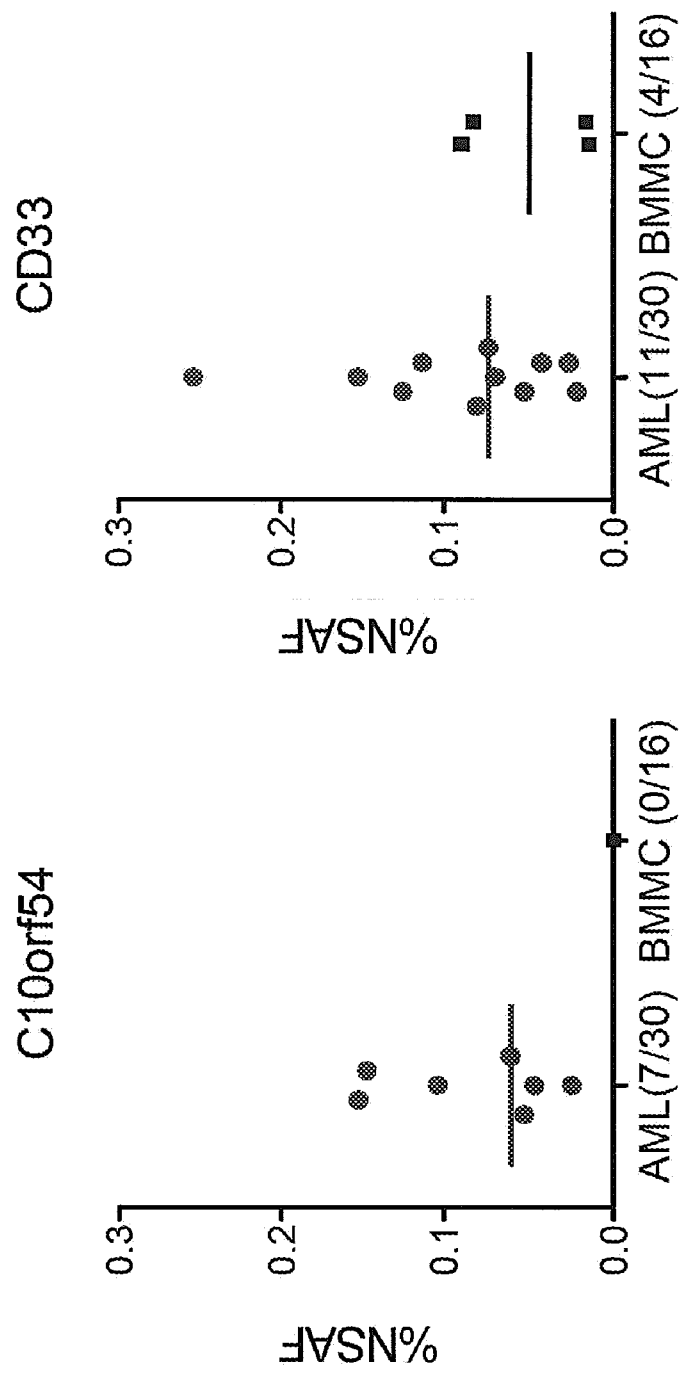

C10orf54
%NSAF
0.3
0.2
0.1
0.0
AML(7/30)
BMMC (0/16)
CD33
%NSAF
0.3
0.2
0.1
0.0
AML(11/30)
BMMC (4/16)

FIG. 1A

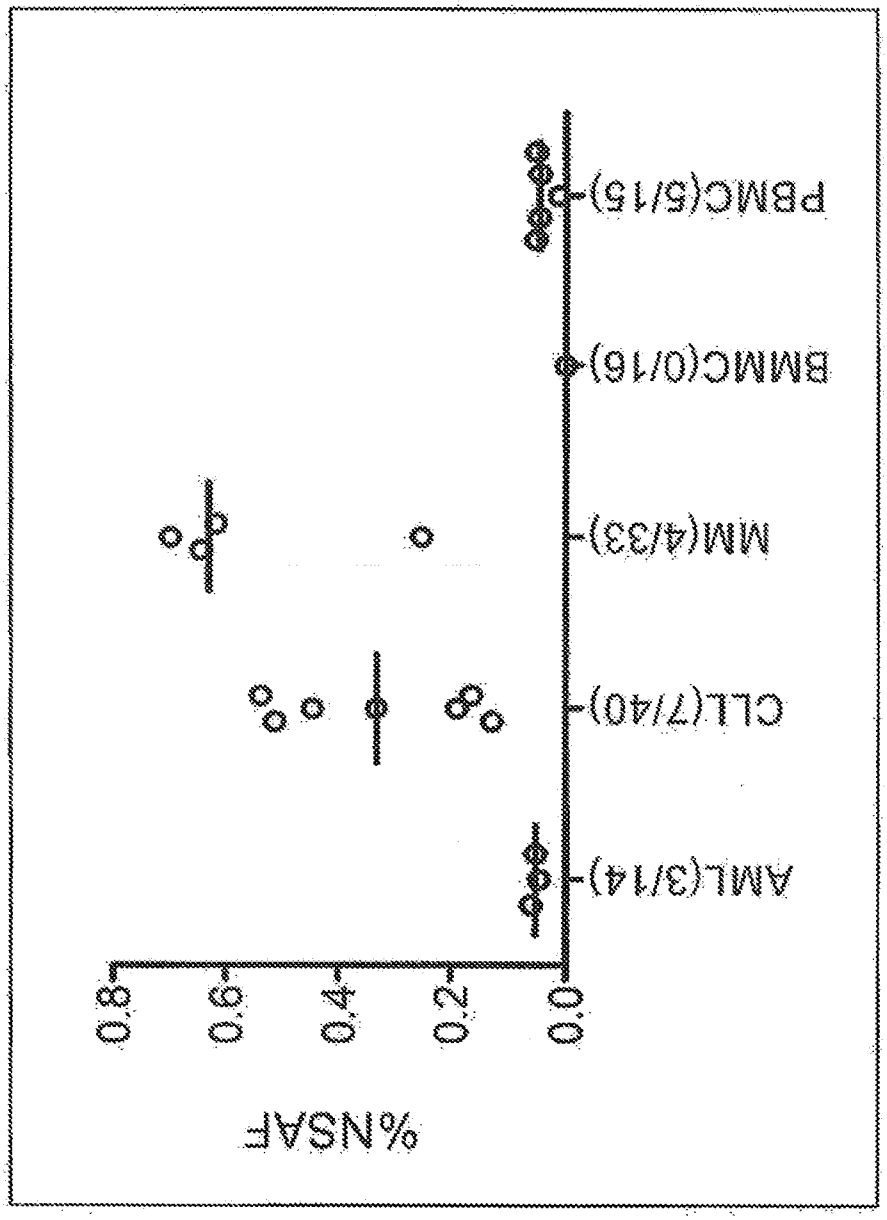


FIG. 1B

C10ORF54	CD13+/CD33+			CD34+/CD33+			CD34+/CD33-		
	Incidence*	Pos, [%]	Fold MFI	Incidence*	Pos, [%]	Fold MFI	Incidence*	Pos, [%]	Fold MFI
AML	18/23 (3 relapses)	31	48.6	10/21 (3 relapses)	41	50.9	9/21 (3 relapses)	25	8.5
BMNC	3/3	75	28.1	1/3	31	0.9	0/3	1.5	0.5

FIG. 2

huVH1
Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)
QVQLVQSGAEVKKPGASVKCKAS **GYTFTSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYAQKLQG** RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

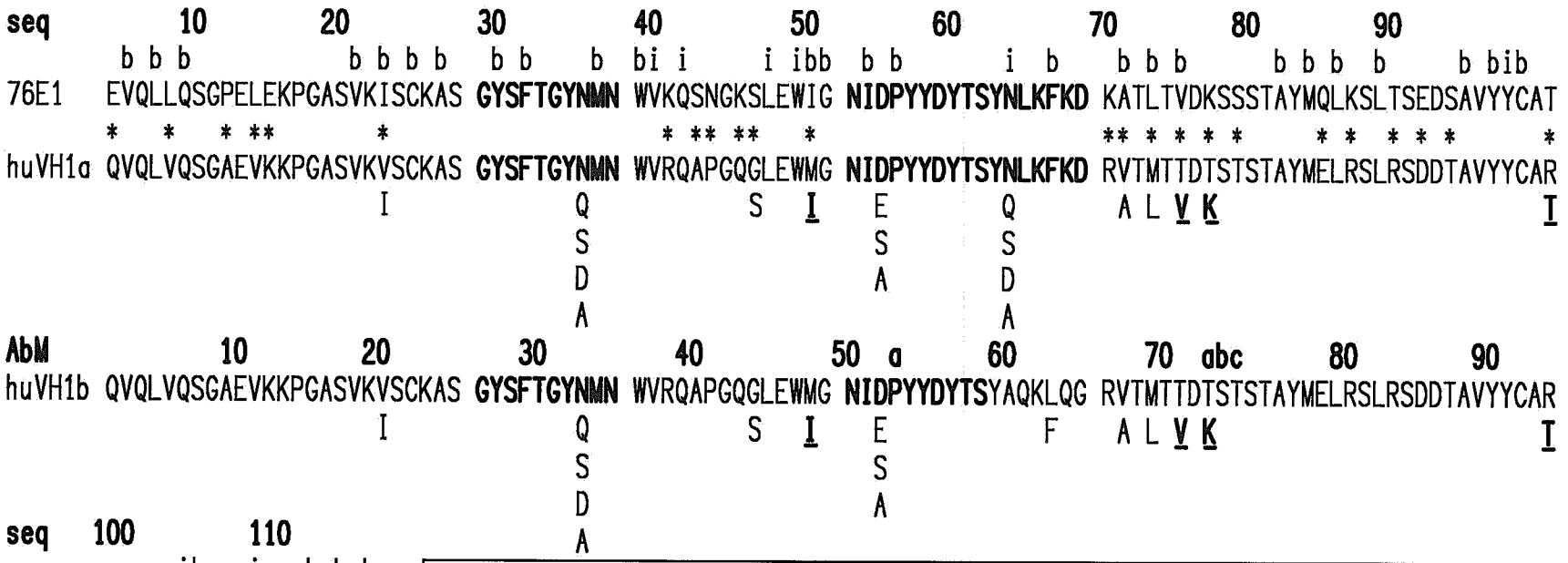
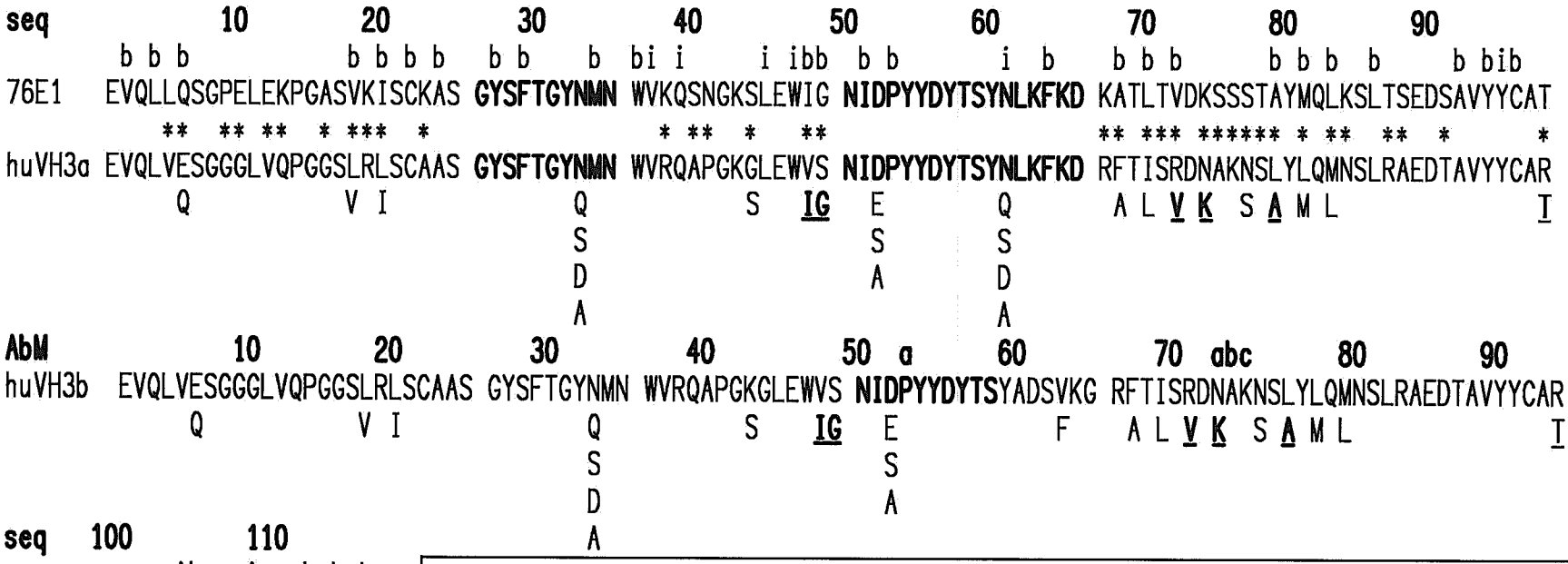


FIG. 3A

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVH3
Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GFTFSSYSMN** WVRQAPGKGLEWVS **YISSSSSTIYYADSVKG** RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS



(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 3B

huVH1
Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)
QVQLVQSGAEVKKPGASVKCKAS **GYTFTSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYAQKLQG** RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

FIG. 4A

Joining region
IMGT 00256|IGHJ4*01|YFDYWGQGTLVTVSS

```
seq              10        20        30        40        50        60        70        80        90
         b b b           b b b b   b b    b  bi i    i ibb  b b      i  b    b b b      b b b  b     b bib
141A     QVQLQQSGAELMKPGASVKISCKAT GYTFSRYWIE WVKQRPGHGLEWIG EILPGSGSTNYNEKFKG KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG
           *     **        *   *             * *  *    *                      ** * *   **    * *  * * *      *
huVH1a   QVQLVQSGAEVKKPGASVKVSCKAS GYTFSRYWIE WVRQAPGQGLEWMG EILPGSGSTNYNEKFKG RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                   M       I                                 I          Q Q       A F A    N                   G
                                                                      S S
                                                                      D D
                                                                      A A
AbM              10        20        30        40        50 a      60        70 abc    80        90
huVH1b   QVQLVQSGAEVKKPGASVKVSCKAS GYTFSRYWIE WVRQAPGQGLEWMG EILPGSGSTNYAQKLQG RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                   M       I                                 I          Q    F    A F A    N                   G
                                                                      S
                                                                      D
                                                                      A
seq   100        110       120
                ib   i   b b b
141A     EEVYDGYPWFGY WGQGTLVTVSA                                      *
huVH1a   EEVYDGYPWFGY WGQGTLVTVSS
           E
           S
           A
AbM        100abcd        110
huVH1b   EEVYDGYPWFGY WGQGTLVTVSS
           E
           S
           A
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVH3
Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GFTFSSYSMN** WVRQAPGKGLEWVS **YISSSSSTIYYADSVKG** RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR

FIG. 4B

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

```
seq              10        20        30        40        50        60        70        80        90
          b b b          b b b b   b b    b  bi i    i ibb  b b      i  b   b b b      b b b  b     b bib
141A      QVQLQQSGAELMKPGASVKISCKAT GYTFSRYWIE WVKQRPGHGLEWIG EILPGSGSTNYNEKFKG KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG
          *   **  ** **  * ***  * *             * *  *    **                     ** *** *** ** * **  **  *      *
huVH3a    EVQLVESGGLVQPGGSLRLSCAAS GYTFSRYWIE WVRQAPGKGLEWVS EILPGSGSTNYNEKFKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
              Q    M    V I                              IG        Q Q      A F A T   A M L            G
                                                                    S S
                                                                    D D
                                                                    A A
AbM              10        20        30        40        50 a      60        70 abc    80        90
huVH3b    EVQLVESGGGLVQPGGSLRLSCAAS GYTFSRYWIE WVRQAPGKGLEWVS EILPGSGSTNYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
              Q    M    V I                              IG        Q   F   A F A T   A M L            G
                                                                    S
                                                                    D
                                                                    A
seq   100       110       120
                ib   i   b b b
141A      EEVYDGYPWFGY WGQGTLVTVSA
                                 *
huVH3a    EEVYDGYPWFGY WGQGTLVTVSS
          E
          S
          A
AbM       100abcd        110
huVH3b    EEVYDGYPWFGY WGQGTLVTVSS
          E
          S
          A
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVH1
Potential humanized sequence based on IMGT IGHV1-18 acceptor framework (method 1)
QVQLVQSGAEVKKPGASVKCKAS **GYTFTSYGIS** WVRQAPGQGLEWMG **WISAYNGNTNYAQKLQG** RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

```
seq              10        20        30        40        50        60        70        80        90
          b b b          b b b b   b b    b  bi i    i ibb  b b      i  b    b b b      b b b  b     b bib
175A      QVQLQQSGAELMKPGASVKISCKAT GYTFSTHWIE WVKQRPGHGLEWIG EILPGSGSTSYNEKFKG KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR
            *     **        *    *              * *  *    *                     ** * *   **    * *  * * *
huVH1a    QVQLVQSGAEVKKPGASVKVSCKAS GYTFSTHWIE WVRQAPGQGLEWMG EILPGSGSTSYNEKFKG RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                          I                                   I           Q       A F A    N
                                                                          S
                                                                          D
                                                                          A
AbM               10        20        30        40        50 a      60        70 abc    80        90
huVH1b    QVQLVQSGAEVKKPGASVKVSCKAS GYTFSTHWIE WVRQAPGQGLEWMG EILPGSGSTSYAQKLQG RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                          I                                   I             F    A F A
```

```
seq   100       110
           ib    i   b b b
175A      WLLYYYAMDY WGQGTSVTVSS
                        *
huVH1a    WLLYYYAMDY WGQGTLVTVSS

AbM        100ab        110
huVH1b    WLLYYYAMDY WGQGTLVTVSS
```

FIG. 5A

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVH3
Potential humanized sequence based on IMGT IGHV3-48 acceptor framework (method 2)
EVQLVESGGGLVQPGGSLRLSCAAS **GFTFSSYSMN** WVRQAPGKGLEWVS **YISSSSSTIYYADSVKG** RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR

Joining region
IMGT J00256|IGHJ4*01|YFDYWGQTLVTVSS

```
seq              10        20        30        40        50        60        70        80        90
          b b b          b b b b   b b    b  bi i     i ibb  b b      i  b    b b b      b b b  b     b bib
175A      QVQLQQSGAELMKPGASVKISCKAT GYTFSTHWIE WVKQRPGHGLEWIG EILPGSGSTSYNEKFKG KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR
          *   **  ** **  * ***  * *             * *  *    **                    ** *** *** ** * **  **  *
huVH3a    EVQLVESGGGLVQPGGSLRLSCAAS GYTFSTHWIE WVRQAPGKGLEWVS EILPGSGSTSYNEKFKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
               Q          V I                            IG          Q       A F A I    A M L
                                                                      S
                                                                      D
                                                                      A
AbM              10        20        30        40        50 a      60        70 abc    80        90
huVH3b    EVQLVESGGGLVQPGGSLRLSCAAS GYTFSTHWIE WVRQAPGKGLEWVS EILPGSGSTSYADSVKG RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
               Q          V I                            IG            F    A F A I    A M L
```

```
seq      100       110
              ib    i   b b b
175A      WLLYYYAMDY WGQGTSVTVSS
                        *
huVH3a    WLLYYYAMDY WGQGTLVTVSS

AbM       100ab     110
huVH3b    WLLYYYAMDY WGQGTLVTVSS
```

FIG. 5B

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVK2
Potential humanized sequence based on IMGT IGKV2-28 acceptor framework (method 1)
DIVMTQSPLSLPVTPGEPASISC **RSSQSLLHSNGYNYLD** WYLQKPGQSPQLLIY **LGSNRAS** GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC **MQALQTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq          10        20        30        40        50        60        70        80        90
AbM          10        20        30abcde         40        50        60        70        80
       b b b   b b     b b b  b   b       bi bi i    ii ibbi     i   b   b       b b b  b    bb bib
76E1   DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KVSNRFS GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC
       **   *      ** **                         *                                 *      *
huVK2  DIVMTQSPLSLPVTPGEPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC
       V                              Q Q                  Q                           L
                                      S S                  S
                                      D D                  D
                                        A                  A
```

```
seq       100       110
AbM    90        100
       ibi   iib i   b b b
76E1   FQGSHVPWT FGGGTKLEIK
                  *
huVK2  FQGSHVPWT FGQGTKLEIK
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 6A

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGDRVTITC **RASQSISSYLN** WYQQKPGKAPKLLIY **AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq          10        20        30        40        50        60        70        80        90
AbM          10        20        30abcde        40        50        60        70        80
       b b b   b b    b b b b  b   b       bi bi i   ii ibbi     i   b   b       b b b  b   bb bib
76E1   DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KVSNRFS GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC
       **   * *  ** *  *** *                    *    **                *              * *****  ***
huVK1  DIQMTQSPSSLSASVGDRVTITC RSSQSIVHSNGNTYLE WYQQKPGKAPKLLIY KVSNRFS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
       V         V    A             Q Q           S        Q                          V   LG
                                      S S                    S
                                      A A                    D
                                        D                    A
```

```
seq        100       110
AbM    90        100
       ibi   iib i   b b b
76E1   FQGSHVPWT FGGGTKLEIK
                 *
huVK1  FQGSHVPWT FGQGTKLEIK
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 6B

huVK3
Potential humanized sequence based on IMGT IGKV3-20 acceptor framework (method 1)
EIVLTQSPGTLSLPGERATLSC **RASQSVSSSYLA** WYQQKPGQAPRLLIY **GASSRAT** GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC **QQYGSSP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq            10        20        30        40        50        60        70        80
AbM            10        20           34     40        50        60        70        80
        b b b    b b     b b b  b   b  bi bi i    ii ibbi      i   b   b       b b b  b     b bib
141A    QIVLSQSPAILSASPGEKVTMTC RASSSLSYMH WYQQKPGSSPKPWIY ATSNLAS GVPARFSGSGSGTSYSLTISRVEAEDAATYYC
        *   *   **  *    ** **                ** ***          * *         ***     * *  * *
huVK3   EIVLTQSPGTLSLSPGERATLSC RASSSLSYMH WYQQKPGQAPRLLIY ATSNLAS GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC
                  A     V M                   S PW     Q    V          Y      V
                                                       S
                                                       D
                                                       A
```

```
seq     90        100
AbM     90        100
        ibi   iib i   b b b
141A    QQWSSNPYT FGGGTKLEIK
                  *
huVK3   QQWSSNPYT FGQGTKLEIK
          Q
          S
          A
```

FIG. 7A

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGDRVTITC **RASQSISSYLN** WYQQKPGKAPKLLIY **AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq          10        20        30        40        50        60        70        80
AbM          10        20           34     40        50        60        70        80
       b b b   b b    b b b  b   b  bi bi i   ii ibbi     i   b   b       b b b  b    b bib
141A   QIVLSQSPAILSASPGEKVTMTC RASSSLSYMH WYQQKPGSSPKPWIY ATSNLAS GVPARFSGSGSGTSYSLTISRVEAEDAATYYC
       * ***   **    * **  *                    **  **          *        ***    ****  *
huVK1  DIQMTQSPSSLSASVGDRVTITC RASSSLSYMH WYQQKPGKAPKLLIY ATSNLAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
         L               M                    S  PW     Q                 Y     V
                                                         S
                                                         D
                                                         A
```

```
seq     90        100
AbM     90        100
        ibi   iib i   b b b
141A    QQWSSNPYT FGGGTKLEIK
                  *
huVK1   QQWSSNPYT FGQGTKLEIK
           Q
           S
           A
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 7B

huVK2
Potential humanized sequence based on IMGT IGKV2-28 acceptor framework (method 1)
DIVMTQSPLSLPVTPGEPASISC **RSSQSLLHSNGYNYLD** WYLQKPGQSPQLLIY **LGSNRAS** GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC **MQALQTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq          10        20        30        40        50        60        70        80        90
AbM          10        20        30abcde         40        50        60        70        80
       b b b   b b     b b b  b   b       bi bi i    ii ibbi     i   b   b       b b b  b    bb bib
175A   DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KLSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC
        **   *      ** **                          *                                        *
huVK2  DIVMTQSPLSLPVTPGEPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KLSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC
       V                              Q Q                Q                                 L
                                      S S                S
                                      A A                D
                                        D                A
```

```
seq       100       110
AbM   90        100
      ibi   iib i   b b b
175A  FQGSHFPYT FGGGTKLEIK
                  *
huVK2 FQGSHFPYT FGQGTKLEIK
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 8A

huVK1
Potential humanized sequence based on IMGT IGKV1-39 acceptor framework (method 2)
DIQMTQSPSSLSASVGDRVTITC **RASQSISSYLN** WYQQKPGKAPKLLIY **AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC **QQSYSTP**

Joining region
IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

```
seq          10        20        30        40        50        60        70        80        90
AbM          10        20        30abcde         40        50        60        70        80
       b b b   b b     b b b  b   b       bi bi i    ii ibbi     i   b   b       b b b  b    bb bib
175A   DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KLSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC
        **   * *  ** *  *** *                  *    **                 *              *  ****  ***
huVK1  DIQMTQSPSSLSASVGDRVTITC RSSQSIVHSNGNTYLE WYQQKPGKAPKLLIY KLSNRFS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
       V         V    A             Q Q          S        Q                      V    LG
                                      S S                   S
                                      A A                   D
                                        D                   A
```

```
seq       100       110
AbM   90        100
      ibi   iib i   b b b
175A  FQGSHFPYT FGGGTKLEIK
                  *
huVK1 FQGSHFPYT FGQGTKLEIK
```

(1) CDR sequences noted in bold.
(2) Human germline and joining sequences from IMGT® the international ImMunoGeneTics information system® www.imgt.org (founder and director: Marie-Paule Lefranc, Montpellier, France).
(3) Residue numbering shown as sequential (seq) or according to website www.bioinf.org.uk/abs/ (AbM).
(4) "b" notes buried sidechain; "i" notes sidechain at interface between VH and VL domains.
(5) Sequence differences between each humanized sequence and murine sequence noted by asterick (*).
(6) Potential humanized framework mutations from human sequence to parental mouse sequence are noted below sequence in red; underlined residues are positions to alter first.
(7) Potential changes in CDR sequence noted below each CDR sequence. These may prevent asparagines (N) deamidation (N), methionine (M) oxidation, Asp-Gly (DG) isoaspartate formation or Asp-Pro (DP) bond cleavage.

FIG. 8B

76E1 VH
EVQLLQSGPELEKPGASVKISCKAS**GYSFAAAAAA**WVKQSNGKSLEWIG**AIAAAAAAAAAAAAAAAA**KATLTVDKSSSTAYMQLKSLTSEDSAVYYC
AT**AAAAAAFDY**WGQGTTLTVSS (SEQ ID NO:1143)
human subgroup I

141A VH
QVQLQQSGAELMKPGASVKISCKAT**GYTFAAAAAA**WVKQRPGHGLEWIG**AIAAAAAAAAAAAAAAAA**KATFTADTSSNTAYMQLSSLTSEDSAVYYC
AG**AAAAAAAAAAAA**WGQGTLVTVSA (SEQ ID NO:1144)
human subgroup I

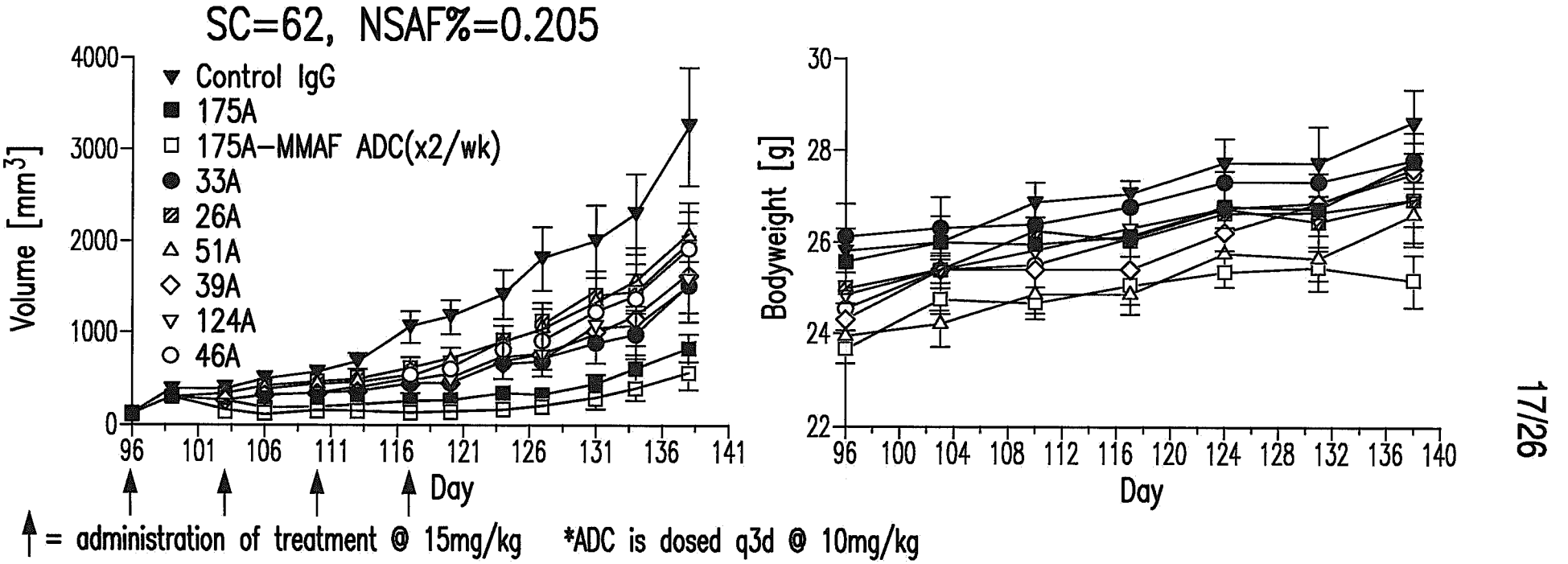
175A VH
QVQLQQSGAELMKPGASVKISCKAT**GYTFAAAAAA**WVKQRPGHGLEWIG**AIAAAAAAAAAAAAAAAA**KATFTADTSSNTAYMQLSSLTSEDSAVYYC
AR**AAAAAYAMDY**WGQGTSVTVSS (SEQ ID NO:1145)
human subgroup I

76E1 VL
DVLMTQTPLSLPVSLGDQASISC**RSSQSAAAAAAAAAAA**WYLQKPGQSPKLLIY**AAAAAAA**GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC**AQA**
AAAPATFGGGTKLEIK (SEQ ID NO:1146)
human kappa II

141A VL
QIVLSQSPAILSASPGEKVTMTC**RASAAAAAAA**WYQQKPGSSPKPWIY**AAANLAS**GVPARFSGSGSGTSYSLTISRVEAEDAATYYC**QQAAAAPAT**
FGGGTKLEIK (SEQ ID NO:1147)
human kappa III

175A VL
DVLMTQTPLSLPVSLGDQASISC**RSSQSAAAAAAAAAAA**WYLQKPGQSPKLLIY**AAAAAAA**GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC**AQA**
AAAPATFGGGTKLEIK (SEQ ID NO:1148)
human kappa II

FIG. 9



Kasumi–3 NOD	Control IgG 2a	175A	175A–MMAF	33A	26A	51A	39A	124A	46A
Volume±SD	3255±1704	833±429	555±511	1514±1156	1982±997	1668±638	2039±1102	1305±674	1925±791
TGI	–	–77	–86	–55	–41	–51	–39	–62	–42
p–Value	–	0.0088	0.0050	0.0447	0.1154	0.0507	0.1370	0.0363	0.0937

FIG. 10

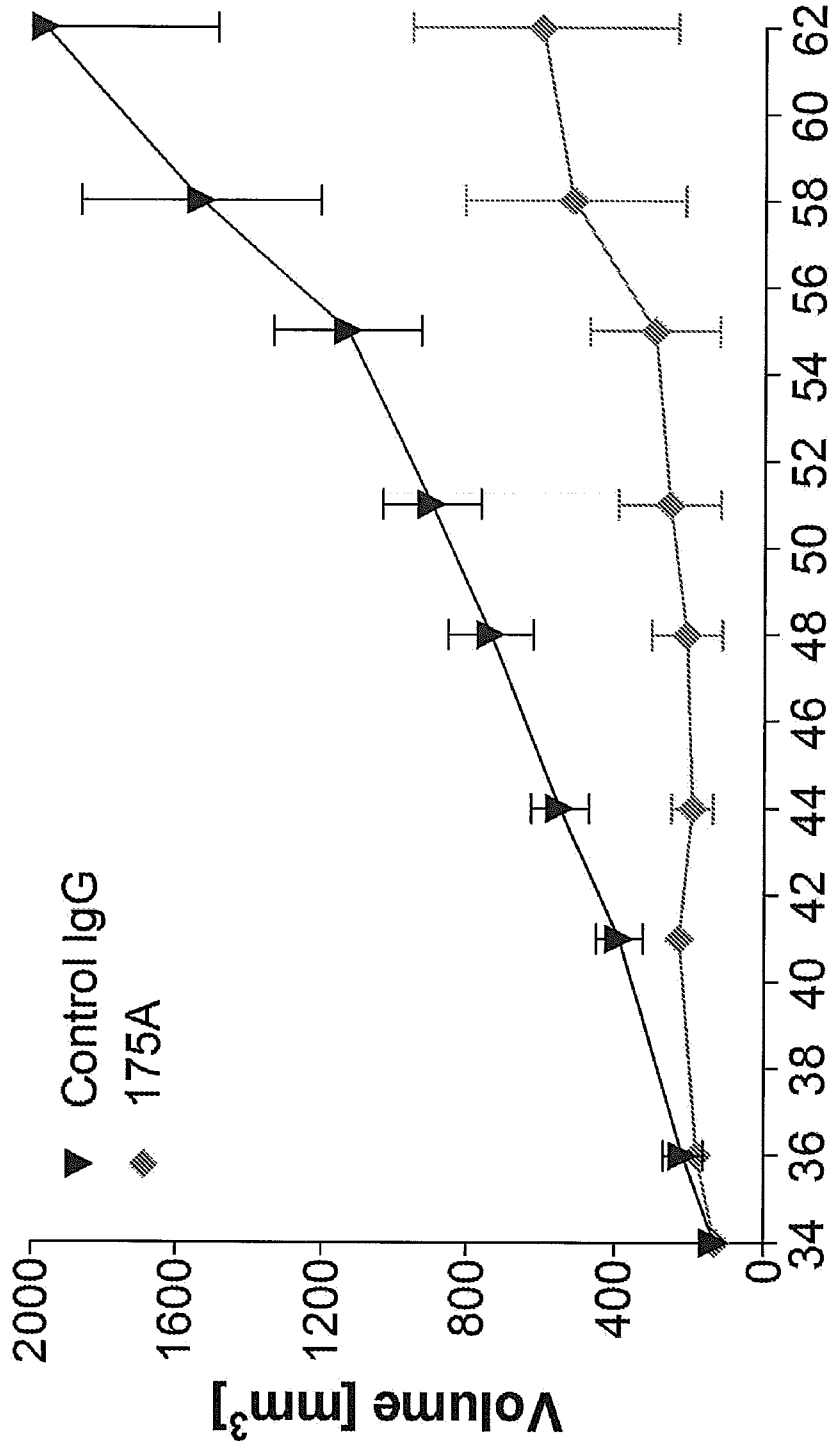

Control IgG
175A
Volume [mm³]
2000
1600
1200
800
400
0
34
36
38
40
42
44
46
48
50
52
54
56
58
60
62
Day

FIG. 11

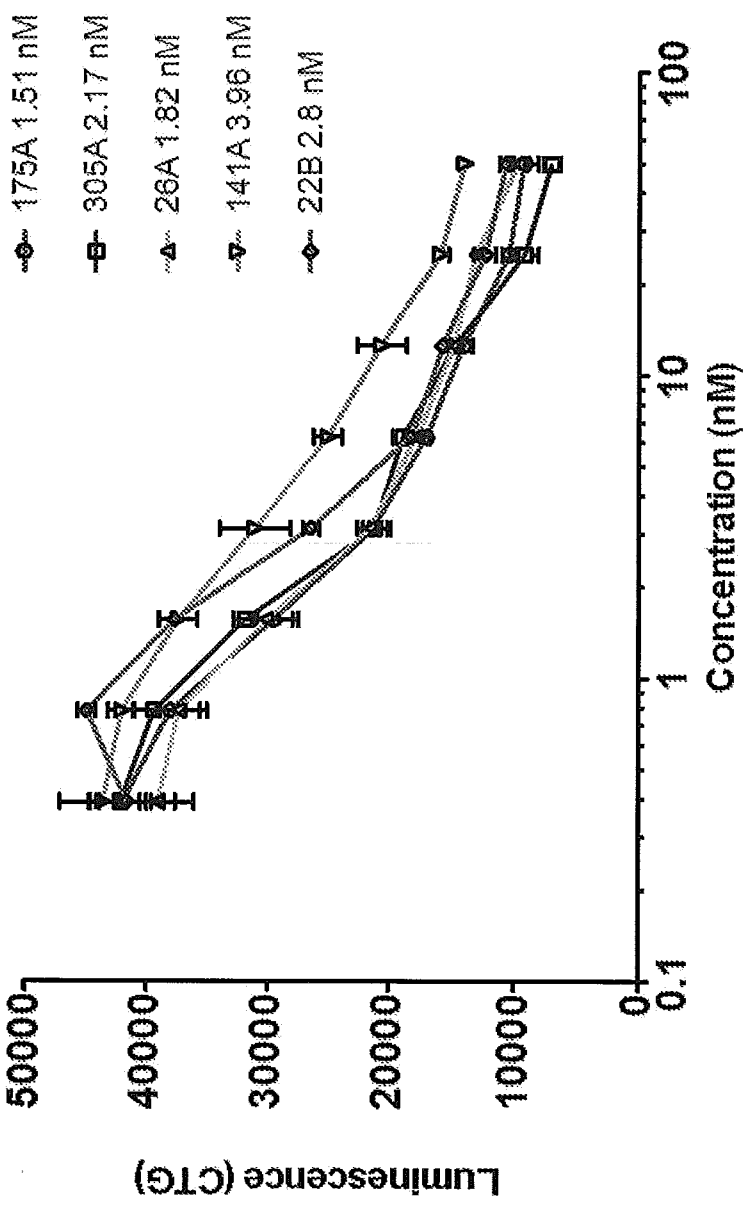
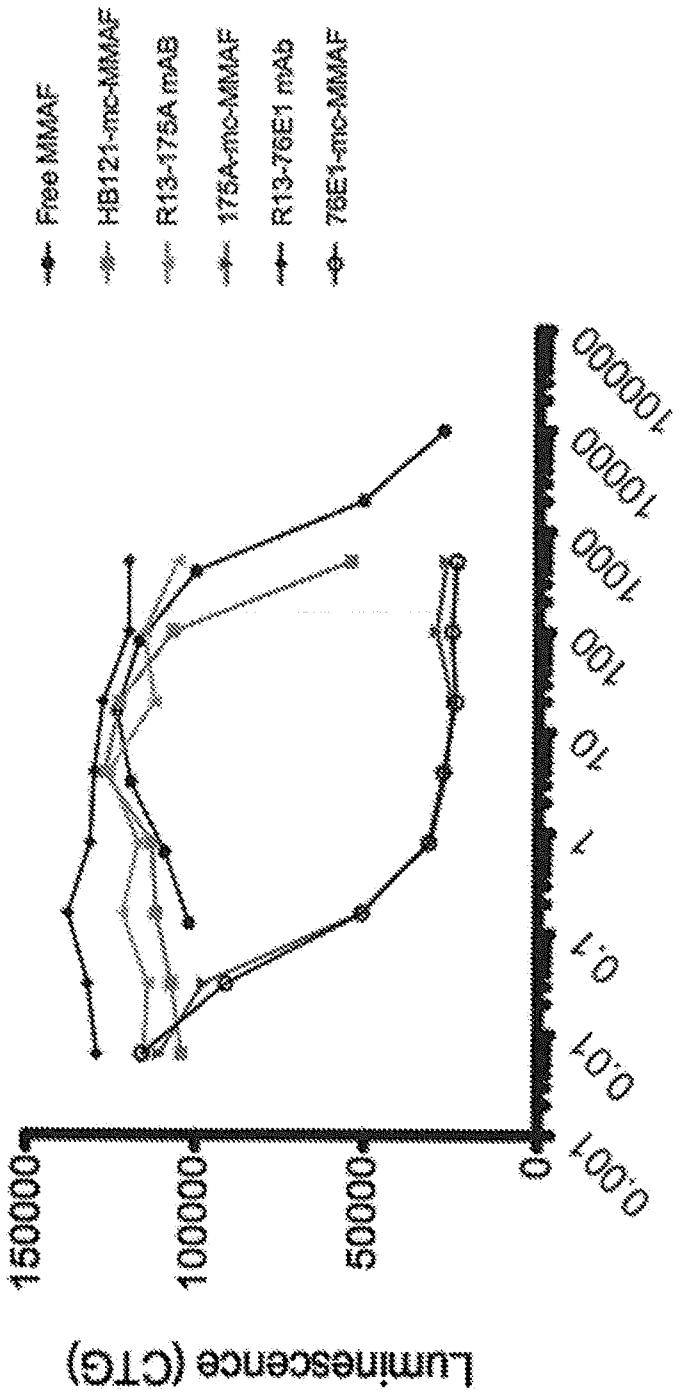

175A 1.51 nM
305A 2.17 nM
26A 1.82 nM
141A 3.96 nM
22B 2.8 nM
Luminescence (CTG)
50000
40000
30000
20000
10000
0
0.1
1
10
100
Concentration (nM)

FIG. 12



	Free MMAF	175A-mc-MMAF	76E1-mc-MMAF
IC50	1560	0.07166	0.05877
R square	0.9504	0.9906	0.9995

FIG. 13

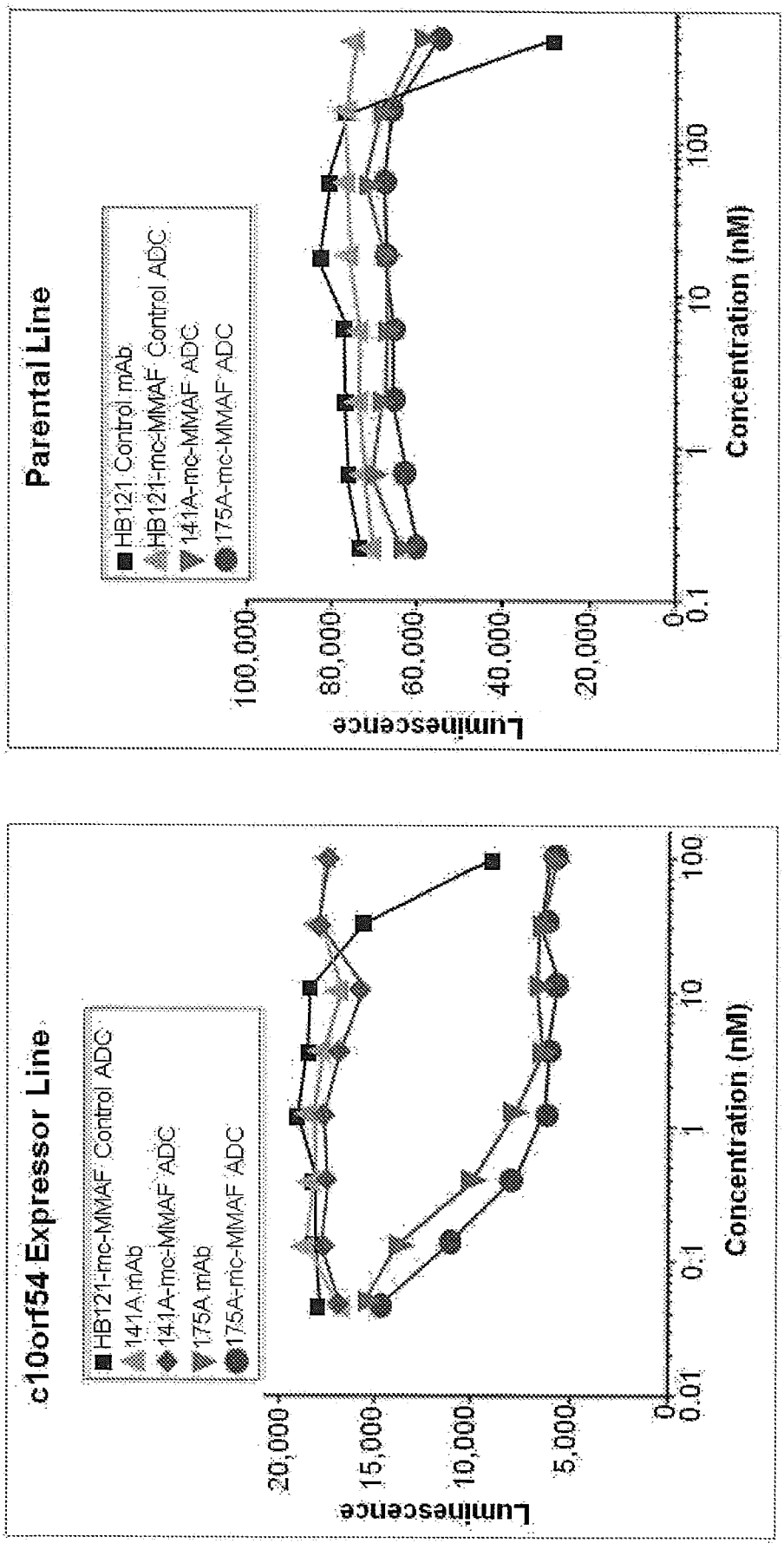
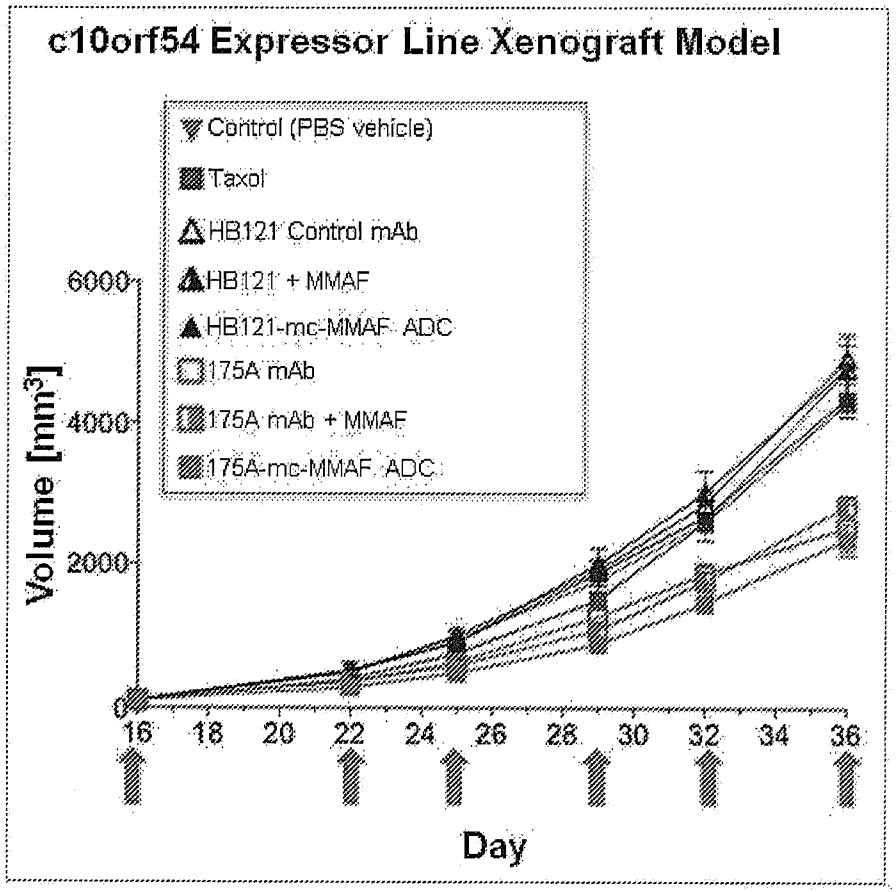
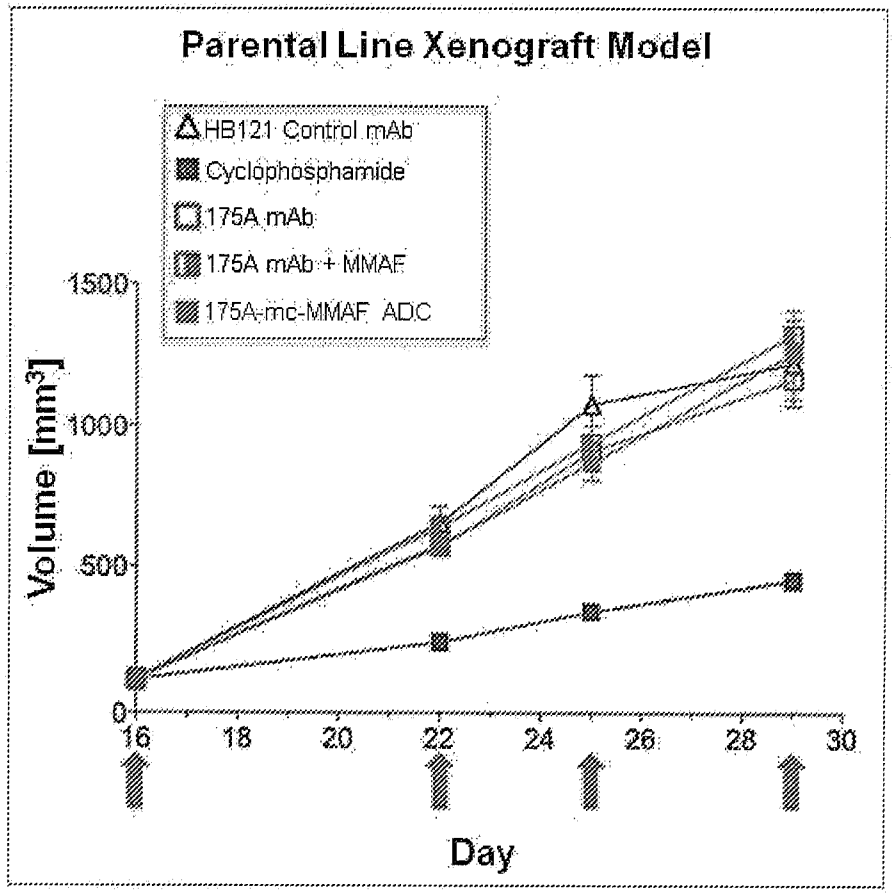

Parental Line
HB121 Control mAb
HB121-mc-MMAF Control ADC
141A-mc-MMAF ADC
175A-mc-MMAF ADC
Luminescence
100,000
80,000
60,000
40,000
20,000
0
0.1
1
10
100
Concentration (nM)
c10orf54 Expressor Line
HB121-mc-MMAF Control ADC
141A mAb
141A-mc-MMAF ADC
175A mAb
175A-mc-MMAF ADC
Luminescence
20,000
15,000
10,000
5,000
0
0.01
0.1
1
10
100
Concentration (nM)

FIG. 14





Treatment: 10mg/kg

FIG. 15

R13 VH

```
R13-3610-76E1   MGWTWIFILILSVTTGVHS
R13-3610-141A   MEWTWVFLFLLSVTAGVHS
R13-3610-175A   MEWTWVFLFLLSVTAGVHS

Kabat   1        10          22        31--35    40          50--a------60---65
AbM     1        10          22     26-------35  40          50--a----58      65
Chothia 1        10          22     26----32     40             a-55          65
Contact 1        10          22        30---35   40      47------a----58      65
IMGT    1                    23     27-----38  41               56-----65      74
76E1    EVQLLQSGPELEKPGASVKISCKAS GYSFTGYNMN WVKQSNGKSLEWIG NIDPYYDYTSYNLKFKD
141A    QVQLQQSGAELMKPGASVKISCKAT GYTFSRYWIE WVKQRPGHGLEWIG EILPGSGSTNYNEKFKG
175A    QVQLQQSGAELMKPGASVKISCKAT GYTFSTHWIE WVKQRPGHGLEWIG EILPGSGSTSYNEKFKG

Kabat       70        80  abc      90    95--100---102      110
AbM         70        80  abc      90    95--100---102      110
Chothia     70        80  abc      90     96-100--101       110
Contact     70        80  abc      90 93-----100--101       110
IMGT   75               89           105-----------117
76E1    KATLTVDKSSSTAYMQLKSLTSEDSAVYYCAT STMITP---FDY WGQGTTLTVSS
141A    KATFTADTSSNTAYMQLSSLTSEDSAVYYCAG EEVYDGYPWFGY WGQGTLVTVSA
175A    KATFTADTSSNTAYMQLSSLTSEDSAVYYCAR WLLYYYA--MDY WGQGTSVTVSS
```

FIG. 16A

R13 VL

```
R13-3610-76E1   MKLPVRLLVLMFWIPASSS
R13-3610-141A   MDFQVQIFSFLLISASVIMSRG
R13-3610-175A   MKLPVRLLVLMFWIPASSS

Kabat   1        10        20   24-27abcd------34     40          50----56
AbM     1        10        20   24----30abcd---34     40          50----56
Chothia 1        10        20     26--30abcd-32       40          50--
Contact 1        10        20         30abcd------36  40    46--------55
IMGT    1                     23   27--------38  41                56-65 69
                                                                    | |
76E1    DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KVSNRFS
141A    QIVLSQSPAILSASPGEKVTMTC RASSSL------SYMH WYQQKPGSSPKPWIY ATSNLAS
175A    DVLMTQTPLSLPVSLGDQASISC RSSQSIVHSNGNTYLE WYLQKPGQSPKLLIY KLSNRFS

Kabat      60        70        80        89------97
AbM        60        70        80        89------97
Chothia    60        70        80          91---96
Contact    60        70        80        89-----96
IMGT   70              89              105-----117
76E1    GVPDRFSGSGSGTDFTLKINRVEAEDLGVYYC FQGSHVPWT FGGGTKLEIK
141A    GVPARFSGSGSGTSYSLTISRVEAEDAATYYC QQWSSNPYT FGGGTKLEIK
175A    GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC FQGSHFPYT FGGGTKLEIK
```

FIG. 16B

R13 VH

```
AbM     1         10          22   26--------35   40            50--a----58      65
hu76E1  QVQLVQSGAEVKKPGASVKVSCKAS GYSFTGYNMN WVRQAPGQGLEWIG NIDPYYDYTSYNLKFKD

hu141A  QVQLVQSGAEVKKPGASVKVSCKAS GYTFSRYWIE WVRQAPGQGLEWIG EILPGSGSTNYNEKFKG
hu175A  QVQLVQSGAEVKKPGASVKVSCKAS GYTFSTHWIE WVRQAPGQGLEWIG EILPGSGSTSYNEKFKG
consen  QVQLVQSGAEVKKPGASVKVSCKAS GYTFSXXWIE WVRQAPGQGLEWIG EILPGSGSTXYNEKFKG
                                       RY                            N
                                       TH                            S

AbM        70        80  abc      90   95--100---102    110
hu76E1  RVTMTVDKSTSTAYMELRSLRSDDTAVYYCAT STMITP---FDY WGQGTLVTVSS (SEQ ID NO: 1135)

hu141A  RVTMTADTSTSTAYMELRSLRSDDTAVYYCAG EEVYDGYPWFGY WGQGTLVTVSS (SEQ ID NO: 1136)
hu175A  RVTMTADTSTSTAYMELRSLRSDDTAVYYCAR WLLYYYA--MDY WGQGTLVTVSS (SEQ ID NO: 1137)
consen  RVTMTADTSTSTAYMELRSLRSDDTAVYYCAR xxxxxxxxxXXY WGQGTLVTVSS (SEQ ID NO: 1138)
                                                  MG
                                                  FD
```

FIG. 17A

```
R13 VL

AbM      1        10         20    24----30abcd---34    40             50----56
hu141A   EIVLTQSPGTLSLSPGERATLSC RASSSL------SYMH WYQQKPGQAPRPWIY ATSNLAS

hu76E1   DIVMTQSPLSLPVTPGEPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KVSNRFS
hu175A   DIVMTQSPLSLPVTPGEPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KLSNRFS
consen   DIVMTQSPLSLPVTPGEPASISC RSSQSIVHSNGNTYLE WYLQKPGQSPQLLIY KXSNRFS
                                                                   V
                                                                   L

AbM        60        70        80       89------97
hu141A   GIPDRFSGSGSGTDYTLTISRLEPEDFAVYYC QQWSSNPYT FGQGTKLEIK (SEQ ID NO: 1139)

hu76E1   GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC FQGSHVPWT FGQGTKLEIK (SEQ ID NO: 1140)
hu175A   GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC FQGSHFPYT FGQGTKLEIK (SEQ ID NO: 1141)
consen   GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC FQGSHXPXT FGQGTKLEIK (SEQ ID NO: 1142)
                                               V W
                                               F Y
```

FIG. 17B