

Figure 1 The cDNA (SEQ ID NO: 1) and amino acid sequence (SEQ ID NO: 2) of human FLT3. The start methionine is underlined. The open reading frame extends from nucleic acid 67-3048 including the stop codon.

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1  GTTTTACACGAGGCGGCATGCGAGGGGCTGGGCGGGCGCGGCTGGGGACCCCGGGGCTCCG
    M P A L A R D G G Q L P L L V V F S
61  GAGGCCATGCCGSCGTTGGCGCGCGACGGCGGCCAGCTGCCGCTGCTCGTTGTTTTTCT
    A M I F G T I T N Q D L P V I K C V L I
121 GCAATGATATTTGGGACTATTACAAATCAAGATCTGCCTGTGATCAAGTGTGTTTAATC
    N H K N N D S S V G K S S S Y P M V S E
181 AATCATAAGAACAATGATTCATCAGTGGGGAAGTCATCATCATATCCCATGGTATCAGAA
    S P E D L G C A L R P Q S S G T V Y E A
241 TCCCCGGAAGACCTCGGGTGTGCGTTGAGACCCAGAGCTCAGGGACAGTGTACGAAGCT
    A A V E V D V S A S I T L Q V L V D A P
301 GCCGCTGTGGAAAGTGGATGTATCTGCTTCCATCACACTGCAAGTGTGCTGGTGGATGCCCCA
    G N I S C L W V F K H S S L N C Q P H F
361 GGGAAACATTTCTGTCTCTGGGTCTTTAAGCACAGCTCCCTGAATTGCCAGCCACATTTT
    D L Q N R G V V S M V I L K M T E T Q A
421 GATTTACAAAACAGAGAGTTGTTTCCATGGTCATTTTGAAAATGACAGAAACCCAAGCT
    G E Y L L F I Q S E A T N Y T I L F T V
481 GGAGAATACCTACTTTTTATTACAGAGTGAAGCTACCAATTACACAATATTGTTTACAGTG
    S I R N T L L Y T L R R P Y F R K M E N
541 AGTATAAGAAATACCCTGCTTTACACATTAAGAAGACCTTACTTTAGAAAAATGGAAAAC
    Q D A L V C I S E S V F E P I V E W V L
601 CAGGACGCGCTGCTGTCATATCTGAGAGCGTTCCAGAGCCGATCGTGGAAATGGCTGCTT
    C D S Q G E S C K E E S P A V V K K E E
661 TGCGATTACAGGGGGAAGCTGTAAAGAAGAAAGTCCAGCTGTTGTTAAAAAGGAGGAA
    K V L H E L F G M D I R C C A R N E L G
721 AAAGTGCTTCATGAATTATTTGGGATGGACATAAGGTGCTGTGCCAGAAATGAAGTGGGC
    R E C T R L F T I D L N Q T P Q T T L P
781 AGGGAATGCACCAGGCTGTTTACAAATAGATCTAAATCAAACCTCCTCAGACCACATTGCCA
    Q L F L K V G E P L W I R C K A V H V N
841 CAATTATTTCTTAAACTAGGGGAACCCCTTATGGATAAGGTGCAAAGCTGTTTATGTGAAC
    H G F G L T W E L E N K A L E E G N Y F
901 CATGGATTCGGGCTCACCTGGGAATTAGAAAACAAAGCACTCGAGGAGGGCAACTACTTT
    E M S T Y S T N R T M I R I L F A F V S
961 GAGATGAGTACCTATTCAACAAACAGAACTATGATACGGATTCTGTTTGTCTTTGTATCA
    S V A R N D T G Y Y T C S S S K H P S Q
1021 TCAGTGGCAAGAAACGACACCGGATACTACACTTGTTTCTCTTCAAAGCATCCCAGTCAA
    S A L V T I V E K G F I N A T N S S E D
1081 TCAGCTTTGGTTACCATCGTAGAAAAGGGATTATATAAATGCTACCAATTCAAGTGAAGAT
    Y E I D Q Y E E F C F S V R F K A Y P Q
1141 TATGAAATTGACCAATATGAAGAGTTTTGTTTTCTGTGAGGTTTAAAGCCTACCCACAA
    I R C T W T F S R K S F P C E Q K G L D
1201 ATCAGATGTACGTGGACCTTCTCTCGAAAATCATTTCTTGTGAGCAAAAGGGTCTTGAT
    N G Y S I S K F C N H K H Q P G E Y I F
1261 AACGGATACAGCATATCCAAGTTTTGCAATCATAAGCACCAGCCAGGAGAATATATATTC

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Figure 1 (Continued)

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      H A E N D D A Q F T K M F T L N I R R K
1321 CATGCAGAAAATGATGATGCCCAATTTACCAAAATGTTACGCTGAATATAAGAAGGAAA
      P Q V L A E A S A S Q A S C F S D G Y P
1381 CCTCAAGTGCTCGCAGAAGCATCGGCAAGTCAGGCGTCTCTGTTCTCGGATGGATACCCA
      L P S W T W K K C S D K S P N C T E E I
1441 TTACCATCTTGGACCTGGAAGAAGTGTTACAGACAAGTCTCCCAACTGCACAGAAGAGATC
      T E G V W N R K A N R K V F G Q W V S S
1501 ACAGAAGGAGTCTGGAATAGAAAGGCTAACAGAAAAGTGTTEGGACAGTGGGTGTCGAGC
      S T L N M S E A I K G F L V K C C A Y N
1561 AGTACTCTAAACATGAGTGAAGCCATAAAAGGGTTCCTGGTCAAGTGCTGTGCATACAAT
      S L G T S C E T I L L N S P G P F P F I
1621 TCCCTTGGCACATCTTGTGAGACGATCCTTTTAAACTCTCCAGGCCCTTCCCTTTTCATC
      Q D N I S F Y A T I G V C L L F I V V L
1691 CAAGACAACATCTCATTCTATGCAACAATTGGTGTFTTGTCTCCTCTTCATTGTGCTTTTA
      T L L I C H K Y K K Q F R Y E S Q L Q M
1741 ACCCTGCTAATTTGTCAACAAGTACAAAAAGCAATTTAGGTATGAAAGCCAGCTACAGATG
      V Q V T G S S D N E Y F Y V D F R E Y E
1801 GTACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTACGTTGATTTACAGAGAATATGAA
      Y D L K W E F P R E N L E F G K V L G S
1861 TATGATCTCAAAATGGAGTTTCCAAGAGAAAATTTAGAGTTTGGGAAGGTACTAGGATCA
      G A F G K V M N A T A Y G I S K T G V S
1921 GGTGCTTTTGGAAAAGTGATGAACGCAACAGCTTATGGAATTAGCAAAACAGGAGTCTCA
      I Q V A V K M L K E K A D S S E R E A L
1981 ATCCAGGTTGCCGTCAAAATGCTGAAAGAAAAAGCAGACAGCTCTGAAAGAGAGGCACTC
      M S E L K M M T Q L G S H E N I V N L L
2041 ATGTGCAAGTCAAGATGATGACCCAGCTGGGAAGCCAGGAGAATATTGTGAACCTGCTG
      G A C T L S G P I Y L I F E Y C C Y G D
2101 GGGGCGTGACACTGTACAGGACCAATTTACTTGATTTTGAATACTGTTGCTATGGTGAT
      L L N Y L R S K R E K F H R T W T E I F
2161 CTTCTCAACTATCTAAGAACTAAAAGAGAAAAATTTACAGGACTTGGACAGAGATTTTC
      K E H N F S F Y P T F Q S H P N S S M P
2221 AAGGAACACAATTTGAGTTTTTACCCCACTTTCCAATCACATCCAAATTCAGCATGCCT
      G S R E V Q I H P D S D Q I S G L H G N
2281 GGTTCAGAGAAGTTCAGATACACCCGGAAGTGGATCAAATCTCAGGGCTTCATGGGAAT
      S F H S E D E I E Y E N Q K R L E E E E
2341 TCATTTCACTCTGAAGATGAAATTGAATATGAAAACCAAAAAAGGCTGGAAGAAGAGGAG
      D L N V L T F E D L L C F A Y Q V A K G
2401 CACTTGAATGTGCTTACATTTCAAGATCTTCTTTGCTTTGCATATCAACTGCCAAAGCA
      M E F L E F K S C V H R D L A A R N V L
2461 ATGGAATTTCTGGAATTTAAGTCGTGTGTTACAGAGACCTGGCCGCCAGGAACGTGCTT
      V T H G K V V K I C D F G L A R D I M S
2521 GTCACCCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAGATATCATGAGT
      D S N Y V V R G N A R L P V K W M A P E
2581 GATTCCAACATATGTTGTGAGGGGCAATGCCCGTCTGCCTGTAAAATGGATGGCCCCCGAA
      S L F E G I Y T I K S D V W S Y G I L L
2641 AGCCTGTTTGAAGGCATCTACACCATTAAAGAGTGATGTCTGGTCATATGGAATATTACTG

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Figure 1 (Continued)

W E I F S L G V N F Y P G I F V D A N F
2701 TGGGAAATCTTCTCACTTGGTGTGAATCCTTACCCTGGCATTCGGGTTGATGCTAACTTC
Y K L I Q N G F K M D Q P F Y A T E E I
2761 TACAAACTGATTCAAAATGGATTAAAATGGATCAGCCATTTTATGCTACAGAAGAAATA
Y I I M Q S C W A F D S R K R P S F P N
2821 TACATTATAATGCAATCCTGCTGGGCTTTTGA CTCAAGGAAACGGCCATCCTTCCCTAAT
L T S F L G C Q L A D A E E A M Y Q N V
2881 TTGACTTCGTTTTTAGGATGTCAGCTGGCAGATGCAGAAGAAGCGATGTATCAGAATGTG
D G R V S E C P H T Y Q N R R P F S R E
2941 GATGGCCGTGTTTCGGAATGTCCTCACACCTACCAAACAGGCGACCTTTCAGCAGAGAG
M D L G L L S P Q A Q V E D S *
3001 ATGGATTGGGGCTACTCTCTCCGCAGGCTCAGGTCGAAGATTCCGTAGAGGAACAATTTA
3061 GTTTTAAGGACTTCATCCCTCCACCTATCCCTAACAGGCTGTAGATTACCAAAACAAGAT
3121 TAATTTTCATCACTAAAAGAAAATCTATTATCAACTGCTGCTTCACCAGACTTTTCTCTAG
3181 AAGCTGTCTGCGTTTACTCTTGTTTTCAAAGGGACTTTTGTAAAATCAAATCATCCTGTC
3241 ACAAGGCAGGAGGAGCTGATAATGAACTTTATTGGAGCATTGATCTGCATCCAAGGCCTT
3301 CTCAGGC

Figure 2A The cDNA (SEQ ID NO: 3) and amino acid sequence (SEQ ID NO: 4) of CHv62.21 heavy chain. Double-underlined is the heavy chain variable region, and underlined is the heavy chain human IgG1 constant region.

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      E V Q L V E S G G G L V R P G G S L R L
1   GAGGTGCAGCTGGTGGACTCTGGGGGAGGCCTGGTCAGGCCTGGGGGTCCCTGAGACTC
      S C A A S G F T F S G Y S I N W V R Q A
61  TCCTGTGCAGCCTCTGGATTACCTTCAGTGGCTATAGCATAAACTGGGTCCGCCAGGCT
      P G K G L E W V S S I S S S S N Y I Y Y
121 CCAGGGAAGGGGCTGGAATGGGTCTCATCCATTAGTAGTAGTAATTACATATACTAC
      A D S V K G R F T I S R D N A K N S L Y
181 GCAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAAGTCACTGTAT
      L Q M N S L R A E D T A V Y Y C A R E G
241 CTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAGGG
      F I A G T T F D A F D I W G Q G T M V T
301 TTTATAGCTGGAAGTACTTTTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACC
      V S S A S T K G P S V F P L A P S S K S
361 GTCTCTTCAGCATCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGC
      T S G G T A A L G C L V K D Y F F E P V
421 ACCTCTGGGGGACACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGACCCGGTG
      T V S W N S G A L T S G V H T F P A V L
481 ACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTA
      Q S S G L Y S L S S V V T V P S S S L G
541 CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC
      T Q T Y I C N V N H K P S N T K V D K K
601 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAA
      V E P K S C D K T H T C P P C P A P E L
661 GTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCCAGCACCTGAAGTC
      L G G P S V F L F P P K P K D T L M I S
721 CTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCC
      R T P E V T C V V V D V S H E D P E V K
781 CGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG
      F N W Y V D G V E V H N A K T K P R E E
841 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
      Q Y N S T Y R V V S V L T V L H Q D W L
901 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACACAGGACTGGCTG
      N G K E Y K C K V S N K A L P A P I E K
961 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAA
      T I S K A K G Q P R E P Q V Y T L P P S
1021 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCC
      R E E M T K N Q V S L T C L V K G F Y P
1081 CGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
      S D I A V E W E S N G Q P E N N Y K T T
1141 AGGACATCGCCGTGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCAGG
      P P V L D S D G S F F L Y S K L T V D K
1201 CCTCCCGTCTGCACTCCGACGGCTCTTCTTCTCTATAGCAAGCTCACCGTGGACAAG
      S R W Q Q G N V F S C S V M H E A L H N

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Figure 2A (Continued)

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1261 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC  
      H Y T Q K S L S L S P G K *  
1321 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAA
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Figure 2B The cDNA (SEQ ID NO : 5) and amino acid sequence (SEQ ID NO: 6) of CHv62.21 light chain. Double-underlined is the light chain variable region, and underlined is the human kappa constant region.

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      D I Q M T Q S P S S L S A S V G D R V T
1  GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTCTGCATCTGTAGGAGACAGAGTCACC
      I T C R A S Q G I R N D L G W Y Q Q K P
61 ATCACTTGCCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCA
      G K A P K R L I Y A A S S L Q S G V P S
121 GGGAAAGCCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
      R F S G S G S G T E F T L T I S S L Q P
181 AGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACCTCTCACAATCAGCAGCCTGCAGCCT
      E D F A T Y Y C L Q H N G F P Y T F G Q
241 GAAGATTTTGCAACTTATTACTGTCTACAGCATAATGGTTTCCCGTACACTTTTGGCCAG
      G T K L E I K R T V A A P S V F I F P P
301 GGGACCAAGCTGGAGATCAAACGGACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA
      S D E Q L K S G T A S V V C L L N N F Y
361 TCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTAT
      P R E A K V Q W K V D N A L Q S G N S Q
421 CCCAGAGAGGCCAAACTACAGTGGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAG
      E S V T E Q D S K D S T Y S L S S T L T
481 GAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACG
      L S K A D Y E K H K V Y A C E V T H Q G
541 CTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
      L S S F V T K S F N R G E C *
601 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAA

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Figure 2C The cDNA (SEQ ID NO : 7) and amino acid sequence (SEQ ID NO: 8) of CHv62.21 heavy chain modified with insertion of a non-natural amino acid. Marked with an X is location of the amber codon for insertion of the non-natural amino acid *para*-acetylphenylalanine (pAF) at nucleic acid residue 371. Double-underlined is the heavy chain variable region, and underlined is the heavy chain human IgG1 constant region.

```

      E V Q L V E S G G G L V R P G G S L R L
1  GAGGTCCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAGGCGCTGGGGGGTCCCTGAGACTC
   S C A A S G E T F S G Y S I N W V R Q A
51 TCCTGTGCAGCCTCTGGATTACCTTCAGTGGCTATAGCATAAACTGGGTCCGCCAGGCT
   P G K G L E W V S S I S S S S N Y I Y Y
121 CCAGGGAAGGGGCTGGGAATGGGTCTCATCCATTAGTAGTAGTAATTACATATACTAC
   A D S V K G R F T I S R D N A K N S L Y
181 GCAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAACTCACTGTAT
   L Q M N S L R A E D T A V Y Y C A R E G
241 CTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTCCGAGAGAAGGG
   F I A G T T F D A F D I W G Q G T M V T
301 TTTATAGCTGGAAGTACTTTTGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACC
   V S S X S T K G P S V F P L A P S S K S
361 GTCTCTTCATAGTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGC
   T S G G T A A L G C L V K D Y F P E P V
421 ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTG
   T V S W N S G A L T S G V H T F P A V L
481 ACGGTGTCGTGGAAGTCAAGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTTA
   Q S S G L Y S L S S V V T V P S S S L G
541 CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC
   T Q T Y I C N V N H K P S N T K V D K K
601 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAA
   V E P K S C D K T H T C P P C P A P E L
661 GTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCCAGCACCTGAAGTC
   L G G P S V F L F P P K P K D T L M I S
721 CTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTCC
   R T P E V T C V V V D V S H E D P E V K
781 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG
   F N W Y V D G V E V H N A K T K P R E E
841 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
   Q Y N S T Y R V V S V L T V L H Q D W L
901 CAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTG
   N G K E Y K C K V S N K A L P A P I E K
961 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAA
   T I S K A K G Q P R E P Q V Y T L P P S
1021 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCATCC
   R E E M T K N Q V S L T C L V K G F Y P
1081 CGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGGCTCAAAGGCTTCTATCCC
   S D I A V E W E S N G Q P E N N Y K T T
1141 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACCAG

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Figure 2C (Continued)

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      P P V L D S D G S F F L Y S K L T V D K  
1201 CCTCCCCTGCTGGACTCCGACGGGCTCCTTCTTCCTCTATAGCAAGCTCAOCCGTGGACAAG  
      S R W Q Q G N V F S C S V M H E A L H N  
1261 AGCAGGTGGCAGCAGGGGAAOCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC  
      H Y T Q K S L S L S P G K *  
1321 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAA
```

Figure 3A The amino acid sequence (SEQ ID NO: 9) of CHv62.21 heavy chain. Double-underlined is the heavy chain variable region, and underlined is the human IgG1 constant region.

1 EVQLVESGGGLVPRPGGSLRLSCAASGFTFSGYSINWVROAPGKGLEWVSS
51 ISSSSNYIYYADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAREG
101 FIAGTTFDAFDINGOGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
151 LVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG
201 TQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTPPCPAPELLGGPSVFLFP
251 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREE
301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
351 EPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
401 PFVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLS
451 FGK

Figure 3B The amino acid sequence (SEQ ID NO: 10) of CHv62.21 light chain. Double-underlined is the light chain variable region, and underlined is the human kappa constant region.

```
1   DIQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQOKPGKAPKRLIYA  
51  ASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNGFPYTFGQ  
101 GTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV  
151 DNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQG  
201 LSSPVTKSFNRGEC
```

Figure 3C The amino acid sequence (SEQ ID NO: 11) of CHv62.21 heavy chain. Amino acid position 124, marked with an X is location of the amber codon for insertion of the non-natural amino acid ("nnAA") *para*-acetylphenylalanine (pAF). Double-underlined is the heavy chain variable region, and underlined is the human IgG1 constant region.

```
1  EVQLVESGGGLVFRPGGSLRLSCAASGFTFSGY SINWVROAPGKGLEWVSS  
51 ISSSSNYIYYADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAREG  
101 FIAGTTFDAFDINGQGTMVTVSSXSTKGPSVFPLAPSSKSTSGGTAALGC  
151 LVKDYFFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG  
201 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP  
251 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE  
301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR  
351 EFQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT  
401 PFVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS  
451 PGK
```

Figure 4A

Alignment of CHV62.21 heavy chain to human Ig germline.

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<-----FR1----->
E V Q L V E S G G G L V R P G S L R L S C A A S G F T F S
1 GAGTTCAGTGGTGGAGTCTGGGGAGTCTGATCAAGGCTGGGGTCTCCCTGAGACTCTCCCTGACAGTCTCGATTCACTTCAGT 90
V 98.3% (231/296) IGHV3-21*01 1 .....A.....
E V Q L V E S G G G L V R P G S L R L S C A A S G F T F S
91 GCTATAGCATTAACCTGGGTCCCGCCGAGCTCCAGGGAGGGCTGGATGGTCTCATCCATTAGTCTAGTATAGTATATATATAC 180
V 98.3% (231/296) IGHV3-21*01 91 A.....G.....G.....G.....
S Y S M N W V R Q A F G K G L E W V S S I S S S S S Y I Y Y
-----CDR1-----FR2-----FR3-----FR4-----
A D S V E G R F T I S R D K A R N S L Y L Q M N S L R A E D
181 GCACACTCAGTCAGAGGCCGATTCACCTCCAGAGACACGCCAGACTCACTGATCTGATGATGATGATGATGATGATGATGATGAT 270
V 98.3% (231/296) IGHV3-21*01 181 .....
A D S V K G R F T I S R D N A K N S L Y L Q M N S L R A E D
271 T A V Y I C A R E G E I A G T I F D A E D I W G Q E I M V T
Query 1 271 ACGCTGTGTTTACTGTGAGAGAGGGTTTATAGTCACTTGTGATCTTTGATTCGTTGATTCGTTGATTCGTTGATTCGTTGATTC 360
V 98.3% (231/296) IGHV3-21*01 271 .....
T A V Y Y C A R
D 100.0% (10/10) IGHV1-7*01 8 .....
J 100.0% (48/48) IGHV3*02 1 .....
J 98.0% (48/49) IGHV3*01 1 .....
----->
V S S
361 GTCTCTTCA 369
J 100.0% (48/49) IGHV3*02 41 ..... 49

```

Alignment of CHv62.21 light chain to human Ig germline.

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Figure 5

SQ 14-019

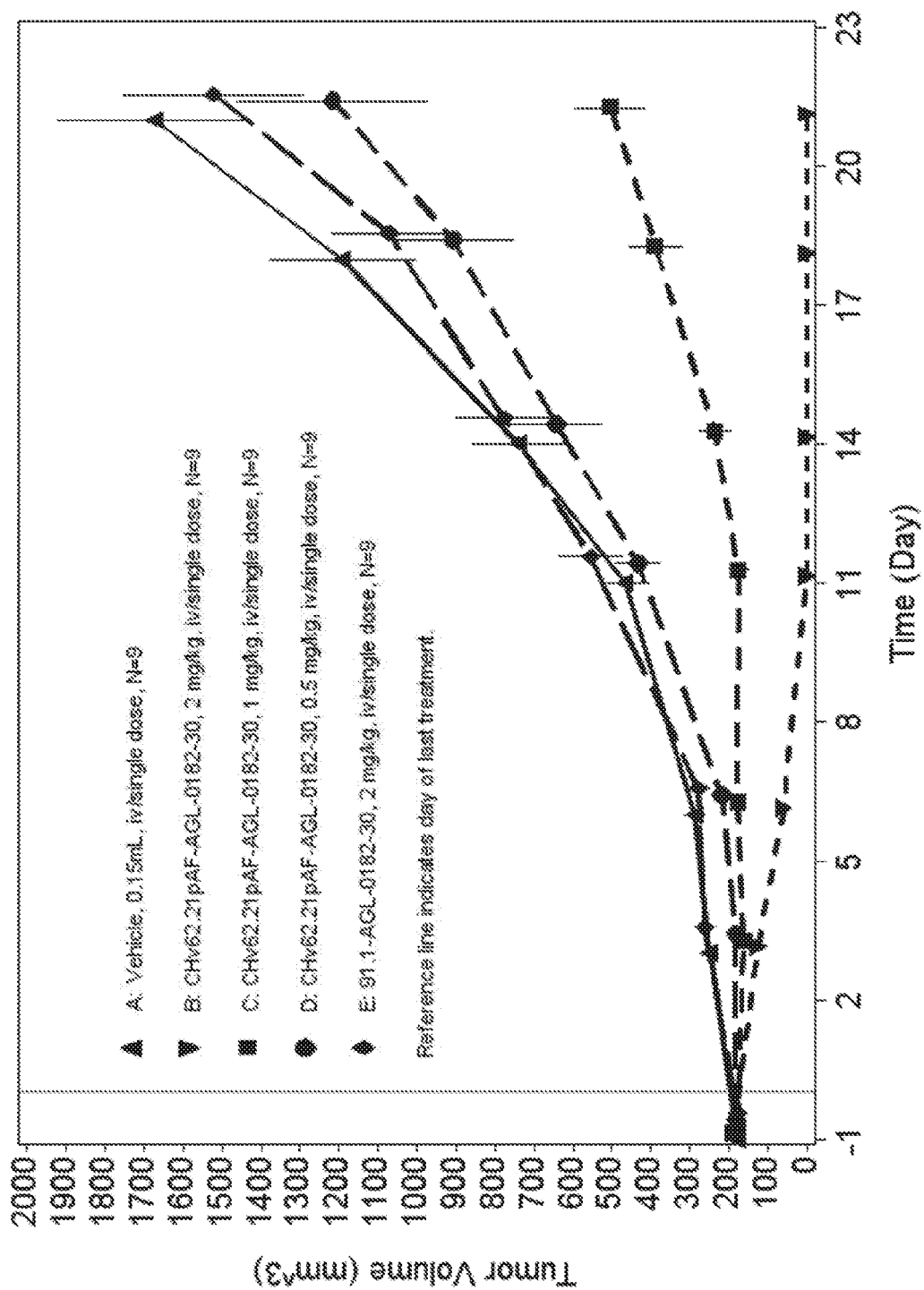


Figure 6
SQ 14-056

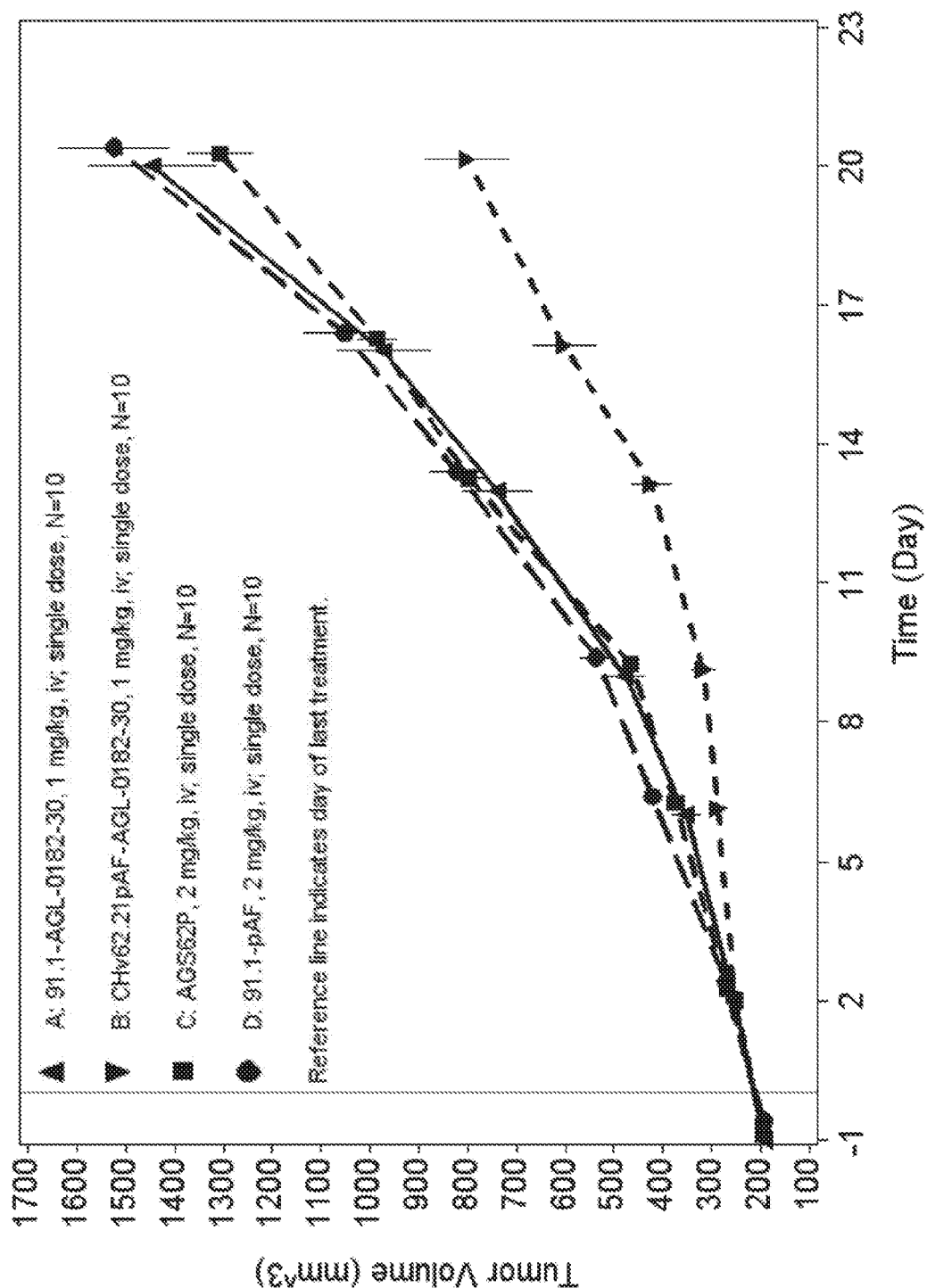


Figure 7

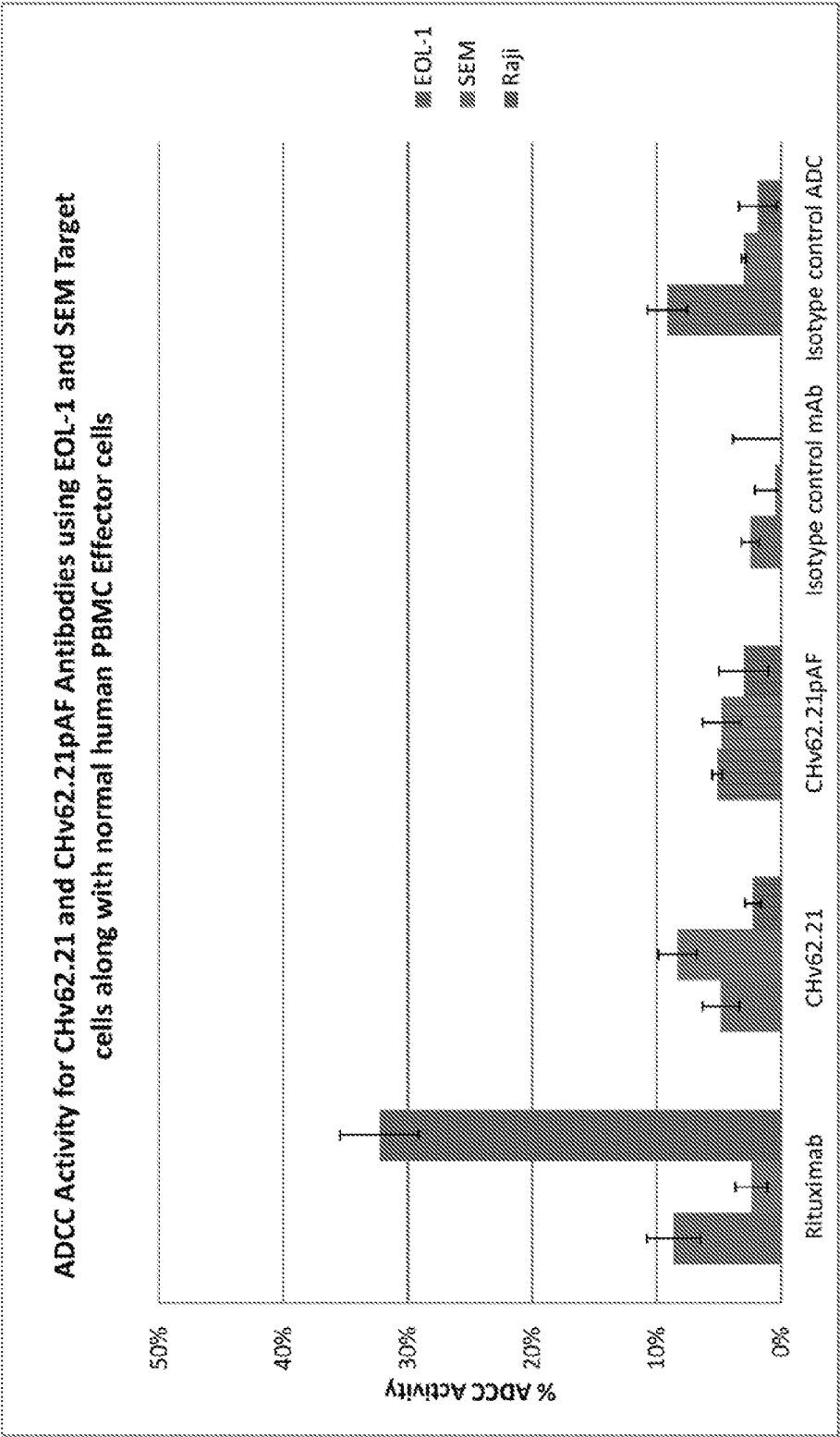


Figure 9

EOL1 Growth + hFL

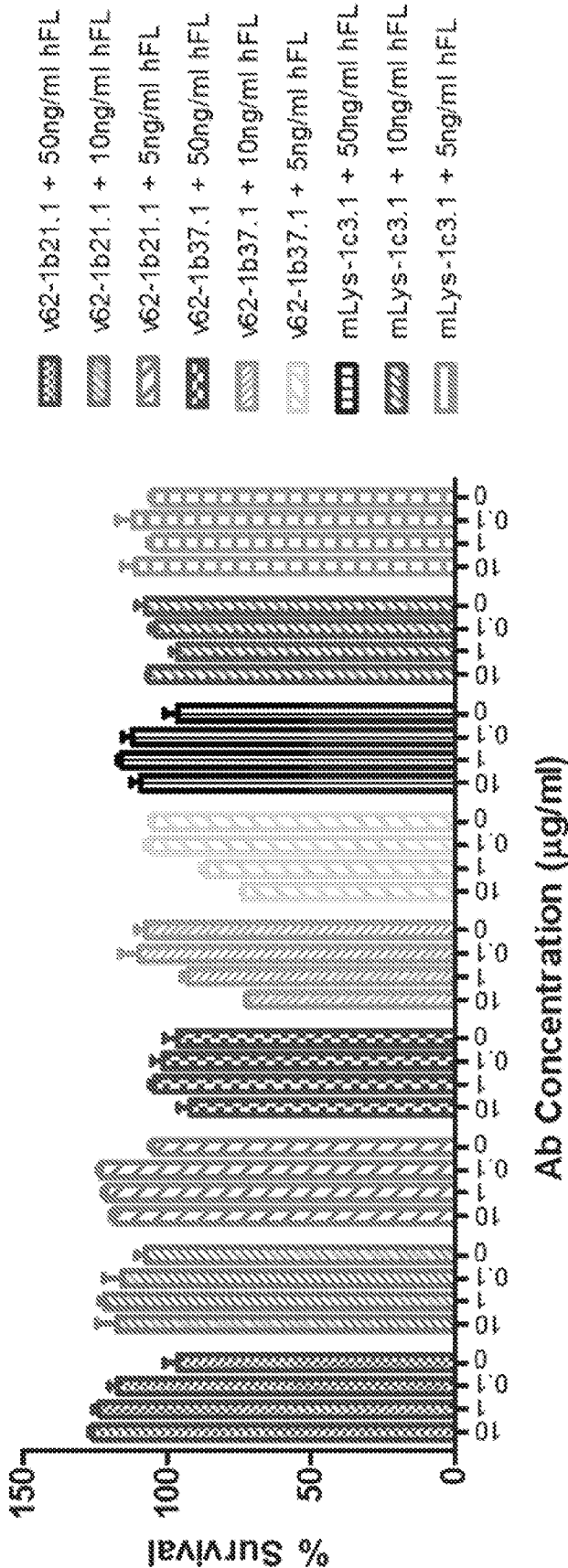


Figure 10

Cytotoxic activity of a 1b37.1 ligand blocking Mab is reduced in the presence of FL

Figure 10A

CHV62.21 (Non ligand blocker)

RS-4-11 Cytotox

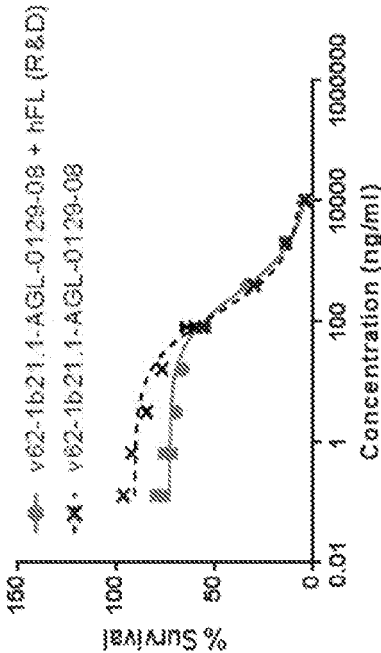
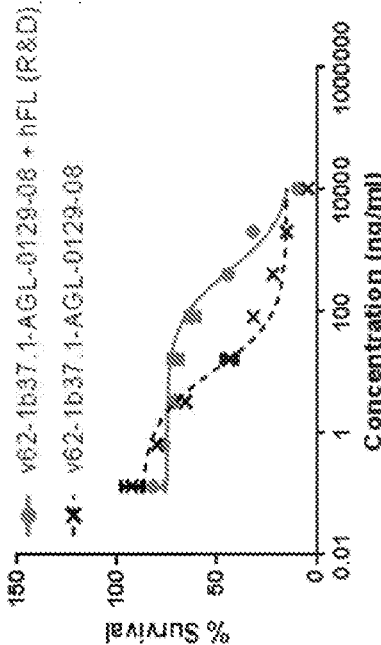


Figure 10B

1b37.1 (Ligand blocker)

RS-4-11 Cytotox



ADC	Ligand	DAR	RS411		
			IC50 (ng/ml)	R ² value	Fold diff
v62 1b21.1-AGL-0129-08	hFLT3 (R&D)	5.3	304	0.984	2.2
	N/A		138.6	0.9865	N/A
1b37.1-AGL-0129-08	hFLT3 (R&D)	3.9	472.3	0.9506	45.5
	N/A		10.37	0.9573	N/A

Figure 11 - FLT3 Ligand does not interfere with CHv62.21pAF-AGL-0182-30 mediated cytotoxicity in MOLM-13 cells

Figure 11A

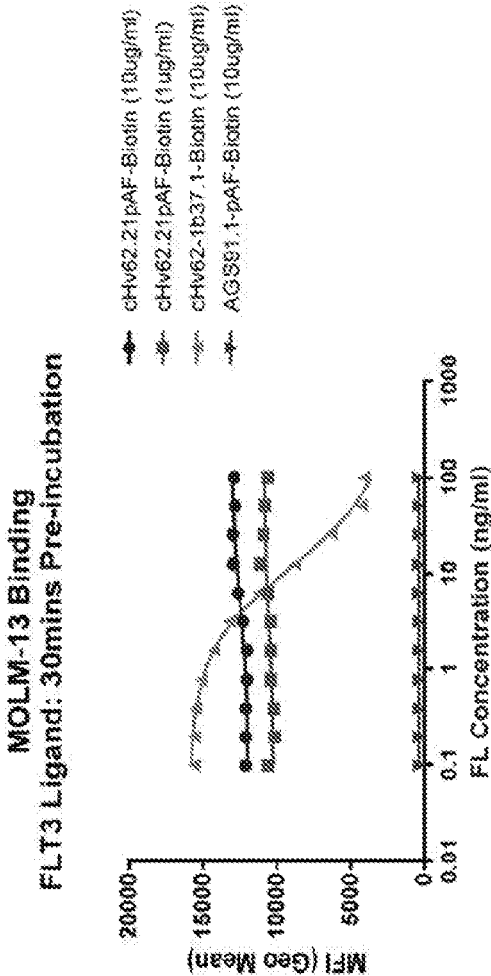


Figure 11B

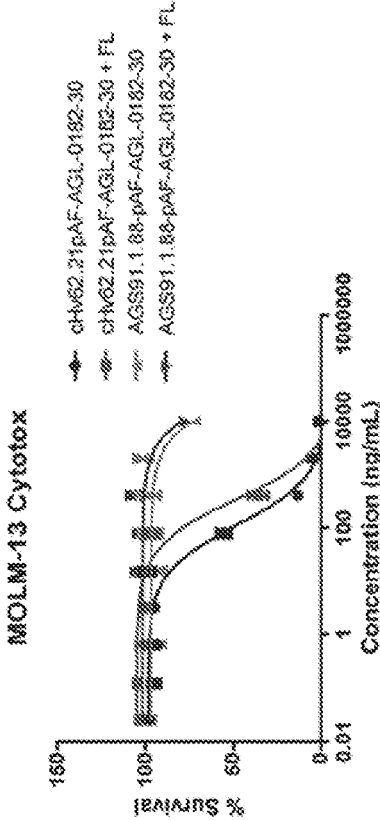


Figure 12
In vitro Stability Comparison of CHv62.21pAF-AGL-0182-30 compared to FLT3 ADC CHv62-1b21-AGL-0301-20

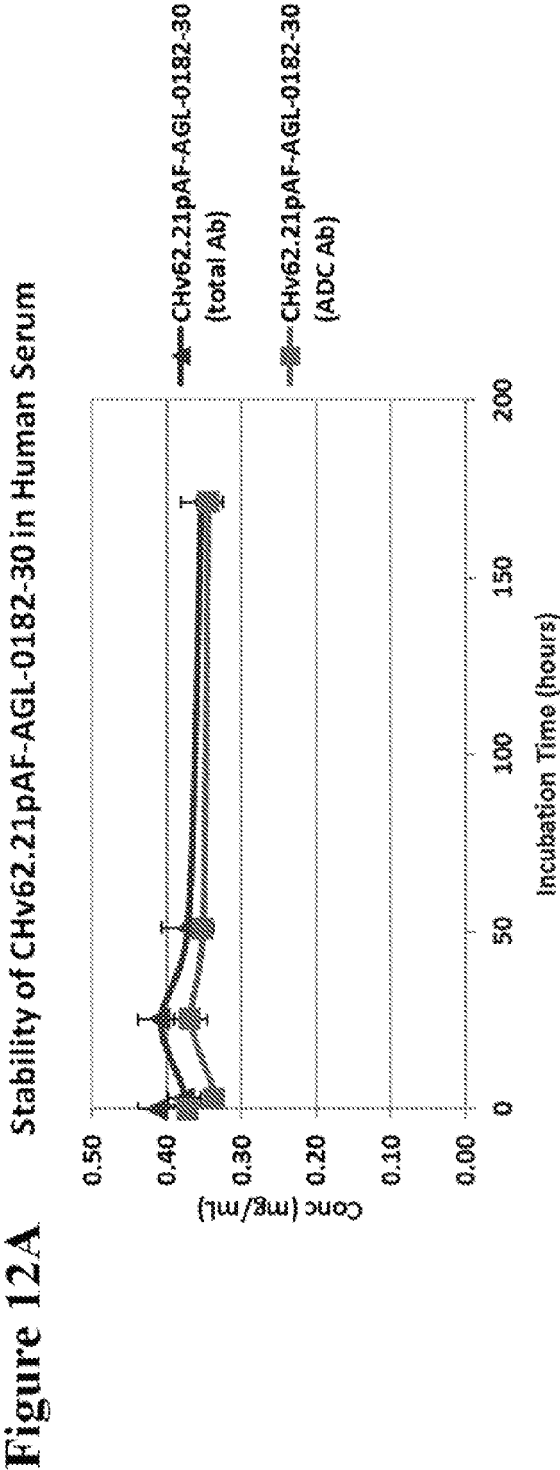


Figure 12B Stability of chV62-1b21-AGL-0301-20 in Human Serum

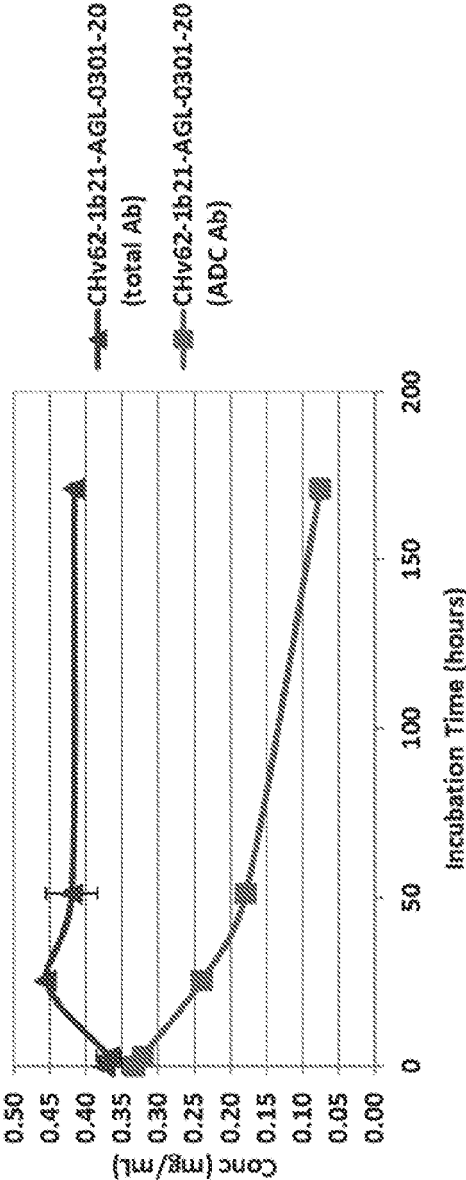


Figure 13

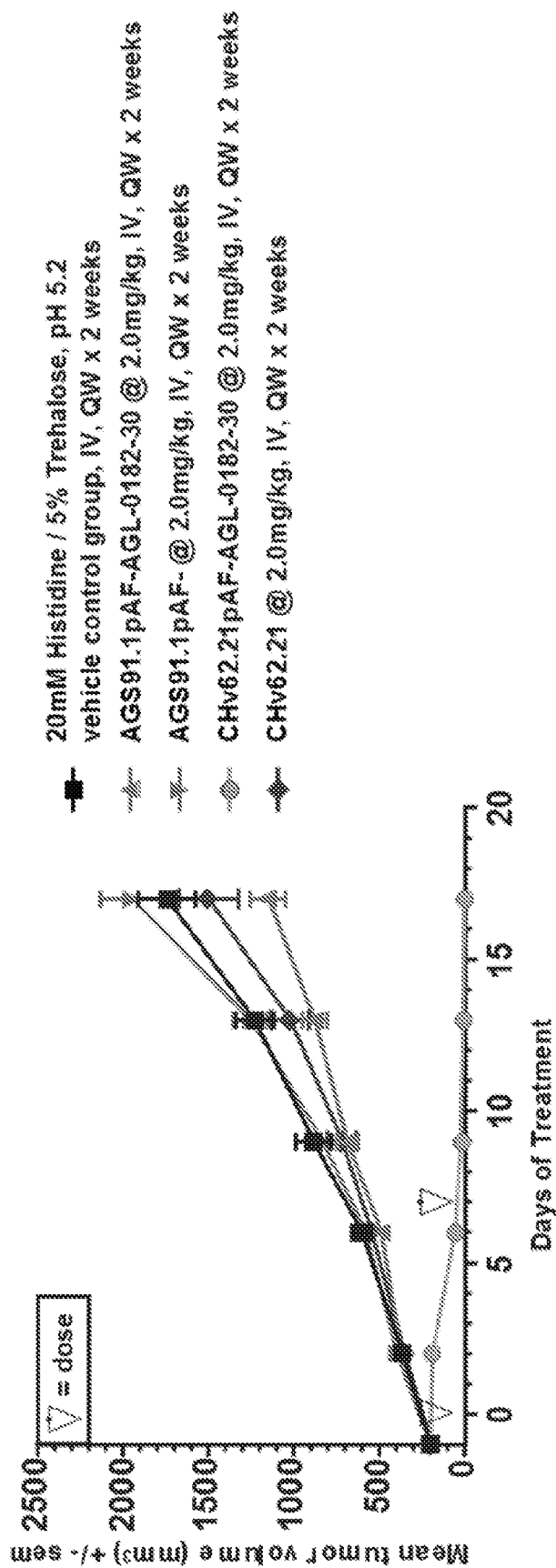


Figure 14

