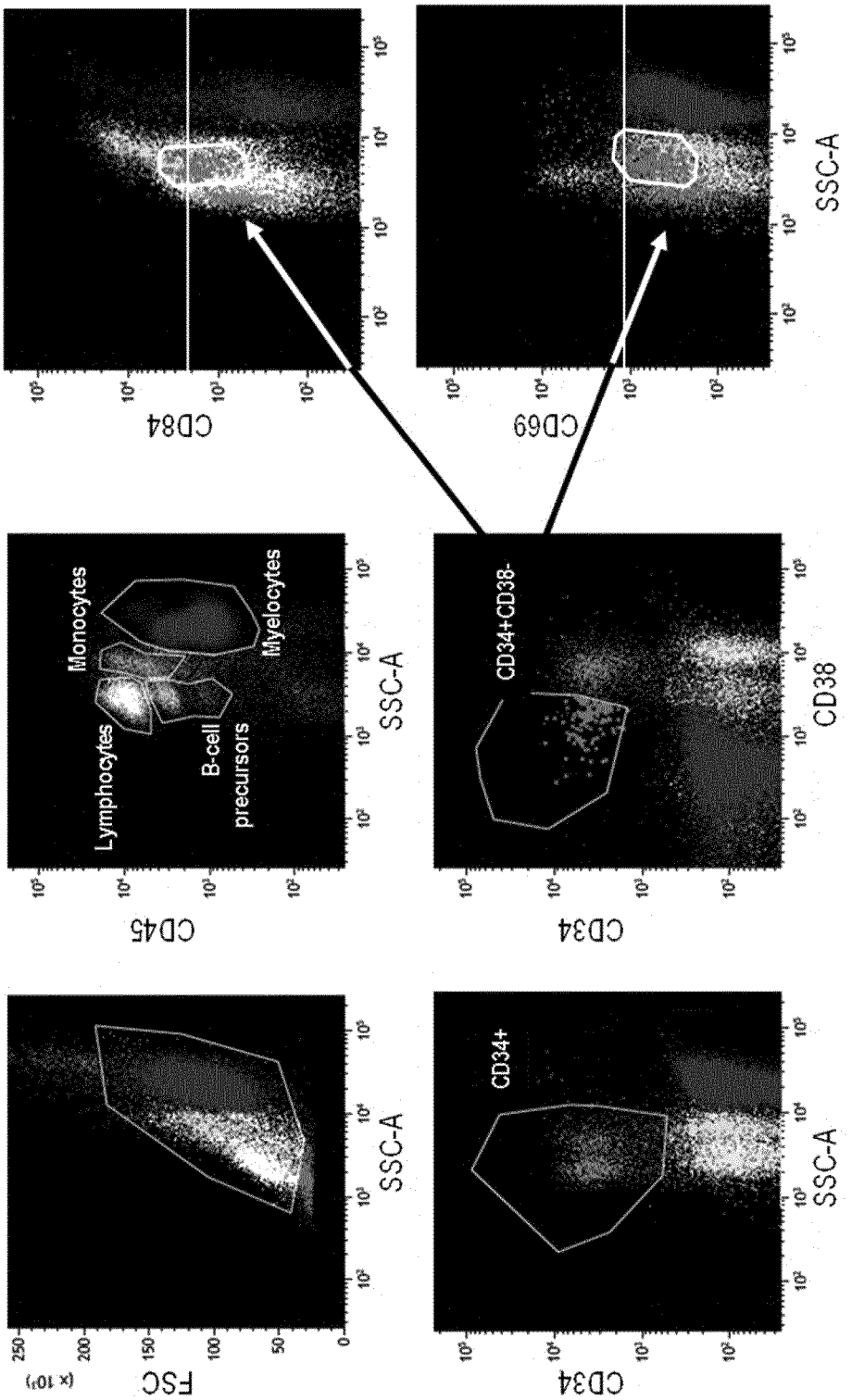

TSA expression in healthy CD34+CD38-
FSC
SSC-A
CD34+
CD34
CD38
CD34+CD38-
CD45
Lymphocytes
Monocytes
B-cell precursors
Myelocytes
CD84
CD69

FIG. 12B

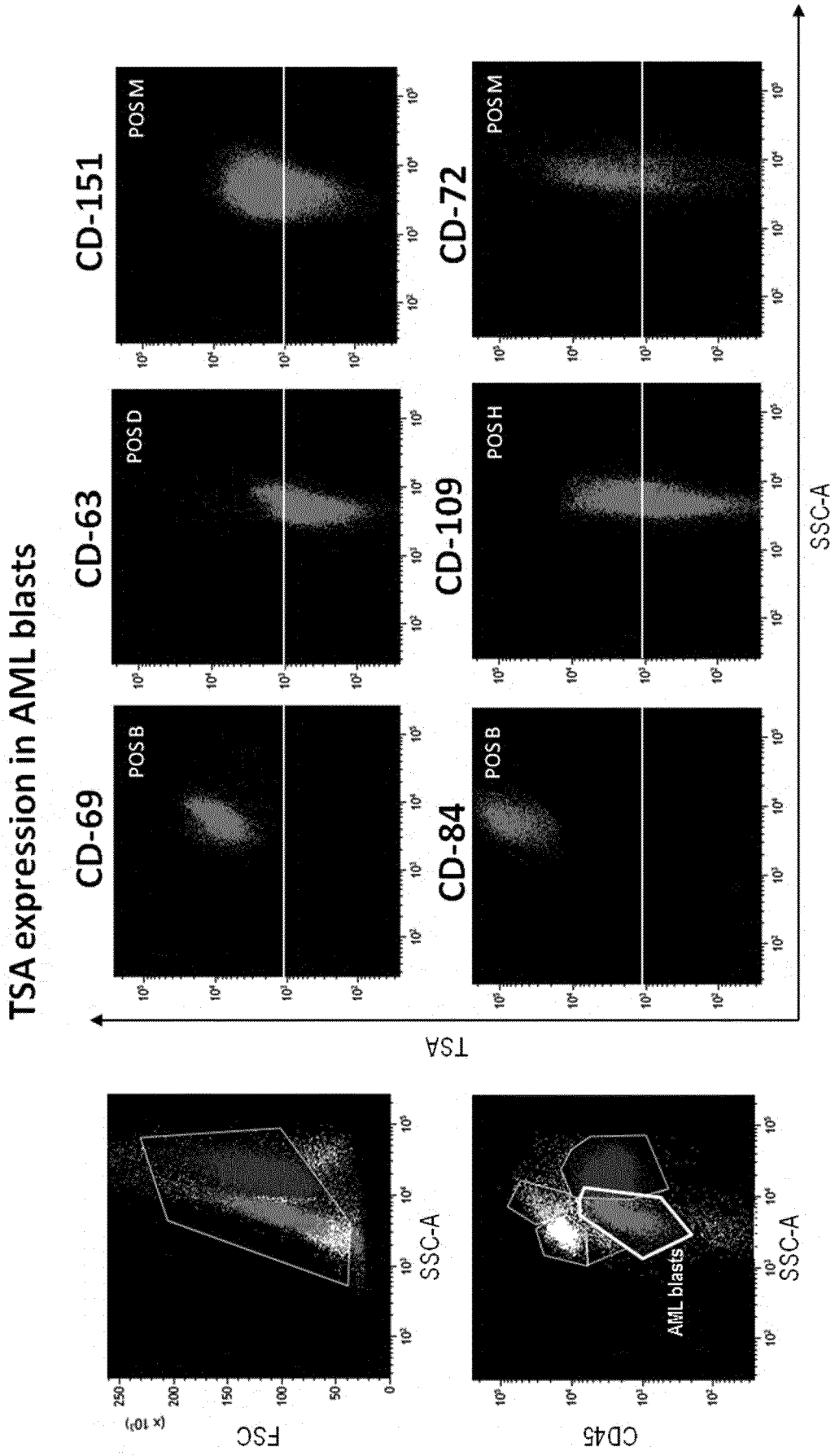

TSA expression in AML blasts
CD-69
POS B
CD-63
POS D
CD-151
POS M
CD-84
POS B
CD-109
POS H
CD-72
POS M
TSA
SSC-A
FSC
SSC-A
CD45
SSC-A
AML blasts

FIG. 13

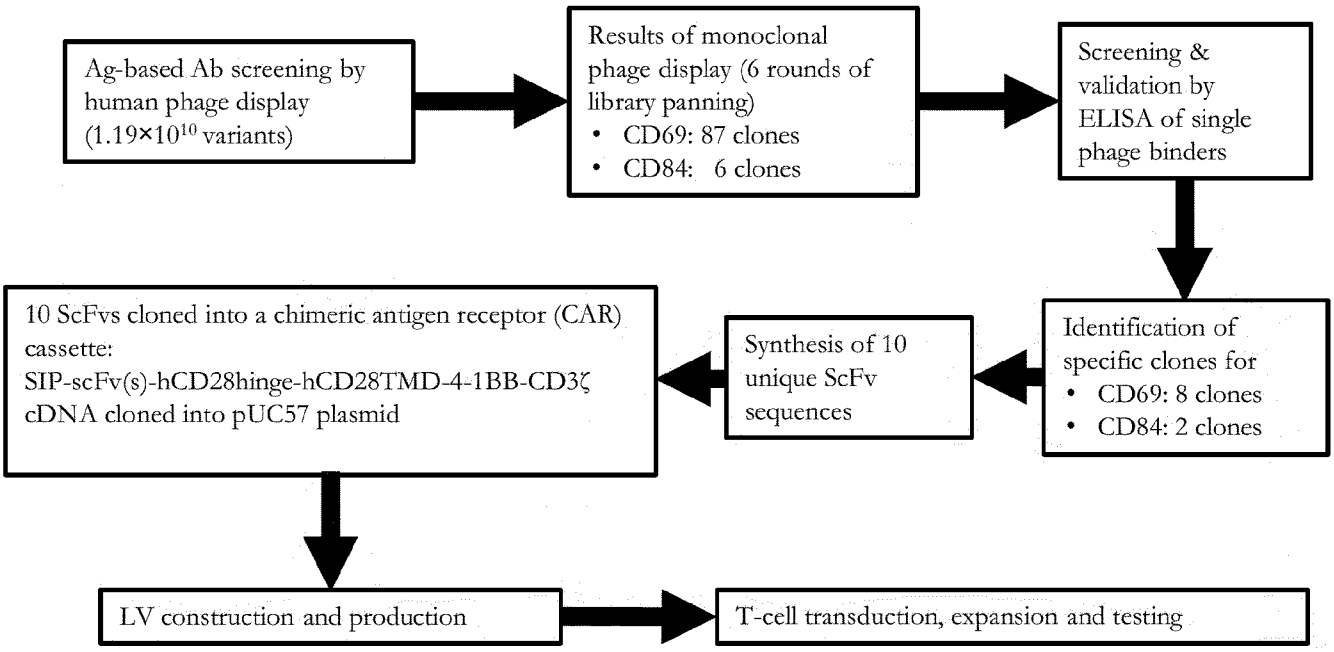

Ag-based Ab screening by human phage display (1.19×10^10 variants)
Results of monoclonal phage display (6 rounds of library panning)
• CD69: 87 clones
• CD84: 6 clones
Screening & validation by ELISA of single phage binders
Identification of specific clones for
• CD69: 8 clones
• CD84: 2 clones
Synthesis of 10 unique ScFv sequences
10 ScFvs cloned into a chimeric antigen receptor (CAR) cassette:
SIP-scFv(s)-hCD28hinge-hCD28TMD-4-1BB-CD3ζ
cDNA cloned into pUC57 plasmid
LV construction and production
T-cell transduction, expansion and testing

FIG. 14

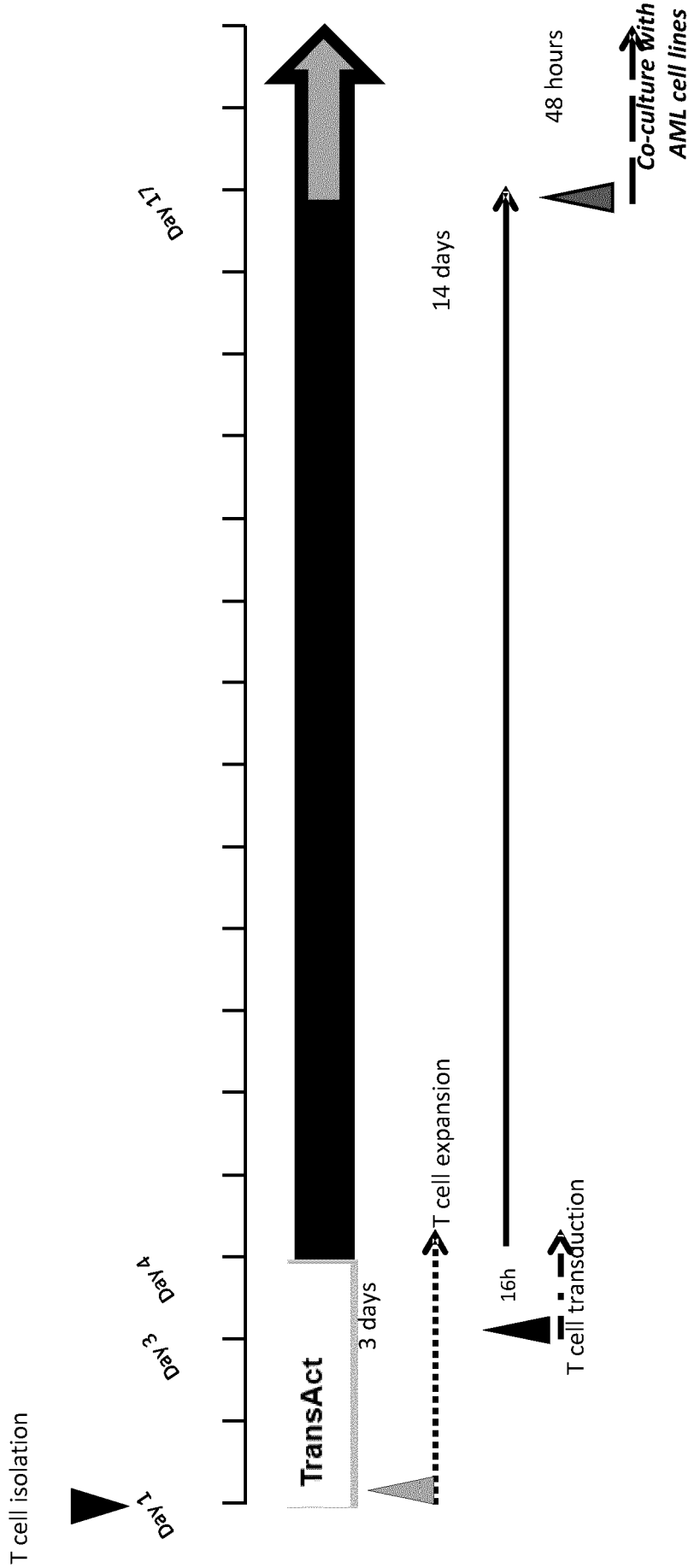

T cell isolation
Day 1
Day 3
Day 4
Day 17
TransAct
3 days
T cell expansion
14 days
16h
T cell transduction
48 hours
Co-culture With
AML cell lines

FIG. 15

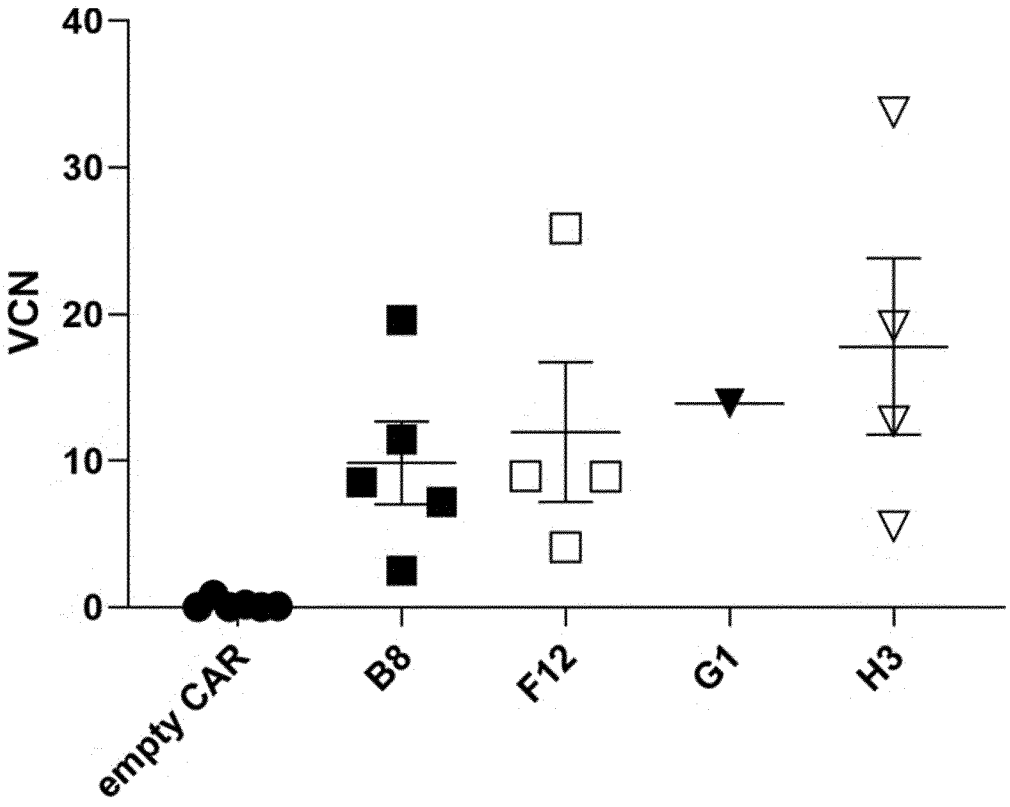


FIG. 16

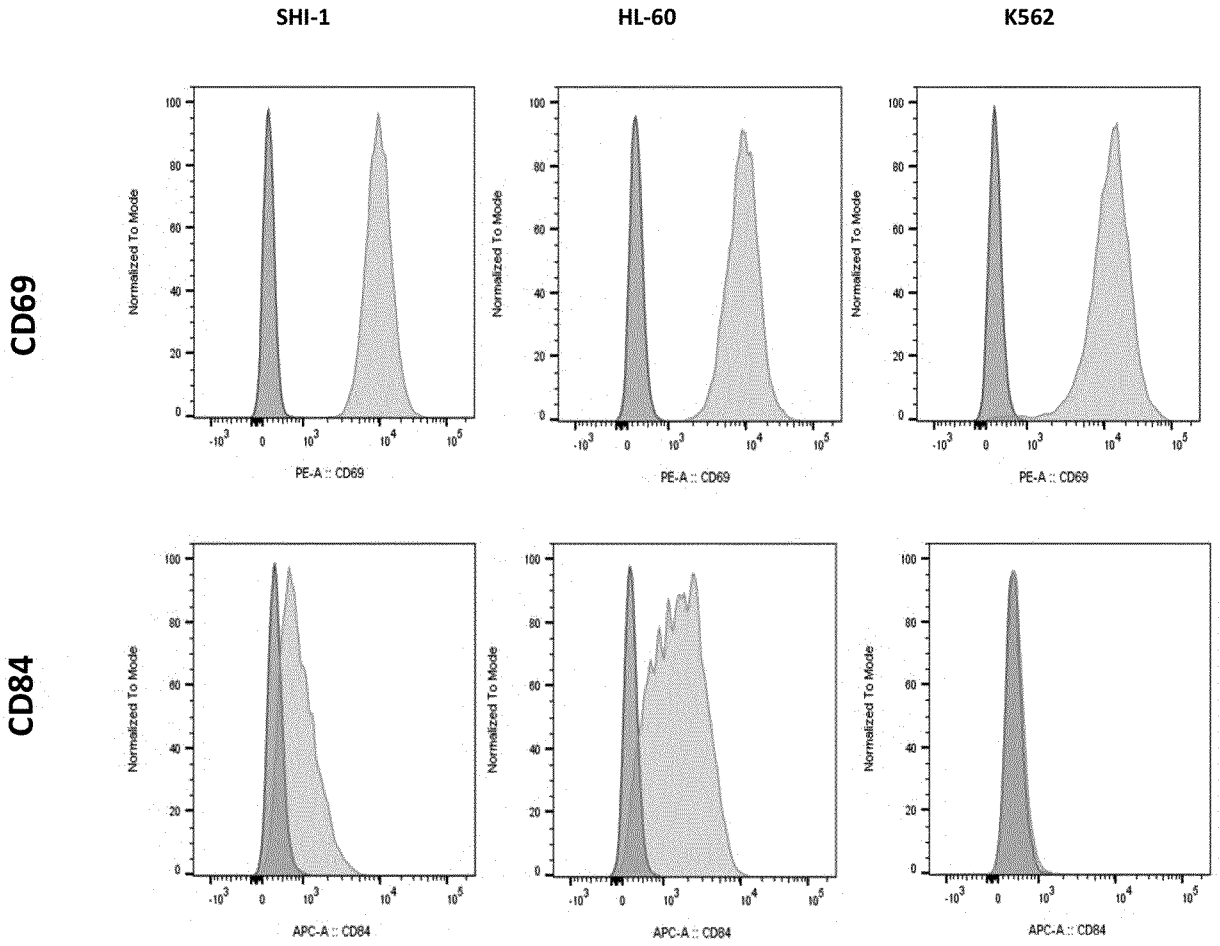

SHI-1
HL-60
K562
CD69
CD84
Normalized To Mode
PE-A :: CD69
APC-A :: CD84

FIG. 16 (continued)

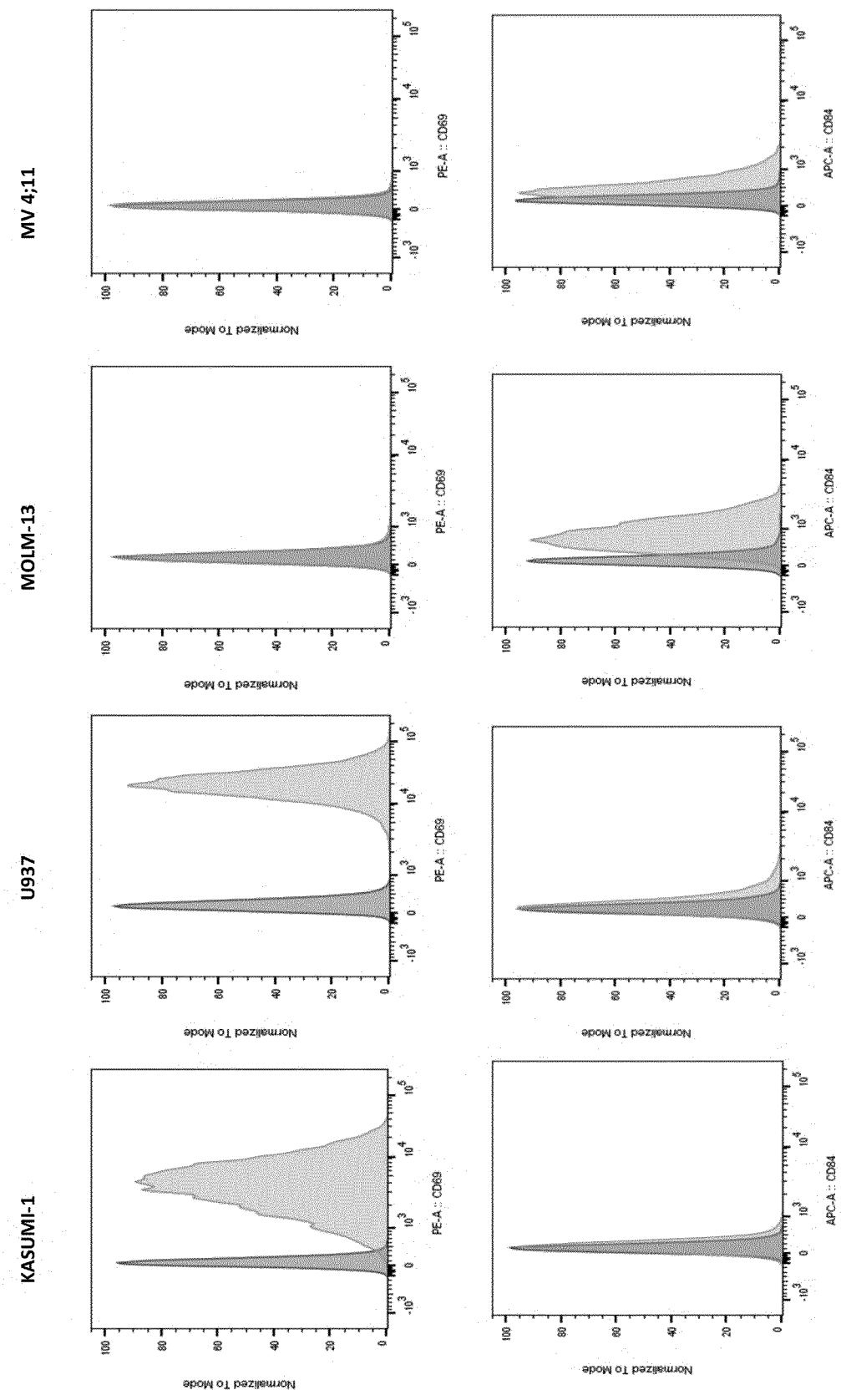


FIG. 17

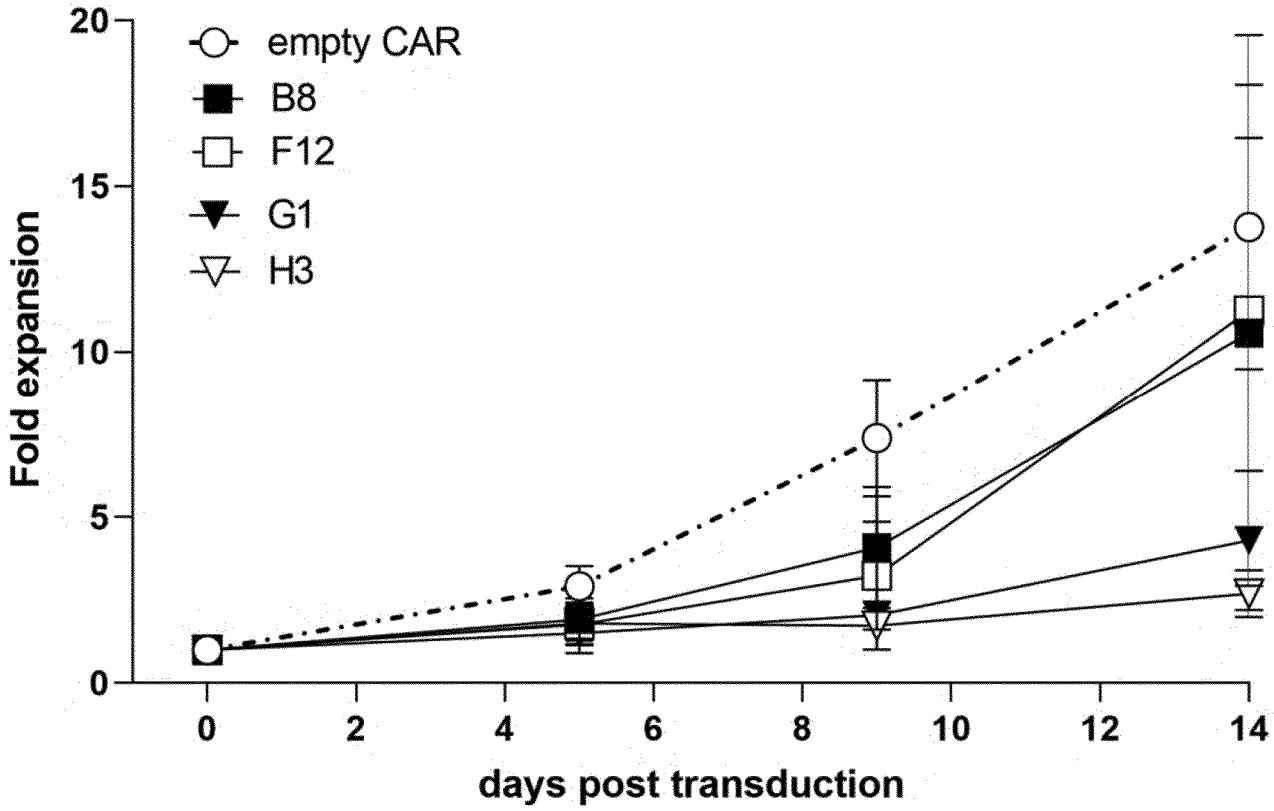

20
15
10
5
0
Fold expansion
empty CAR
B8
F12
G1
H3
0
2
4
6
8
10
12
14
days post transduction

FIG. 18A

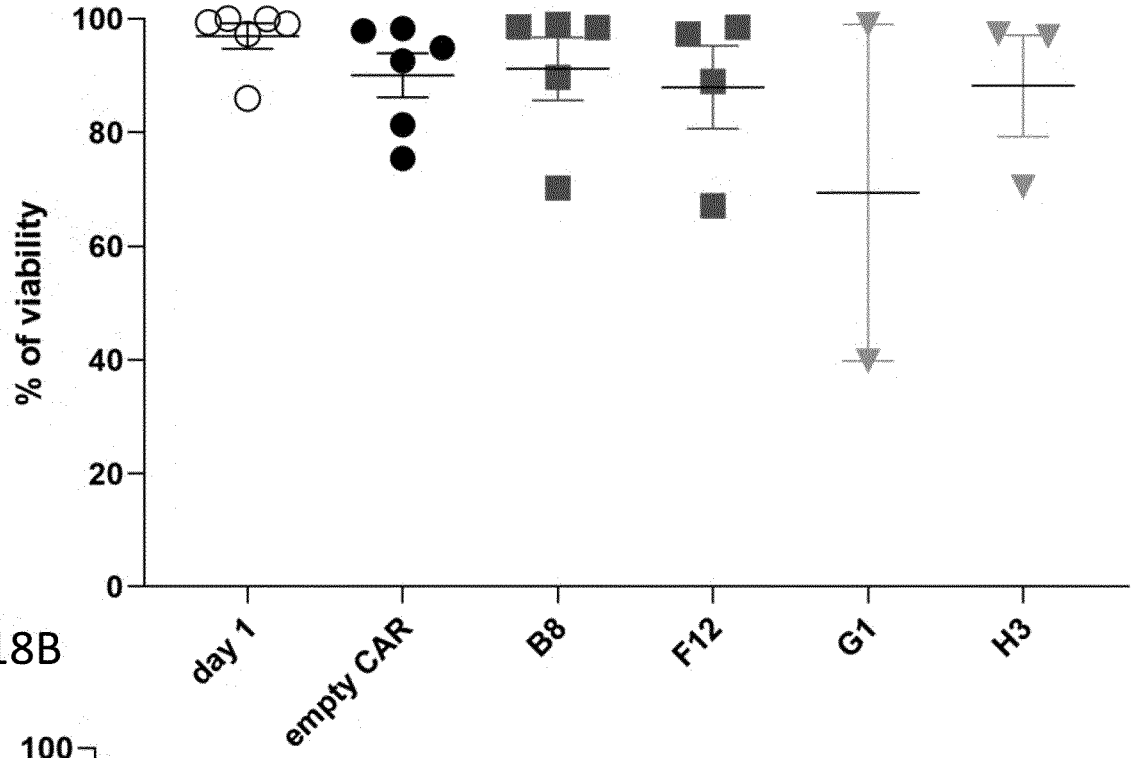


FIG. 18B

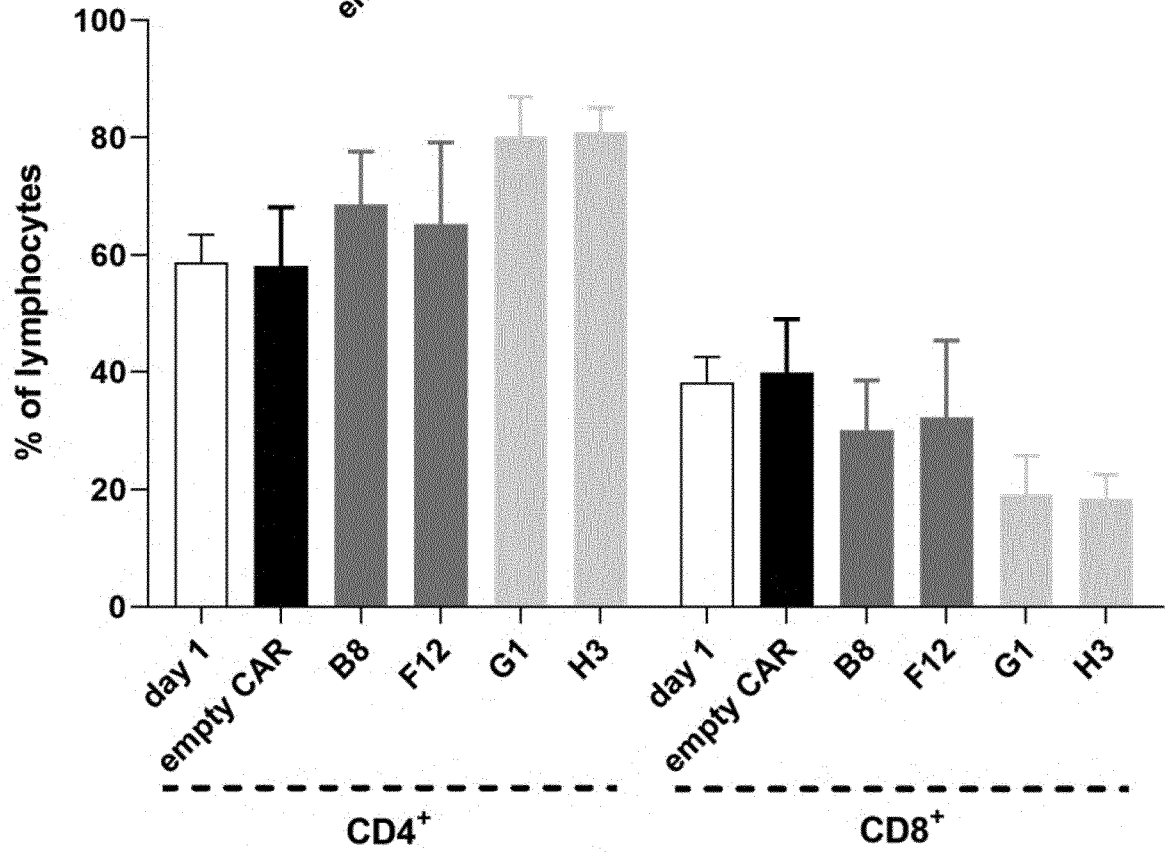


FIG. 19A

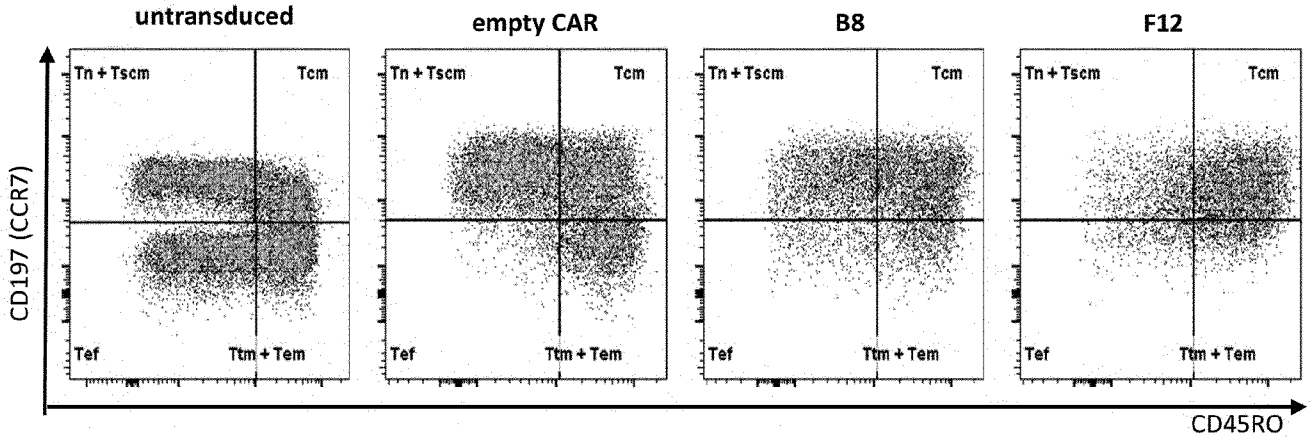


FIG. 19B

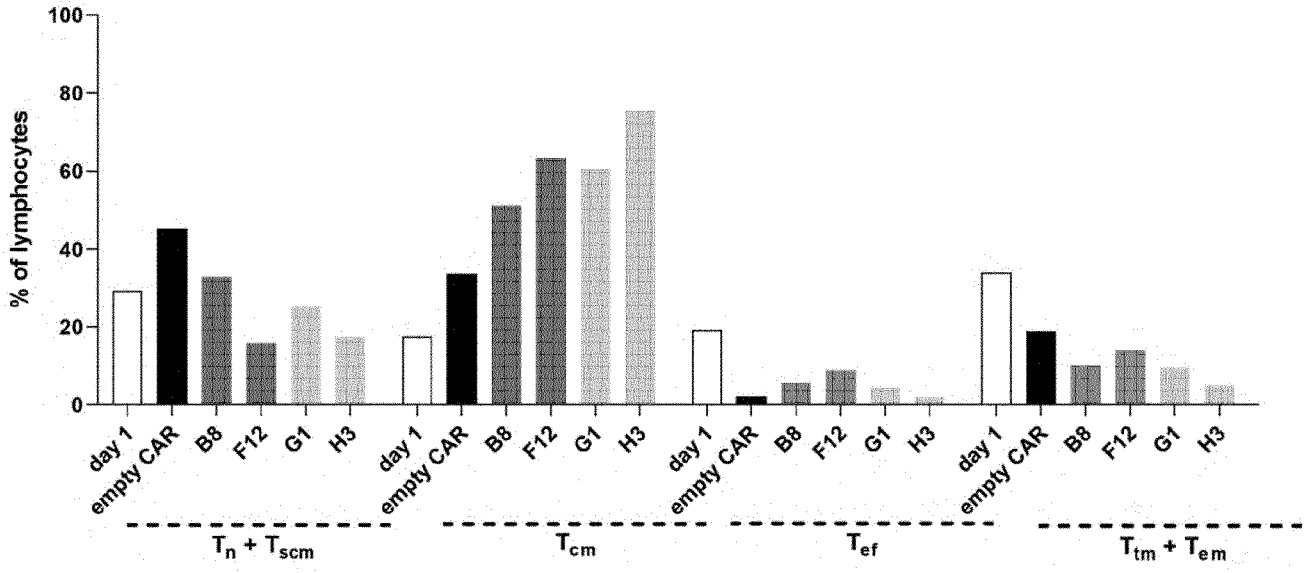


FIG. 20A

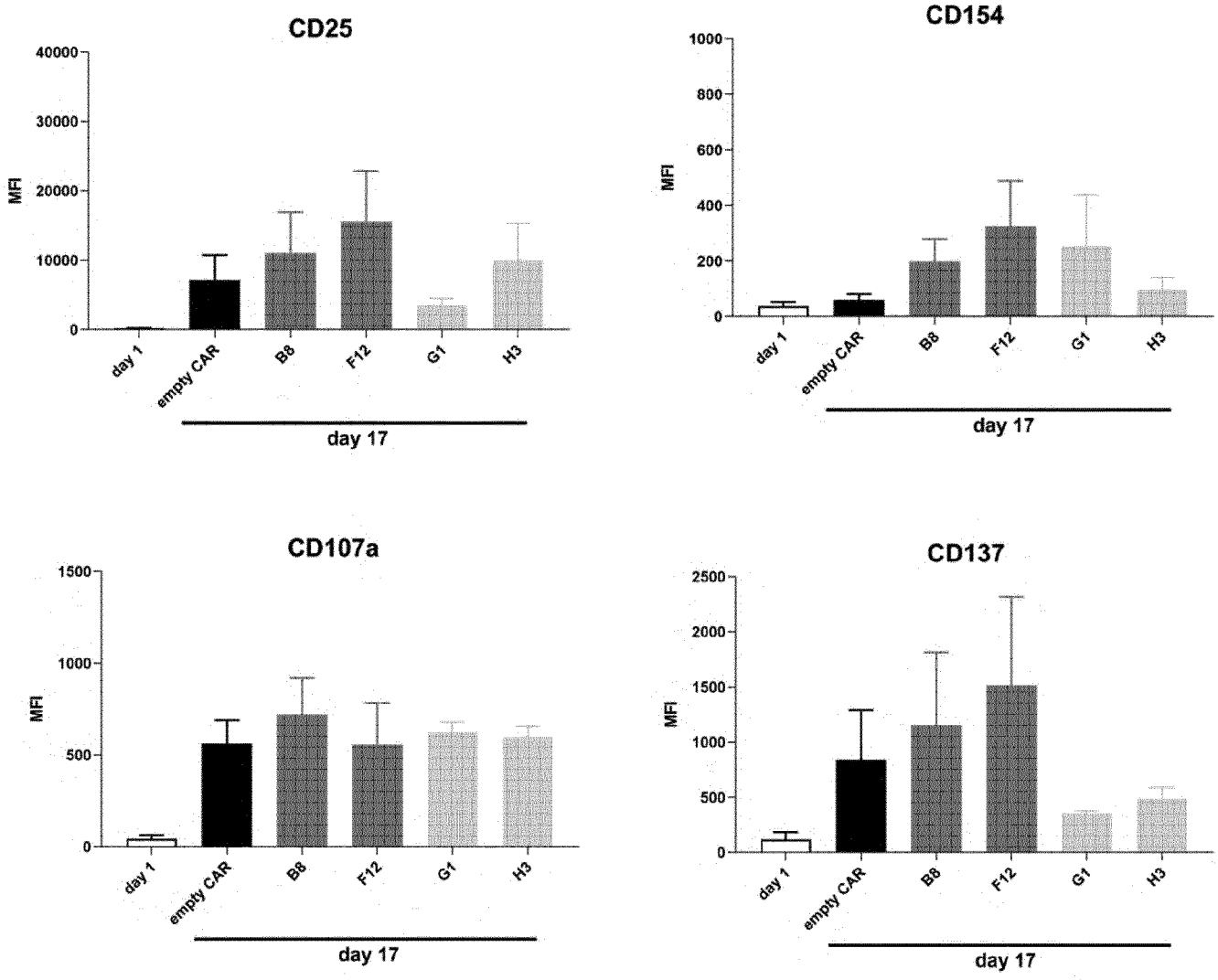

CD25
MFI
40000
30000
20000
10000
0
day 1
empty CAR
B8
F12
G1
H3
day 17
CD154
MFI
1000
800
600
400
200
0
day 1
empty CAR
B8
F12
G1
H3
day 17
CD107a
MFI
1500
1000
500
0
day 1
empty CAR
B8
F12
G1
H3
day 17
CD137
MFI
2500
2000
1500
1000
500
0
day 1
empty CAR
B8
F12
G1
H3
day 17

FIG. 20B

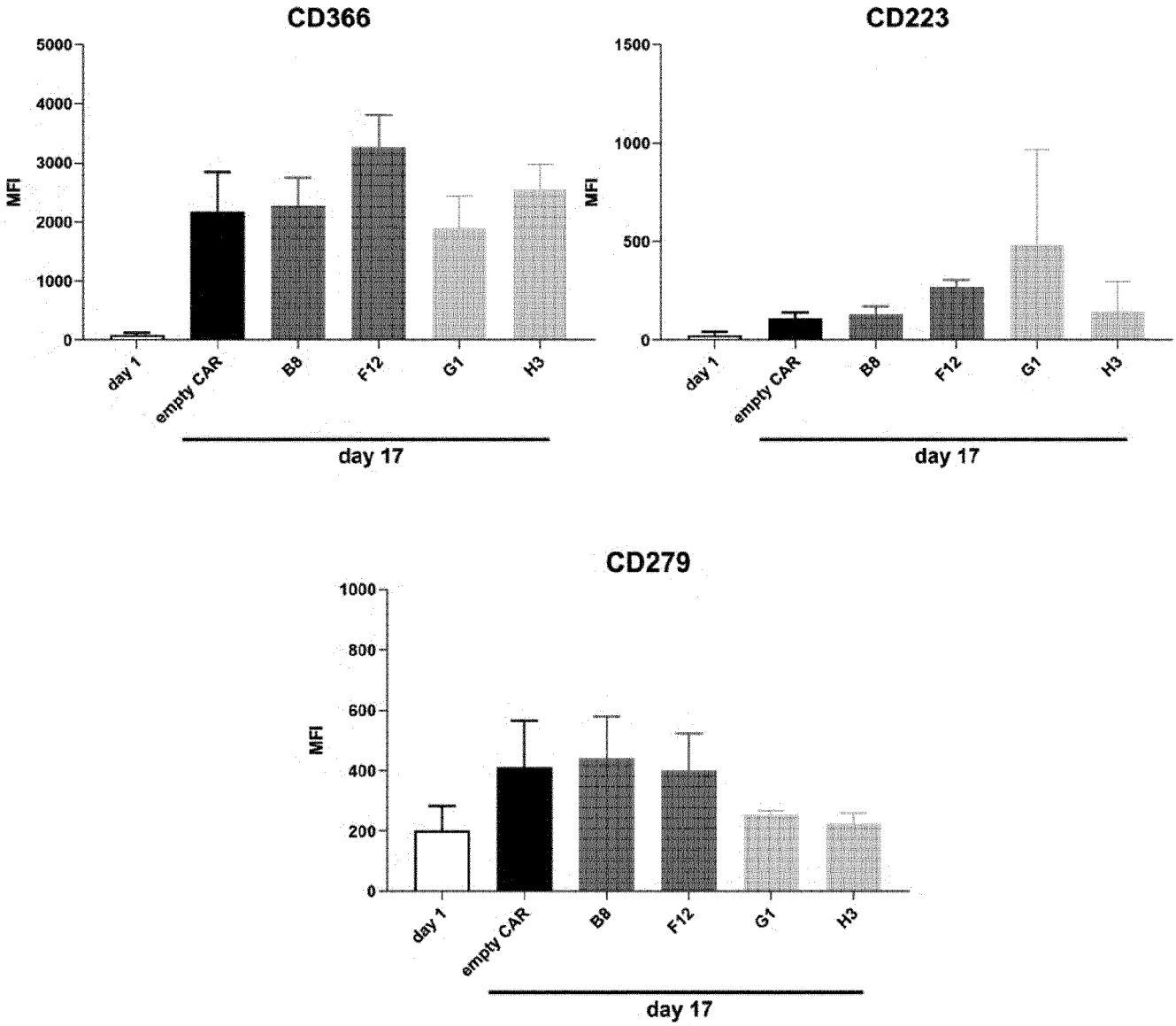

CD366
MFI
5000
4000
3000
2000
1000
0
day 1
empty CAR
B8
F12
G1
H3
day 17
CD223
MFI
1500
1000
500
0
day 1
empty CAR
B8
F12
G1
H3
day 17
CD279
MFI
1000
800
600
400
200
0
day 1
empty CAR
B8
F12
G1
H3
day 17

FIG. 21

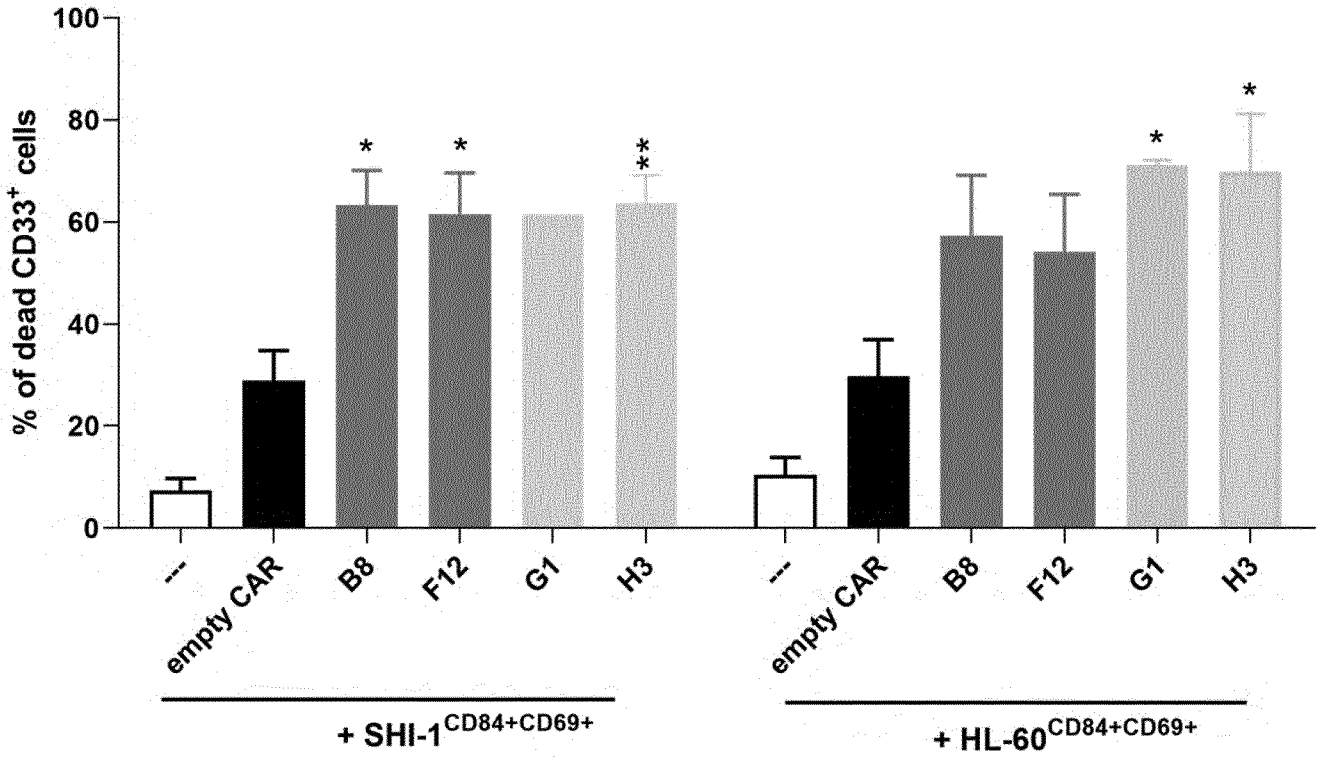

100
80
60
40
20
0
% of dead CD33+ cells
*
*
**
*
*
---
empty CAR
B8
F12
G1
H3
---
empty CAR
B8
F12
G1
H3
+ SHI-1CD84+CD69+
+ HL-60CD84+CD69+

FIG. 22

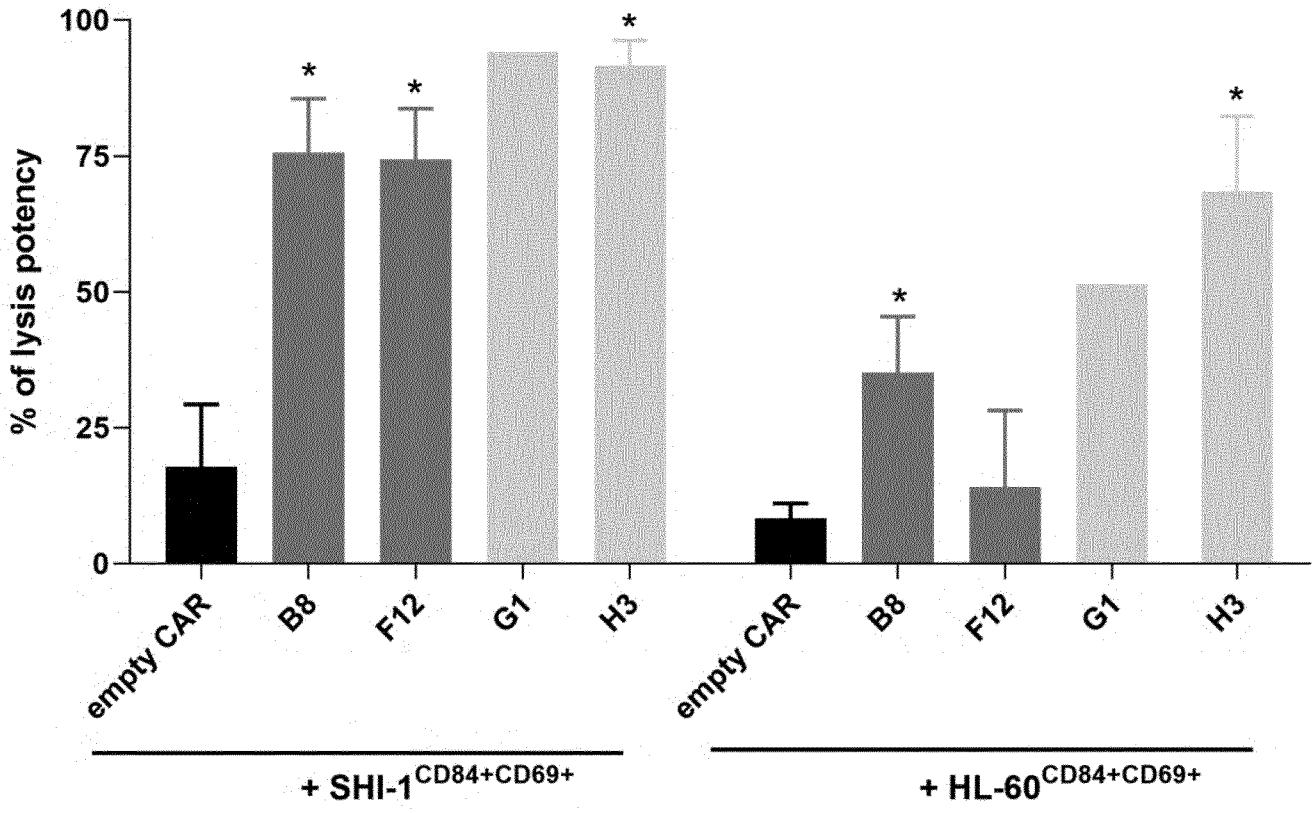

100
75
50
25
0
% of lysis potency
*
*
*
*
*
empty CAR
B8
F12
G1
H3
empty CAR
B8
F12
G1
H3
+ SHI-1CD84+CD69+
+ HL-60CD84+CD69+

FIG. 23

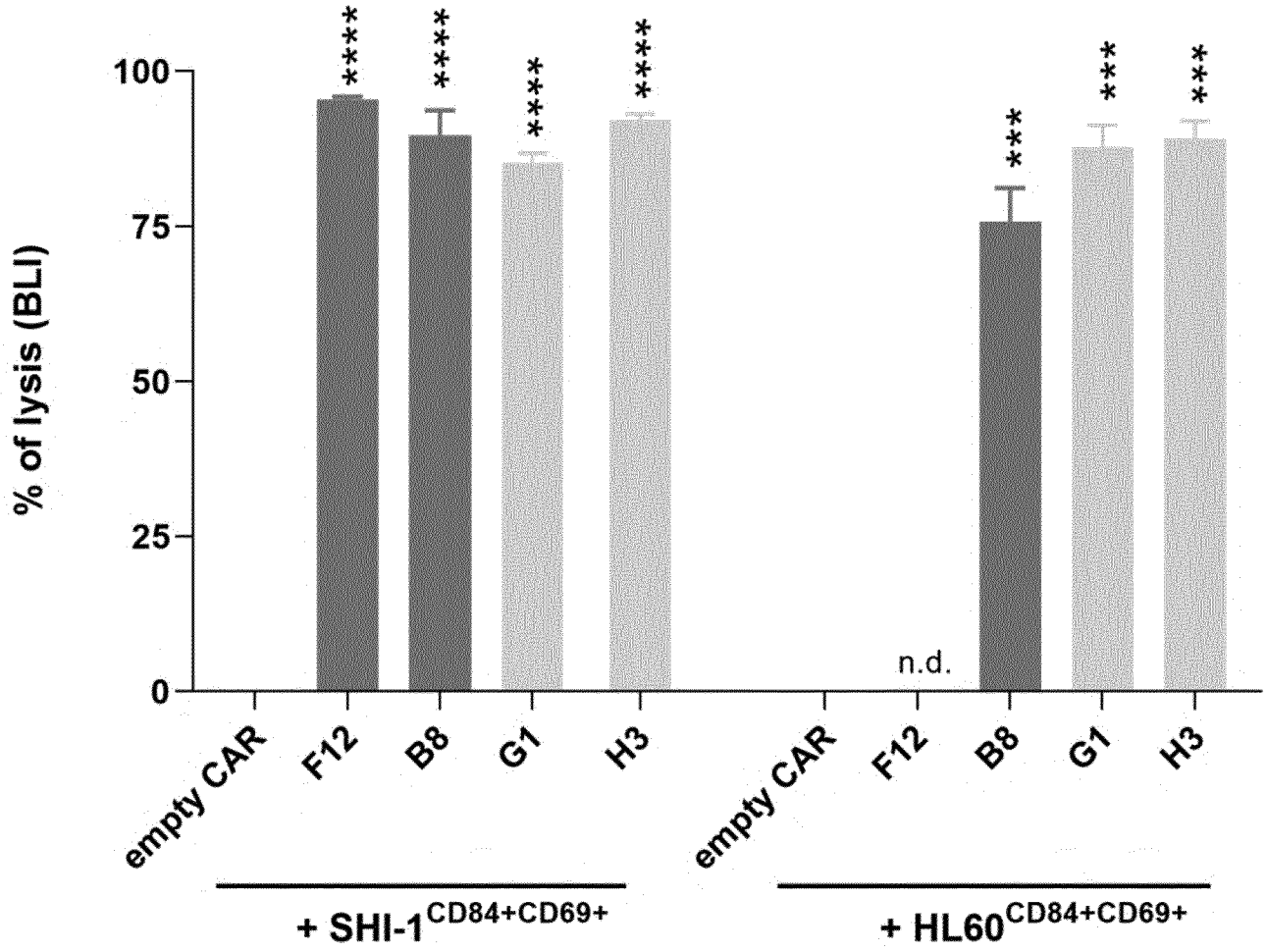

% of lysis (BLI)
100
75
50
25
0
****
****
****
****
***
***
***
n.d.
empty CAR
F12
B8
G1
H3
empty CAR
F12
B8
G1
H3
+ SHI-1CD84+CD69+
+ HL60CD84+CD69+

FIG. 24

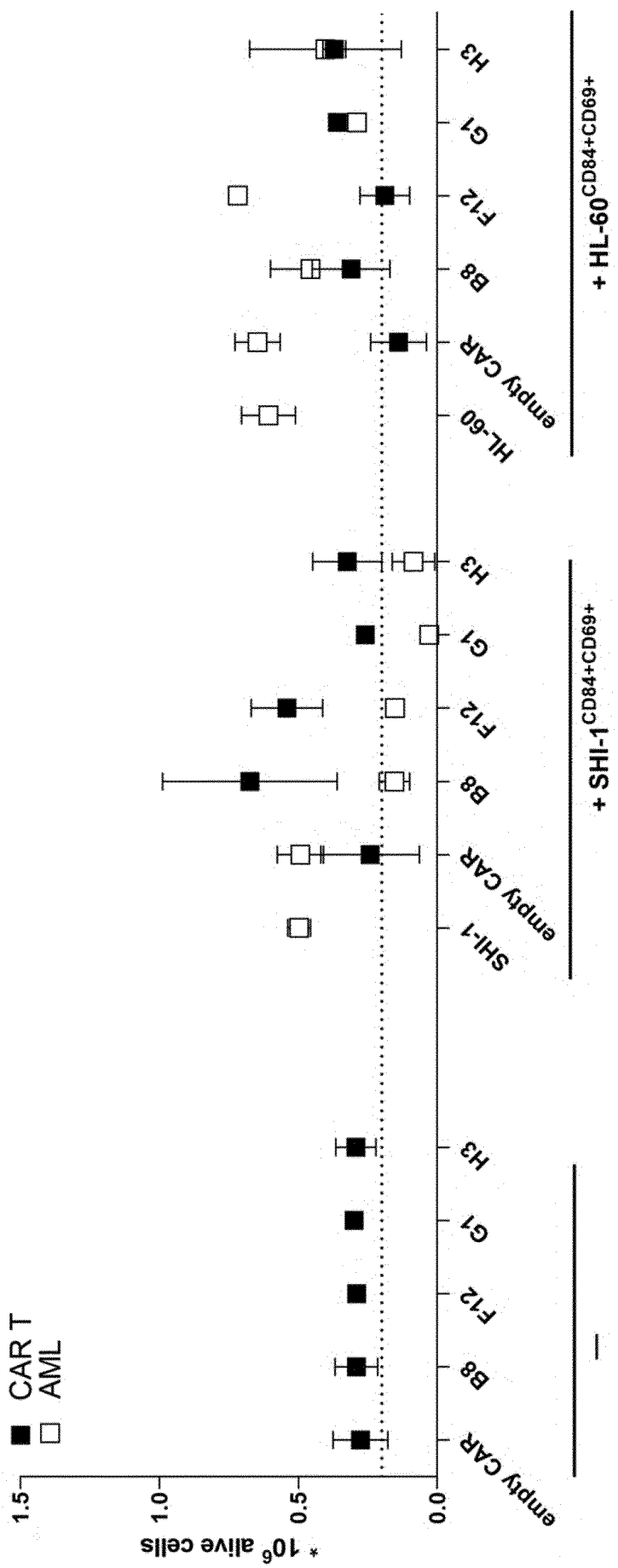

CAR T
AML
* 10^6 alive cells
1.5
1.0
0.5
0.0
—
+ SHI-1CD84+CD69+
+ HL-60CD84+CD69+
empty CAR
B8
F12
G1
H3
SHI-1
HL-60

FIG. 25A

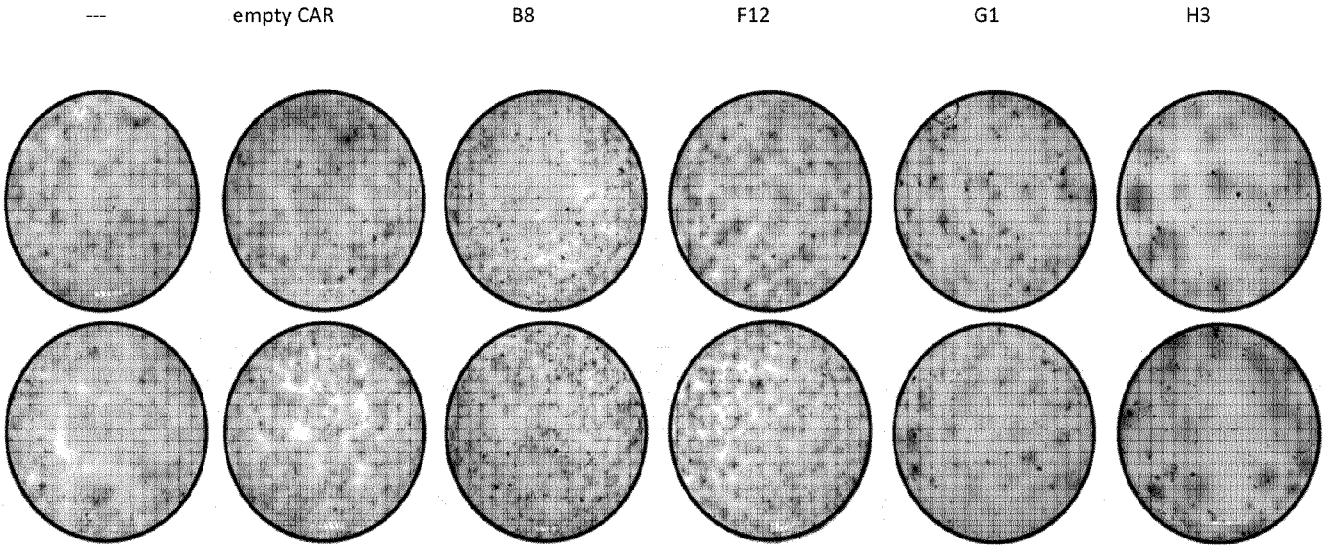


FIG. 25B

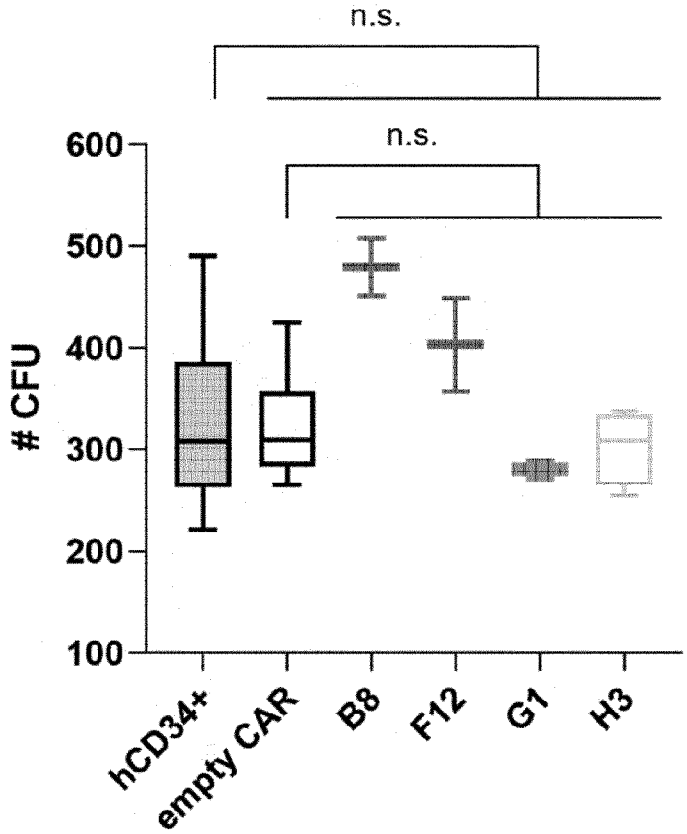


FIG. 26A

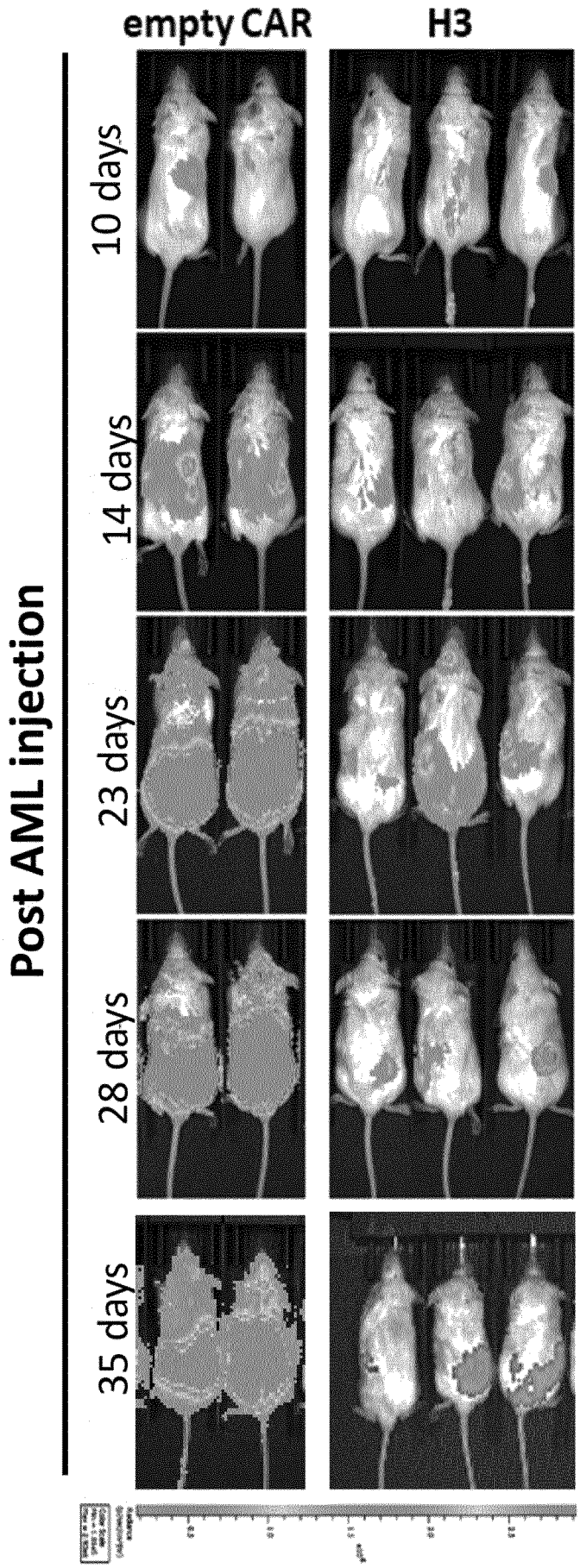

empty CAR
H3
Post AML injection
10 days
14 days
23 days
28 days
35 days

FIG. 26B

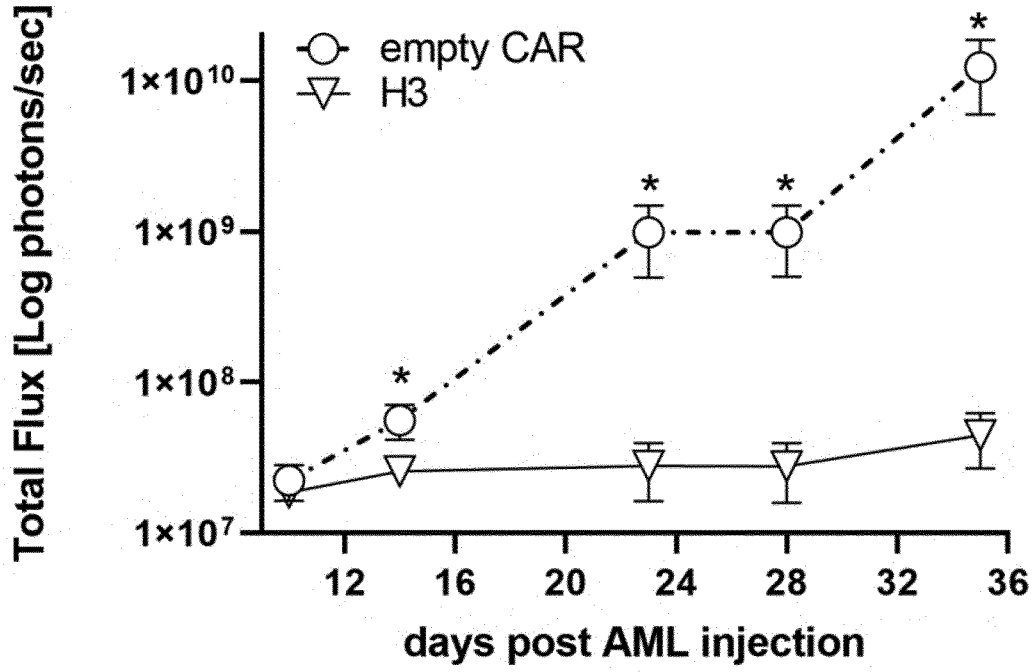


FIG. 26C

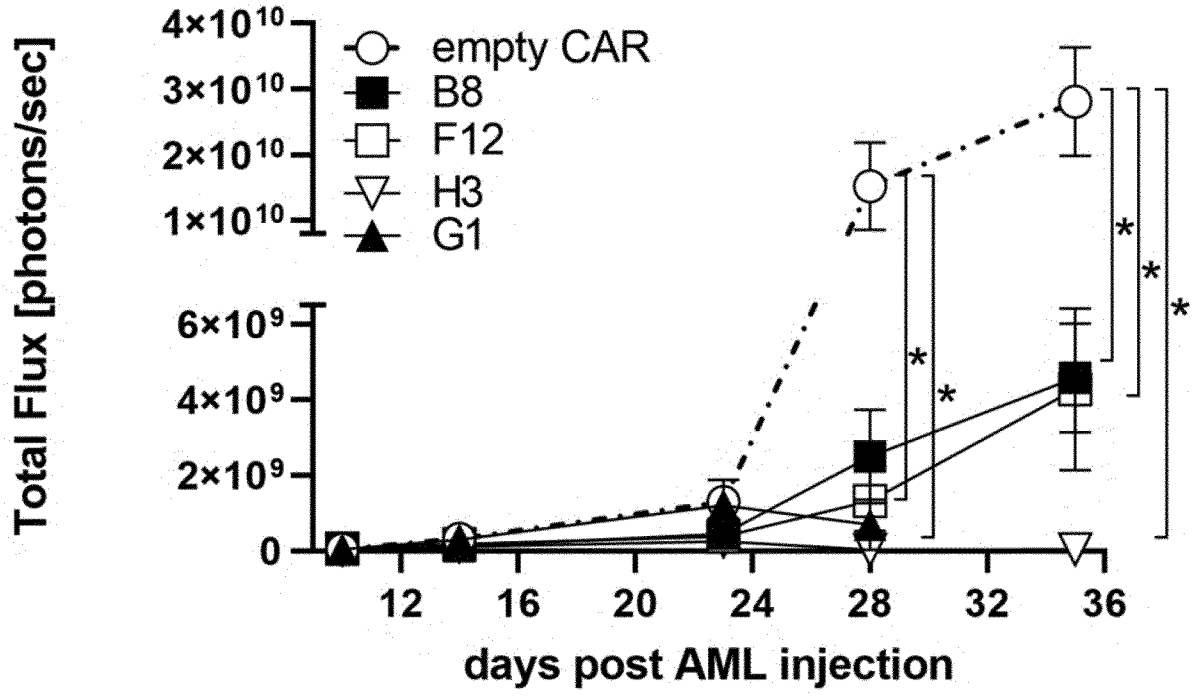


FIG 27

Gene Synthesis of optimized sequences for expression in Mammalian cells

SIP-scFv(14721-P1-A1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp

ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCCAGGTGGGTTCTGAGCCAGG
TGCAGCTGCAGCAGTCCGGCCCTGGCCTGGTGCAGCCTAGCAGAACCCTGAGCCTGACATGTGCCATCAGCGGCGA
TTCCATCTCCAGCAATACCGCCTCCTGGAACTGGATCAGACAGAGCCCTAGCAGGGGCCTGGAGTGGGTGGGCAAG
ACAGAGTACAGATCCGGCTGGTTCTTCGAGTACGCCCCCTCCGTGGGCGGCAGAGTGAATATCTCCCCCGATACAA
GCAAGAACCAGTTCAGCCTGCAGCTGAATAGCGTGACACCTGAGGATACAGCCGTGTACTTCTGCGCCAGGGACTC
CTACAATGACTACGATAACGACGGCTTTGACATCTGGGGCCAGGGCACACTGGTGACAGTGAGCAGCGGCGGCGGC
GGAAGCGGAGGAGGAGGATCTGGCGGCGGCGGTAGCGGAGGAGGTGGATCTCAGTCCGTGCTGACCCAGCCCCCC
A GCGTGTCCGCTGCTCCTGGACAGAAGGTGACCATCAGCTGCAGCGGCTCCTCCTCCAATATCGGCTCCAACTACGT
GGCCTGGTACCAGCAGCTGCCCGGCACAGCCCCCAAGCTGCTGATCTACGACACCAACAAGAGGCCCAGCGGCATC
CCCGATAGGTTTAGCGGCTCCAAGAGCGGCACATCCGCCACCCTGGGCATCACCGGCCTGCAGACAGGCGATGAGG
CCGACTACTACTGTGGCACATGGGACAGCTCCCTGAGCGCCGAGGTGTTCGGCACAGGCACAAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 24)

SIP-scFv(14721-P1-C1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp

ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCTAGATGGGTGCTGTCCCAGG
TGCAGCTGCAGCAGAGCGGCCCTGGCCTGGTGAAGCCCAGCCAGACCCTGTCCCTGACCTGCGCCATCAGCGGCGA
TAGCGTGAGCAGCAACTCCGCCAGCTGGAATTGGATCAGGCAGTCCCCCAGCAGGGGCCTGGAGTGGCTGGGAAAG
ACAGAGTACAGATCCAAGTGGTACTACGAGTTTGCCCCTAGCGTGAAGAGCAGAATCACCATCACCCCTGATACCA
GCAAGAACCAGTTTTCCCTGCAGCTGAATTCCGTGACCCCTGAGGACACCGCCGTGTACTACTGCGTGAGAGACTC
CTACAACGGCTACGATTTTGACGGCTTCGATATCTGGGGCCAGGGCACCCTGGTGACCGTGTCCAGCGGCGGAGGC
GGAAGCGGAGGAGGAGGAAGCGGCGGAGGAGGCAGCGGAGGAGGTGGAAGCCAGAGCGTGCTGACACAGCCCCC
TA GCGTGTCCGCCGCCCCAGGACAAAAGGTGACAATCAGCTGCTCCGGCTCCTCCTCCAATATCGGCAGCAACTACGT
GGCCTGGTACCAGCAGCTGCCTGGCACAGCCCCCAAGCTGCTGATCTACGACACCAATAAGAGGCCCTCCGGCATC
CCCGATAGATTCTCCGGCTCCAAGAGCGGCACATCCGCCACCCTGGGCATCACCGGCCTGCAGACAGGCGATGAGG
CCGACTACTACTGTGGCACATGGGATTCCTCCCTGTCCGCCGAGGTGTTTGGCACCGGCACAAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 25)

SIP-scFv(14721-P1-F1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp

ggatccgccgccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCCCCTAGATGGGTGCTGAGCCAGG
TGCAGCTGCAGCAGTCCGGCCCTGGCCTGGTGAAGCCTTCCCAGACACTGTCCCTGACATGTGCCATCAGCGGCGA
CTCCGTGTTCTCCAATAGCGCCAGCTGGAATTGGATCAGACAGAGCCCCTCCAGAGGCCTGGAGTGGCTGGGCAAG

FIG 27 continued

ACAGAGTACAGGTCCAAGTGGTTTGACGAGTACGCCCCCAGCGTGAAGGGCAGAATCGCCATCAGACCTGACACCT
CCAAGAACCAGGTGTCCCTGCAGCTGAATAGCGTGACCCCCGAGGACACCGCCGTGTACTACTGTGTGAGAGATAG
CTACAACGGCTACGATTTTGATGGCTTTGACATCTGGGGCCAGGGCACCCTGGTGACCGTGAGCTCCGGCGGAGGC
GGAAGCGGAGGAGGAGGAAGCGGCGGAGGCGGTAGCGGAGGAGGTGGAAGCCAGAGCGTGCTGACCCAGCCTCC
TAGCGTGAGCGCCGCCCCTGGACAGCAGGTGATCATCTCCTGCAGCGGCTCCAGCTCCAACGTGGGCAATAACTACG
T GGCCTGGTACCAGCAGGTGCCCGGCGCTGCTCCCAGGCTGCTGATCTACGACAACTACAAGAGACCCTCCGGCATC
CCCGACAGGTTTTCCGGCAGCAAGTCCGGCACCTCCGCCACCCTGGGCATCACCGGACTGCAGAGCGGCGACGAGG
CCGACTACTACTGTGGCAGCTGGGATAGCTCCCTGAGCGCCGAGGTGTTTGGCGGCGGCACCAAGCTGACAGCCCT
GATCGAGGTGATGTACCCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 26)

SIP-scFv(14721-P1-G1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCCAGGTGGGTTCTGAGCCAGG
TGCAGCTGCAGCAGTCCGGCCCTGGCCTGGTGAAGCCCTCCCAGACACTGAGCCTGACATGCGCCATCTCCGGCGA
CAGCGTGTTCAGCACCACCGCCAGCTGGAATTGGATCAGACAGAGCCCCAGCAGAGGCCTGGAGTGGCTGGGCAAG
ACCGAGTACAGGAGCAAGTGGTTCGACGAGTACGCCCCCAGCGTGAAGGGCAGGATCGCCATCAGACCTGACACAT
CCAGAAATCAGGTGAGCCTGCAGCTGAATAGCATGACACCCGAGGATACCGCCGTGTACTTCTGTGTGAGAGACAG
CTACAACGGCTACGACTTCGACGGCTTCGACATCTGGGGCCAGGGCACAACAGTGACAGTGAGCTCCGGCGGCGGC
GGCTCTGGAGGAGGAGGATCTGGCGGCGGCGGAAGCGGAGGAGGAGGTTCTCAGAGCGTGGTGACACAGCCCCCC
A GCGTGAGCGCCGCTCCTGGACAAAAGGTGACCATCTCCTGCTCCGGCAGCAGCAGCAACATCGGCAATAACTACGT
GTCCTGGTACCAGCAGCTGCCTGGCACCGCCCCCAAGCTGCTGATCTACGACAACAATAAGAGGCCCAGCGGCATC
CCTGACAGATTCTCCGGCTCCAAGAGCGGCACCTCCGCCACCCTGGGCATCACAGGCCTGCAGACAGGCGACGAGG
CCGACTACTACTGTGGCACATGGGATAGCTCCCTGTCCGCCGAGATGTTTGGCGGCGGCACCAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 27)

SIP-scFv(14721-P1-C2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCTAGGTGGGTGCTGAGCCAGG
TGCAGCTGCAGCAGAGCGGCCCTGGCCTGGTGAAGCCCAGCCAGACCCTGTCCCTGACATGCGCCATCAGCGGCGA
TAGCGTGTCCAGCAATAGCGCCTCCTGGAATTGGATCAGACAGAGCCCTAGCAGAGGCCTGGAGTGGCTGGGCAAG
GTGGAGTACAGGTCCAAGTGGTACGATGAGTACGCCCCCTCCGTGAAGAGCAGAATCGCCATCAGACCTGACACAT
CCAAGAACCAGGTGAGCCTGCACCTGATCTCCGTGACACCTGATGATACAGCCGTGTACTACTGCGCCAGGGACTC
CTACAACGGCCACGCCTTCGATGGCTTTGATGTGTGGGGCCAGGGCACACTGGTGACCGTGTCCAGCGGCGGCGGC
GGATCTGGAGGAGGAGGAAGCGGCGGCGGAGGCTCTGGAGGAGGTGGAAGCCAGTCCGTGCTGACCCAGCCCCCC
T CCGTGAGCGCTGCTCCAGGACAGAAGGTGACAATCAGCTGCTCCGGCTCCAGCTCCAACATCGGCGATAATCTGGT
GAGCTGGTACCAGCAGCTGCCTGGCACAGCCCCTAAGCTGCTGATCTACGATAACAATAAGAGACCCTCCGGCATC

FIG 27 continued

CCCGACAGGTTCAGCGGCAGCAAGTCCGGCACCTCCGCCACACTGGACATCACAGGCCTGCAGACCGGCGACGAGG
CCGACTACTACTGCGAGAGCTGGGATAACAACCTGACCGCCGAGGTGTTCGGCACCGGCACAAAGGTGACAGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 28)

SIP-scFv(14721-P1-F2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTCTTCCTGCTGCTGGTGGCCGCCCCCAGATGGGTGCTGTCCCAGG
TGCAGCTGCAGCAGTCCGGCCCCGGACTGGTGAAGCCTTCCCAGACCCTGAGCCTGACCTGCGCCATCAGCGGCGA
CTCCGTGTTTAGCAACTCCGCCTCCTGGAACTGGATCAGACAGTCCCCCTCCAGAGGCCTGGAGTGGCTGGGCAAG
ACAGAGTACAGGAGCAAGTGGTTTGACGAGTACGCCCCTTCCGTGAAGGGCAGGATCGCCATCAGACCCGATACCT
CCAAGAATCAGGTGAGCCTGCAGCTGAATAGCGTGACACCCGAGGACACCGCCGTGTACTACTGTGTGAGAGACTC
CTACAATGGCTACGACTTCGACGGCTTTGACATCTGGGGCCAGGGCACCCTGGTGACCGTGTCCAGCGGCGGAGGC
GGAAGCGGAGGAGGAGGAAGCGGCGGAGGAGGCTCCGGAGGAGGAGGTTCCCAGAGCGTGCTGACCCAGCCCCCT
AGCGTGAGCGCCGCTCCTGGACAGAAGGTGACCATCAGCTGCTCCGGCGGCTCCAGCAACATCGAGAAGAACTACGT
GAGCTGGTACCAGCAGCTGCCTGGCACAGCCCCTAAGCTGCTGATCTACGACACCAATAAGAGGCCTAGCGGCATC
CCCGACAGATTCAGCGGCTCCAAGTCCGGCACAAGCGCCACACTGGGCATCACCGGCCTGCAGACCGGCGACGAGG
CCGATTACTACTGTGGCGCCTGGGATAATATCCTGAACTCCGAGATGTTCGGCGGCGGCACAAAGCTGACAGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 29)

SIP-scFv(14721-P1-H2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCCCCCAGATGGGTGCTGAGCCAGG
TGCAGCTGCAGCAGAGCGGCCCTGGCCTGGTGAAGCCTTCCCAGACACTGAGCCTGACCTGTGCCATCAGCGGCGA
TAGCGTGTTTAGCAACAGCGCCAGCTGGAATTGGATCAGGCAGAGCCCTTCCAGGGGCCTGGAGTGGCTGGGCAAG
ACCGAGTACAGGTCCAAGTGGTTCGATGAGTACGCCCCTAGCGTGAAGGGCAGGATCGCCATCAGGCCTGACACCT
CCAAGAACCAGGTGTCCCTGCAGCTGAATTCCGTGACACCTGAGGATACCGCCGTGTACTACTGCGTGAGGGATTC
CTACAACGGCTACGACTTCGACGGCTTTGATATCTGGGGCCAGGGCACACTGGTGACAGTGTCCTCCGGCGGCGGC
GGAAGCGGAGGAGGAGGATCTGGCGGCGGCGGTTCCGGAGGAGGAGGTTCTCAGTCCGTGGTGACCCAGCCTCCC
A GCGTGAGCGCCGCTCCTGGACAGAAGGTGACCATCAGCTGTAGCGGCAGCTCCTCCAACATCGGCAACAACTACGT
GTCCTGGTACCAGCAGCTGCCCGGCACCGCCCCAAAGCTGCTGATCTACGATAATAATAAGAGACCTTCCGGCATC
CCCGATAGATTTTCCGGCAGCAAGAGCGGCACAAGCGCCACCCTGGGCATCACAGGCCTGCAGACCGGCGACGAGG
CCGATTACTACTGCGGCACCTGGGATAGCAGCCTGTCCGCCGAGGTGTTTGGCGGCGGCACCAAGCTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG

FIG 27 continued

GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 30)

SIP-scFv(14721-P1-H3)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCCAGGTGGGTTCTGTCCCAGG
TGCAGCTGCAGCAGAGCGGCCCCGGACTGGTGAAGCCCAGCCAGACACTGAGCCTGACATGTGACATCTCCGGCGA
TTCCGTGTTCTCCAACACAGCCAGCTGGAATTGGATCAGGCAGAGCCCCAGCAGGGGCCTGGAGTGGCTGGGAAAG
ACAGAGTACAGATCCCAGTGGCTGCACGAGTACGCCCCTTCCGTGAGATCCAGGATCGCCATCAGACCCGACACCT
CCAAGAACCAGGTGTCCCTGCAGCTGTCCTTCGTGACCCCCGAGGACACCGCCGTGTACTACTGTGTGAGGGATTC
CTACAATGGCTACGCCTTCGATGGCTTTGACACCTGGGGCCAGGGCACCCTGGTGACCGTGAGCAGCGGCGGAGGC
GGAAGCGGAGGAGGAGGAAGCGGCGGAGGAGGCTCCGGAGGAGGAGGTAGCCAGAGCGTGGTGACCCAGCCCCC
CA GCGTGTCCGCTGCTCCTGGACAGAAGGTGACCATCAGCTGTTCCGGCAGGAACTCCAACATCGCCAACAACTTTGT
GTCCTGGTACAGACAGCTGCCTGGCACCGCCCCTAAGCTGCTGATCTACGACAATAATAAGAGGCCTAGCGGCATC
CCCGATAGATTCTCCGGCTCCAAGAGCGGCACATCCGCCACCCTGGCCATCACCGGCCTGCAGACCGGCGACGAGG
CCGATTACTACTGCGAGTCCTGGGATAGCTCCCTGACCGCCGAGGTGTTTGGCACCGGCACCAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 31)

SIP-scFv(14722-P1-F12)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp
ggatccgccgccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCCCCTAGGTGGGTGCTGAGCCAGG
TGCAGCTGCAGCAGTCCGGCCCTGGCCTGGTGAAGCCCAGCCAGACACTGAGCCTGACCTGTGCCATCTCCGGCGA
CTCCGTGTCCAGCAACAGCGCCTCCTGGAACTGGATCAGACAGTCCCCTAGCAGGGGCCTGGAGTGGCTGGGCAAG
GTGGAGTACAGATCCAAGTGGTACGATGAGTACGCCCCCAGCGTGAAGAGCAGAATCGCCATCAGACCTGACACCA
GCAAGAACCAGGTGTCCCTGCACCTGATCAGCGTGACCCCTGATGACACAGCCGTGTACTACTGCGCCAGAGATAG
CTACAACGGCCACGCCTTTGATGGCTTTGATGTGTGGGGCCAGGGCACAATGGTGACCGTGAGCTCCGGCGGCGGC
GGATCTGGAGGAGGAGGAAGCGGCGGCGGCGGTTCTGGAGGAGGTGGAAGCCAGAGCGTGGTGACACAGCCTCCC
T CCGTGTCCGCCGCCCCTGGACAAAAGGTGACCATCTCCTGCAGCGGCAGCAGCAGCAACATCGGCAATAACTACGT
GTCCTGGTACCAGCAGCTGCCTGGCACAGCCCCCAAGCTGCTGATCTACGACAACAATAAGAGGCCCAGCGGCATC
CCCGACAGGTTCTCCGGCTCCAAGTCCGGCACCTCCGCCACACTGGGCATCACAGGCCTGCAGACCGGCGACGAGG
CCGACTACTACTGTGGCACCTGGGATTCCAGCCTGAGCGCCGAGGTGTTTGGCGGCGGCACAAAGGTGACAGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 32)

FIG 27 continued

SIP-scFv(14722-P2-B8)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp

ggatccgccgccaccATGAAGCACCTGTGGTTTTTTCTGCTGCTGGTGGCCGCCCCCAGATGGGTGCTGAGCCAGG
TGCAGCTGCAGCAGTCCGGCCCTGGCCTGGTGAAGCCTTCCCAGACACTGTCCCTGACCTGCGCCATCAGCGGCGA
CAGCGTGAGCAGCAATTCCGCCAGCTGGAACTGGATCAGGCAGTCCCCCAGCAGGGGCCTGGAGTGGCTGGGAAAG
GTGGAGTACAGGAGCAAGTGGTACGACGAGTACGCCCCCAGCGTGAAGAGCAGAATCGCCATCAGGCCCGACACAT
CCAAGAATCAGGTGAGCCTGCACCTGATCAGCGTGACCCCCGATGACACAGCCGTGTACTACTGCGCCAGAGACTC
CTACAACGGCCACGCCTTCGACGGCTTTGACGTGTGGGGCCAGGGCACAATGGTGACAGTGAGCTCCGGCGGCGGC
GGCTCTGGAGGAGGAGGATCTGGCGGCGGCGGAAGCGGAGGAGGAGGTTCTCAGAGCGTGCTGACCCAGCCCCCT
A GCCTGAGCGCCGCTCCTGGACAGAGAGTGACCATCAGCTGCTCCGGCACAACCTCCAATATCGCCAATAATTTCGT
GTCCTGGTACCAGCAGCTGTCCGGCTCCGCCCCCAAGCTGCTGATCAATGACAATAACAAGAGACCCTCCGGCATC
CCCGATAGGTTCTCCGGCAGCAAGTCCGGCGCCTCCGCCACACTGGCCATCACCGGACTGCAGACAGAGGACGAGG
CCGACTACTACTGTGGCGTGTGGGACAACAGCCTGAATGCCGAGGTGTTTGGCGGCGGCACCAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 33)

SIP-scFv(14722-P2-B11)-hCD28hinge-hCD28TMD-4IBB-CD3zeta cDNA – 1 506bp

ggatccgccgccaccATGAAGCACCTGTGGTTTTTCCTGCTGCTGGTGGCCGCCCCTAGGTGGGTGCTGTCCCAGG
TGCAGCTGCAGCAGTCCGGCCCCGGACTGGTGAAGCCTTCCCAGACCCTGAGCCTGACATGTGCCATCTCCGGCGA
CAGCGTGTCCTCCAACTCCGCCAGCTGGAACTGGATCAGGCAGTCCCCTTCCAGAGGCCTGGAGTGGCTGGGCAAG
ACAGAGTACAGAAGCAAGTGGTACTACGAGTTTGCCCCTAGCGTGAAGTCCAGAATCACCATCACCCCCGACACCA
GCAAGAATCAGTTTAGCCTGCAGCTGAATAGCGTGACCCCTGAGGATACAGCCGTGTACTACTGCGTGAGGGATAG
CTACAACGGCTACGACTTCGACGGCTTTGATATCTGGGGCCAGGGCACACTGGTGACCGTGTCCAGCGGCGGCGGC
GGATCTGGAGGAGGAGGAAGCGGCGGCGGAGGCTCTGGAGGAGGTGGAAGCCAGAGCGTGCTGACCCAGCCCCCT
A GCGTGAGCGCCGCTCCTGGACAGAAGGTGACAATCAGCTGCTCCGGCTCCAGCAGCAACATCGGCAGCAATTACGT
GGCCTGGTACCAGCAGCTGCCTGGCACCGCCCCCAAGCTGCTGATCTACGACACAAACAAGAGGCCCAGCGGCATC
CCTGACAGGTTCAGCGGCAGCAAGAGCGGCACCAGCGCCACCCTGGGCATCACCGGACTGCAGACAGGCGACGAGG
CCGATTACTACTGTGGCACCTGGGACTCCAGCCTGAGCGCCGAGGTGTTTGGCACAGGCACAAAGGTGACCGTGCT
GATCGAGGTGATGTACCCCCCCCCCTACCTGGACAATGAGAAGTCCAACGGCACAATCATCCACGTGAAGGGCAAG
CACCTGTGTCCCAGCCCCCTGTTTCCCGGCCCTAGCAAGCCCTTCTGGGTGCTGGTGGTGGTGGGCGGCGTGCTGG
CTTGTTACAGCCTGCTGGTGACAGTCGCCTTCATCATCTTTTGGGTGAAGAGGGGCAGGAAGAAGCTGCTGTACAT
CTTTAAGCAGCCCTTTATGAGGCCCGTGCAGACAACCCAGGAGGAGGACGGCTGTAGCTGCAGGTTTCCTGAGGAG
GAGGAGGGCGGCTGTGAGCTGAGAGTGAAGTTCAGCAGGTCCGCCGACGCCCCCGCCTACCAACAGGGACAGAATC
AGCTGTACAATGAGCTGAACCTGGGCAGAAGAGAGGAGTACGACGTGCTGGATAAGAGGAGAGGCAGGGACCCTG
AGATGGGCGGCAAGCCTAGAAGAAAGAACCCCCAGGAGGGCCTGTACAATGAACTGCAGAAGGACAAGATGGCCG
AGGCCTACAGCGAGATCGGCATGAAGGGCGAGAGAAGGAGGGGCAAGGGCCACGATGGCCTGTACCAGGGCCTGT
CCA CAGCCACCAAGGACACATACGACGCCCTGCACATGCAGGCCCTGCCCCCAAGGtgagtcgac (SEQ ID NO: 34)

3. Expected protein sequence

SIP-scFv(14721-P1-A1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.75kDa

FIG 27 continued

MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVQPSRTLSLTCAISGDSISSNTASWNWIRQSPSRGLEWVGKTEYRS
GWFFEYAPSVGGRVNISPDTSKNQFSLQLNSVTPEDTAVYFCARDSYNDYDNDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGSNYVAWYQQLPGTAPKLLIYDTNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGTGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 35)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-C1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.93kDa

MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSASWNWIRQSPSRGLEWLGKTEYRS
KWYYEFAPSVKSRITITPDTSKNQFSLQLNSVTPEDTAVYYCVRDSYNGYDFDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGSNYVAWYQQLPGTAPKLLIYDTNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGTGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 36)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-F1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.87kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVFSNSASWNWIRQSPSRGLEWLGKTEYRS
KWFDEYAPSVKGRIAIRPDTSKNQVSLQLNSVTPEDTAVYYCVRDSYNGYDFDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQQVIISCSGSSSNVGNNYVAWYQQVPGAAPRLLIYDNYKRPSGIPDRFS
GSKSGTSATLGITGLQSGDEADYYCGSWDSSLSAEVFGGGTKLTALIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 37)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-G1)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.95kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVFSTTASWNWIRQSPSRGLEWLGKTEYRS
KWFDEYAPSVKGRIAIRPDTSRNQVSLQLNSMTPEDTAVYFCVRDSYNGYDFDGFDIWGQGTTVTVSSGGGGSGGG
GSGGGGSGGGGSQSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEMFGGGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 38)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-C2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.94kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSASWNWIRQSPSRGLEWLGKVEYRS
KWYDEYAPSVKSRIAIRPDTSKNQVSLHLISVTPDDTAVYYCARDSYNGHAFDGFDVWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGDNLVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFS

FIG 27 continued

GSKSGTSATLDITGLQTGDEADYYCESWDNNLTAEVFGTGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 39)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-F2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=54.06kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVFSNSASWNWIRQSPSRGLEWLGKTEYRS
KWFDEYAPSVKGRIAIRPDTSKNQVSLQLNSVTPEDTAVYYCVRDSYNGYDFDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGGSSNIEKNYVSWYQQLPGTAPKLLIYDTNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGAWDNILNSEMFGGGTKLTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 40)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-H2)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.90kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVFSNSASWNWIRQSPSRGLEWLGKTEYRS
KWFDEYAPSVKGRIAIRPDTSKNQVSLQLNSVTPEDTAVYYCVRDSYNGYDFDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGGGTKLTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 41)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14721-P1-H3)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=54.22kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCDISGDSVFSNTASWNWIRQSPSRGLEWLGKTEYRS
QWLHEYAPSVRSRIAIRPDTSKNQVSLQLSFVTPEDTAVYYCVRDSYNGYAFDGFDTWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVVTQPPSVSAAPGQKVTISCSGRNSNIANNFVSWYRQLPGTAPKLLIYDNNKRPSGIPDRFS
GSKSGTSATLAITGLQTGDEADYYCESWDSSLTAEVFGTGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 42)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14722-P1-F12)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.77kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSASWNWIRQSPSRGLEWLGKVEYRS
KWYDEYAPSVKSRIAIRPDTSKNQVSLHLISVTPDDTAVYYCARDSYNGHAFDGFDVWGQGTMVTVSSGGGGSGGG
GSGGGGSGGGGSQSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGGGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 43)

FIG 27 continued

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14722-P2-B8)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.89kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSASWNWIRQSPSRGLEWLGKVEYRS
KWYDEYAPSVKSRIAIRPDTSKNQVSLHLISVTPDDTAVYYCARDSYNGHAFDGFDVWGQGTMVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSLSAAPGQRVTISCSGTTSNIANNFVSWYQQLSGSAPKLLINDNNKRPSGIPDRFS
GSKSGASATLAITGLQTEDEADYYCGVWDNSLNAEVFGGGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 44)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494]

> SIP-scFv(14722-P2-B11)-hCD28hinge-hCD28TMD-4IBB-CD3zeta – 494AAs MW=53.93kDa
MKHLWFFLLLVAAPRWVLSQVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSASWNWIRQSPSRGLEWLGKTEYRS
KWYYEFAPSVKSRITITPDTSKNQFSLQLNSVTPEDTAVYYCVRDSYNGYDFDGFDIWGQGTLVTVSSGGGGSGGG
GSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGSNYVAWYQQLPGTAPKLLIYDTNKRPSGIPDRFS
GSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGTGTKVTVLIEVMYPPPYLDNEKSNGTIIHVKGKHLCPS
PLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC
ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 36)

Features : SIP : [1 : 19] scFv : [20 : 274] hCD28hinge-hCD28TMD-4IBB-CD3zeta : [275 : 494