CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGGCCCTCACCTGCGCTGTCTCT
GGTGGGTCCTTCACTGATCATTACTGGAGTTGGATCCGTCAGGCCCCAGGGAAGGGGCTGGAGTGGATTGGAGAA
ATCAATCATAGTGGAGTCACCAACTACAACCCGTCCCTCAAGAGTCGACTCACCATATCAGTAGACACGTCCAAG
AGCCAGTTCTCCCTGAGGCTGACCTCTGTGACCGCCGCGGACACGGCTCTGTACTACTGTGCGAAAACTGGCCTG
TATTATGATGACGTTTGGGGGACTTTTCGTCCACGGGGCGGGTTCGACTCCTGGGGCCAGGGAACCCTGGTCACC
GTCTCCTCA (SEQ ID NO: 1)

FIG. 1

Q	V	Q	L	Q	Q	W	G	A	G	L	L	K	P	S	E	T	L	A	L	T	C	A	V	S
G	G	S	F	T	D	H	Y	W	S	W	I	R	Q	A	P	G	K	G	L	E	W	I	G	E
I	N	H	S	G	V	T	N	Y	N	P	S	L	K	S	R	L	T	I	S	V	D	T	S	K
S	Q	F	S	L	R	L	T	S	V	T	A	A	D	T	A	L	Y	Y	C	A	K	T	G	L
Y	Y	D	D	V	W	G	T	F	R	P	R	G	G	F	D	S	W	G	Q	G	T	L	V	T
V	S	S	(SEQ ID NO: 2)																				

FIG. 2

GACATCGTGATGACCCAGTCTCCGGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCC
AGCCAGAGTATTTTATATAGCTCCGACAATAAGAATTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCT
AAGCTGCTCTTTACTGGGCATCTATCCGGGAATCCGGGTCCCTGACCGATTCAGTGGCGGGTCTGGGACA
GATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTCCT
CCTTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCCAA (SEQ ID NO: 10)

FIG. 3

D I V M T Q S P D S L A V S L G E R A T I N C K S
S Q S I L Y S S D N K N Y L A W Y Q H K P G Q P P
K L L F Y W A S I R E S G V P D R F S G S G S G T
D F T L T I S S L Q A E D V A V Y Y C Q Q Y Y S P
P C S F G Q G T K L E I Q (SEQ ID NO: 11)

FIG. 4

```
1    GAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGAGACTC
61   TCCTGTGCAG CCTCTGGATT CACCTTTAGT AGTTATGCCA TGAGCTGGGT CCGCCAGGCT
121  CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT ATTTATTGGA GTGGTGGTAG CACATACTAC
181  GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCAGAGACA TATCCAAGAA CACGCTGTAT
241  CTGCAAATGA ACAGTCTGAG AGCCGACGAC ACGGCCGTGT ATTACTGTGC GAGAGGCGAT
301  TACTATGGTT CGGGGGCTCA CTTTGACTAC TGGGGCCAGG GAACCCTGGT CACCGTCTCC
361  TCA    (SEQ ID NO: 19)
```

FIG. 5

```
1    EVQLVESGGG LVQPGGSLRL
21   SCAASGFTFS SYAMSWVRQA CDR1
41   PGKGLEWVSG IYWSGGSTYY CDR2
61   ADSVKGRFTI SRDISKNTLY
81   LQMNSLRADD TAVYYCARGD CDR3
101  YYGSGAHFDY WGQGTLVTVS
121  S    (SEQ ID NO: 20)
```

FIG. 6

```
1    GATATTGTGA TGACCCAGAC TCCACTCTCC TCACCTGTCA CCCTTGGACA GCCGGCCTCC
61   ATCTCCTGCA GGTCTAGCCA AAGCCTCGTA CACAGTGATG GAAACACCTA CTTGAGTTGG
121  CTTCAGCAGA GGCCAGGCCA GCCTCCAAGA CTCCTAATTT ATCAGATTTC TAACCGGTTC
181  TCTGGGGTCC CAGACAGATT CAGTGGCAGT GGGGCAGGGA CAGATTTCAC ACTGAAAATC
241  AGCAGGGTGG AAGCTGAGGA TGTCGGGGTT TACTACTGCA TGCAAGGTAC ACAATTTCCT
301  CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAA          (SEQ ID NO: 28)
```

FIG. 7

```
1    DIVMTQTPLS SPVTLGQPAS
21   ISCRSSQSLV HSDGNTYLSW CDR1
41   LQQRPGQPPR LLIYQISNRF CDR2
61   SGVPDRFSGS GAGTDFTLKI
81   SRVEAEDVGV YYCMQGTQFP CDR3
101  RTFGQGTKVE IK          (SEQ ID NO: 29)
```

FIG. 8

```
1    GAGGTGCAGC TGGTGGAGTC CGGGGGAGGC TTAGTTCAGC CTGGGGGATC CCTGAGACTC
61   TCCTGTGCAG CCTCAGGGTT CACCTTTAGT AATAACTGGA TGCACTGGGT CCGCCAGGCT
121  CCAGGGAAGG GGCTGGAGTG GATCTCAGAG ATTAGAAGTG ATGGGAATTT CACAAGGTAC
181  GCGGACTCCA TGAAGGGCCG ATTCACCATC TCCAGAGACA ACGCCAAGAG CACACTGTAT
241  TTGCAAATGA ACAGTCTGAG AGTCGAGGAC ACGGGTCTGT ATTACTGTGC AAGAGACTAC
301  CCCTATAGCA TTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC A    (SEQ ID NO: 37)
```

FIG. 9

```
1    EVQLVESGGG LVQPGGSLRL
21   SCAAS GFTFS NNWMHWVRQA CDR1
41   PGKGLEWISE IRSDGNFTRY CDR2
61   ADSMKGRFTI SRDNAKSTLY
81   LQMNSLRVED TGLYYC ARDY CDR3
101  PYSIDYWGQG TLVTVSS    (SEQ ID NO: 38)
```

FIG. 10

```
1       GATATTGTGA TGACCCAGAC TCCACTCTCC TCACCTGTCA CCCTTGGACA GCCGGCCTCC
61      ATCTCCTGCA CATCTAGTCA AAGCCTCGTA CACAGTAATG GAAACACCTA CTTGAGTTGG
121     CTTCAGCAGA GGCCAGGCCA GCCCCCAAGA CTCCTAATTT ATGAGATTTC TAAGCGGGTC
181     TCTGGGGTCC CAGACAGATT CAGTGGCAGT GGGGCAGGGA CAGATTTCAC ACTGAAAATC
241     AGCAGGGTGG AAGCTGAGGA TGTCGGGGTT TATTACTGCA TGCAAGGTAA ACAACTTCGG
301     ACTTTTGGCC AGGGGACCAA GCTGGAGATC AAA
```

(SEQ ID NO: 46)

FIG. 11


```
1       DIVMTQTPLS SPVTLGQPAS
21      ISCTSSQSLV HSNGNTYLSW CDR1
41      LQQRPGQPPR LLIYEISKRV CDR2
61      SGVPDRFSGS GAGTDFTLKI
81      SRVEAEDVGV YYCMQGKQLR CDR3
101     TFGQGTKLEI K
```

(SEQ ID NO: 47)

FIG. 12

```
1       GAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGCTC CGTGAGACTG
61      TCTTGTGCGG CCTCAGGCTT CATTCTTAGC AACTTTGCCA TGAGTTGGGT CCGCCAGGCT
121     CCAGGGAAGG GGCTGGACTG GGTCTCAGGT AATTTTGGTG GTCGTGAAAA TACATATTAC
181     GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCAGAGACA GTTCCAAGAG CACACTGTAT
241     CTGCAAATGA ACAATTTGAG AGCCGAGGAC ACGGCCGTAT ATTACTGTGC GCGAGGCGAT
301     TACCATGGTT CGGGGGCTCA CTTTGACTAC TGGGGCCAGG GAATACTGGT CACCGTCTCC
361     TCA    (SEQ ID NO: 55)
```

FIG. 13


```
1       EVQLVESGGG LVQPGGSVRL
21      SCAASGFILS NFAMSWVRQA CDR1
41      PGKGLDWVSG NFGGRENTYY CDR2
61      ADSVKGRFTI SRDSSKSTLY
81      LQMNNLRAED TAVYYCARGD CDR3
101     YHGSGAHFDY WGQGILVTVS
121     S
```

(SEQ ID NO: 56)

FIG. 14

```
1    GATATTGTGA TGACCCAGAG TCCACTCTCC TCACCTGTCA TCCTTGGACA GCCGGCCTCC
61   ATCTCCTGCA GGTCTAGTCA AAGCCTCCTA CACAGTGATG GAAACACCTA CTTGAGTTGG
121  CTTCACCAGA GGCCAGGCCA GCCTCCTAGA CTCCTAATTT ATCAGATTTC TAACCGGTTC
181  TCTGGGGTCC CAGACAGATT CAGTGGCAGT GGGACAGGGA CAGATTTCAC ACTGAAAATC
241  AGCAGGGTGG AAGCTGAGGA TGCCGGGATT TATTACTGCA TGCAAGGTAC AGAATTTCCT
301  CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAA   (SEQ ID NO: 64)
```

FIG. 15

```
1    DIVMTQSPLS SPVILGQPAS
21   ISCRSSQSLL HSDGNTYLSW CDR1
41   LHQRPGQPPR LLIYQISNRF CDR2
61   SGVPDRFSGS GTGTDFTLKI
81   SRVEAEDAGI YYCMQGTEFP CDR3
101  RTFGQGTKVE IK   (SEQ ID NO: 65)
```

FIG. 16

```
1       GAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGATACAGC CTGGGGGGTC CCTGAGACTC
61      TCCTGTGCAA CCTCTGGATT CACCTTTAGA ACTTCTTCCA TGAGTTGGGT CCGTCGGGCT
121     CCAGGGAAGG GGCTGGAATG GGTCTCAGCT ATTGGTGCTG AAAGTCATGA CACGCACTAC
181     ACAGACTCCG CGGAGGGCCG GTTCACCATC TCCAAAGACT ATTCAAAGAA CACAGTATAT
241     CTGCAGATGA ACGGCCTGAG AGTCGACGAC ACGGCCATAT ATTATTGTGC CCATCACTAT
301     TACTATGGCT CGCGGCAGAA ACCCAAAGAT TGGGGAGATG CTTTTGATAT GTGGGGCCAG
361     GGGACAATGG TCTCCGTCTC TTCA
```

(SEQ ID NO: 73)

FIG. 17


```
1       EVQLVESGGG LIQPGGSLRL
21      SCATSGFTFR TSSMSWVRRA CDR1
41      PGKGLEWVSA IGAESHDTHY CDR2
61      TDSAEGRFTI SKDYSKNTVY
81      LQMNGLRVDD TAIYYCAHHY CDR3
101     YYGSRQKPKD WGDAFDMWGQ
121     GTMVSVSS
```

(SEQ ID NO: 74)

FIG. 18

```
1       GACATCCAGA TGACCCAGTC TCCATCTTCT GTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61      ATCACTTGTC GGGCGAGTCA GGATATTAGC ACCTGGTTAA CCTGGTATCA GCAGAGAGCA
121     GGGAAGGCCC CTAACCTCCT GATCTATGGT GCATCCACTT TGGAAGATGG GGTCCCATCC
181     AGGTTCAGCG GCAGTGGATC CGGGACAGAT TTCACTCTCA CTATCGACAG CCTGCAGCCT
241     GACGATTTTG CAACTTACTA TTGTCAACAG TCTCACAGTT TCCCCTACAC TTTTGGCCAG
301     GGGACCCAGC TGGGGATCTC A
```

(SEQ ID NO: 82)

FIG. 19


```
1           DIQMTQSPSS VSASVGDRVT
21          ITCRASQDIS TWLTWYQQRA CDR1
41          GKAPNLLIYG ASTLEDGVPS CDR2
61          RFSGSGSGTD FTLTIDSLQP
81          DDFATYYCQQ SHSFPYTFGQ CDR3
101         GTQLGIS
```

(SEQ ID NO: 83)

FIG. 20

FIG. 21A

FIG. 21B

FIG. 21C

FIG. 21D

FIG. 21E

FIG. 21F

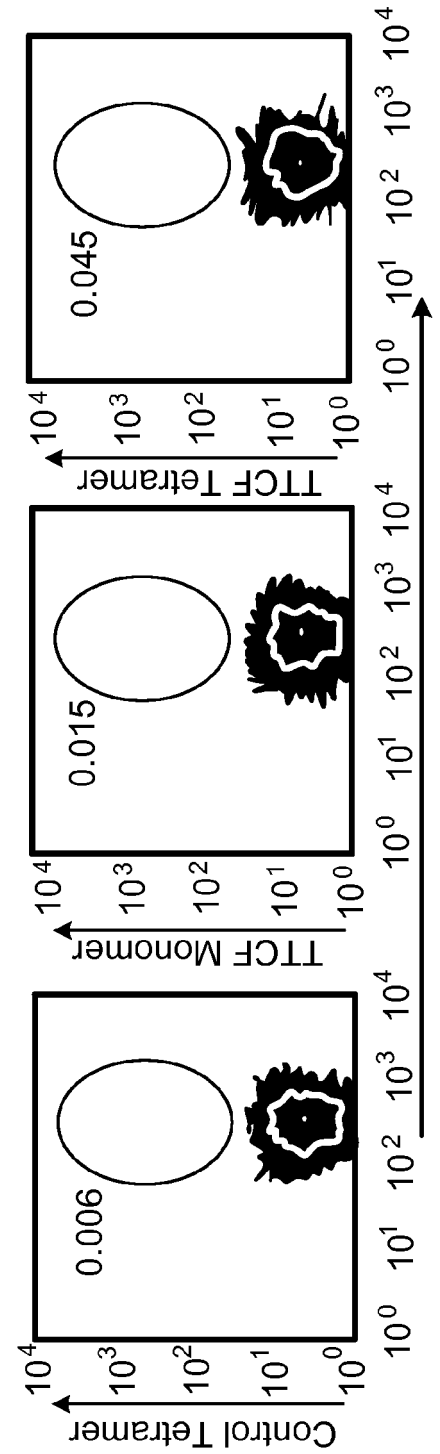


FIG. 22A

	Control Tet/ 10^5 B cells	TTCF Moncmen/ 10^4 B cells	TTCF Tet/# 10^4 B cells	#Tet/#Mono Foldchange
Donor 1	3.98	2.53	18.41	7.3
Donor 2	15.03	38.64	117.18	3.1
Donor 3	4.14	48.92	77.55	1.6

FIG. 22B

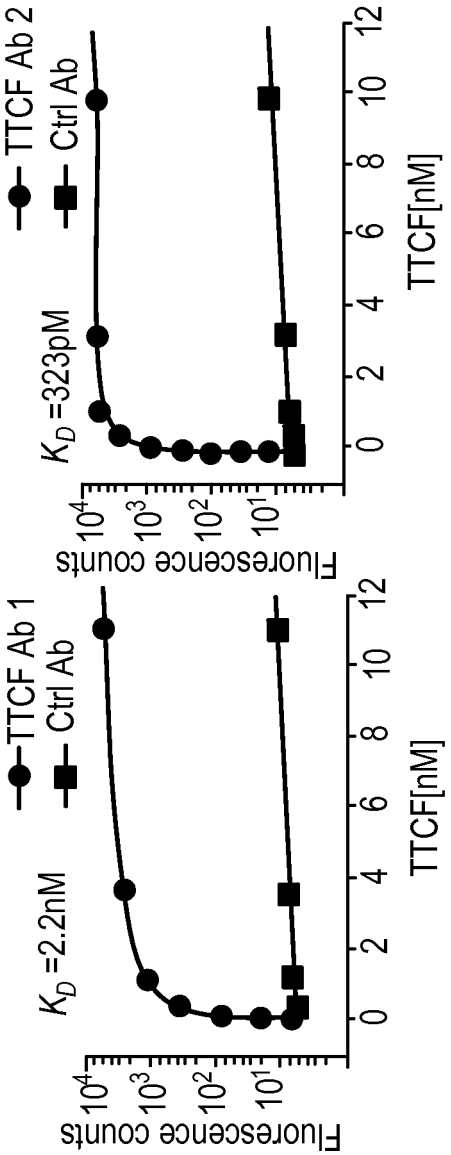


FIG. 23A

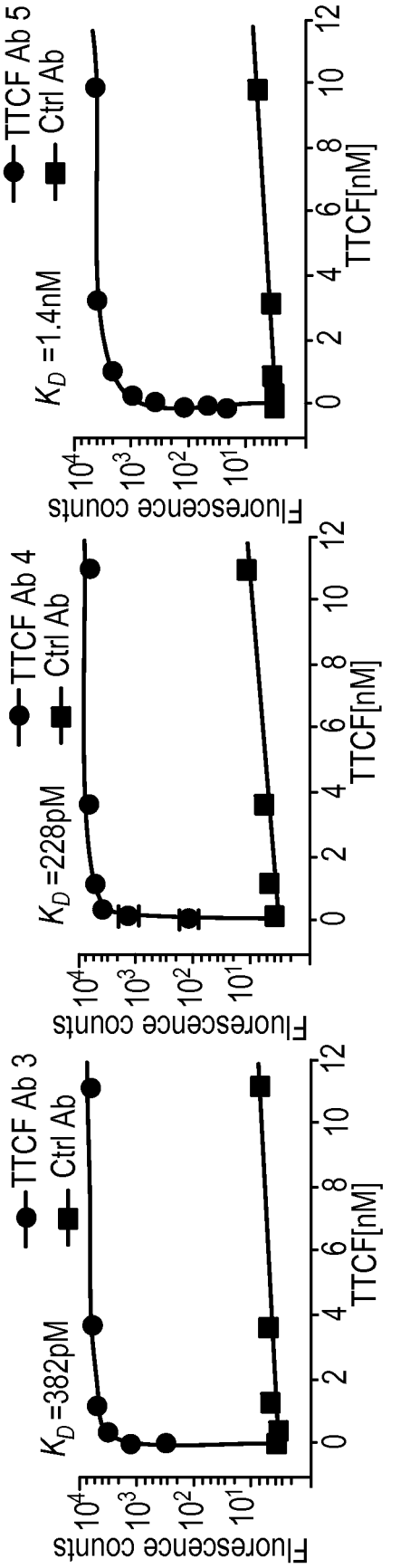


FIG. 23B

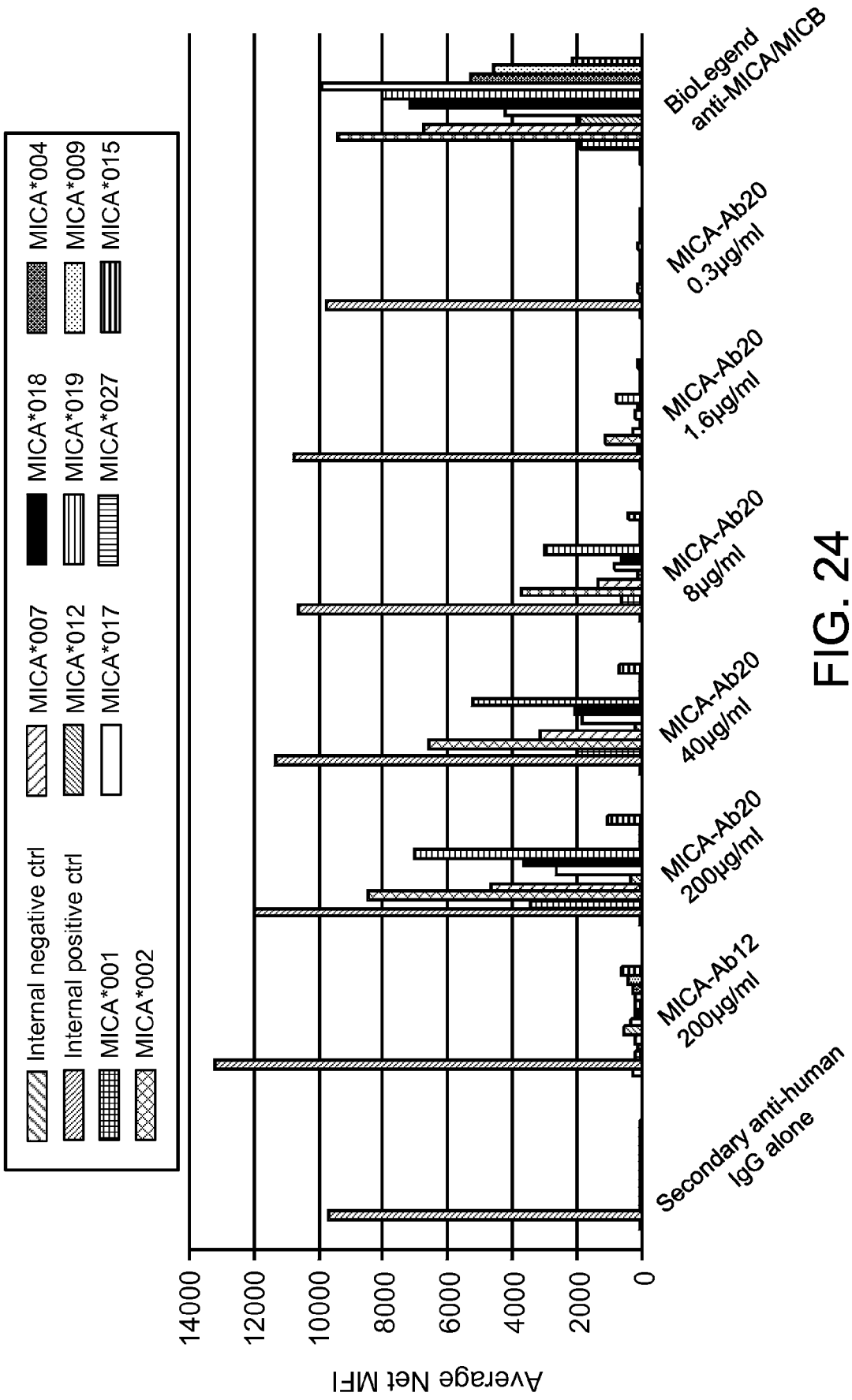

Internal negative ctrl
Internal positive ctrl
MICA*001
MICA*002
MICA*007
MICA*012
MICA*017
MICA*018
MICA*019
MICA*027
MICA*004
MICA*009
MICA*015
Average Net MFI
14000
12000
10000
8000
6000
4000
2000
0
Secondary anti-human IgG alone
MICA-Ab12 200µg/ml
MICA-Ab20 200µg/ml
MICA-Ab20 40µg/ml
MICA-Ab20 8µg/ml
MICA-Ab20 1.6µg/ml
MICA-Ab20 0.3µg/ml
BioLegend anti-MICA/MICB

FIG. 24

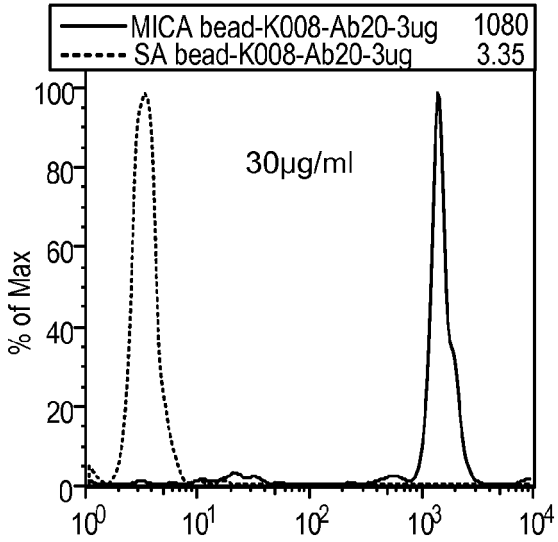


FIG. 25A

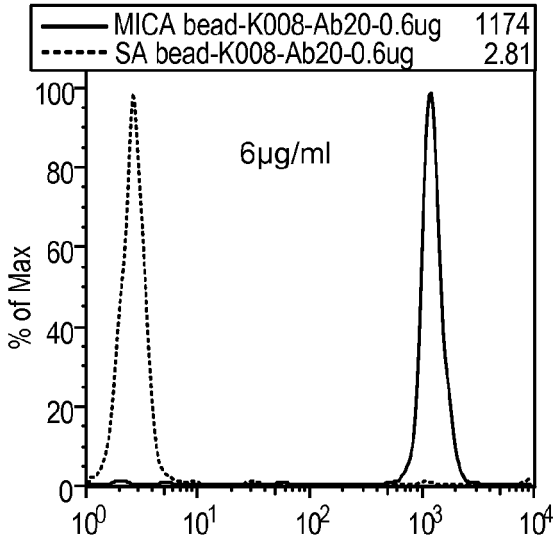
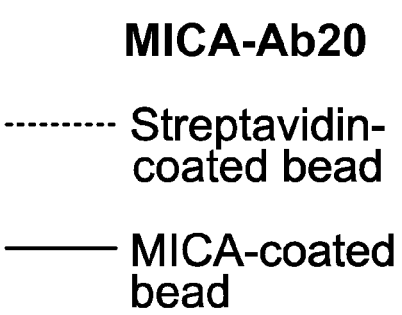


FIG. 25B



MICA

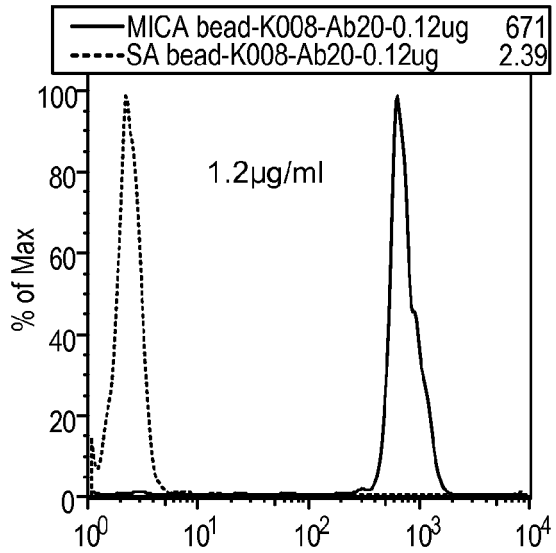


FIG. 25C

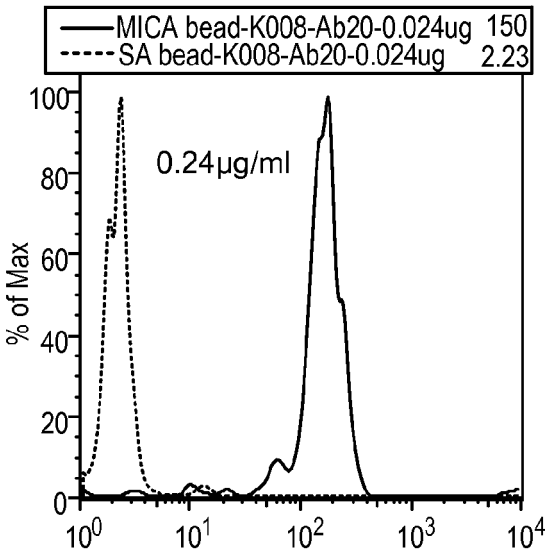


FIG. 25D

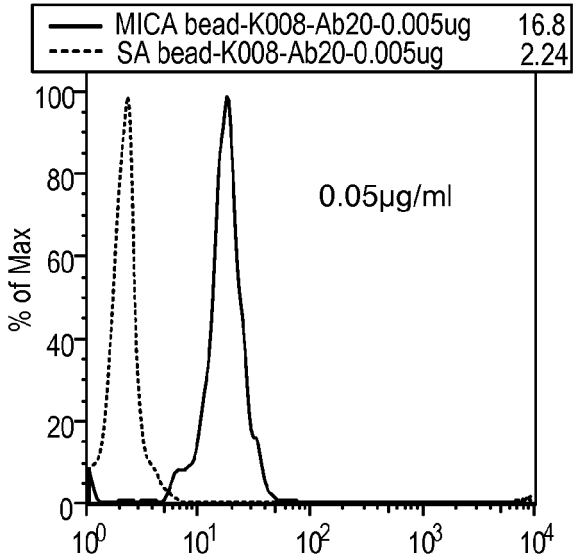


FIG. 25E

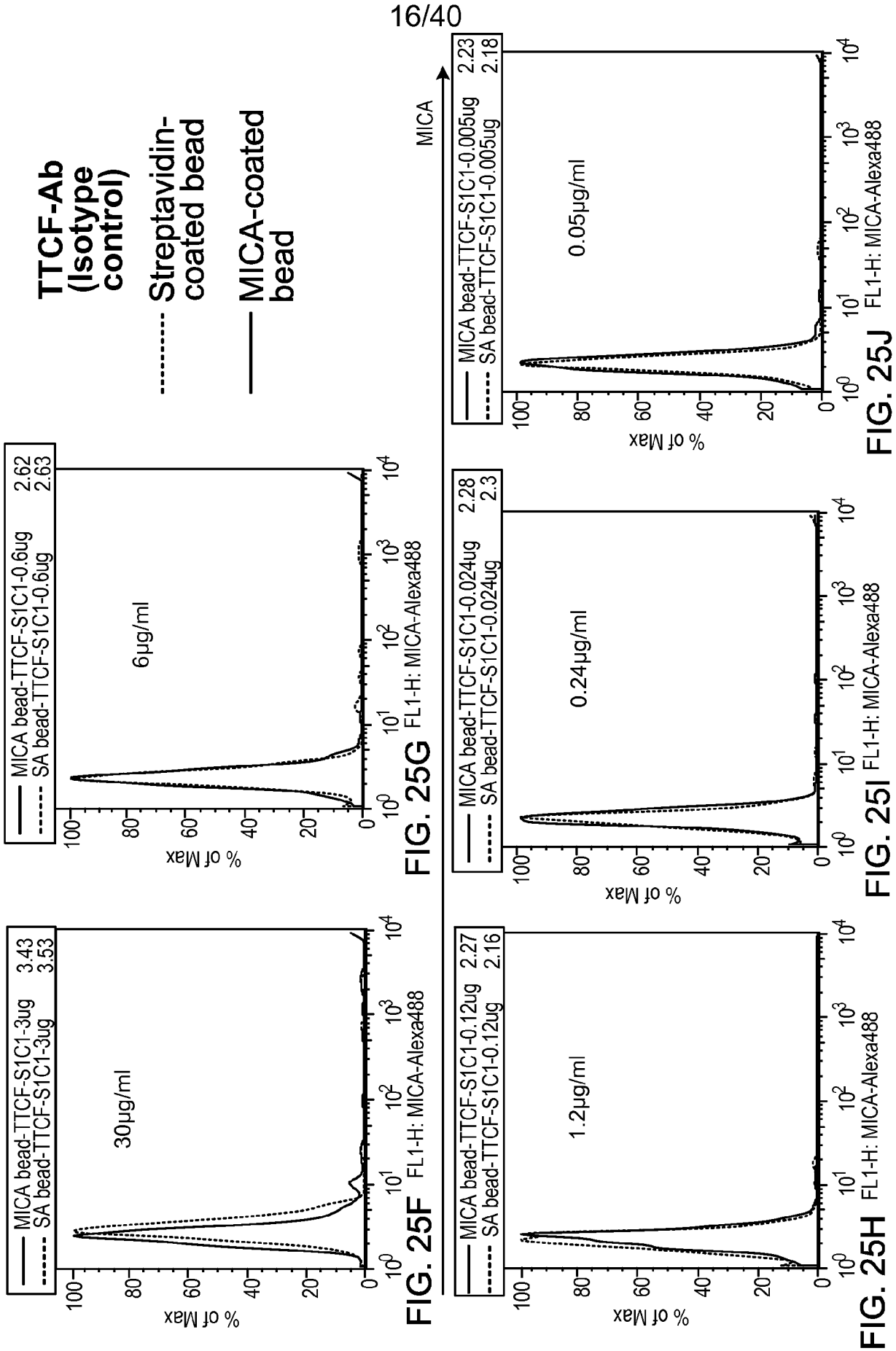


FIG. 25F FIG. 25G FIG. 25H FIG. 25I FIG. 25J

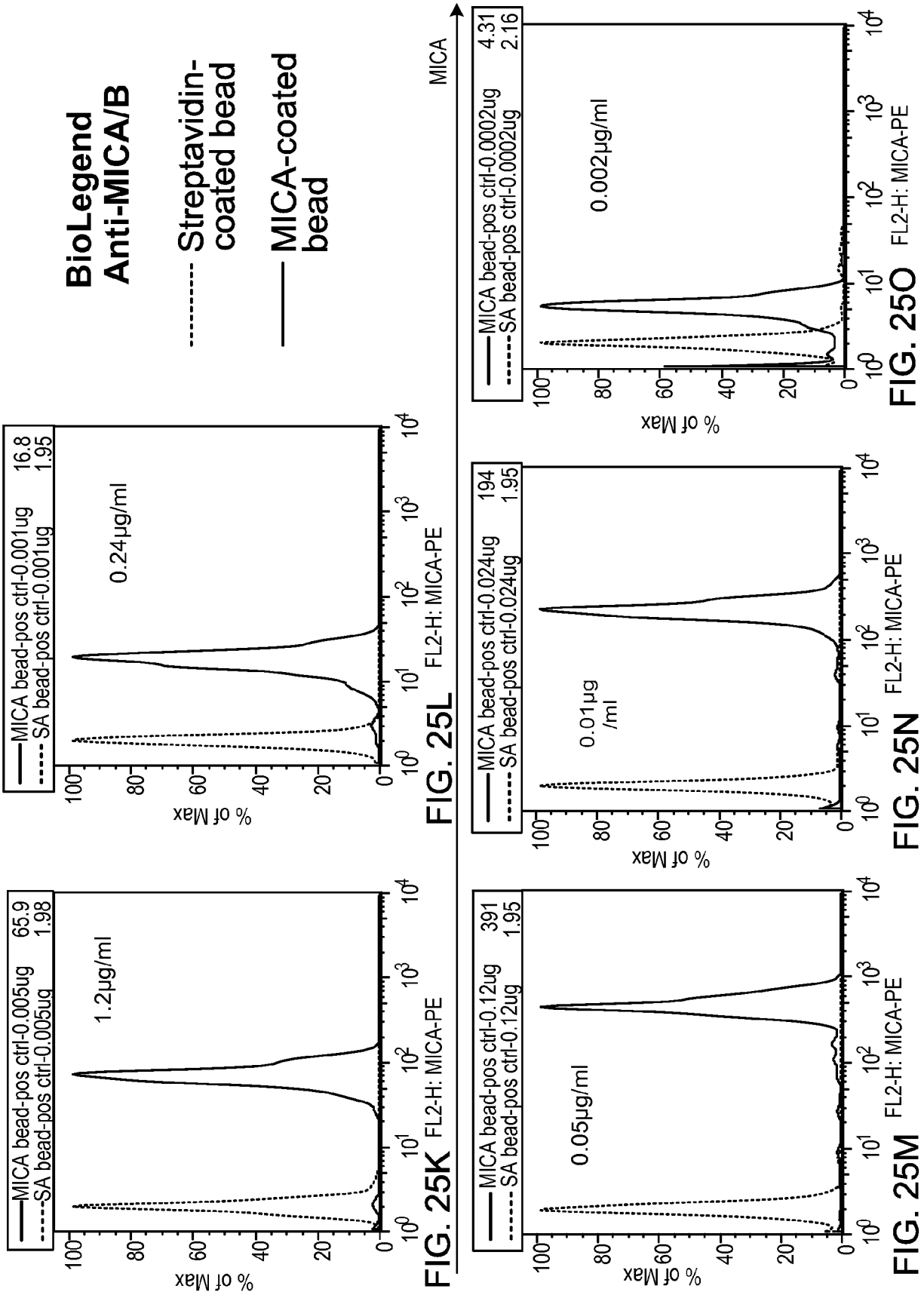
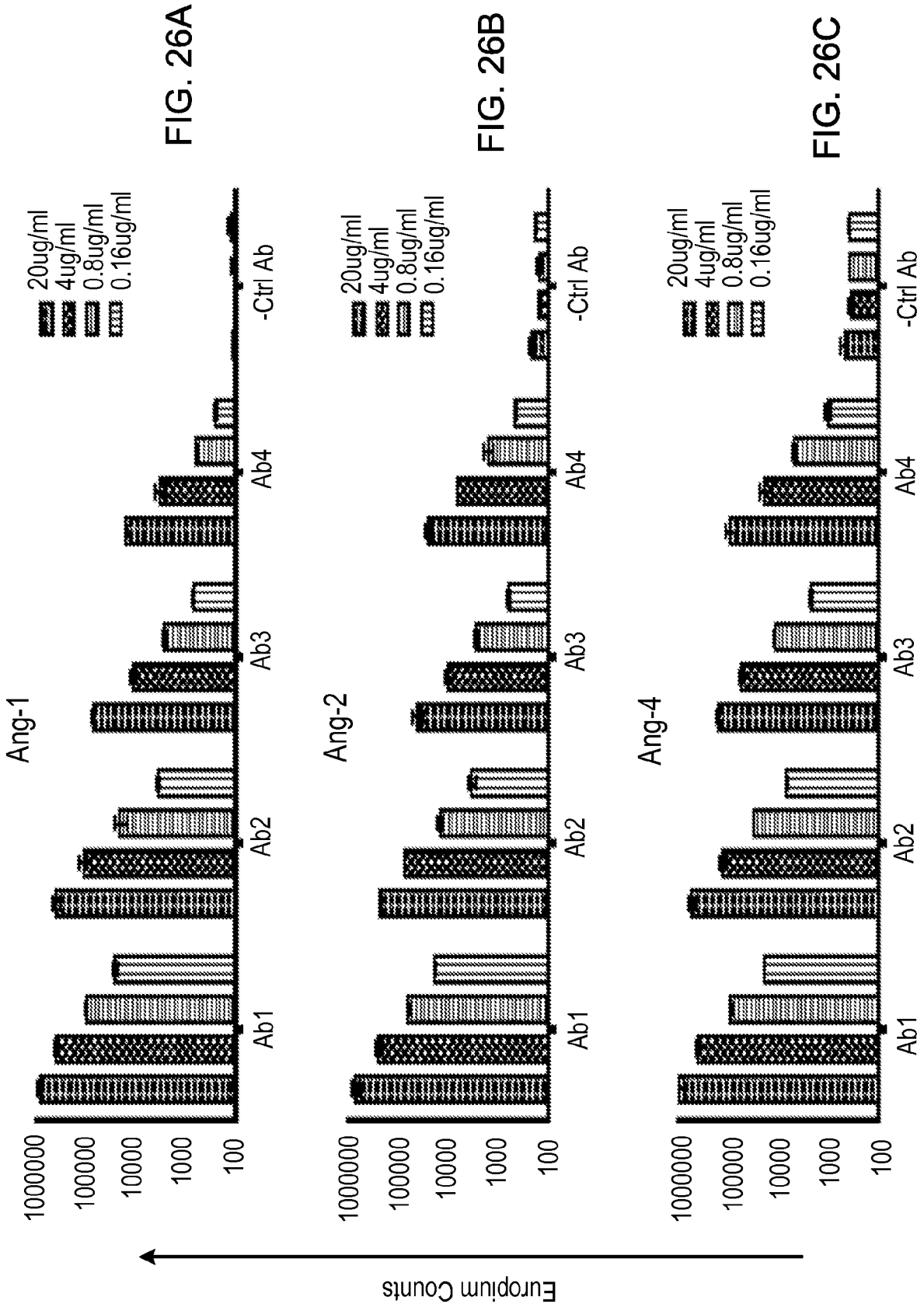


FIG. 25K FIG. 25L FIG. 25M FIG. 25N FIG. 25O


FIG. 26A
FIG. 26B
FIG. 26C
Ang-1
Ang-2
Ang-4
20ug/ml
4ug/ml
0.8ug/ml
0.16ug/ml
Ab1
Ab2
Ab3
Ab4
-Ctrl Ab
1000000
100000
10000
1000
100
Europium Counts


Ang-like-3
20ug/ml
4ug/ml
0.8ug/ml
0.16ug/ml
1000000
100000
10000
1000
100
Ab1
Ab2
Ab3
Ab4
-Ctrl Ab

FIG. 26D

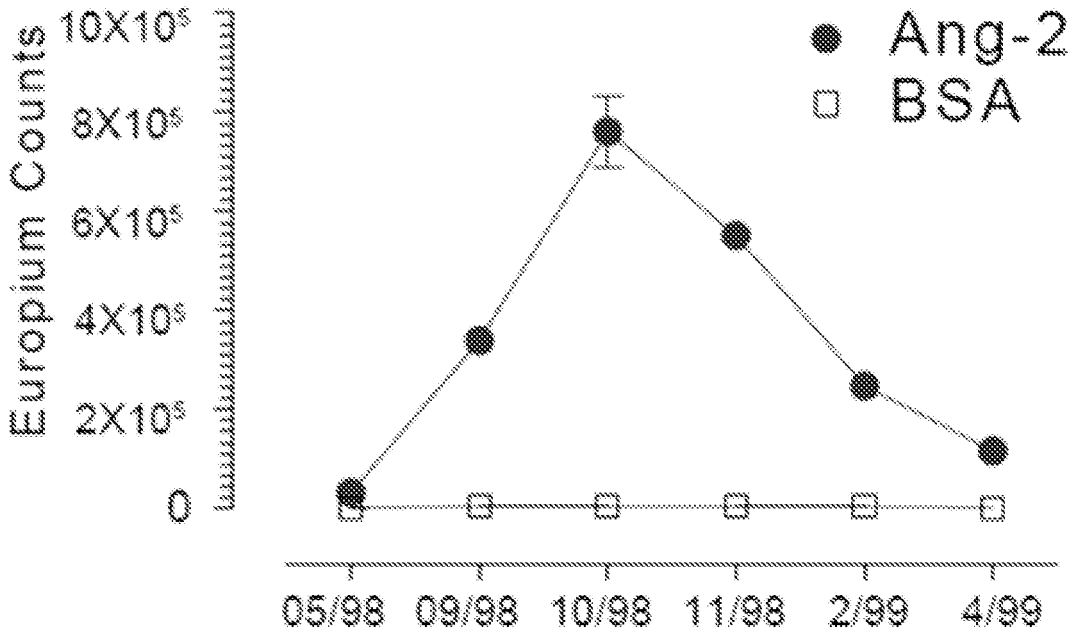


FIG. 27A

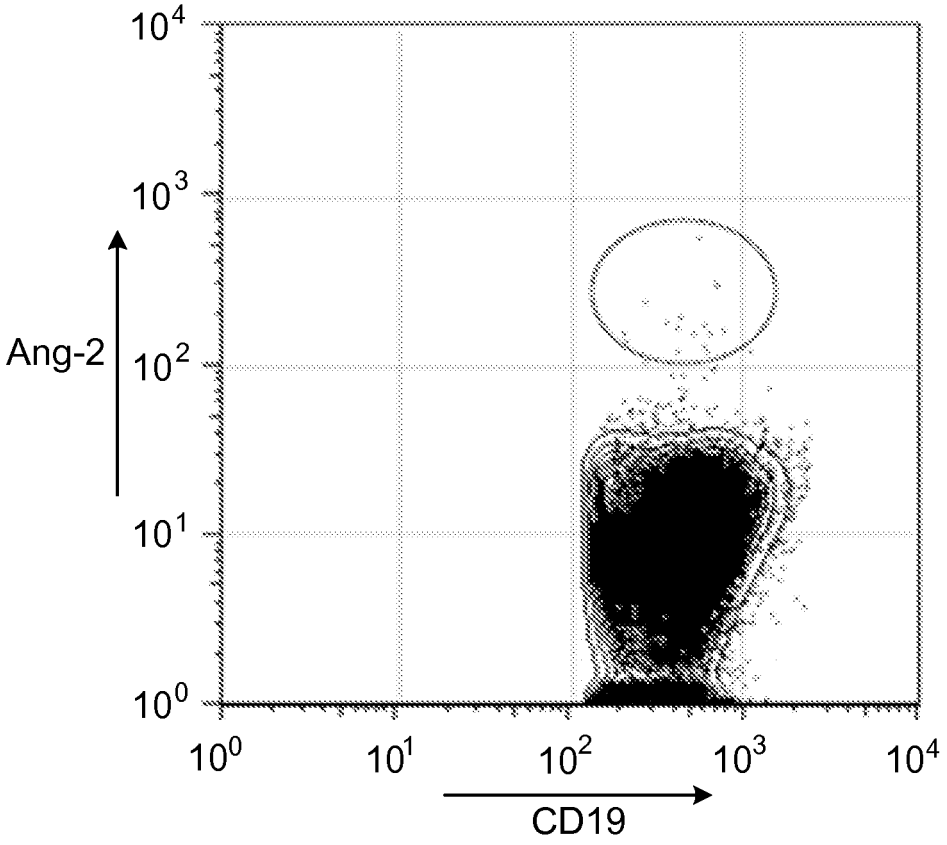


FIG. 27B

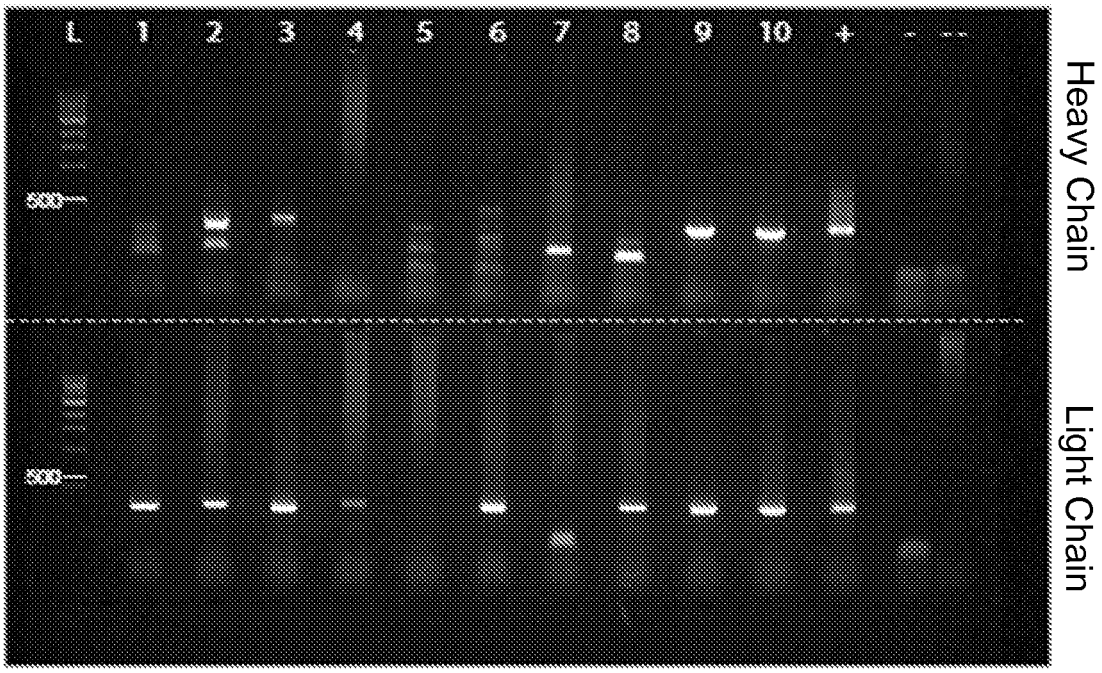


FIG. 27C

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGGAGCCTTCGGGGACCCTGTCCCT
CACCTGCACTGTGTCTGGTGGCTCCATCAGCAGGAGTAACTGGTGGAGTTGGGTCCGCC
AGCCCCCAGGGGAGGGGCTGGAATGGATTGGAGAAATCCATCACATTGGGAGGTCCAGC
TACAATCCGTCCCTCAAGAGTCGAGTCACCATGTCTGTAGACAAGTCCCAGAACCAGTT
CTCCCTGAGGCTGACCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAAAA
ATGGCTACTACGCTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCG
(SEQ ID NO. 148)

FIG. 28

QVQLQESGPGLVEPSGTLSLTCTVSGGSISRSNWWSWVRQPPGEGLEWIGEIHHIGRSS
YNPSLKSRVTMSVDKSQNQFSLRLTSVTAADTAVYYCAKNGYYAMDVWGQGTTVTVSS
(SEQ ID NO. 149)

FIG. 29

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCGACTTCCTAGCCTGGTACCAGCAGA
AACCTGGCCAGGCTCCCAGGCTCCTCATCTACGCTACATCCTTCAGGGCCACTGGCATC
TCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCTCTCTCACCATCAACAGACT
GGAACCTGAAGATTTTGCAGTGTATTACTGTCAGCACTATCGTAGTTCACCTCCGTGGT
ACACTTTTGCCCAGGGGACCAAGCTGGACATGAGACGTACGGTGGCTGCACCATCTGTC
(SEQ ID NO. 150)

FIG. 30

EIVLTQSPGTLSLSPGERATLSCRASQSVSSDFLAWYQQKPGQAPRLLIYATSFRATGI
SDRFSGSGSGTDFSLTINRLEPEDFAVYYCQHYRSSPPWYTFAQGTKLDMRRTVAAPSV
(SEQ ID NO. 151)

FIG. 31

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCTC ACCTGCGCTGTCTCTGGTGCCTCCATTACCAATGGTGCCTGGTGGAGTTGGGTCCGCCAG CCCCCAGGGAAGGGGCTGGAGTGGATTGGAGAAATCTATCTTAATGGGAACACCAACTCC AACCCGTCCCTGAAGAGTCGAGTCATCATATCAGTGGACAAGTCCAAGAACCACTTCTCG CTGACCCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAAGAACGCT GCCTACAACCTTGAGTTCTGGGGCCAGGGAGCCCTGGTCACCGTCTCCTCA (SEQ ID NO: 167)

FIG. 32

QVQLQESGPGLVKPSGTLSLTCAVSGASITNGAWWSWVRQPPGKGLEWIGEIYLNGNTNS NPSLKSRVIISVDKSKNHFSLTLNSVTAADTAVYYCAKNAAYNLEFWGQGALVTVSS (SEQ ID NO: 168)

FIG. 33

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC
CTCTCCTGCAGGGCCAGTCAGACTGTTAGCAGCCCCTACGTAGCCTGGTACCAGCAGAAA
CGTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACCGGCATCCCAG
ACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC
CTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGATAGATCATACTATTACACTTTT
GGCCAGGGGACCAAGCTGGAGATCAAA (SEQ ID NO: 169)

FIG. 34

EIVLTQSPGTLSLSPGERATLSCRASQTVSSPYVAWYQQKRGQAPRLLIYGASTRATGIPDR
FSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSYYYTFGQGTKLEIK (SEQ ID NO: 170)

FIG. 35

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAACCTGTCGCTC
ACCTGCACTGTCTCTGATGCCTCCATGAGTGATTATCACTGGAGCTGGATCCGGCAGGCC
GCCGGGAAGGGACTGGAGTGGATTGGGCGTATGTACAGCACTGGGAGTCCCTACTACAA
ACCCTCCCTCAAAGGTCGGGTCACCATGTCAATAGACACGTCCAAGAACCAGTTCTCCCT
GAAGCTGGCCTCTGTGACCGCCGCAGACACGGCCATCTATTATTGTGCGAGCGGACAACA
TATTGGTGGCTGGGTCCCCCCTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC
A (SEQ ID NO: 185)

FIG. 36

QVQLQESGPGLVKPSENLSLTCTVSDASMSDYHWSWIRQAAGKGLEWIGRMYSTGSPYY
KPSLKGRVTMSIDTSKNQFSLKLASVTAADTAIYYCASGQHIGGWVPPDFWGQGTLVTVS
S (SEQ ID NO: 186)

FIG. 37

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCA
TCTCCTGCAGGTCTAGTGAAGGCCTCGTATATAGTGATGGAGACACCTACTTGAGTTGGT
TTCACCAGAGGCCAGGCCAGCCTCCAAGACTCCTGATTTATAAAATTTCTAACCGGTTCT
CTGGGGTCCCCGACAGATTCAGTGGCAGTGGGGCAGGCACAGATTTCACACTGAAAATCA
GCAGGGTGGAGGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGCTACACATTTTCCGT
GGACGTTCGGCCAGGGGACCAAAGTGGAAGTCAAACGT (SEQ ID NO: 187)

FIG. 38

DIVMTQTPLSSPVTLGQPASISCRSSEGLVYSDGDTYLSWFHQRPGQPPRLLIYKISNRFSG
VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATHFPWTFGQGTKVEVKR (SEQ ID NO:
188)

FIG. 39

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC
TCCTGTGCAGCCTCTGGATTCACCTTTAGTTCATATGGCTTGACCTGGATACGCCAGGCT
CCGGGGAAGGGCCTGGAGTGGGTCTCAAGTATCAGTGGCAGTGGCAATAACACATACTA
CGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCAGAGACAAAGTCAAGAAGACACTATA
TCTACAAATGGACAGCCTGACAGTCGGAGACACGGCCGTCTATTACTGCTTAGGAGTCGG
TCAGGGCCACGGAATTCCGGTCATCGTCTCCTCA (SEQ ID NO. 203)

FIG. 40

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGLTWIRQAPGKGLEWVSSISGSGNNTYYA
DSVKGRFTISRDKVKKTLYLQMDSLTVGDTAVYYCLGVGQGHGIPVIVSS (SEQ ID NO.
204)

FIG. 41

GATATTGTGATGACCCAGACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCA
TCTCCTGCAGGTCTAGTCAGAGCCTCGTACACCGTGATGGAAACACCTACTTGAGTTGGT
TTCTGCAGAGGCCAGGCCAGGCTCCAAGACTCCTAATTTATCGGATTTCTAACCGGTTCT
CTGGGGTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACGGATTTCACACTGAAAATC
AGCAGGGTGGAAGCTGAGGATGTCGGCGTTTACTACTGCATGCAAGCTACACAAATCCCC
AACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAG (SEQ ID NO. 205)

FIG. 42

DIVMTQTPLSSPVTLGQPASISCRSSQSLVHRDGNTYLSWFLQRPGQAPRLLIYRISNRFSG
VPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQIPNTFGQGTKLEIK (SEQ ID NO.
206)

FIG. 43

GAGGTGCAGCTGGTGGAGTCTGGAGGAGGCTTAATCCAGCCGGGGGGGTCCCTAAGACT
CTCCTGTGCAGCCTCGGGCTTCCTCATCAGTAGTTATTTCATGAGCTGGGTCCGCCAGG
CTCCAGGGAAGGGGCCGGAGTGGGTCTCAGTTATTTATAGCGATGGTAGTACATATTAC
GTAGACTCCGTGAAGGGCCGATTCACCATCTCCACAGACAATTCCAAGAACACACTATA
TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCCGATATTACTGTGCGACACGGC
ATTTGAATTATGACGGTGACCACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
TCCACCAAG (SEQ ID NO: 221)

FIG. 44

EVQLVESGGGLIQPGGSLRLSCAASGFLISSYFMSWVRQAPGKGPEWVSVIYSDGSTYY
VDSVKGRFTISTDNSKNTLYLQMNSLRAEDTARYYCATRHLNYDGDHWGQGTLVTVSSA
STK (SEQ ID NO: 222)

FIG. 45

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTC
CATCTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTGACGGAAACACCTACTTGAATT
GGTTTCACCAGAGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAAGCGG
GACTCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGTAGTGATTTCACACTGAA
AATCAGCAGGGTGGAGGCTGAGGATGTTGGAATTTATTACTGCATGCAAGGTACACATT
GGCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCA (SEQ
ID NO: 223)

FIG. 46

DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNWFHQRPGQSPRRLIYKVSKR
DSGVPDRFSGSGSGSDFTLKISRVEAEDVGIYYCMQGTHWPTFGQGTKVEIKRTVAA
(SEQ ID NO: 224)

FIG. 47

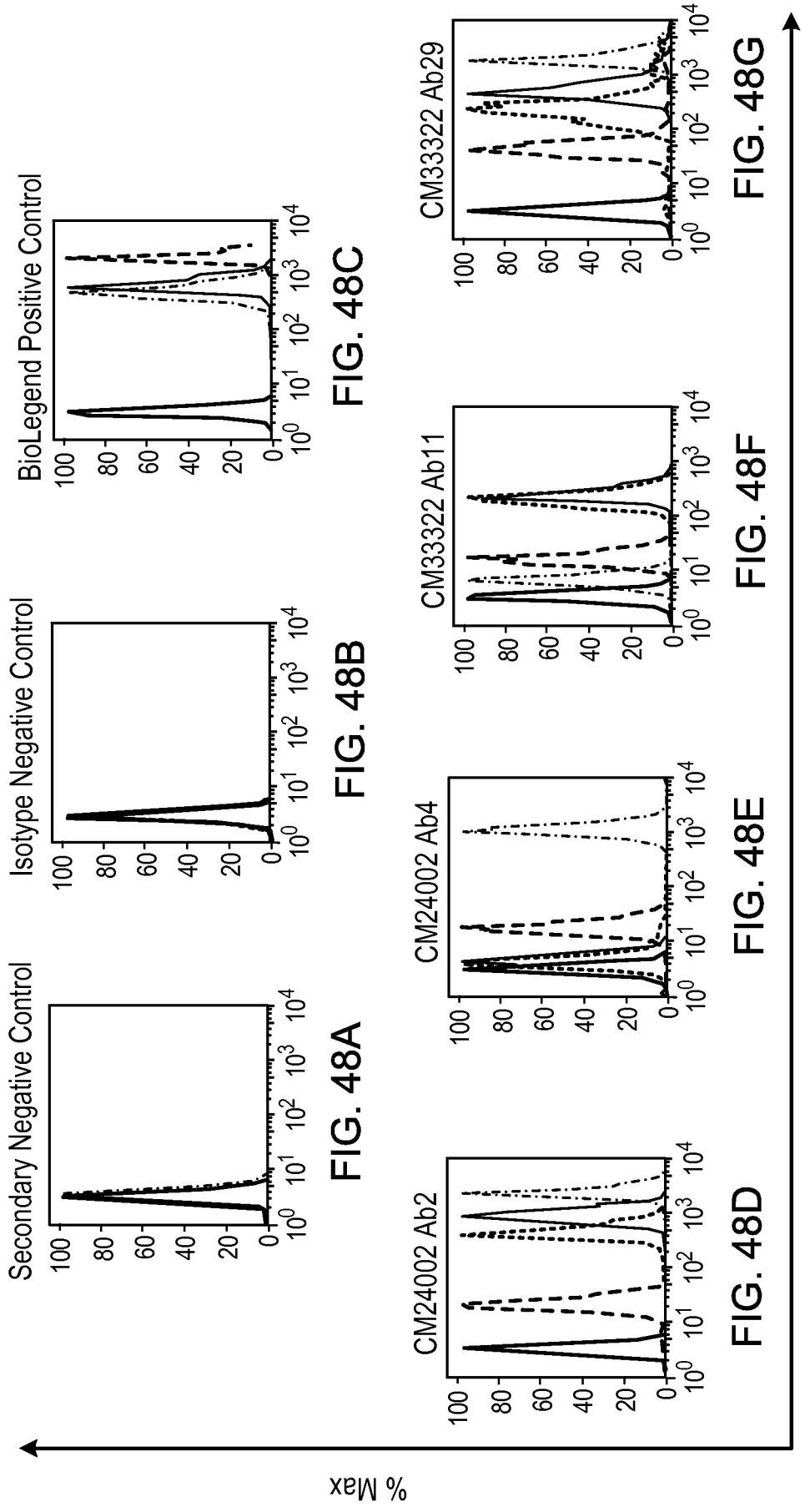


FIG. 48A FIG. 48B FIG. 48C

FIG. 48D FIG. 48E FIG. 48F FIG. 48G

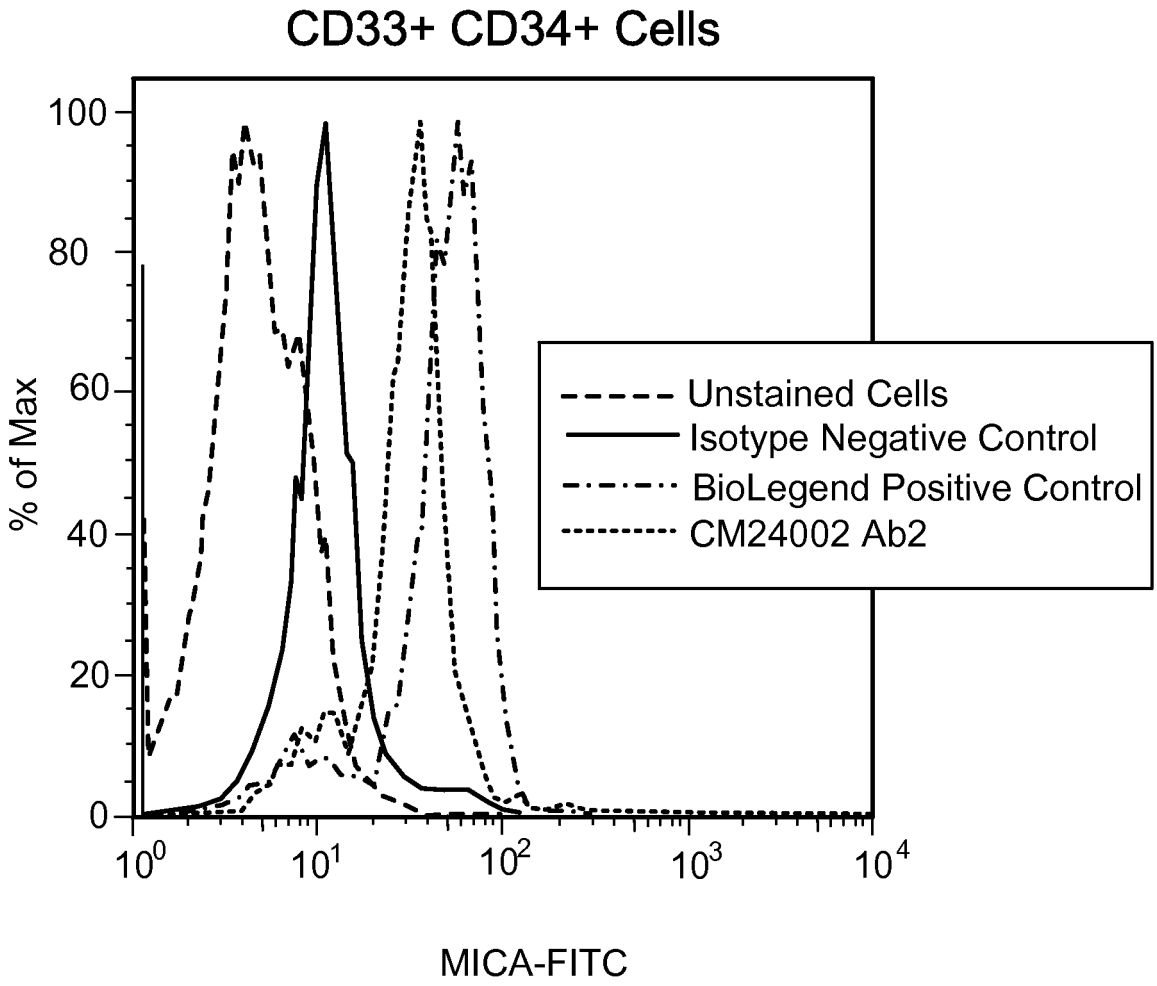

CD33+ CD34+ Cells
% of Max
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
MICA-FITC
Unstained Cells
Isotype Negative Control
BioLegend Positive Control
CM24002 Ab2

FIG. 49

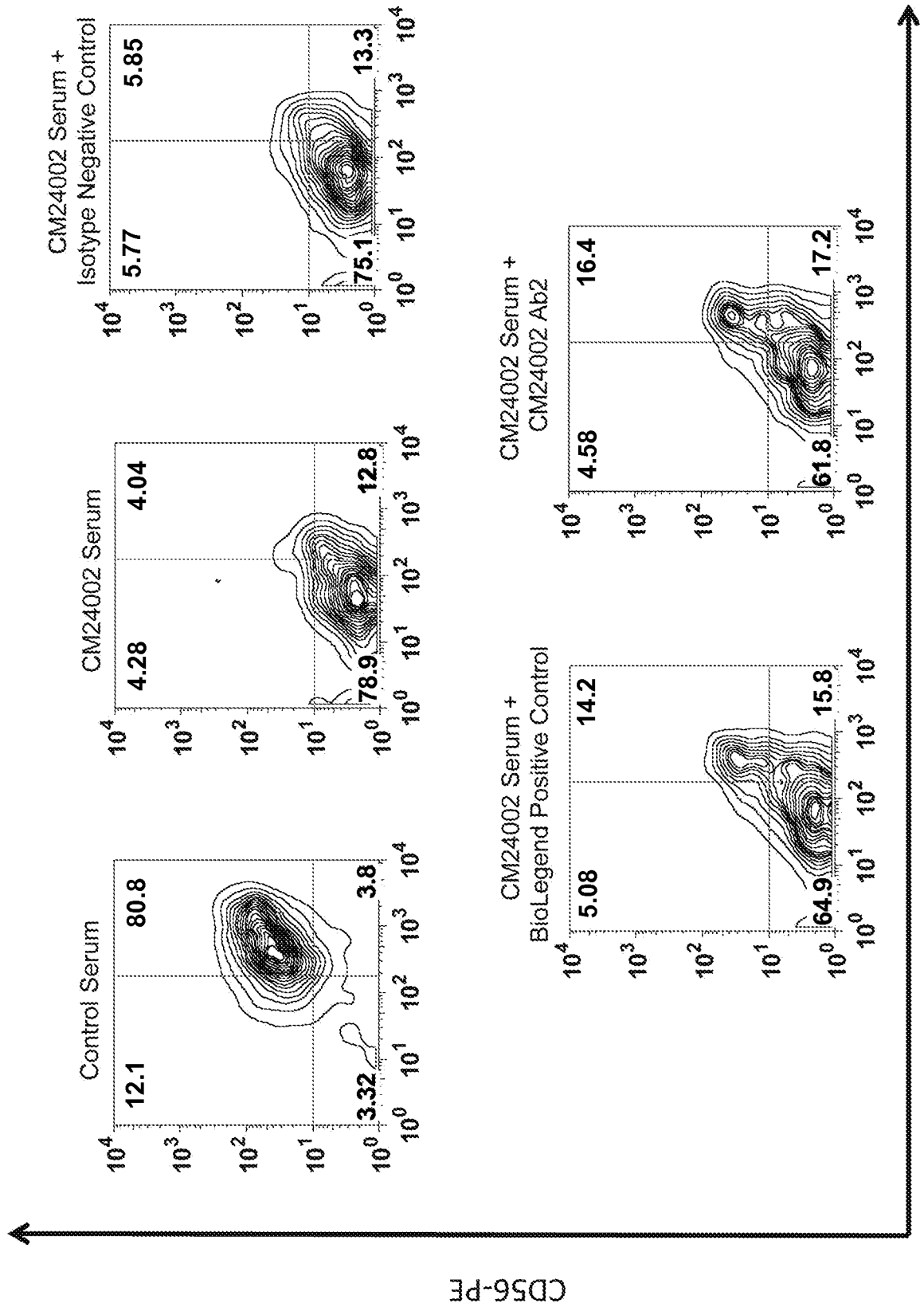

Control Serum
12.1
80.8
3.32
3.8
CM24002 Serum
4.28
4.04
78.9
12.8
CM24002 Serum +
Isotype Negative Control
5.77
5.85
75.1
13.3
CM24002 Serum +
BioLegend Positive Control
5.08
14.2
64.9
15.8
CM24002 Serum +
CM24002 Ab2
4.58
16.4
61.8
17.2
CD56-PE
NKG2D-APC

FIG. 50

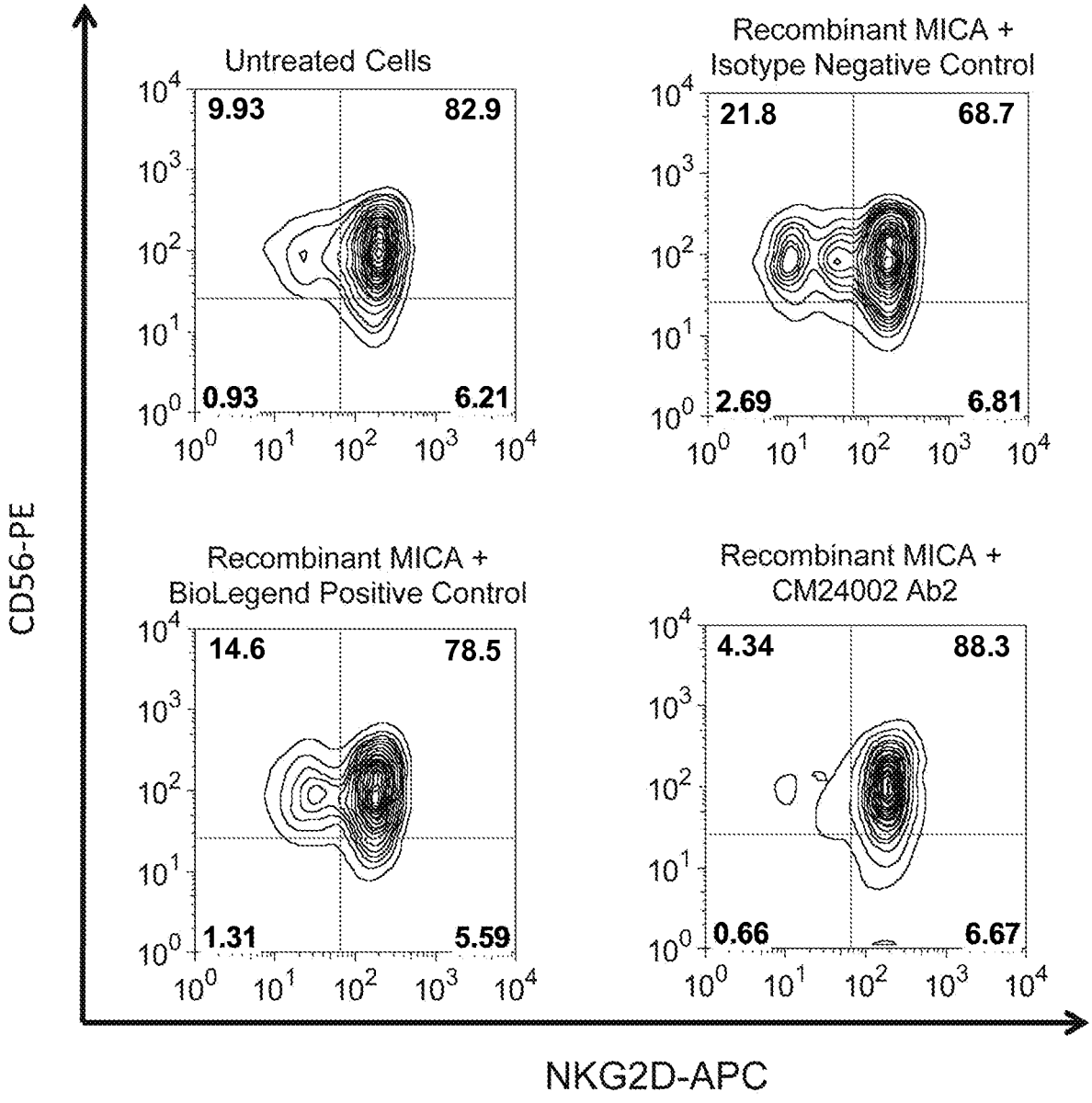

Untreated Cells
9.93
82.9
0.93
6.21
Recombinant MICA +
Isotype Negative Control
21.8
68.7
2.69
6.81
Recombinant MICA +
BioLegend Positive Control
14.6
78.5
1.31
5.59
Recombinant MICA +
CM24002 Ab2
4.34
88.3
0.66
6.67
CD56-PE
NKG2D-APC

FIG. 51

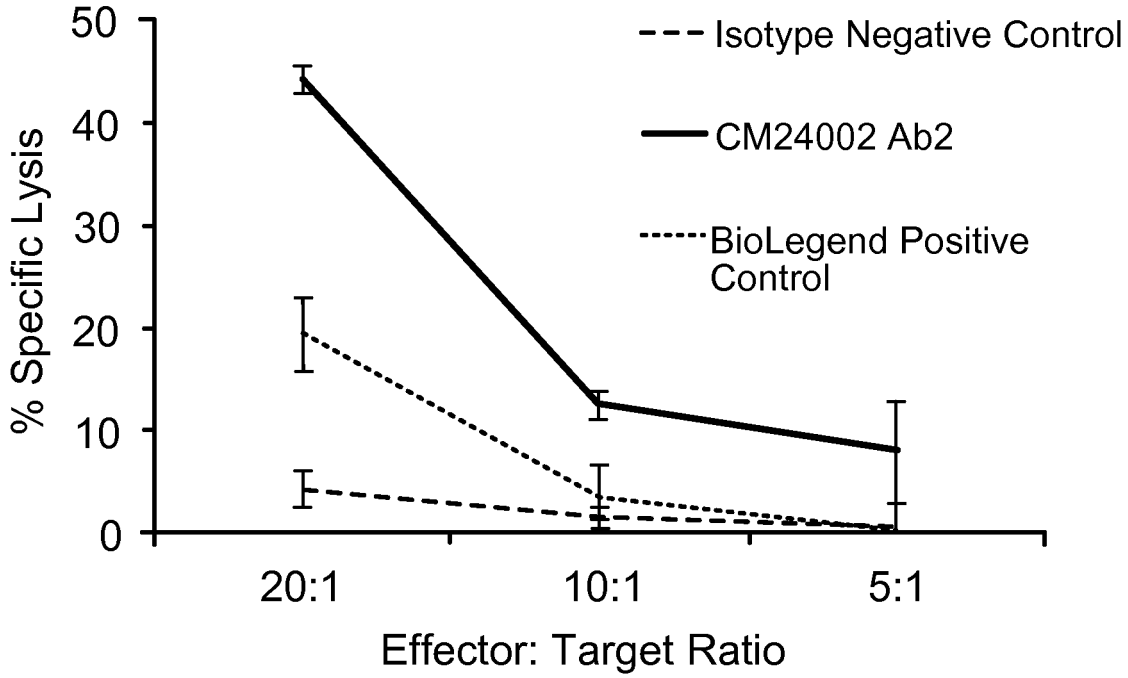

50
40
30
20
10
0
% Specific Lysis
Isotype Negative Control
CM24002 Ab2
BioLegend Positive Control
20:1
10:1
5:1
Effector: Target Ratio

FIG. 52

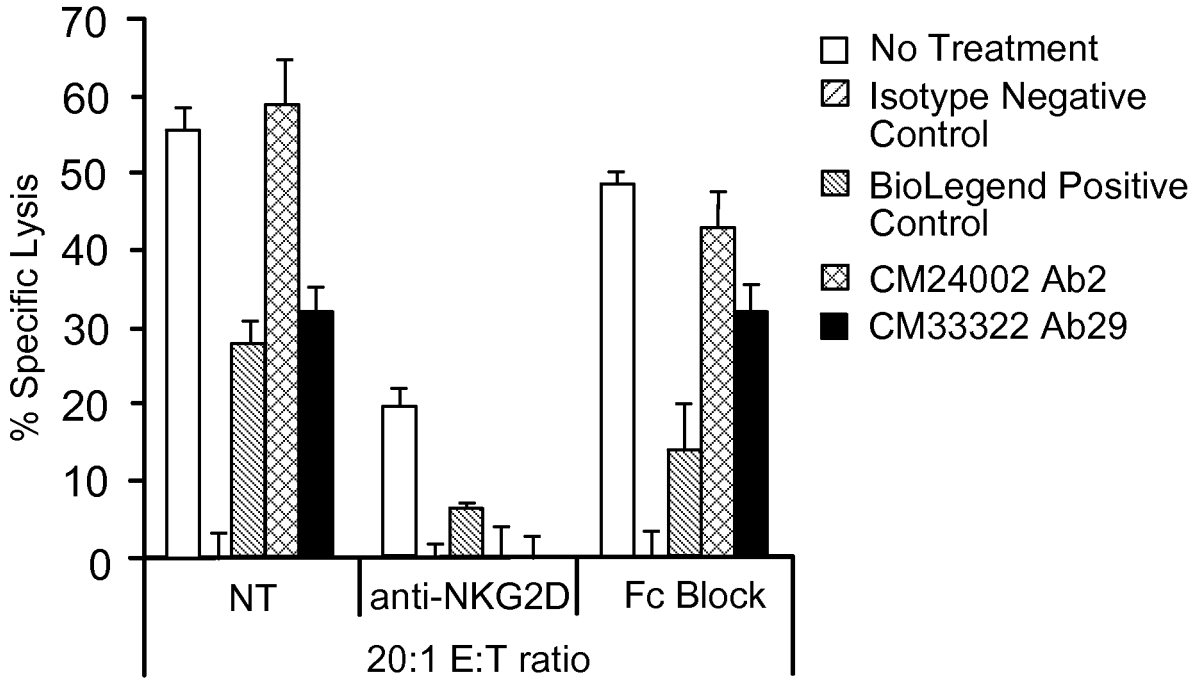

70
60
50
40
30
20
10
0
% Specific Lysis
No Treatment
Isotype Negative Control
BioLegend Positive Control
CM24002 Ab2
CM33322 Ab29
NT
anti-NKG2D
Fc Block
20:1 E:T ratio

FIG. 53

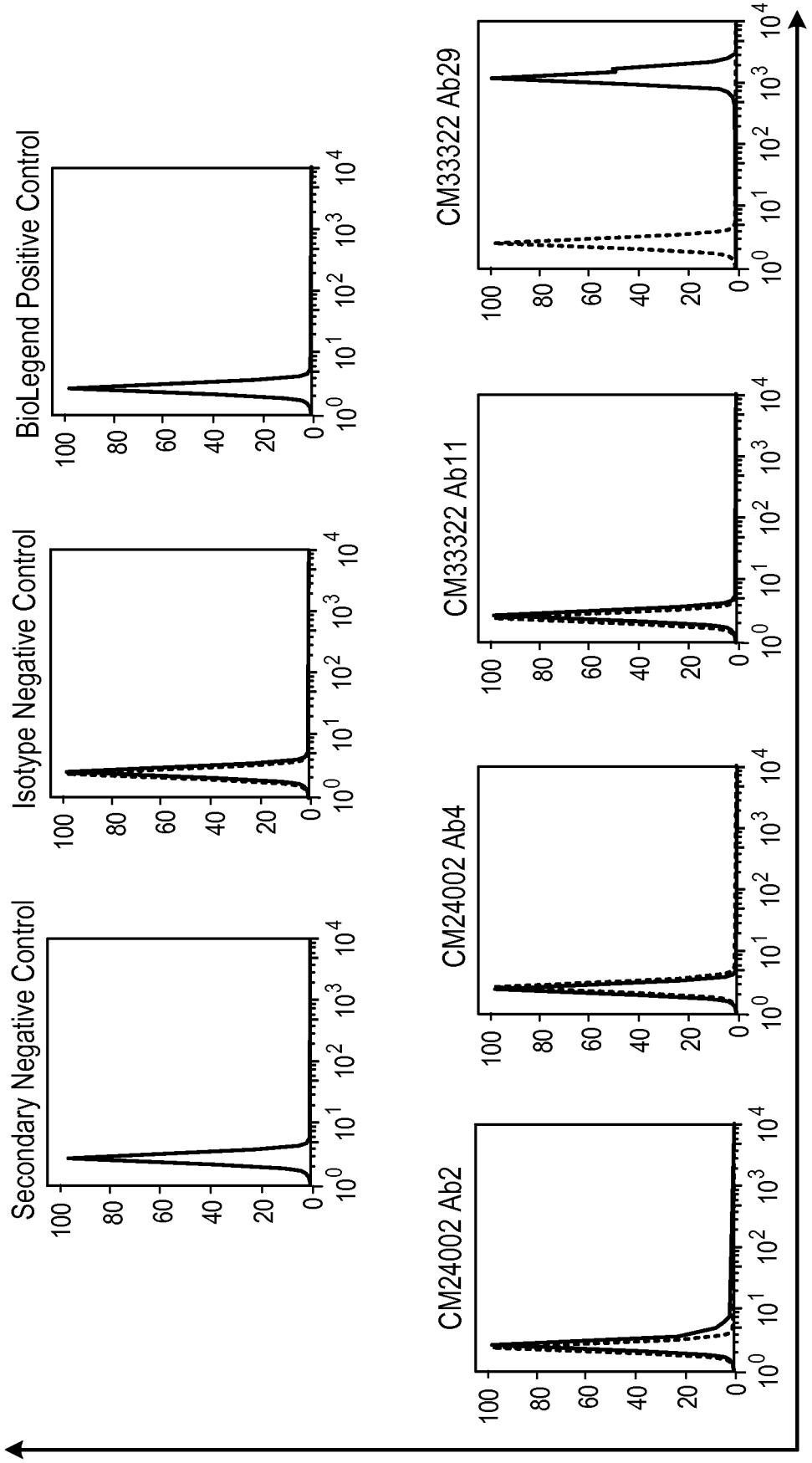

% Max
MICA-α3 DOMAIN-FITC
Streptavidin Negative Control
MICA α3 Domain
Secondary Negative Control
Isotype Negative Control
BioLegend Positive Control
CM24002 Ab2
CM24002 Ab4
CM33322 Ab11
CM33322 Ab29

FIG. 54

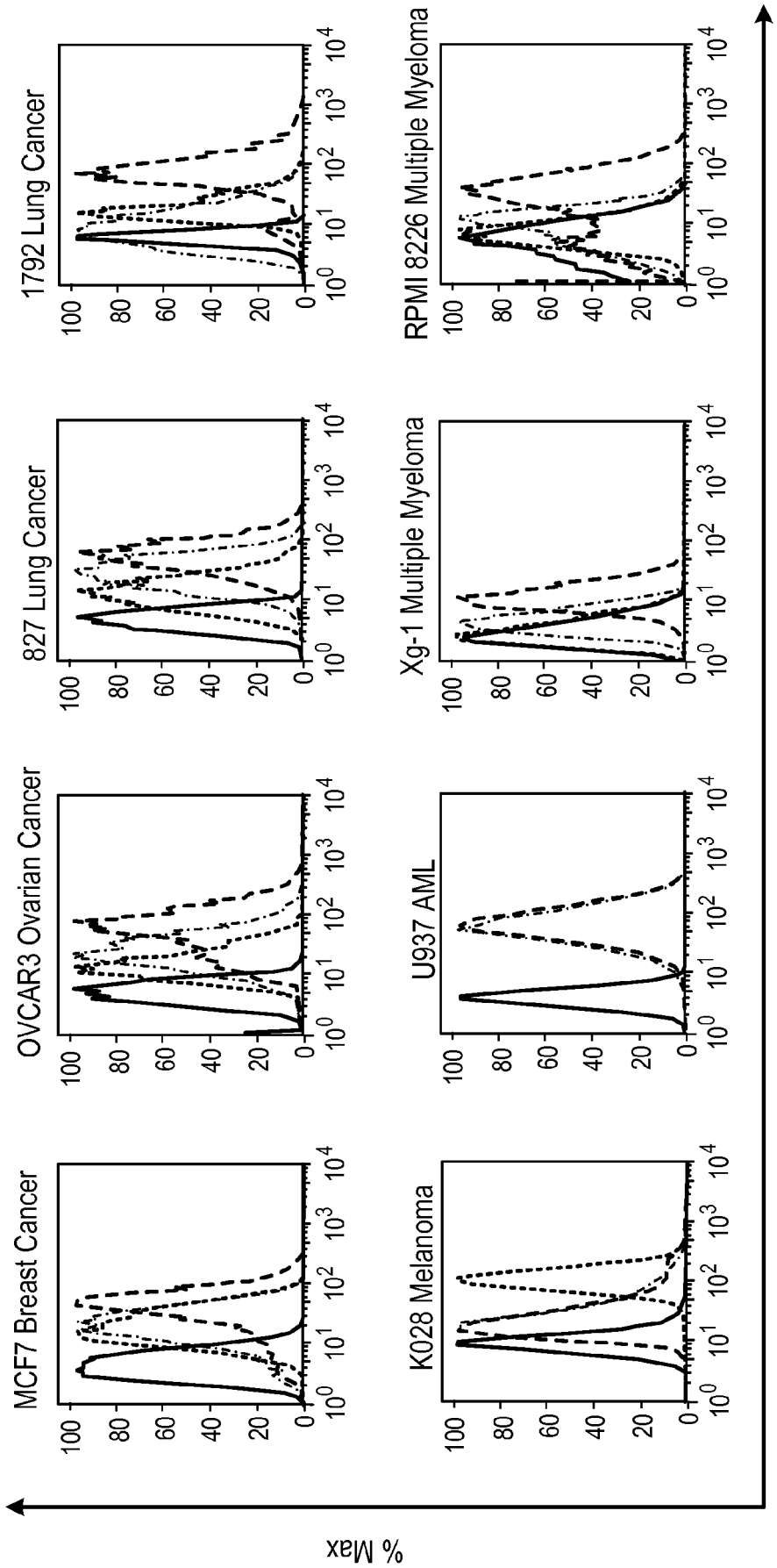

MCF7 Breast Cancer
OVCAR3 Ovarian Cancer
827 Lung Cancer
1792 Lung Cancer
K028 Melanoma
U937 AML
Xg-1 Multiple Myeloma
RPMI 8226 Multiple Myeloma
% Max
MICA-FITC
Unstained Cells
Isotype Negative Control
BioLegend Positive Control
CM24002 Ab2
CM33322 Ab29

FIG. 55

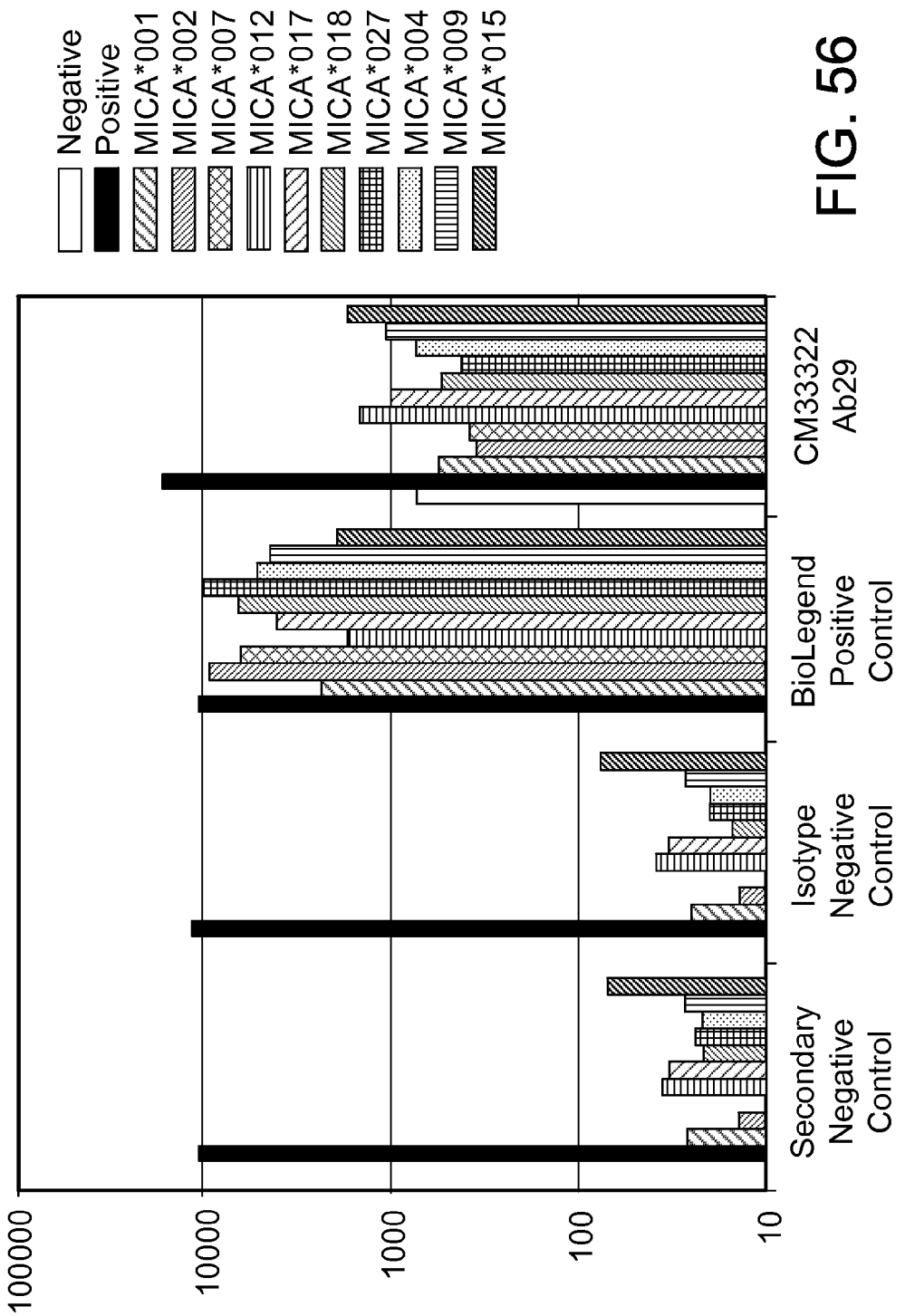

Negative
Positive
MICA*001
MICA*002
MICA*007
MICA*012
MICA*017
MICA*018
MICA*027
MICA*004
MICA*009
MICA*015
100000
10000
1000
100
10
Secondary Negative Control
Isotype Negative Control
BioLegend Positive Control
CM33322 Ab29

FIG. 56

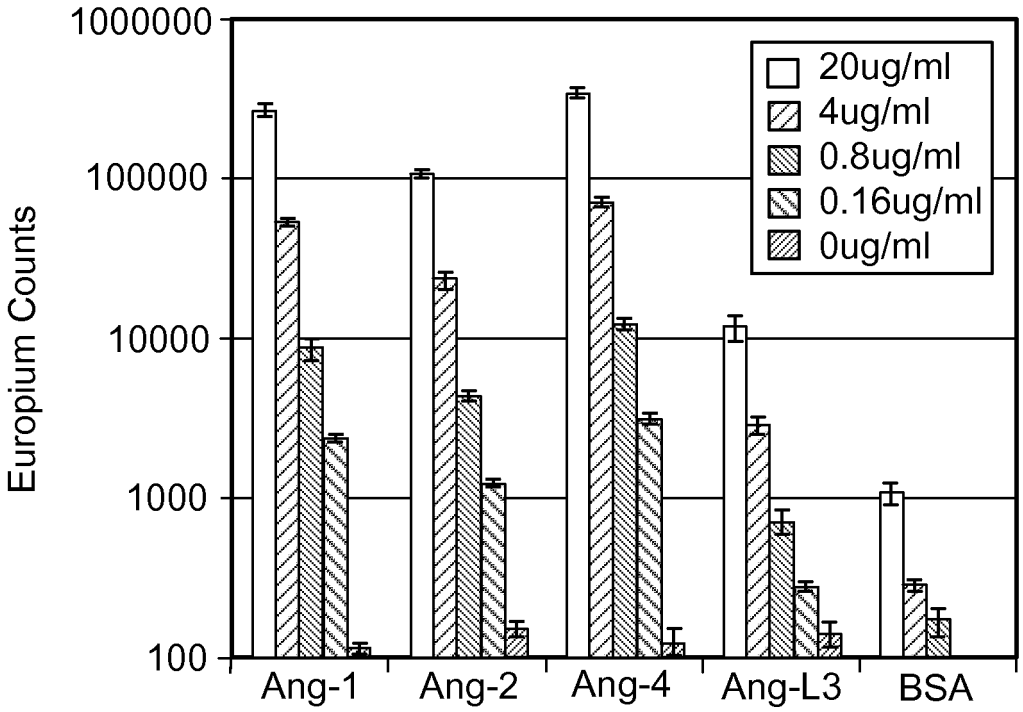

1000000
100000
10000
1000
100
Europium Counts
20ug/ml
4ug/ml
0.8ug/ml
0.16ug/ml
0ug/ml
Ang-1
Ang-2
Ang-4
Ang-L3
BSA

FIG. 57