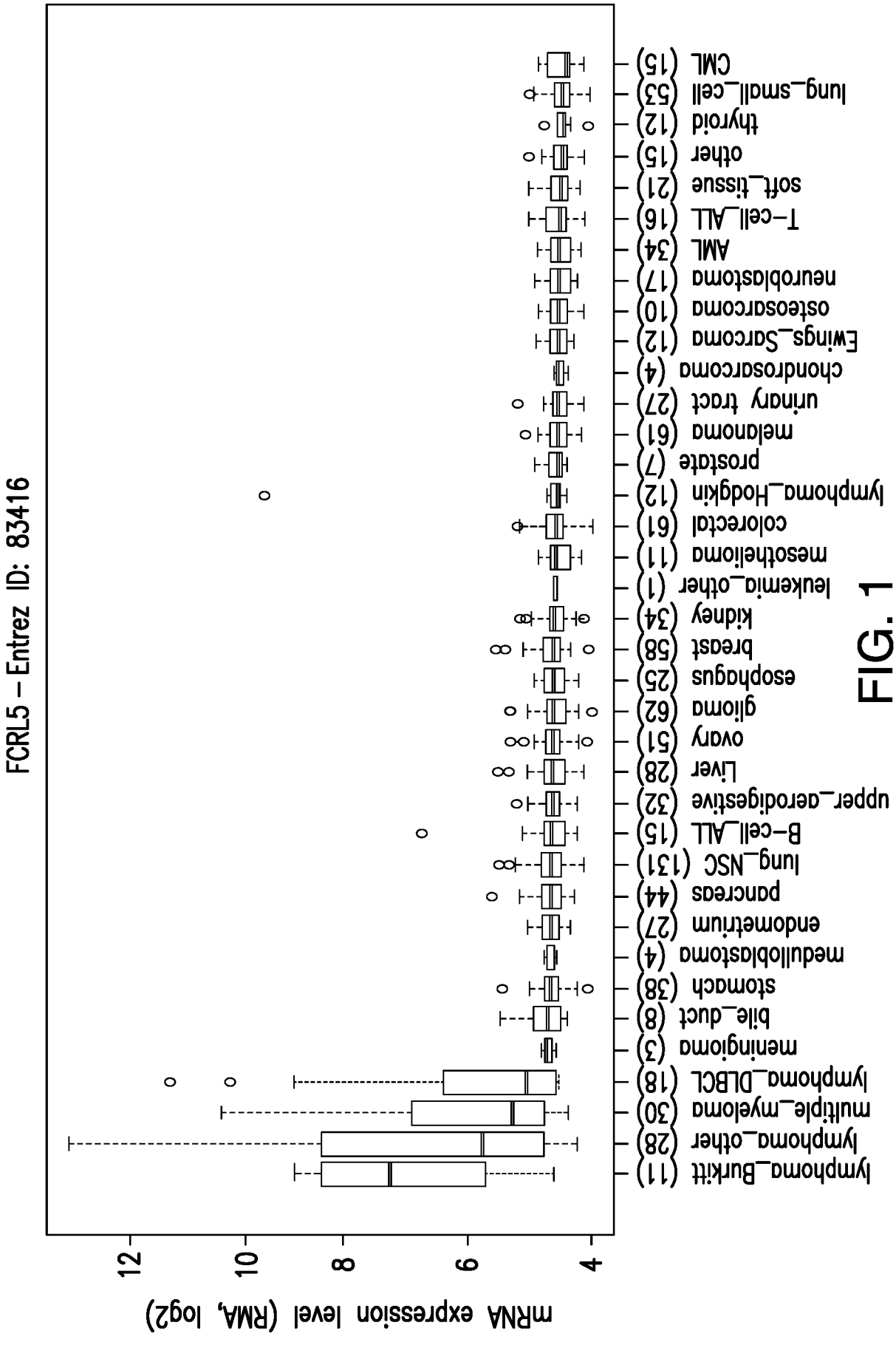

FCRL5 – Entrez ID: 83416
mRNA expression level (RMA, log2)
4
6
8
10
12
lymphoma_Burkitt (11)
lymphoma_other (28)
multiple_myeloma (30)
lymphoma_DLBCL (18)
meningioma (3)
bile_duct (8)
stomach (38)
medulloblastoma (4)
endometrium (27)
pancreas (44)
lung_NSC (131)
B–cell_ALL (15)
upper_aerodigestive (32)
Liver (28)
ovary (51)
glioma (62)
esophagus (25)
breast (58)
kidney (34)
leukemia_other (1)
mesothelioma (11)
colorectal (61)
lymphoma_Hodgkin (12)
prostate (7)
melanoma (61)
urinary tract (27)
chondrosarcoma (4)
Ewings_Sarcoma (12)
osteosarcoma (10)
neuroblastoma (17)
AML (34)
T–cell_ALL (16)
soft_tissue (21)
other (15)
thyroid (12)
lung_small_cell (53)
CML (15)

FIG. 1

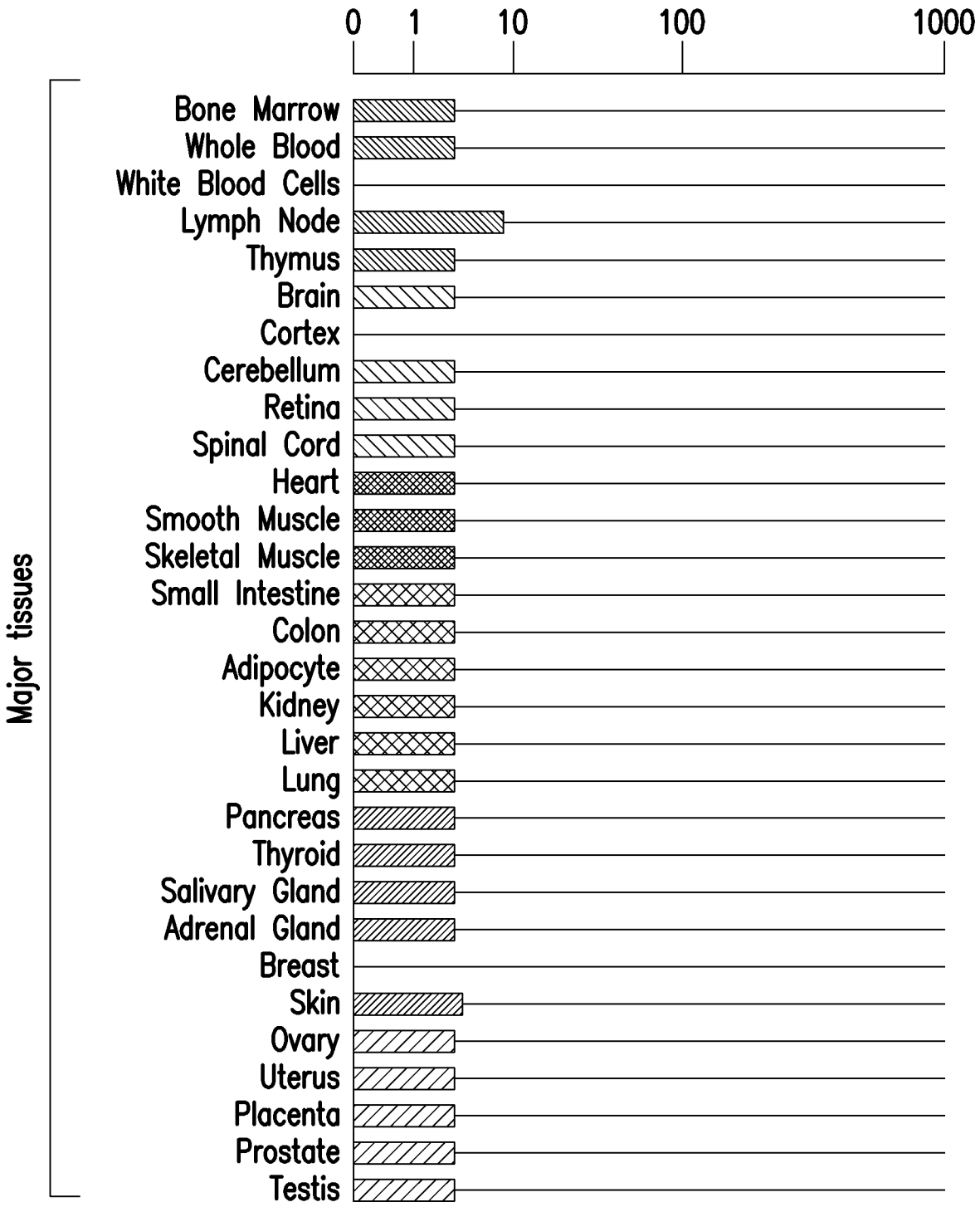


FIG. 1 (continued)

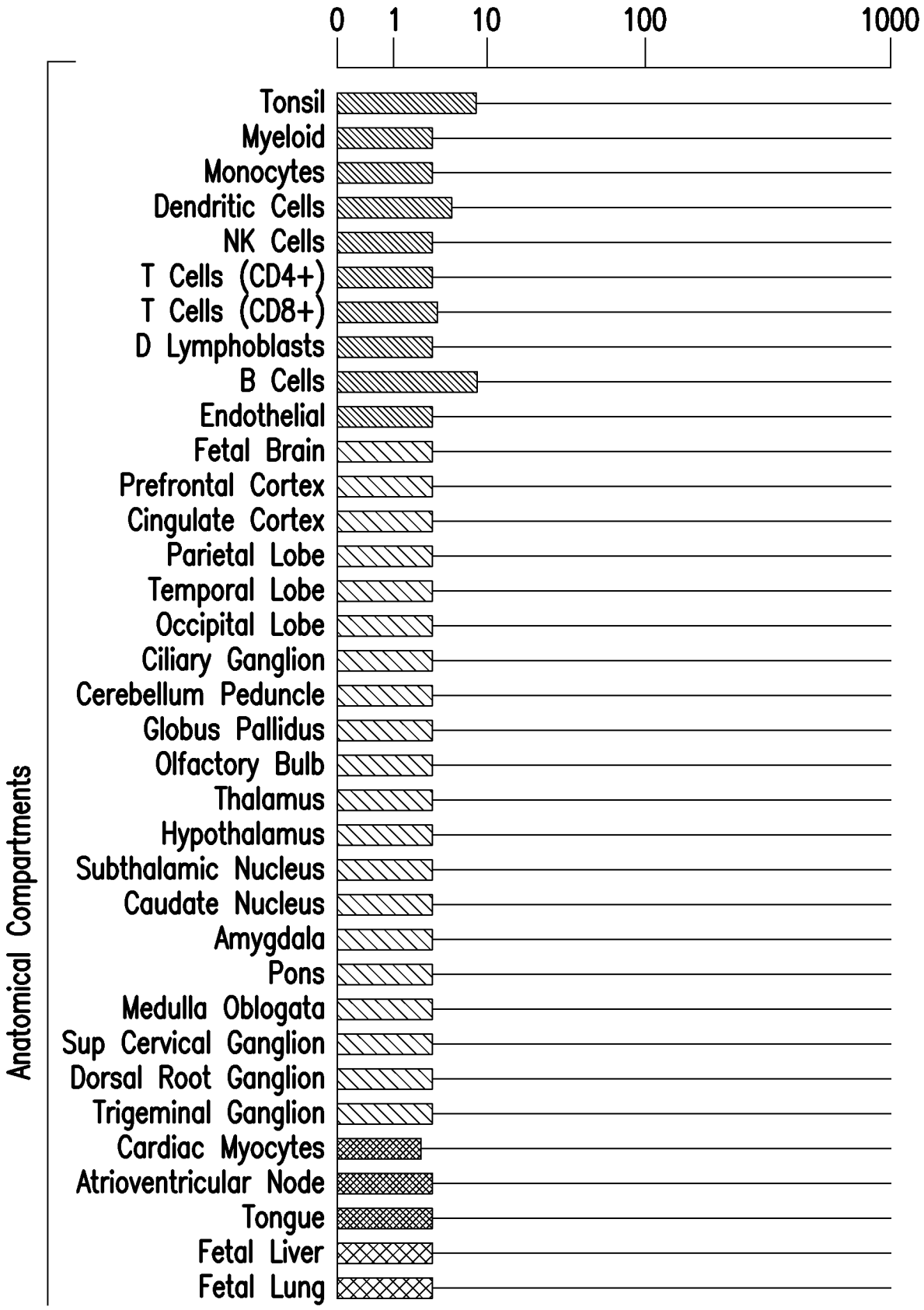


FIG. 1 (continued)

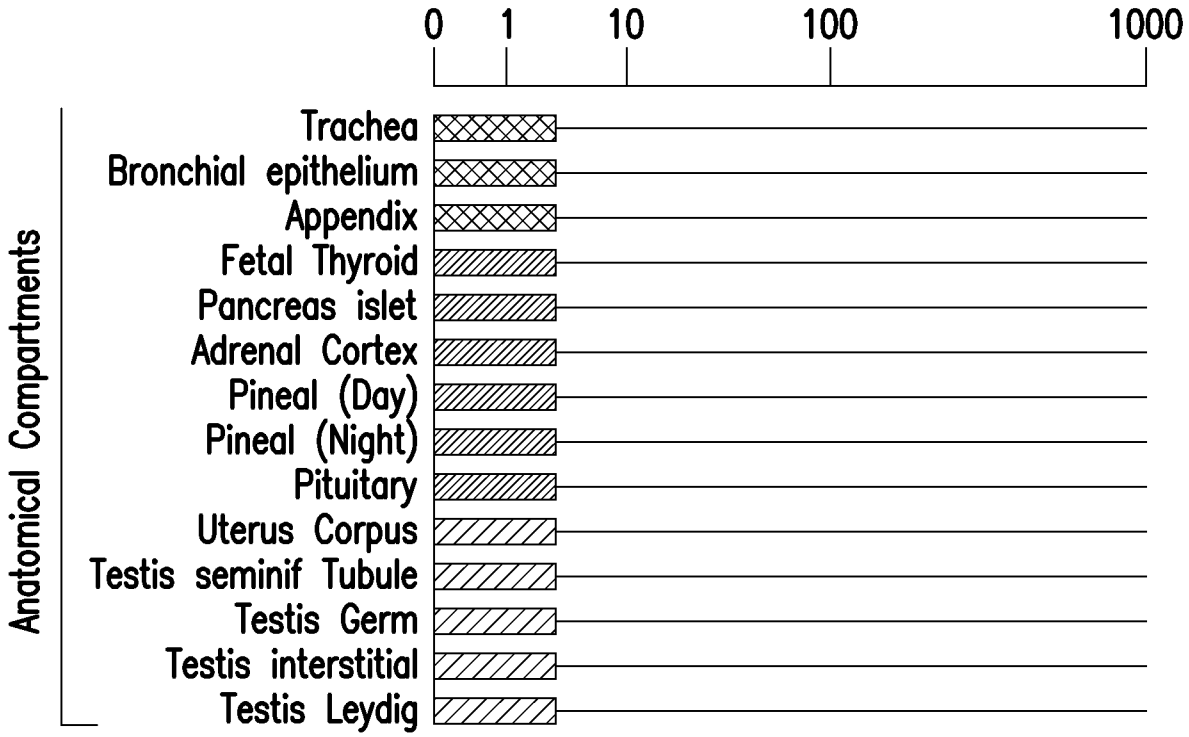
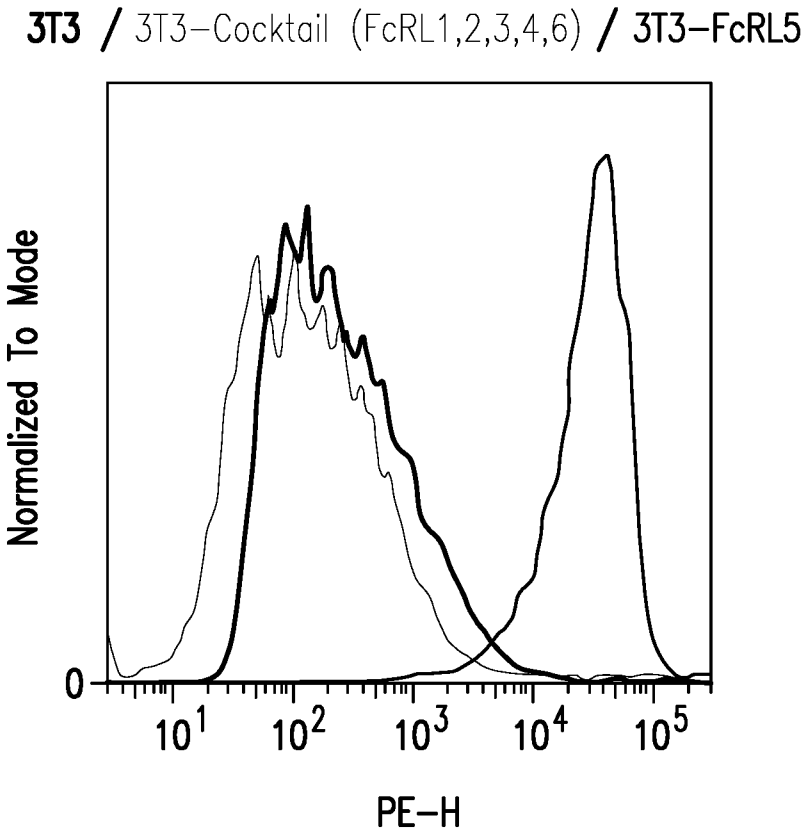
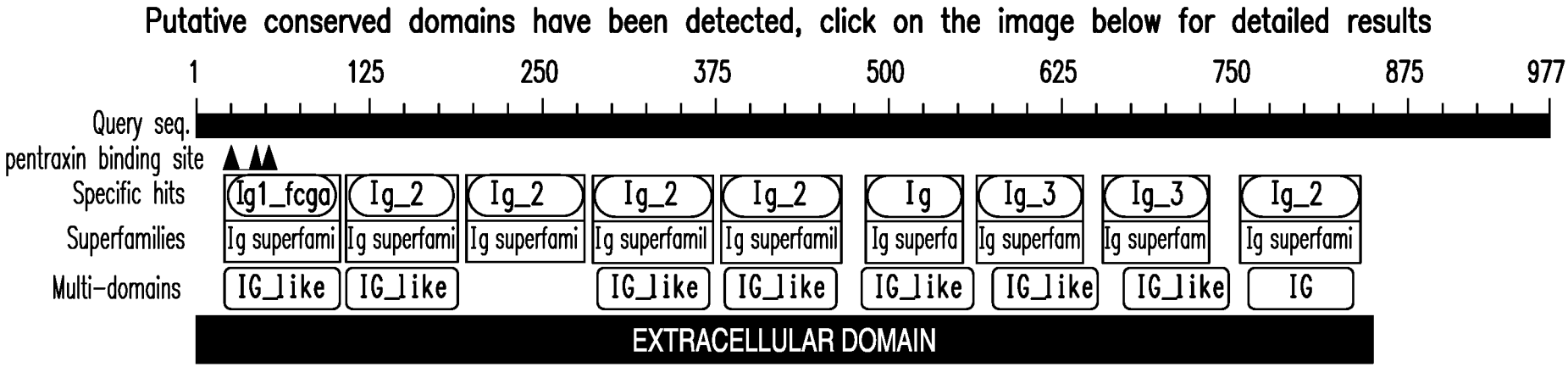


FIG. 1 (continued)



	Sample Name	Median, PE-H
———	Plate1 E12.fcs	124
———	Plate1 E11.fcs	3.15E4
———	Plate1 E10.fcs	216

FIG. 2



Epitope locations of anti-CD307(IRTA2/FcRH5/FCRL5) MAbs (Satoshi Nagata 070201)

IRTA2-structure

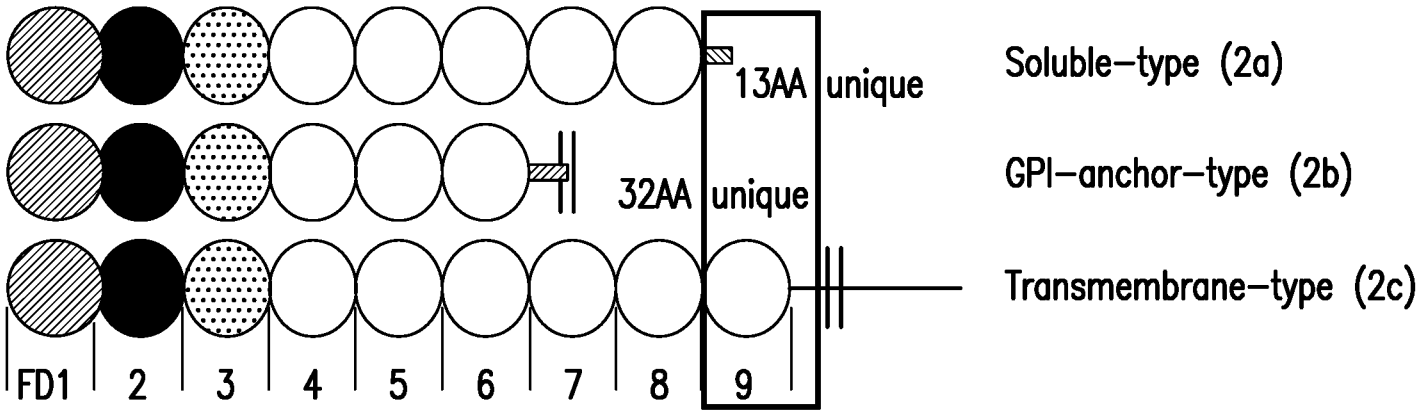


FIG. 3A

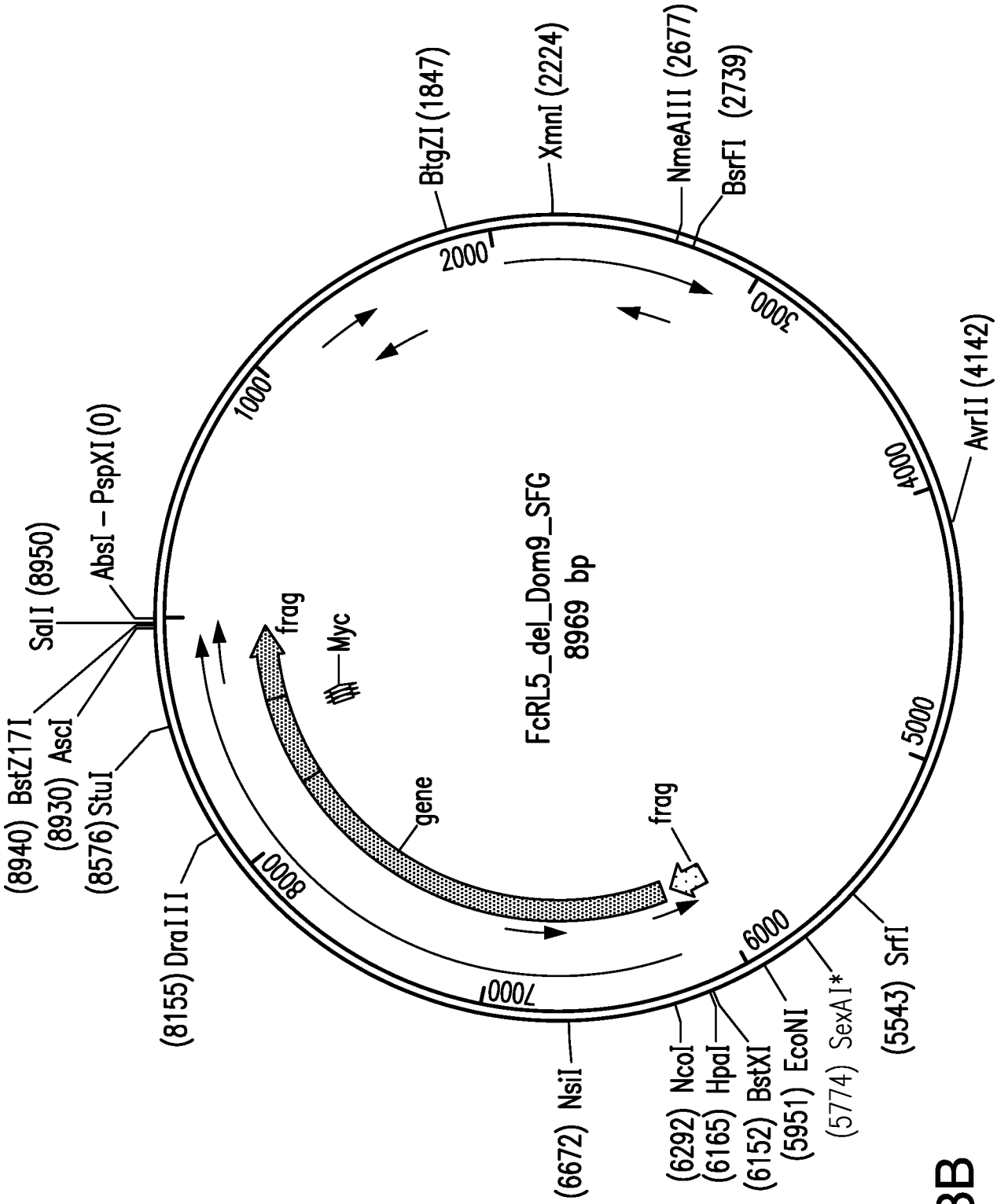

FcRL5_del_Dom9_SFG
8969 bp
1000
2000
3000
4000
5000
6000
7000
8000
BtgZI (1847)
XmnI (2224)
NmeAIII (2677)
BsrFI (2739)
AvrII (4142)
SrfI (5543)
SexAI* (5774)
EcoNI (5951)
BstXI (6152)
HpaI (6165)
NcoI (6292)
NsiI (6672)
DraIII (8155)
StuI (8576)
AscI (8930)
BstZ17I (8940)
SalI (8950)
AbsI – PspXI (0)
frag
Myc
gene
frag

FIG. 3B

Domain 1-8
Domain 9
TM
Myc3

>MSK_delDOM9_myc_mCD8

MLLWVILLVLAPVSGQFARTPR**PIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYLGKEILRET**
PDNILEVQESGEYRCQAQGSPLSSPVHLDFSSAS**LILQAPLSVFEGDSVVLRCRAKAEVTLNNTIYKNDN**
VLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSNTVKIQVQEPFT**RPVLRASSFQPISGNPVTLT**
CETQLSLERSDVPLRFRFFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQV
QIPASH**PVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENS**
GNYYCTADNGLGAKPSKAVSLSVTVPVSH**PVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA**
LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHP**VLTLSSAEALTFEGATV**
TLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYYCTADNGFGPQRSEVVSLFVT
VPVS**RPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGEASFNLSLTAEHSG**
NYSCEANNGLVAQHSDTISLSVIVPVS**RPILTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTL**
GKISAPSGGGASFNLSLTTEHSGIYSC**EADN**GLEAQRSEMVTLKVAAAA[EQKLISEEDLEQKLISEEDLE
QKLISEEDL]TGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPSDSDSQEPTYHNVPAWEELQP
VYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVASTPVSGSLFL
ASSAPHR*

>gi|14278719|gb|AAK50059.2|AF369794_1 B cell crosslinked IgM-activating sequence protein [Homo sapiens]

MLLWVILLVLAPVSGQFARTPR**PIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYLGKEILRET**
PDNILEVQESGEYRCQAQGSPLSSPVHLDFSSAS**LILQAPLSVFEGDSVVLRCRAKAEVTLNNTIYKNDN**
VLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSNTVKIQVQEPFT**RPVLRASSFQPISGNPVTLT**
CETQLSLERSDVPLRFRFFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQV
QIPASH**PVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENS**
GNYYCTADNGLGAKPSKAVSLSVTVPVSH**PVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA**
LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHP**VLTLSSAEALTFEGATV**
TLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYYCTADNGFGPQRSEVVSLFVT
VPVS**RPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGEASFNLSLTAEHSG**
NYSCEANNGLVAQHSDTISLSVIVPVS**RPILTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTL**
GKISAPSGGGASFNLSLTTEHSGIYSCEADNGPEAQRSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLLE
LHCEALRGSPLILYRFFHEDVTLGNRSSPSGGASLNLSLTAEHSGNYSCEADNGLGAQRSETVTLYITGL
TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPPDSDSQEPTYHNVPAWEELQP
VYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVASTPVSGSLFLASSAPHR

FIG. 3C

MSK_delDOM9_myc3_mCD8	MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHR
gi|14278719|gb|AAK50059.2|AF3697	MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHR

MSK_delDOM9_myc3_mCD8	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVV
gi|14278719|gb|AAK50059.2|AF3697	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVV

MSK_delDOM9_myc3_mCD8	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSMT
gi|14278719|gb|AAK50059.2|AF3697	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDFHIPHACLKDNGAYRCTGYKESCCPVSSMT

MSK_delDOM9_myc3_mCD8	VKIQVQEPFTRPVLRASSFQPISGNPVTLTCETQLSLERSDVPLRFRFFRDDQTLGLGWS
gi|14278719|gb|AAK50059.2|AF3697	VKIQVQEPFTRPVLRASSFQPISGNPVTLTCETQLSLERSDVPLRFRFFRDDQTLGLGWS

MSK_delDOM9_myc3_mCD8	LSPNFQITAMWSKDSGFYWCKAATMPHSIISDSPRSWIQVQIPASHPVLTLSPEKALNFE
gi|14278719|gb|AAK50059.2|AF3697	LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE

MSK_delDOM9_myc3_mCD8	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYYCTADNG
gi|14278719|gb|AAK50059.2|AF3697	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYYCTADNG

MSK_delDOM9_myc3_mCD8	LGAKPSKAVSLSVTVPVSHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA
gi|14278719|gb|AAK50059.2|AF3697	LGAKPSKAVSLSVTVPVSHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA

MSK_delDOM9_myc3_mCD8	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSSA
gi|14278719|gb|AAK50059.2|AF3697	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSSA

FIG. 3D

MSK_delDOM9_myc3_mCD8	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYY
gi|14278719|gb|AAK50059.2|AF3697	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSGNYY

MSK_delDOM9_myc3_mCD8	CTADNGFGPQRSEVVSLFVTVPVSRPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWF
gi|14278719|gb|AAK50059.2|AF3697	CTADNGFGPQRSEVVSLFVTVPVSRPILTLRVPRAQAVVGDLLELHCEAPRGSPPILYWF

MSK_delDOM9_myc3_mCD8	YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVAQHSDTISLSVIVPVSRPI
gi|14278719|gb|AAK50059.2|AF3697	YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVAQHSDTISLSVIVPVSRPI

MSK_delDOM9_myc3_mCD8	LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTTE
gi|14278719|gb|AAK50059.2|AF3697	LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTTE

MSK_delDOM9_myc3_mCD8	HSGIYSCEADNGlEAQRSEMVTLKVAaaaaQkLIS----------
gi|14278719|gb|AAK50059.2|AF3697	HSGIYSCEADNGpEAQRSEMVTLKVAvpvsRpVLTlrapgthaavgdllelhcealrgsp

MSK_delDOM9_myc3_mCD8	----------eedLeqkLiSEedleqkliSEedL----------
gi|14278719|gb|AAK50059.2|AF3697	lilyrffhedvtlgnrsspsggasLnlsLtAEhsgnysceADngLgaqrsetvtlyitgl

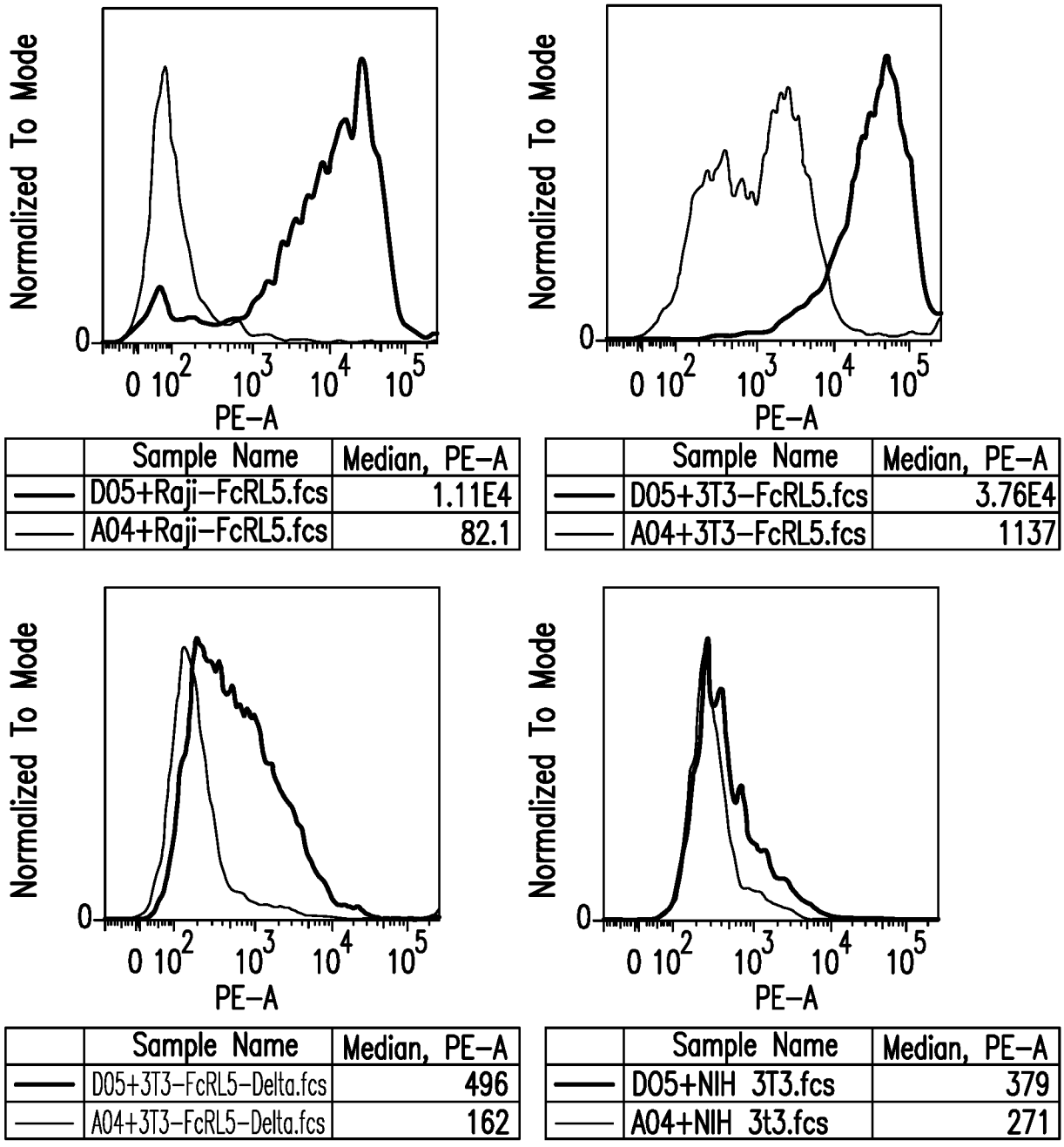
MSK_delDOM9_myc3_mCD8	---------TGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPsDSDSQEPTYH
gi|14278719|gb|AAK50059.2|AF3697	tanrsgpfaTGVAGGLLSIAGLAAGALLLYCWLSRKAGRKPASDPARSPpDSDSQEPTYH

MSK_delDOM9_myc3_mCD8	NVPAWEELQPVYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA
gi|14278719|gb|AAK50059.2|AF3697	NVPAWEELQPVYTNANPRGENVVYSEVRIIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA

MSK_delDOM9_myc3_mCD8	STPVSGSLFLASSAPHR
gi|14278719|gb|AAK50059.2|AF3697	STPVSGSLFLASSAPHR

FIG. 3D (continued)

ET200-39



	Sample Name	Median, PE-A
——	D05+Raji-FcRL5.fcs	1.11E4
——	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
——	D05+3T3-FcRL5.fcs	3.76E4
——	A04+3T3-FcRL5.fcs	1137

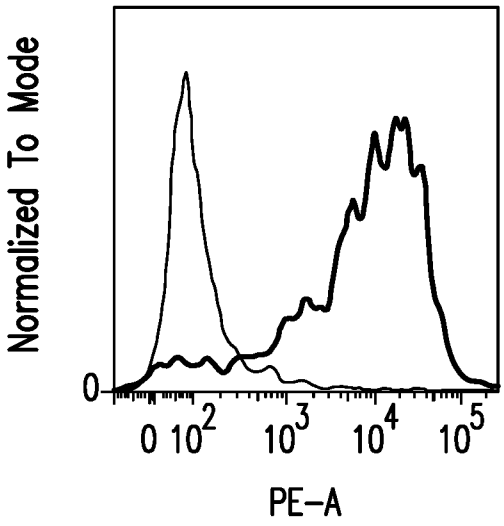
	Sample Name	Median, PE-A
——	D05+3T3-FcRL5-Delta.fcs	496
——	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
——	D05+NIH 3T3.fcs	379
——	A04+NIH 3t3.fcs	271

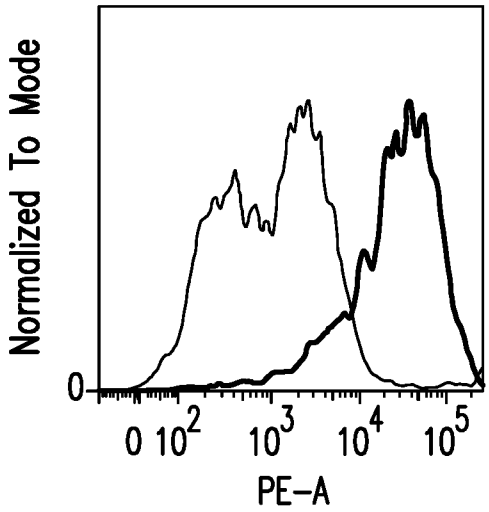
—— Negative control phage
—— ET200 phage

FIG.4

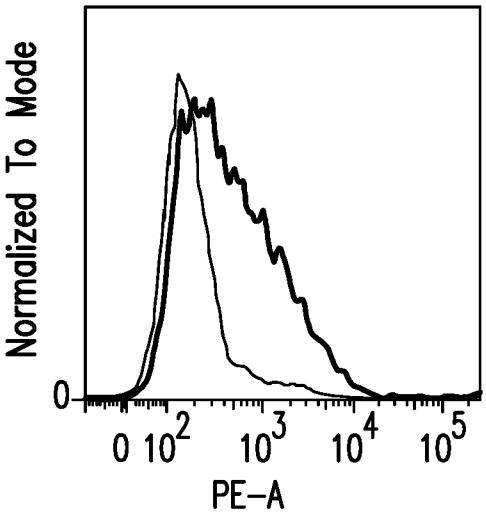
ET200-104



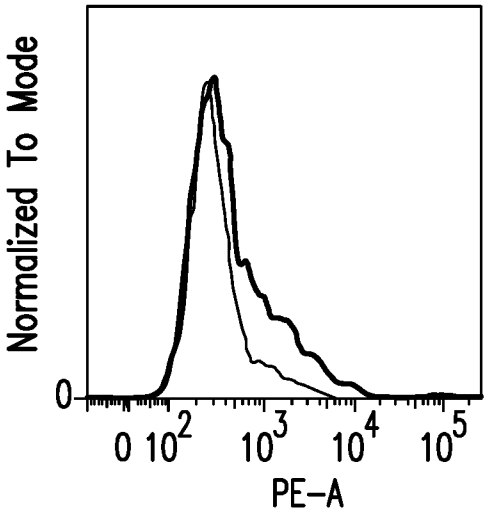
	Sample Name	Median, PE-A
——	E11+Raji-FcRL5.fcs	9165
——	A04+Raji-FcRL5.fcs	82.1



	Sample Name	Median, PE-A
——	E11+3T3-FcRL5.fcs	2.91E4
——	A04+Raji-FcRL5.fcs	1137



	Sample Name	Median, PE-A
——	E11+3T3-FcRL5-Delta.fcs	387
——	A04+3T3-FcRL5-Delta.fcs	162

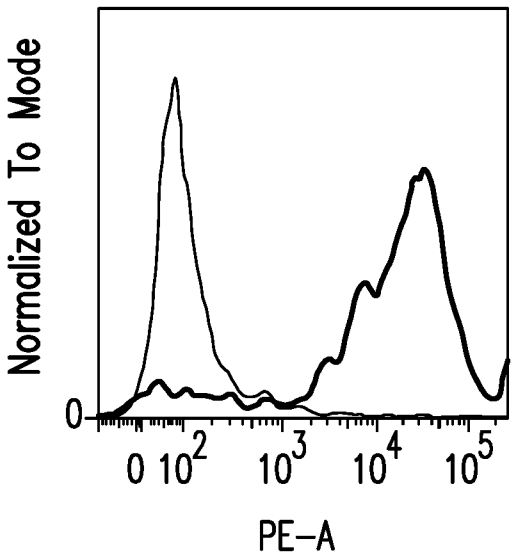


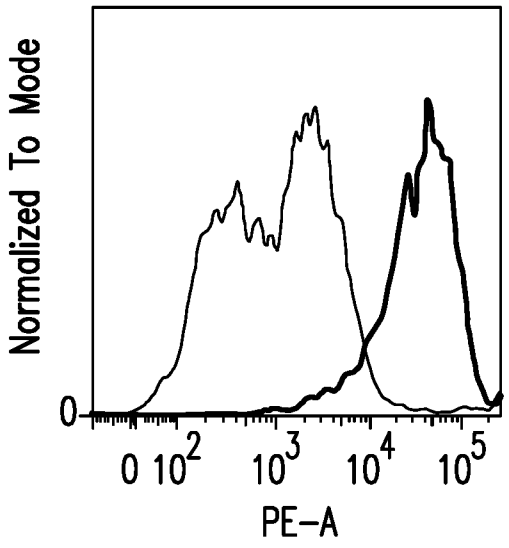
	Sample Name	Median, PE-A
——	E11+NIH 3T3.fcs	360
——	A04+NIH 3T3.fcs	271

—— Negative control phage
—— ET200 phage

FIG. 5

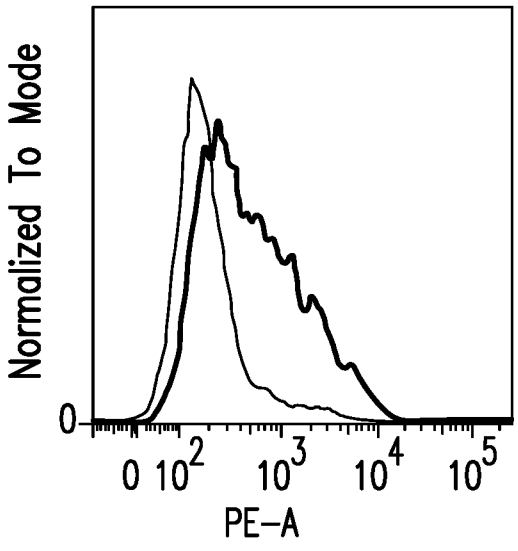
ET200-105

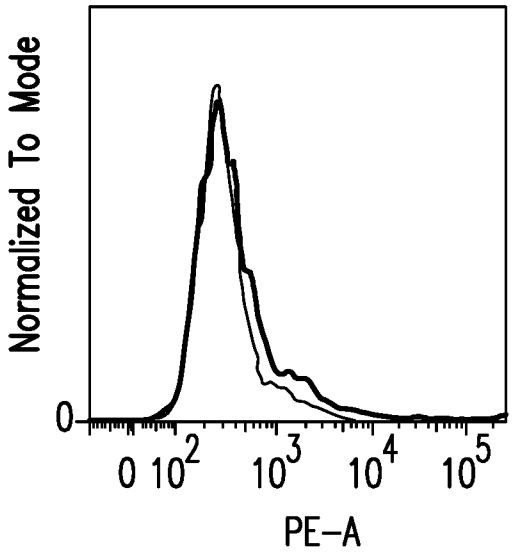




	Sample Name	Median, PE-A
——	E12+Raji-FcRL5.fcs	1.80E4
——	A04+Raji-FcRL5.fcs	82.1

	Sample Name	Median, PE-A
——	E12+3T3-FcRL5.fcs	3.52E4
——	A04+3T3-FcRL5.fcs	1137



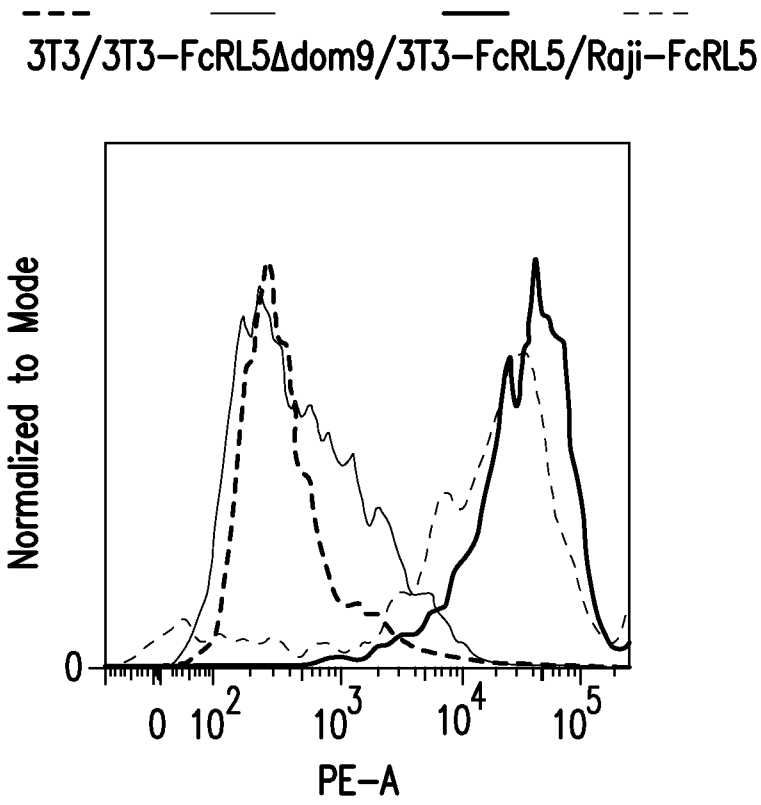


	Sample Name	Median, PE-A
——	E12+3T3-FcRL5-Delta.fcs	415
——	A04+3T3-FcRL5-Delta.fcs	162

	Sample Name	Median, PE-A
——	E12+NIH 3T3.fcs	309
——	A04+NIH 3T3.fcs	271

—— Negative control phage —— ET200 phage

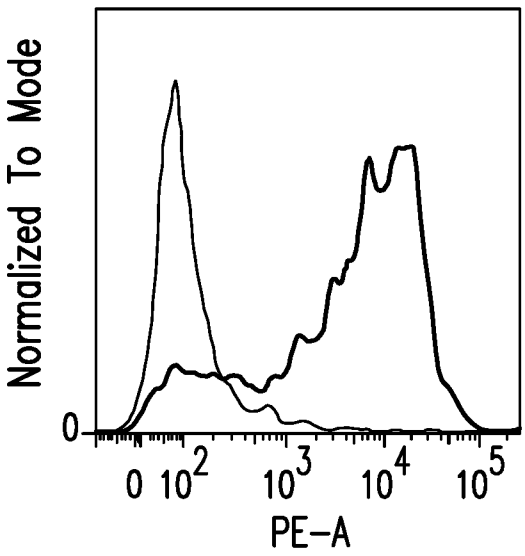
FIG. 6



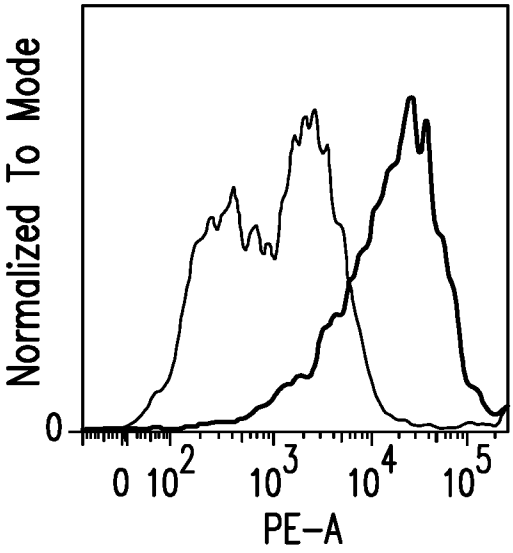
	Sample Name	Median, PE-A
- - -	E12+Raji-FcRL5.fcs	1.80E4
- - -	E12+NIH 3T3.fcs	309
——	E12+3T3-FcRL5-Delta.fcs	415
——	E12+3T3-FcRL5.fcs	3.52E4

FIG. 6 (continued)

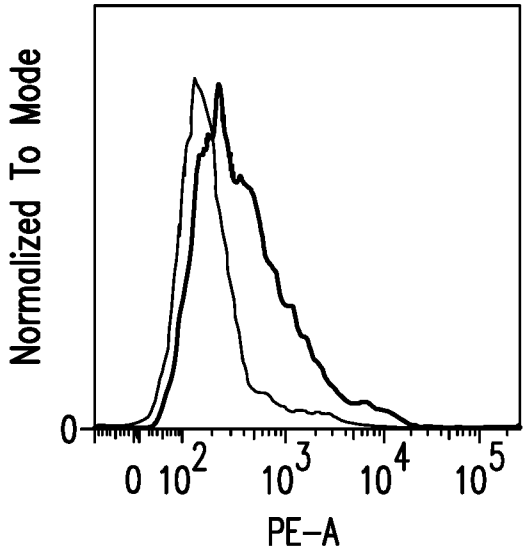
ET200-109



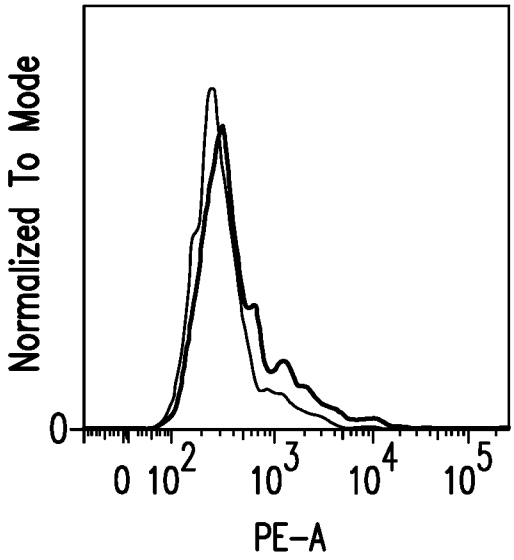
	Sample Name	Median, PE-A
——	F04+Raji-FcRL5.fcs	6161
——	A04+Raji-FcRL5.fcs	82.1



	Sample Name	Median, PE-A
——	F04+3T3-FcRL5.fcs	1.75E4
——	A04+3T3-FcRL5.fcs	1137



	Sample Name	Median, PE-A
——	F04+3T3-FcRL5-Delta.fcs	328
——	A04+3T3-FcRL5-Delta.fcs	162

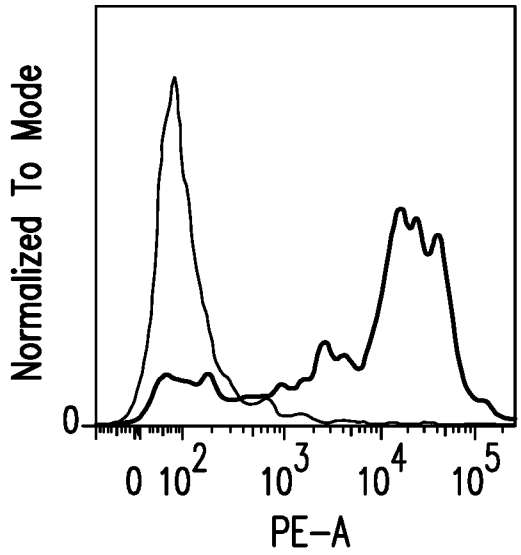


	Sample Name	Median, PE-A
——	F04+NIH 3T3.fcs	343
——	A04+NIH 3T3.fcs	271

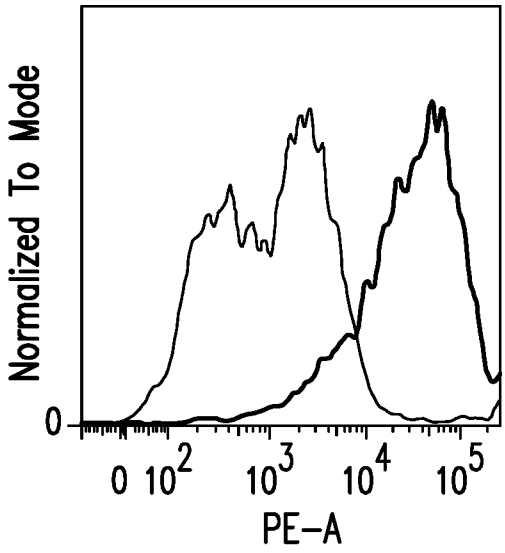
—— Negative control phage —— ET200 phage

FIG. 7

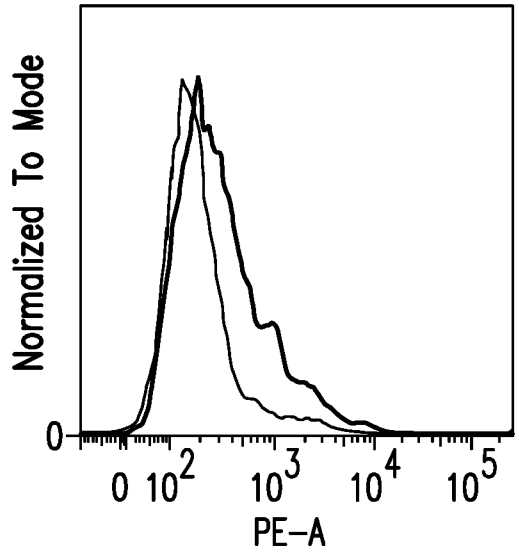
ET200-117



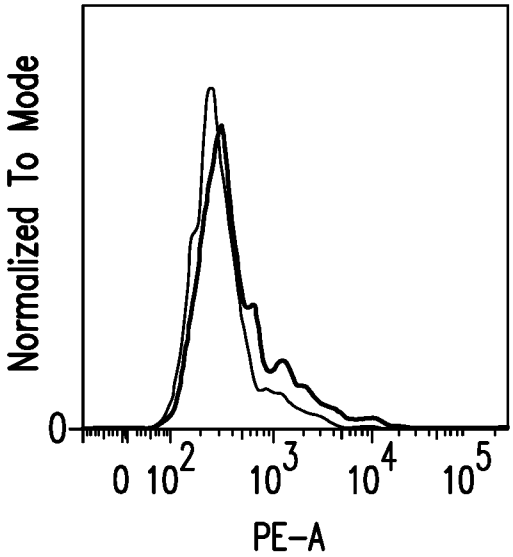
	Sample Name	Median, PE-A
——	F12+Raji-FcRL5.fcs	1.27E4
——	A04+Raji-FcRL5.fcs	82.1



	Sample Name	Median, PE-A
——	F12+3T3-FcRL5.fcs	3.23E4
——	A04+3T3-FcRL5.fcs	1137



	Sample Name	Median, PE-A
——	F12+3T3-FcRL5-Delta.fcs	260
——	A04+3T3-FcRL5-Delta.fcs	162



	Sample Name	Median, PE-A
——	F12+NIH 3T3.fcs	317
——	A04+NIH 3T3.fcs	271

—— Negative control phage —— ET200 phage

FIG. 8

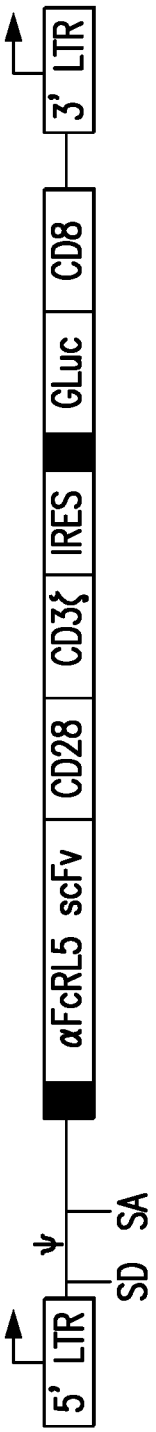

5' LTR
SD
SA
ψ
αFcRL5 scFv
CD28
CD3ζ
IRES
GLuc
CD8
3' LTR

FIG. 9A

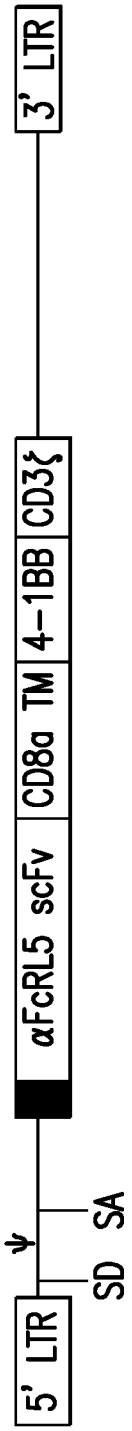

5' LTR
SD
SA
ψ
αFcRL5 scFv
CD8α TM
4-1BB
CD3ζ
3' LTR

FIG. 9B

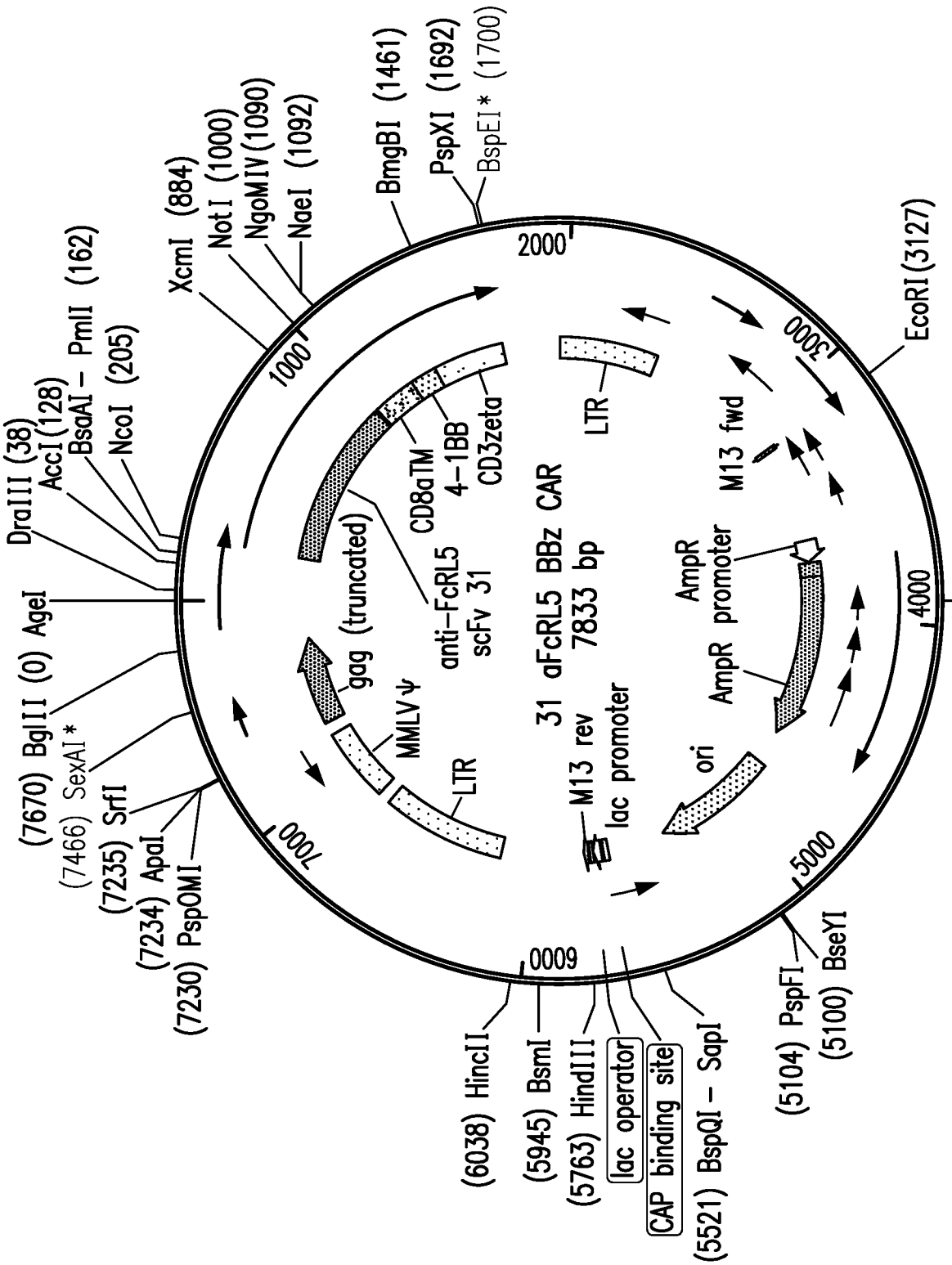

DraIII (38)
AccI (128)
BsaAI – PmlI (162)
NcoI (205)
XcmI (884)
NotI (1000)
NgoMIV (1090)
NaeI (1092)
BmgBI (1461)
PspXI (1692)
BspEI* (1700)
EcoRI (3127)
XmnI (3916)
(7670) BglII (0) AgeI
(7466) SexAI*
(7235) SrfI
(7234) ApaI
(7230) PspOMI
(6038) HincII
(5945) BsmI
(5763) HindIII
lac operator
CAP binding site
(5521) BspQI – SapI
(5104) PspFI
(5100) BseYI
LTR
MMLV ψ
gag (truncated)
anti–FcRL5 scFv 31
CD8aTM
4–1BB
CD3zeta
LTR
31 aFcRL5 BBz CAR
7833 bp
M13 rev
lac promoter
ori
AmpR
AmpR promoter
M13 fwd
1000
2000
3000
4000
5000
6000
7000

FIG. 10

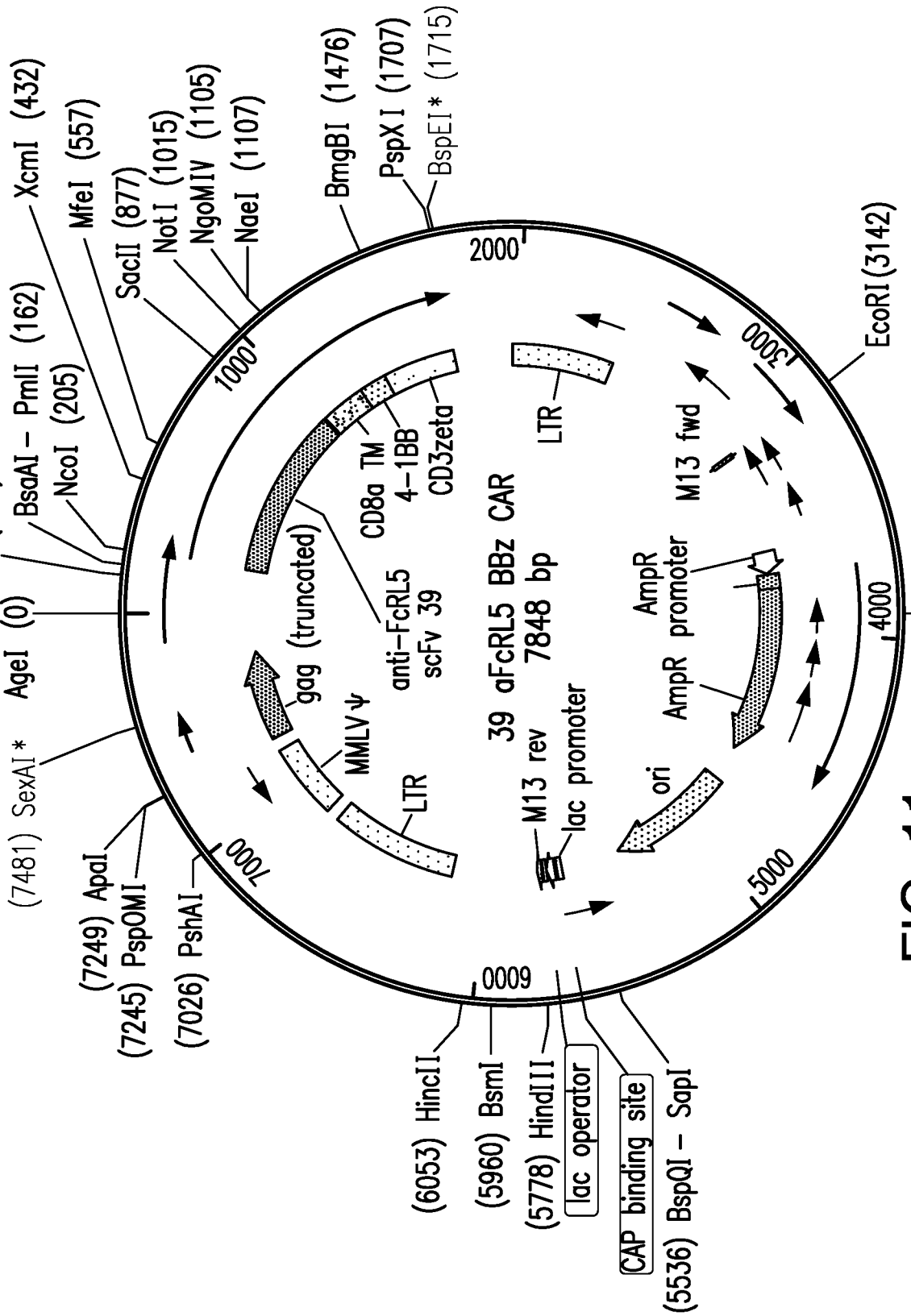

AccI (128)
BsaAI – PmlI (162)
NcoI (205)
MfeI (557)
SacII (877)
NotI (1015)
NgoMIV (1105)
NaeI (1107)
BmgBI (1476)
PspXI (1707)
BspEI* (1715)
EcoRI (3142)
XmnI (3931)
AgeI (0)
SexAI* (7481)
ApaI (7249)
PspOMI (7245)
PshAI (7026)
HincII (6053)
BsmI (5960)
HindIII (5778)
lac operator
CAP binding site
SapI (5536) BspQI –
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
MMLV ψ
LTR
anti-FcRL5 scFv 39
CD8a TM
4-1BB
CD3zeta
LTR
M13 fwd
AmpR promoter
AmpR
ori
M13 rev
lac promoter
39 aFcRL5 BBz CAR
7848 bp

FIG. 11

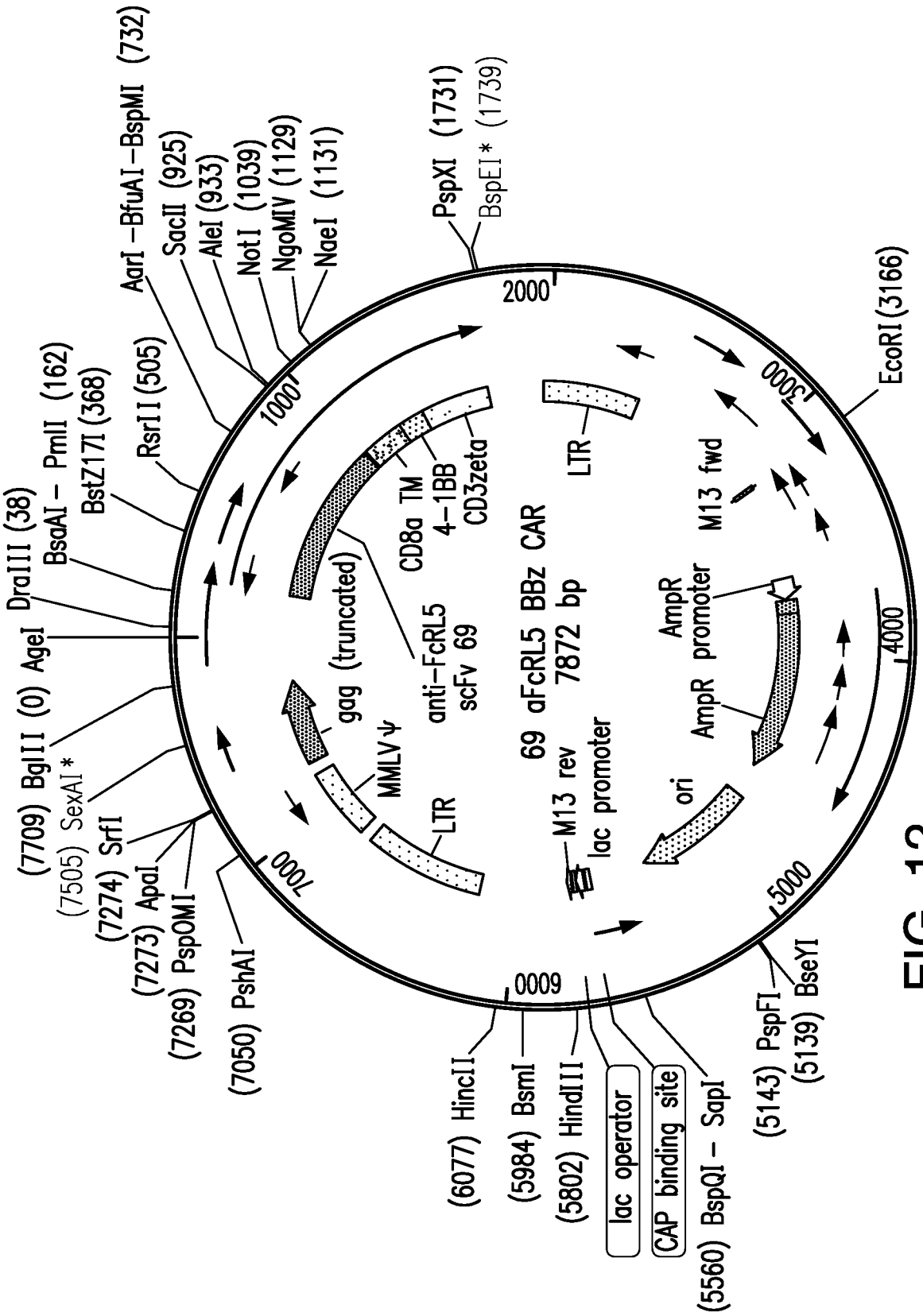

(7709) BglII (0) AgeI
DraIII (38)
BsaAI – PmlI (162)
BstZ17I (368)
RsrII (505)
AarI –BfuAI–BspMI (732)
SacII (925)
AleI (933)
NotI (1039)
NgoMIV (1129)
NaeI (1131)
PspXI (1731)
BspEI* (1739)
EcoRI (3166)
(7505) SexAI*
SrfI (7274)
ApaI (7273)
PspOMI (7269)
PshAI (7050)
HincII (6077)
BsmI (5984)
HindIII (5802)
lac operator
CAP binding site
BspQI – SapI (5560)
PspFI (5143)
BseYI (5139)
1000
2000
3000
4000
5000
6000
7000
LTR
MMLV ψ
gag (truncated)
anti–FcRL5 scFv 69
CD8a TM
4–1BB
CD3zeta
69 aFcRL5 BBz CAR
7872 bp
M13 rev
lac promoter
ori
AmpR
AmpR promoter
LTR
M13 fwd

FIG. 12

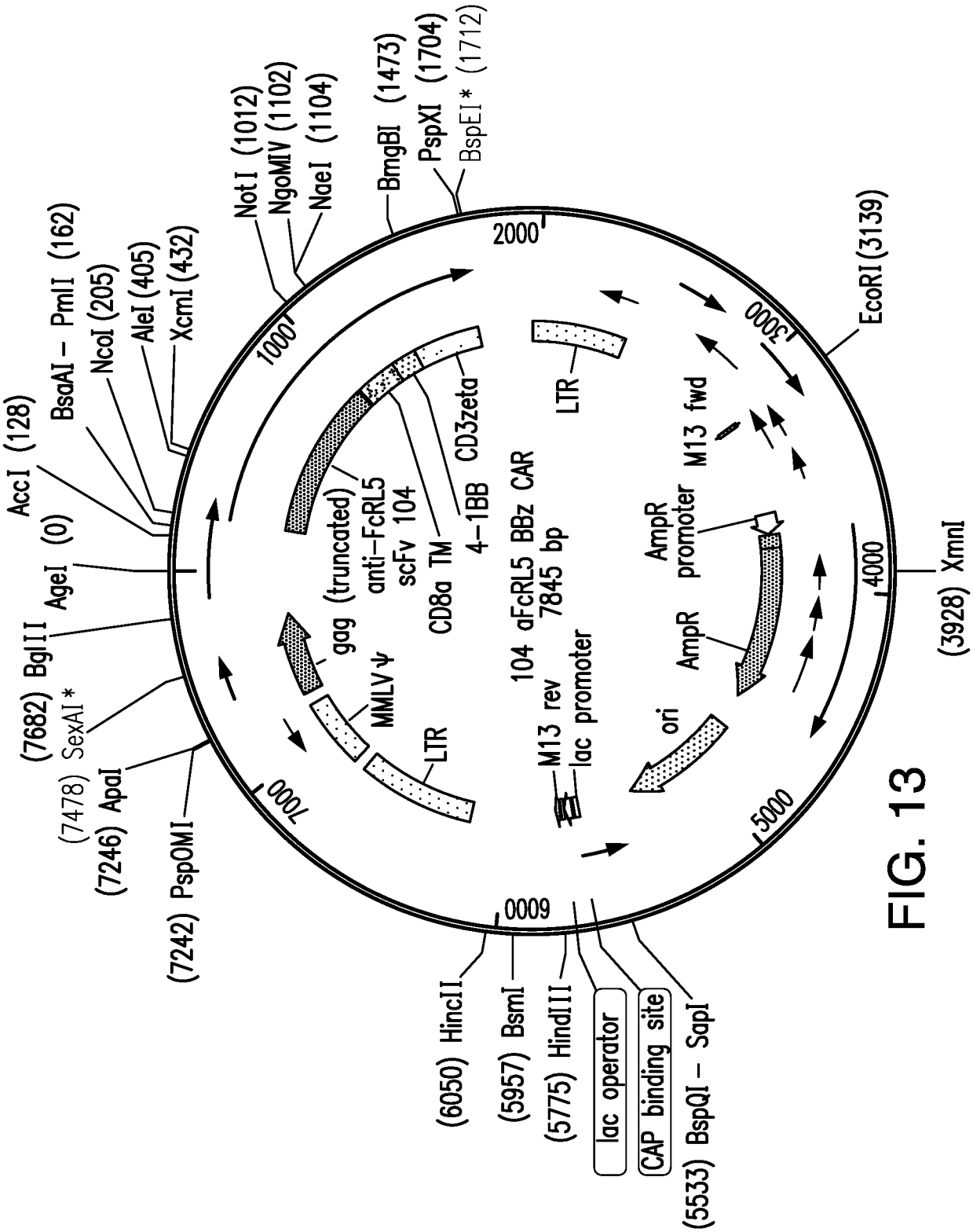

AccI (128)
BsaAI – PmlI (162)
NcoI (205)
AleI (405)
XcmI (432)
NotI (1012)
NgoMIV (1102)
NaeI (1104)
BmgBI (1473)
PspXI (1704)
BspEI* (1712)
EcoRI (3139)
XmnI (3928)
(7682) BglII
AgeI (0)
(7478) SexAI*
(7246) ApaI
(7242) PspOMI
(6050) HincII
(5957) BsmI
(5775) HindIII
lac operator
CAP binding site
(5533) BspQI – SapI
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
anti-FcRL5 scFv 104
CD8a TM
4-1BB
CD3zeta
LTR
MMLV ψ
LTR
104 aFcRL5 BBz CAR
7845 bp
M13 rev
lac promoter
ori
AmpR
AmpR promoter
M13 fwd

FIG. 13

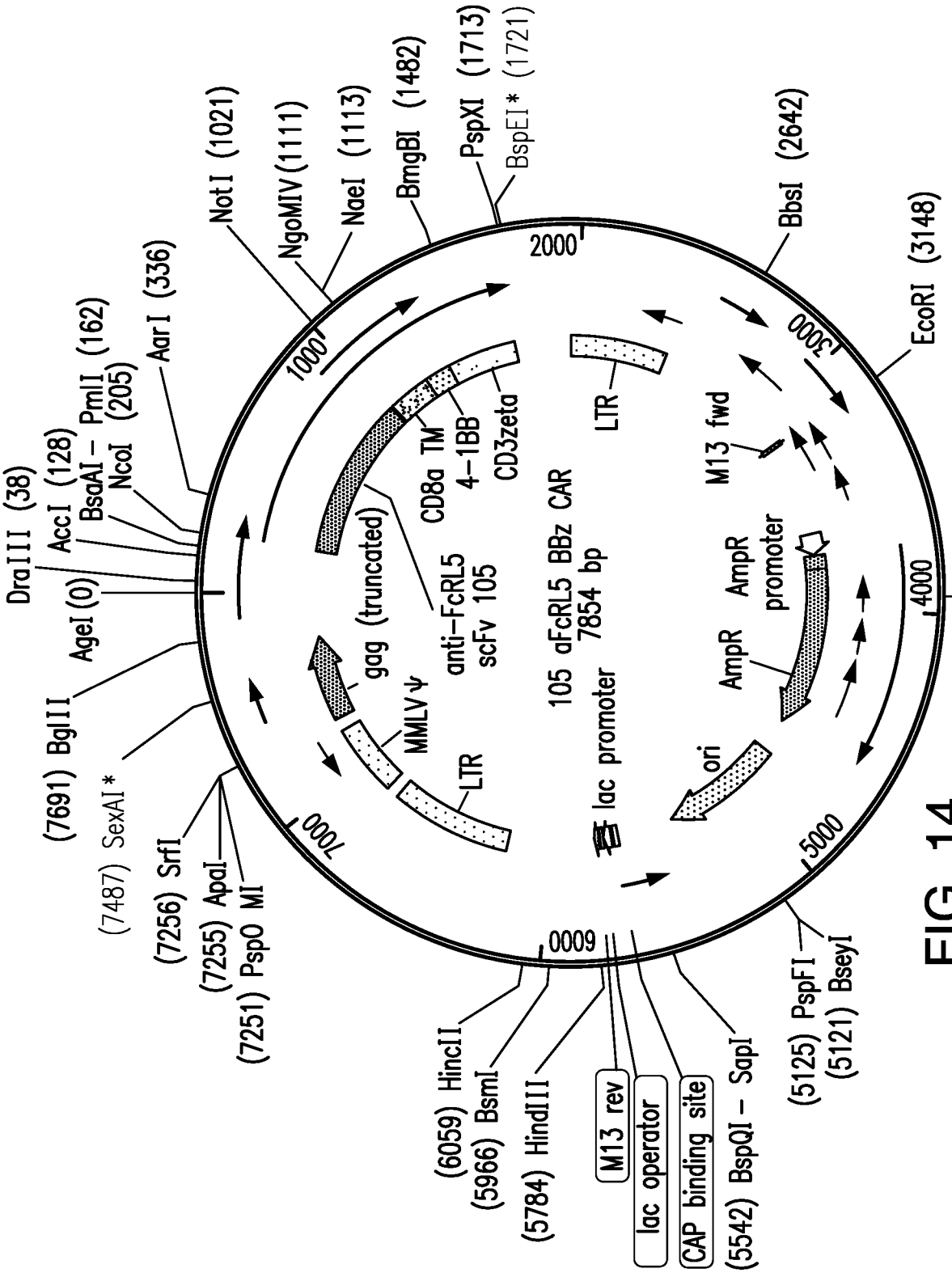

DraIII (38)
AccI (128)
BsaAI – PmlI (162)
NcoI (205)
AarI (336)
NotI (1021)
NgoMIV (1111)
NaeI (1113)
BmgBI (1482)
PspXI (1713)
BspEI* (1721)
BbsI (2642)
EcoRI (3148)
XmnI (3937)
PspFI (5125)
BseyI (5121)
BspQI – SapI (5542)
CAP binding site
lac operator
M13 rev
HindIII (5784)
BsmI (5966)
HincII (6059)
PspOMI (7251)
ApaI (7255)
SrfI (7256)
SexAI* (7487)
BglII (7691)
AgeI (0)
1000
2000
3000
4000
5000
6000
7000
LTR
MMLV ψ
gag (truncated)
anti-FcRL5 scFv 105
CD8a TM
4-1BB
CD3zeta
105 aFcRL5 BBz CAR 7854 bp
lac promoter
ori
AmpR
AmpR promoter
LTR
M13 fwd

FIG. 14

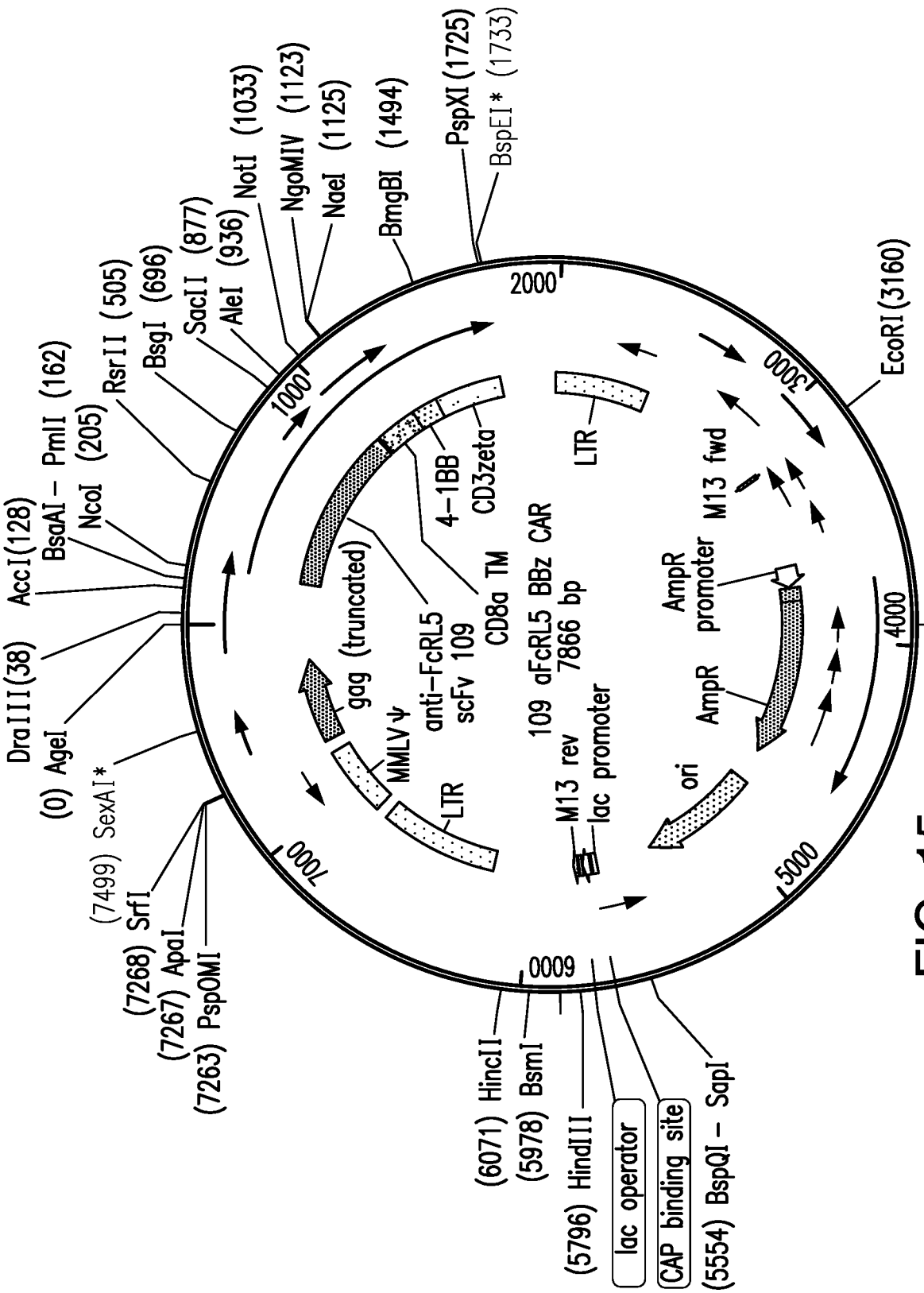

1000
2000
3000
4000
5000
6000
7000
(0) AgeI
DraIII(38)
AccI(128)
BsaAI – PmlI (162)
NcoI (205)
RsrII (505)
BsgI (696)
SacII (877)
AleI (936)
NotI (1033)
NgoMIV (1123)
NaeI (1125)
BmgBI (1494)
PspXI (1725)
BspEI* (1733)
EcoRI(3160)
(3949) XmnI
(7499) SexAI*
(7268) SrfI
(7267) ApaI
(7263) PspOMI
(6071) HincII
(5978) BsmI
(5796) HindIII
(5554) BspQI – SapI
LTR
MMLV ψ
gag (truncated)
anti-FcRL5 scFv 109
CD8a TM
4-1BB
CD3zeta
109 aFcRL5 BBz CAR
7866 bp
M13 rev
lac promoter
lac operator
CAP binding site
ori
AmpR
AmpR promoter
LTR
M13 fwd

FIG. 15

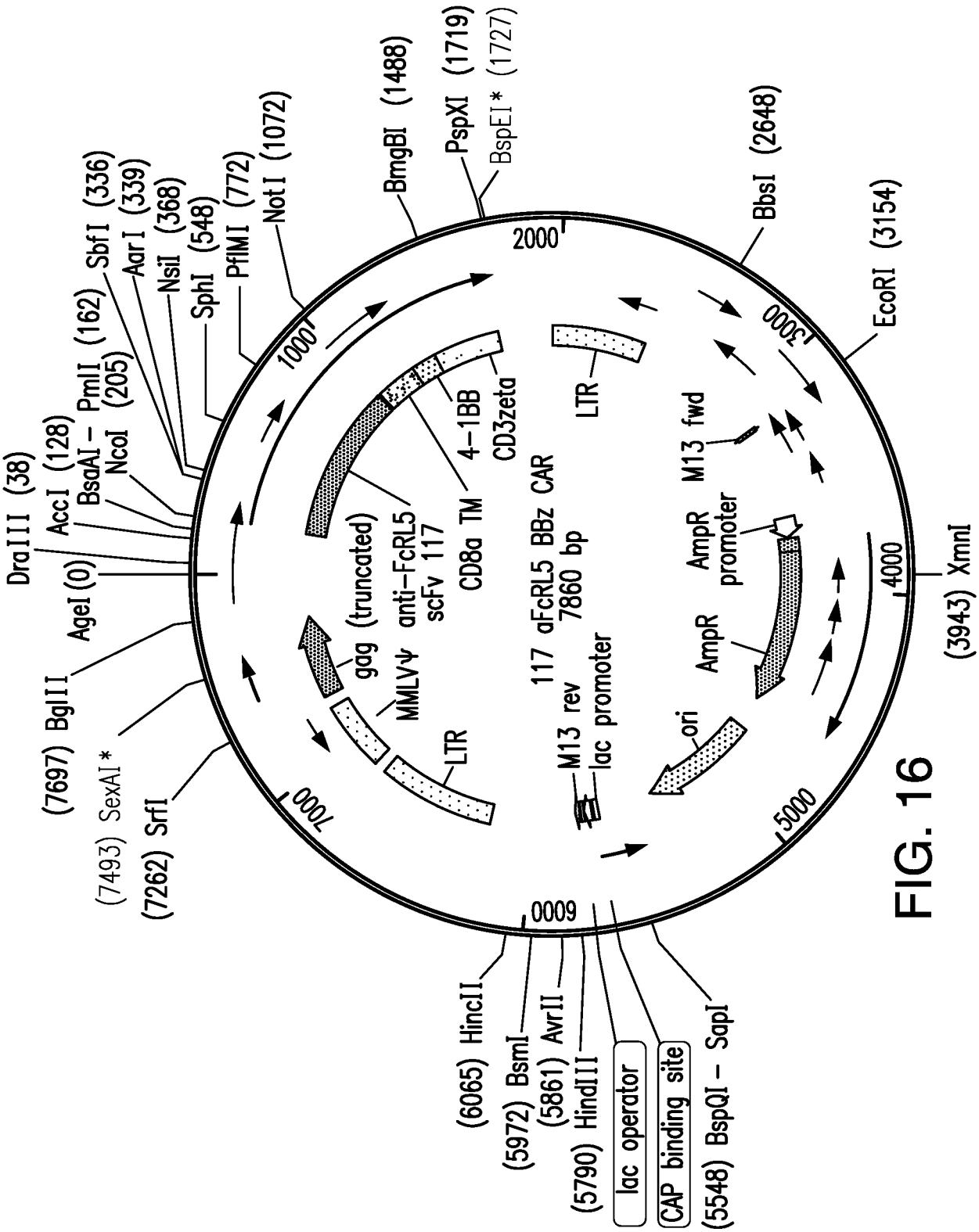

DraIII (38)
AccI (128)
BsaAI – PmlI (162)
NcoI (205)
AgeI (0)
(7697) BglII
(7493) SexAI*
(7262) SrfI
SbfI (336)
AarI (339)
NsiI (368)
SphI (548)
PflMI (772)
NotI (1072)
BmgBI (1488)
PspXI (1719)
BspEI* (1727)
BbsI (2648)
EcoRI (3154)
(3943) XmnI
1000
2000
3000
4000
5000
6000
7000
gag (truncated)
MMLVψ
LTR
anti-FcRL5 scFv 117
CD8a TM
4-1BB
CD3zeta
117 aFcRL5 BBz CAR
7860 bp
M13 rev
lac promoter
LTR
M13 fwd
AmpR promoter
AmpR
ori
(6065) HincII
(5972) BsmI
(5861) AvrII
(5790) HindIII
lac operator
CAP binding site
(5548) BspQI – SapI

FIG. 16

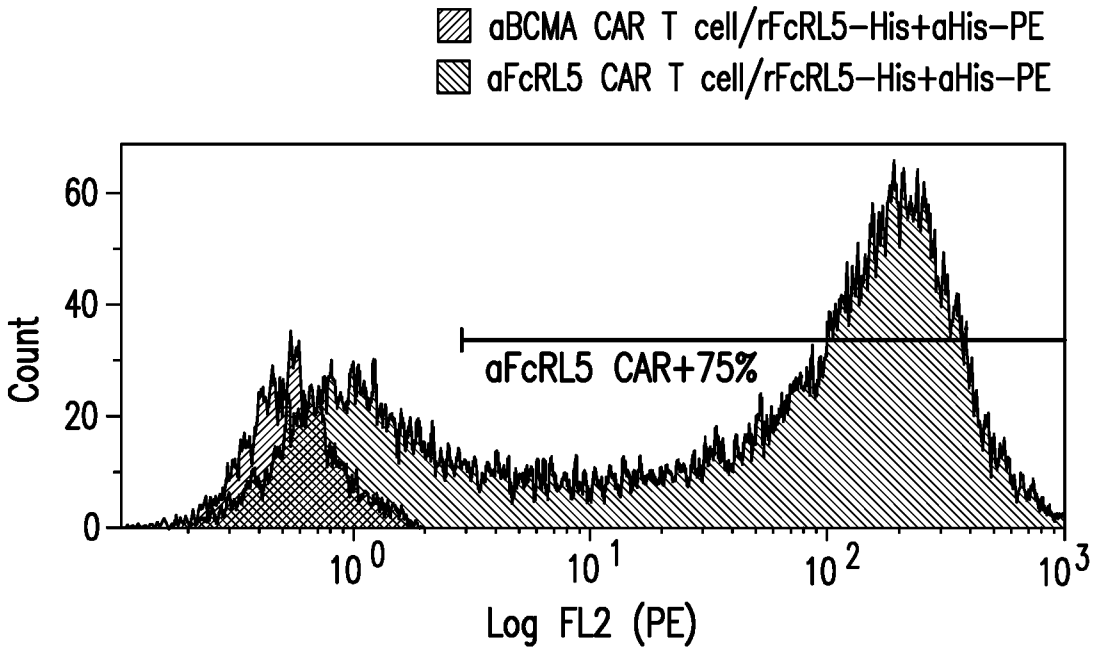

aBCMA CAR T cell/rFcRL5-His+aHis-PE
aFcRL5 CAR T cell/rFcRL5-His+aHis-PE
Count
60
40
20
0
aFcRL5 CAR+75%
10 0
10 1
10 2
10 3
Log FL2 (PE)

FIG. 17

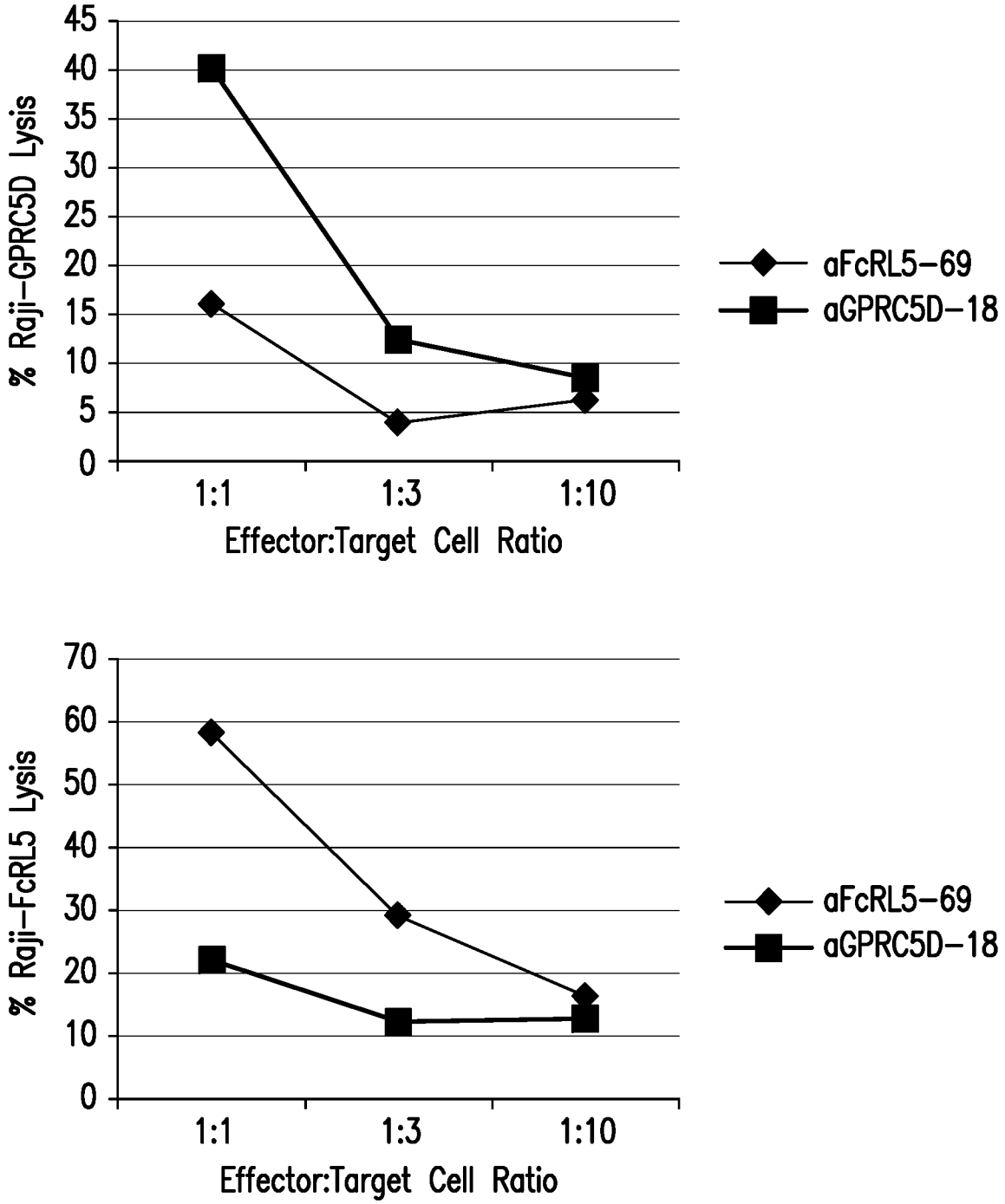

% Raji-GPRC5D Lysis
45
40
35
30
25
20
15
10
5
0
1:1
1:3
1:10
Effector:Target Cell Ratio
aFcRL5-69
aGPRC5D-18
% Raji-FcRL5 Lysis
70
60
50
40
30
20
10
0
1:1
1:3
1:10
Effector:Target Cell Ratio
aFcRL5-69
aGPRC5D-18

FIG. 18

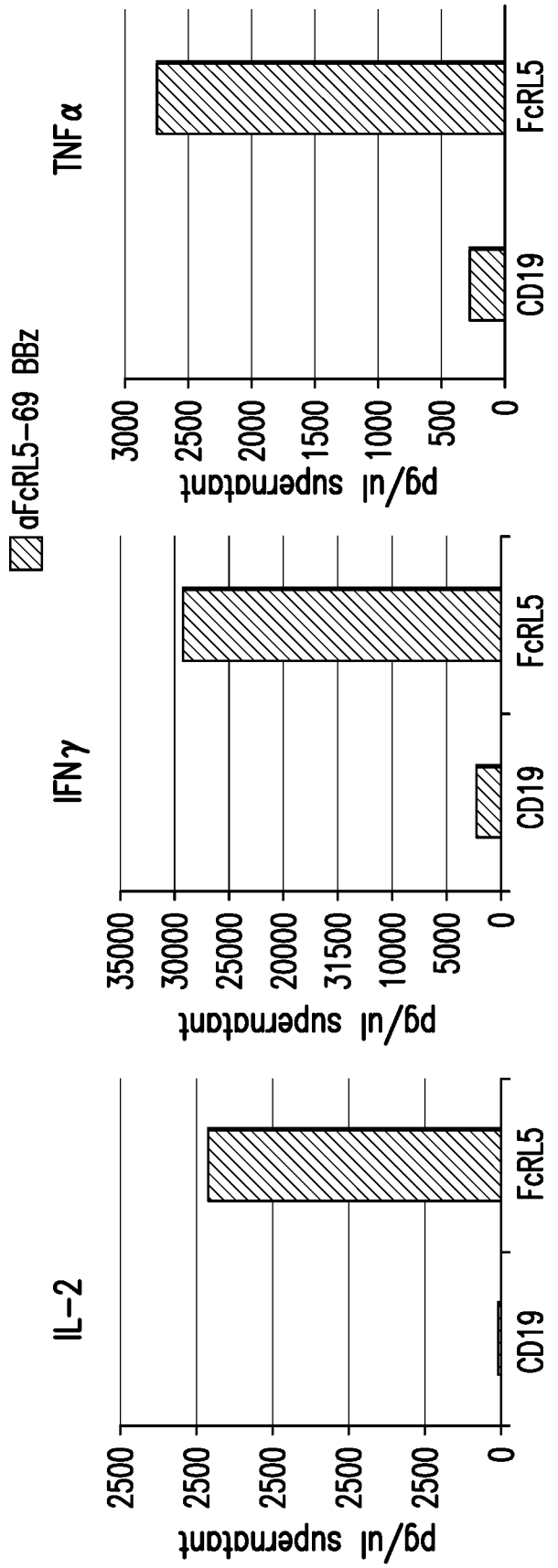

αFcRL5-69 BBz
IL-2
IFNγ
TNFα
pg/ml supernatant
2500
2500
2500
2500
2500
0
CD19
FcRL5
35000
30000
25000
20000
31500
10000
5000
0
CD19
FcRL5
3000
2500
2000
1500
1000
500
0
CD19
FcRL5

FIG. 19

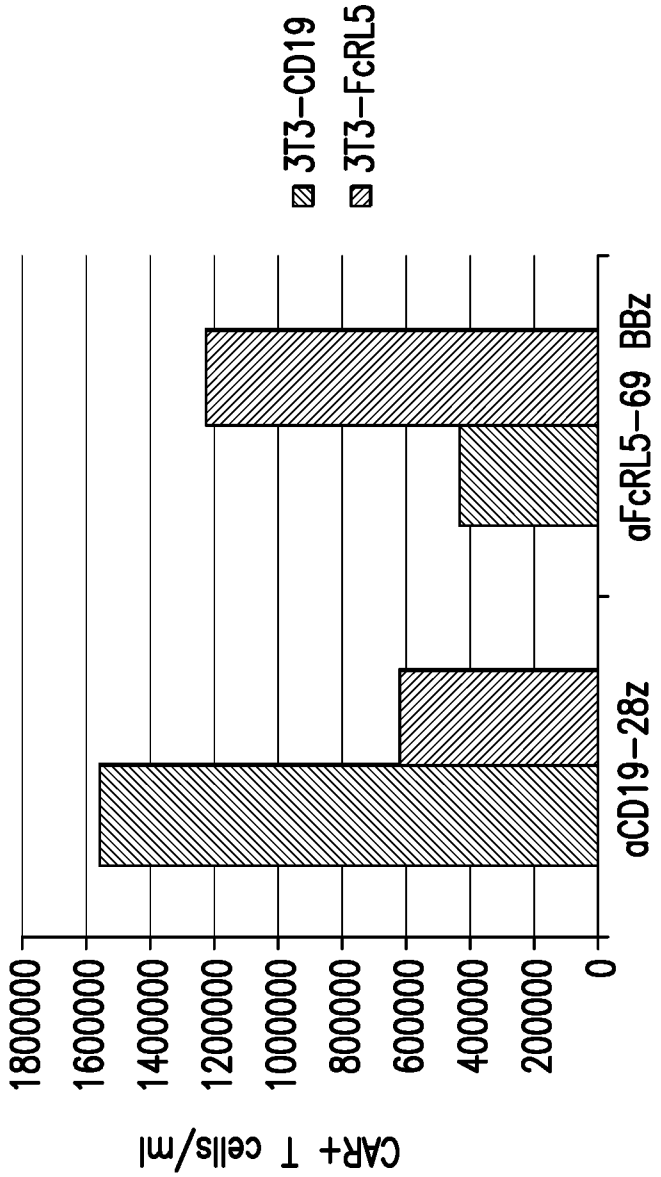

3T3-CD19
3T3-FcRL5
CAR+ T cells/ml
1800000
1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
αCD19-28z
αFcRL5-69 BBz

FIG. 20

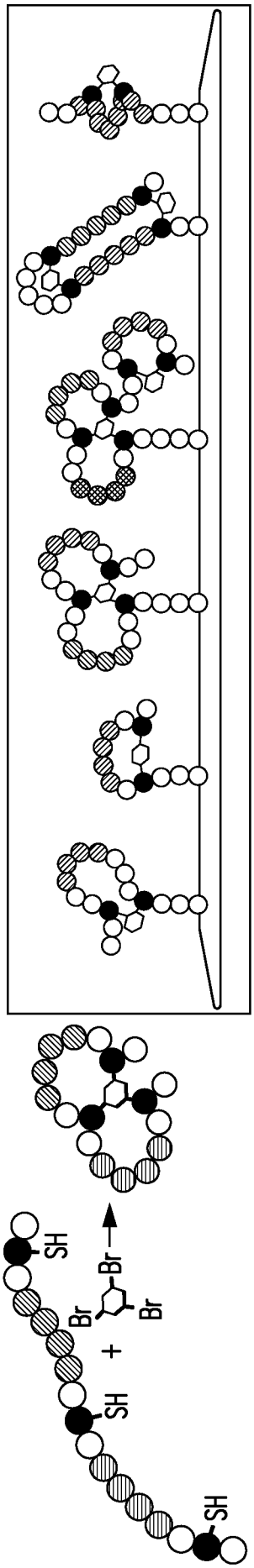


FIG. 21

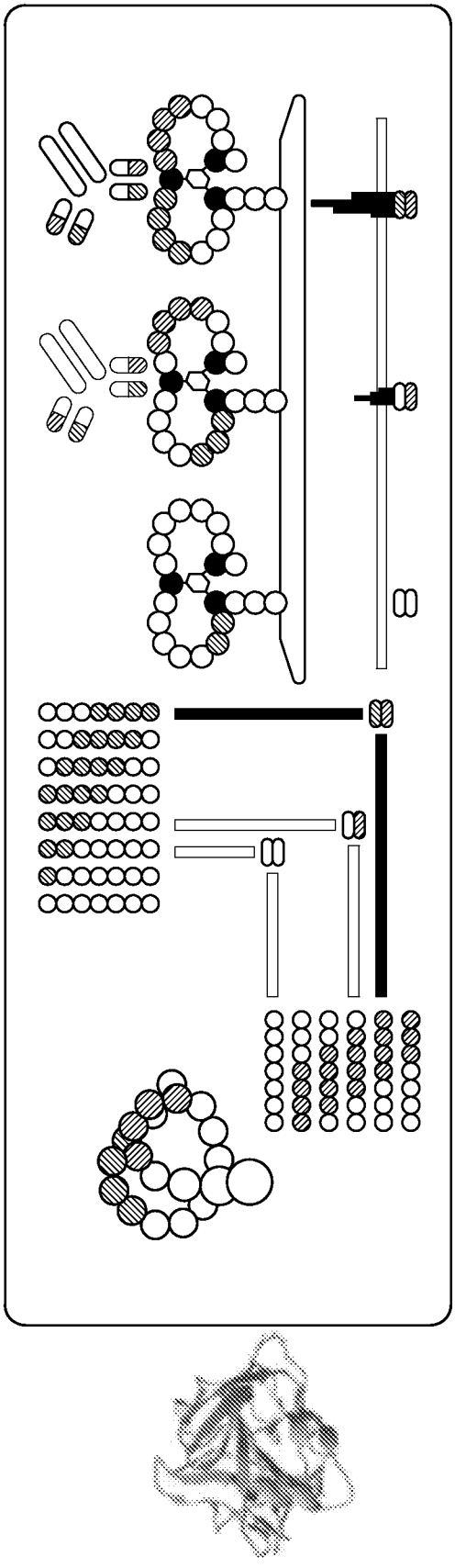


FIG. 22

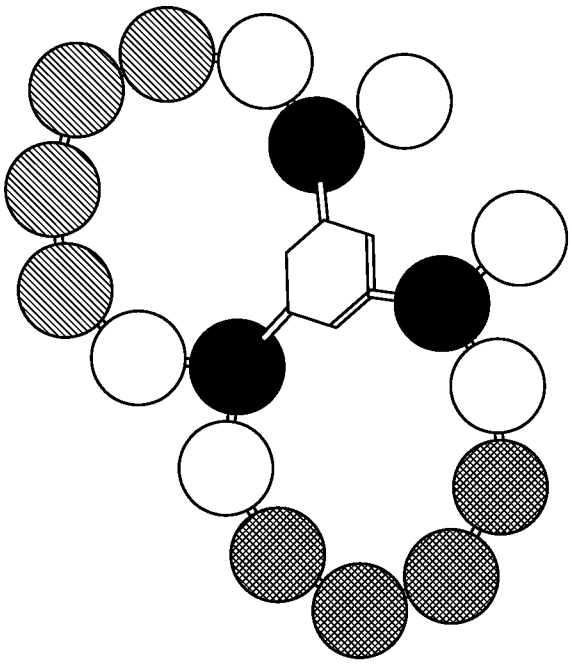


FIG. 23

Loop 1	Loop 2	ELISA
CMDYDFKVKLSSERERC	WAIGCIFAELLTSEPC	−0.01
CMDYDFKVKLSSERERC	CIFAELLTSEPIFHCC	0.79
CMDYDFKVKLSSERERC	ELLTSEPIFHCRQEDC	1.21
CMDYDFKVKLSSERERC	SEPIFHCRQEDIKTSC	0.36
CFKVKLSSERERVEDLC	WAIGCIFAELLTSEPC	0.17
CFKVKLSSERERVEDLC	CIFAELLTSEPIFHCC	1.19
CFKVKLSSERERVEDLC	ELLTSEPIFHCRQEDC	1.24
CFKVKLSSERERVEDLC	SEPIFHCRQEDIKTSC	0.56
CLSSERERVEDLFEYEC	WAIGCIFAELLTSEPC	0.61
CLSSERERVEDLFEYEC	CIFAELLTSEPIFHCC	1.21
CLSSERERVEDLFEYEC	ELLTSEPIFHCRQEDC	1.41
CLSSERERVEDLFEYEC	SEPIFHCRQEDIKTSC	0.58
CRERVEDLFEYEGCKVC	WAIGCIFAELLTSEPC	0.10
CRERVEDLFEYEGCKVC	CIFAELLTSEPIFHCC	0.83
CRERVEDLFEYEGCKVC	ELLTSEPIFHCRQEDC	1.21
CRERVEDLFEYEGCKVC	SEPIFHCRQEDIKTSC	−0.02

FIG. 24A

Loop 1	WAIGCIFAELLTSEP	CIFAELLTSEPIFHC	ELLTSEPIFHCRQED	SEPIFHCRQEDIKTS
MDYDFKVKLSSERER	−0.01	0.79	1.21	0.36
FKVKLSSERERVEDL	0.17	1.19	1.24	0.56
LSSERERVEDLFEYE	0.61	1.21	1.41	0.58
RERVEDLFEYEGCKV	0.10	0.83	1.21	−0.02

Loop 2

FIG. 24B



FIG. 24C

	WAIGCIFAELLTSEP	CIFAELLTSEPIFHC	ELLTSEPIFHCRQED	SEPIFHCRQEDIKTS
MDYDFKVKLSSERER	−0.01	0.79	1.21	0.36
FKVKLSSERERVEDL	0.17	1.19	1.24	0.56
LSSERERVEDLFEYE	0.61	1.21	1.41	0.58
RERVEDLFEYEGCKV	0.10	0.83	1.21	−0.02

FIG. 24D

FIGURE 25



FIGURE 26



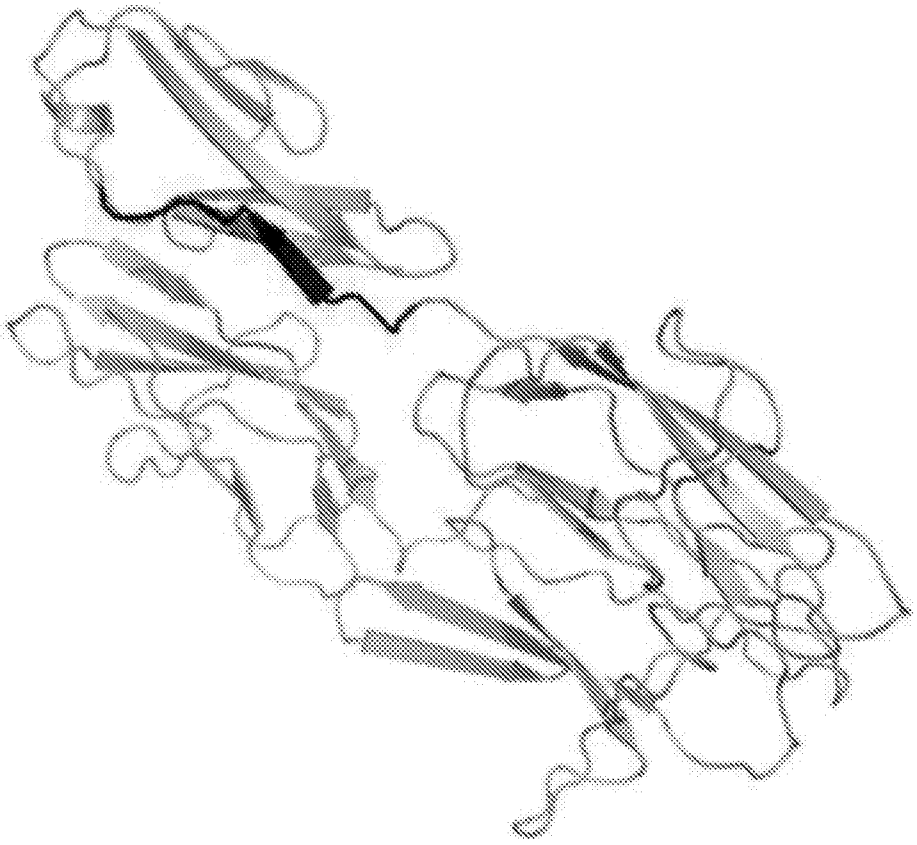


FIG. 27