

FIG. 1A: The cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of 191P4D12. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

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1  ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61  acggcttcttggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
121  tcccctagtggagaccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
181  cagttccttattcaagtctgcagccggctcccaggagatctcggtggaacttcagaaac
1      M P L S L G A E M W G P E
241  gctgggcagctctgcctttcaaccATGCCCTGTCCCTGGGAGCCGAGATGTGGGGCCTG
14   A W L L L L L L L A S F T G R C P A G E
301  AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTCCCCCGGGTG
34   L E T S D V V T V V L G Q D A K L P C F
361  AGCTGGAGACCTCAGACGTGGTAAGTGTGGTGTGGGCCAGGACGCAAACTGCCCTGCT
54   Y R G D S G E Q V G Q V A W A R V D A G
421  TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
74   E G A Q E L A L L H S K Y G L H V S P A
481  GCGAAGGCGCCCAGGAAGTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94   Y E G R V E Q P P P P R N P L D G S V L
541  CTTACGAGGGCCCGTGGAGCAGCCCGCCCGCCACGCAACCCCTGGACGGCTCAGTGC
114  L R N A V Q A D E G E Y E C R V S T F P
601  TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
134  A G S F Q A R L R L R V L V P P L P S L
661  CCGCCGGCAGCTTCCAGGCGGGCTGCGGCTCCGAGTGTGGTGCCTCCCCTGCCCTCAC
154  N P G P A L E E G Q G L T L A A S C T A
721  TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174  E G S P A P S V T W D T E V K G T T S S
781  CTGAGGGCAGCCAGCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194  R S F K H S R S A A V T S E F H L V P S
841  GCCGTTCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214  R S M N G Q P L T C V V S H P G L L Q D
901  GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234  Q R I T H I L H V S F L A E A S V R G L
961  ACCAAAGGATCACCCACATCCTCCACGTGTCTTCTTCTGCTGAGGCCTCTGTGAGGGGCC
254  E D Q N L W H I G R E G A M L K C L S E
1021  TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274  G Q P P P S Y N W T R L D G P L P S G V
1081  AAGGGCAGCCCCCTCCCTCATACAAGTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294  R V D G D T L G F P P L T T E H S G I Y
1141  TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314  V C H V S N E F S S R D S Q V T V D V L
1201  ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTT
334  D P Q E D S G K Q V D L V S A S V V V V
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gtgga
tacat

FIG. 1A
(Continued)

FIG. 1B: The cDNA (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region.

M E L G L C W V F L V A I L E

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1  GGTGATCAGCACTGAACACAGAGGACTCAACATGGAGTTGGGGCTGTGCTGGGTTTCCTTGTGCTATTTTAGA
   ·G V Q C E V Q L V E S G G G L V Q P G G S L R L S
76  AGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTC
   ·C A A S S G F T F S S Y N M N W V R Q A P G K G L E
151  CTGTGCAGCCTCTGGATTCACTTCAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCAACCATCTC
   ·W V S Y I S S S S S S T I Y Y A D S V K G R F T I S
226  GTGGGTTTCATACATTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCAACCATCTC
   ·R D N A K N S L S L Q M N S L R D E D T A V Y Y C
301  CAGAGACAATGCCAAGAACTCACTGTCTCTGCAAAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTG
   ·A R A Y Y Y G M D V W G Q G T T V T V S S A S T K
376  TCGCAGACCATACTACTACGGTATGGAGCTCTGGGGCCAGGACACGGTCAACGCTCTCTCAGCCTCCACCAA
   ·G P S V F P L A P S S K S T S G G T A A L G L V
451  GGGCCCATCGCTCTTCCCTTGGCAGCCTCTTCCAAGAGCACTCTGGGGCCACAGCGCCCTGGGCTGGCTGGT
   ·K D Y F P E P V T F V W N S G A L T S G V H T F P
526  CAAGGACTACTTCCCGAACCCTGAGCTGTGTTGGAATCAGGCGCCCTGACAGCGCGCTGACACCTTCC
   ·A V L Q S S G L Y S L S S V V T V P S S S L G T Q
601  GGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCCCTCCAGCAGCTTGGGCCACCA
   ·T Y I C N V N H K P S N T R V D K R V E P K S C D
676  GACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGGTTGAGCCAAATCTTGTGA
   ·K T H T C F P P C F A P E L L G G P S V F L F P P K
751  CAAAATCACAATGCCAACCCTGGCCAGCACTGAACCTCTGGGGGACCGTCAGTCTCTCTTCCCGCCAAA
   ·P K D T L M I S R T P E V T C V V V D V S H E D P
826  ACCCAAGCACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGTGAAGTGAAGCCAGCAAGACCC
   ·E V K F N W Y V D G V E V H N A K T K P R E E Q Y
901  TGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTA
   ·N S T Y R V V S V L T V L H Q D W L N G K E Y K C
976  CAACAGCAGTACCGGTGTGGTCAAGCTCTGCAACCTCTGGGGGACCGTCAGTCTCTCTTCCCGCCAAA
   ·K V S N K A L P A P I E K T I S K A K G Q P R E P
1051  CAGGCTCTCCAAACAAAGCCCTCCCGGACCCCTGAGCAAAACCACTCTCCAAAGCCAAAGCCCGCCCGAGAACCC
   ·Q V Y T L P P S R E E M T K N Q V S L T C L V K G
1126  ACAGGTGTACACCTTCCCGCATCCCGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGCTGCTCAAGG
   ·F Y P S D I A V E W E S N G Q P E N N Y K T T P P
1201  CTCTATCCAGCGACATCCCGTGGAGTGGGAGCAATGGGAGCCGAGCAACTACAGAGCAACCCCTCC
   ·V L D S D G S F F L Y S K L T V D K S R W Q Q G N
1276  CGTGTGCACTCCAGCGCTCTCTCTCTATAGCAAGCTCAGCGTGGACBAGAGCAGGTGGCAGCGGGAA
   ·V F S C S V M H E A L H N H Y T Q K S L S L S P G
1351  CGTCTCTCATCTCTCGTATGATGAGGCTCTGCACACCACTACACACAGAGAGCTCTCCCTGTCCCGGG
   ·K *
1426  TAAATGA

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FIG. 1C: The cDNA (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

M D M R V P A Q L L G L L L L W F

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1  AGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTGCTCTGGGTTC
   P G S R C D I Q M T Q S P S S V S A S V G D R V T
76  CCAGGTTCACATGGACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGCATCTGTGGAGACAGAGTCACC
   I T C R A S Q G I S G W L A W Y Q Q K P G K A P K
151  ATCAGTCTTGGGGCAGTCAAGGTATTAGCGGCTGGTTAGCTGTATCAGCAGAAACAGGCAAGCCCTAAG
   F L I Y A A S T L Q S G V P S R F S G S G S G T D
226  TTCTGATCTATGCTGCATCCACTTTGCAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGGACAGAT
   F T L T I S S L Q P E D F A T Y Y C Q Q A N S F P
301  TTCCTCTCACCCTCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGCTTCCCT
   P T F G G G T K V E I K R T V A A P S V F I F P P
376  CCCACTTTTGGGGAGGACCAAGGTGGAGATCAAAAGCACTGTGGCTGCACCATCTGTCTTCTCTTCCCGCA
   S D E Q L K S G T A S V V C L L N N F Y P R E A K
451  TCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCGAAA
   V Q W K V D N A L Q S G N S Q E S V T E Q D S K D
526  GTACAGTGGAGGTGGATAACCGCTCCATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGGCAAGGAC
   S T Y S L S S T L T L S K A D Y E K H K V Y A C E
601  AGCACCTACAGCCTCAGAGCACCTGACCTGAGCAAGCAGACTACAGAGAAACAAAGTCTTACGCTGCGAA
   V T H Q G L S S P V T K S F N R G E C *
676  GTCACCCATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTAG

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FIG. 1D: The amino acid sequence (SEQ ID NO:7) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, (SEQ ID NO:22, which is the sequence ranging from the 20th to the 136th amino acid of SEQ ID NO:7) and underlined with a dashed line is the human IgG1 constant region.

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1  MELGLCWVFLVAILEGVQCEVQVLESGGGLVQPGGSLRLSCAASGFTFS
51 YNMNVWRQAPGKGLEWVSYIISSSSTIYYADSVKGRFTISRDNAKNSLSL
101 QMNSLRDEDTAVYYCARAYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
151 SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS
201 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA
251 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
301 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP
351 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
401 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
451 LHNHYTQKSLSLSPGK

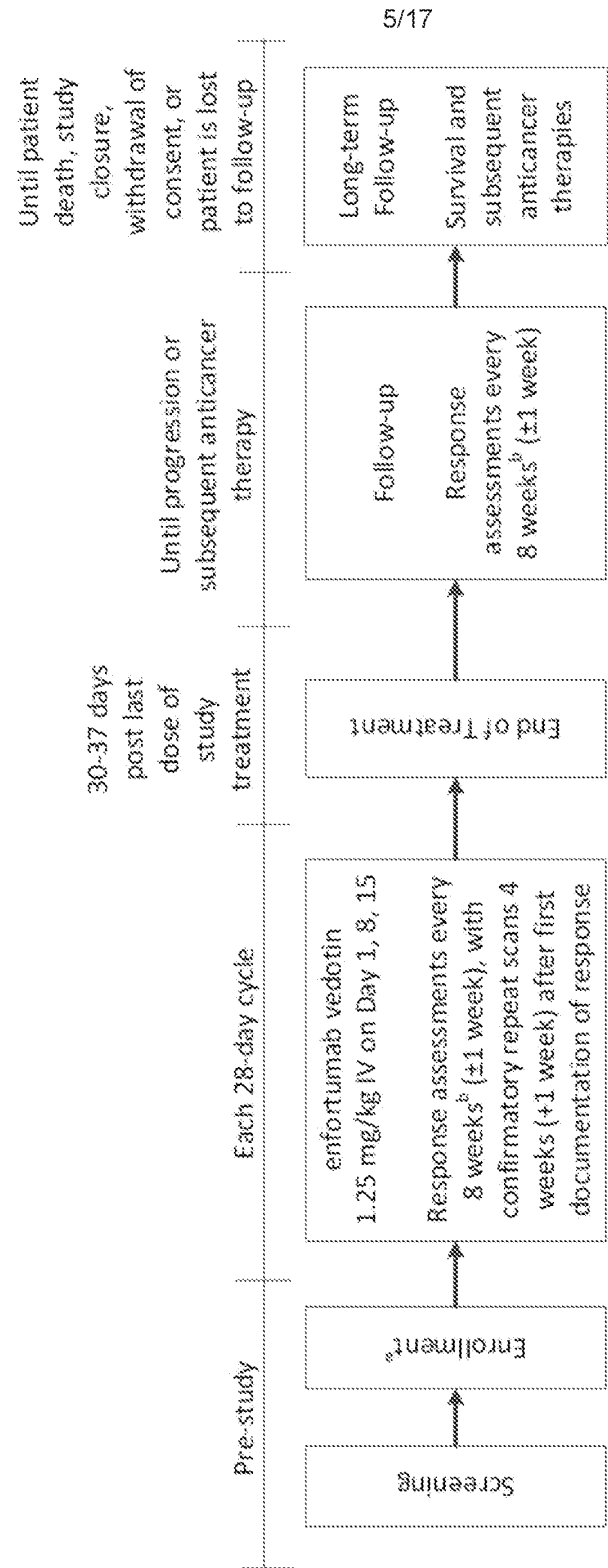
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FIG. 1E: The amino acid sequence (SEQ ID NO:8) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region (SEQ ID NO:23, which is the sequence ranging from the 23rd to the 130th amino acid of SEQ ID NO:8), and underlined with a dashed line is the human kappa constant region.

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1  MDMRVPAQLLGLLLLWEPGSRCDIQMTQSPSSVSASVGDRVTITCRASQG
51 ISGWLAWYQQKPKAPKFLIYAASTLQSGVPSRFSGSGSGTDFTLTISL
101 QPEDFATYYCQANSFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
151 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTLSST
201 LTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

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a There are 2 cohorts of CPI-treated patients in the study: Cohort 1) platinum-treated patients, and Cohort 2) platinum-naïve/cisplatin-ineligible patients.

b After 1 year on study, the frequency of response assessments will be reduced to every 12 weeks (±1 week).

FIG. 2

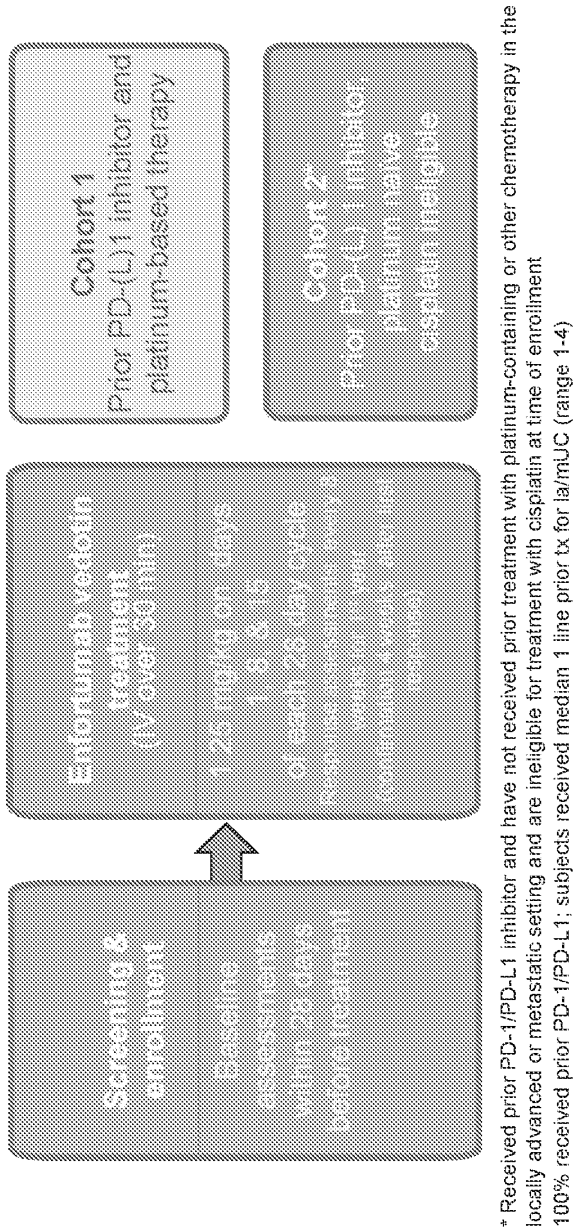


FIG. 3

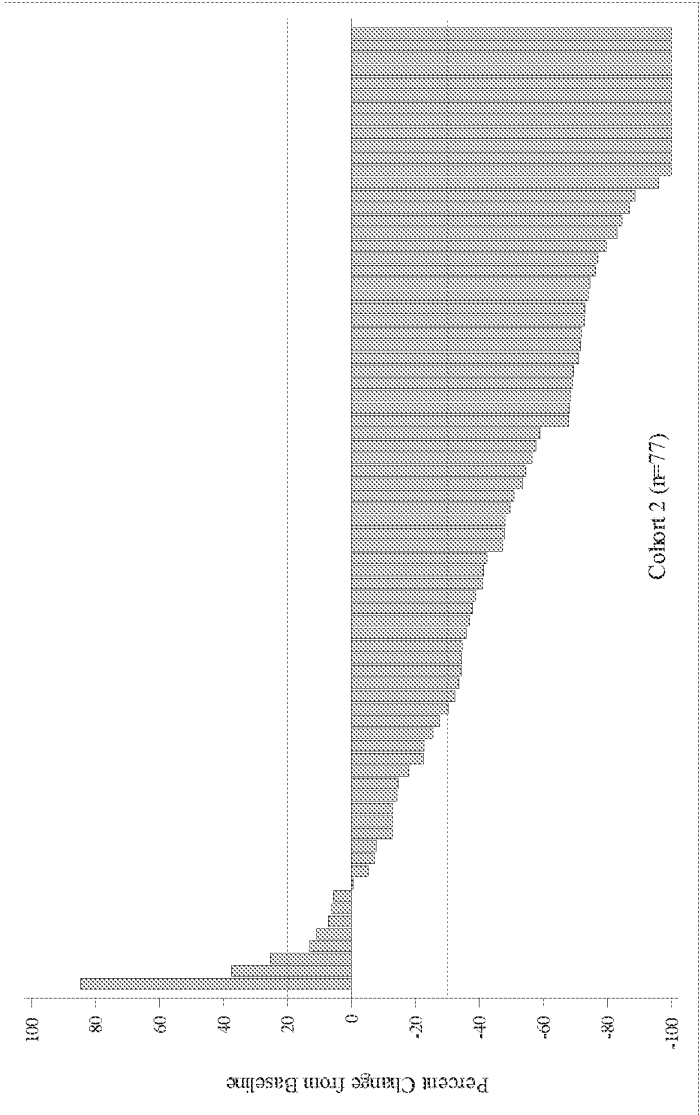


FIG. 4

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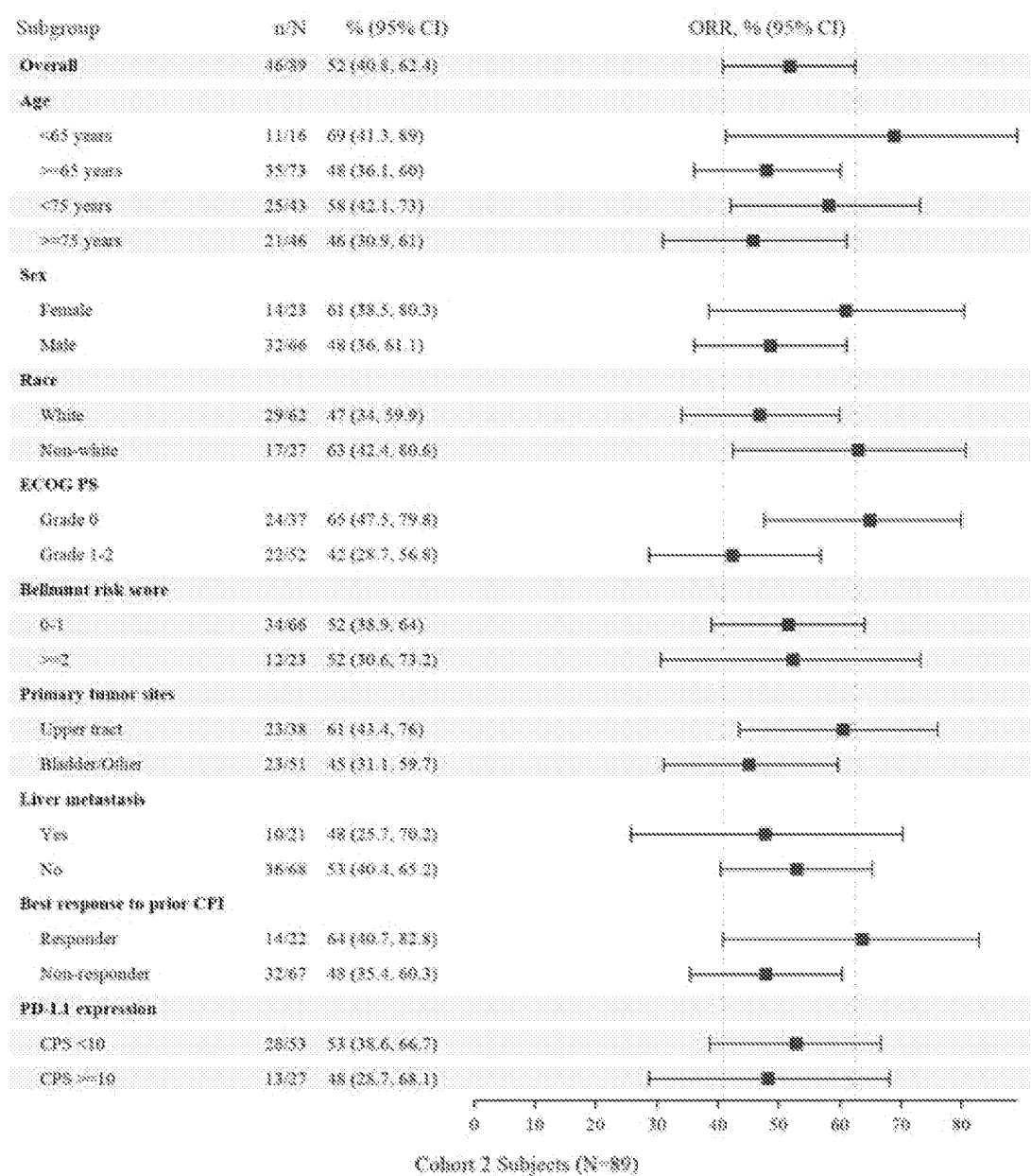


FIG. 5

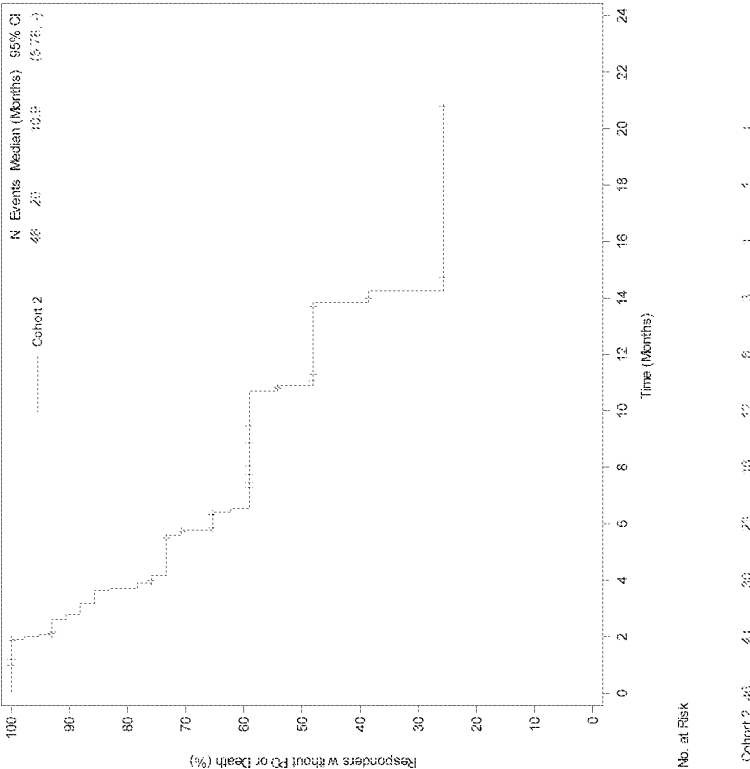


FIG. 6

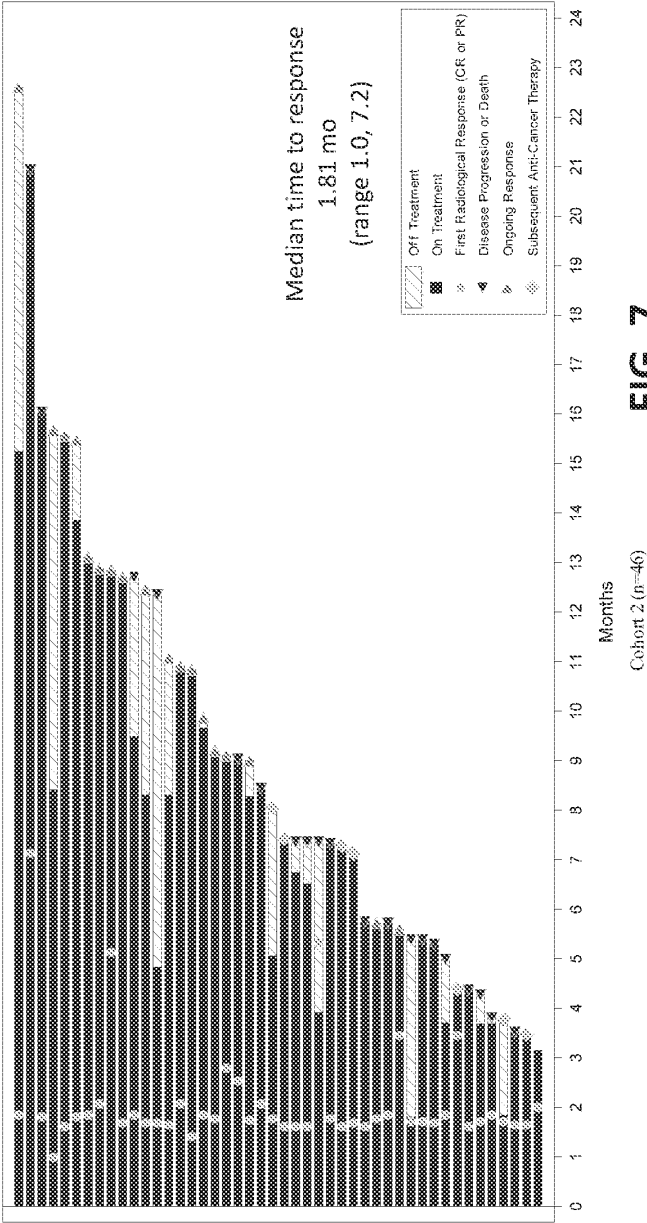


FIG. 7

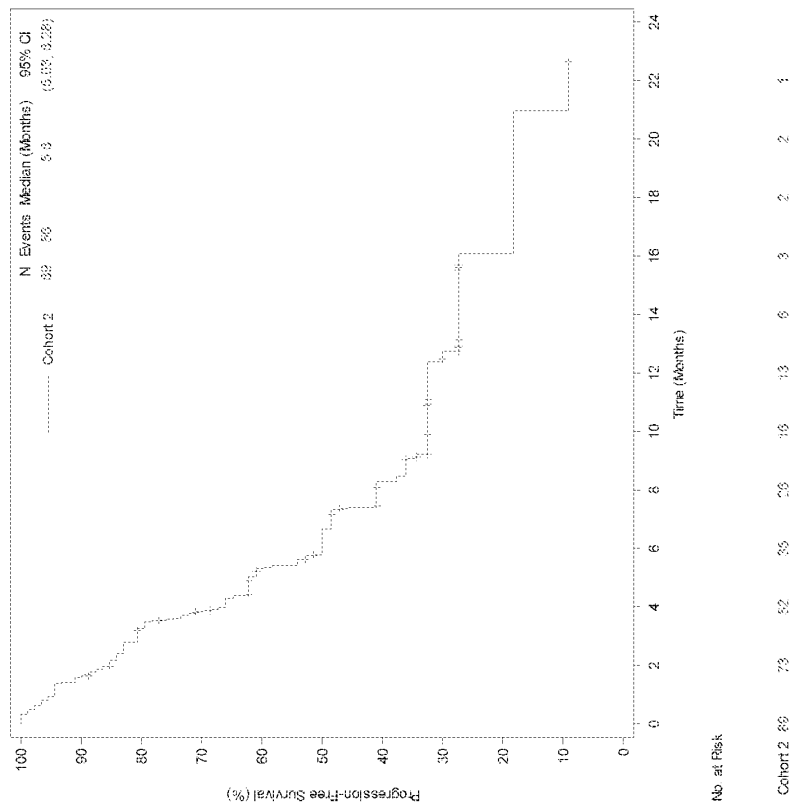


FIG. 8

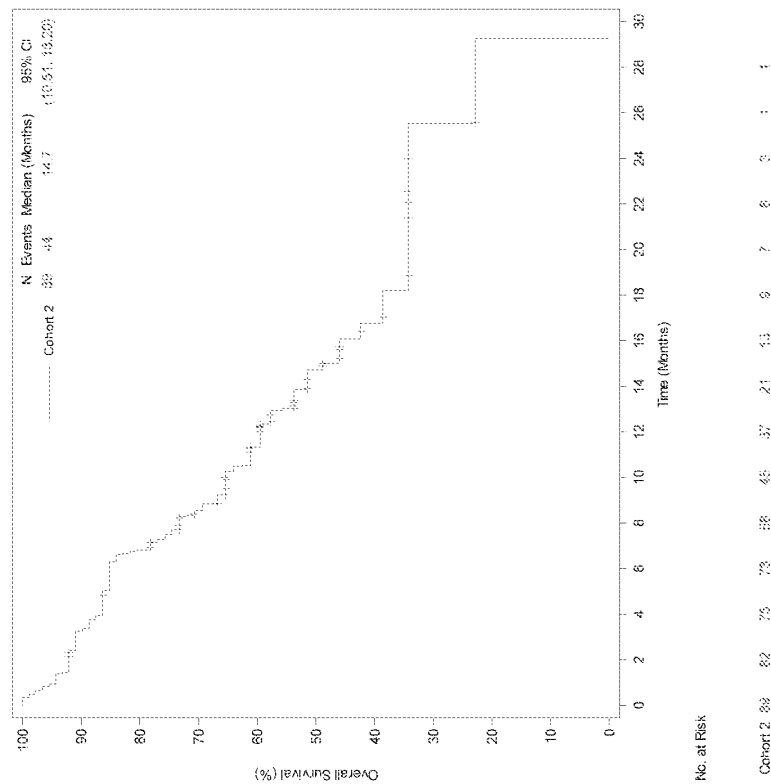


FIG. 9

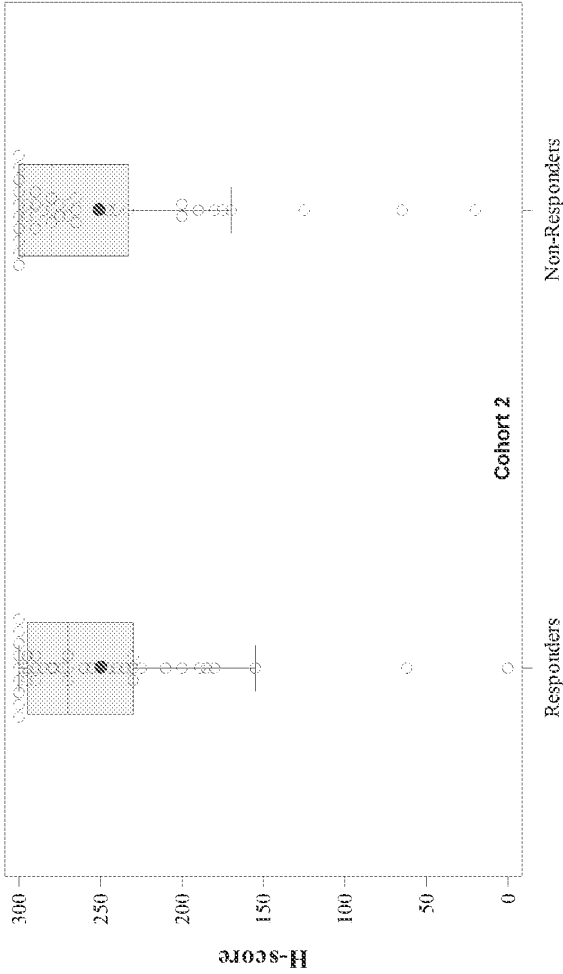


FIG. 10

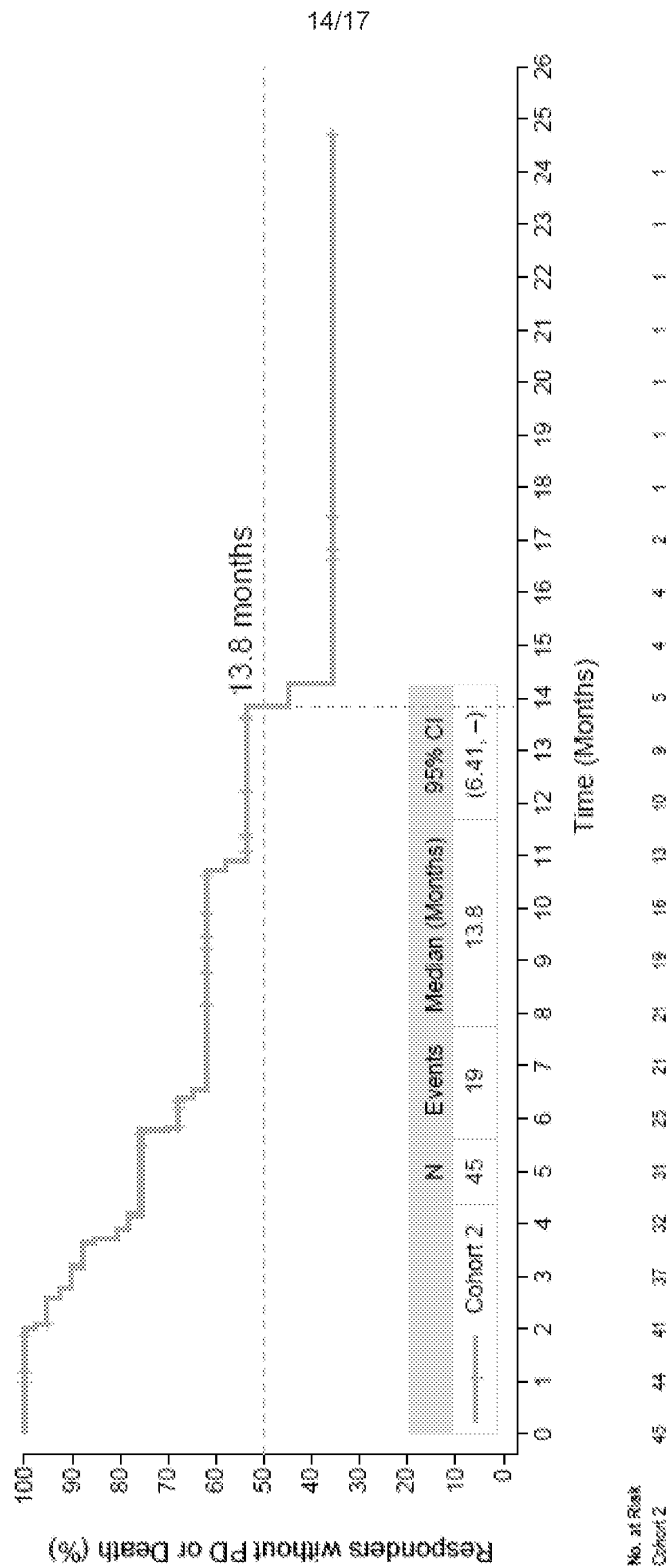
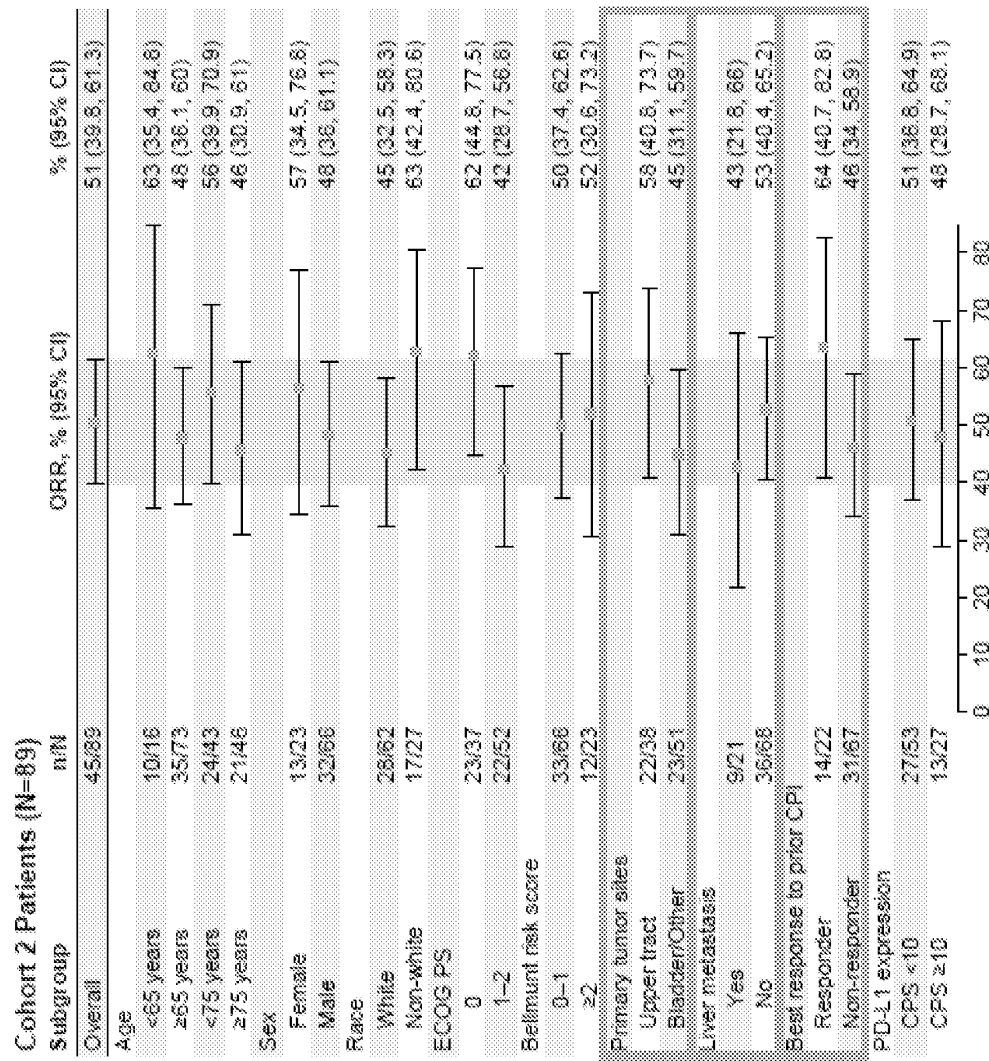


FIG. 11



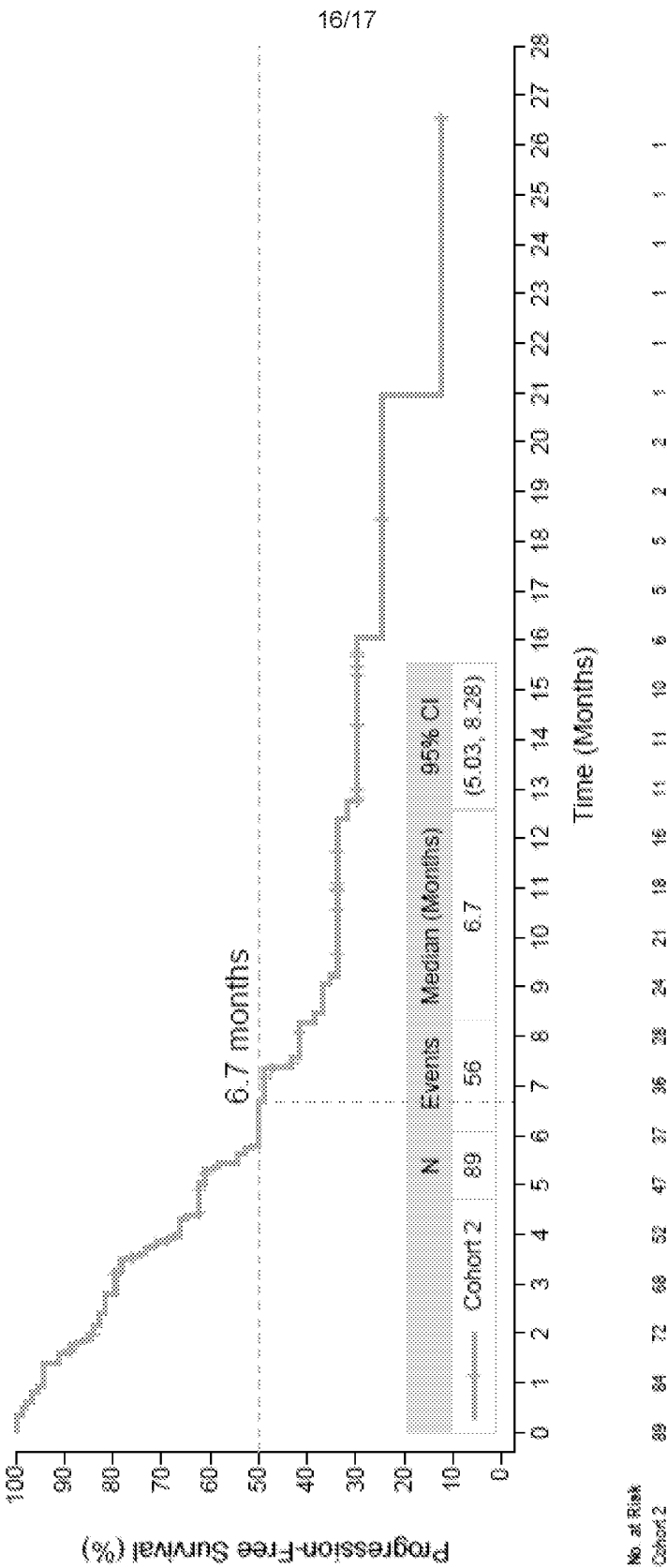


FIG. 13

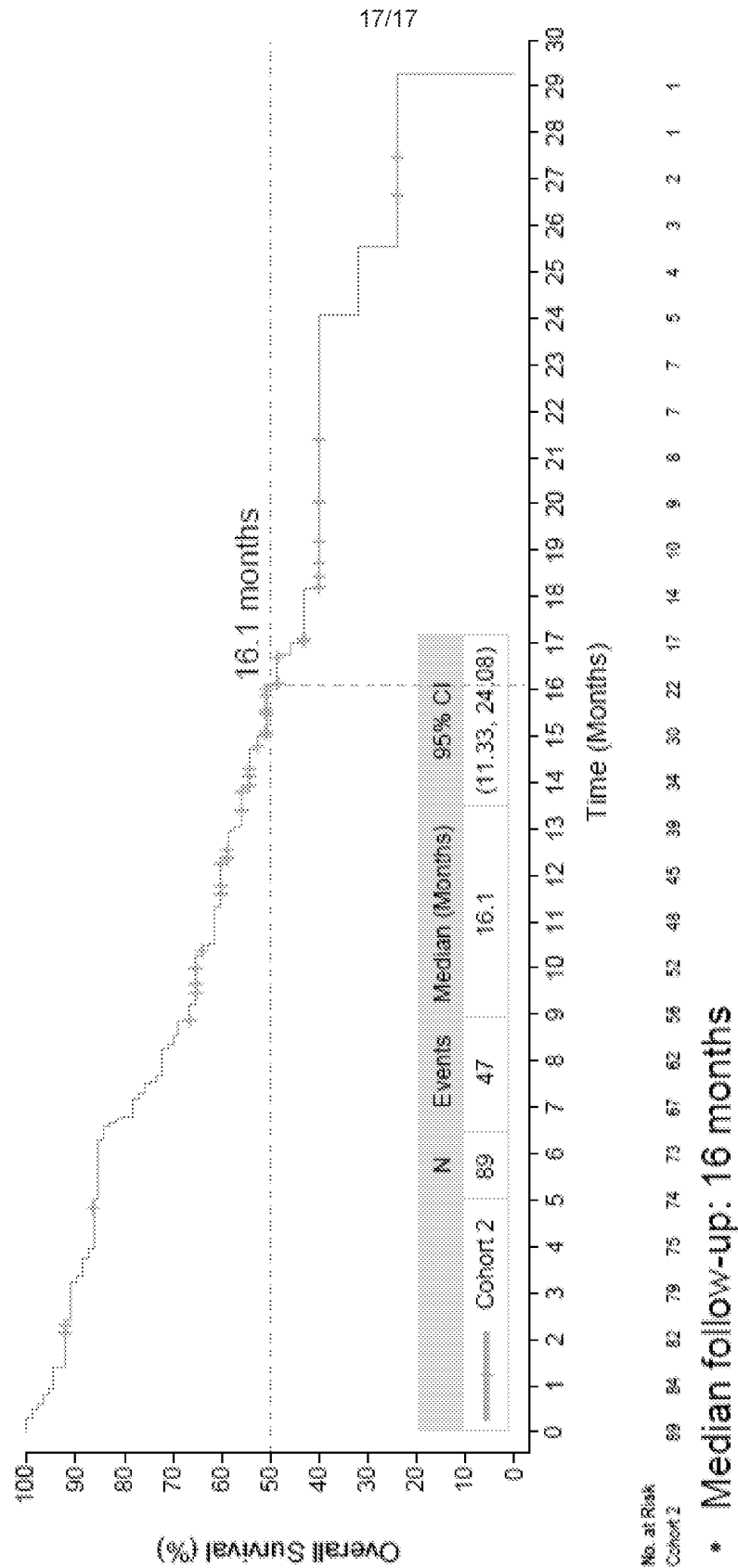


FIG. 14