Figure1

MF nr	Specificity	VH Sequence
1337	TT	EVQLVETGAEVKKPGASVKVSCKASDYIFTKYDINWVRQAPGQGLEWMGWMSANTGNTGYAQKFQGRVTMTRDTSINTAYMELSSLTSGDTAVYFCARSSLFKTETAPYYHFALDVWGQGTTVTVSS
3370	EGFR	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRHWHWWLDAFDYWGQGTLVTVSS
3755	EGFR	QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGWINANTGDPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGQGTLVTVSS
4297	cMet	EVQLVESGGGLVKPGGSLRLSCAASGFTFSKAWMNWVRQAPGKGLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTASSMITFGGVIVSWFDPWGQGTLVTVSS
4356	cMet	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYSMNWVRQAPGQGLEWMGWINTYTGDPTYAQGFTGRYVFSLDTSVNTAYLQISSLKAEDTAVYYCARETYYYDRGGYPFDPWGQGTLVTVSS
2708	RSV-G	EVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGSTKYSADSLKGRFTISRDNSKNTLYLQMNSLRADDTAVYYCAKEGWSFDSSGYRSWFDSWGQGTLVTVSS

MF nr:	Specificity	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
1337	TT	EVQLVETGAEVKKPG ASVKVSCKASDYIFT	KYDIN	WVRQAPGQGLEWMG	WMSANTGNTGYAQKFQG	RVTMTRDTSINTAYMEL SSLTSGDTAVYFCAR	SSLFKTETAPYYHFALDV	WGQGTTVTVSS
3370	EGFR	QVQLVQSGAEVKKPG ASVKVSCKASGYTFT	SYGIS	WVRQAPGQGLEWMG	WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMEL RSLRSDDTAVYYCAK	DRHWHWWLDAFDY	WGQGTLVTVSS
3755	EGFR	QVQLVQSGSELKKPG ASVKISCKASGYDFT	NYAMN	WVRQAPGHGLEWMG	WINANTGDPTYAQGFTG	RFVFSLDTSVSTAYLQI SSLKAEDSAVYYCTR	ERFLEWLHFDY	WGQGTLVTVSS
4297	cMET	EVQLVESGGGLVKPG GSLRLSCAASGFTFS	KAWMN	WVRQAPGKGLEWVG	RIKSKTDGGTTDYAAPVKG	RFTISRDDSKNTLYLQM NSLKTEDTAVYYCTT	ASSMITFGGVIVSWFDP	WGQGTLVTVSS
4356	cMET	QVQLVQSGSELKKPG ASVKVSCKASGYTFT	SYSMN	WVRQAPGQGLEWMG	WINTYTGDPTYAQGFTG	RYVFSLDTSVNTAYLQI SSLKAEDTAVYYCAR	ETYYYDRGGYPFDP	WGQGTLVTVSS
2708	RSV-G	EVQLVESGGGVVQPG RSLRLSCAASGFTFS	NYGMH	WVRQAPGKGLEWVA	VISYDGSTKYSADSLKG	RFTISRDNSKNTLYLQM NSLRADDTAVYYCAK	EGWSFDSSGYRSWFDS	WGQGTLVTVSS

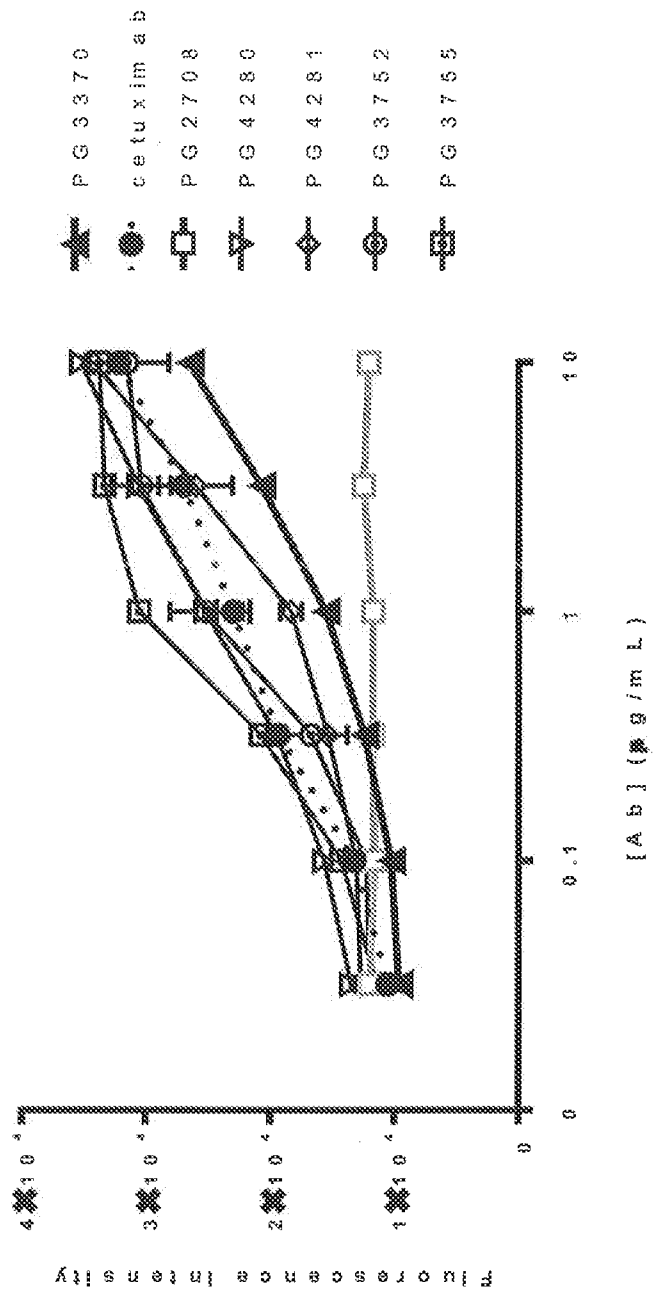

PG3370
cetuximab
PG2708
PG4280
PG4281
PG3752
PG3755
fluorescence intensity
4*10^4
3*10^4
2*10^4
1*10^4
0
0
0.1
1
10
[Abl] (μg/mL)

Figure 2

Figure 3

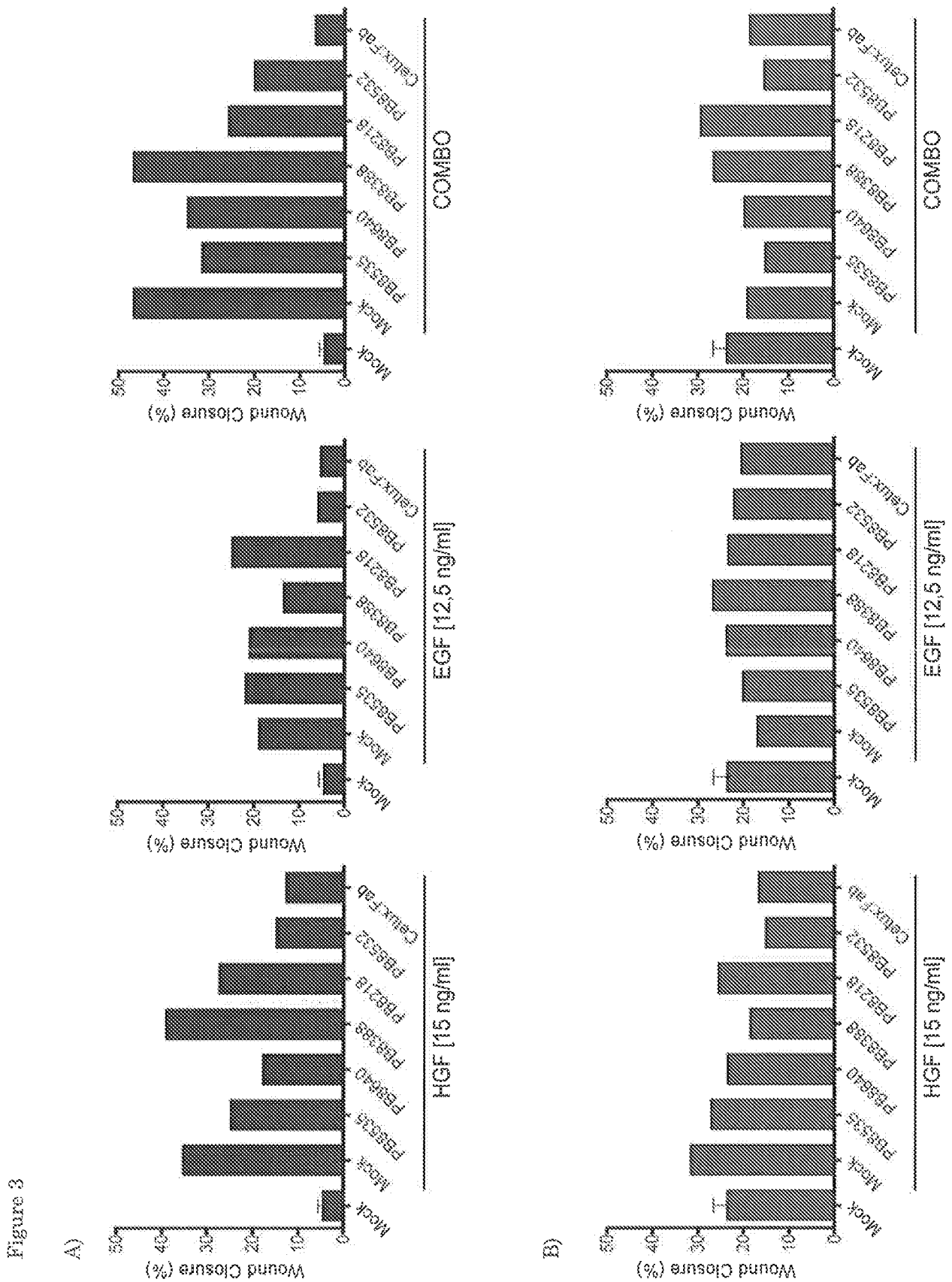

A)
B)
Wound Closure (%)
HGF [15 ng/ml]
EGF [12,5 ng/ml]
COMBO
Mock
Mock
PBS535
PBS540
PBS358
PBS218
PBS532
Celux'Fab

Figure 4

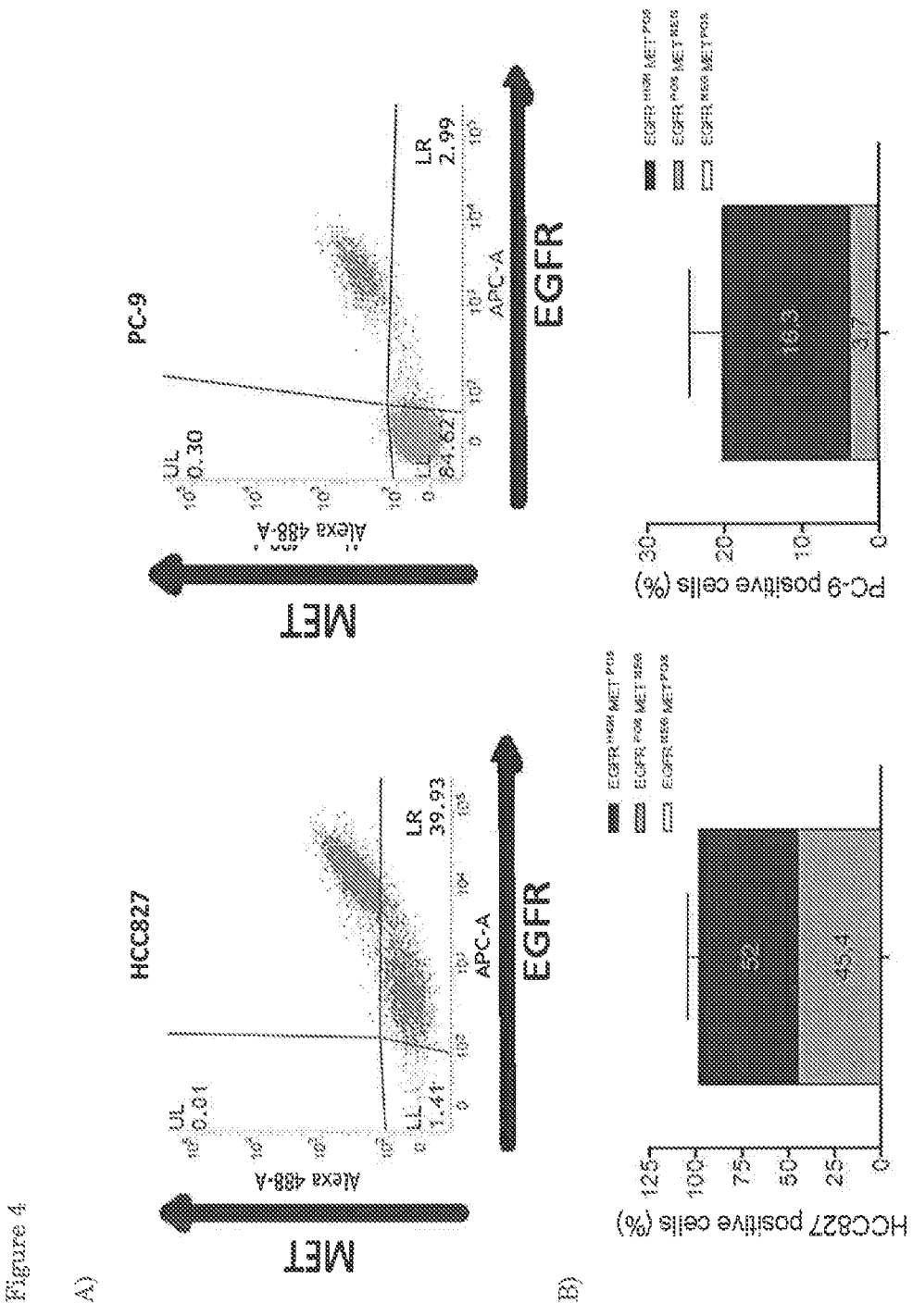
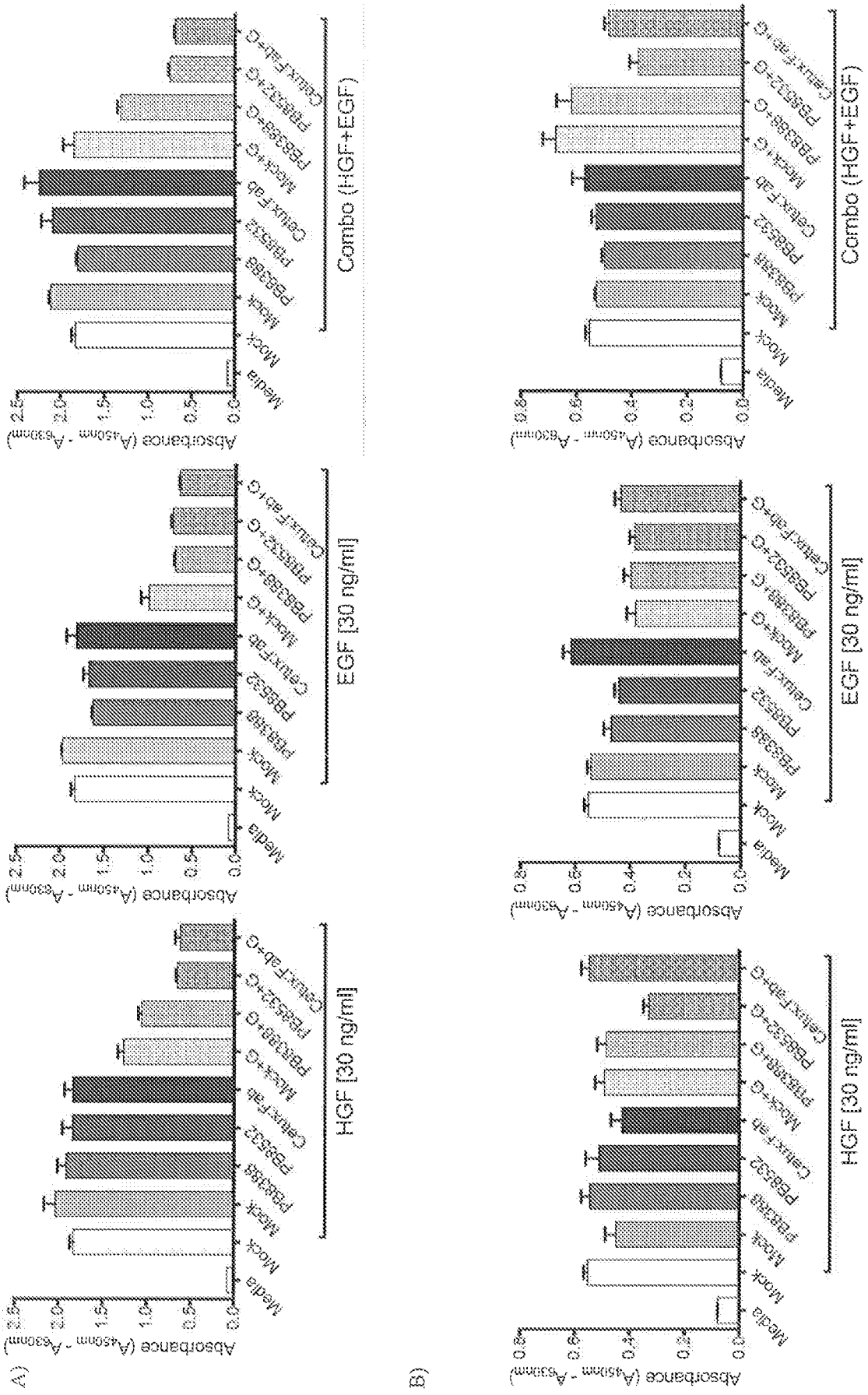

A)
HCC827
PC-9
MET
EGFR
Alexa 488-A
APC-A
UL 0.01
LL 1.41
LR 39.93
UL 0.30
LL 84.62
LR 2.99
B)
HCC827 positive cells (%)
PC-9 positive cells (%)
EGFR HIGH MET POS
EGFR POS MET HIGH
EGFR HIGH MET POS
EGFR POS MET HIGH
EGFR HIGH MET POS
EGFR POS MET HIGH

Figure 5


A)
B)
Absorbance (A_{450nm} - A_{630nm})
Media
Mock
Mock
PB8388
PB8532
Cetux.Fab
Mock+G
PB8388+G
PB8532+G
Cetux.Fab+G
HGF [30 ng/ml]
EGF [30 ng/ml]
Combo (HGF+EGF)

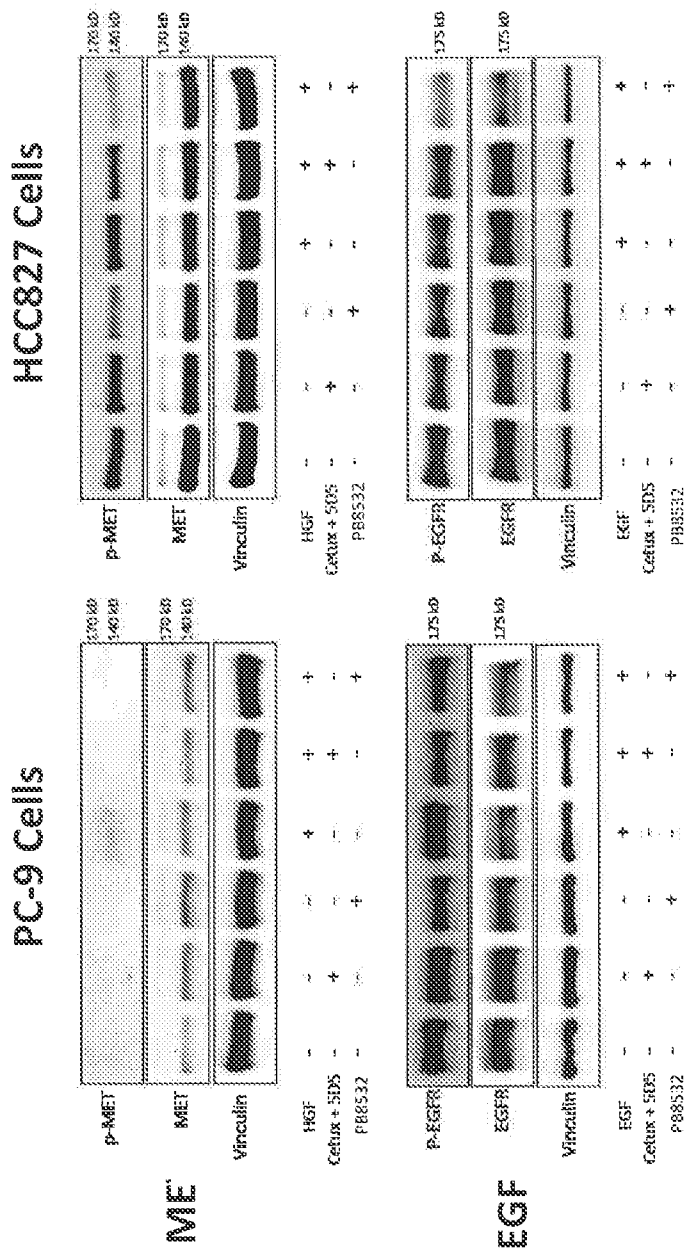

PC-9 Cells
HCC827 Cells
MET
EGF
p-MET
MET
Vinculin
p-EGFR
EGFR
HGF
Cetux + SDS
PBS532
EGF

Figure 6

Figure 7

```
MF3353          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8229          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8228          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF3370          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8233          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8232          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF3393          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8227          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
MF8226          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
                ************************************************

MF3353          ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDS
MF8229          ISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDS
MF8228          ISAYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDS
MF3370          ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDR
MF8233          ISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDR
MF8232          ISAYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDR
MF3393          ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGY
MF8227          ISAYNANTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGY
MF8226          ISAYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGY
                ****.**********************************************.

MF3353          YWHWWLGAFDYWGQGTLVTVSS
MF8229          YWHWWLGAFDYWGQGTLVTVSS
MF8228          YWHWWLGAFDYWGQGTLVTVSS
MF3370          HWHWWLDAFDYWGQGTLVTVSS
MF8233          HWHWWLDAFDYWGQGTLVTVSS
MF8232          HWHWWLDAFDYWGQGTLVTVSS
MF3393          LDHWWLGAFDYWGQGTLVTVSS
MF8227          LDHWWLGAFDYWGQGTLVTVSS
MF8226          LDHWWLGAFDYWGQGTLVTVSS
                  ****.***************
```

Figure 8

```
MF8225          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYSLNWVRQAPGQGLEWMGW
MF8243          QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAPGQGLEWMGW
MF8224          QVQLMQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8239          QVQLVQSGSELKKPGASVKVSCKASGYTFTDYAMNWVRQVPGQGLEWMGW
MF8242          QVQLVQSGSELKKPGASVKVSCKASGYTFTNYAMNWVRQAPGQGLEWMGW
MF8237          QVQLVQSGSELKKPGASVKVSCKASGYTFTSFGMSWVRQAPGQGLEWMGW
MF8240          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8234          QVQLVQSGSELEKPGASVKVSCKASGYTFISYAMNWVRQAPGQGLEWMGW
MF8245          QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAVNWVRQAPGQGLEWMGW
MF8231          QVQVVQSGSEVKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8247          QVQLVQSGSELKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGW
MF8238          QVQLVQSGSELEKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8230          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8248          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYAINWVRQAPGQGLEWMGW
MF8246          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYAMNWVRQAPGQGLEWMGW
MF8223          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYAMNWVRQAPGQGLEWMGW
MF8222          QVELVQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8235          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8236          QVQLVQSGSELKKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8241          QVQLVQSGSELEKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8244          QVQLVQSGSELEKPGASVKVSCKASGYTFTTYSMNWVRQAPGQGLEWMGW
MF8221          QVQLVQSGSELKKPGASVKVSCKASGYTFTDYAMNWVRQAPGQGLEWMGW
MF4356          QVQLVQSGSELKKPGASVKVSCKASGYTFTSYSMNWVRQAPGQGLEWMGW
                **:::*****;;******************  :.:.****.**********

MF8225          INTYTGNPTYAQGFTGRFVFFLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8243          INTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8224          INTNTGNPTYAQDFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8239          INTYTGNPTYVQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8242          INTNTGNPTYAQGFTGRFVFPLDTSVSTTYLQISSLKAEDTAVYYCARET
MF8237          INTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQINSLKAEDTAVYYCARES
MF8240          INTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLNTEDTAVYYCARET
MF8234          INTYTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8245          INTYTGNPTYAQGFTGRFVFSSDTSVNTAYLQISSLKAEDTAVYYCARET
MF8231          INTYTGDPTYVQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8247          INTYTGNPTYVQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8238          INTYTGSPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAIYYCARET
MF8230          INTYTGDPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8248          INTNTGNPTYAQGFTGRFVFSLDTSVSTAHLQISSLKAEDTAVYYCARET
MF8246          INTYTGDPTYAQGFTGRFVFSLDTSVNTAYLQISSLKAEDTAVYYCARET
MF8223          INTNTGNPTYAQGFTGRFVFSLDTSDSTAFLQISSLKAEDTAVYYCARET
MF8222          INTNTGTPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8235          INTNTGTPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8236          INTYTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLTTEDTAVYYCARET
MF8241          INTYTGSPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF8244          INTYTGSPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
```

```
MF8221          INTYTGNPTYVQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARET
MF4356          INTYTGDPTYAQGFTGRYVFSLDTSVNTAYLQISSLKAEDTAVYYCARET
                *** ** ***.*.****:**  *** .*:.***.**.:****:******:

MF8225          YYYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 1)
MF8243          YYYDRGGYPFDPWGQGTLVTVSS (SEQ ID NO: 2)
MF8224          YYYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 3)
MF8239          YYYDSSGFPFDPWGQGTLVTVSS (SEQ ID NO: 4)
MF8242          YYYQSSGYLFDPWGQGTLVTVSS (SEQ ID NO: 5)
MF8237          YYYDRNDYPFDPWGQGTLVTVSS (SEQ ID NO: 6)
MF8240          YYYDVGGYPFDPWGQGTLVTVSS (SEQ ID NO: 7)
MF8234          YYYDSGGYPFDPWGQGTLVTVSS (SEQ ID NO: 8)
MF8245          YFYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 9)
MF8231          YFYDRGGYPFDPWGQGTLVTVSS (SEQ ID NO: 10)
MF8247          YYYDSSAYPFDPWGQGTLVTVSS (SEQ ID NO: 11)
MF8238          FYFDSGGYPFDPWGQGTLVTVSS (SEQ ID NO: 12)
MF8230          YFYDRGGYPFDPWGQGTLVTVSS (SEQ ID NO: 13)
MF8248          YYYATSGYPFDPWGQGALVTVSS (SEQ ID NO: 14)
MF8246          SYYDRTGYPFDPWGQGTLVTVSS (SEQ ID NO: 15)
MF8223          YYYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 16)
MF8222          YYYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 17)
MF8235          YYYGSSGYPFAPWGQGTLVTVSS (SEQ ID NO: 18)
MF8236          YYYESSGYPFDPWGQGTLVTVSS (SEQ ID NO: 19)
MF8241          YYFDSGDYPFDPWGQGTLVTVSS (SEQ ID NO: 20)
MF8244          YYFDSGGYPFDPWGQGTLVTVSS (SEQ ID NO: 21)
MF8221          YYYDSSGYPFDPWGQGTLVTVSS (SEQ ID NO: 22)
MF4356          YYYDRGGYPFDPWGQGTLVTVSS (SEQ ID NO: 23)
                 ::    : * *****:******
```

Figure 9A:

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYSTPPTFGQGTKVEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 9B:

gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacagagtcacc
D I Q M T Q S P S S L S A S V G D R V T
atcacttgccgggcaagtcagagcattagcagctacttaaattggtatcagcagaaacca
I T C R A S Q S I S S Y L N W Y Q Q K P
gggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatca
G K A P K L L I Y A A S S L Q S G V P S
aggttcagtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacct
R F S G S G S G T D F T L T I S S L Q P
gaagattttgcaacttactactgtcaacagagttacagtaccccctccaacgttcggccaa
E D F A T Y Y C Q Q S Y S T P P T F G Q
gggaccaaggtggagatcaaa
G T K V E I K

Figure 9C:

cgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct
R T V A A P S V F I F P P S D E Q L K S
ggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacag
G T A S V V C L L N N F Y P R E A K V Q
tggaaggtggataacgccctccaatcgggtaactcccaggagagtgtcacagagcaggac
W K V D N A L Q S G N S Q E S V T E Q D
agcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagactacgag
S K D S T Y S L S S T L T L S K A D Y E
aaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaag
K H K V Y A C E V T H Q G L S S P V T K
agcttcaacaggggagagtgttag
S F N R G E C -

Figure 9D

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCQQSYSTPPITFGQGTRLEIK

Figure 9E

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCQQSYSTP

Figure 10A
CH1:

```
gctagcaccaagggcccatcggtcttccccctggcaccctcctccaagagcacctctggg
 A  S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G
ggcacagcggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtgtcg
 G  T  A  A  L  G  C  L  V  K  D  Y  F  P  E  P  V  T  V  S
tggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtcctacagtcctca
 W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S
ggactctactccctcagcagcgtcgtgaccgtgccctccagcagcttgggcacccagacc
 G  L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T
tacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagtt
 Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  R  V
```

Figure 10B
Hinge:

```
gagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca
 E  P  K  S  C  D  K  T  H  T  C  P  P  C  P
```

Figure 10C
CH2:

```
gcacctgaactcctgggggggaccgtcagtcttcctcttccccccaaaacccaaggacacc
 A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T
ctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagac
 L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D
cctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaag
 P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T  K
ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
 P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
 Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A
cccatcgagaaaaccatctccaaagccaaa
 P  I  E  K  T  I  S  K  A  K
```

Figure 10D
CH2 containing L235G and G236R silencing substitutions:

```
gcacctgaactcggcaggggaccgtcagtcttcctcttccccccaaaacccaaggacacc
 A  P  E  L  G  R  G  P  S  V  F  L  F  P  P  K  P  K  D  T
ctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagac
 L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D
cctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaag
 P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T  K
ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
 P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
 Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A
cccatcgagaaaaccatctccaaagccaaa
 P  I  E  K  T  I  S  K  A  K
```

Figure 10E
CH3: KK of DEKK

```
gggcagccccgagaaccacaggtgtacaccaagccccccatcccgggaggagatgaccaag
 G  Q  P  R  E  P  Q  V  Y  T  K  P  P  S  R  E  E  M  T  K
aaccaggtcagcctgaagtgcctggtcaaaggcttctatcccagcgacatcgccgtggag
 N  Q  V  S  L  K  C  L  V  K  G  F  Y  P  S  D  I  A  V  E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
 W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S
gacggctccttcttcctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
 D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
 N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S
ctctccctgtctccgggttga
 L  S  L  S  P  G  -
```

Figure 10F
CH3: DE of DEKK

```
gggcagccccgagaaccacaggtgtacaccgacccccccatcccgggaggagatgaccaag
 G  Q  P  R  E  P  Q  V  Y  T  D  P  P  S  R  E  E  M  T  K
aaccaggtcagcctgacctgcgaggtcaaaggcttctatcccagcgacatcgccgtggag
 N  Q  V  S  L  T  C  E  V  K  G  F  Y  P  S  D  I  A  V  E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
 W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S
gacggctccttcttcctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
 D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
 N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S
ctctccctgtctccgggttga
 L  S  L  S  P  G  -
```

Figure 11

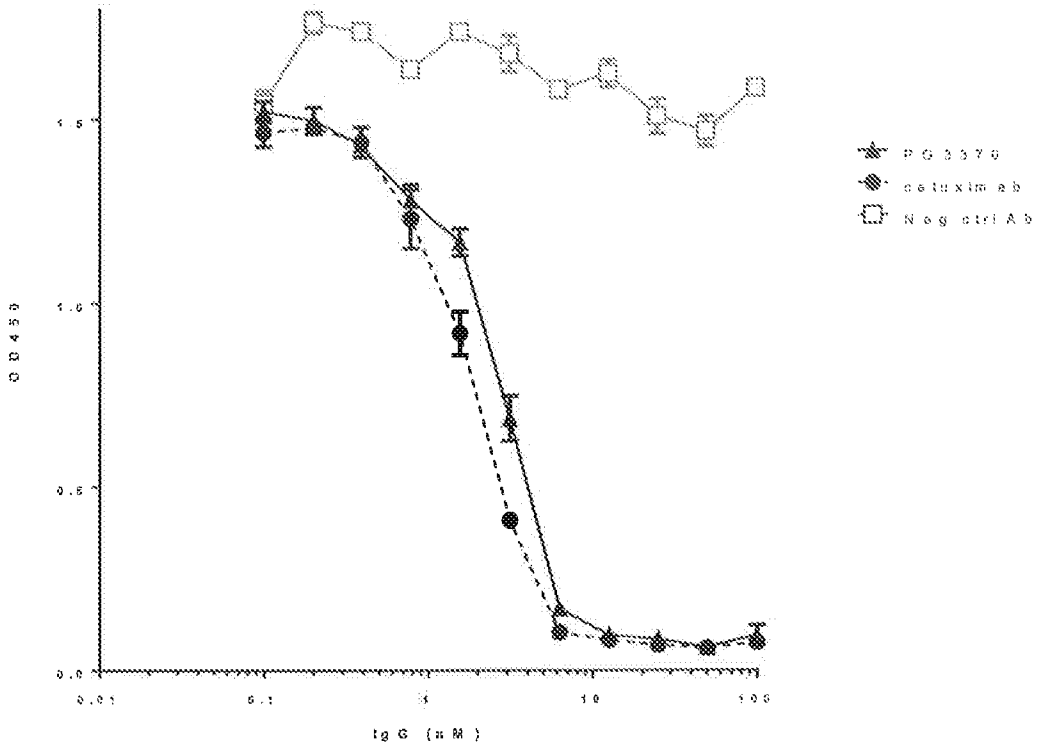
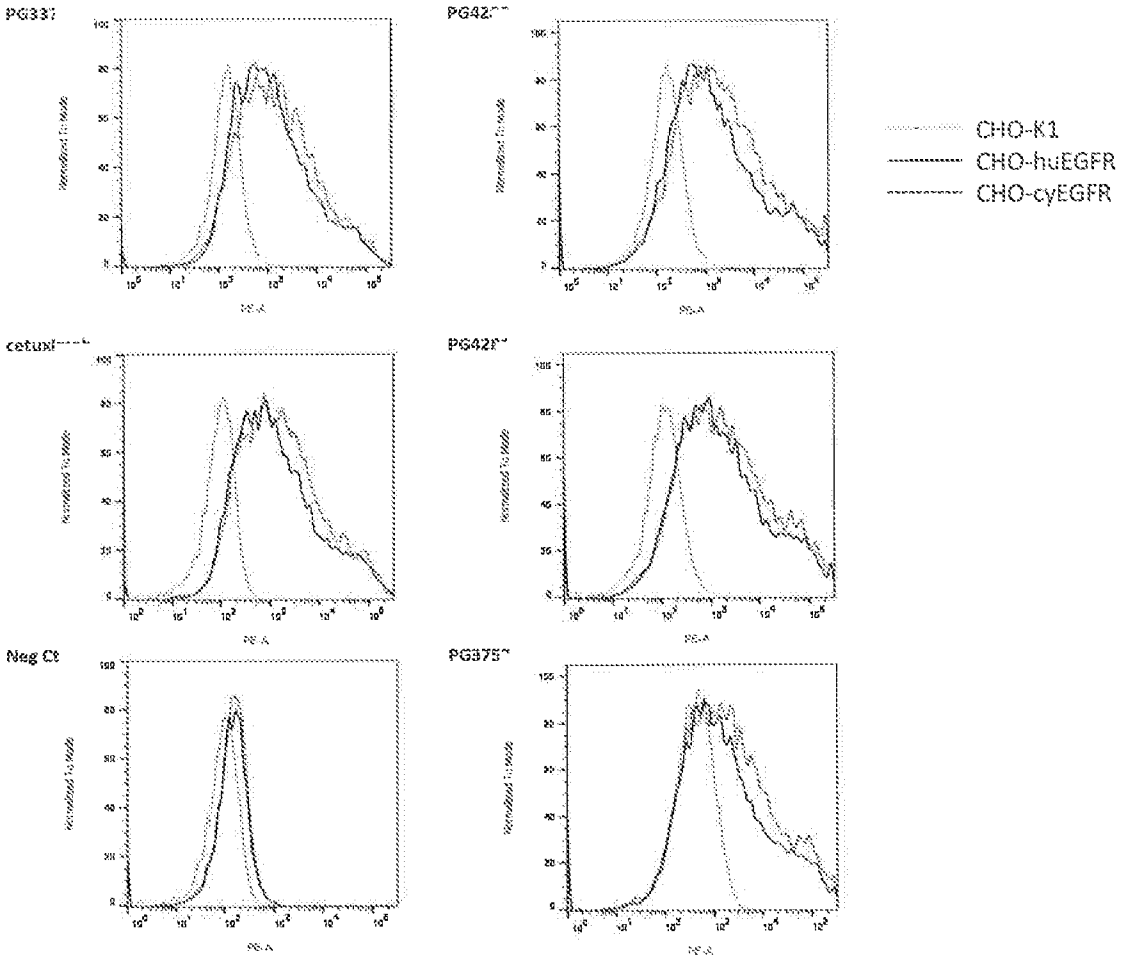

OD450
1.5
1.0
0.5
0.0
0.01
0.1
1
10
100
IgG (nM)
PG3370
cetuximab
Neg ctrl Ab

Figure 12


PG337
PG42
cetuxi
PG42
Neg Ct
PG375
CHO-K1
CHO-huEGFR
CHO-cyEGFR

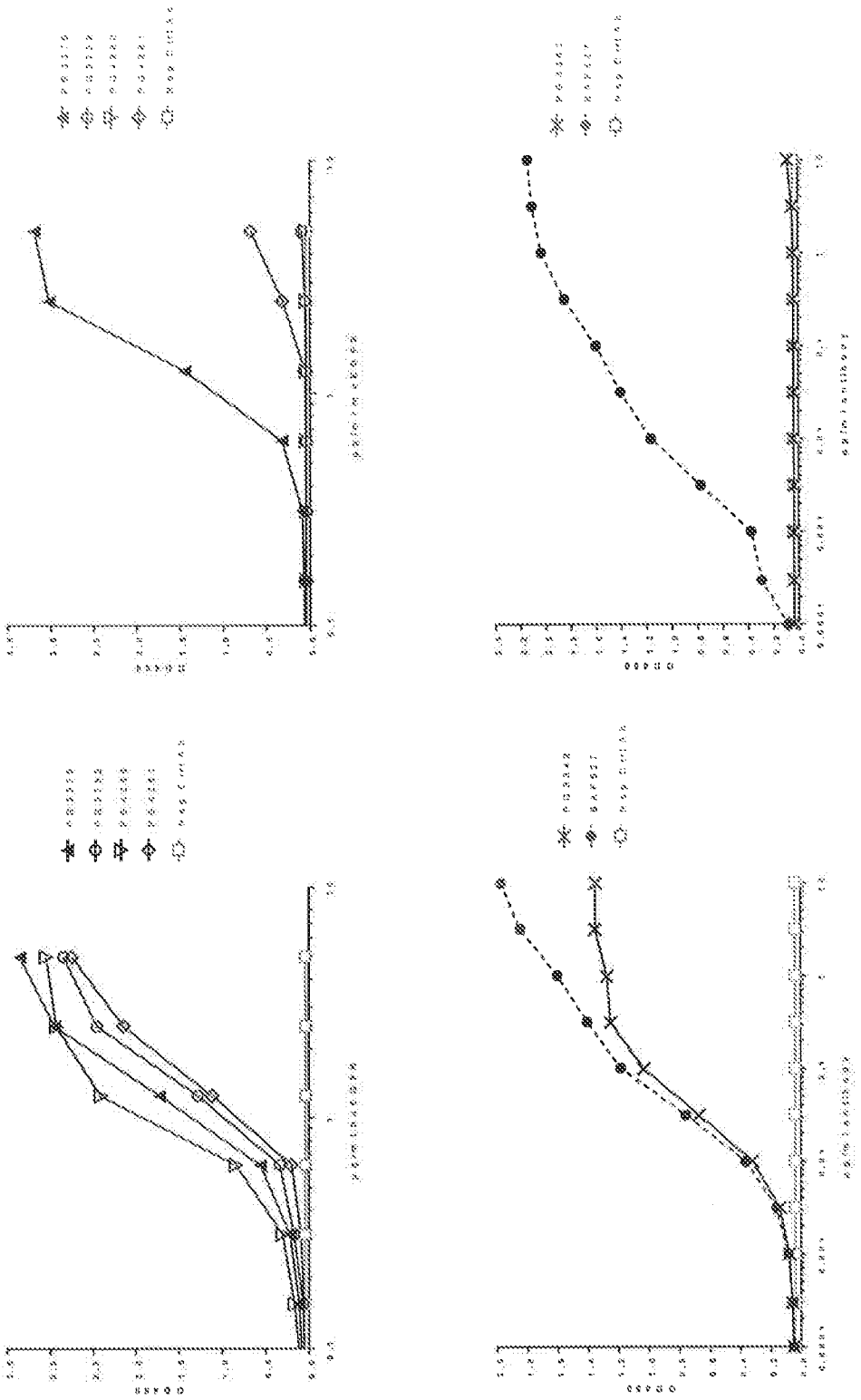


Figure 13

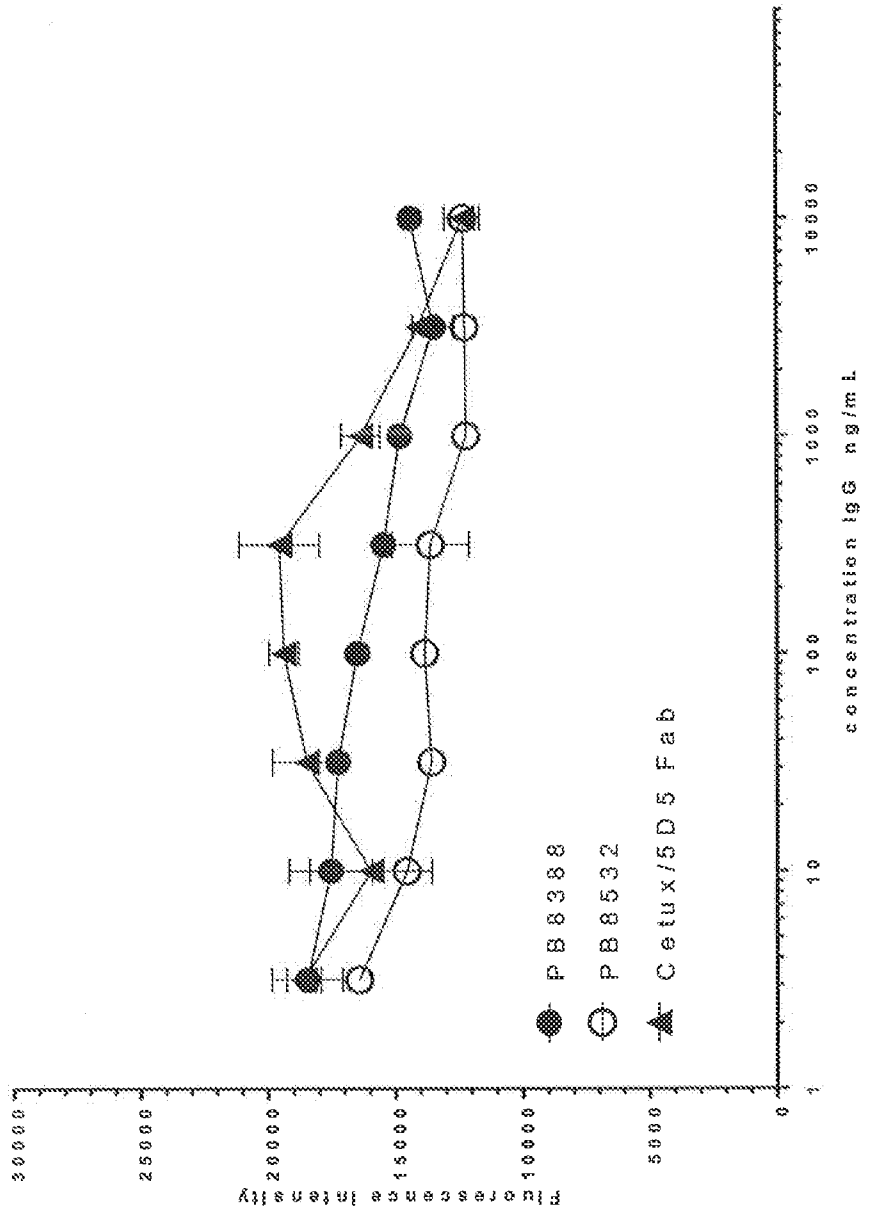

fluorescence intensity
30000
25000
20000
15000
10000
5000
0
1
10
100
1000
10000
concentration IgG ng/mL
PB8388
PB8532
Cetux/5D5 Fab

Figure 14A

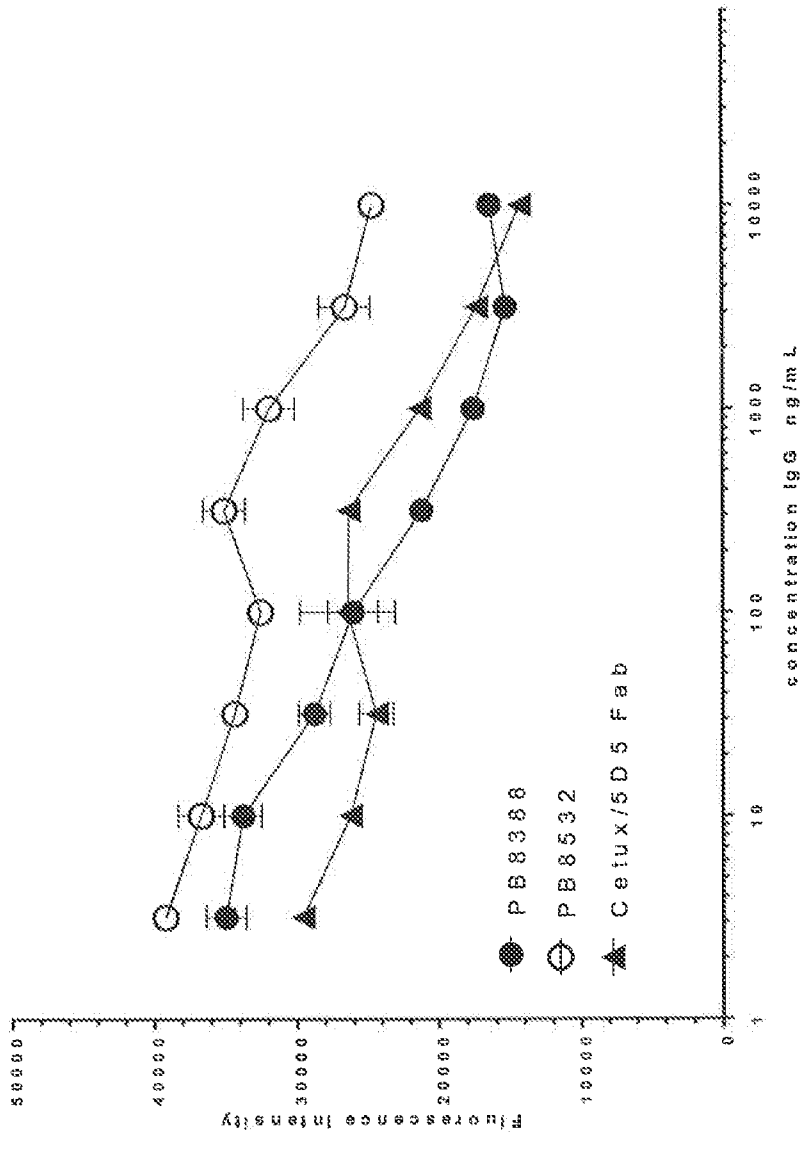

fluorescence intensity
50000
40000
30000
20000
10000
0
1
10
100
1000
10000
concentration IgG ng/mL
PB8386
PB8532
Cetux/5D5 Fab

Figure 14B

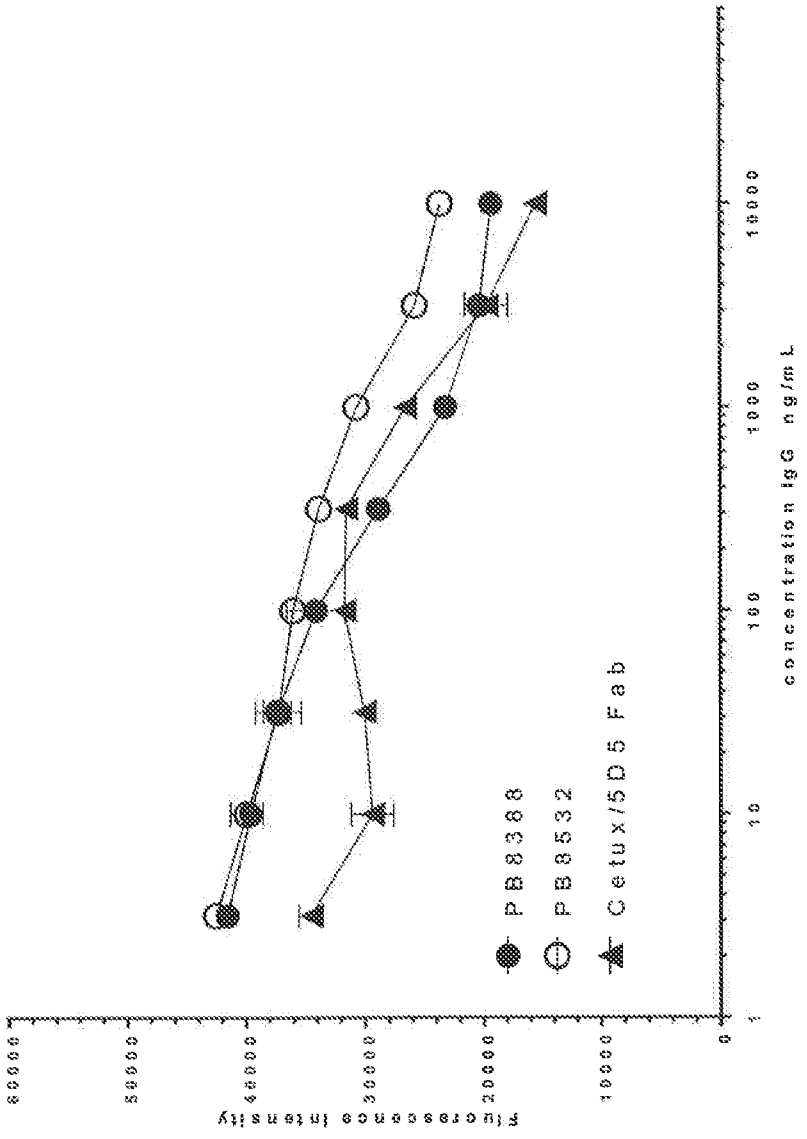
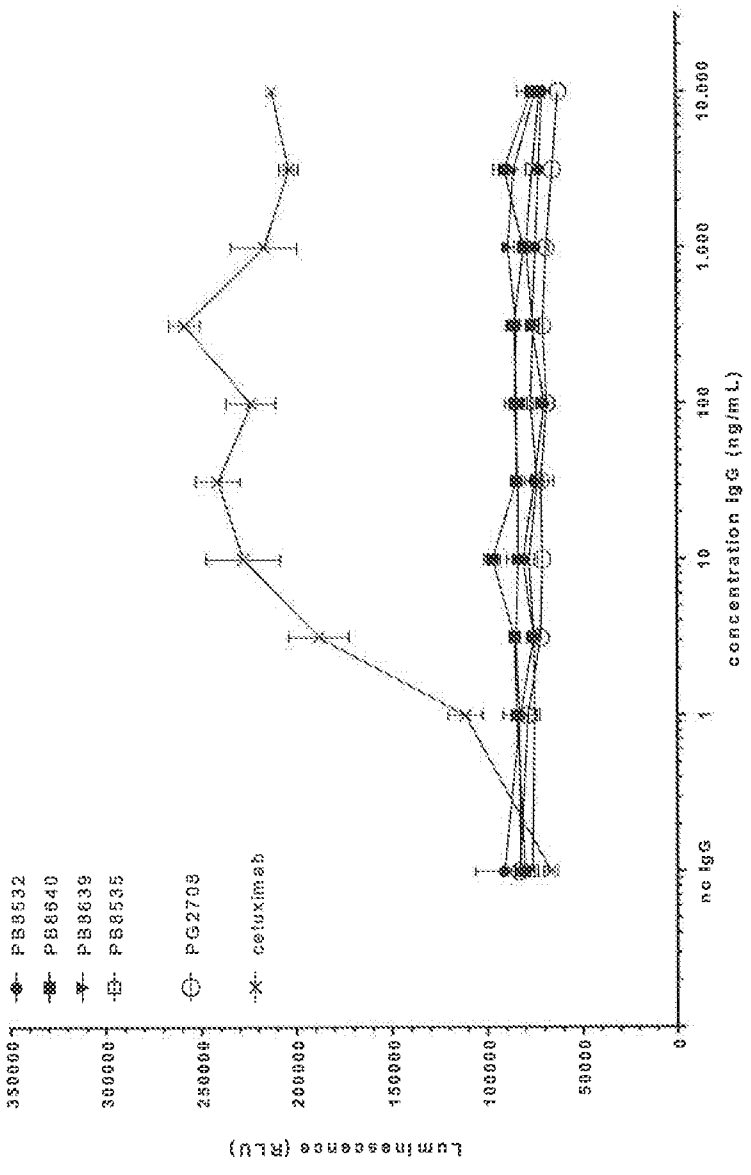

fluorescence intensity
80000
60000
40000
30000
20000
10000
0
1
10
100
1000
10000
concentration IgG ng/mL
PB8368
PB8532
Cetux/5D5 Fab

Figure 14C

Figure 15A


PB3532
PB3540
PB3639
PB3535
PG2703
cetuximab
luminescence (RLU)
350000
300000
250000
200000
150000
100000
50000
0
no IgG
1
10
100
1.000
10.000
concentration IgG (ng/mL)

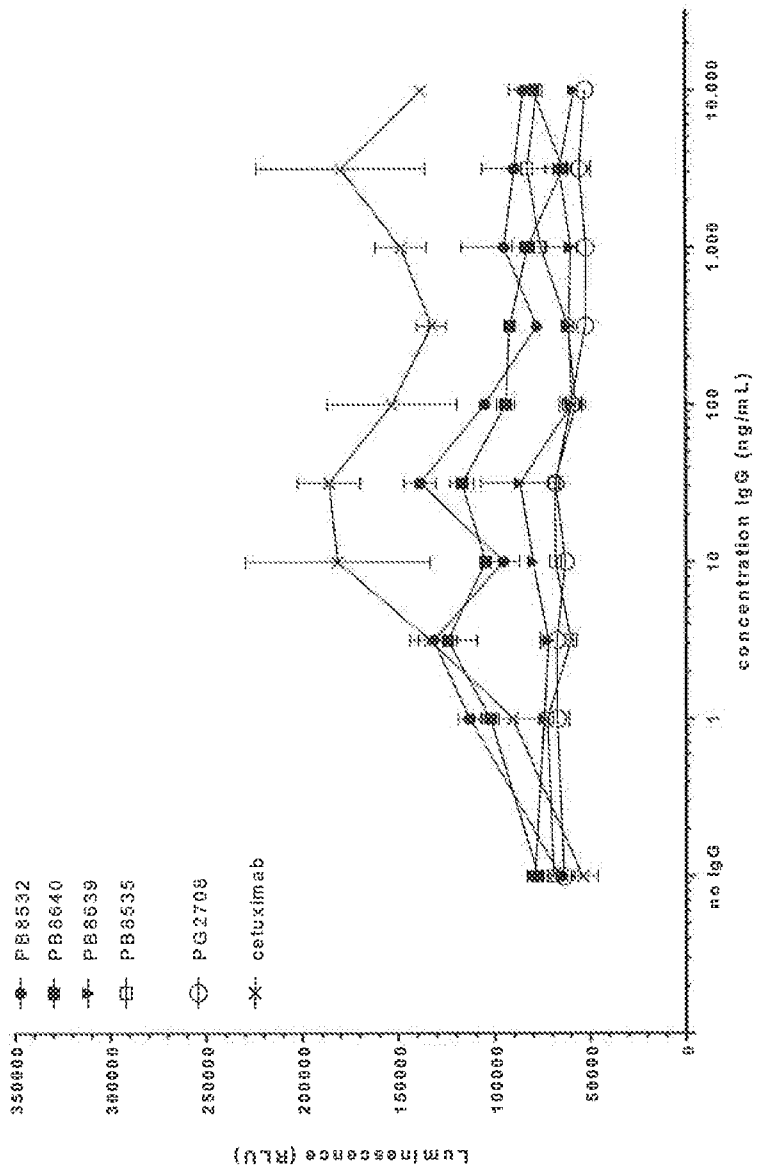

PB8532
PB8640
PB8639
PB8535
PG2705
cetuximab
luminescence (RLU)
350000
300000
250000
200000
150000
100000
50000
0
no IgG
1
10
100
1.000
10.000
concentration IgG (ng/mL)

Figure 15B

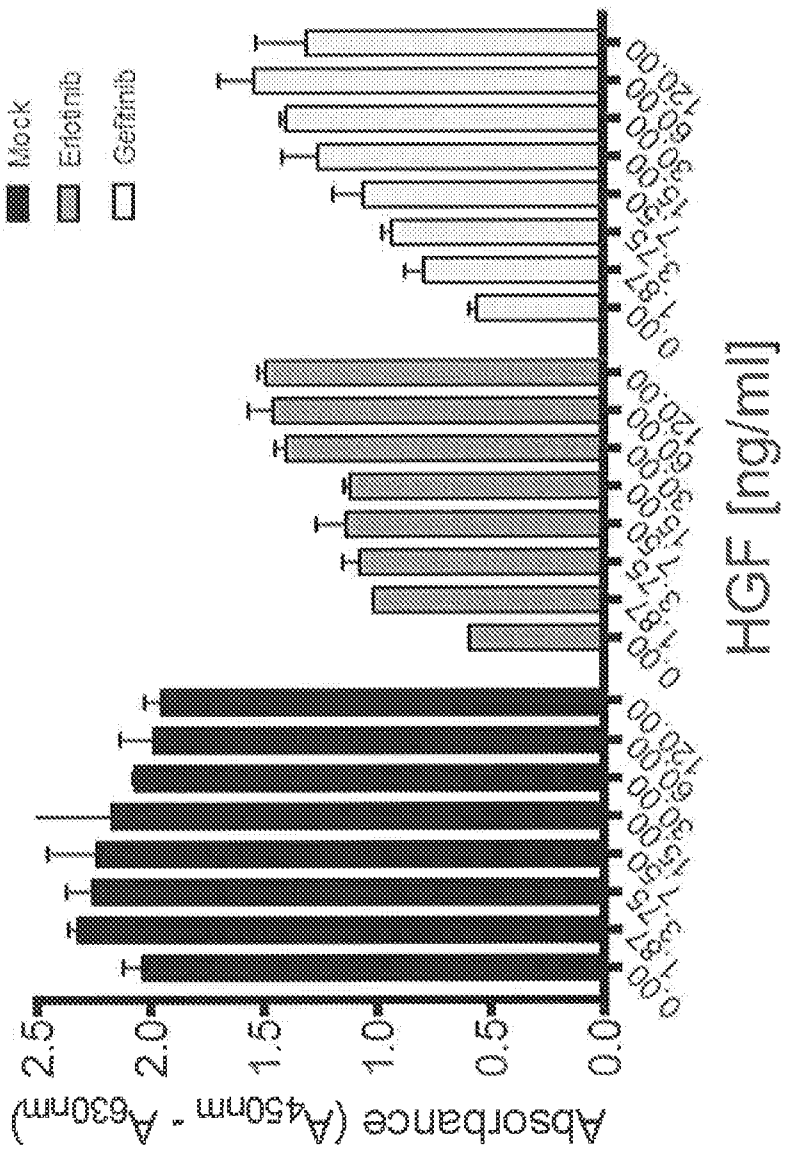

Mock
Erlotinib
Gefitinib
Absorbance (A450nm - A630nm)
2.5
2.0
1.5
1.0
0.5
0.0
0
0.187
0.375
0.75
1.5
3
6
12
24
48
HGF [ng/ml]

Figure 16A

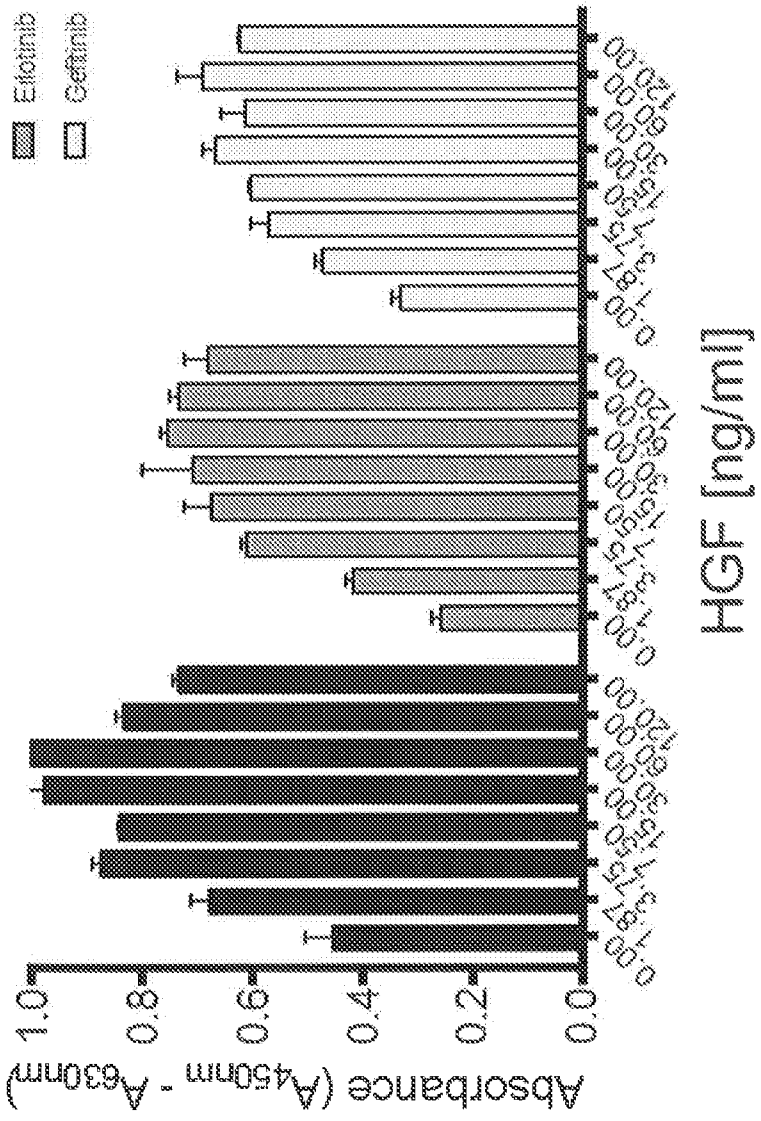

Mock
Erlotinib
Cetuximab
Absorbance (A450nm - A630nm)
1.0
0.8
0.6
0.4
0.2
0.0
0.00
0.78
3.75
7.50
15.00
30.00
60.00
120.00
HGF [ng/ml]

Figure 16B

Figure 17A

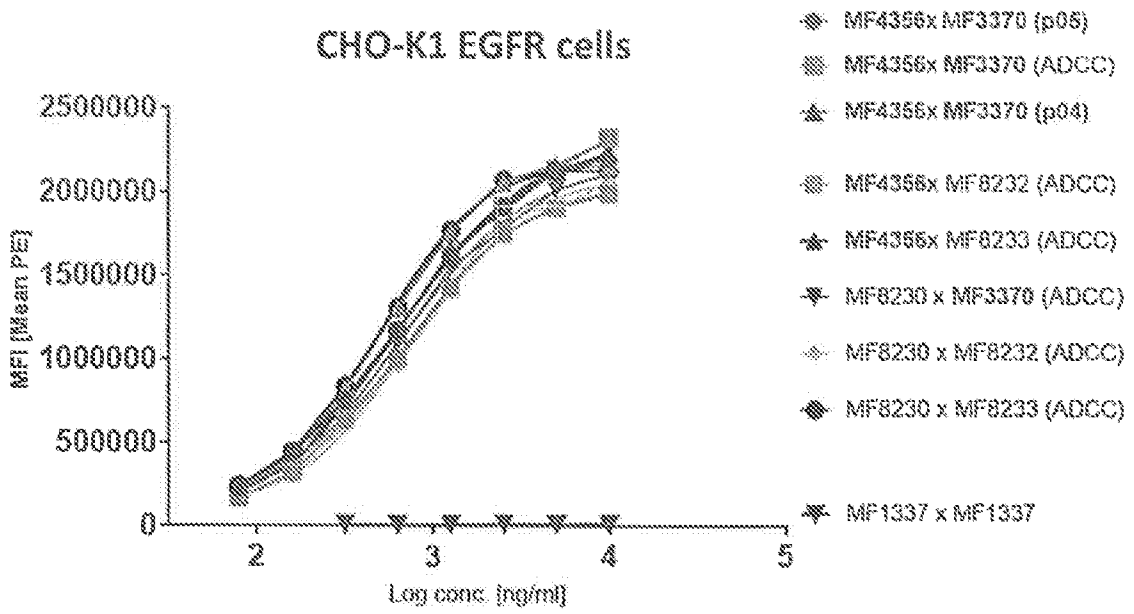


Figure 17B

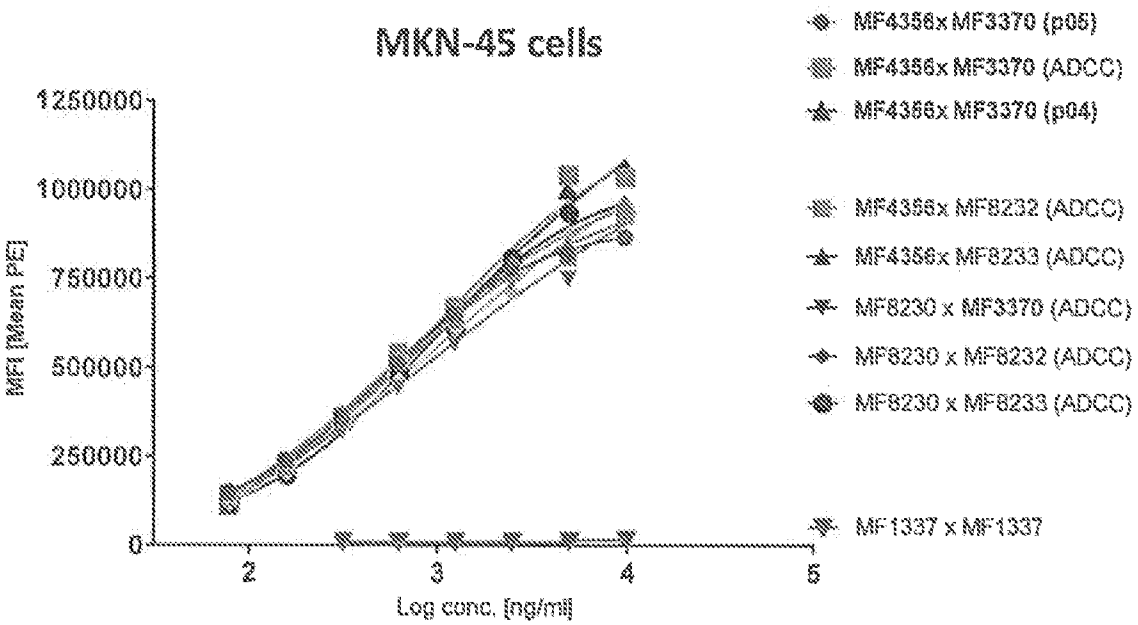


Figure 18

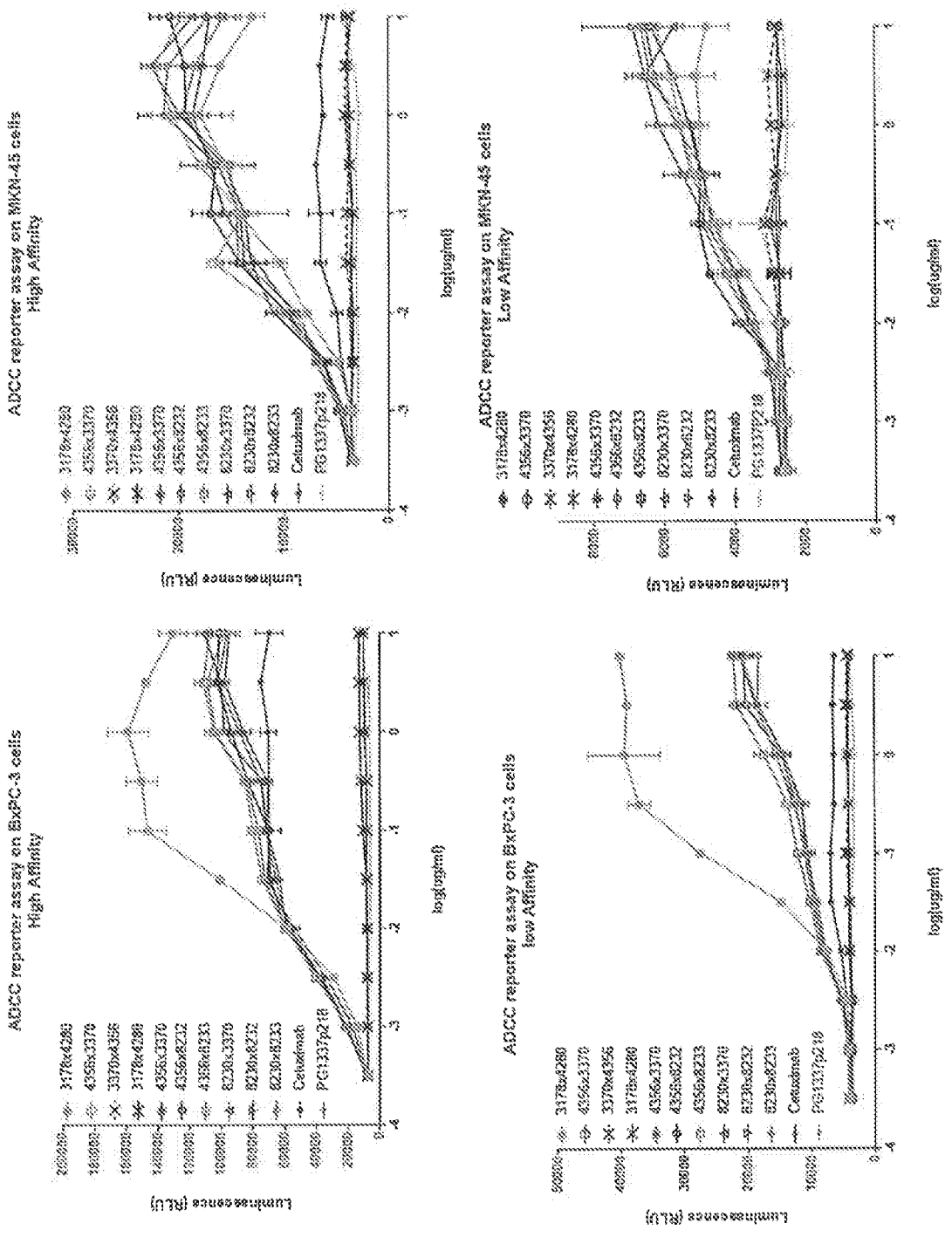

ADCC reporter assay on BxPC-3 cells
High Affinity
ADCC reporter assay on MKN-45 cells
High Affinity
ADCC reporter assay on BxPC-3 cells
low Affinity
ADCC reporter assay on MKN-45 cells
Low Affinity
luminescence (RLU)
log(ug/ml)
3178x4280
4356x3370
3370x4356
3178x4280
4356x3370
4356x8232
4356x8233
8230x3370
8230x8232
8230x8233
Cetuximab
PG1337p218

Figure 19

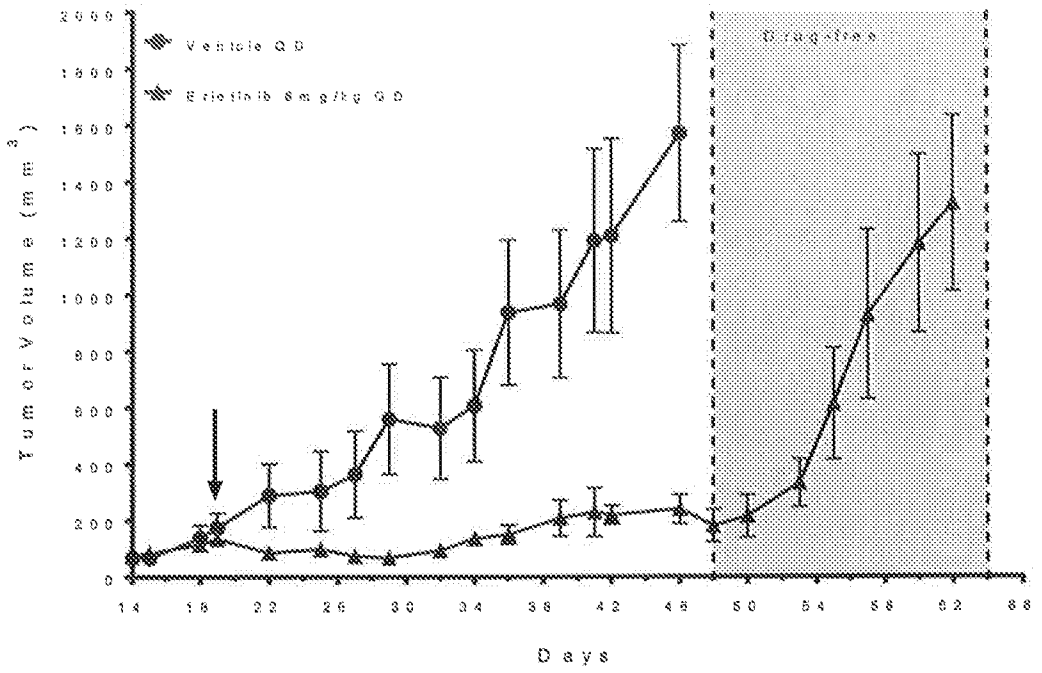


Figure 20

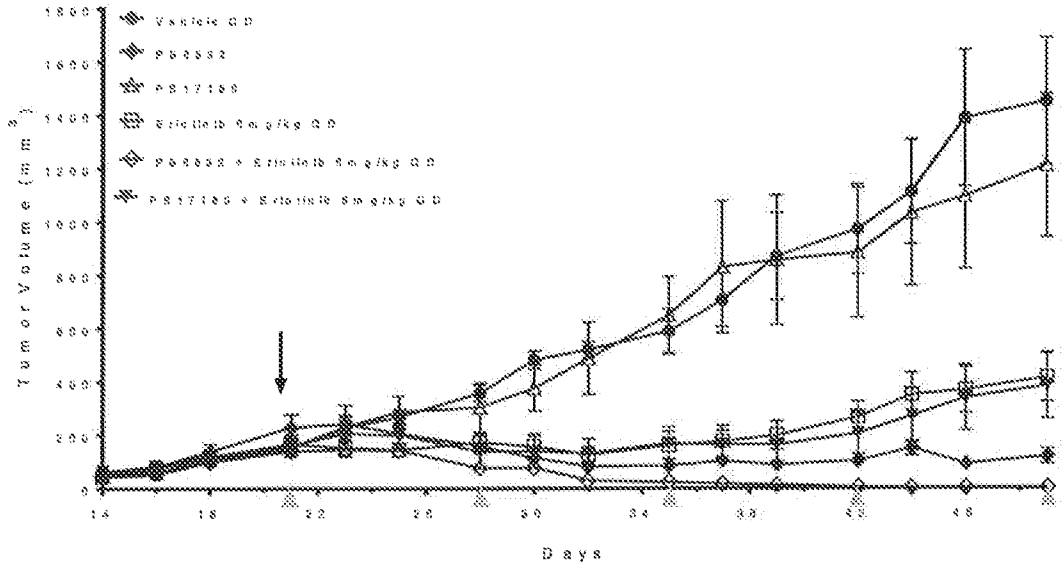


Figure 21

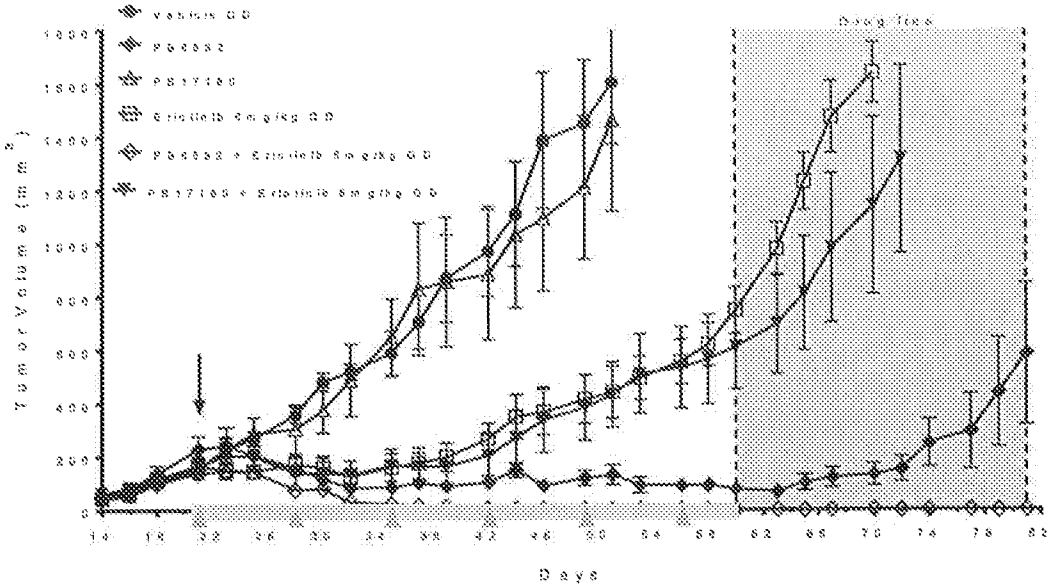


Figure 22

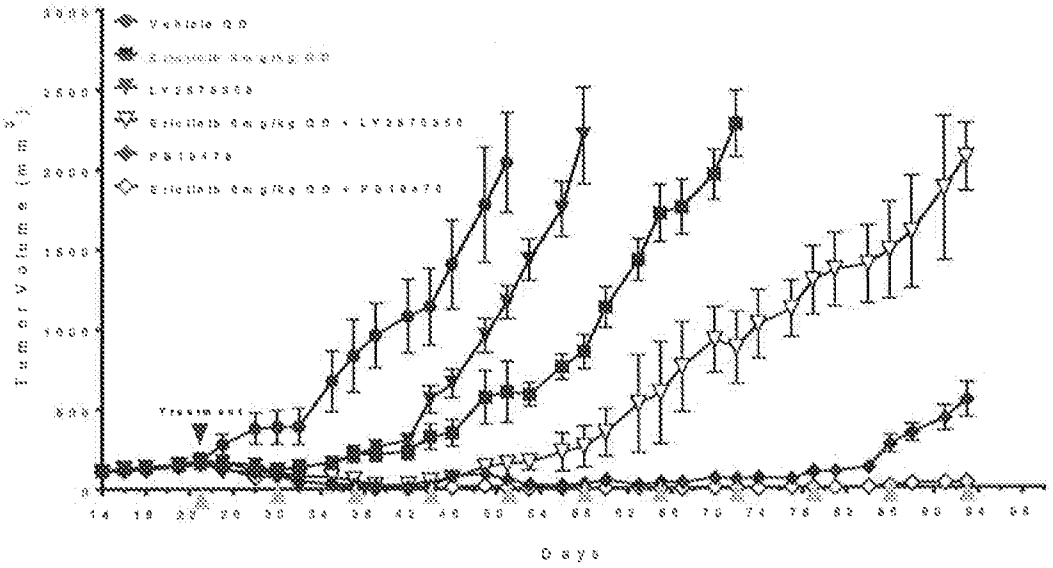


Figure 23

