Figure 1:

Figure 1. The cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of 158P1D7. The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

```
   1                                M  K  L  W  I  H  L  F  Y  S  S  L  L
   1 tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
  14  A  C  I  S  L  H  S  Q  T  P  V  L  S  S  R  G  S  C  D  S
  61 TGCCTGTATATCTTTACACTCCCAAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
  34  L  C  N  C  E  E  K  D  G  T  M  L  I  N  C  E  A  K  G  I
 121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
  54  K  M  V  S  E  I  S  V  P  P  S  R  P  F  Q  L  S  L  L  N
 181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACTAAGCTTATTAAA
  74  N  G  L  T  M  L  H  T  N  D  F  S  G  L  T  N  A  I  S  I
 241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
  94  H  L  G  F  N  N  I  A  D  I  E  I  G  A  F  N  G  L  G  L
 301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
 114  L  K  Q  L  H  I  N  H  N  S  L  E  I  L  K  E  D  T  F  H
 361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
 134  G  L  E  N  L  E  F  L  Q  A  D  N  N  F  I  T  V  I  E  P
 421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
 154  S  A  F  S  K  L  N  R  L  K  V  L  I  L  N  D  N  A  I  E
 481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
 174  S  L  P  P  N  I  F  R  F  V  P  L  T  H  L  D  L  R  G  N
 541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA
 194  Q  L  Q  T  L  P  Y  V  G  F  L  E  H  I  G  R  I  L  D  L
 601 TCAATTACAAACATTGCCTTATGTTGGTTTTCTCGAACACATTGGCCGAATATTGGATCT
 214  Q  L  E  D  N  K  W  A  C  N  C  D  L  L  Q  L  K  T  W  L
 661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAAACTTGGTT
 234  E  N  M  P  P  Q  S  I  I  G  D  V  V  C  N  S  P  P  F  F
 721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
 254  K  G  S  I  L  S  R  L  K  K  E  S  I  C  P  T  P  P  V  Y
 781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
 274  E  E  H  E  D  P  S  G  S  L  H  L  A  A  T  S  S  I  N  D
 841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
 294  S  R  M  S  T  K  T  T  S  I  L  K  L  P  T  K  A  P  G  L
 901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT
```

Figure 1-2

```
 314  I  P  Y  I  T  K  P  S  T  Q  L  P  G  P  Y  C  P  I  P  C
 961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCCTTG
 334  N  C  K  V  L  S  P  S  G  L  L  I  H  C  Q  E  R  N  I  E
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
 354  S  L  S  D  L  R  P  P  P  Q  N  P  R  K  L  I  L  A  G  N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
 374  I  I  H  S  L  M  K  S  D  L  V  E  Y  F  T  L  E  M  L  H
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA
 394  L  G  N  N  R  I  E  V  L  E  E  G  S  F  M  N  L  T  E  L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
 414  Q  K  L  Y  L  N  G  N  H  L  T  K  L  S  K  G  M  F  L  G
1261 ACAAAAACTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCCTTGG
 434  L  N  N  L  E  Y  L  Y  L  E  Y  N  A  I  K  E  I  L  P  G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
 454  T  F  N  P  M  P  K  L  K  V  L  Y  L  N  N  N  L  L  Q  V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
 474  L  P  P  N  I  F  S  G  V  P  L  T  K  V  N  L  K  T  N  Q
1441 TTTACCACCACATATTTTTTCAGGGGTTCCTCTAACTAAGGTAAATCTTAAAACAAACCA
 494  F  T  H  L  P  V  S  N  I  L  D  D  L  D  L  L  T  Q  I  D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTACTAACCCAGATTGA
 514  L  E  D  N  P  W  D  C  S  C  D  L  V  G  L  Q  Q  W  I  Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
 534  K  L  S  K  N  T  V  T  D  D  I  L  C  T  S  P  G  H  L  D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGGCATCTCGA
 554  K  K  E  L  K  A  L  N  S  E  I  L  C  P  G  L  V  N  N  P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
 574  S  M  P  T  Q  T  S  Y  L  M  V  T  T  P  A  T  T  T  N  T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
 594  A  D  T  I  L  R  S  L  T  D  A  V  P  L  S  V  L  I  L  G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
 614  L  L  I  M  F  I  T  I  V  F  C  A  A  G  I  V  V  L  V  L
1861 ACTTCTGATTATGTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTCT
 634  H  R  R  R  R  Y  K  K  K  Q  V  D  E  Q  M  R  D  N  S  P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
 654  V  H  L  Q  Y  S  M  Y  G  H  K  T  T  H  H  T  T  E  R  P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
 674  S  A  S  L  Y  E  Q  H  M  V  S  P  M  V  H  V  Y  R  S  P
```

Figure 1-3

```
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
 694  S  F  G  P  K  H  L  E  E  E  E  E  R  N  E  K  E  G  S  D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
 714  A  K  H  L  Q  R  S  L  L  E  Q  E  N  H  S  P  L  T  G  S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGAAAATCATTCACCACTCACAGGGTC
 734  N  M  K  Y  K  T  T  N  Q  S  T  E  F  L  S  F  Q  D  A  S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
 754  S  L  Y  R  N  I  L  E  K  E  R  E  L  Q  Q  L  G  I  T  E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACTTCAGCAACTGGGAATCACAGA
 774  Y  L  R  K  N  I  A  Q  L  Q  P  D  M  E  A  H  Y  P  G  A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
 794  H  E  E  L  K  L  M  E  T  L  M  Y  S  R  P  R  K  V  L  V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
 814  E  Q  T  K  N  E  Y  F  E  L  K  A  N  L  H  A  E  P  D  Y
2461 GGAACAGACAAAAAATGAGTATTTTGAACTTAAAGCTAATTTACATGCTGAACCTGACTA
 834  L  E  V  L  E  Q  Q  T  *
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga
```

Figure 2: **Nucleic Acid and Amino Acid Sequences of 158P1D7 Antibodies**

Figure 2A. **The cDNA (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of Ha15-10ac12 heavy chain. Double-underlined is the heavy chain variable region, and underlined is the heavy chain human IgG2 constant region.**

```
     Q  V  Q  L  V  E  S  G  G  G  V  V  Q  P  G  R  S  L  R  L
   1 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC
     S  C  A  A  S  G  F  T  F  S  S  Y  G  M  H  W  V  R  Q  A
  61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT
     P  G  K  G  L  E  W  V  A  V  I  W  Y  D  G  S  N  Q  Y  Y
 121 CCAGGCAAGGGGCTGGAATGGGTGGCAGTTATATGGTATGATGGAAGTAATCAATATTAT
     A  D  S  V  K  G  R  F  T  I  S  R  D  N  S  K  N  T  L  F
 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTT
     L  Q  M  H  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R  G  L
 241 CTGCAAATGCACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTCTG
     T  S  G  R  Y  G  M  D  V  W  G  Q  G  T  T  V  T  V  S  S
 301 ACTTCTGGACGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
     A  S  T  K  G  P  S  V  F  P  L  A  P  C  S  R  S  T  S  E
 361 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG
     S  T  A  A  L  G  C  L  V  K  D  Y  F  P  E  P  V  T  V  S
 421 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG
     W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S
 481 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA
     G  L  Y  S  L  S  S  V  V  T  V  P  S  S  N  F  G  T  Q  T
 541 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC
     Y  T  C  N  V  D  H  K  P  S  N  T  K  V  D  K  T  V  E  R
 601 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC
     K  C  C  V  E  C  P  P  C  P  A  P  P  V  A  G  P  S  V  F
 661 AAATGTTGTGTCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTC
     L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C
 721 CTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGC
     V  V  V  D  V  S  H  E  D  P  E  V  Q  F  N  W  Y  V  D  G
 781 GTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC
     V  E  V  H  N  A  K  T  K  P  R  E  E  Q  F  N  S  T  F  R
 841 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGT
     V  V  S  V  L  T  V  V  H  Q  D  W  L  N  G  K  E  Y  K  C
 901 GTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGC
     K  V  S  N  K  G  L  P  A  P  I  E  K  T  I  S  K  T  K  G
 961 AAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG
     Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  E  E  M  T  K  N
1021 CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAC
     Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W
1081 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG
     E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  M  L  D  S  D
1141 GAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGAC
     G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N
1201 GGCTCCTTCTTCCTTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
     V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L
1261 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
     S  L  S  P  G  K  *
1321 TCCCTGTCTCCGGGTAAATAA
```

Figure 2B. **The cDNA (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6) of Ha15-10ac12 light chain. Double-underlined is the light chain variable region, and underlined is the human kappa constant region.**

```
      D  I  V  M  T  Q  S  P  L  S  L  P  V  T  P  G  E  P  A  S
   1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
      I  S  C  R  S  S  Q  S  L  L  L  S  N  G  F  N  Y  L  D  W
  61  ATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCTTAGTCATGGATTCAACTATTTGGATTGG
      Y  L  Q  K  P  G  Q  S  P  Q  L  L  I  Y  L  G  S  S  R  A
 121  TACCTGCAGAAGCCAGGGCAGTCTCCACAACTCCTGATCTATTTGGGTTCTAGTCGGGCC
      S  G  V  P  D  R  F  S  G  S  G  S  G  T  D  F  T  L  K  I
 181  TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC
      S  R  V  E  A  E  D  V  G  L  Y  Y  C  M  Q  P  L  Q  I  P
 241  AGCAGAGTGGAGGCTGAGGATGTTGGGCTTTATTACTGCATGCAACCCCTACAAATTCCG
      W  T  F  G  Q  G  T  K  V  E  I  K  R  T  V  A  A  P  S  V
 301  TGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTC
      F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L
 361  TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
      L  N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q
 421  CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
      S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y  S  L
 481  TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
      S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E
 541  AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA
      V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R  G  E  C  *
 601  GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
```

Figure 3: Amino Acid Sequences of 158P1D7 Antibodies

Figure 3A. The amino acid sequence (SEQ ID NO:7) of Ha15-10ac12 heavy chain. Double-underlined is the heavy chain variable region, and underlined is the human IgG2 constant region.

```
  1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAV
 51 IWYDGSNQYYADSVKGRFTISRDNSKNTLFLQMHSLRAEDTAVYYCARGL
101 TSGRYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK
151 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQT
201 YTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL
251 MISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
301 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
351 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSD
401 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
```

Figure 3B. **The amino acid sequence (SEQ ID NO:8) of Ha15-10ac12 light chain. Double-underlined is the light chain variable region, and underlined is the human kappa constant region.**

```
  1   DIVMTQSPLSLPVTPGEPASISCRSSQSLLLSHGFNYLDWYLQKPGQSPQ
 51   LLIYLGSSRASGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQPLQIP
101   WTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
151   VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
201   VTHQGLSSPVTKSFNRGEC
```

Figure 4: Alignment of Ha15-10ac12 Antibodies to Human Ig Germline

Figure 4A. Alignment of Ha15-10ac12 Heavy Chain to Human Ig Germline.

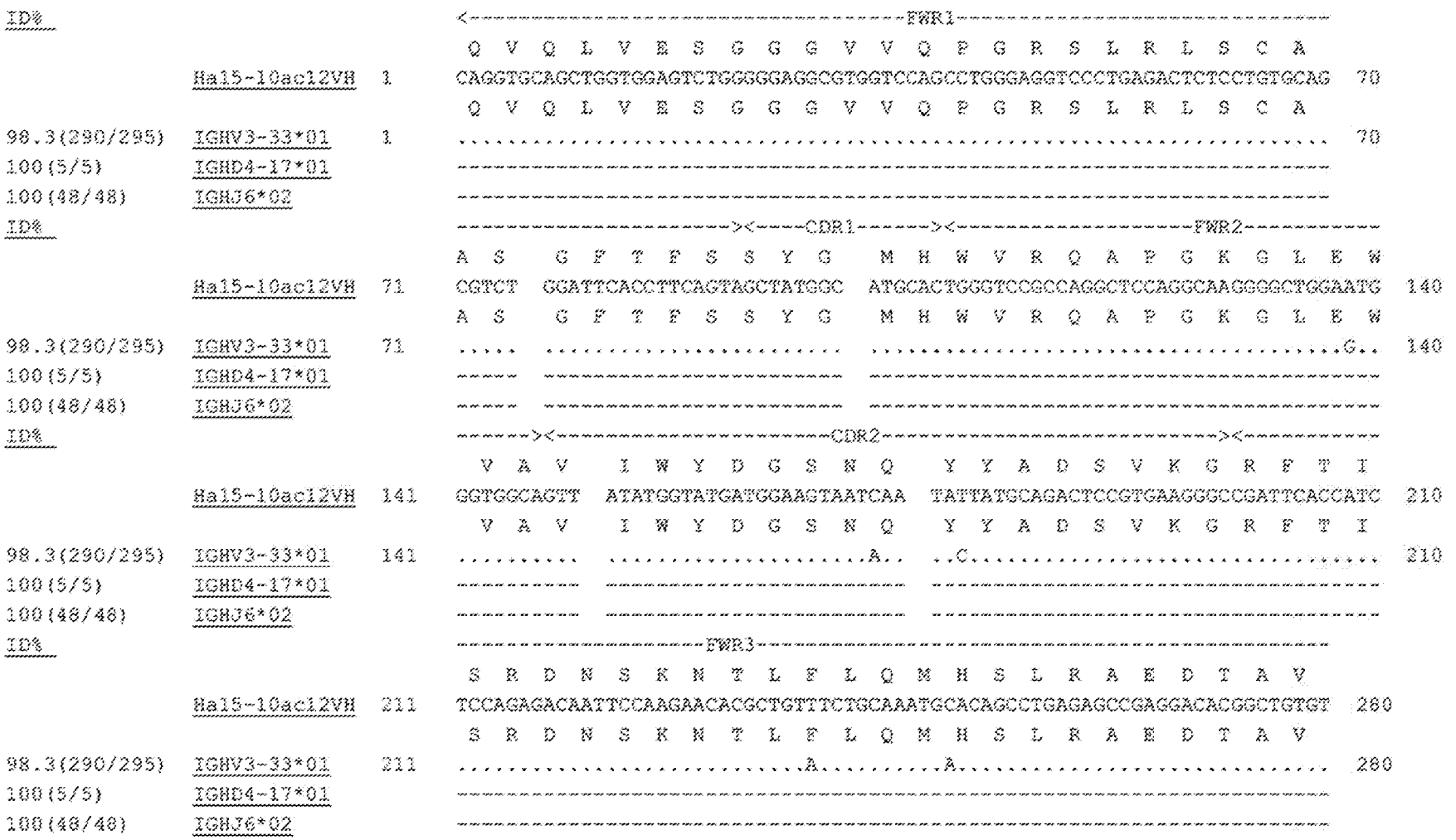


Figure 4A-2

```
                                   Y  Y  C   A  R  G  L  T  S  G  R  Y  G  M  D  V  W  G  Q  G  T  T  V  T
               Ha15-10ac12VH  281  ATTACTGT  GCGAGAGGTCTGACTTCTGGACGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  350

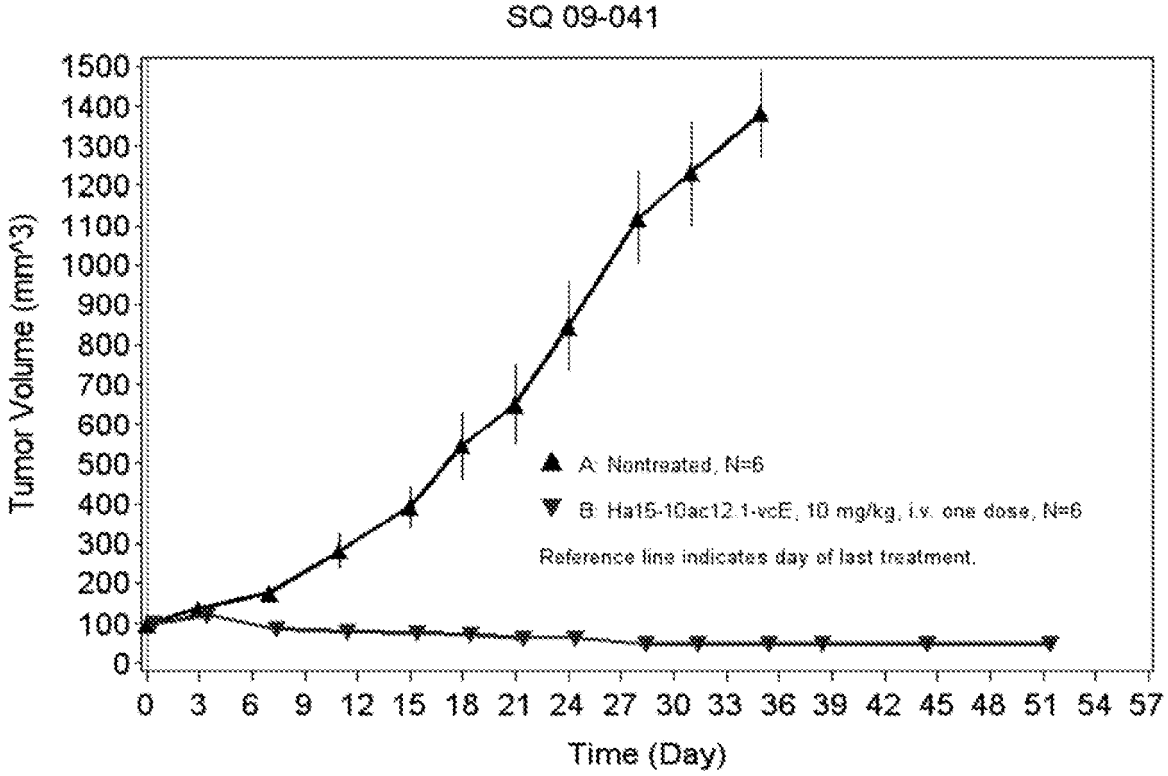
                                   Y  Y  C   A  R  G  L  T  S  G  R  Y  G  M  D  V  W  G  Q  G  T  T  V  T
98.3(290/295)  IGHV3-33*01    281  ........  .......-------------------------------------------------------  295
100(5/5)       IGHD4-17*01    1    --------  ----------.....-----------------------------------------------  5
100(48/48)     IGHJ6*02       15   --------  ------------------------......................................  52
ID%

                                    V  S  S
               Ha15-10ac12VH  351  CGTCTCCTCA  360
                                    V  S  S
98.3(290/295)  IGHV3-33*01         ----------
100(5/5)       IGHD4-17*01         ----------
100(48/48)     IGHJ6*02       53   ..........  62
```

Figure 4B. Alignment of Ha15-10ac12 Light Chain to Human Ig Germline.

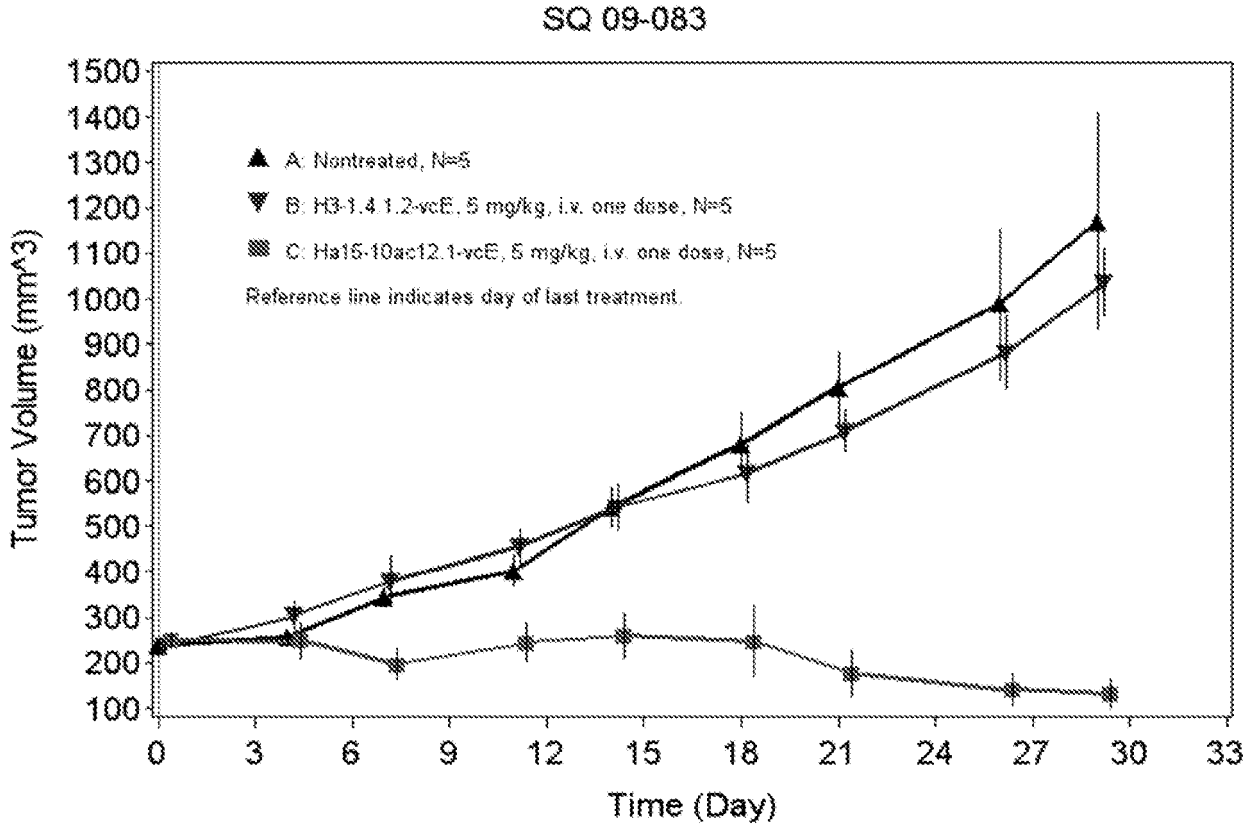
```
ID%                                  <-----------------------------------------FWR1------------------------------>
                                      D  I  V  M  T  Q  S  P  L  S  L  P  V  T  P  G  E  P  A  S  I  S  C
                Ha15-10ac12VL   1    GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCA  70
                                      D  I  V  M  T  Q  S  P  L  S  L  P  V  T  P  G  E  P  A  S  I  S  C
97.0(290/299)   IGKV2D-28*01    1    ..........................................................................  70
100(38/38)      IGKJ1*01        ----------------------------------------------------------------------------
ID%                                  <-----------------CDR1-----------------------------------> <------------FWR2--
                                      R  S  S     Q  S  L  L  L  S  H     G  F  N  Y    L  D  W  Y  L  Q  K  P  G
                Ha15-10ac12VL   71   GGTCTAGT  CAGAGCCTCCTGCTTAGTCATG---GATTCAACTAT  TTGGATTGGTACCTGCAGAAGCCAGG  137
                                      R  S  S     Q  S  L  L  H  S  N     G  Y  N  Y    L  D  W  Y  L  Q  K  P  G
97.0(290/299)   IGKV2D-28*01    71   ........  ..............A....A...---...A.......  ...........................  137
100(38/38)      IGKJ1*01        --------  ------------------------------------------  ---------------------------
ID%                                  --------------------------->  <---------CDR2-------->  <-----------------------
                                       Q  S  P  Q  L  L  I  Y    L  G  S    S  R  A  S  G  V  P  D  R  F  S  G
                Ha15-10ac12VL   138  GCAGTCTCCACAACTCCTGATCTAT  TTGGGTTCT  AGTCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGC  207
                                       Q  S  P  Q  L  L  I  Y    L  G  S    N  R  A  S  G  V  P  D  R  F  S  G
97.0(290/299)   IGKV2D-28*01    138  ............G.............  .........  .A.....................................  207
100(38/38)      IGKJ1*01        ---------------------------  ---------  -------------------------------------
ID%                                  ------------------FWR3-------------------------------------------------
                                      S  G  S  G  T  D  F  T  L  K  I  S  R  V  E  A  E  D  V  G  L  Y  Y
                Ha15-10ac12VL   208  AGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGCTTTATTACT  277
                                      S  G  S  G  T  D  F  T  L  K  I  S  R  V  E  A  E  D  V  G  V  Y  Y
97.0(290/299)   IGKV2D-28*01    208  ..........................................................G.........  277
100(38/38)      IGKJ1*01        ----------------------------------------------------------------------------
ID%                                  ->  <-------------CDR3---------->
                                      C    M  Q  P  L  Q  I  P  W  T  F  G  Q  G  T  K  V  E  I  K
                Ha15-10ac12VL   278  GC  ATGCAACCCCTACAAATTCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC  337
                                      C    M  Q  A  L  Q  T  P
97.0(290/299)   IGKV2D-28*01    278  ..  ......G.T.......C...----------------------------------------  299
100(38/38)      IGKJ1*01        1    --  --------------------.....................................  38
```

Figure 5. Efficacy of Ha15-10ac12vcMMAE in a Subcutaneously Established Xenograft Model of Human Bladder Cancer AG-B7 in SCID Mice



Note. Extraneous treatment arms in this experiment are not shown in this figure.

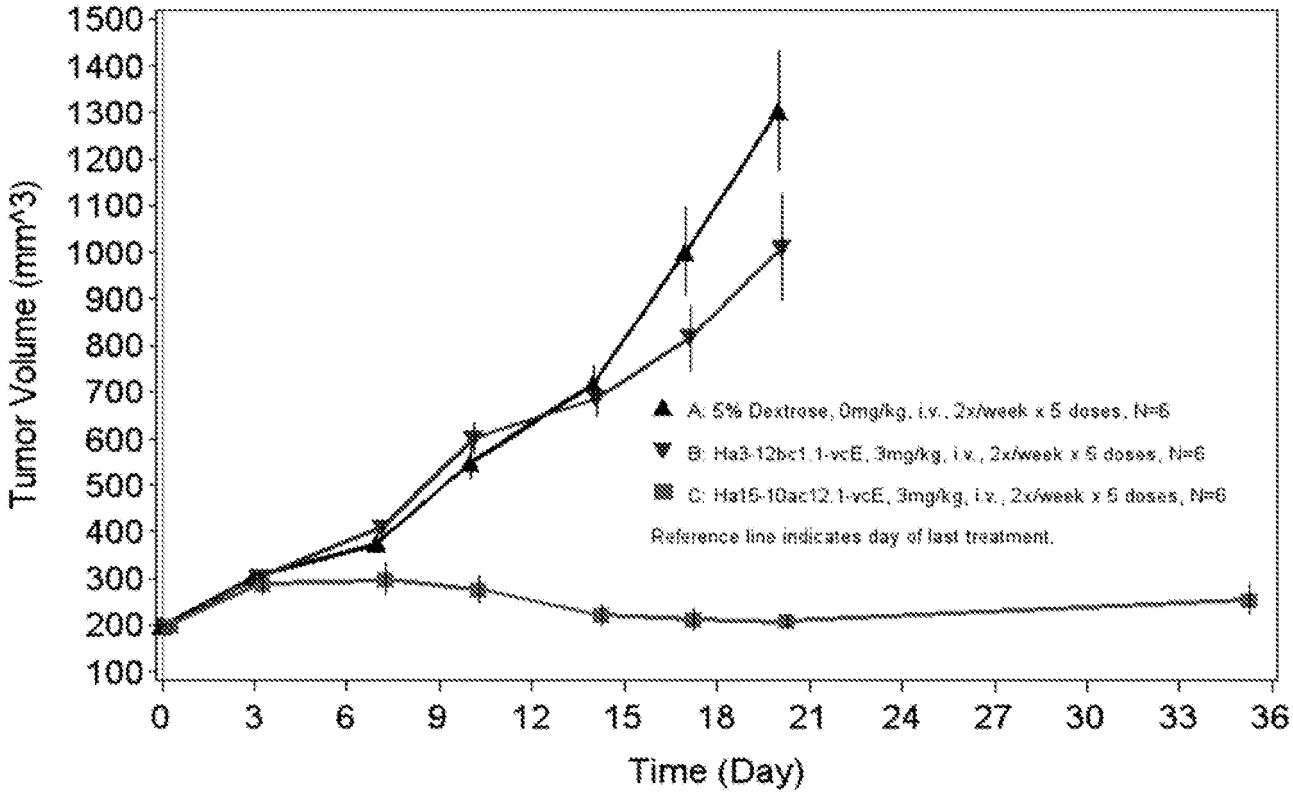
Figure 6. Efficacy of Ha15-10ac12vcMMAE in Subcutaneously Established Human Bladder Cancer RT-4-XCL Implanted in SCID Mice



Note: Extraneous treatment arms in this experiment are not shown in this figure.

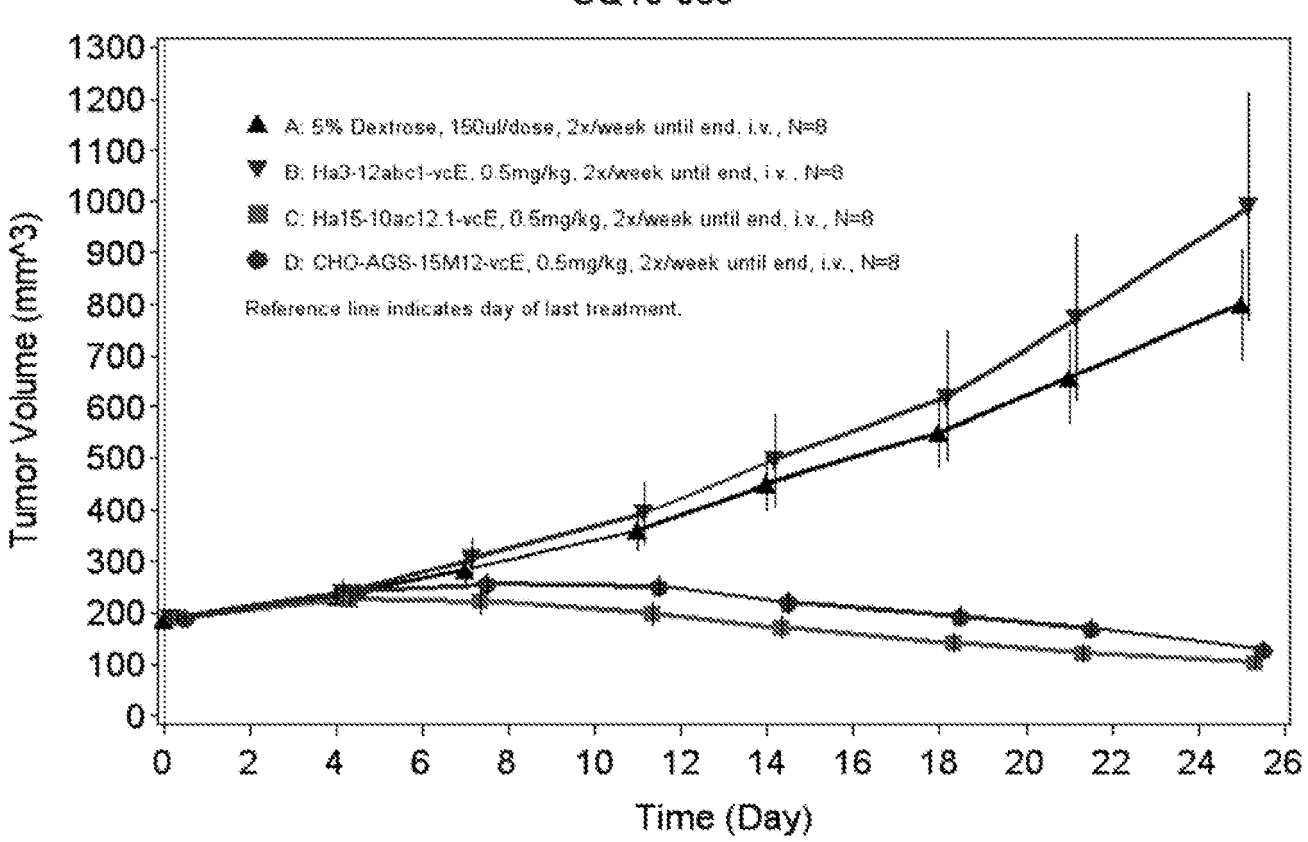
Figure 7. Efficacy of Ha15-10ac12vcMMAE in Subcutaneously Established Human Lung Cancer NCI-H322M-XCL Implanted in SCID Mice

SQ 11-031



Note: Extraneous treatment arms in this experiment are not shown in this figure.

Figure 8. Efficacy of Ha15-10ac12vcMMAE in a Subcutaneously Established Xenograft Model of Human Bladder Cancer AG-B7 in SCID Mice



Note: Extraneous treatment arms in this experiment are not shown in this figure.

Figure 9. Detection of 158P1D7 Protein by Immunohistochemistry.

Figure 9A-9B – Detection of 158P1D7 Protein in Bladder Cancer.

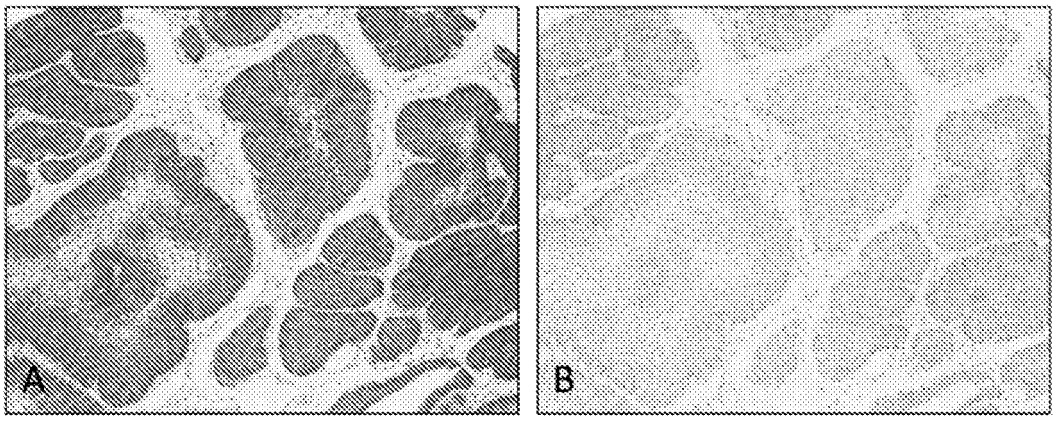


Figure 9C-9D – Detection of 158P1D7 Protein in Breast Cancer.

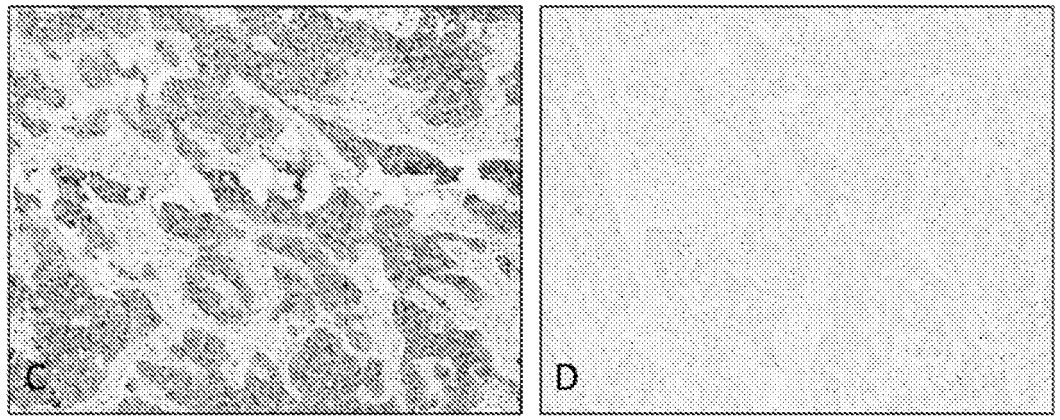


Figure 9E-9F – Detection of 158P1D7 Protein in Lung Cancer.

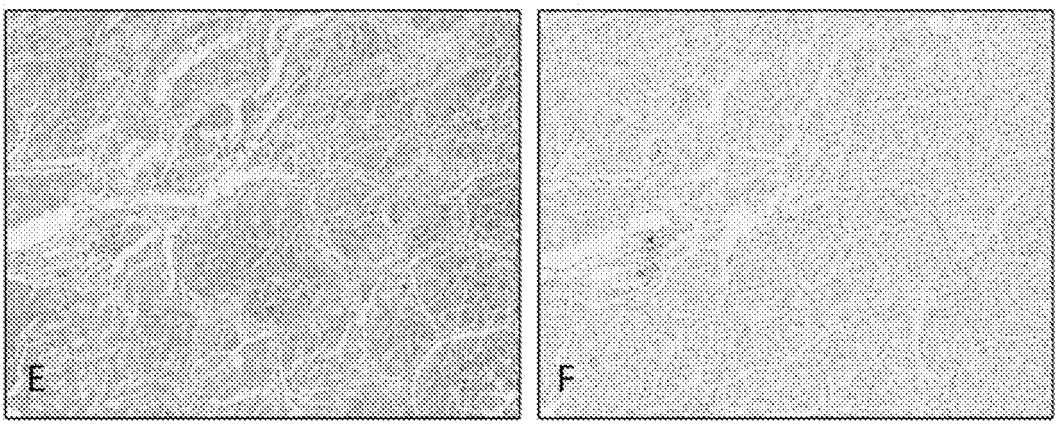


Figure 9G-9H – Detection of 158P1D7 Protein in Glioblastoma.

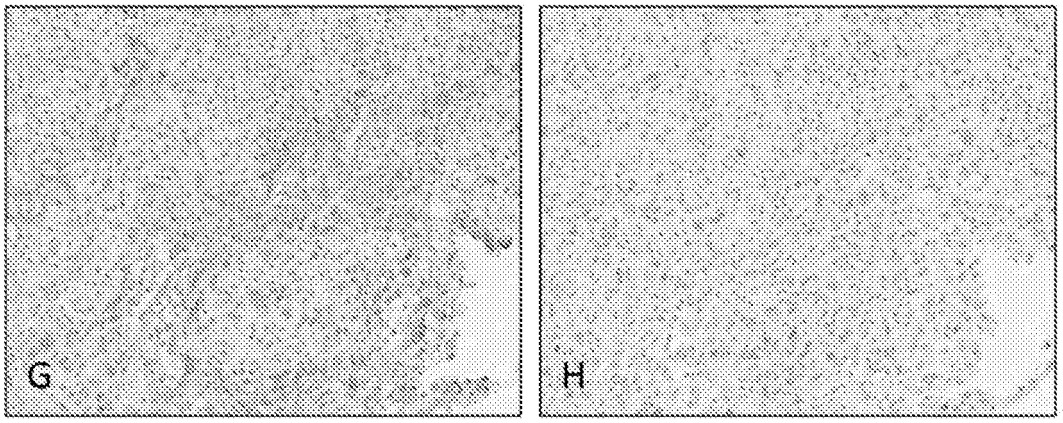


Figure 10. Efficacy of Ha15-10ac12vcMMAE in Subcutaneous established Xenograft model of human bladder cancer SW780 in SCID mice

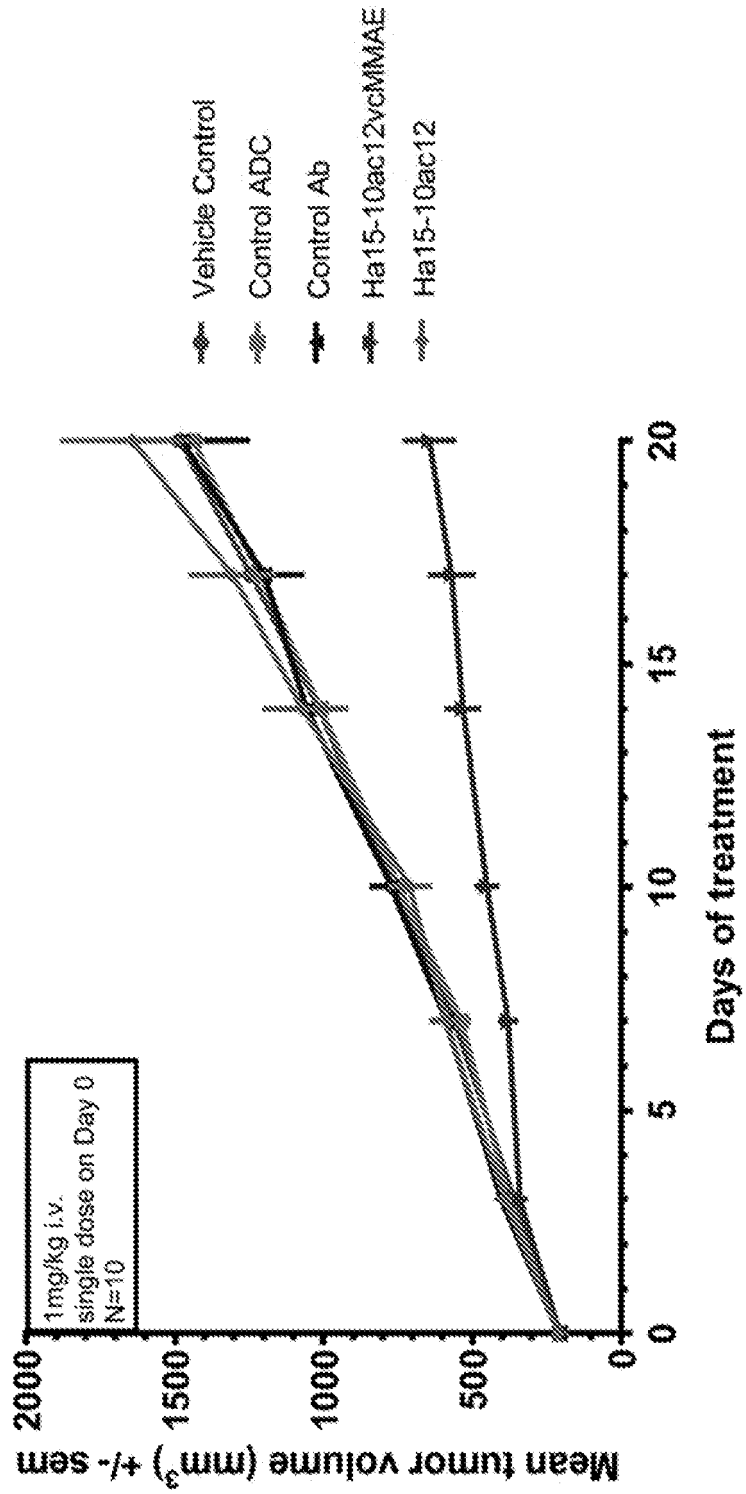


Figure 11. *In vitro* efficacy of Ha15-10ac12vcMMAE in CHP-212 cytotoxicity assay compared with M15-68(2)18 (a.k.a. 68(18)1.1)

	g2-non ADC control	g2-vcE control	M15-68(2)18.1.1	Ha15-10ac12vcMMAE
IC50 (nM)				
CHP212	Low confidence	65.64	Low confidence	0.9076
IGROV1	Not converged	Low confidence	Low confidence	Not converged

Figure 12. Efficacy of Ha15-10ac12vcMMAE in Subcutaneous established Xenograft model of Patient Derived human bladder cancer AG-B8 in SCID mice

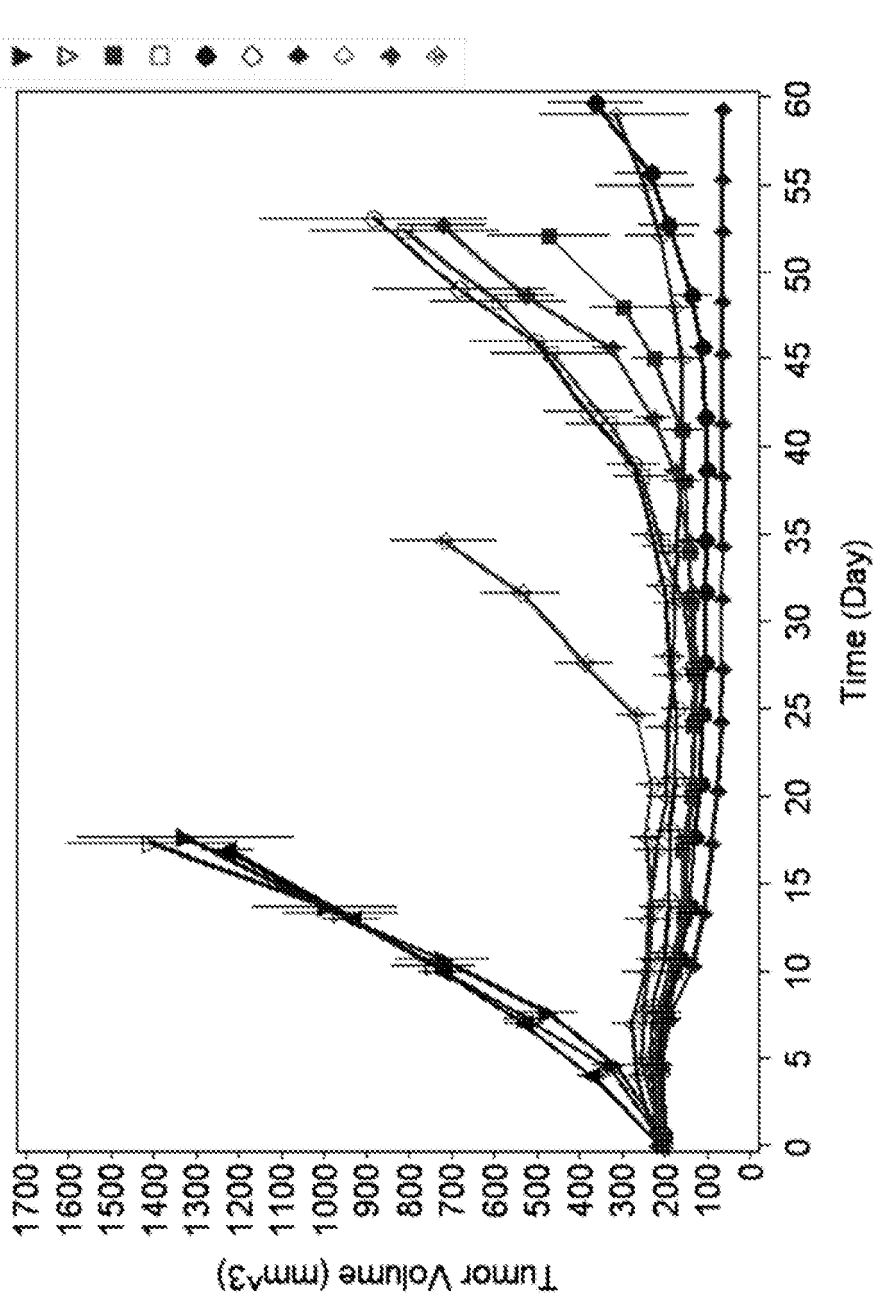
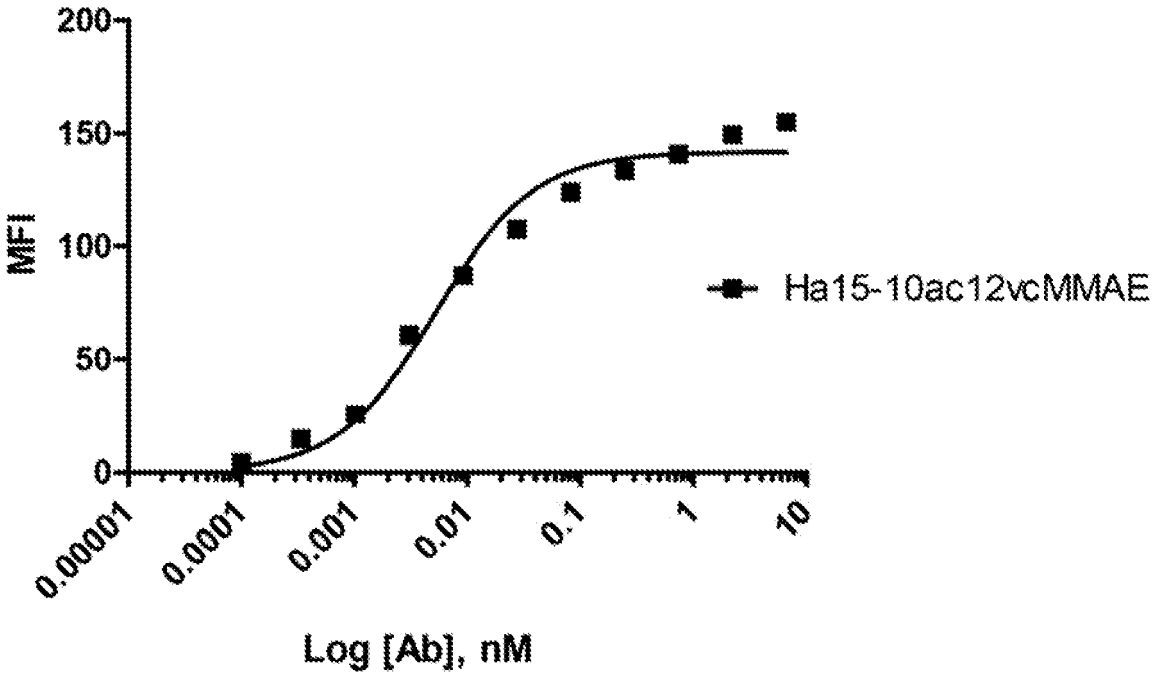


Figure 13. Ha15-10ac12vcMMAE Saturation Curve using SW780 Cells



	Ha15-10ac12vcMMAE
Bmax	141.9
Kd	0.005286

Figure 14. Ha15-10ac12vcMMAE binding to UMUC-AGS15, SW780 and CHP-212 cells by FACS

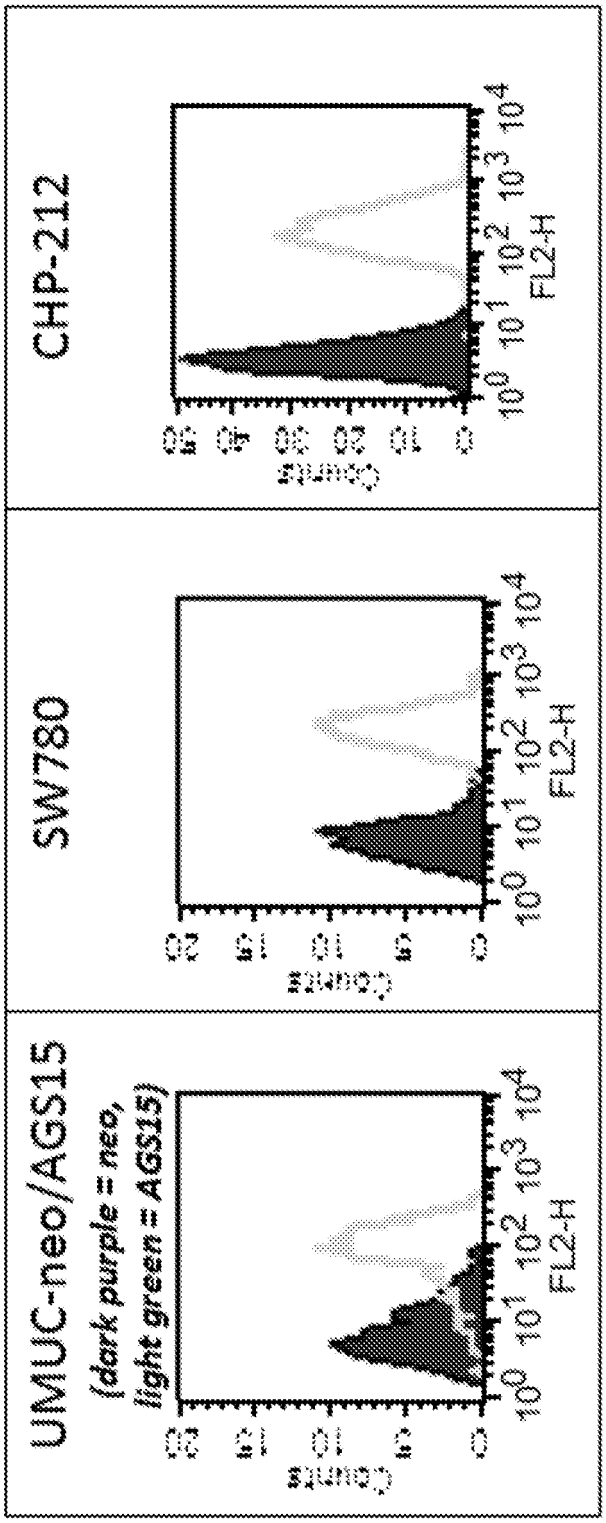


Figure 15A. Evaluation of the *In-vitro* cytotoxicity of Ha15-10ac12vcMMAE on CHP-212 and IGROV-1 cells

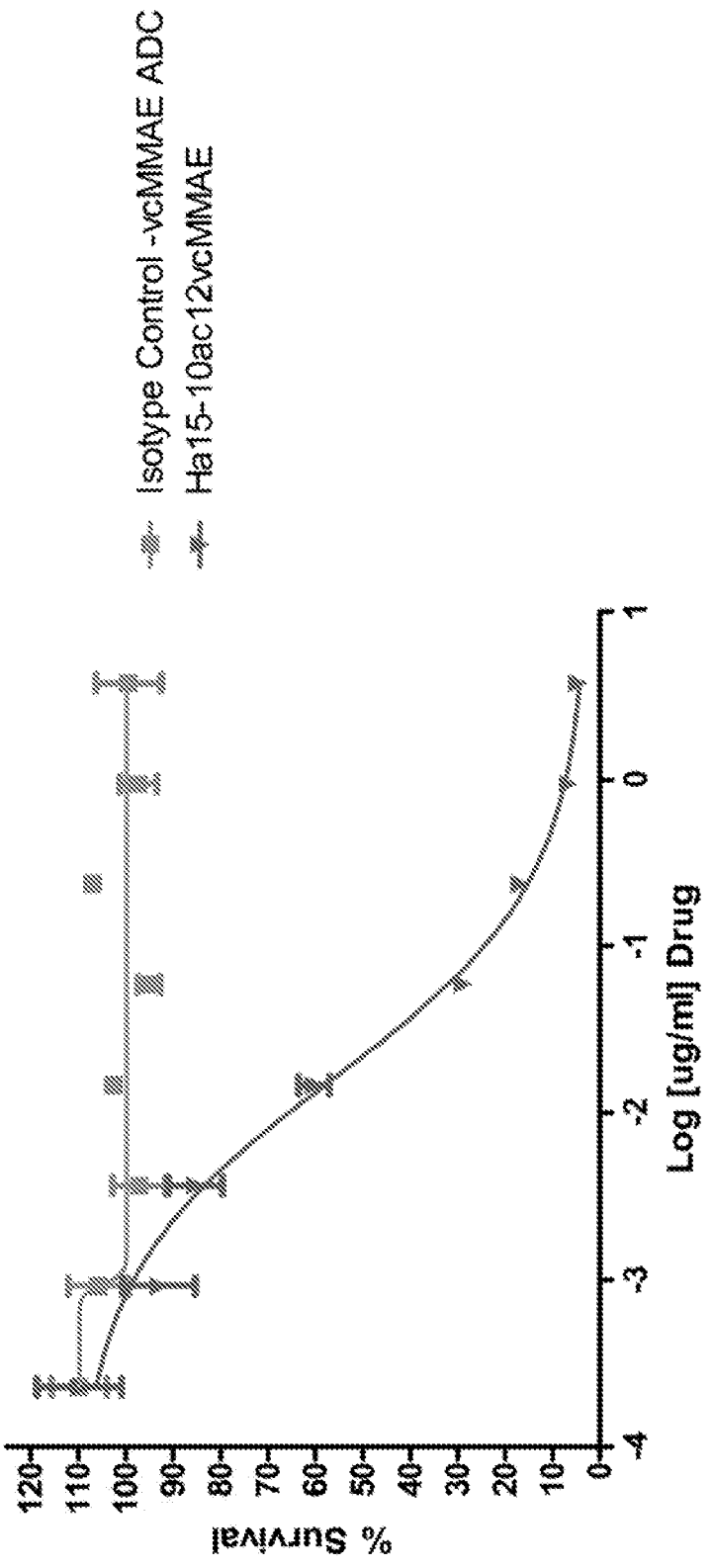


Figure 15B. Evaluation of the *In-vitro* cytotoxicity of Ha15-10ac12vcMMAE on CHP-212 and IGROV-1 cells

