FIG. 1

GCTAGCacc atggggcccagcggcaccgccggcgccgccctgctggccctgctggcc
A S T M G P S G T A G A A L L A L L A
Gccctgtgccccgccagccgggcc ctggaggagaagaaggtgtgccagggcaccagcaac
A L C P A S R A **L** E E K K V C Q G T S N
aagctgacccagctgggcaccttcgaggaccacttcctgagcctgcagcggatgttcaac
K L T Q L G T F E D H F L S L Q R M F N
aactgcgaggtggtgctgggcaacctggagatcacctacgtgcagcggaactacgacctg
N C E V V L G N L E I T Y V Q R N Y D L
agcttcctgaagaccatccaggaggtggccggctacgtgctgatcgccctgaacaccgtg
S F L K T I Q E V A G Y V L I A L N T V
gagcggatccccctggagaacctgcagatcatccggggcaacatgtactacgagaacagc
E R I P L E N L Q I I R G N M Y Y E N S
tacgccctggccgtgctgagcaactacgacgccaacaagaccggcctgaaggagctgccc
Y A L A V L S N Y D A N K T G L K E L P
atgcggaacctgcaggagatcctgcacggcgccgtgcggttcagcaacaaccccgccctg
M R N L Q E I L H G A V R F S N N P A L
tgcaacgtggagagcatccagtggcgggacatcgtgagcagcgagttcctgagcaacatg
C N V E S I Q W R D I V S S E F L S N M
agcatggacttccagaaccacctgggcagctgccagaagtgcgaccccagctgccccaac
S M D F Q N H L G S C Q K C D P S C P N
ggcagctgctggggcgccggcgaggagaactgccagaagctgaccaagatcatctgcgcc
G S C W G A G E E N C Q K L T K I I C A
cagcagtgcagcggccggtgccggggcaagagccccagcgactgctgccacaaccagtgc
Q Q C S G R C R G K S P S D C C H N Q C
gccgccggctgcaccggcccccgggagagcgactgcctggtgtgccggaagttccgggac
A A G C T G P R E S D C L V C R K F R D
gaggccacctgcaaggacacctgccccccccctgatgctgtacaaccccaccacctaccag
E A T C K D T C P P L M L Y N P T T Y Q
atggacgtgaaccccgagggcaagtacagcttcggcgccacctgcgtgaagaagtgcccc
M D V N P E G K Y S F G A T C V K K C P
cggaactacgtggtgaccgaccacggcagctgcgtgcgggcctgcggcgccgacagctac
R N Y V V T D H G S C V R A C G A D S Y
gagatggaggaggacggcgtgcggaagtgcaagaagtgcgagggcccctgccggaaggtg
E M E E D G V R K C K K C E G P C R K V
tgcaacggcatcggcatcggcgagttcaaggacaccctgagcatcaacgccaccaacatc
C N G I G I G E F K D T L S I N A T N I
aagcacttcaagaactgcaccagcatcagcggcgacctgcacatcctgcccgtggccttc
K H F K N C T S I S G D L H I L P V A F
cggggcgacagcttcacccacaccccccccctggaccccaggagctggacatcctgaag
R G D S F T H T P P L D P Q E L D I L K
accgtgaaggagatcaccggcttcctgctgatccaggcctggcccgagaaccggaccgac
T V K E I T G F L L I Q A W P E N R T D
ctgcacgccttcgagaacctggagatcatccggggccggaccaagcagcacggccagttc
L H A F E N L E I I R G R T K Q H G Q F
agcctggccgtggtgagcctgaacatcaccagcctgggcctgcggagcctgaaggagatc
S L A V V S L N I T S L G L R S L K E I

FIG. 1, Cont'd

agcgacggcgacgtgatcatcagcggcaacaagaacctgtgctacgccaacaccatcaac
S D G D V I I S G N K N L C Y A N T I N
tggaagaagctgttcggcaccagcagccagaagaccaagatcatcagcaaccggggcgag
W K K L F G T S S Q K T K I I S N R G E
aacagctgcaaggccaccggccaggtgtgccacgccctgtgcagccccgagggctgctgg
N S C K A T G Q V C H A L C S P E G C W
ggccccgagccccgggactgcgtgagctgccagaacgtgagccggggccgggagtgcgtg
G P E P R D C V S C Q N V S R G R E C V
gacaagtgcaacatcctggagggcgagccccgggagttcgtggagaacagcgagtgcatc
D K C N I L E G E P R E F V E N S E C I
cagtgccaccccgagtgcctgccccaggtgatgaacatcacctgcaccggccggggcccc
Q C H P E C L P Q V M N I T C T G R G P
gacaactgcatccagtgcgcccactacatcgacggcccccactgcgtgaagacctgcccc
D N C I Q C A H Y I D G P H C V K T C P
gccggcgtgatgggcgagaacaacaccctggtgtggaagtacgccgacgccggccacgtg
A G V M G E N N T L V W K Y A D A G H V
tgccacctgtgccaccccaactgcacctacggctgcaccggccccggcctggagggctgc
C H L C H P N C T Y G C T G P G L E G C
gcccggaacggccccaagatccccagcatcgccaccggcatgctgggcgccctgctgctg
A R N G P K I P S I A T ***G M L G A L L L***
ctgctggtggtggccctgggcatcggcctgttcatgcggcggcggcacatcgtgcggaag
L L V V A L G I G L F M R R R H I V R K
cggaccctgcggcggctgctgcaggagcgggagctggtggagcccctgaccccagcggc
R T L R R L L Q E R E L V E P L T P S G
gaggcccccaaccaggccctgctgcggatcctgaaggagaccgagttcaagaagatcaag
E A P N Q A L L R I L K E T E F K K I K
gtgctgggcagcggcgccttcggcaccgtgtacaagggcctgtggatccccgagggcgag
V L G S G A F G T V Y K G L W I P E G E
aaggtgaagatccccgtggccatcaaggagctgcgggaggccaccagccccaaggccaac
K V K I P V A I K E L R E A T S P K A N
aaggagatcctggacgaggcctacgtgatggccagcgtggacaaccccccacgtgtgccgg
K E I L D E A Y V M A S V D N P H V C R
ctgctgggcatctgcctgaccagcaccgtgcagctgatcacccagctgatgcccttcggc
L L G I C L T S T V Q L I T Q L M P F G
tgcctgctggactacgtgcgggagcacaaggacaacatcggcagccagtacctgctgaac
C L L D Y V R E H K D N I G S Q Y L L N
tggtgcgtgcagatcgccaagggcatgaactacctggaggaccggcggctggtgcaccgg
W C V Q I A K G M N Y L E D R R L V H R
gacctggccgcccggaacgtgctggtgaagacccccagcacgtgaagatcaccgacttc
D L A A R N V L V K T P Q H V K I T D F
ggcctggccaagctgctgggcgccgaggagaaggagtaccacgccgagggcggcaaggtg
G L A K L L G A E E K E Y H A E G G K V
cccatcaagtggatggccctggagagcatcctgcaccggatctacacccaccagagcgac
P I K W M A L E S I L H R I Y T H Q S D
gtgtggagctacggcgtgaccgtgtgggagctgatgaccttcggcagcaagccctacgac
V W S Y G V T V W E L M T F G S K P Y D

FIG. 1, Cont'd

```
ggcatccccgccagcgagatcagcagcatcctggagaagggcgagcggctgccccagccc
 G  I  P  A  S  E  I  S  S  I  L  E  K  G  E  R  L  P  Q  P
cccatctgcaccatcgacgtgtacatgatcatggtgaagtgctggatgatcgacgccgac
 P  I  C  T  I  D  V  Y  M  I  M  V  K  C  W  M  I  D  A  D
agccggcccaagttccgggagctgatcatcgagttcagcaagatggcccgggacccccag
 S  R  P  K  F  R  E  L  I  I  E  F  S  K  M  A  R  D  P  Q
cggtacctggtgatccagggcgacgagcggatgcacctgcccagccccaccgacagcaac
 R  Y  L  V  I  Q  G  D  E  R  M  H  L  P  S  P  T  D  S  N
ttctaccgggccctgatggacgaggaggacatggacgacgtggtggacgccgacgagtac
 F  Y  R  A  L  M  D  E  E  D  M  D  D  V  V  D  A  D  E  Y
ctgatcccccagcagggcttcttcagcagccccagcaccagccggacccccctgctgagc
 L  I  P  Q  Q  G  F  F  S  S  P  S  T  S  R  T  P  L  L  S
agcctgagcgccaccagcaacaacagcaccgtggcctgcatcgaccggaacggcctgcag
 S  L  S  A  T  S  N  N  S  T  V  A  C  I  D  R  N  G  L  Q
agctgccccatcaaggaggacagcttcctgcagcggtacagcagcgaccccaccggcgcc
 S  C  P  I  K  E  D  S  F  L  Q  R  Y  S  S  D  P  T  G  A
ctgaccgaggacagcatcgacgacaccttcctgcccgtgcccgagtacatcaaccagagc
 L  T  E  D  S  I  D  D  T  F  L  P  V  P  E  Y  I  N  Q  S
gtgcccaagcggcccgccggcagcgtgcagaaccccgtgtaccacaaccagcccctgaac
 V  P  K  R  P  A  G  S  V  Q  N  P  V  Y  H  N  Q  P  L  N
cccgcccccagccgggaccccccactaccaggacccccacagcaccgccgtgggcaacccc
 P  A  P  S  R  D  P  H  Y  Q  D  P  H  S  T  A  V  G  N  P
gagtacctgaacaccgtgcagcccacctgcgtgaacagcaccttcgacagccccgcccac
 E  Y  L  N  T  V  Q  P  T  C  V  N  S  T  F  D  S  P  A  H
tgggcccagaagggcagccaccagatcagcctggacaaccccgactaccagcaggacttc
 W  A  Q  K  G  S  H  Q  I  S  L  D  N  P  D  Y  Q  Q  D  F
ttccccaaggaggccaagcccaacggcatcttcaagggcagcaccgccgagaacgccgag
 F  P  K  E  A  K  P  N  G  I  F  K  G  S  T  A  E  N  A  E
tacctgcgggtggccccccagagcagcgagttcatcggcgcctgaGCGGCCGC
 Y  L  R  V  A  P  Q  S  S  E  F  I  G  A  -  A  A  A
```

FIG. 2

EGFR HER3 swap varII ECD

LEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLEN
LQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMD
FQNHLCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFN
DSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCG
GLCPKACEGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWP
ENRTDLHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKTKIIS
NRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVENSECIQCHPECLPQAM
NITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGP
KIPS

EGFR HER3 swap varIII ECD

LEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLEN
LQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMD
FQNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKF
RDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGSCVRACGADSYEMEEDGVRKCKK
CEGPCRKVCNGIGIGEFKDSLSINATNIKHFKNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNIQ
SWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTKVLGTSG
QKTKIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVENSECIQCHPE
CLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLE
GCPTNGPKIPS

EGFR HER3 swap varIV ECD

LEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLEN
LQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMD
FQNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKF
RDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTDHGSCVRACGADSYEMEEDGVRKCKK
CEGPCRKVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQA
WPENRTDLHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKT
KIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVEECFSCHPECQPME
GTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTN
GPKIPS

FIG. 3

		Competition of phages with				
			Domain I	**Domain II**	**Domain III**	**Domain III**
Cluster nr.	**MF tested**	**no IgG**	**ICR10**	**EGFR.1**	**Cetuximab**	**MatuzuMab**
1	3998	2.494	2.227	2.343	0.101	0.671
2	4289	2.278	2.046	2.226	2.222	2.356
3	4000	2.597	1.736	2.604	2.533	0.345
4	4016	2.184	0.088	2.129	2.135	2.133
5	4029	1.898	2.193	1.256	1.235	1.938
6	4034	1.747	1.42	0.108	1.62	1.776
7	4035	1.594	0.951	1.554	1.079	1.309
8	4032	2.276	2.145	2.057	1.996	0.099
9	4284	2.04	2.212	1.776	2.08	1.226
10	4358	1.631	1.704	1.833	1.991	0.066
11	4280	2.549	2.302	2.135	1.141	0.613
12	4283	2.827	2.336	2.889	0.265	0.122
13	4281	2.107	2.195	1.968	1.589	1.255
14	4286	1.589	1.723	1.66	0.272	0.247
15	4285	2.176	2.332	1.599	2.369	2.285
16	4287	2.052	1.825	1.711	1.187	1.705
17	4359	ND	ND	ND	ND	ND

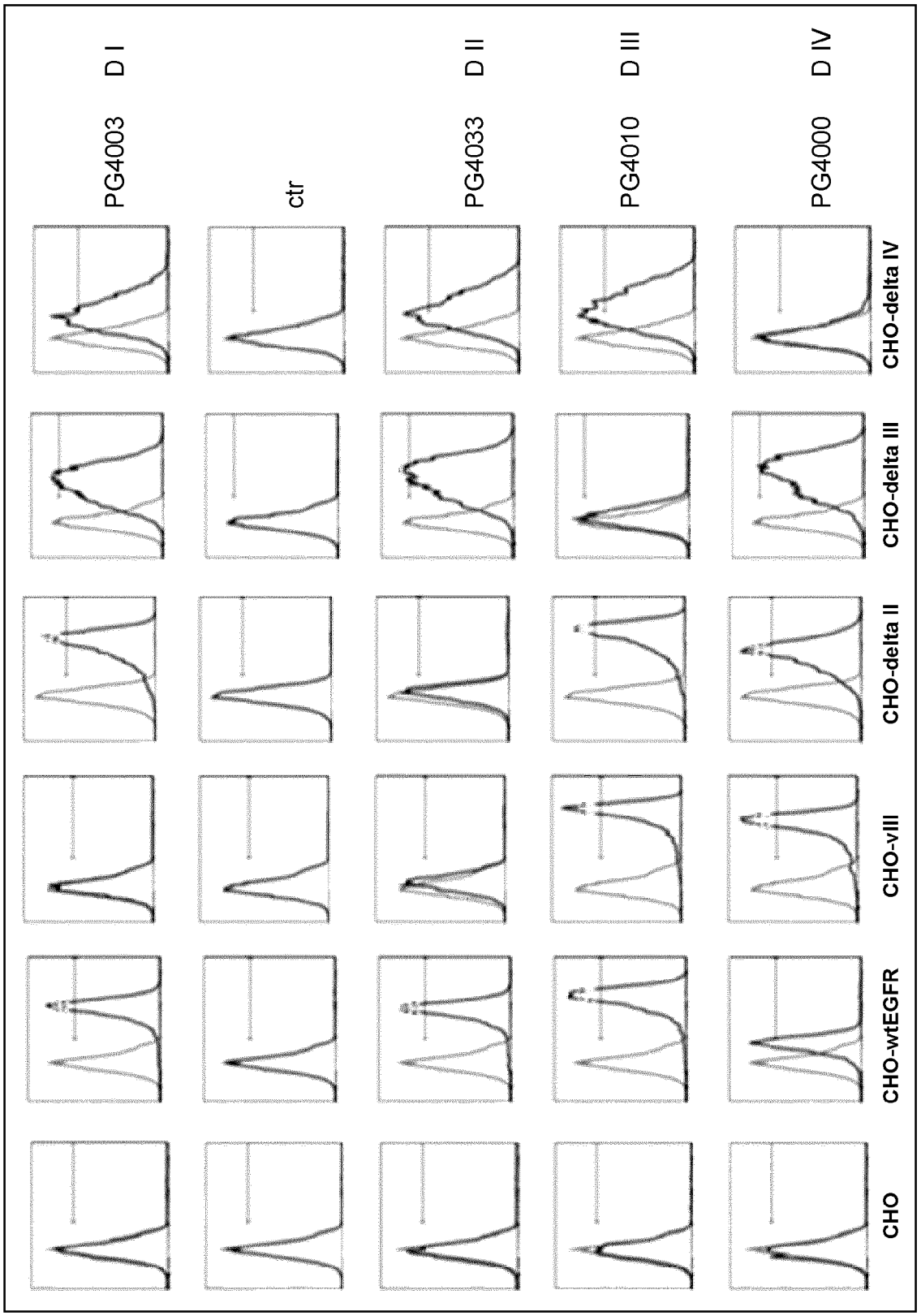

PG4003
D I
ctr
PG4033
D II
PG4010
D III
PG4000
D IV
CHO-delta IV
CHO-delta III
CHO-delta II
CHO-vIII
CHO-wtEGFR
CHO

FIG. 4

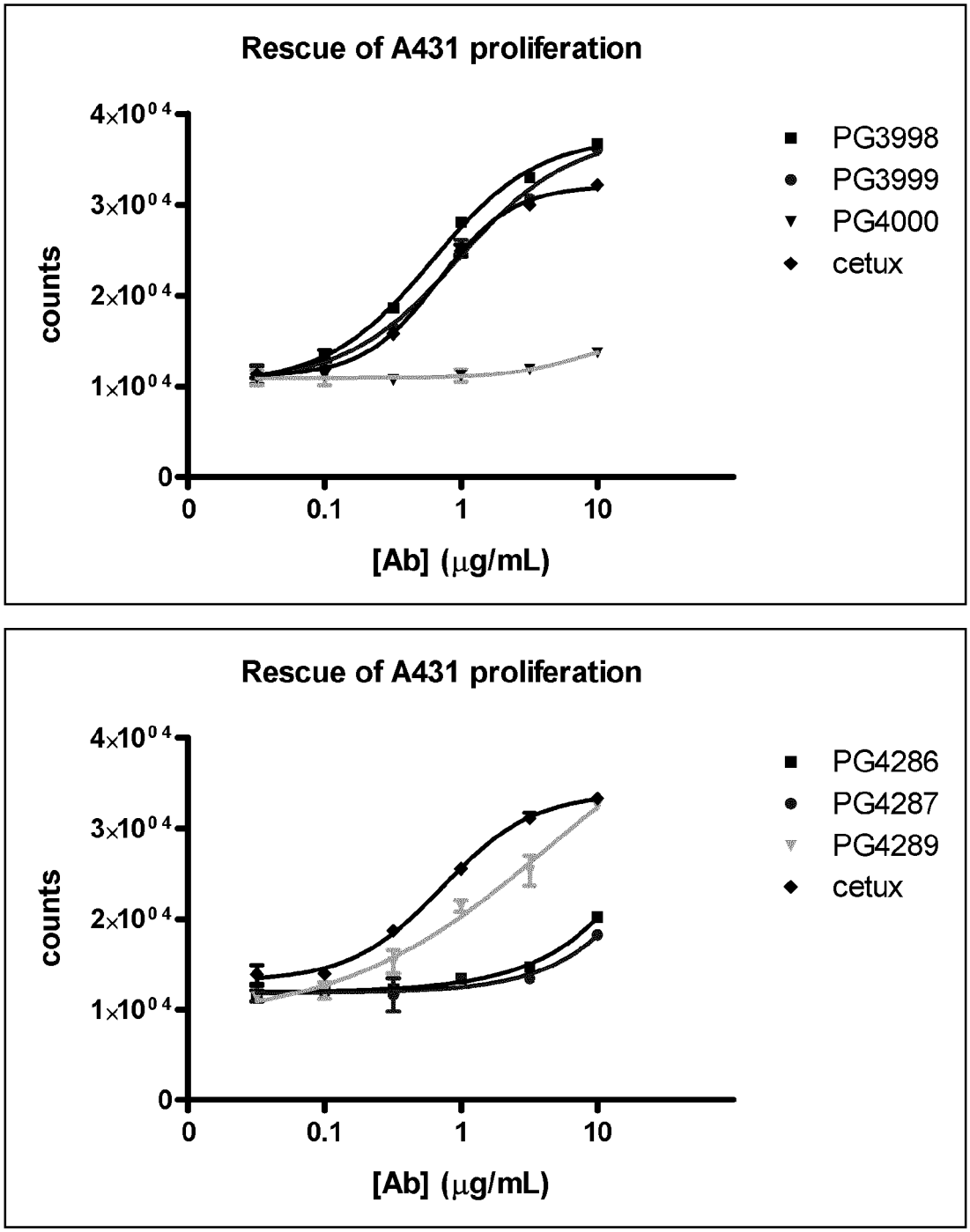

Rescue of A431 proliferation
counts
4x10^04
3x10^04
2x10^04
1x10^04
0
0
0.1
1
10
[Ab] (μg/mL)
PG3998
PG3999
PG4000
cetux
Rescue of A431 proliferation
counts
4x10^04
3x10^04
2x10^04
1x10^04
0
0
0.1
1
10
[Ab] (μg/mL)
PG4286
PG4287
PG4289
cetux

FIG. 5

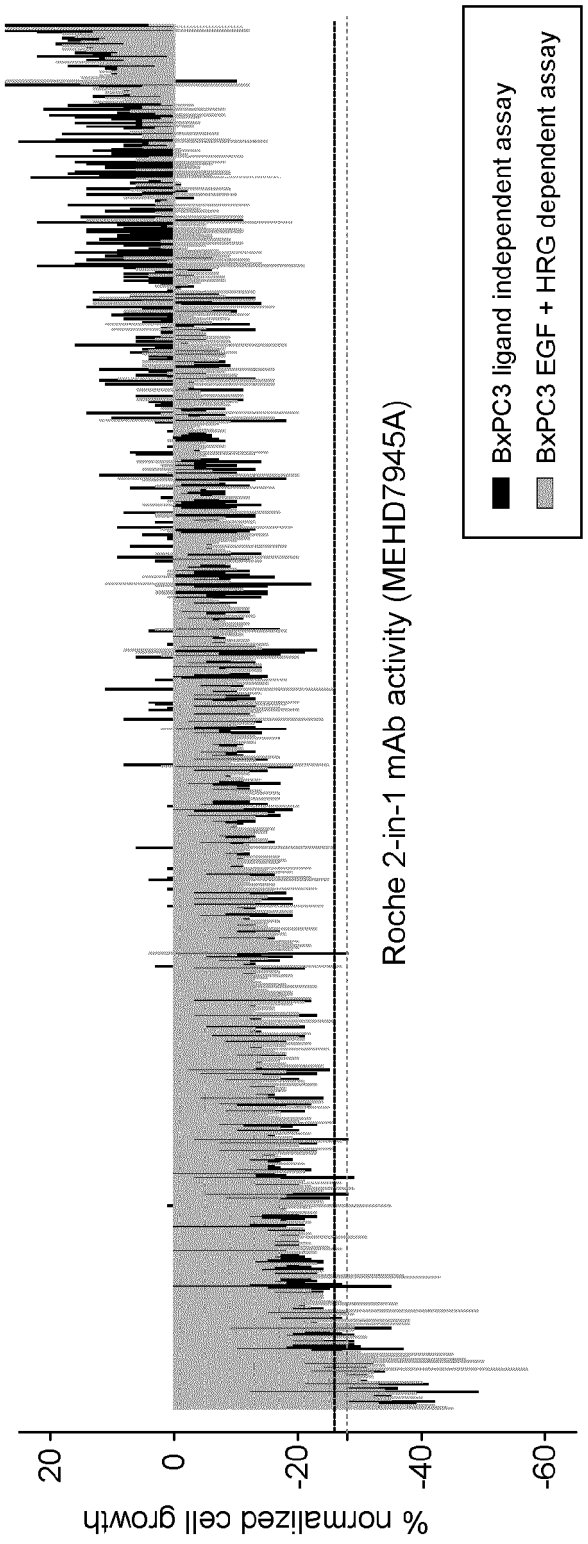

BxPC3 ligand independent assay
BxPC3 EGF + HRG dependent assay
Roche 2-in-1 mAb activity (MEHD7945A)
% normalized cell growth
20
0
-20
-40
-60

FIG. 6

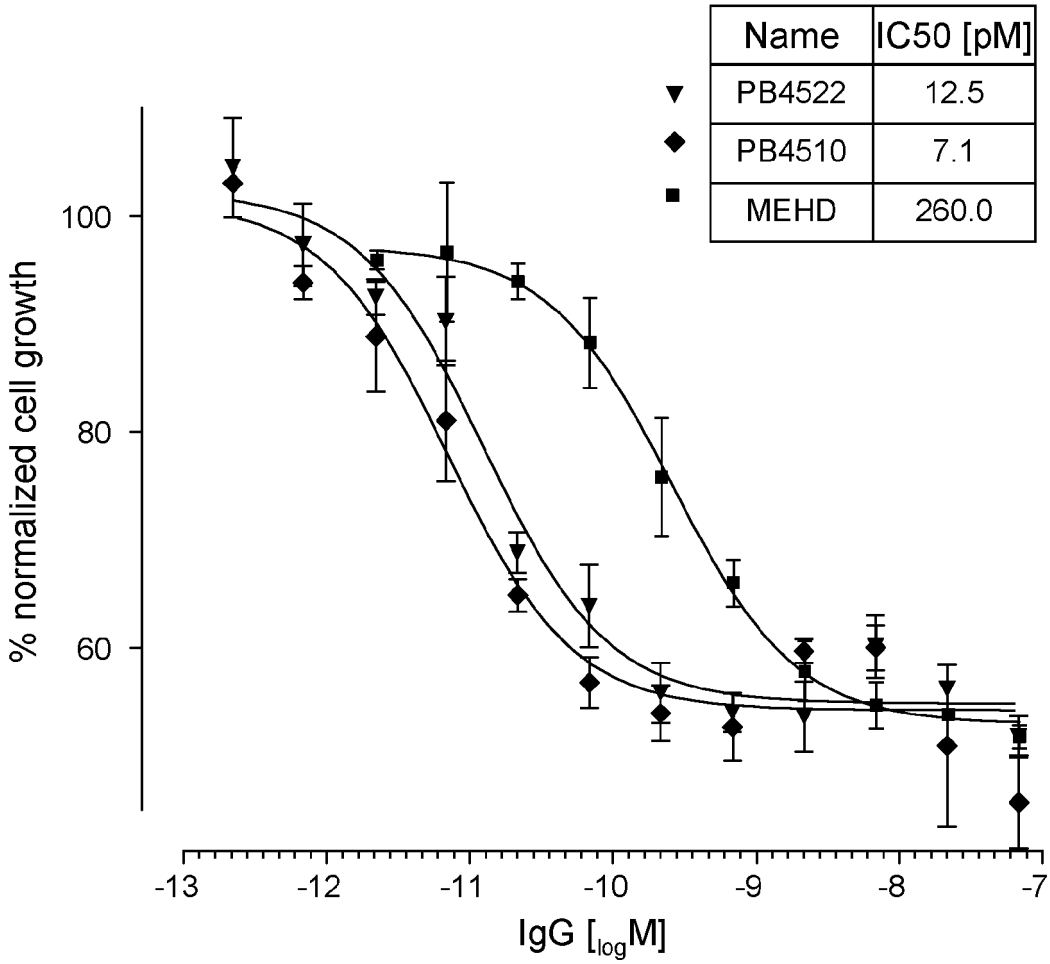
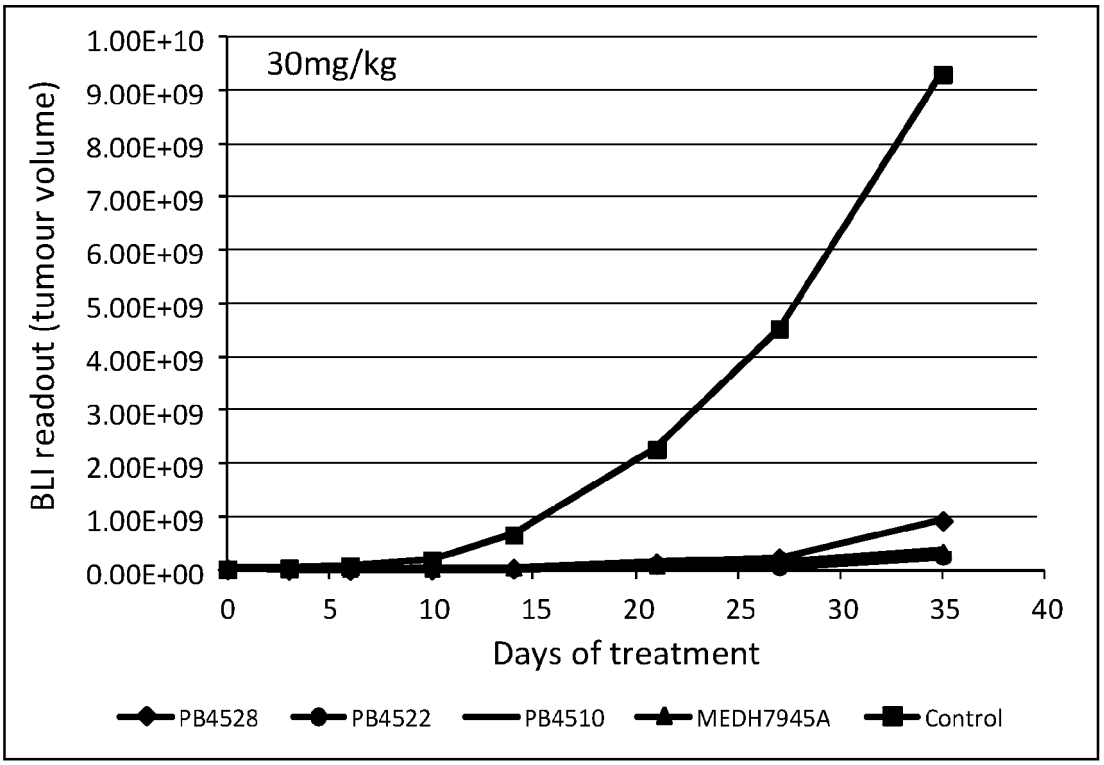

Name
IC50 [pM]
PB4522
12.5
PB4510
7.1
MEHD
260.0
% normalized cell growth
100
80
60
-13
-12
-11
-10
-9
-8
-7
IgG [log M]

FIG. 7


30mg/kg
BLI readout (tumour volume)
1.00E+10
9.00E+09
8.00E+09
7.00E+09
6.00E+09
5.00E+09
4.00E+09
3.00E+09
2.00E+09
1.00E+09
0.00E+00
0
5
10
15
20
25
30
35
40
Days of treatment
PB4528
PB4522
PB4510
MEDH7945A
Control

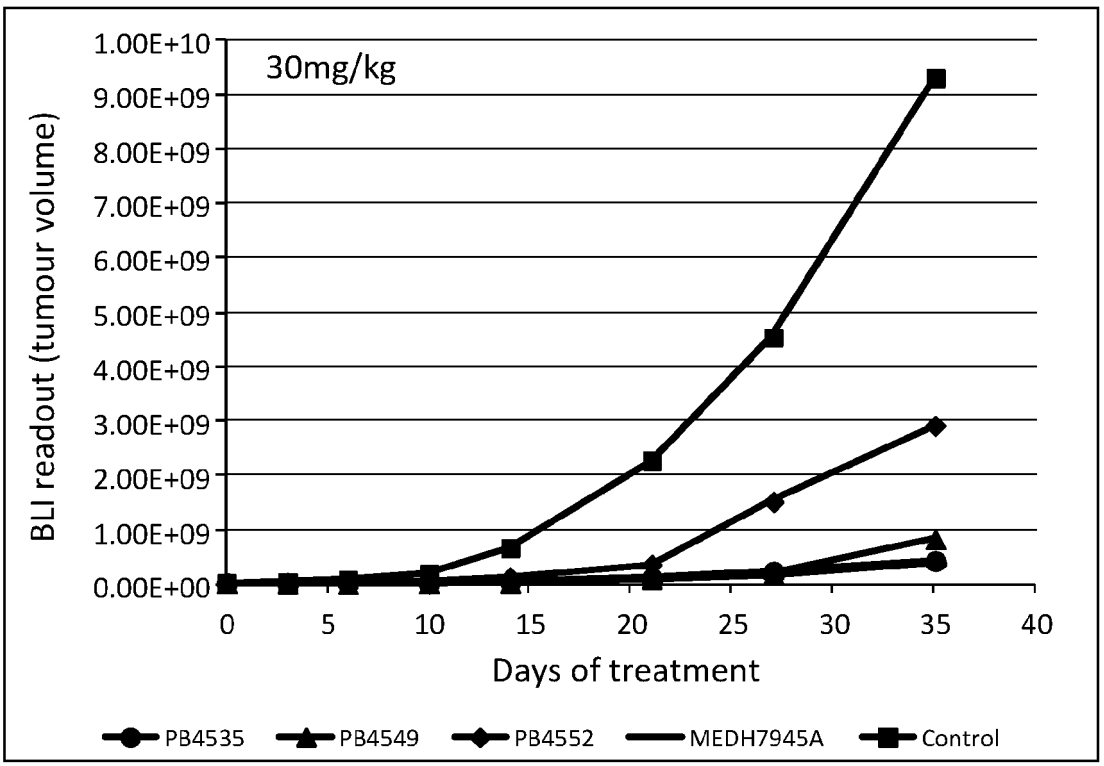

30mg/kg
BLI readout (tumour volume)
1.00E+10
9.00E+09
8.00E+09
7.00E+09
6.00E+09
5.00E+09
4.00E+09
3.00E+09
2.00E+09
1.00E+09
0.00E+00
0
5
10
15
20
25
30
35
40
Days of treatment
PB4535
PB4549
PB4552
MEDH7945A
Control

FIG. 8

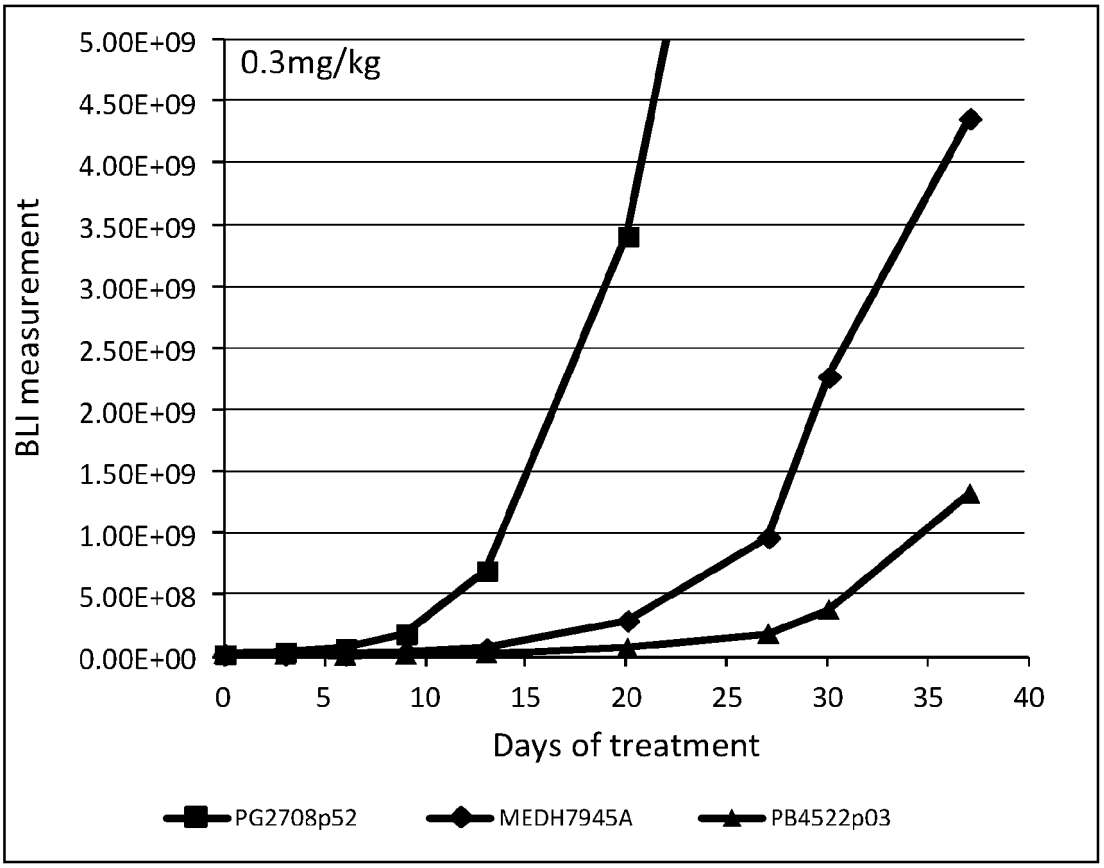

0.3mg/kg
BLI measurement
5.00E+09
4.50E+09
4.00E+09
3.50E+09
3.00E+09
2.50E+09
2.00E+09
1.50E+09
1.00E+09
5.00E+08
0.00E+00
0
5
10
15
20
25
30
35
40
Days of treatment
PG2708p52
MEDH7945A
PB4522p03

FIG. 9

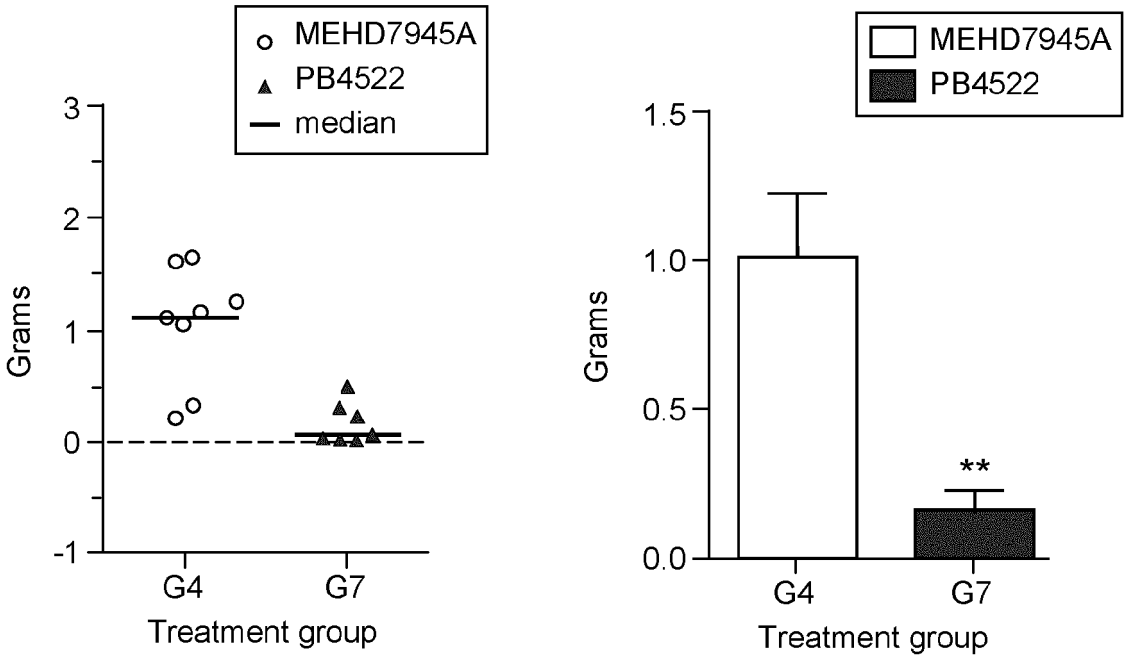

MEHD7945A
PB4522
median
Grams
3
2
1
0
-1
G4
G7
Treatment group
MEHD7945A
PB4522
Grams
1.5
1.0
0.5
0.0
**
G4
G7
Treatment group

FIG. 10

FIG. 11A

MF4280: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEY
GKTFFAQNFQGRVTMTEDTSADTAYMELSSLRSEDTAVYYCATEGYYETTTYYYNLF
DSWGQGTLVTVSS

FR1: QVQLVQSGAEVKKPGASVKVSCKVSGYTLT

CDR1: ELSMH

FR2: WVRQAPGKGLEWMG

CDR2: GFDPEYGKTFFAQNFQG

FR3: RVTMTEDTSADTAYMELSSLRSEDTAVYYCAT

CDR3: EGYYETTTYYYNLFDS

FR4: WGQGTLVTVSS

Annotated nucleotide sequence

```
CAGGTGCAGCTG
 Q  V  Q  L
GTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGCGCCTCAGTGAAGGTCTCCTGCAAGGTT
 V  Q  S  G  A  E  V  K  K  P  G  A  S  V  K  V  S  C  K  V
TCCGGATACACCCTCACTGAATTATCCATGCACTGGGTGCGACAGGCTCCTGGTAAAGGG
 S  G  Y  T  L  T  E  L  S  M  H  W  V  R  Q  A  P  G  K  G
CTTGAATGGATGGGAGGCTTTGATCCTGAGTATGGTAAAACATTCTTCGCACAGAACTTC
 L  E  W  M  G  G  F  D  P  E  Y  G  K  T  F  F  A  Q  N  F
CAGGGCAGAGTCACCATGACCGAGGACACATCTGCAGACACAGCCTACATGGAGCTAAGC
 Q  G  R  V  T  M  T  E  D  T  S  A  D  T  A  Y  M  E  L  S
AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAACAGAGGGGTATTATGAGACT
 S  L  R  S  E  D  T  A  V  Y  Y  C  A  T  E  G  Y  Y  E  T
ACTACTTATTACTACAACCTTTTTGACTCCTGGGGCCAGGGAACCCTGGTCACCGTCTCA
 T  T  Y  Y  Y  N  L  F  D  S  W  G  Q  G  T  L  V  T  V  S
AGC
 S
```

FIG. 11A, Cont'd

MF3998: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

QVQLVQSGSELKKPGASVKVSCKASGYTFTNNAINWVRQAPGQGLEWMGWINTITG
DPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTGVYYCAREEFLEWLFFDYWGQG
TLVTVSS

FR1: QVQLVQSGSELKKPGASVKVSCKASGYTFT

CDR1: NNAIN

FR2: WVRQAPGQGLEWMG

CDR2: WINTITGDPTYAQGFTG

FR3: RFVFSLDTSVSTAYLQISSLKAEDTGVYYCAR

CDR3: EEFLEWLFFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence

```
CAGGTGCAGCTGGTGCAGTCTGGGTCTGAGTTGAAGAAG
 Q  V  Q  L  V  Q  S  G  S  E  L  K  K
CCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACTAACAATGCC
 P  G  A  S  V  K  V  S  C  K  A  S  G  Y  T  F  T  N  N  A
ATAAATTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAACACC
 I  N  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  N  T
ATCACTGGGGACCCAACGTATGCCCAGGGCTTCACAGGACGGTTTGTCTTCTCCTTGGAC
 I  T  G  D  P  T  Y  A  Q  G  F  T  G  R  F  V  F  S  L  D
ACCTCTGTCAGCACGGCATATCTGCAGATCAGCAGCCTGAAGGCTGAGGACACTGGCGTG
 T  S  V  S  T  A  Y  L  Q  I  S  S  L  K  A  E  D  T  G  V
TATTACTGTGCGAGAGAGGAATTTTTGGAGTGGTTATTCTTTGACTACTGGGGCCAGGGA
 Y  Y  C  A  R  E  E  F  L  E  W  L  F  F  D  Y  W  G  Q  G
ACCCTGGTCACCGTCTCAAGC
 T  L  V  T  V  S  S
```

FIG. 11A, Cont'd

MF4010: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

QVQLVQSGSELKKPGASVKVSCKASGYTFTNNAMNWVRQAPGQGLEWMGWINTIT
GDPSYAQGFTGRFVFSLDTSVNTAYLQISSLKAEDTAVYYCAREEFLEWLFFDYWGQ
GTLVTVSS

FR1: QVQLVQSGSELKKPGASVKVSCKASGYTFT

CDR1: NNAMN

FR2: WVRQAPGQGLEWMG

CDR2: WINTITGDPSYAQGFTG

FR3: RFVFSLDTSVNTAYLQISSLKAEDTAVYYCAR

CDR3: EEFLEWLFFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
caggtgcagctggtgcagtctgggtctgagttgaagaagcct
  Q  V  Q  L  V  Q  S  G  S  E  L  K  K  P
ggggcctcagtgaaggtttcctgcaaggcttctggatacaccttcactaacaatgccatg
 G  A  S  V  K  V  S  C  K  A  S  G  Y  T  F  T  N  N  A  M
aattgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaacaccatc
 N  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  N  T  I
actggggacccatcgtatgcccagggcttcacaggacggtttgtcttctccctggacacc
 T  G  D  P  S  Y  A  Q  G  F  T  G  R  F  V  F  S  L  D  T
tctgtcaacacggcatatctgcagatcagcagcctgaaggctgaggacactgccgtatat
 S  V  N  T  A  Y  L  Q  I  S  S  L  K  A  E  D  T  A  V  Y
tactgtgcgagagaggaatttttggagtggttattctttgactactggggccagggaacc
 Y  C  A  R  E  E  F  L  E  W  L  F  F  D  Y  W  G  Q  G  T
ctggtcaccgtctcaagcgtctccagt
 L  V  T  V  S  S  V  S  S
```

FIG. 11A, Cont'd

MF4003: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

QVQLVQSGSELKKPGASVKVSCKASGYTFPSFAMNWLRQAPGQGLEWMGWITTNTG
DPTYAQGFSGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARVYNWIRGFDYWGQGTL
VTVSS

FR1: QVQLVQSGSELKKPGASVKVSCKASGYTFP

CDR1: SFAMN

FR2: WLRQAPGQGLEWMG

CDR2: WITTNTGDPTYAQGFSG

FR3: RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR

CDR3: VYNWIRGFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
caggtgcagctggtgcaatctgggtctgagttgaagaagcct
 Q  V  Q  L  V  Q  S  G  S  E  L  K  K  P
ggggcctcagtgaaggtttcctgcaaggcttctggatacaccttccctagttttgctatg
 G  A  S  V  K  V  S  C  K  A  S  G  Y  T  F  P  S  F  A  M
aattggcttcgacaggcccctggacaagggcttgagtggatgggatggatcaccaccaac
 N  W  L  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  T  T  N
actggggacccaacgtatgcccagggcttcacaggacggtttgtgttccctggacacc
 T  G  D  P  T  Y  A  Q  G  F  S  G  R  F  V  F  S  L  D  T
tctgtcagcacggcatatctgcagatcagcagcctaaaggctgaggacactgccgtgtat
 S  V  S  T  A  Y  L  Q  I  S  S  L  K  A  E  D  T  A  V  Y
tactgtgcgagagtttataactggataaggggatttgactactggggccagggaaccctg
 Y  C  A  R  V  Y  N  W  I  R  G  F  D  Y  W  G  Q  G  T  L
gtcaccgtctcaagcgtctccagt
 V  T  V  S  S  V  S  S
```

FIG. 11A, Cont'd

MF4289: heavy chain variable region sequence of an EGFR binding antibody:

Complete VH sequence:

QVQLVQSGSELKKPGASVKVSCKTSGYTFTDYAMTWVRQAPGQGLEWMGWITTNTG
DPTYAPGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARVYHWIRGFEFWGQGTL
VTVSS

FR1: QVQLVQSGSELKKPGASVKVSCKTSGYTFT

CDR1: DYAMT

FR2: WVRQAPGQGLEWMG

CDR2: WITTNTGDPTYAPGFTG

FR3: RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR

CDR3: VYHWIRGFEF

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
ggcccagccggccalggcccagglgcagclgglgcaalclggglclgaallgaagaagccl
  A  Q  P  A  M  A  Q  V  Q  L  V  Q  S  G  S  E  L  K  K  P
ggggcctcagtgaaggtttcctgcaagacttctggatacaccttcactgactatgctatg
 G  A  S  V  K  V  S  C  K  T  S  G  Y  T  F  T  D  Y  A  M
acttgggtgcgacaggcccctggacaagggcttgaatggatgggatggatcaccaccaac
 T  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  T  T  N
actggggacccaacgtatgccccgggcttcacaggacggtttgtcttctccttggacacc
 T  G  D  P  T  Y  A  P  G  F  T  G  R  F  V  F  S  L  D  T
tctgtcagcacggcatatctgcagatcagcagcctaaaggccgaggacactgccgtatat
 S  V  S  T  A  Y  L  Q  I  S  S  L  K  A  E  D  T  A  V  Y
tactgtgcgagagtgtatcattggatacggggatttgagttttggggccagggaaccctg
 Y  C  A  R  V  Y  H  W  I  R  G  F  E  F  W  G  Q  G  T  L
gtcaccgtctcaagcgtctccagt
 V  T  V  S  S  V  S  S
```

FIG. 11A, Cont'd

MF3370: heavy chain variable region sequence of an EGFR binding antibody:

Complete VH sequence:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNG
NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRHWHWWLDAFDY
WGQGTLVTVSS

FR1: QVQLVQSGAEVKKPGASVKVSCKASGYTFT

CDR1: SYGIS

FR2: WVRQAPGQGLEWMG

CDR2: WISAYNGNTNYAQKLQG

FR3: RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAK

CDR3: DRHWHWWLDAFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
caggttcagctggtgcagtctggagctgagggtgaagaagcct
 Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P
ggggcctcagtgaaggtctcctgcaaggcttctggttacacctttaccagctatggtatc
 G  A  S  V  K  V  S  C  K  A  S  G  Y  T  F  T  S  Y  G  I
agctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcagcgcttac
 S  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  S  A  Y
aatggtaacacaaactatgcacagaagctccagggcagagtcaccatgaccacagacaca
 N  G  N  T  N  Y  A  Q  K  L  Q  G  R  V  T  M  T  T  D  T
tccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggctgtgtat
 S  T  S  T  A  Y  M  E  L  R  S  L  R  S  D  D  T  A  V  Y
tactgtgcaaaagatcgtcattggcattggtggctggacgcctttgattattggggccaa
 Y  C  A  K  D  R  H  W  H  W  W  L  D  A  F  D  Y  W  G  Q
ggtaccctggtcaccgtctccagt
 G  T  L  V  T  V  S  S
```

FIG. 11A, Cont'd

MF4002: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

QVQLVQSGSELKKPGSSVKVSCKASGYTFTNYAMNWVRQAPGQGLEWMGWITTNT
GDPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCVRVYNWIRGFDYWGQG
TLVTVSS

FR1: QVQLVQSGSELKKPGSSVKVSCKASGYTFT

CDR1: NYAMN

FR2: WVRQAPGQGLEWMG

CDR2: WITTNTGDPTYAQGFTG

FR3: RFVFSLDTSVSTAYLQISSLKAEDTAVYYCVR

CDR3: VYNWIRGFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
caggtgcagctggtgcaatctgggtctgagttgaagaagcct
 Q  V  Q  L  V  Q  S  G  S  E  L  K  K  P
gggtcctcagtgaaggtttcctgcaaggcttctggatacaccttcactaactatgctatg
 G  S  S  V  K  V  S  C  K  A  S  G  Y  T  F  T  N  Y  A  M
aattgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaccaccaac
 N  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  W  I  T  T  N
actggggacccaacgtatgcccagggcttcacaggacgttttgtcttctccttggacacc
 T  G  D  P  T  Y  A  Q  G  F  T  G  R  F  V  F  S  L  D  T
tctgtcagtacggcatatctgcagatcagcagcctaaaggctgaggacactgccgtatat
 S  V  S  T  A  Y  L  Q  I  S  S  L  K  A  E  D  T  A  V  Y
tactgtgtgagagtgtataactggataaggggatttgactactggggccagggaaccctg
 Y  C  V  R  V  Y  N  W  I  R  G  F  D  Y  W  G  Q  G  T  L
gtcaccgtctcaagcgtctccagt
 V  T  V  S  S  V  S  S
```

FIG. 11A, Cont'd

MF3751: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGTINPSG
GSTYYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDRNWGWDFDYWGQ
GTLVTVSS

FR1: QVQLVQSGAEVKKPGASVKVSCKASGYTFT

CDR1: GYYMH

FR2: WVRQAPGQGLEWMG

CDR2: TINPSGGSTYYAQKFQG

FR3: RVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR

CDR3: DRNWGWDFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
 cagglgcagclg
  Q  V  Q  L
gtacagtctggggctgaggtgaagaagcctggggcctcagtgaaggtttcctgcaaggca
 V  Q  S  G  A  E  V  K  K  P  G  A  S  V  K  V  S  C  K  A
tctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaaggg
 S  G  Y  T  F  T  G  Y  Y  M  H  W  V  R  Q  A  P  G  Q  G
cttgagtggatgggaacaatcaaccctagtggtggtagcacatactacgcacagaagttc
 L  E  W  M  G  T  I  N  P  S  G  G  S  T  Y  Y  A  Q  K  F
cagggcagagtcaccatgaccagggacacgtccacgagcacagtctacatggagctgagc
 Q  G  R  V  T  M  T  R  D  T  S  T  S  T  V  Y  M  E  L  S
agcctgagatctgaggacacggccgtgtattactgtgcgagagatcggaactggggatgg
 S  L  R  S  E  D  T  A  V  Y  Y  C  A  R  D  R  N  W  G  W
Gactttgactactggggccagggaaccctggtcaccgtctccagt
 D  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S
```

FIG. 11A, Cont'd

MF3752: heavy chain variable region sequence of an EGFR binding antibody

Complete VH sequence:

EVQLVESGPEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGTINPSGG
STYYAQKFQGRVTLTRDTSTSTVYMVLSSLRSEDTAVYYCARDRNWGWDFDYWGQG
TLVTVSS

FR1: EVQLVESGPEVKKPGASVKVSCKASGYTFT

CDR1: SYYMH

FR2: WVRQAPGQGLEWMG

CDR2: TINPSGGSTYYAQKFQG

FR3: RVTLTRDTSTSTVYMVLSSLRSEDTAVYYCAR

CDR3: DRNWGWDFDY

FR4: WGQGTLVTVSS

Annotated nucleotide sequence:

```
  gaggtgcagctggtggagtctgggcctgaggtgaagaagcct
   E  V  Q  L  V  E  S  G  P  E  V  K  K  P
ggggcctcagtgaaggtttcctgcaaggcatctggatacaccttcaccagctactatatg
 G  A  S  V  K  V  S  C  K  A  S  G  Y  T  F  T  S  Y  Y  M
cactgggtgcgacaggcccctggacaagggcttgagtggatgggaacaatcaaccctagt
 H  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  T  I  N  P  S
ggtggtagcacatactacgcacagaagttccagggcagagtcaccctgaccagggacacg
 G  G  S  T  Y  Y  A  Q  K  F  Q  G  R  V  T  L  T  R  D  T
tccacgagcacagtctacatggtgctgagcagcctgagatctgaggacacggccgtgtat
 S  T  S  T  V  Y  M  V  L  S  S  L  R  S  E  D  T  A  V  Y
tactgtgcgagagatcggaactggggatgggactttgactactggggccagggaaccctg
 Y  C  A  R  D  R  N  W  G  W  D  F  D  Y  W  G  Q  G  T  L
gtcaccgtctcaagcgtctccagt
 V  T  V  S  S  V  S  S
```

FIG. 11B

MF3178: heavy chain variable region sequence of an erbB-3 binding antibody

Nucleic acid sequence (underlined sequence encodes end of leader peptide):

```
  1 GGCCCAGCCG GCCATGGCCC AGGTGCAGCT GGTGCAGTCT GGGGCTGAGG TGAAGAAGCC
 61 TGGGGCCTCA GTGAAGGTCT CCTGCAAGGC TTCTGGATAC ACCTTCACCG GCTACTATAT
121 GCACTGGGTG CGACAGGCCC CTGGACAAGG GCTTGAGTGG ATGGGATGGA TCAACCCTAA
181 CAGTGGTGGC ACAAACTATG CACAGAAGTT TCAGGGCAGG GTCACGATGA CCAGGGACAC
241 GTCCATCAGC ACAGCCTACA TGGAGCTGAG CAGGCTGAGA TCTGACGACA CGGCTGTGTA
301 TTACTGTCCA ACACATCATC CTTCTCCTCA TTTCTCGTCT TACTCCCCCT TTCATTATTC
361 GGGCCAAGGT ACCCTGGTCA CCGTCTCCAG T
```

Amino acid sequence:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNS
GGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDHGSRHFWSYWGF
DYWGQGTLVTVSS

CDR1: GYYMH

CDR2: WINPNSGGTNYAQKFQG

CDR3: DHGSRHFWSYWGFDY

FIG. 11B, Cont'd

MF3176: heavy chain variable region sequence of an erbB-3 binding antibody

Nucleic acid sequence (underlined sequence encodes end of leader peptide):

```
   1 GGCCCAGCCG GCCATGGCCG AGGTGCAGCT GTTGGAGTCT GGGGGAGGCT TGGTACAGCC
  61 TGGGGGGTCC CTGAGACTCT CCTGTGCAGC CTCTGGATTC ACCTTTAGCA GCTATGCCAT
 121 GAGCTGGGTC CGCCAGGCTC CAGGGAAGGG GCTGGAGTGG GTCTCAGCTA TTAGTGGTAG
 181 TGGTGGTAGC ACATACTACG CAGACTCCGT GAAGGGCCGG TTCACCATCT CCAGAGACAA
 241 TTCCAAGAAC ACGCTGTATC TGCAAATGAA CAGCCTGAGA GCCGAGGACA CGGCTGTGTA
 301 TTACTGTGCA ACACATTGGT CGTACCCCCC CTACTACTGC GGCTTTGATT ATTGGGGCCA
 361 AGGTACCCTG GTCACCGTCT CCAGT
```

Amino acid sequence:

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS
TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWWYPPYYWGFDYWG
QGTLVTVSS

CDR1: SYAMS

CDR2: AISGSGGSTYYADSVKG

CDR3: DWWYPPYYWGFDY

FIG. 11B, Cont'd

MF3163: heavy chain variable region sequence of an erbB-3 binding antibody

Nucleic acid sequence (underlined sequence encodes end of leader peptide):

```
   1 GGCCCAGCCG GCCATGGCCC AGGTGCAGCT GGTGCAGTCT GGGGCTGAGG TGAAGAAGCC
  61 TGGGGCCTCA GTGAAGGTCT CCTGCAAGGC TTCTGGATAC ACCTTCACCG GCTACTATAT
 121 GCACTGGGTG CGACAGGCCC CTGGACAAGG GCTTGAGTGG ATGGGATGGA TCAACCCTAA
 181 CAGTGGTGGC ACAAACTATG CACAGAAGTT TCAGGGCAGG GTCACGATGA CCAGGGACAC
 241 GTCCATCAGC ACAGCCTACA TGGAGCTGAG CAGGCTGAGA TCTGACGACA CGGCCGTGTA
 301 TTACTGTGCA AAACATTCTT ACTCTCCTCA TTTCTACTCT TGGTGCCCCT TTGATTATTG
 361 GGGCCAAGGT ACCCTGGTCA CCGTCTCCAG T
```

Amino acid sequence:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNS
GGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAKDSYSRHFYSWWAF
DYWGQGTLVTVSS

CDR1: GYYMH

CDR2: WINPNSGGTNYAQKFQG

CDR3: DSYSRHFYSWWAFDY

FIG. 11B, Cont'd

MF3307: heavy chain variable region sequence of an erbB-3 binding antibody

Nucleic acid sequence (underlined sequence encodes end of leader peptide):

```
  1 GGCCCAGCCG GCCATGGCCC AGGTGCAGCT GGTGCAGTCT GGGGCTGAGG TGAAGAAGCC
 61 TGGGGCCTCA GTGAAGGTCT CCTGCAAGGC TTCTGGATAC ACCTTCACCG GCTACTATAT
121 GCACTGGGTG CGACAGGCCC CTGGACAAGG GCTTGAGTGG ATGGGATGGA TCAACCCTAA
181 CAGTGGTGGC ACAAACTATG CACAGAAGTT TCAGGGCAGG GTCACGATGA CCAGGGACAC
241 GTCCATCAGC ACAGCCTACA TGGAGCTGAG CAGGCTGAGA TCTGACGACA CGGCCGTGTA
301 TTACTGTGCA AGAGGTTCTC GTAAACGTCT GTCTAACTAC TTCAACGCCT TTGATTATTG
361 GGGCCAAGGT ACCCTGGTCA CCGTCTCCAG T
```

Amino acid sequence:

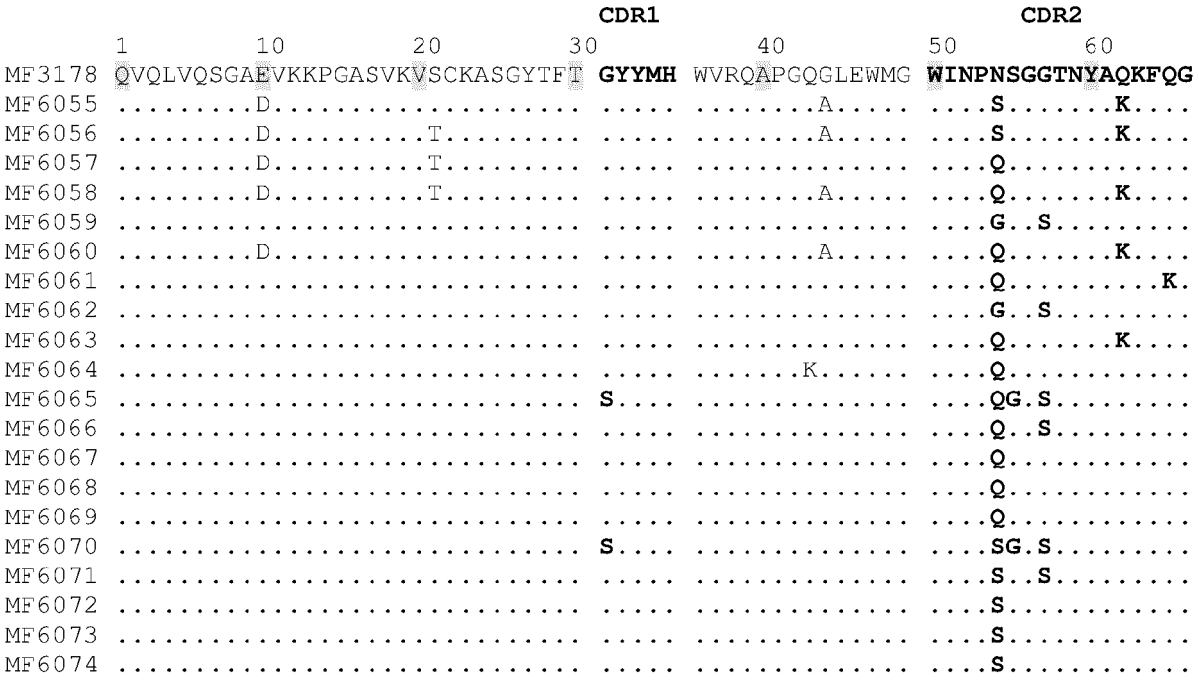
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNS
GGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGSRKRLSNYFNAFD
YWGQGTLVTVSS

CDR1: GYYMII

CDR2: WINPNSGGTNYAQKFQG

CDR3: GSRKRLSNYFNAFDY

FIG. 11B, Cont'd



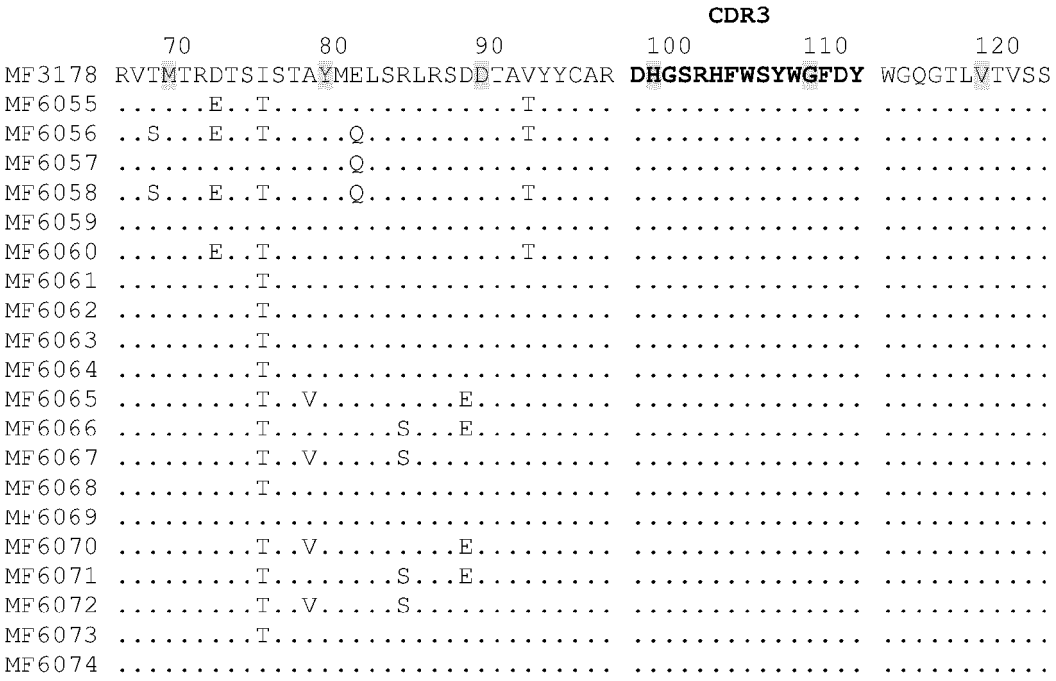


FIG. 11B, Cont'd

DNA sequences of MF3178 variants (without sequence encoding leader peptide)

>MF6055_VH

caggtgcagctggtgcagtctggggctgacgtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagctcttgagtg
gatgggatggatcaacccttctagtggtggcacaaactatgcaaagaagtttcagggcagggtcacgatg
accagggagacgtccacaagcacagcctacatggagctgagcaggctgagatctgacgacacggctacgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccc tggtc accgt ctcca gt

>MF6056_VH

caggtgcagctggtgcagtctggggctgacgtgaagaagcctggggcctcagtgaaggtcacgtgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagctcttgagtg
gatgggatggatcaacccttctagtggtggcacaaactatgcaaagaagtttcagggcagggtctctatg
accagggagacgtccacaagcacagcctacatgcagctgagcaggctgagatctgacgacacggctacgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6057_VH

caggtgcagctggtgcagtctggggctgatgtgaagaagcctggggcctcagtgaaggtcacgtgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccatcagcacagcctacatgcagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6058_VH

caggtgcagctggtgcagtctggggctgacgtgaagaagcctggggcctcagtgaaggtcacgtgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagctcttgagtg
gatgggatggatcaaccctcaaagtggtggcacaaactatgcaaagaagtttcagggcagggtctctatg
accagggagacgtccacaagcacagcctacatgcagctgagcaggctgagatctgacgacacggctacgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6059_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctggcagtggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6060_VH

caggtgcagctggtgcagtctggggctgacgtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagctcttgagtg
gatgggatggatcaaccctcaaagtggtggcacaaactatgcaaagaagtttcagggcagggtcacgatg
accagggagacgtccacaagcacagcctacatggagctgagcaggctgagatctgacgacacggctacgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6061_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttaagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6062_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctggcagtggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccacaagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6063_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcaaagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6064_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggaaaggggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccacgagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6065_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcacctcttactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcaggggggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagtgtacatggagctgagcaggctgagatctgaggacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6066_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagctctctgagatctgaggacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6067_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagtctacatggagctgagctctctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6068_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6069_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaaccctcagagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6070_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcacctcttactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaacccttctgggggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagtgtacatggagctgagcaggctgagatctgaggacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6071_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaacccttctagtggttctacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagctctctgagatctgaggacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6072_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaacccttctagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagtctacatggagctgagctctctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

>MF6073_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaacccttctagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccaccagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

>MF6074_VH

caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
cttctggatacaccttcaccggctactatatgcactgggtgcgacaggcccctggacaagggcttgagtg
gatgggatggatcaacccttctagtggtggcacaaactatgcacagaagtttcagggcagggtcacgatg
accagggacacgtccatcagcacagcctacatggagctgagcaggctgagatctgacgacacggctgtgt
attactgtgcaagagatcatggttctcgtcatttctggtcttactggggctttgattattggggccaagg
taccctggtcaccgtctccagt

FIG. 11B, Cont'd

Nucleic acid alignment (*without* end of leader sequence)

```
MF3178 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAG
MF6058 ............................C.............................A.G......
MF6061 ............................................................................
MF6065 ............................................................................

                                    CDR1
MF3178 GCTTCTGGATACACCTTCACC GGCTACTATATGCAC TGGGTGCGACAGGCCCCTGGACAAGGGCTTG
MF6058 ..................... ............... ..........................CT....
MF6061 ..................... ............... ..............................
MF6065 ..................... TCT............ ..............................

                                                CDR2
MF3178 AGTGGATGGGA TGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGT
MF6058 ..........  ............C.A.....................A.............. .....
MF6061 ..........  ............C.G...............................A..... .....
MF6065 ..........  ............C.GG.G...TCT.......................... .....

MF3178 CACGATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGAGCAGGCTGAGATCTGACGACAC
MF6058 .T.T...........G.......CA..............C.............................
MF6061 ........................C.....................................................
MF6065 ........................C........TG.............................G.....

                                                          CDR3
MF3178 GGCTGTGTATTACTGTGCAAGA GATCATGGTTCTCGTCATTTCTGGTCTTACTGGGGCTTTGATTAT
MF6058 ....AC.............. ..........................................
MF6061 ..................... ..........................................
MF6065 ..................... ..........................................

MF3178 TGGGGCCAAGGTACCCTGGTCACCGTCTCCAGT
MF6058 ................................
MF6061 ................................
MF6065 ................................
```

FIG. 11C

a) Common Light Chain

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPPTFGQGTKVEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 11D

heavy chain for EGFR binding

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEY
GKTFFAQNFQGRVTMTEDTSADTAYMELSSLRSEDTAVYYCATEGYYETTTYYYNLF
DSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

heavy chain for erbB-3 binding

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNS
GGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDHGSRHFWSYWGF
DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

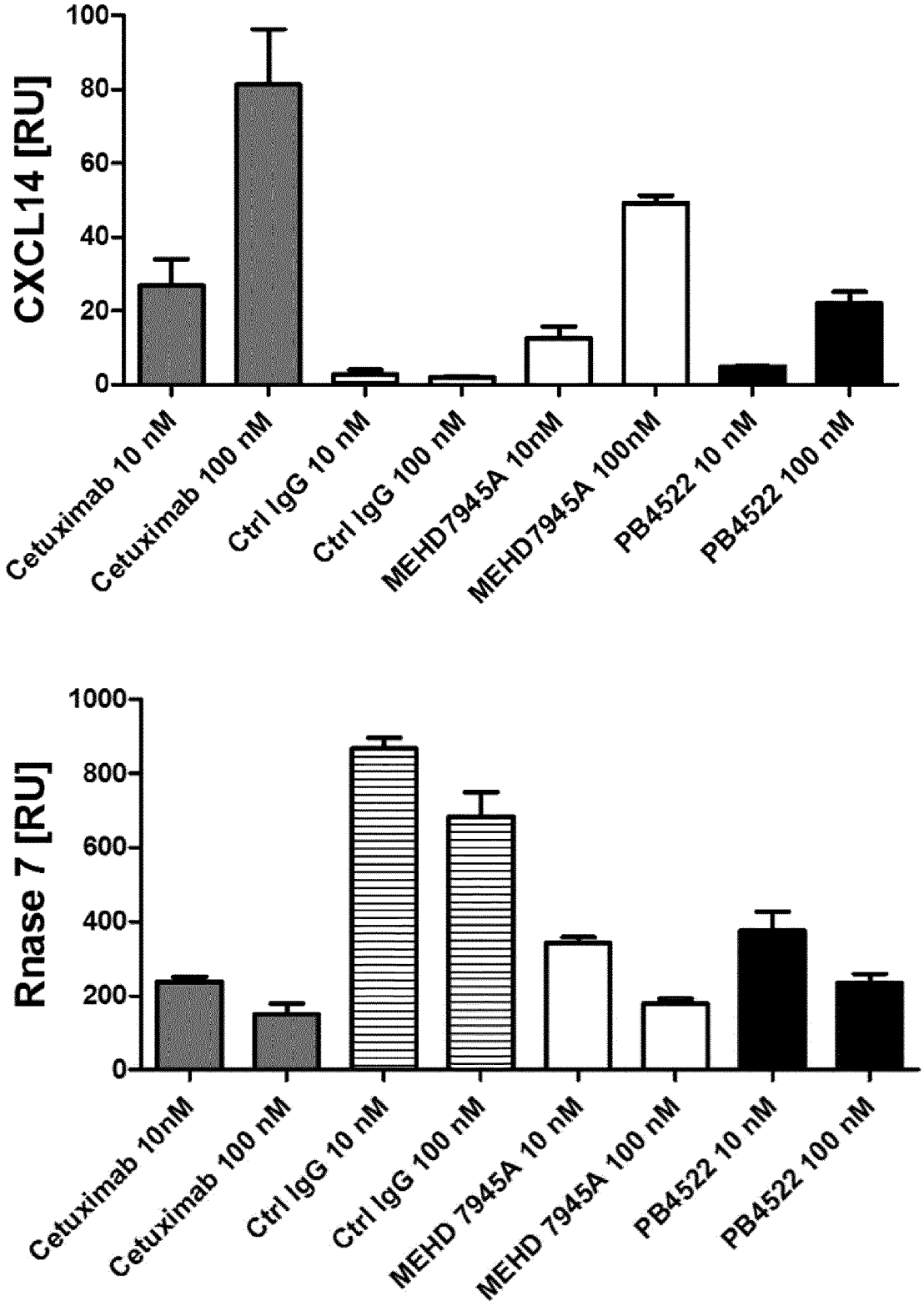

CXCL14 [RU]
100
80
60
40
20
0
Cetuximab 10 nM
Cetuximab 100 nM
Ctrl IgG 10 nM
Ctrl IgG 100 nM
MEHD7945A 10nM
MEHD7945A 100nM
PB4522 10 nM
PB4522 100 nM
Rnase 7 [RU]
1000
800
600
400
200
0
Cetuximab 10nM
Cetuximab 100 nM
Ctrl IgG 10 nM
Ctrl IgG 100 nM
MEHD 7945A 10 nM
MEHD 7945A 100 nM
PB4522 10 nM
PB4522 100 nM

FIG. 12

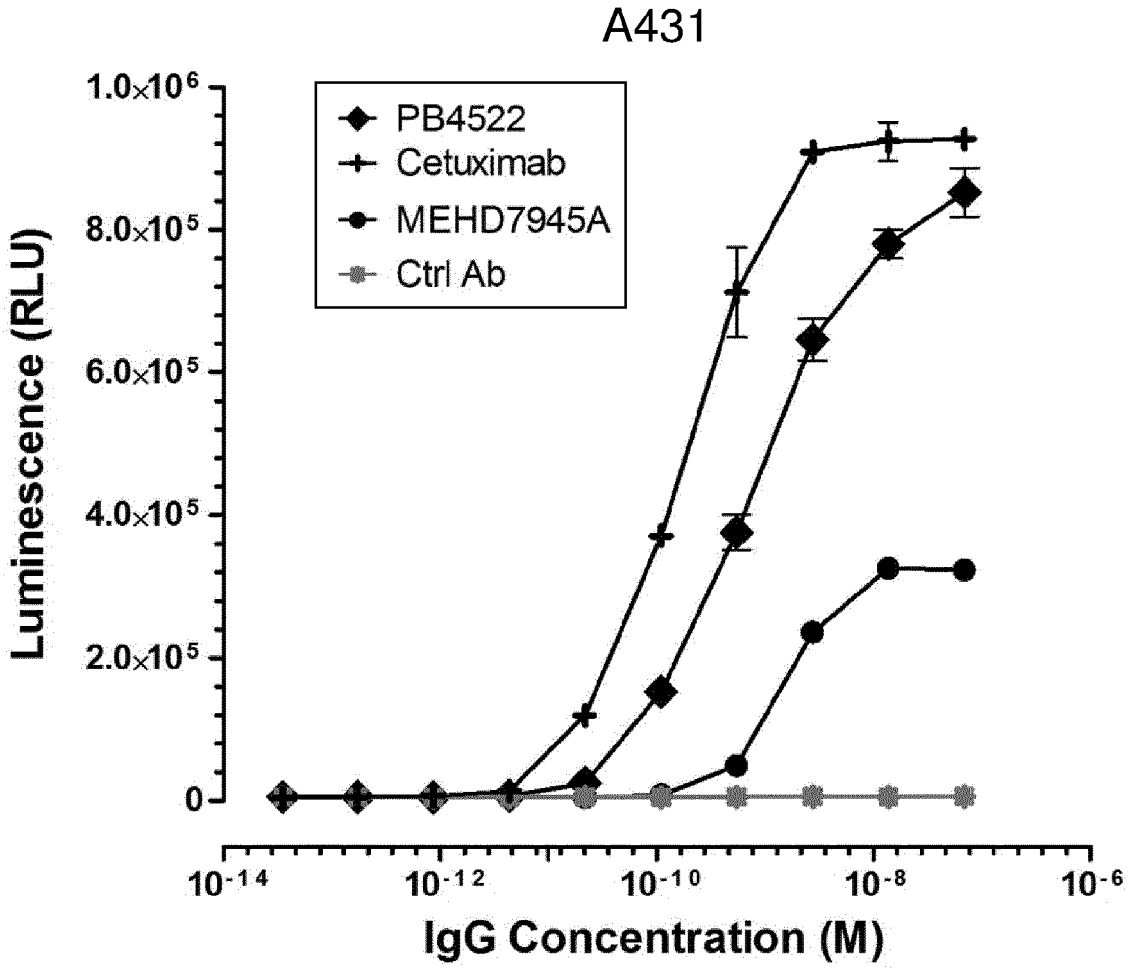

A431
PB4522
Cetuximab
MEHD7945A
Ctrl Ab
Luminescence (RLU)
1.0×10⁶
8.0×10⁵
6.0×10⁵
4.0×10⁵
2.0×10⁵
0
10⁻¹⁴
10⁻¹²
10⁻¹⁰
10⁻⁸
10⁻⁶
IgG Concentration (M)

FIG. 13

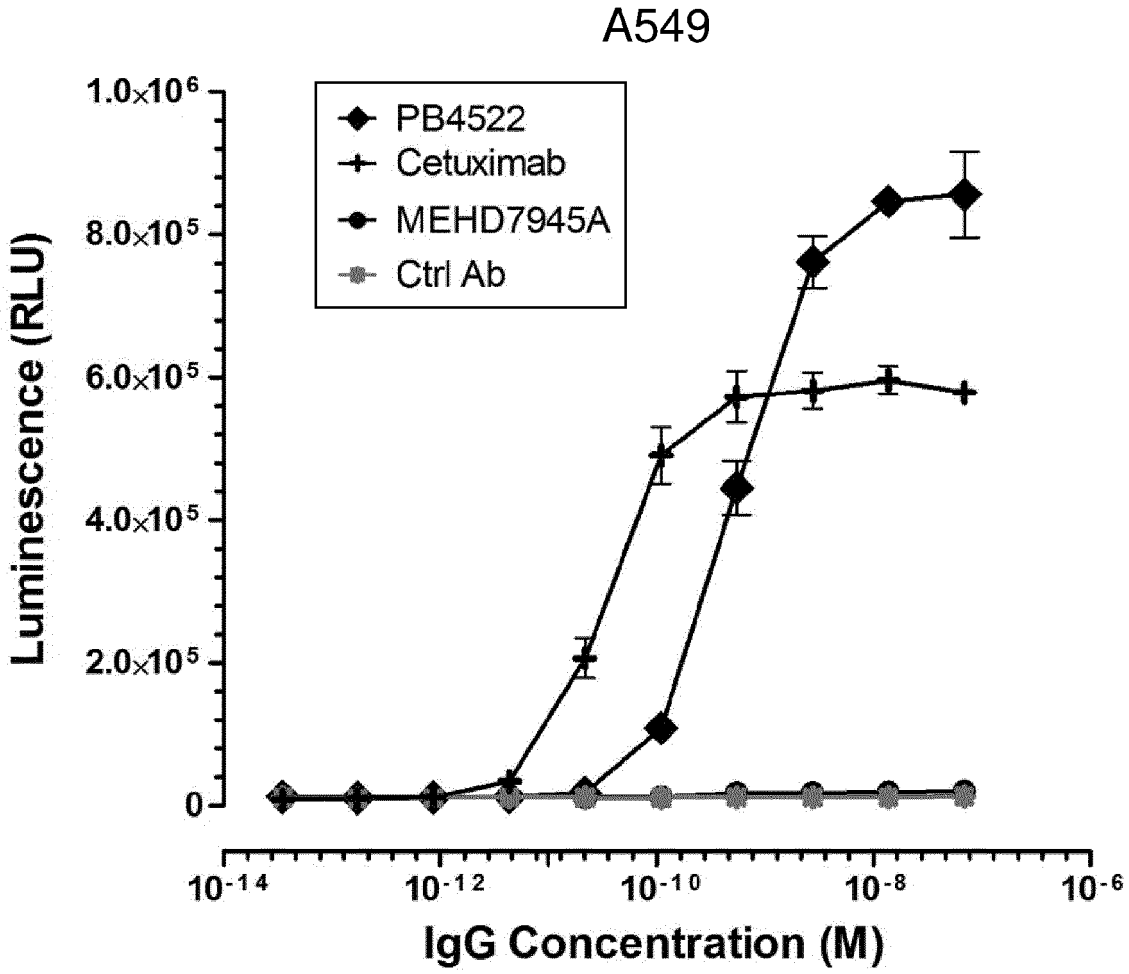

A549
PB4522
Cetuximab
MEHD7945A
Ctrl Ab
Luminescence (RLU)
1.0×10⁶
8.0×10⁵
6.0×10⁵
4.0×10⁵
2.0×10⁵
0
10⁻¹⁴
10⁻¹²
10⁻¹⁰
10⁻⁸
10⁻⁶
IgG Concentration (M)

FIG. 13, Cont'd

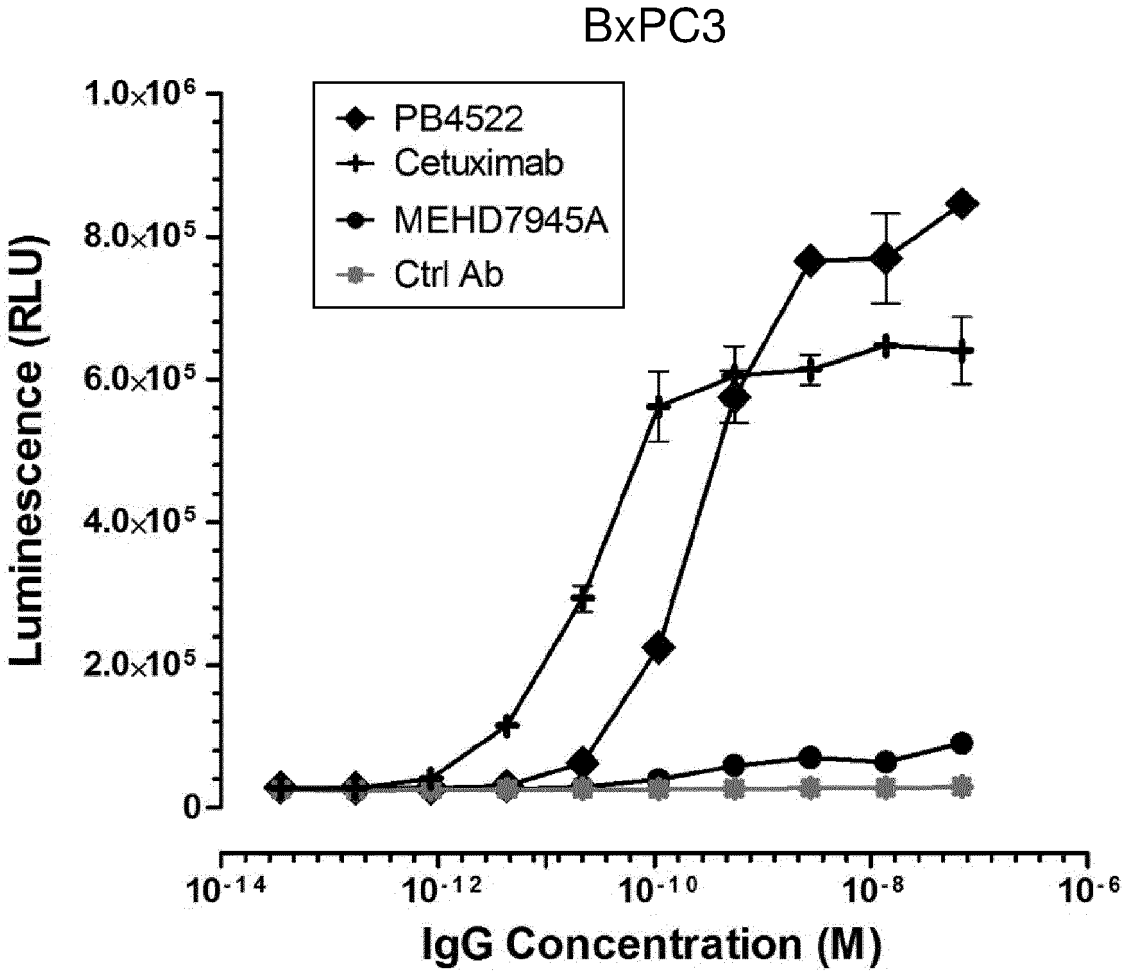

BxPC3
PB4522
Cetuximab
MEHD7945A
Ctrl Ab
Luminescence (RLU)
1.0x10^6
8.0x10^5
6.0x10^5
4.0x10^5
2.0x10^5
0
10^-14
10^-12
10^-10
10^-8
10^-6
IgG Concentration (M)

FIG. 13, Cont'd

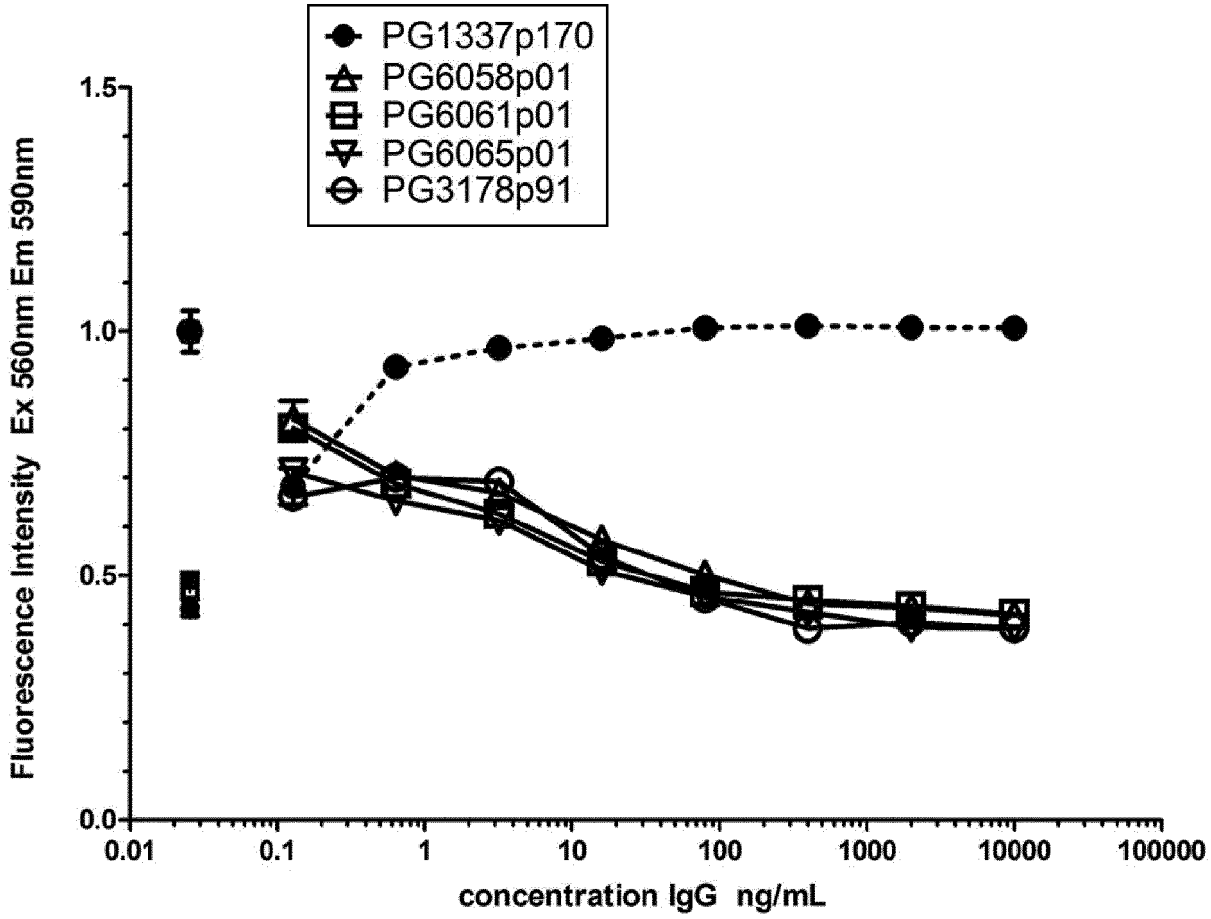

PG1337p170
PG6058p01
PG6061p01
PG6065p01
PG3178p91
Fluorescence Intensity Ex 560nm Em 590nm
1.5
1.0
0.5
0.0
0.01
0.1
1
10
100
1000
10000
100000
concentration IgG ng/mL

FIG. 14

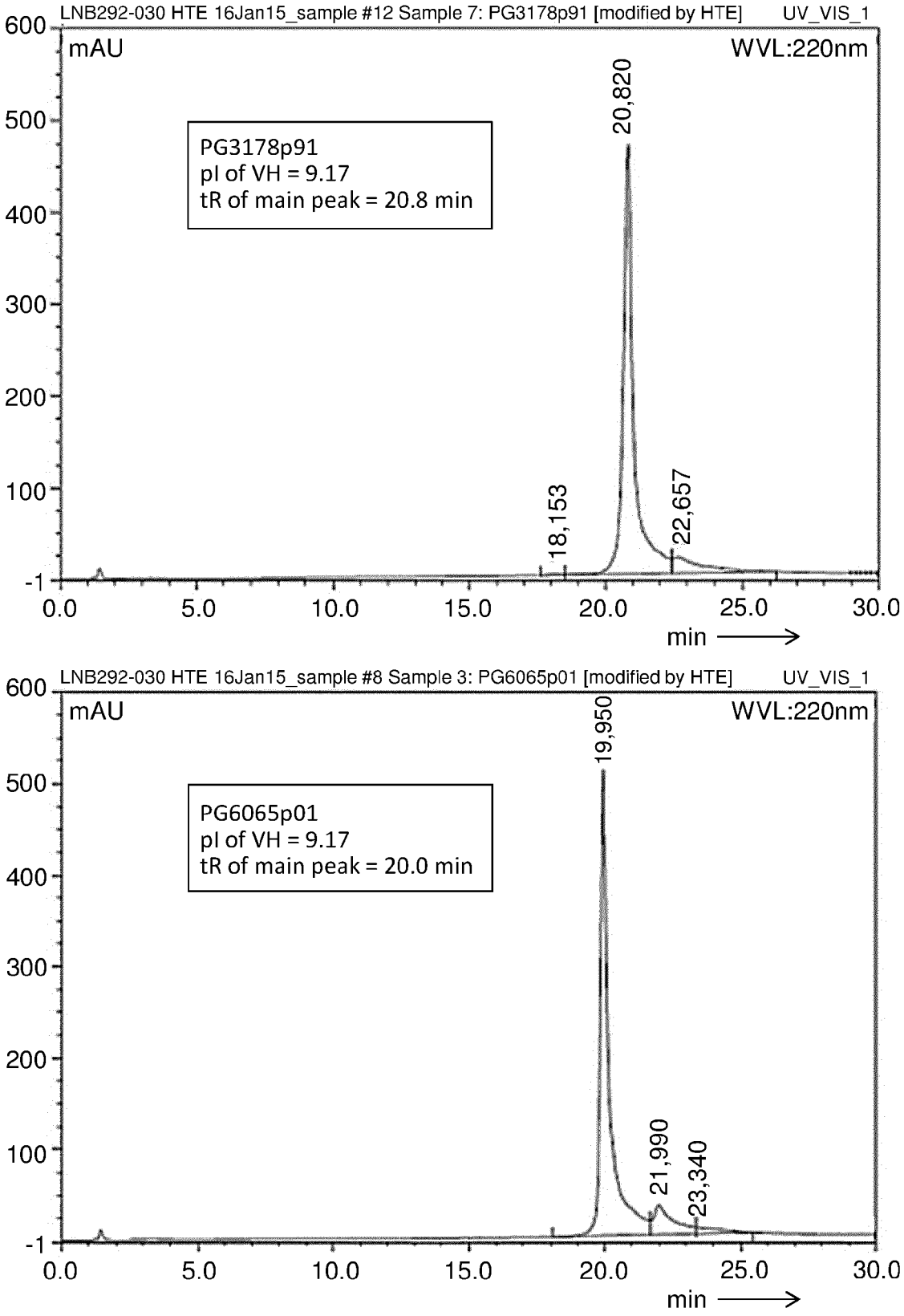

LNB292-030 HTE 16Jan15_sample #12 Sample 7: PG3178p91 [modified by HTE] UV_VIS_1
mAU
WVL:220nm
PG3178p91
pI of VH = 9.17
tR of main peak = 20.8 min
20,820
18,153
22,657
600
500
400
300
200
100
-1
0.0
5.0
10.0
15.0
20.0
25.0
30.0
min
LNB292-030 HTE 16Jan15_sample #8 Sample 3: PG6065p01 [modified by HTE] UV_VIS_1
mAU
WVL:220nm
PG6065p01
pI of VH = 9.17
tR of main peak = 20.0 min
19,950
21,990
23,340
600
500
400
300
200
100
-1
0.0
5.0
10.0
15.0
20.0
25.0
30.0
min

FIG. 15

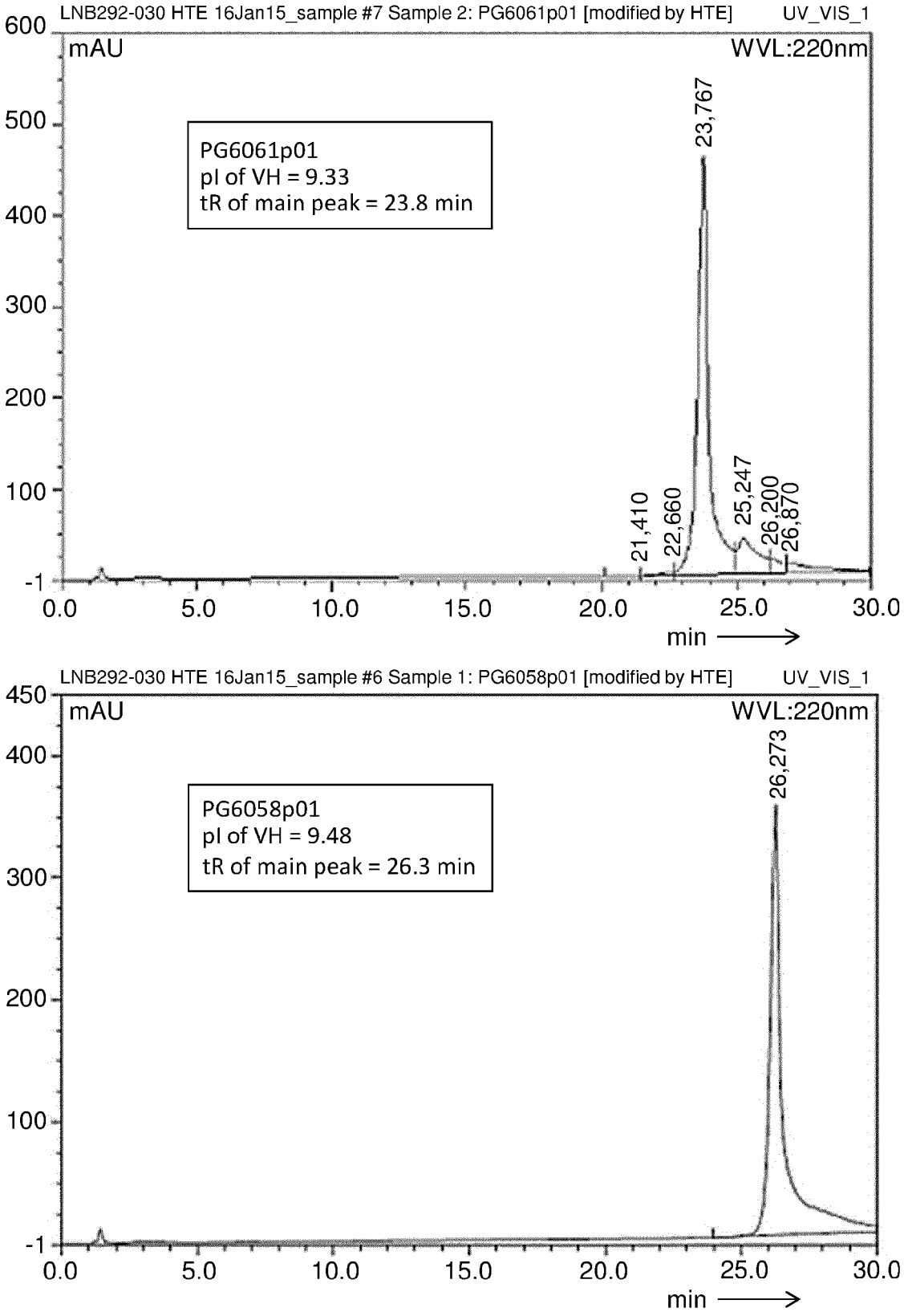

LNB292-030 HTE 16Jan15_sample #7 Sample 2: PG6061p01 [modified by HTE]
UV_VIS_1
mAU
WVL:220nm
PG6061p01
pI of VH = 9.33
tR of main peak = 23.8 min
23,767
21,410
22,660
25,247
26,200
26,870
min
LNB292-030 HTE 16Jan15_sample #6 Sample 1: PG6058p01 [modified by HTE]
UV_VIS_1
mAU
WVL:220nm
PG6058p01
pI of VH = 9.48
tR of main peak = 26.3 min
26,273
min

FIG. 15, Cont'd



FIG. 16a

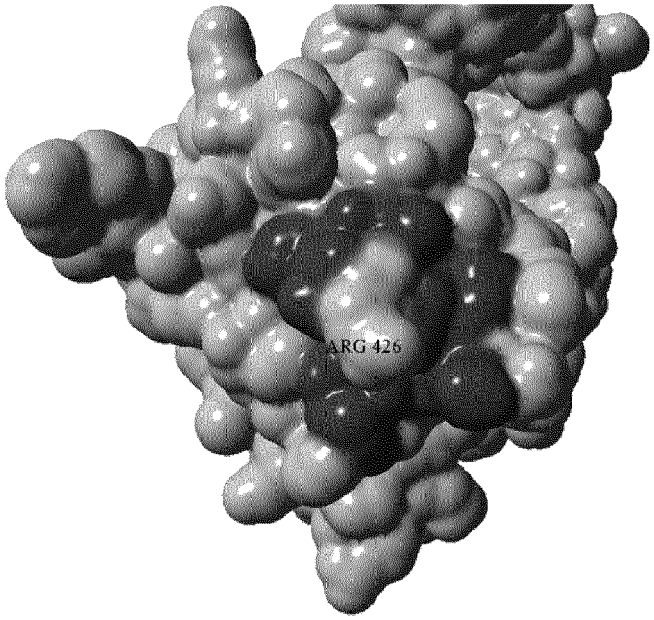


FIG. 16b

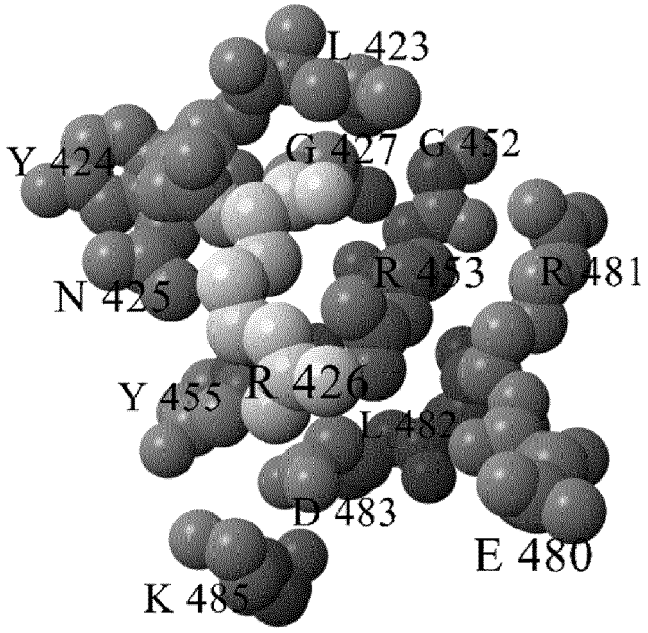


FIG. 16c

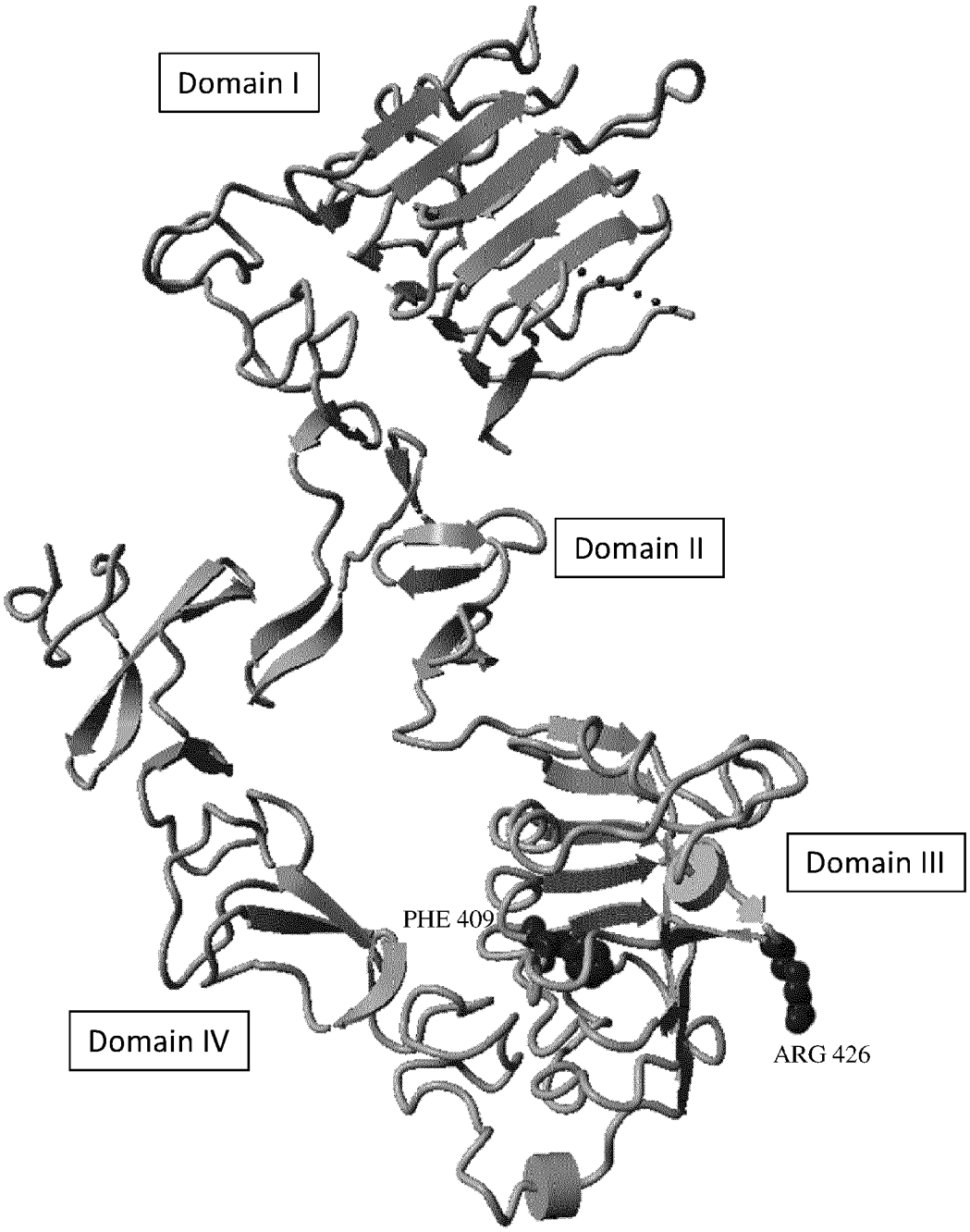


FIG. 17

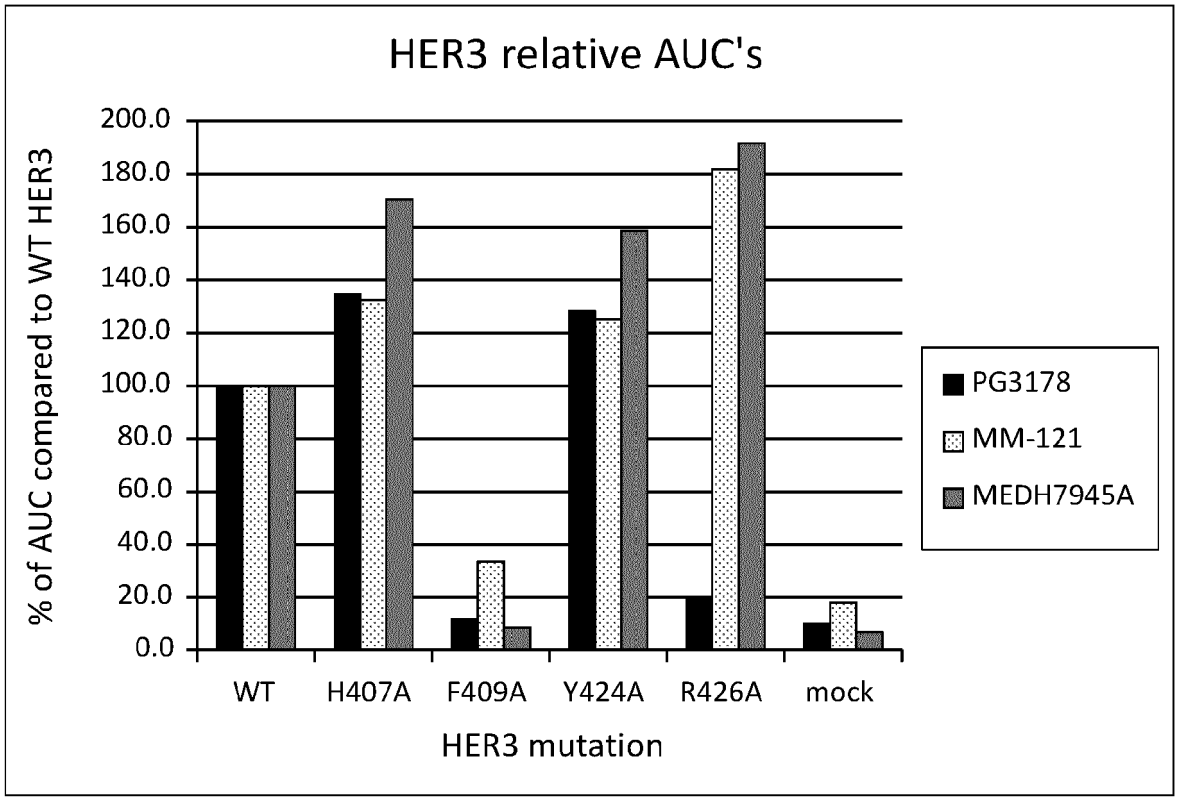

HER3 relative AUC's
% of AUC compared to WT HER3
200.0
180.0
160.0
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
WT
H407A
F409A
Y424A
R426A
mock
HER3 mutation
PG3178
MM-121
MEDH7945A

FIG. 18