ROR1 mAbs

V_K	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 23	35 49	57 88			98 107	
EAR1-324	EIVLTQTPSPVSAAVGGTVTIKC	QASQSVYGNNELA	WYQQKPGQPPKLLIY	RASTLTS	GVPSRFKGSGSGTQFTLTISGVQCADAATYYC	LGGYVSDSYRAA	FGGGTELEIL
EAR1-TOP40	DIVLTQTPSSTSAAVGGTVTIKC	QASQSISSY--LA	WYQQKRGQPPKLLIY	GASTLAS	GVPSRFSGSRSGTEYTLTISGVQCEDAATYYC	LGGIDWTSRTA	FGGGTKLEIK
V_λ	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 23	35 49	57 88			98 107	
KSR1-402	SYELTQLPSVSVSLGQTARITC	EGNNIGSKAVH--	WYQQKPGLAPGLLIY	DDDERPS-----	GVPDRFSGSNSGNT---ATLTISGAQAEDEADYYC	QVWDSSAVV--	FGGGTQLTVTG
EAR1-301	SYELTQLPSVSVSLGQTARITC	GGNSIGSKAVH--	WYQQKPGLAPGLLIY	DDDERPS-----	GVPDRFSASNSGNT---ATLTISGAQAEDEADYYC	QVWDSSAVAVV	FGGGTQLTVTG
EAR1-306	QFVLTQSPSVSAALGASAKLTC	TLSSEHKTYTID-	WYQQQQEAPRYLMK	LKSDGSYTKGT	GVPSRFSGSSSGAD---RYLIISSVQAEDEAEYYC	GTHYSGGVV--	FGGGTQLTVTG
EAR1-316	SYELTQLPSVSVSLGQTARITC	GGNSICSKAVH--	WYQQKPGLAPGLLIY	GDDERPS-----	GVPDRFSGSNSGNT---ATLTISGAQAGDEADYYC	QLWDSSTGAYA	FGGGTQLTVTG
EAR1-403	SYELTQLPSVSVSLGQTARITC	GGNSIGSKAVH--	WYQQKPGLAPGLLIY	GDDERPS-----	GVPARFSGSNSGNT---ATLTISGAQAGDEADYYC	QLWDSSAGAYV	FGGGTQLTVTG
EAR1-409	QFVLTQPQSVSGSLGQTVSISC	WDSSNIGDYYVH	WYQQHPGKAPTVVIY	NDNQRPS-----	GVPDRFSGSIDSTSNSASLTISGLLAEDEADYYC	LSSNSSAVV--	FGGGTQLTVTG
EAR1-TOP4	SYELTQLPSVSVSLGQTARITC	GGSSIESKAVH--	WYQQKPGLAPGLLVY	NDDERPS-----	GVPDRFSGSNSGDT---ATLTISGAQAGDEADYYC	QAWDSAVV--	FGGGTQLTVTG
EAR1-TOP15	SYELTQLPSVSVSLGQTARITC	GGNSIGSKAVH--	WYQQKPGLAPGLLIY	DDDERPS-----	GVPDRFSGSNSGDT---ATLTISGAQAGDEADYYC	QLWDSSAGAYV	FGGGTQLTVTG
EAR1-TOP22	SYELTQLPSVSVSLGQTARITC	GGNSIGSKAVH--	WYQQKPGLAPGLLIY	NDDERPS-----	GVPDRFSGSNSGDT---ATLTISGAQAGDEADYYC	QLWDNNAAV--	FGGGTQLTVTG
EAR1-TOP43	SYELTQLPSVSVSLGQTARITC	GGNNIGSKAVH--	WYQQKPGLAPGLLIY	WDSERPS-----	GVPERFSGSNSGDT---ATLTISGAQAGDEADYYC	QLWDSSAGAYV	FGGGTQLTVTG
EAR1-TOP54	SYELTQLPSVSVSLGQTARITC	GGNSIGSKAVH--	WYQQKPGLAPGLLIY	DDDERPS-----	GVPTRFSGSNSGDT---ATLTISGAQAGDEADYYC	QLWDSSAWAFV	FGGGTQLTVTG

V_H	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 30	36 49	66 94			103 113	
KBA1-402	QEQLKESGGGLVTPTGTLTLTCTASGFDIS	SYWMS	WVRQAPGKGLEWIG	AIGISGNAYYASWAKS-	RSTITKNTNLKT-VTLKMTSLTAADTATYFCAR	GEPTYGMDL----------	WGPGTLVTVSS
EAR1-301	QEQLEESGGGLVTPGGSLTLTCTASGFTIS	TYWMS	WVRQAPGKGLEWIG	SIYAGSSTYYASWVNG	RFTISKTTQWT-VSLQMNSLTVADTATYFCAR	GRTSYGMDL----------	WGPGTLVTVSS
EAR1-306	QEQLKESGGGLVKPGGSLKLSCKASGFDLS	WIGVS	WVRQAPGKGLEWIG	YIDPTFDYTTYASWVNG	RFSISRDNTQWT-VSLQLNSLTTADTATYFCAR	WFYGFDIWGQGTMVTVSS	WGQGTLVTISS
EAR1-316	QEQLEESGGRLVTPGTPLTLTCTASGFTLS	SYVVS	WVRQAPGKGLEWIG	AIGNGGSAYYASWAKS-	RSTITKNTNLST-VTLKMTSLTAADTATYFCAR	DRTWYGMDL----------	WGPGTLVTVSS
EAR1-324	QS-LEESGGRLVKPGESLTLTCTVSGFSLS	RWSMT	WVRQAPGKGLEWIG	LITSGGDKTYYATWAKG-	RFTISKT---SSTTVDLKMTSLTTEDTATYFCAR	GTVSSDI----------	WGPGTLVTISS
EAR1-403	QEQLKESGPALVKPTQTLTLTCTFSGFSLS	GMYMT	WVRQPPGKALEWLA	HIFWDDDKRYNPSLKS	RLTISKDTSKNQVVLTMTNMDPVDTATYYCVR	GSDYYDL----------	WGQGTMVTISS
EAR1-409	QEQLVESGGRLVTPGGSLRLTCTASGFTFS	SYGMS	WVRQAPGKGLEWVG	TIYNGSGTWYASWVNG	RFTISKT---S-TSVDLKITSPTTEDTATYFCAR	SYTGWTTPFFDY----	WGQGTLVTVSS
EAR1-TOP4	QS-VESGGRLVTPGTPLTLTCTASGIDLS	RYAVM	WVRQAPGKGLEWIG	VISGSGTTYYASWAKG-	RFTISKT---S-TTVTLKITSPTTEDTATYFCAR	GWATDSIDYDGYFWL	WGPGTLVTVSS
EAR1-TOP15	QEQVVESGGRLVTPGGSLRLTCTASGFSFS	SYWMS	WVRQAPGKGLEWVG	AIYVNSGSAYYASWAKS	RFTISKT---SSTTVDLKMTSLTTEDTAIYYCAR	DGWSSDY----------	WGPGTLVTISS
EAR1-TOP22	QS-LEESGGRLVTPGTPLTLTCTVSGFSLS	SYMMS	WVRQAPGKGLEWVG	TISSGSTYYASWVKG-	RFTISKT---S-TTVDLKMTSLTTEDTATYFCAR	DLDYDMDL----------	WGPGTLVTVSS
EAR1-TOP40	QEQLEESGGRLVTPGTPLTLTCTASGFSLS	WYTMS	WVRQAPGKGLEYIG	IISSSGSTYYASWAKG-	RFTISKT---SSTTVDLKITSPTTEDTATYFCAR	LYYSDSTAWL----------	WGPGTLVTVSS
EAR1-TOP43	QS-LEESGGRLVTPGTPLTLTCTVSGFSLS	SYMMS	WVRQAPGKGLEWIG	AIYSGSWTYYASWAKG-	RFTISKT---S-TTVDLKITSPTTEDTATYFCAR	DVRSTAIDL----------	WGPGTLVTISS
EAR1-TOP54	QS-LEESGGRLVTPGTPLTLTCTASGFSLS	GYYMS	WVRQAPGKGLEWIG	TIYGGSGWTAYWAKG	RFTISKT---S-TTVDLKITSPTTEDTATYFCAR	DPGLSTGGL----------	WGPGTLVTISS

FIG. 1

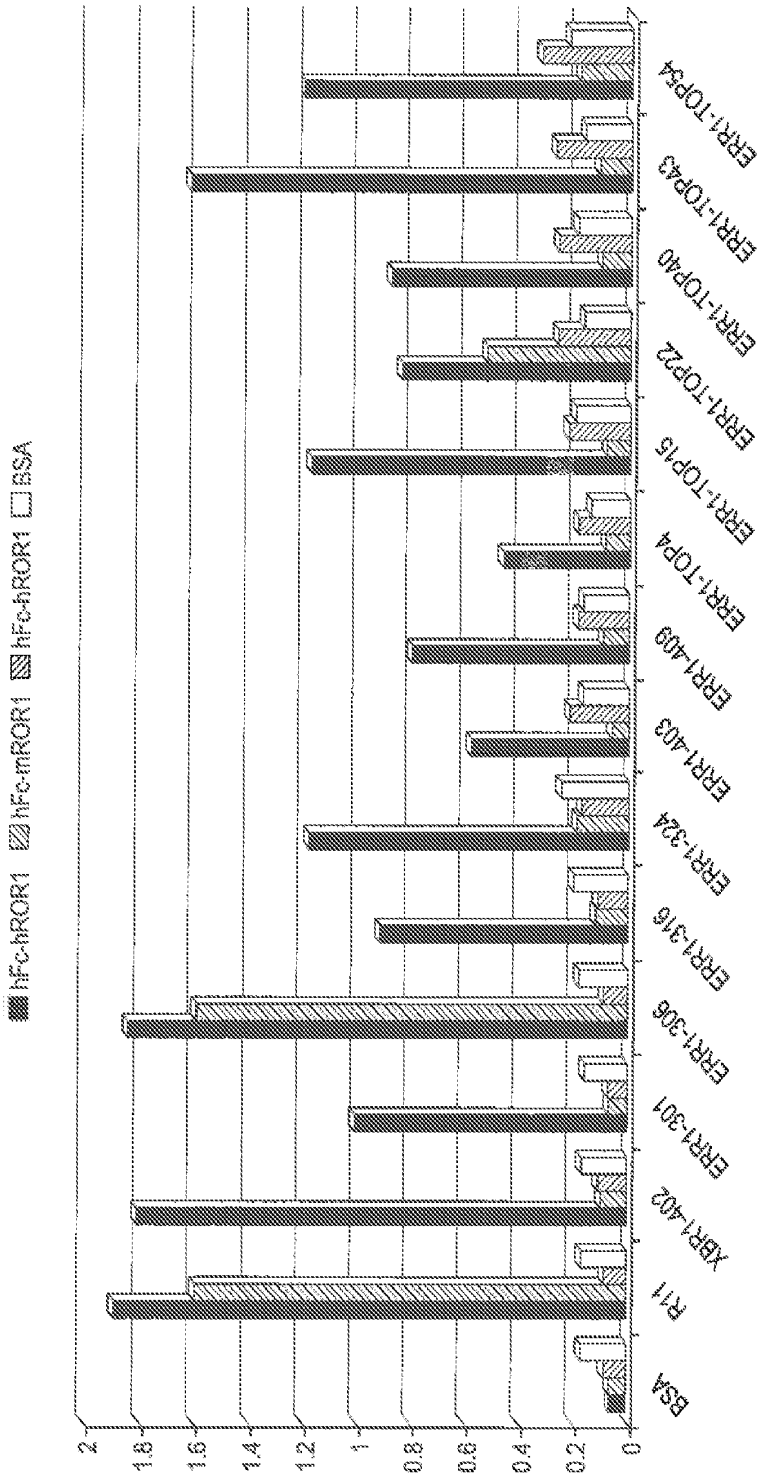

hFc-hROR1
hFc-mROR1
hFc-hROR1
BSA
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
BSA
R11
XBR1-402
ERR1-301
ERR1-306
ERR1-316
ERR1-324
ERR1-403
ERR1-409
ERR1-TOP4
ERR1-TOP15
ERR1-TOP22
ERR1-TOP40
ERR1-TOP43
ERR1-TOP54

FIG. 2

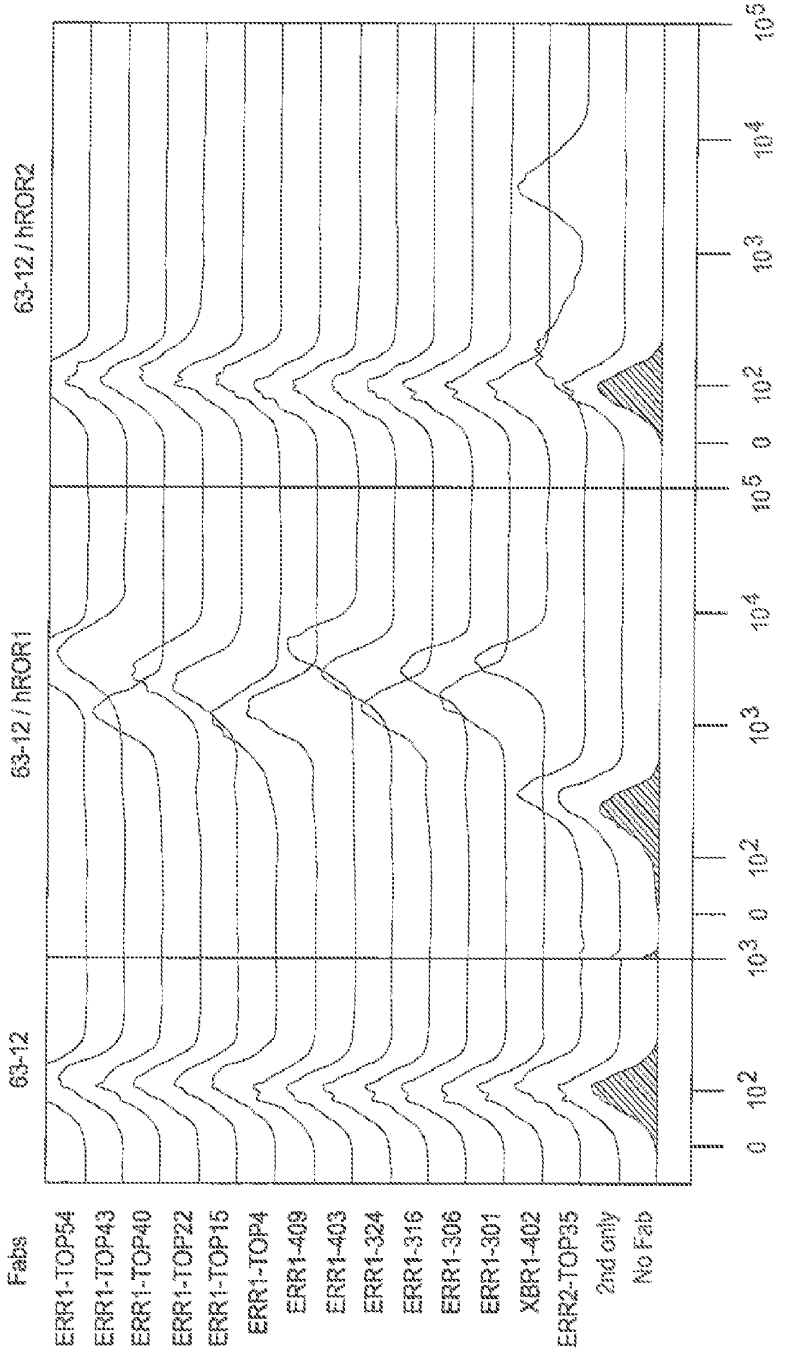

Fabs
ERR1-TOP54
ERR1-TOP43
ERR1-TOP40
ERR1-TOP22
ERR1-TOP15
ERR1-TOP4
ERR1-409
ERR1-403
ERR1-324
ERR1-316
ERR1-306
ERR1-301
XBR1-402
ERR2-TOP35
2nd only
No Fab
63-12
63-12 / hROR1
63-12 / hROR2
0
10^2
10^3
0
10^2
10^3
10^4
10^5
10^5
0
10^2
10^3
10^4
10^5

FIG. 3

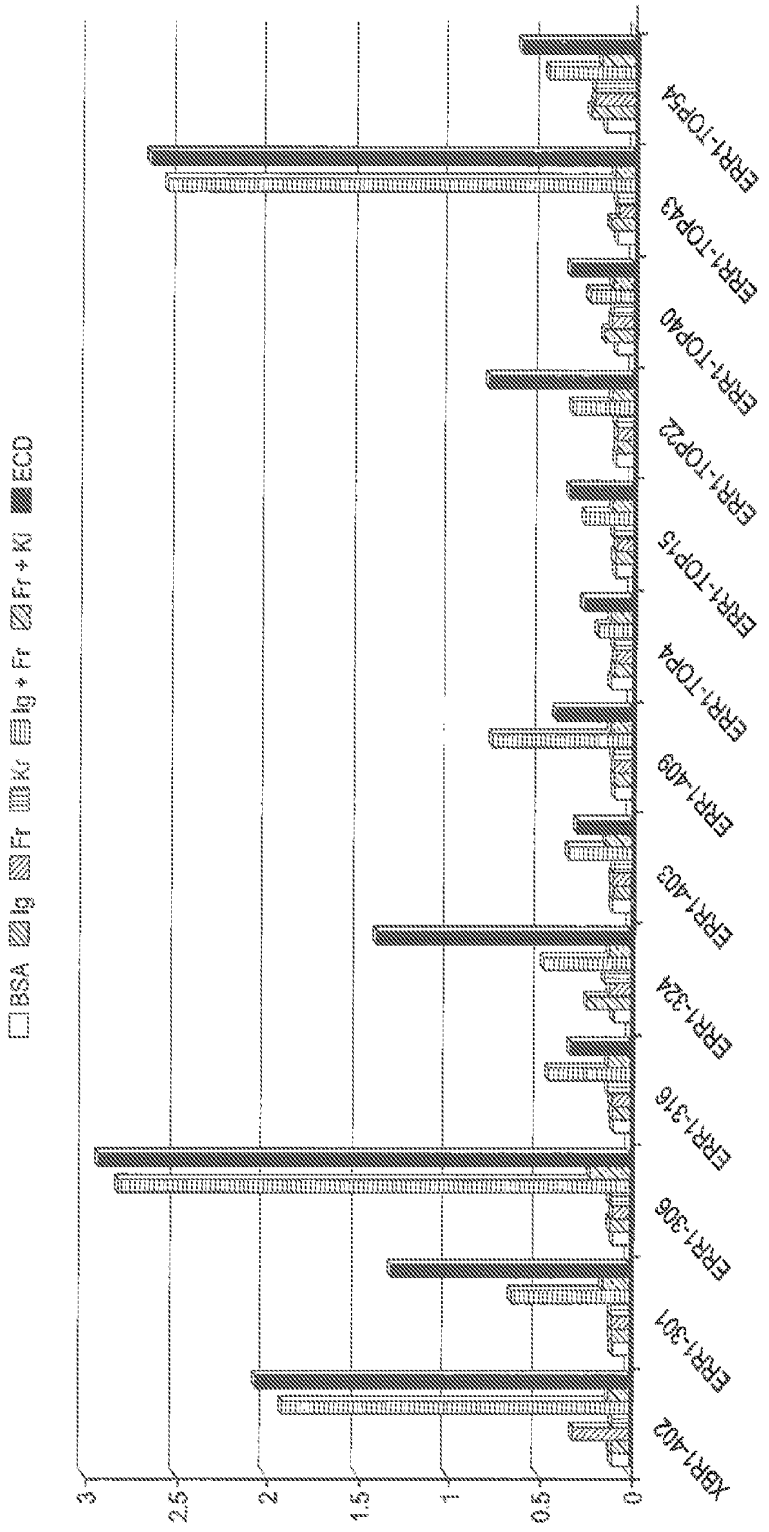

BSA
Ig
Fr
Kr
Ig + Fr
Fr + Kr
ECD
3
2.5
2
1.5
1
0.5
0
XBR1-402
ERR1-301
ERR1-306
ERR1-316
ERR1-324
ERR1-403
ERR1-409
ERR1-TOP4
ERR1-TOP15
ERR1-TOP22
ERR1-TOP40
ERR1-TOP43
ERR1-TOP54

FIG. 4

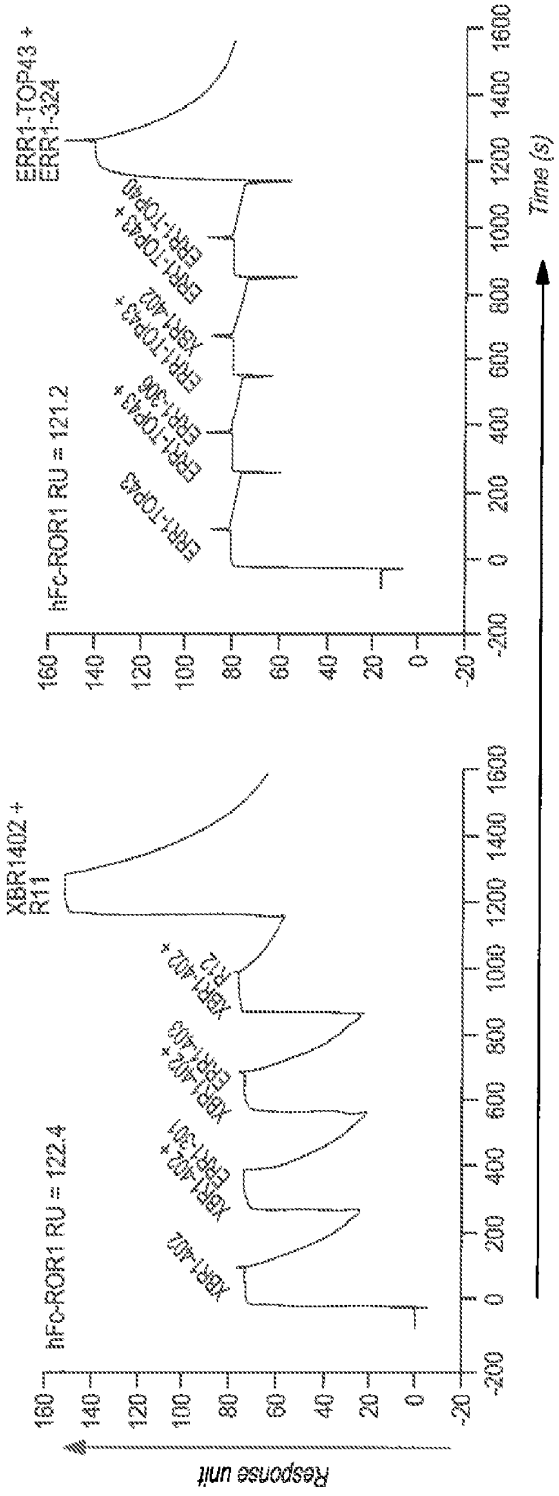
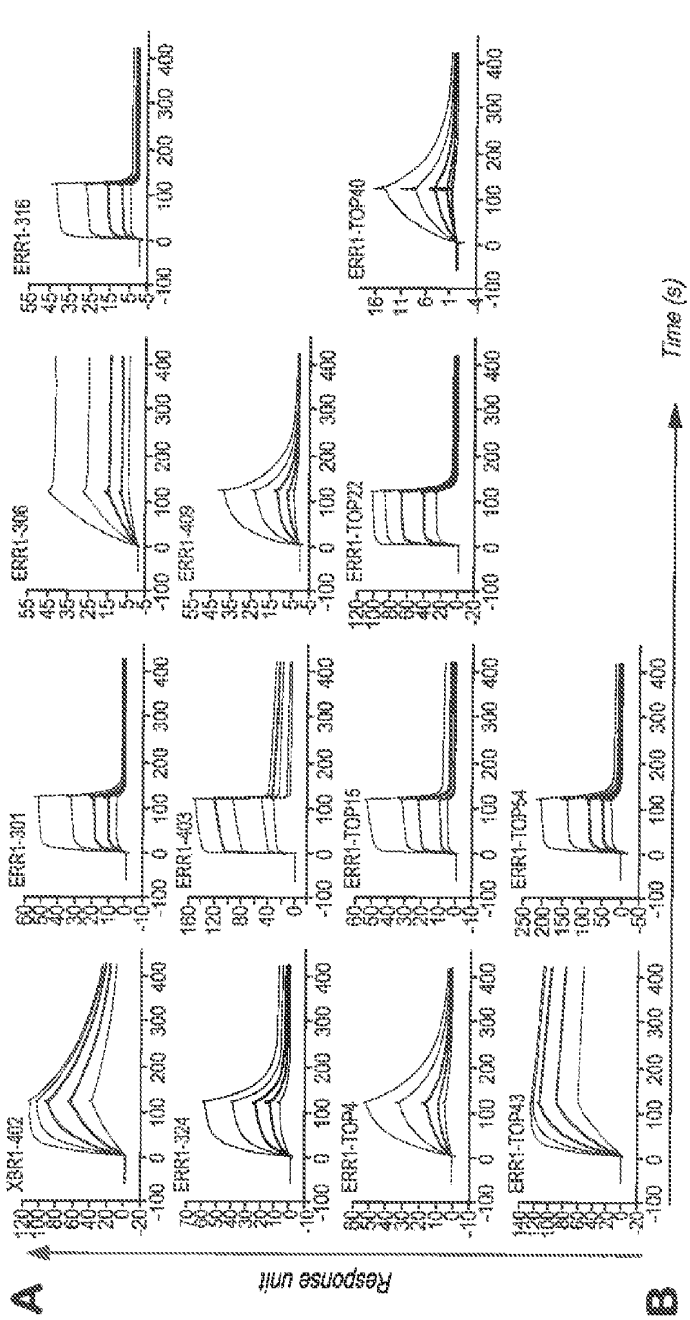

ERR1-TOP43 +
ERR1-324
hFc-ROR1 RU = 121.2
ERR1-TOP43
ERR1-TOP43 +
ERR1-306
ERR1-TOP43 +
XBR1402
ERR1-TOP43 +
ERR1-TOP40
XBR1402 +
R11
hFc-ROR1 RU = 122.4
XBR1402
XBR1402 +
ERR1-304
XBR1402 +
ERR1-303
XBR1402 +
R12
Response unit
Time (s)

FIG. 6



clone	XBR1-402	ERR1-201	ERR1-306	ERR1-316	ERR1-324	ERR1-403	ERR1-409	ERR1-TOP4	ERR1-TOP15	ERR1-TOP22	ERR1-TOP40	ERR1-TOP43	ERR1-TOP54
immobilization RU	5000	5000	5000	5000	5000	5000	5000	5000	5000	5000	5000	5000	5000
hFc-RORt RU	203.8	203	169.4	198.7	179.3	326.4	186.8	172.2	167.9	209.2	184.9	200.3	77.8
Fab. Con.[a] (nM)	100	100	500	100	200	1000	200	200	200	500	500	200	200
k_{on} (10^4 $M^{-1}s^{-1}$)	111	84.9	1.51	110	11.5	3.08	5.75	24.7	46.9	73.7	3.18	45.1	47.5
K_{off} (10^{-3} s^{-1})	6.43	100	0.146	132.6	12.51	1.28	16.16	59.24	65.36	81.26	26.19	0.501	68.85
K_d (nM)	5.81	118	9.66	121	108	41.6	281	240	139	110	636	1.11	145
Chi 2	0.616	0.922	0.137	1.85	4.64	16.7	0.302	0.403	9	14.9	0.14	1.17	54.7

FIG. 6

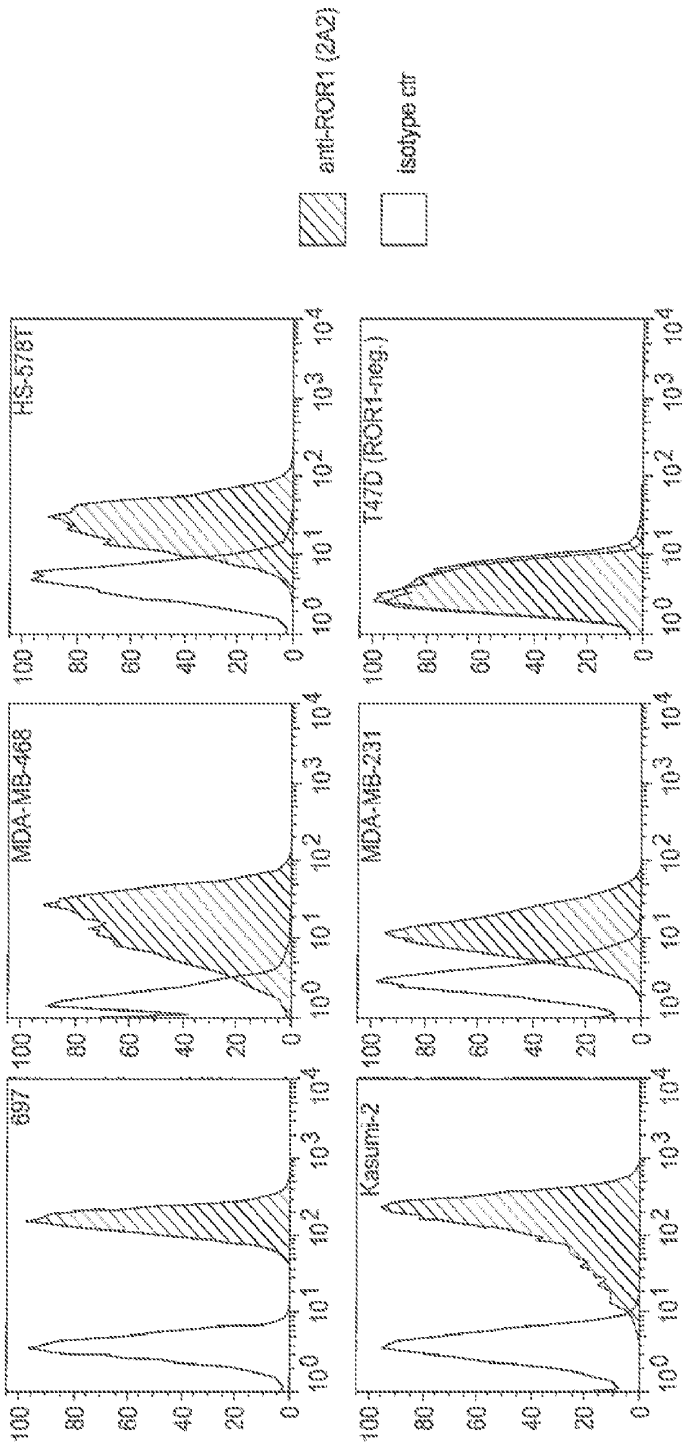

anti-ROR1 (2A2)
isotype ctr
HS-578T
MDA-MB-468
T47D (ROR1-neg.)
697
MDA-MB-231
Kasumi-2

FIG. 7

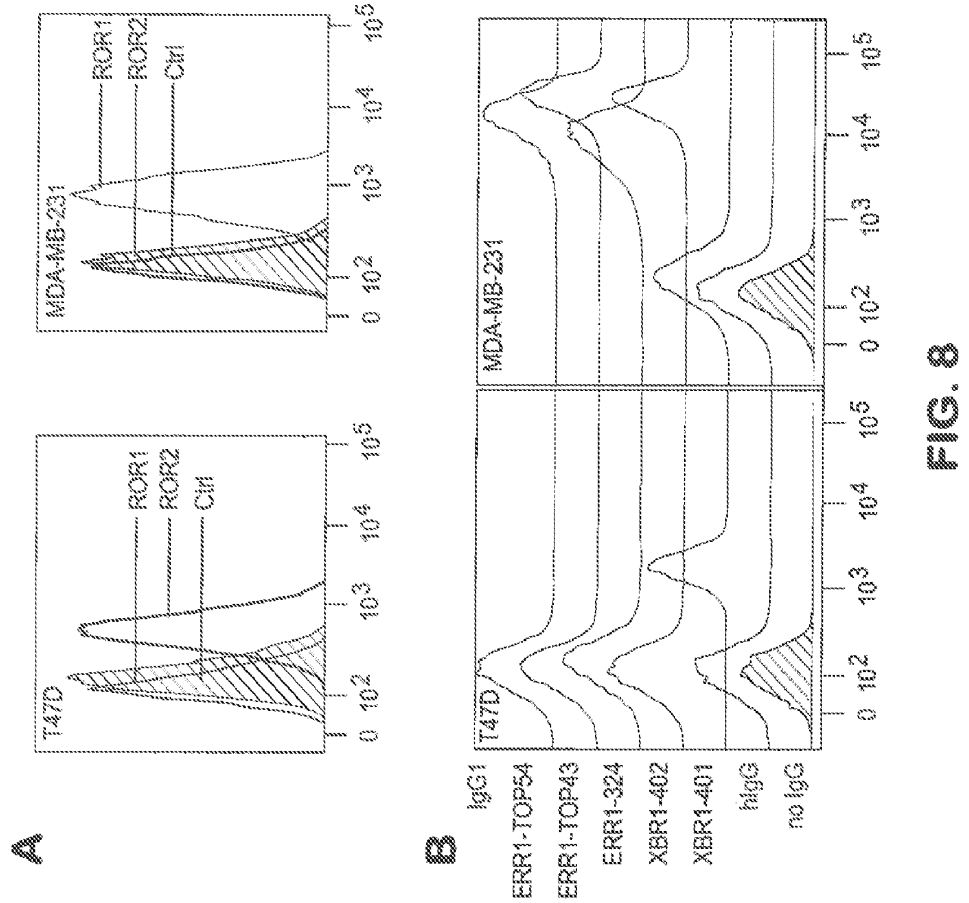

A
T47D
MDA-MB-231
ROR1
ROR2
Ctrl
0
10^2
10^3
10^4
10^5
B
IgG1
ERR1-TOP54
ERR1-TOP43
ERR1-324
XBR1-402
XBR1-401
hIgG
no IgG

FIG. 8

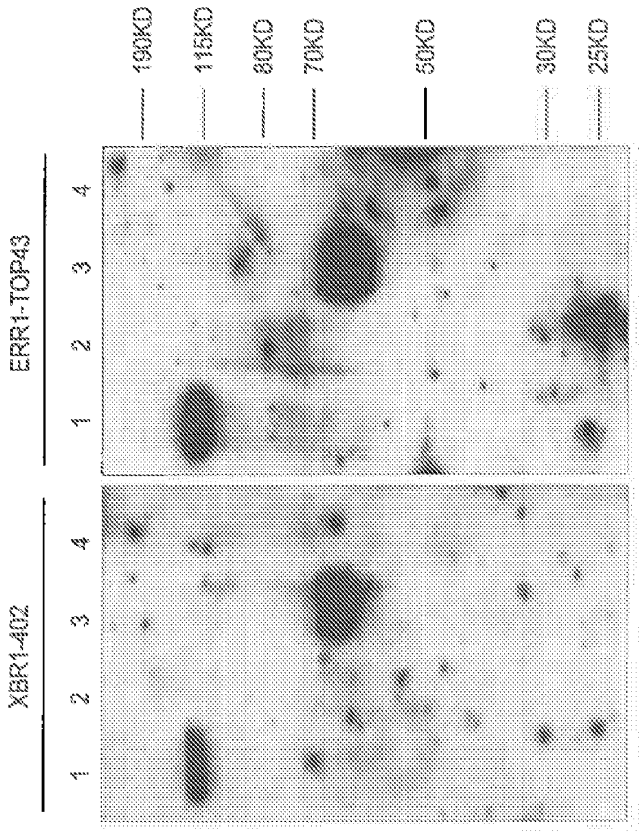

190KD
115KD
80KD
70KD
50KD
30KD
25KD
ERR1-TOP43
1 2 3 4
XBR1-402
1 2 3 4
Lane 1: K562-hROR1
Lane 2: K562
Lane 3: hROR1-ECD-HIS
Lane 4: hROR2-ECD-HIS

FIG. 9

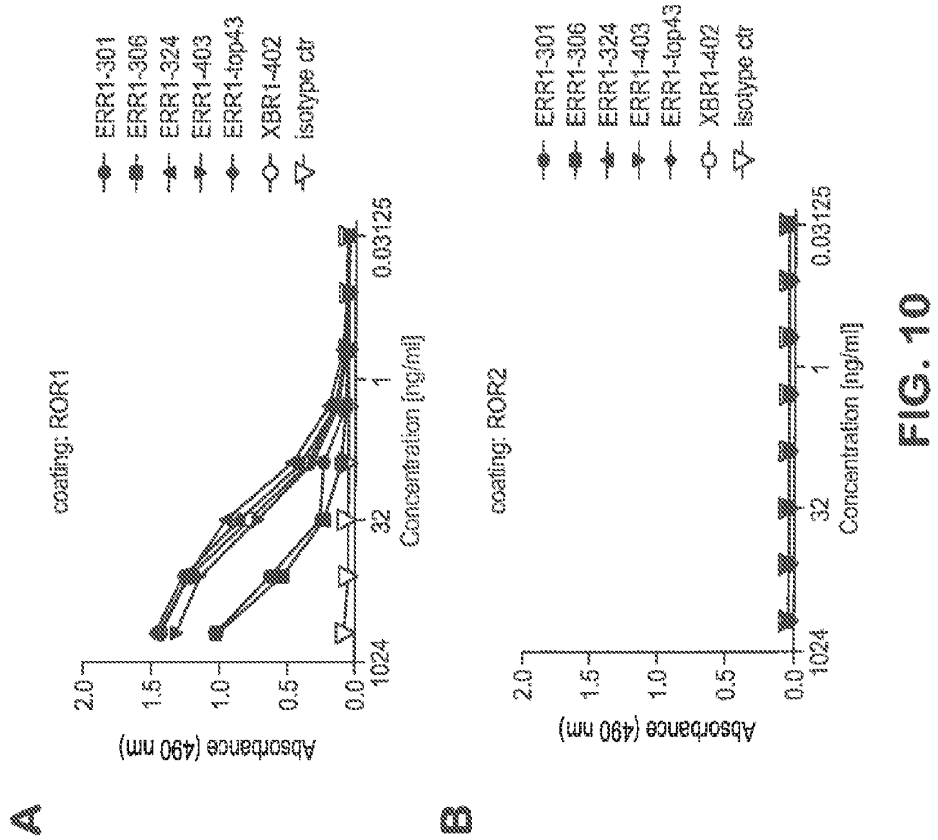

A
coating: ROR1
ERR1-301
ERR1-306
ERR1-324
ERR1-403
ERR1-top43
XBR1-402
isotype ctr
Absorbance (490 nm)
2.0
1.5
1.0
0.5
0.0
1024
32
1
0.03125
Concentration [ng/ml]
B
coating: ROR2
ERR1-301
ERR1-306
ERR1-324
ERR1-403
ERR1-top43
XBR1-402
isotype ctr
Absorbance (490 nm)
2.0
1.5
1.0
0.5
0.0
1024
32
1
0.03125
Concentration [ng/ml]

FIG. 10

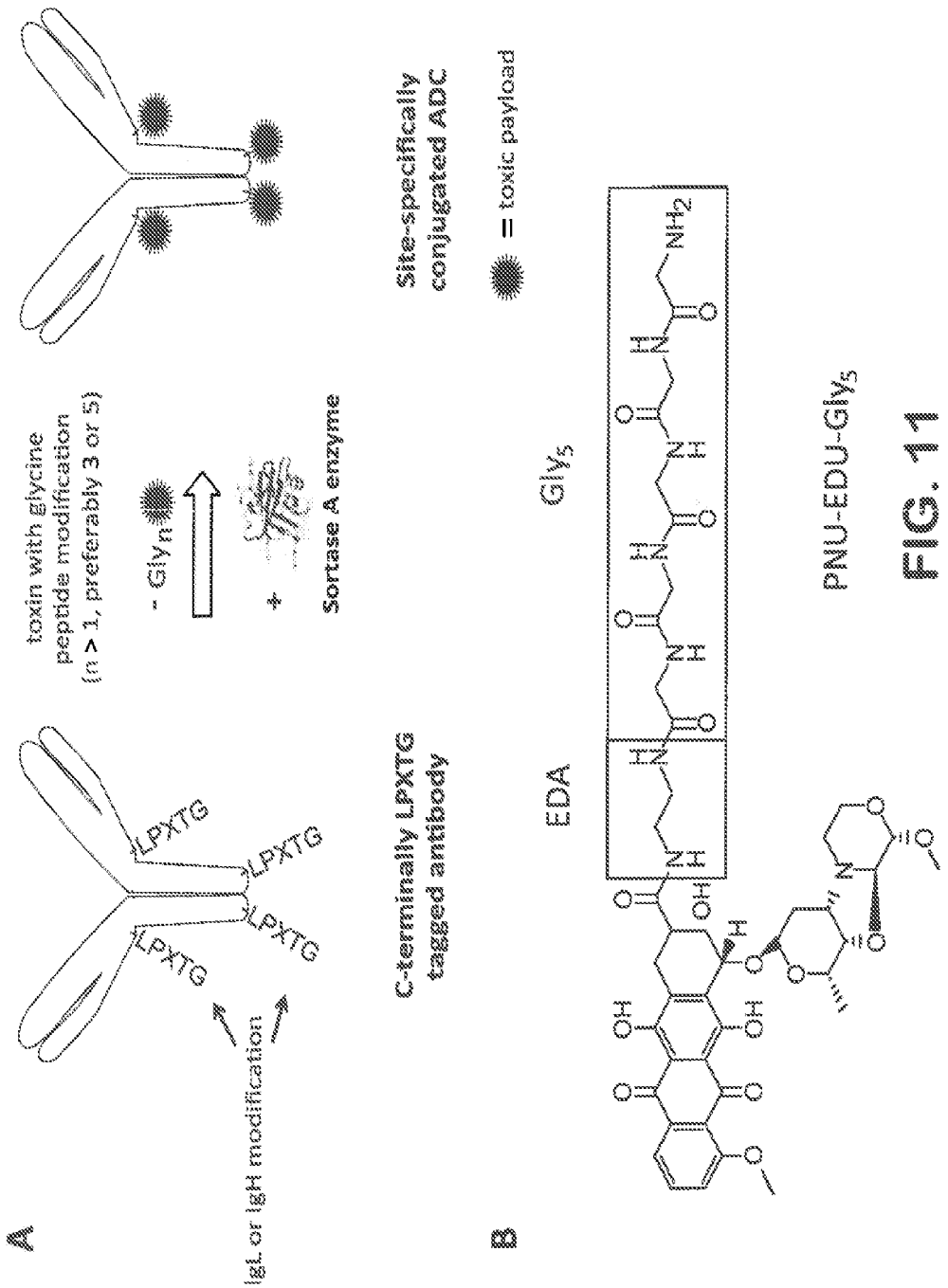

A
toxin with glycine peptide modification (n > 1, preferably 3 or 5)
- Gly$_n$
+
Sortase A enzyme
LPXTG
LPXTG
LPXTG
LPXTG
IgL or IgH modification
C-terminally LPXTG tagged antibody
Site-specifically conjugated ADC
= toxic payload
B
Gly$_5$
EDA
PNU-EDU-Gly$_5$

FIG. 11

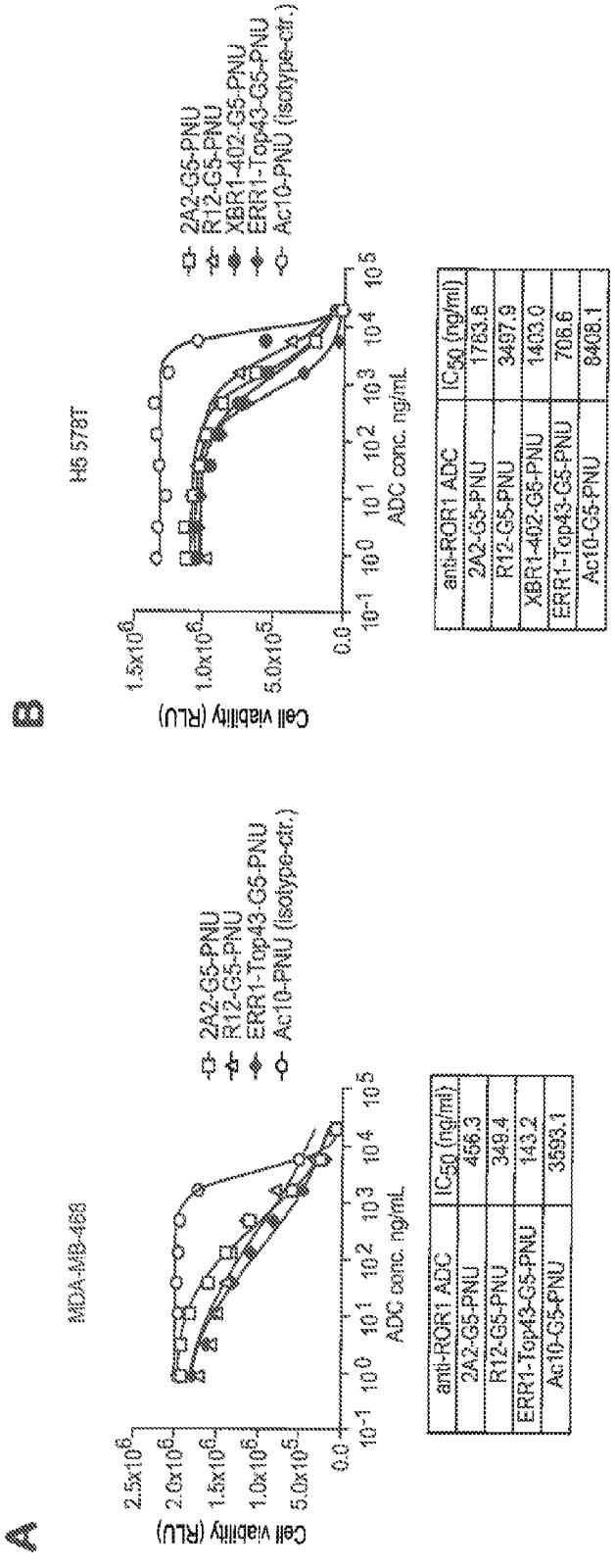
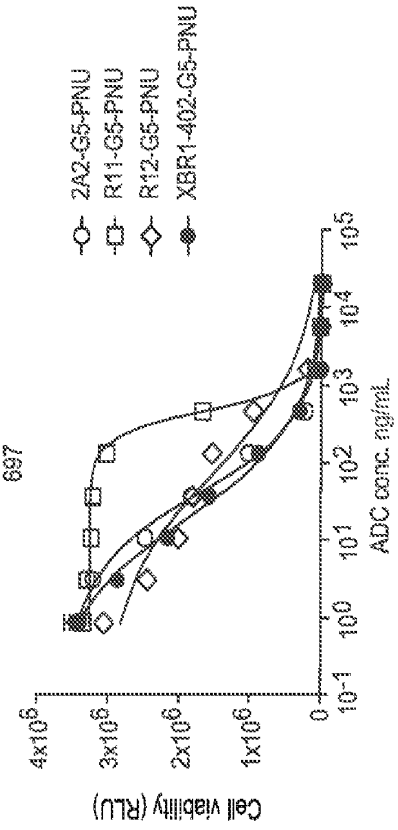

A
MDA-MB-468
Cell viability (RLU)
2.5x10^6
2.0x10^6
1.5x10^6
1.0x10^6
5.0x10^5
0.0
10^-1 10^0 10^1 10^2 10^3 10^4 10^5
ADC conc. ng/mL
2A2-G5-PNU
R12-G5-PNU
ERR1-Top43-G5-PNU
Ac10-PNU (isotype-ctr.)
anti-ROR1 ADC | IC50 (ng/ml)
2A2-G5-PNU | 456.3
R12-G5-PNU | 349.4
ERR1-Top43-G5-PNU | 143.2
Ac10-G5-PNU | 3593.1
B
H6 578T
Cell viability (RLU)
1.5x10^6
1.0x10^6
5.0x10^5
0.0
10^-1 10^0 10^1 10^2 10^3 10^4 10^5
ADC conc. ng/mL
2A2-G5-PNU
R12-G5-PNU
XBR1-402-G5-PNU
ERR1-Top43-G5-PNU
Ac10-PNU (isotype-ctr.)
anti-ROR1 ADC | IC50 (ng/ml)
2A2-G5-PNU | 1783.6
R12-G5-PNU | 3497.9
XBR1-402-G5-PNU | 1403.0
ERR1-Top43-G5-PNU | 706.6
Ac10-G5-PNU | 8408.1

FIG. 12

A



B

anti-ROR1 ADC	IC 50 (ng/ml)
2A2	38.0
R11	469.4
R12	72.1
XBR1-402	17.6

FIG. 13

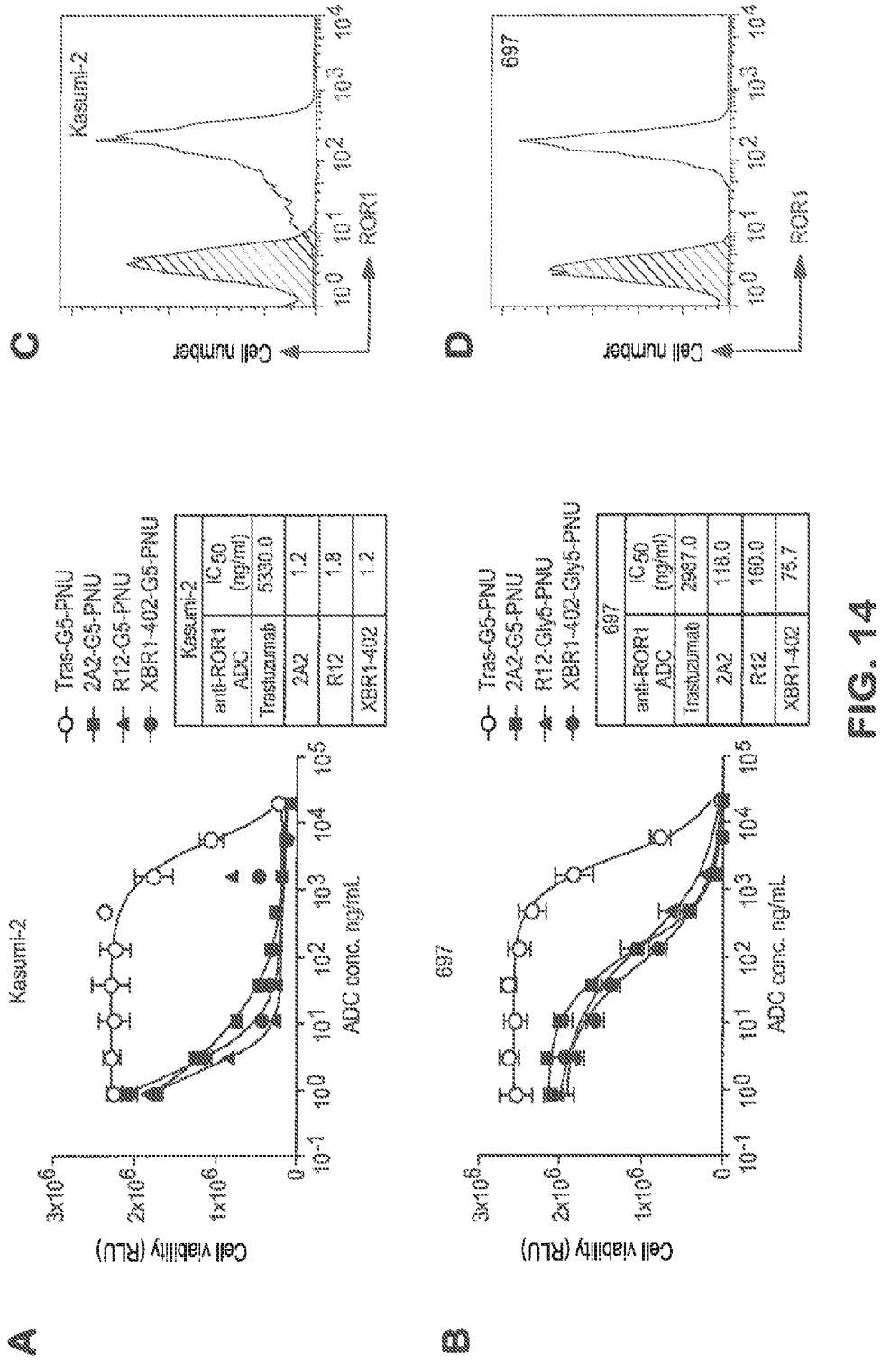

A
Kasumi-2
Cell viability (RLU)
ADC conc. ng/mL
Tras-G5-PNU
2A2-G5-PNU
R12-G5-PNU
XBR1-402-G5-PNU
Kasumi-2
anti-ROR1 ADC
IC50 (ng/ml)
Trastuzumab 5330.0
2A2 1.2
R12 1.8
XBR1-402 1.2
B
697
Cell viability (RLU)
ADC conc. ng/mL
Tras-G5-PNU
2A2-G5-PNU
R12-Gly5-PNU
XBR1-402-Gly5-PNU
697
anti-ROR1 ADC
IC50 (ng/ml)
Trastuzumab 2987.0
2A2 118.0
R12 160.0
XBR1-402 75.7
C
Kasumi-2
Cell number
ROR1
D
697
Cell number
ROR1

FIG. 14

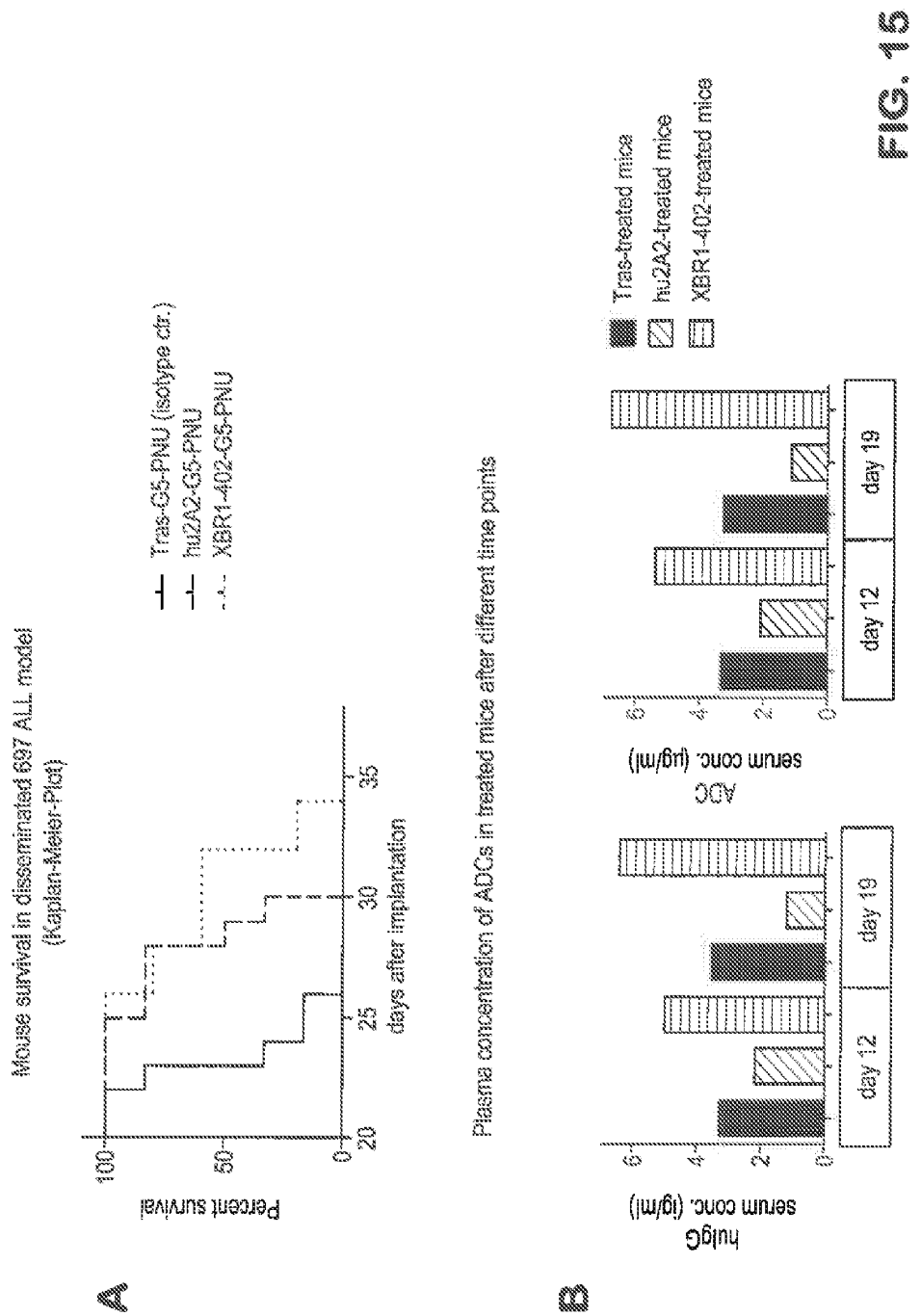

A
Mouse survival in disseminated 697 ALL model
(Kaplan-Meier-Plot)
Tras-G5-PNU (isotype ctr.)
hu2A2-G5-PNU
XBR1-402-G5-PNU
Percent survival
100
50
0
20
25
30
35
days after implantation
B
Plasma concentration of ADCs in treated mice after different time points
Tras-treated mice
hu2A2-treated mice
XBR1-402-treated mice
huIgG
serum conc. (µg/ml)
6
4
2
0
day 12
day 19
ADC
serum conc. (µg/ml)
6
4
2
0
day 12
day 19

FIG. 15

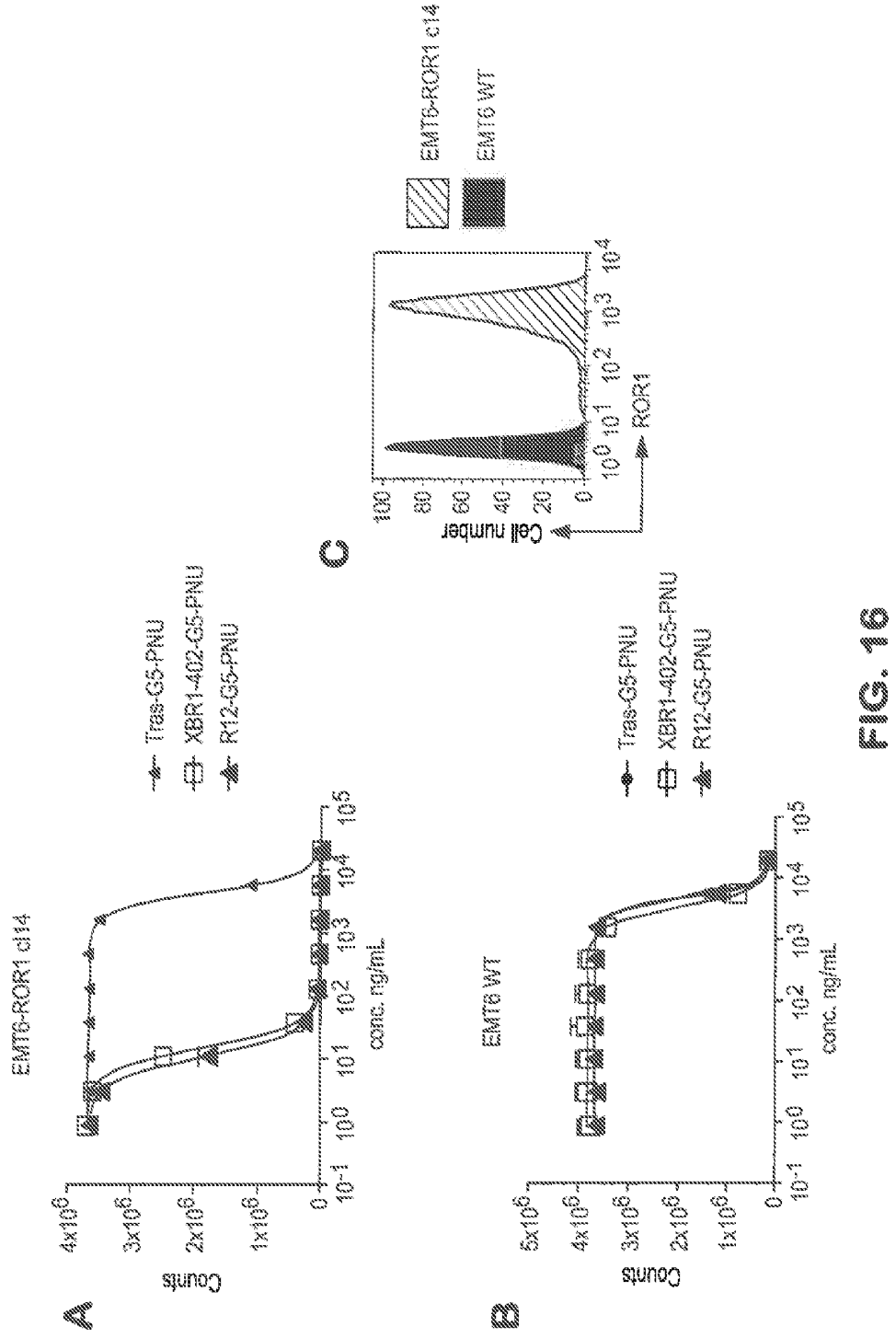

A
EMT6-ROR1 cl14
Tras-G5-PNU
XBR1-402-G5-PNU
R12-G5-PNU
Counts
conc. ng/mL
B
EMT6 WT
C
EMT6-ROR1 c14
EMT6 WT
Cell number
ROR1

FIG. 16

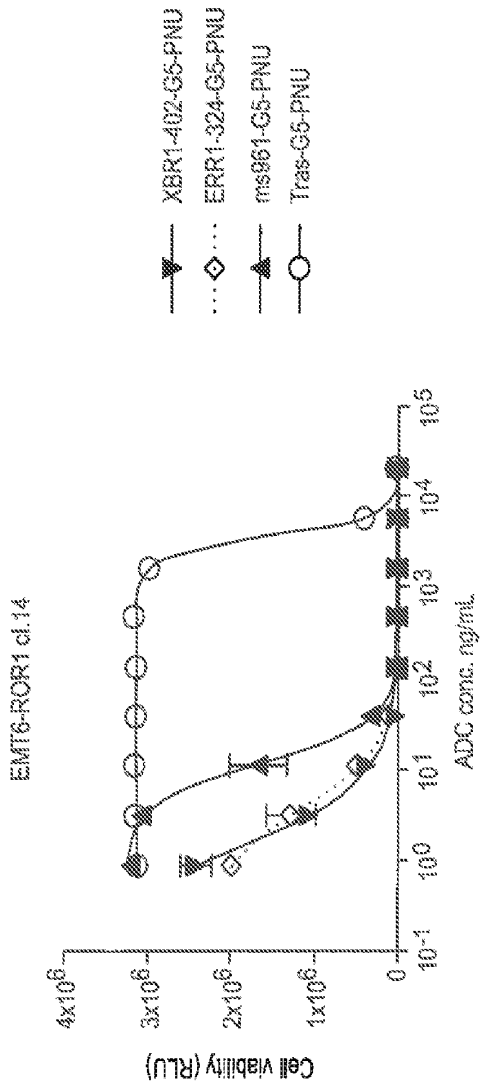

XBR1-402-G5-PNU
ERR1-324-G5-PNU
ms361-G5-PNU
Tras-G5-PNU
EMT6-ROR1 cl.14
Cell viability (RLU)
4x10^6
3x10^6
2x10^6
1x10^6
0
10^-1
10^0
10^1
10^2
10^3
10^4
10^5
ADC conc. ng/mL

FIG. 17

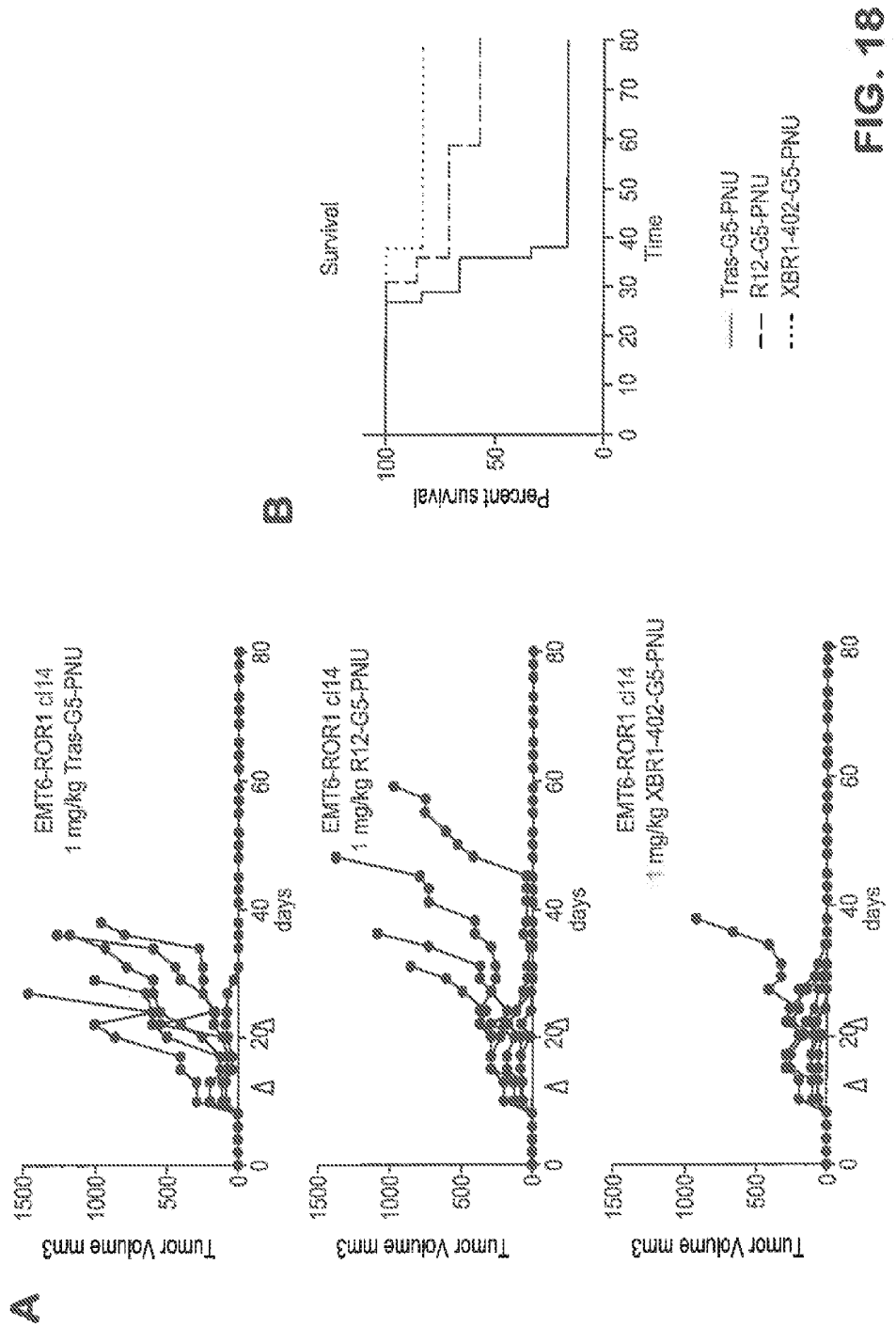

A
EMT6-ROR1 cl14
1 mg/kg Tras-G5-PNU
EMT6-ROR1 cl14
1 mg/kg R12-G5-PNU
EMT6-ROR1 cl14
1 mg/kg XBR1-402-G5-PNU
Tumor Volume mm3
days
B
Survival
Percent survival
Time
Tras-G5-PNU
R12-G5-PNU
XBR1-402-G5-PNU

FIG. 18

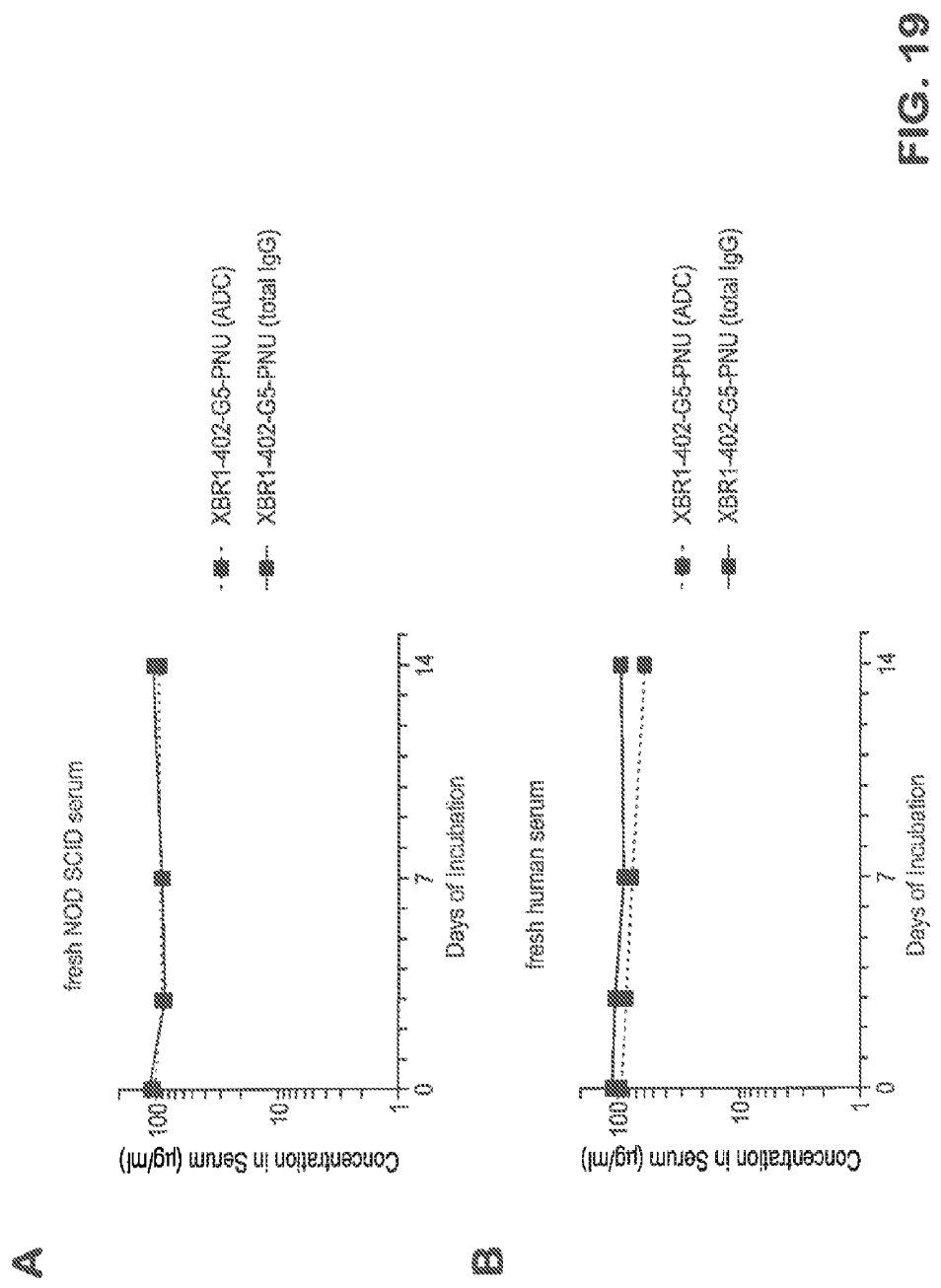

A
fresh NOD SCID serum
Concentration in Serum (µg/ml)
100
10
1
0
7
14
Days of Incubation
XBR1-402-G5-PNU (ADC)
XBR1-402-G5-PNU (total IgG)
B
fresh human serum
Concentration in Serum (µg/ml)
100
10
1
0
7
14
Days of Incubation
XBR1-402-G5-PNU (ADC)
XBR1-402-G5-PNU (total IgG)

FIG. 19

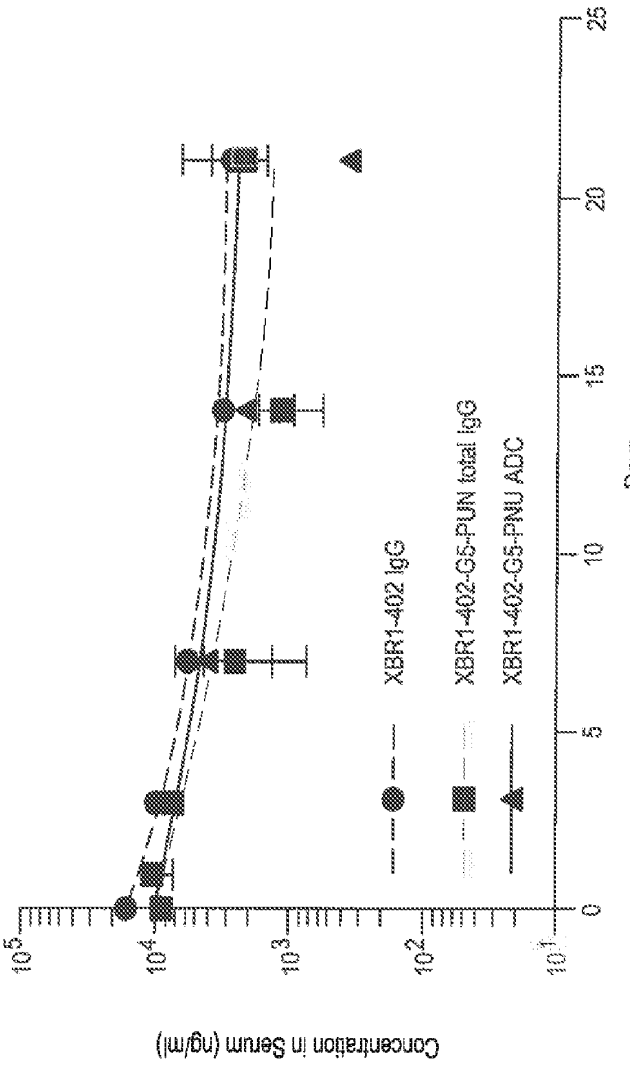

Concentration in Serum (ng/ml)
10^5
10^4
10^3
10^2
10^1
0
5
10
15
20
25
Days
XBR1-402 IgG
XBR1-402-G6-PUN total IgG
XBR1-402-G5-PNU ADC

FIG. 20

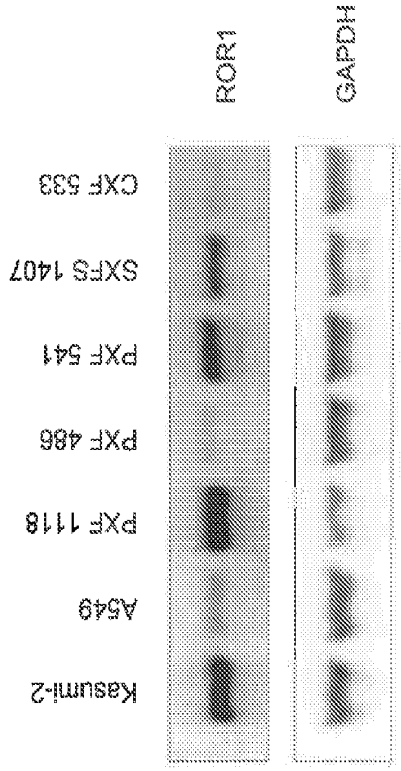

ROR1
GAPDH
CXF 533
SXFS 1407
PXF 541
PXF 486
PXF 1118
A549
Kasumi-2

FIG. 21

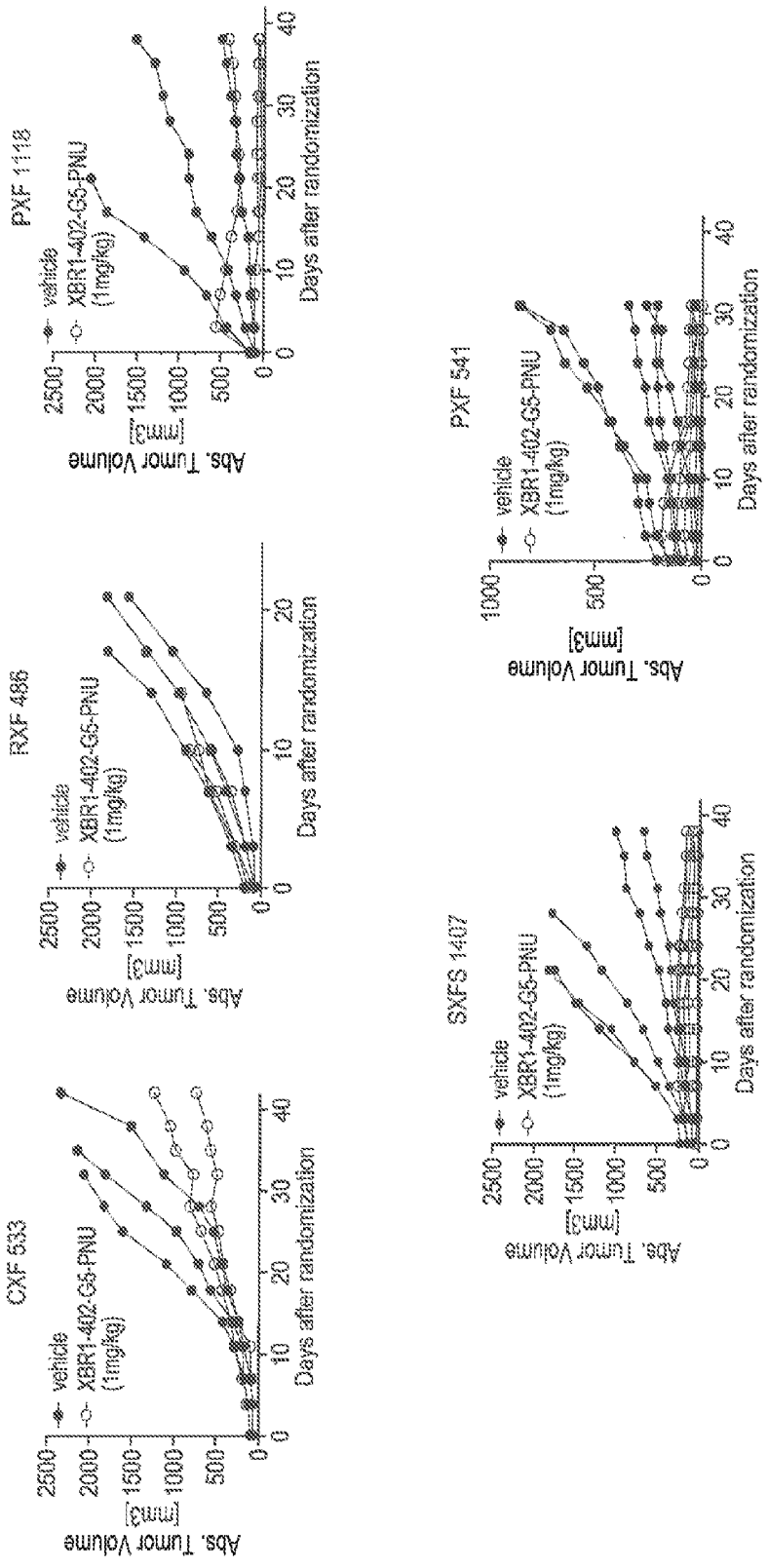

CXF 533
RXF 486
PXF 1118
SXFS 1407
PXF 541
vehicle
XBR1-402-G5-PNU (1mg/kg)
Abs. Tumor Volume [mm3]
Days after randomization

FIG. 22

ROR1 mAbs

V_λ

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 22	34	46	56	87	97 107	
XBR1-402	SYELTQPLSVSVALGQTARITC	EGNNIGSKAVH	WYQQKPGQAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRAQAGDEADYYC	QVWDSSAYV	FGSGTKLTVLG
huXBR1-402-3	SYELTQPLSVSVALGQTARITC	EGNNIGSKAVH	WYQQKPGQAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRAQAGDEADYYC	QVWDSSAYV	FGSGTKLTVLG
huXBR1-402-8	SYELTQPSVSVAPGETAIITC	EGNNIGSKAVH	WYQQKPGLSVVLVIY	EDSERPS	GIPERFSGSNSGNTATLTVSGTQAMDEADYYC	QVWDSSAYV	FGSGTKLTVLG
huXBR1-402-15	SYELTQPSVSVAPGQTARITC	EGNNIGSKAVH	WYQQKPGQAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRVEAGDEADYYC	QVWDSAYV	FGSGTKLTVLG
huXBR1-402-17	SYELTQPPSVSVAPGQTARITC	EGNNIGSKAVH	WYQQKPGQAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRVEAGDEADYYC	QVWDSSAYV	FGSGTKLTVLS
huXBR1-402-19	SYELTQPDVSVSPGETAIITC	EGNNIGSKAVH	WYQQKPGQAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRVEAGDEADYYC	QVWDSSAYV	FGSGTKLTVLG
huXBR1-402-26	SYELTQLLSVSVALGQTARITC	EGNNIGSKAVH	WYQQKPGLAPVLVIY	EDSERPS	GIPERFSGSNSGNTATLTISRAQAGDEADYYC	QVWDSSAYV	FGSGTKLTVLG

V_H

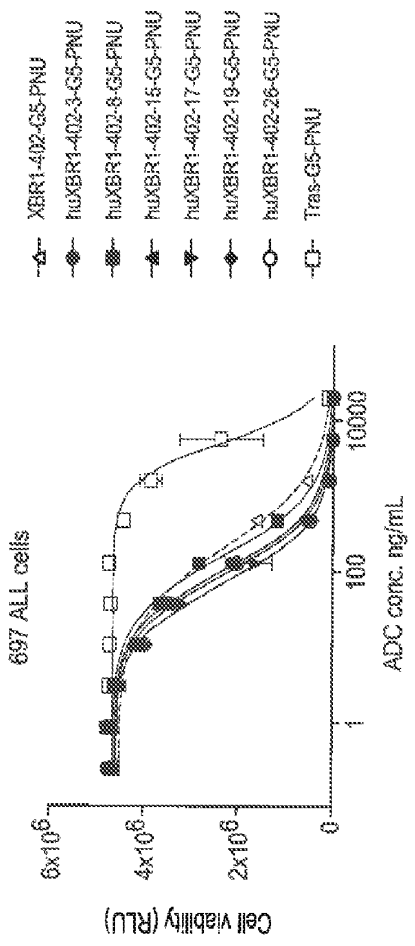
	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	1 30	36	49	66	97	107	117
XBR1-402	QEQQKESGGRLVKPTDTLTLTCTASGFDIS	SYYMS	WVRQAPGKGLEWIG	AIGISGMAYYASWAKG	RSTTRNTMDLKMTSLTTADTATYFCAR	DMPTYGMDL	WGPGTLVTVSS
huXBR1-402-3	QVQLRESGPGLVKPSETLSLTCTVSGFDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKS	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTMVTVSS
huXBR1-402-8	QVQLQESGPGLVKPSETLSLTCTVSGTDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKS	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTLVTVSS
huXBR1-402-15	QVQLQESGPGLVKPSETLSLTCTVSGFDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKG	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTLVTVSS
huXBR1-402-17	QVQLQESGPGLVKPSETLSLTCTVSGFDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKG	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTLVTVSS
huXBR1-402-19	QVQLQESGPGLVKPSETLSLTCTVSGFDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKS	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTLVTVSS
huXBR1-402-26	QVQLQESGPGLVKPSETLSLTCTVSGFDIS	SYYMS	WVRQPPGKGLEWIG	AIGISGMAYYASWAKS	RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR	DMPTYGMDL	WGPGTLVTVSS

FIG. 23

ADC clone	T20 score HC	T20 score LC	K_{on} ($10^{4}M^{-1}s^{-1}$)	K_{off} ($10^{-3}s^{-1}$)	K_D (nM)
XBR1-402*1	60.64	78.85	116	5.91	5.1
XBR1-402*1	60.64	78.85	110	5.56	5.1
huXBR1-402-3	80.34	89.26	119	3.75	3.2
huXBR1-402-8	81.20	82.75	129	2.76	2.1
huXBR1-402-15	81.20	91.15	111	3.94	3.5
huXBR1-402-17	80.34	91.15	96	3.22	3.4
huXBR1-402-19	80.30	91.15	111	3.32	3.0
huXBR1-402-28	80.30	86.56	105	3.28	3.1

*1: two independent measurements

FIG. 24



B

ADC clone	IC_{50}
XBR1-402-G5-PNU	211.6
huXBR1-402-3-G5-PNU	98.1
huXBR1-402-8-G5-PNU	164.2
huXBR1-402-15-G5-PNU	105.6
huXBR1-402-17-G5-PNU	70.6
huXBR1-402-19-G5-PNU	91.7
huXBR1-402-26-G5-PNU	93.9
Trastuzumab-G5-PNU	5214

FIG. 25

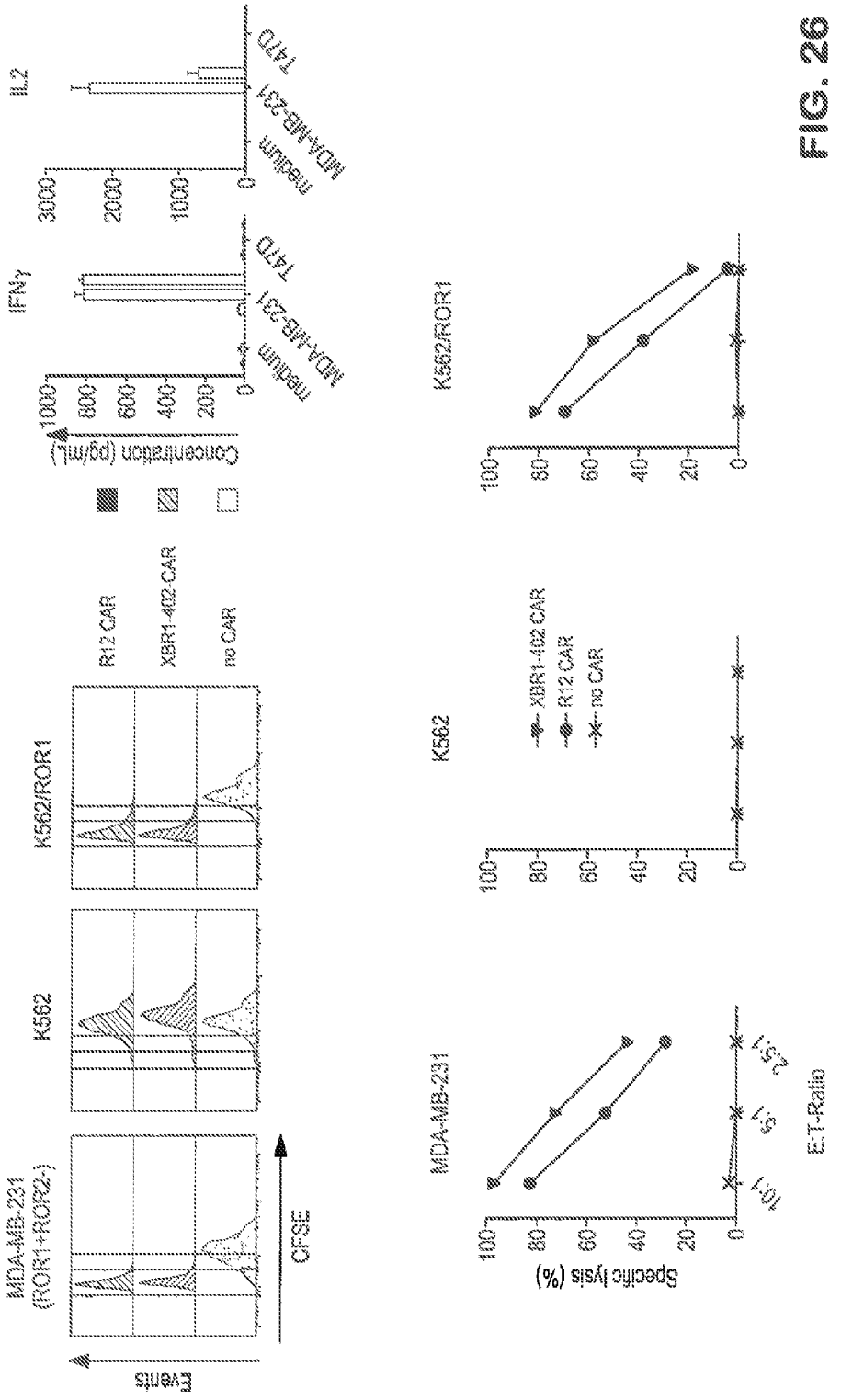

MDA-MB-231 (ROR1+ROR2-)
K562
K562/ROR1
R12 CAR
XBR1-402-CAR
no CAR
CFSE
Events
Concentration (pg/mL)
IFNγ
IL2
medium
MDA-MB-231
1:1
MDA-MB-231
K562/ROR1
K562
XBR1-402 CAR
R12 CAR
no CAR
Specific lysis (%)
E:T-Ratio
10:1
5:1
2.5:1

FIG. 26

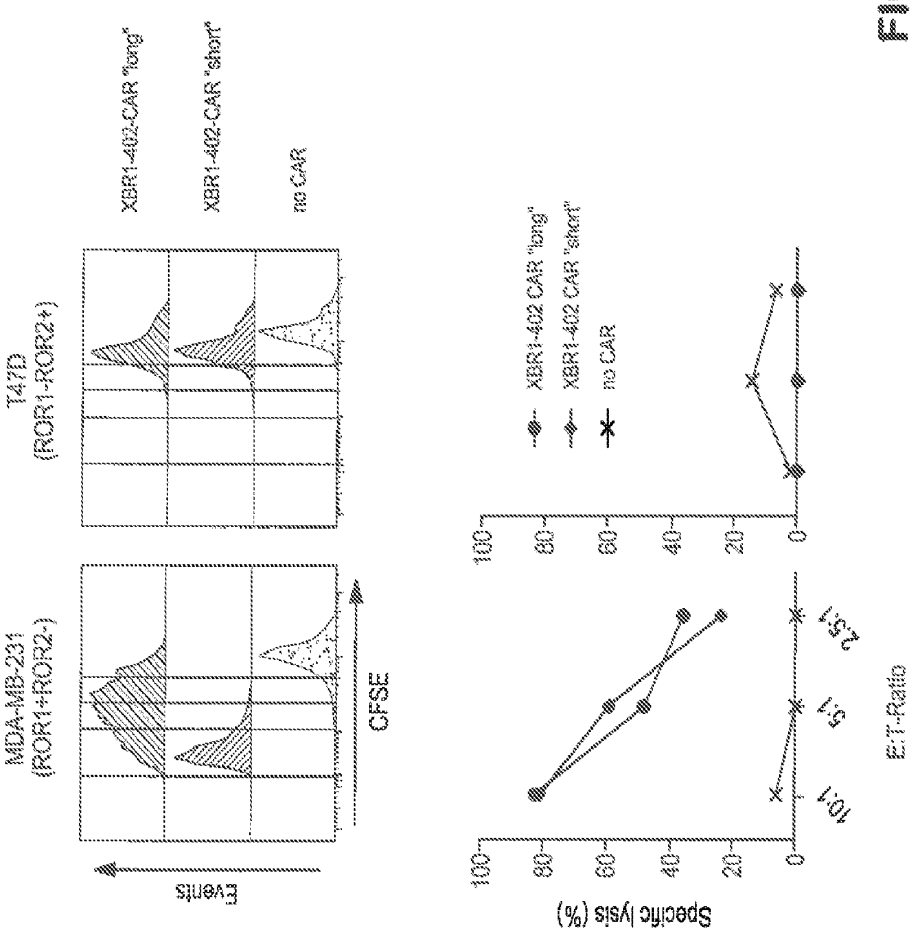

XBR1-402-CAR "long"
XBR1-402-CAR "short"
no CAR
T47D
(ROR1-ROR2+)
MDA-MB-231
(ROR1+ROR2-)
CFSE
Events
XBR1-402 CAR "long"
XBR1-402 CAR "short"
no CAR
Specific lysis (%)
E:T-Ratio
10:1
5:1
2.5:1
0
20
40
60
80
100

FIG. 27

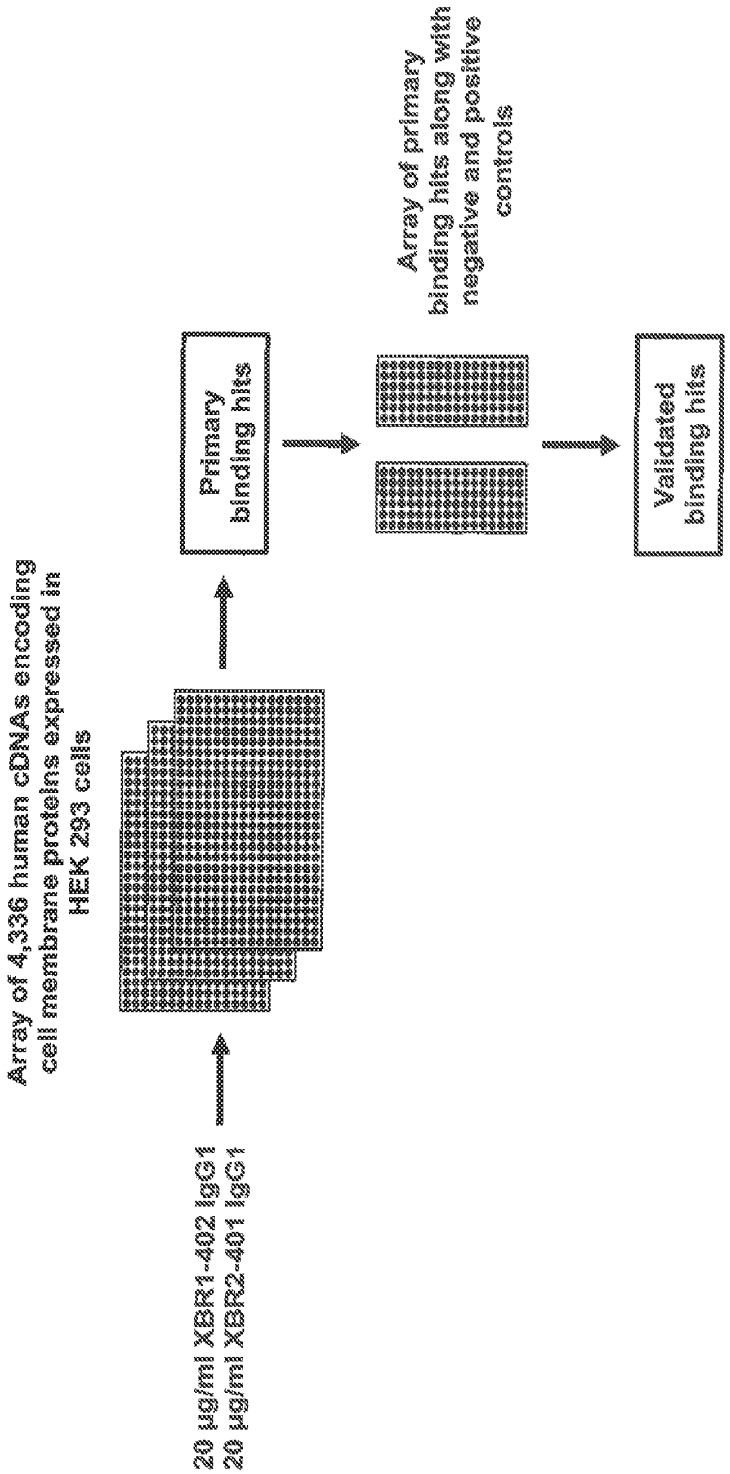

20 µg/ml XBR1-402 IgG1
20 µg/ml XBR2-401 IgG1
Array of 4,336 human cDNAs encoding cell membrane proteins expressed in HEK 293 cells
Primary binding hits
Array of primary binding hits along with negative and positive controls
Validated binding hits

FIG. 28

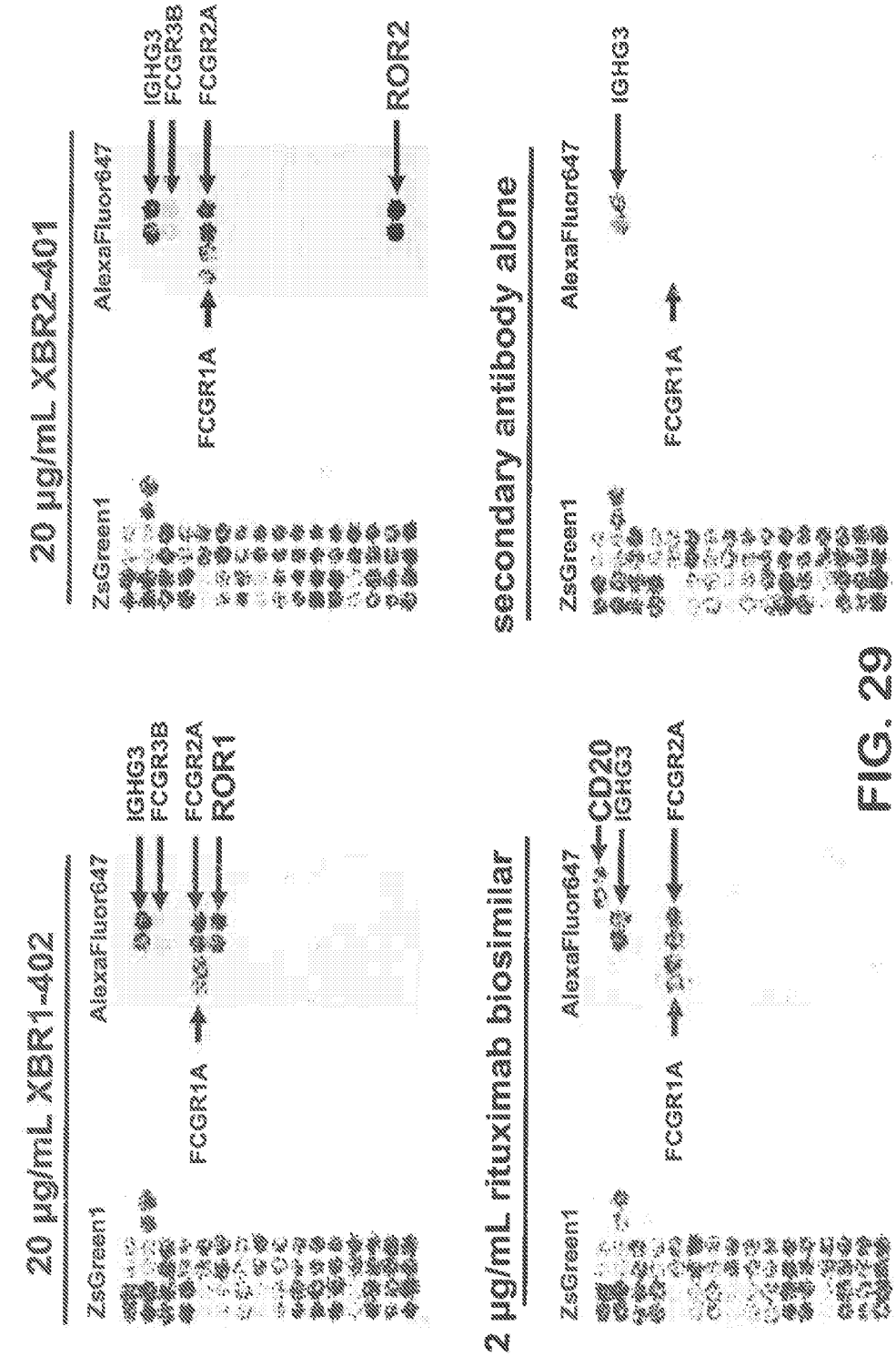

20 µg/mL XBR1-402
ZsGreen1
AlexaFluor647
IGHG3
FCGR3B
FCGR2A
ROR1
FCGR1A
20 µg/mL XBR2-401
ZsGreen1
AlexaFluor647
IGHG3
FCGR3B
FCGR2A
FCGR1A
ROR2
2 µg/mL rituximab biosimilar
ZsGreen1
AlexaFluor647
CD20
IGHG3
FCGR1A
FCGR2A
secondary antibody alone
ZsGreen1
AlexaFluor647
IGHG3
FCGR1A

FIG. 29