

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.

```
1 ggccgtcgttggttgccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61 acggcttcttggggtagctacggctgggtgtgtagaacggggccgggctgggctggg
121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttctgccttctgggt
181 cagttccttattcaagtctgcagccggctcccaggagatctcggtggaacttcagaaac
1      M P L S L G A E M W G P E
241 gctgggcagctctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGCCTG
14  A W L L L L L L L A S F T G R C P A G E
301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGTG
34  L E T S D V V T V V L G Q D A K L P C F
361 AGCTGGAGACCTCAGACGTGTAAGTGTGGTGTGGGCCAGGACGAAAAGTGCCTGCT
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 GCGAAGGCGCCAGGAAGTACGCTACTGCACTCCAATACGGGCTTCATGTGAGCCCGG
94  Y E G R V E Q P P P P R N P L D G S V L
541 CTTACGAGGGCCGCGTGGAGCAGCCGCGCCCGCCACGCAACCCCTGGACGGCTCAGTGC
114 L R N A V Q A D E G E Y E C R V S T F P
601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGGCGGTGAGCACCTTCC
134 A G S F Q A R L R L R V L V P P L P S L
661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGTGGTGCCTCCCCTGCCCTCAC
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 GCCGTTCTTCAAGCACTCCCGCTCTGCTGCCGTACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGACGATGAATGGGCAGCCACTGACTTGTGTGGTGTCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
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 AAGGGCAGCCCCCTCCCTCATACAAGTGGACACGGCTGGATGGGCCTCTGCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
```

FIG. 1A

1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACGTGTGGATGTTCC  
334 D P Q E D S G K Q V D L V S A S V V V V V  
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTACGCCTCGGTGGTGGTGG  
354 G V I A A L L F C L L V V V V V V L M S R  
1321 TGGGTGTGATCGCCGCACTCTTGTCTGCCCTTCTGGTGGTGGTGGTGGTGGTGCATGTCCC  
374 Y H R R K A Q Q M T Q K Y E E E E L T L T  
1381 GATACCATCGGCGCAAGGCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA  
394 R E N S I R R L H S H H T D P R S Q P E  
1441 CCAGGGAGAACTCCATCCGAGGCTGCATTCCCATCACACGGACCCAGGAGCCAGCCGG  
414 E S V G L R A E G H P D S L K D N S S C  
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCTGATAGTCTCAAGGACAACAGTAGCT  
434 S V M S E E P E G R S Y S T L T T V R E  
1561 GCTCTGTGATGAGTGAAGAGCCCCGAGGGCCGAGTTACTCCACGCTGACCACGGTGAGGG  
454 I E T Q T E L L S P G S G R A E E E E D  
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG  
474 Q D E G I K Q A M N H F V Q E N G T L R  
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC  
494 A K P T G N G I Y I N G R G H L V \*  
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGACACCTGGTCTGAccca  
1801 ggcctgcctcccttcccttaggcctggctccttctgttgacatgggagattttagctcatc  
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg  
1921 cttagacctttacctccaaccttctgttcatcgggagggctccaccaattgagtcctcc  
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtggtgactgactg  
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg  
2101 ctgtcatatcagagtcagtgactgtggtgtatgtgccacgggatttgagtggttgctg  
2161 gggcaacactgtcaggggttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa  
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga  
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc  
2341 ggtgtgaggggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca  
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgcctcttggtggcctc  
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg  
2521 aatactgctccgaatcacttttaattttttctttttttttcttgcctttccattagt  
2581 tgtattttttattttattttttatttttttttttagagatggagctctcactatgttgc  
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc  
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa  
2761 attaaagaaagccttttagatttatccaatgtttactactgggatttgcctaaagtgaagcc

**FIG. 1A Continued**

2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggtacttccaaggcatctt  
2881 catgcaggcagccccctgggagggcacctgagagctggtagagtctgaaattagggatgt  
2941 gagcctcgtgggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg  
3001 gaattgcttggacctgggtgacaagggctcctgttcaatagtgggtgtggggagagagaga  
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg  
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc  
3181 tctgggttggggctggagttcaatgaggtttatTTTTtagctggcccaccagatacactc  
3241 agccagaatacctagatttagtaccctaacctcttcttagtctgaaatctgctggatttct  
3301 ggcctaaggagagggctcccatccttcgttccccagccagcctaggacttcgaatgtgga  
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcataattgtacat  
3421 aaaatgatattctgttttttaataaacagacaaaacttgaaaaa

## FIG. 1A Continued

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

1 GGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCTTGCTATTTTAGA  
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 AGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGTTACAGCCTGGGGGTCCCTGAGACTCTC  
C A A S G F T F S S Y N M N W V R Q A P G K G L E

151 CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATAACATGAACTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA  
W V S Y I S S S S S T I Y Y A D S V K G R F T I S

226 GTGGGTTTCATACATTAGTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTACCATCTC  
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 CAGAGACAATGCCAAGAACTCACTGTCTCTGCAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTG  
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 TGCGAGAGCATACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAA  
G P S V F P L A P S S K S T S G G T A A L G C L V

451 GGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT  
K D Y F P E P V T V S W N S G A L T S G V H T F P

526 CAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTGCACACCTTCCC  
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 GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCA  
T Y I C N V N H K P S N T K V D K R V E P K S C D

676 GACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGA  
K T H T C P P C P A P E L L G G P S V F L F P P K

751 CAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAA  
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 ACCCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC  
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 TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA  
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 CAACAGCAGTACCGTGTGGTCAAGCTCCTACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT  
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

FIG. 1B

1051 CAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACC  
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 ACAGGTGTACACCCTGCCCCATCCCGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG  
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 CTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC  
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 CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA  
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 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGG  
K \*  
1426 TAAATGA

## FIG. 1B Continued

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

1 AGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTC  
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 CCAGGTTCCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGCTGTCATCTGTTGGAGACAGAGTCACC  
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 ATCACTTGTCGGGCGAGTCAGGGTATTAGCGCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAG  
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 TTCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTACGGCGCAGTGGATCTGGGACAGAT  
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 TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCT  
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 CCCCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAAGTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA  
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 TCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAA  
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 GTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC  
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 AGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAAGTCTACGCCTGCCAA  
V T H Q G L S S P V T K S F N R G E C \*

676 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

FIG. 1C

**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.**

```

1  MELGLCWVFLVAILEGVOCEVOLVESGGGLVQPGGSLRLSCAASGFTFSS
51  YNMNVWRQAPGKGLEWVSYISSSSSTIYYADSVKGRFTISRDNAKNSLSL
101 QMNSLRDEDTAVYYCARAYYYGMDVWGQGTITVTVSSASTKGPSVFPLAPS
151 SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS
201 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA
251 PELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
301 VEVHNAKTKPREEQYNSTYRVVSVLTVQLQDWLNKEYCKVSNKALPAP
351 IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
401 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEA
451 LHNHYTQKSLSLSPGK

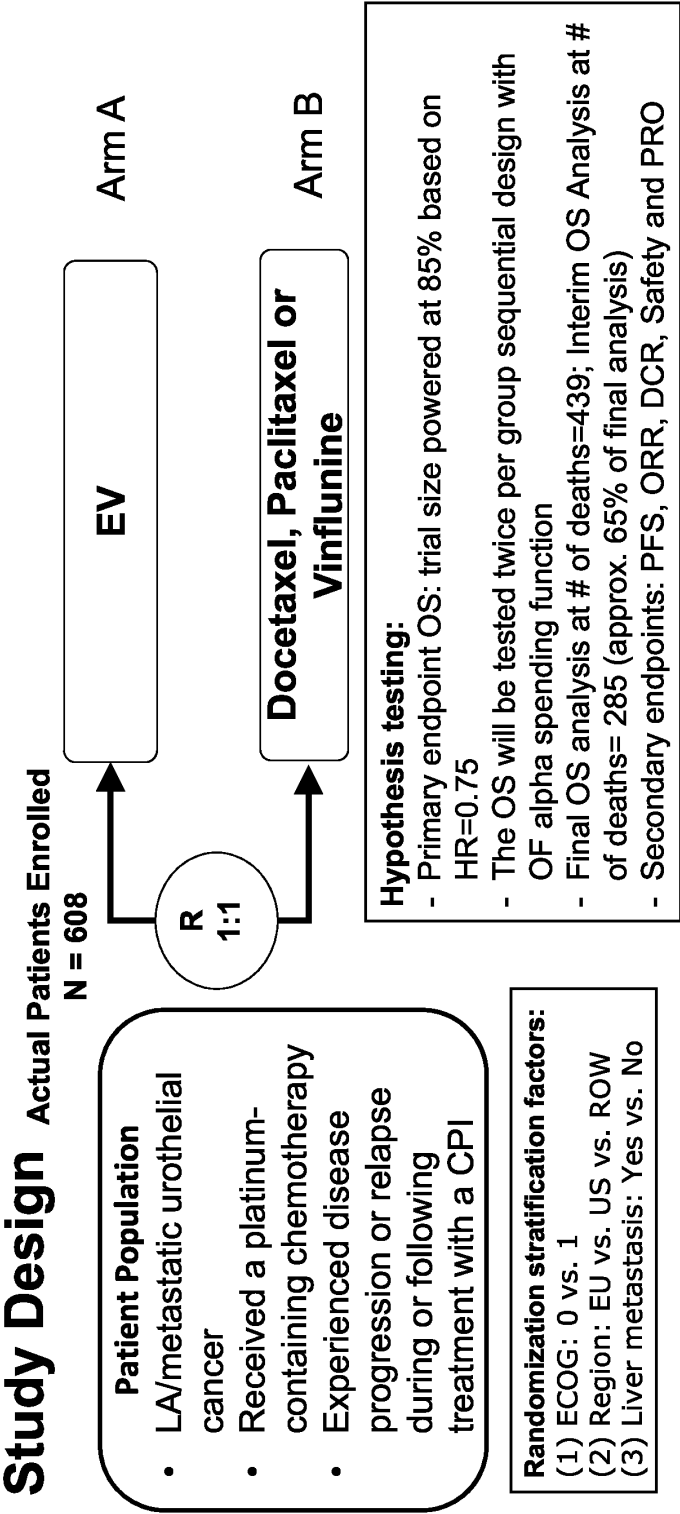
```

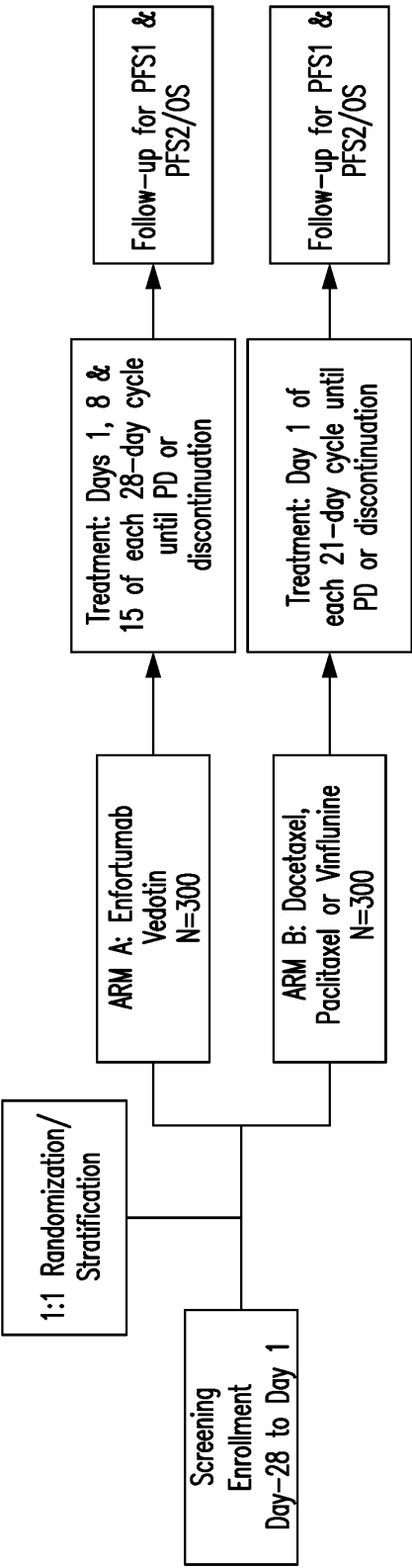
**FIG. 1E: The amino acid sequence (SEQ ID NO:8) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region (SEQ ID NO:23, which is the sequence ranging from the 23rd to the 130th amino acid of SEQ ID NO:8), and underlined with a dashed line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

```

1  MDMRVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRTITCRASQG
51  ISGWLAWYQQKPGKAPKFLIYAASLTQSGVPSRFSGSGSGTDFTLTISSL
101 QPEDFATYYCQQANSFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
151 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS
201 LTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

```





OS: overall survival; PD: progressive disease; PFS: progression free survival;  
PFS1: progression free survival on study therapy; PFS2: progression free  
survival on subsequent therapy

\*Imaging for both Arms was performed at baseline and every 56 days ( $\pm$  7 days) from the first dose of study treatment throughout the study until radiological disease progression, lost to follow-up, withdrawal of study consent, or start of a subsequent anti-cancer therapy. If a subject discontinues study drug prior to radiographic disease progression (i.e., PFS1), the subject should continue to undergo imaging assessment (including brain/bone imaging when indicated and collection of tumor measurements) every 56 days ( $\pm$  7 days) in the post treatment follow-up period until PFS1 is documented per the investigator or the subject starts another cancer treatment, whichever occurs earlier. After PFS1, subjects will be followed in the long-term follow-up period per institutional guidelines, but not less frequently than every 3 months to confirm survival status and collect subsequent anticancer treatment details and progression status until PFS2 is documented or the subject starts another cancer treatment, whichever occurs earlier. Phone contact with subject is sufficient for follow-up. Additional follow-up contacts may be required per sponsor request for analysis purposes.

FIG. 2B

Under each heading, please check the ONE box  
that best describes your health TODAY.

#### MOBILITY

- I have no problems walking ☐
- I have slight problems walking ☐
- I have moderate problems walking ☐
- I have severe problems walking ☐
- I am unable to walk ☐

#### SELF-CARE

- I have no problems washing or dressing myself ☐
- I have slight problems washing or dressing myself ☐
- I have moderate problems washing or dressing myself ☐
- I have severe problems washing or dressing myself ☐
- I am unable to wash or dress myself ☐

#### USUAL ACTIVITIES (*e.g. work, study, housework, family or leisure activities*)

- I have no problems doing my usual activities ☐
- I have slight problems doing my usual activities ☐
- I have moderate problems doing my usual activities ☐
- I have severe problems doing my usual activities ☐
- I am unable to do my usual activities ☐

#### PAIN / DISCOMFORT

- I have no pain or discomfort ☐
- I have slight pain or discomfort ☐
- I have moderate pain or discomfort ☐
- I have severe pain or discomfort ☐
- I have extreme pain or discomfort ☐

#### ANXIETY / DEPRESSION

- I am not anxious or depressed ☐
- I am slightly anxious or depressed ☐
- I am moderately anxious or depressed ☐
- I am severely anxious or depressed ☐
- I am extremely anxious or depressed ☐

USA (English)© 2009 EuroQol Group EQ-5D™ is a trade mark of the EuroQol group

**FIG. 2C**

SUBSTITUTE SHEET (RULE 26)

- We would like to know how good or bad your health is TODAY.
- This scale is numbered from 0 to 100.
- 100 means the best health you can imagine.  
0 means the worst health you can imagine.
- Mark an X on the scale to indicate how your health is TODAY.
- Now, please write the number you marked on the scale in the box below.

YOUR HEALTH TODAY =

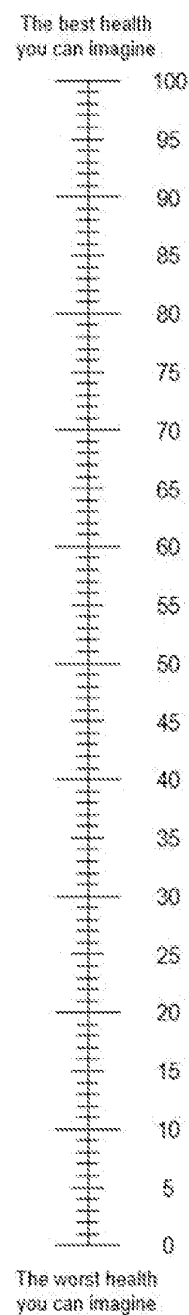
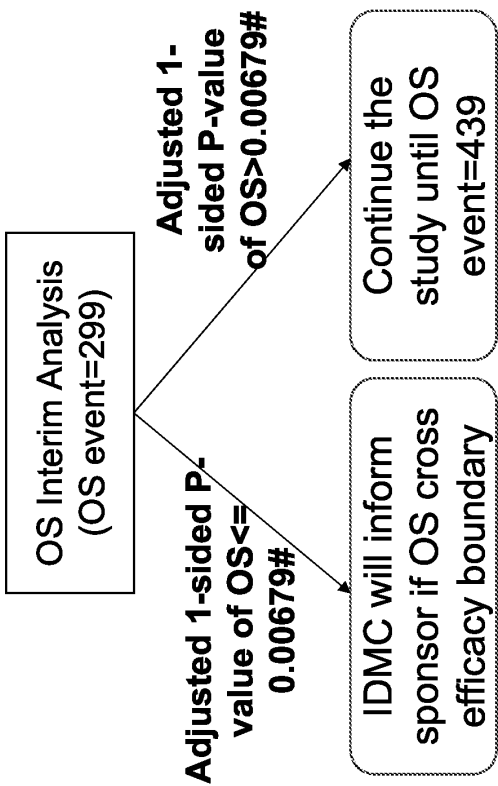


FIG. 2C (Continued)



Interim analysis decision rule is based on OS analysis result, IDAC (Axio) will perform the statistical analysis per interim analysis plan.

- **Primary analysis endpoint:** OS
  - **Analysis population:** Full Analysis Set (FAS), i.e. all randomized subjects
  - **Analysis timing:** Cutoff date of 15Jul2020, when approx. 65% of total planned events (~ 285). Efficacy boundary is adjusted per observed OS events (=301#).
  - **Analysis method:** Stratified log-rank test, HR is estimated by cox proportional hazard model
  - **Secondary analysis endpoints:** PFS1, ORR and DCR per investigator assessment
- FIG. 3

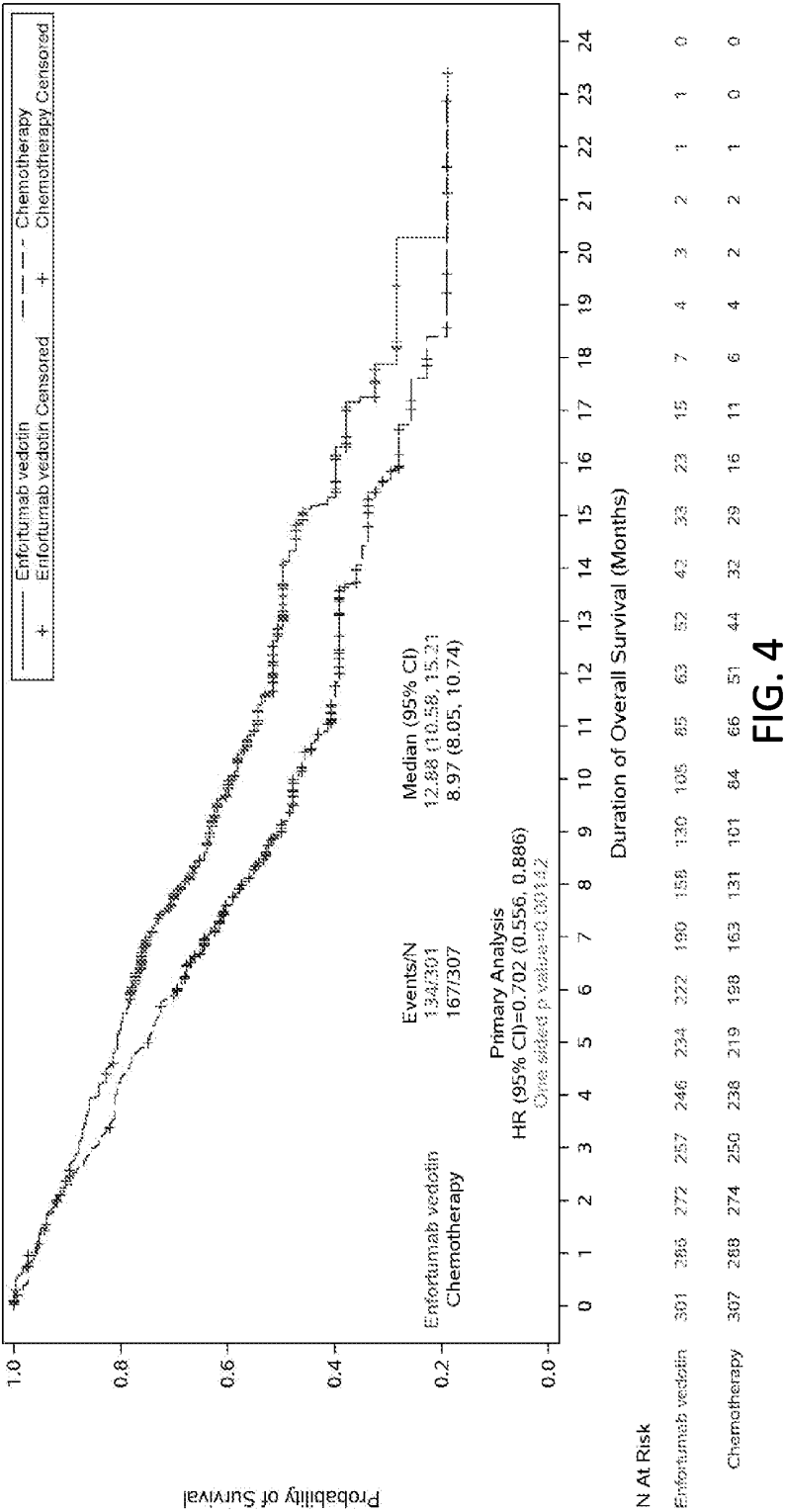


FIG. 4

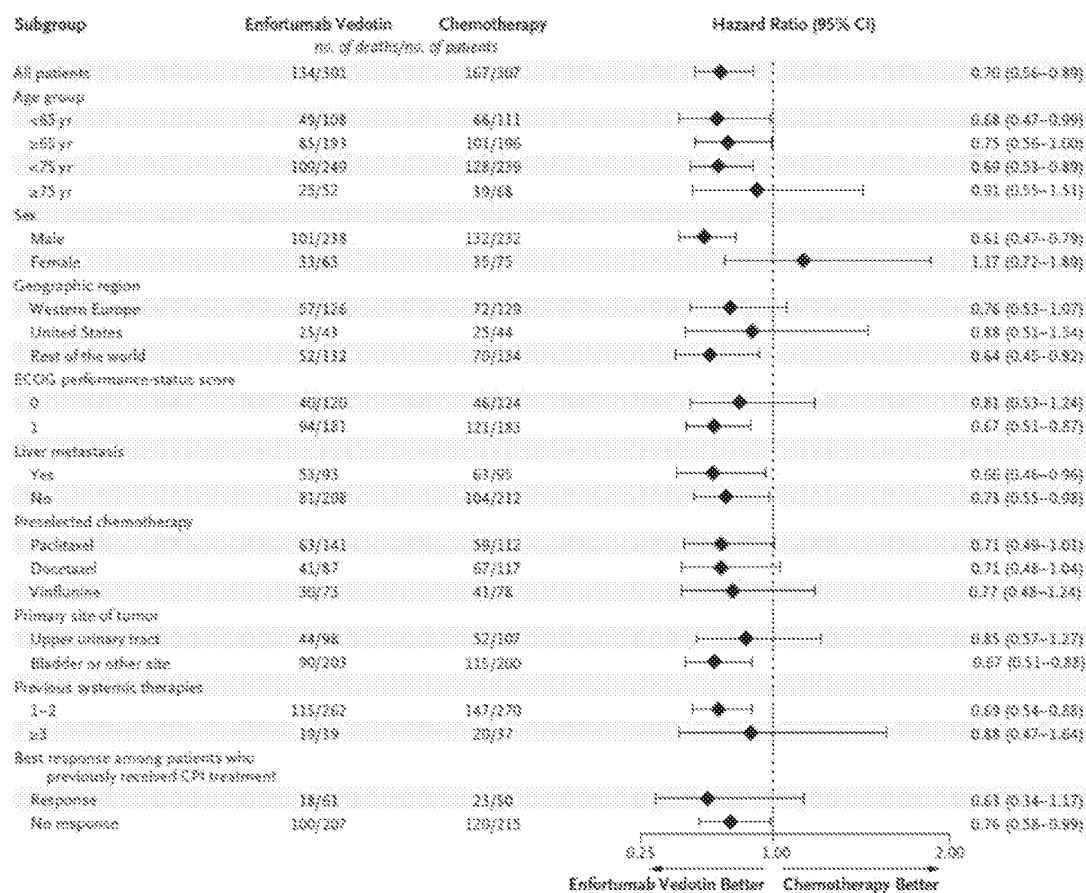
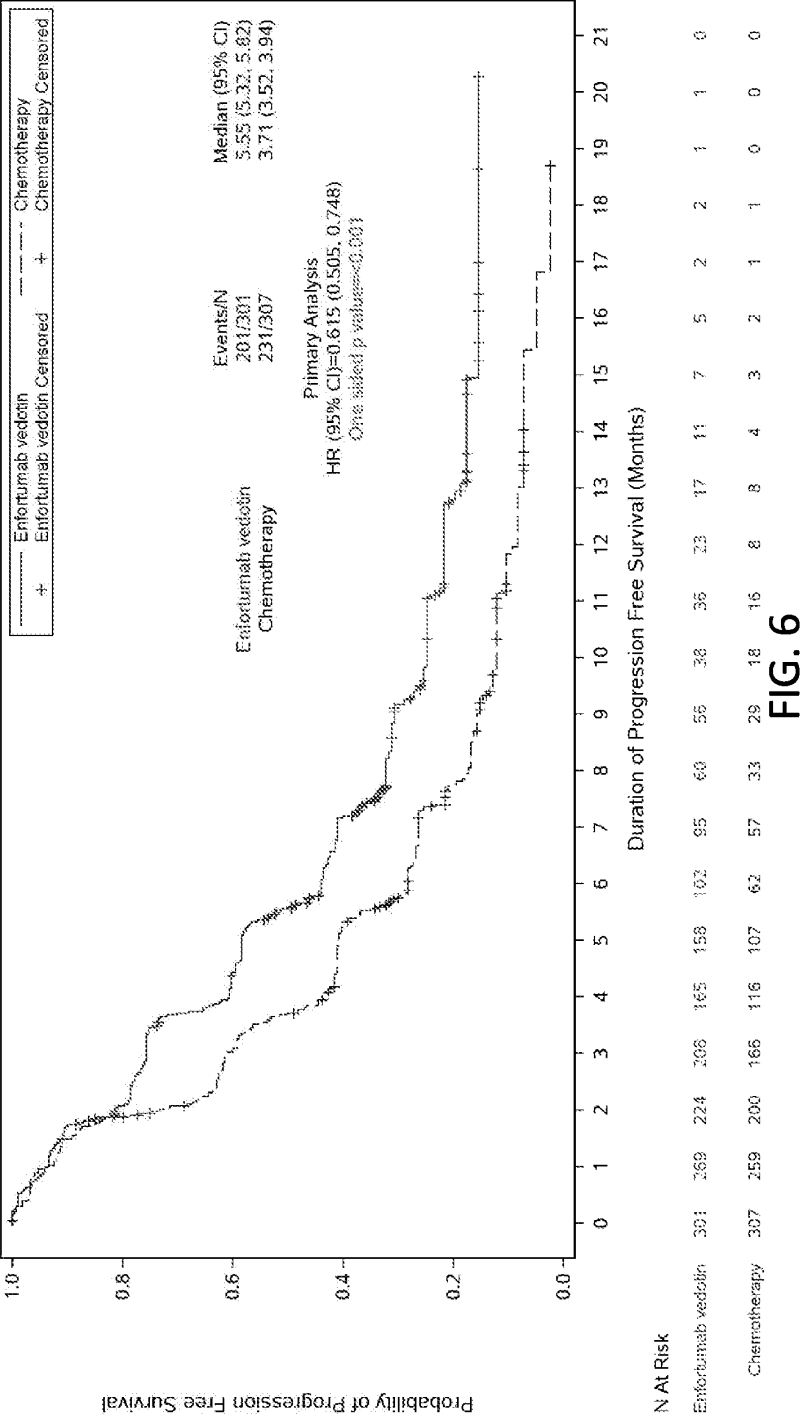


FIG. 5



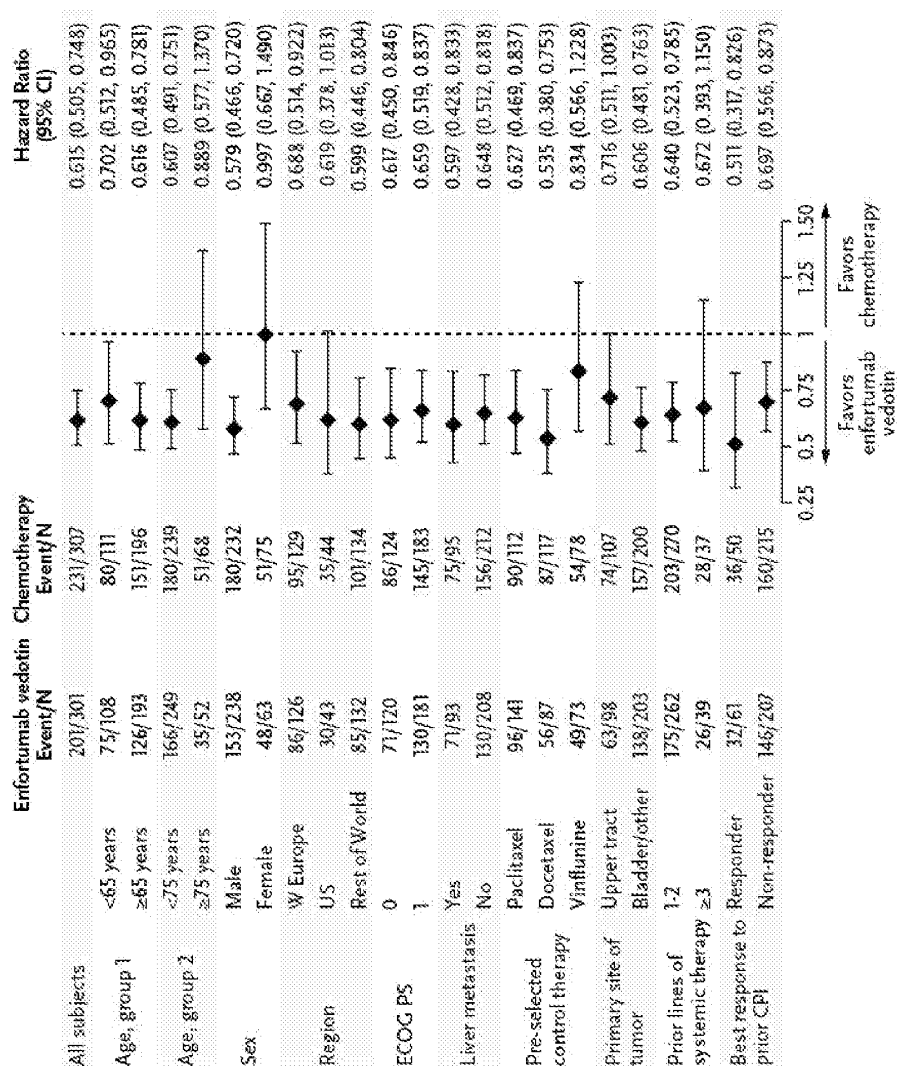


FIG. 7

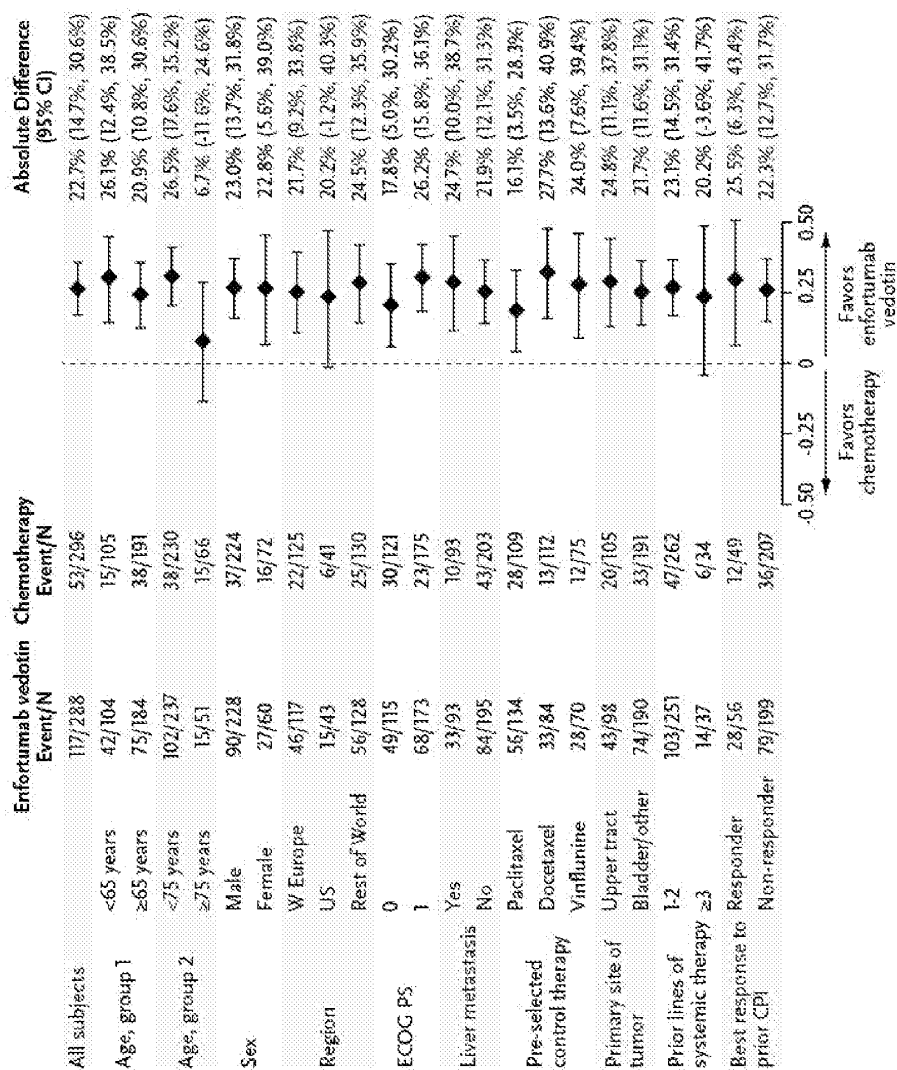


FIG. 8

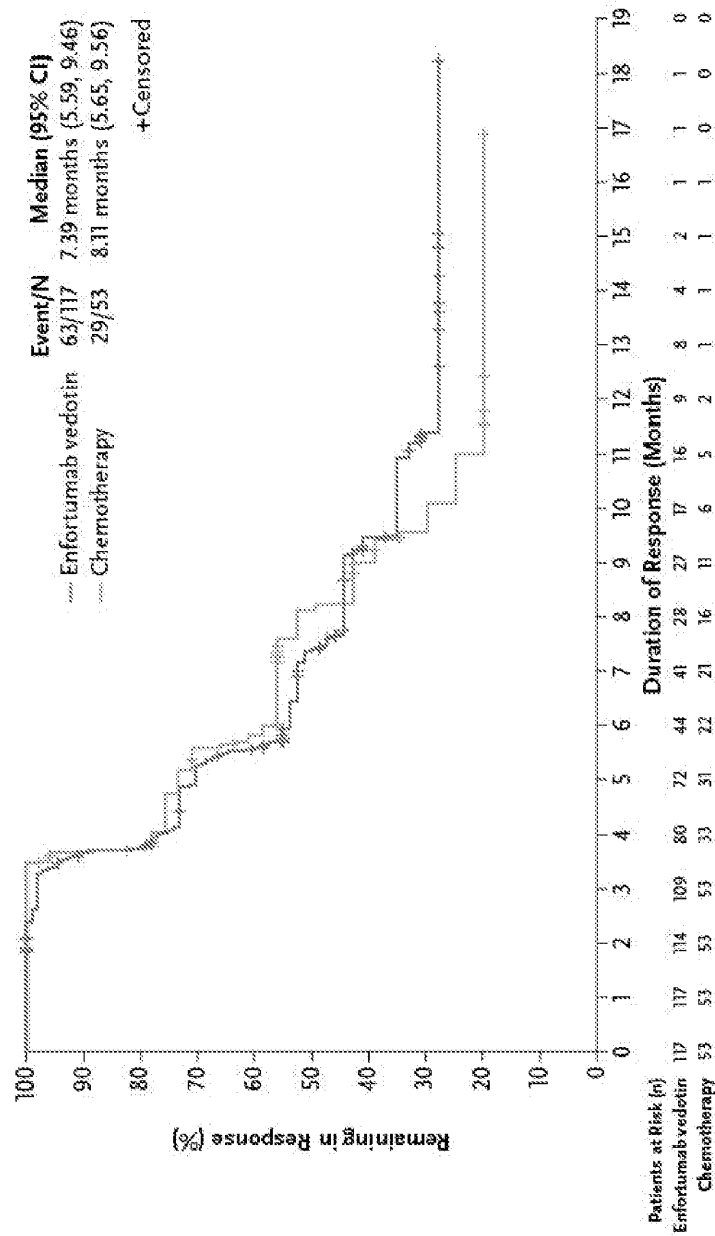


FIG. 9

FIG. 10A

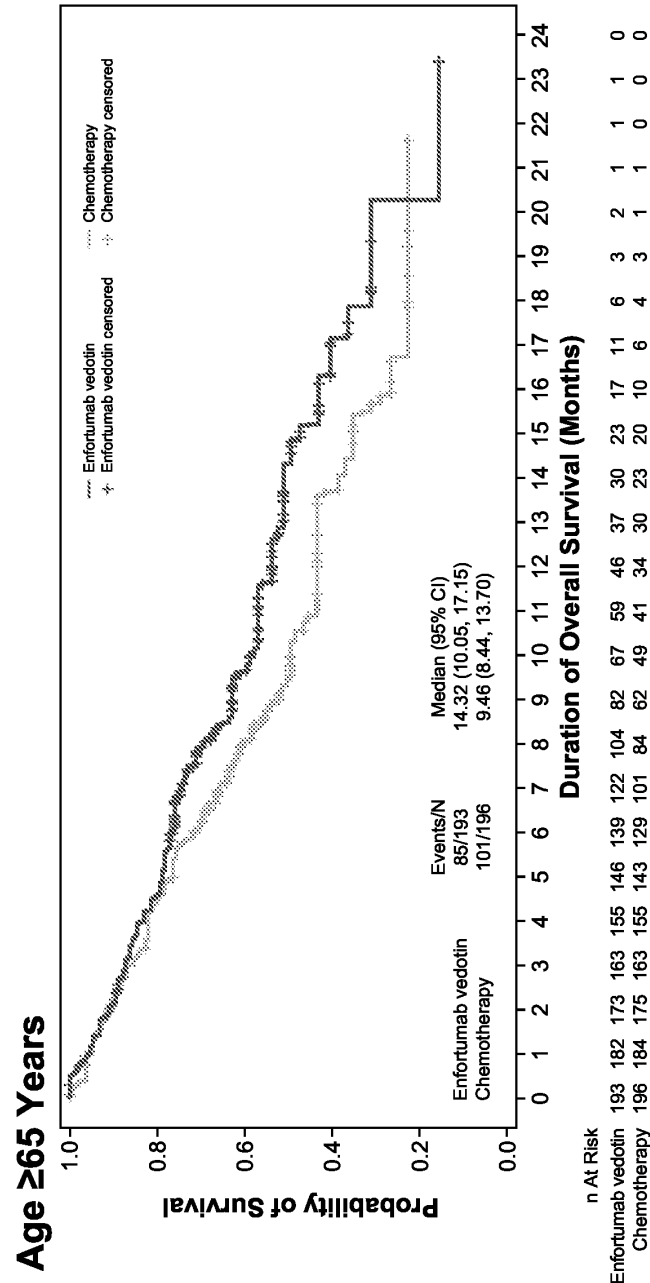


FIG. 10B

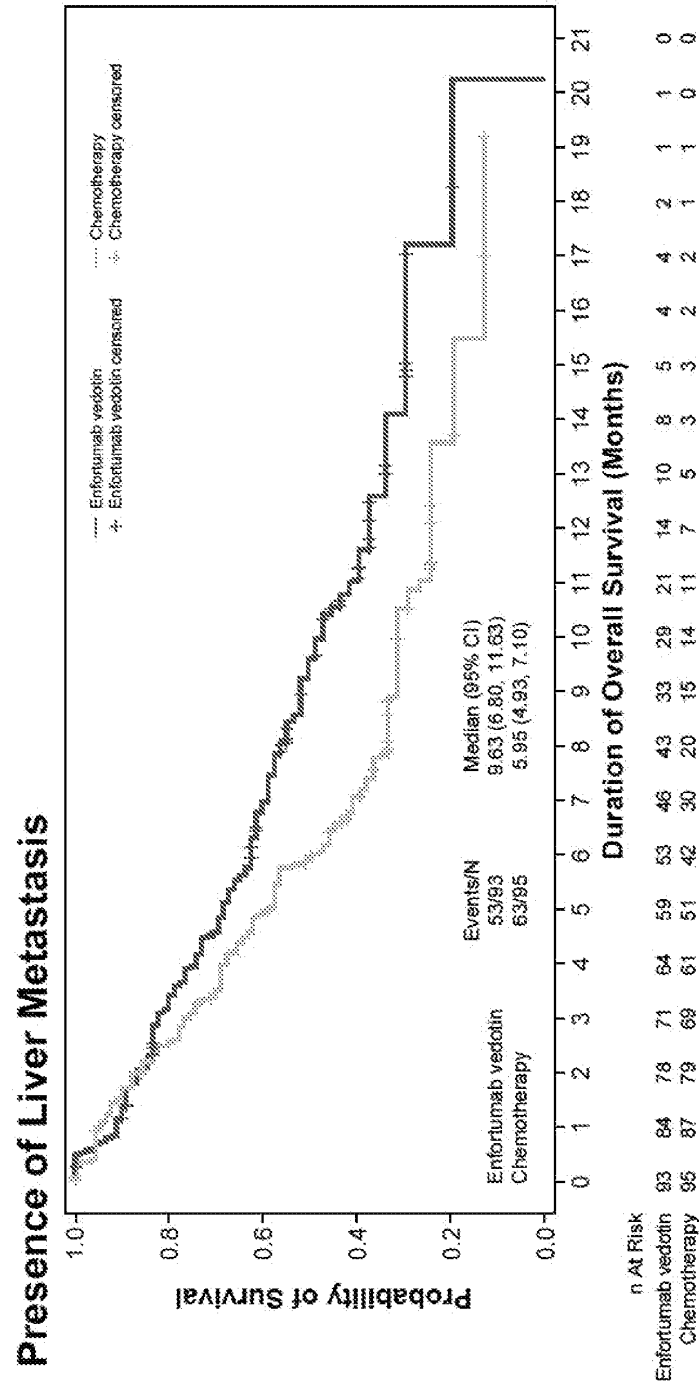


FIG. 10C

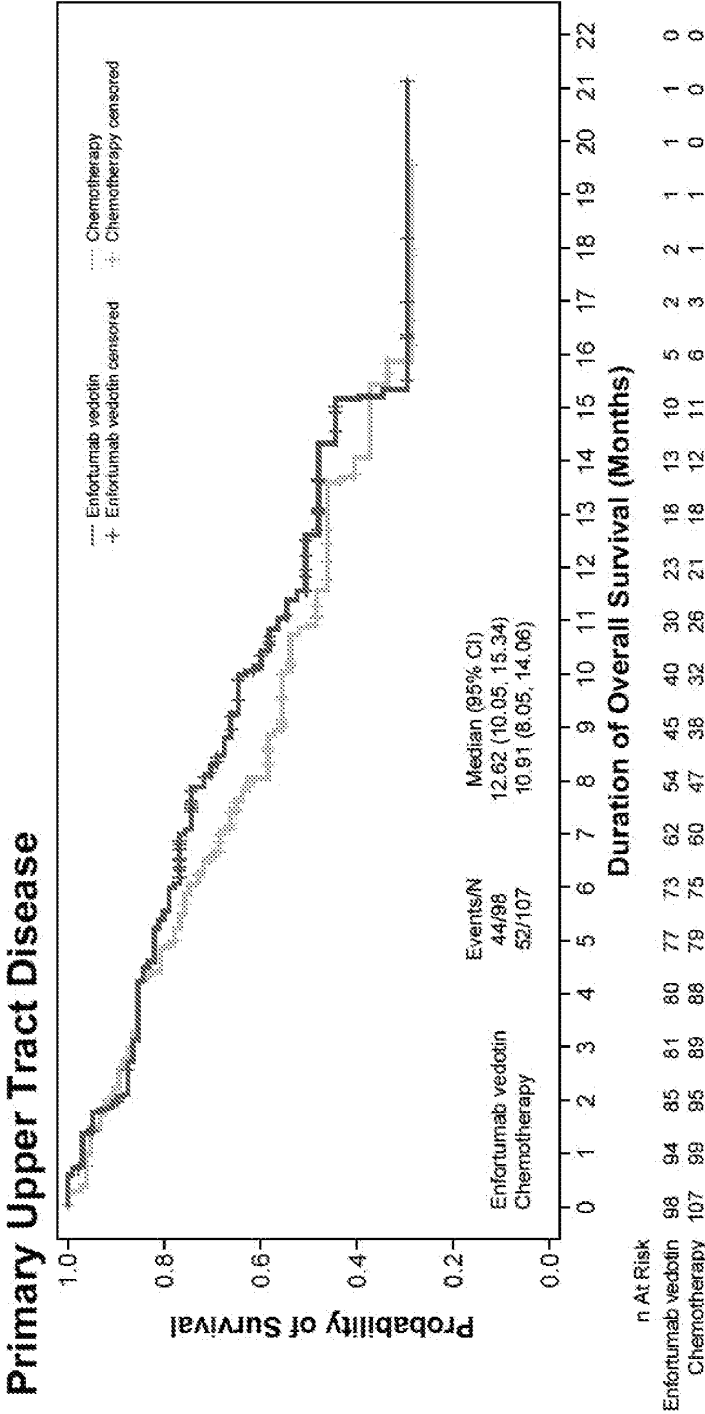


FIG. 10D

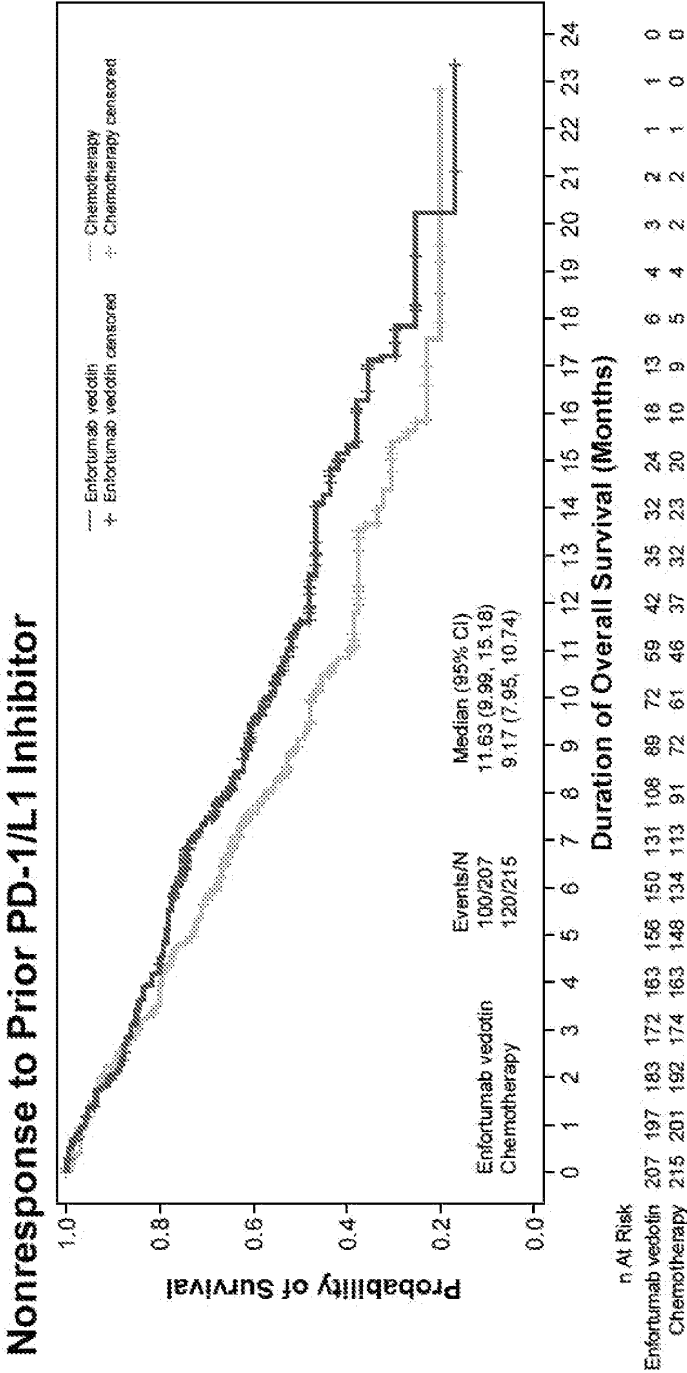


FIG. 11A

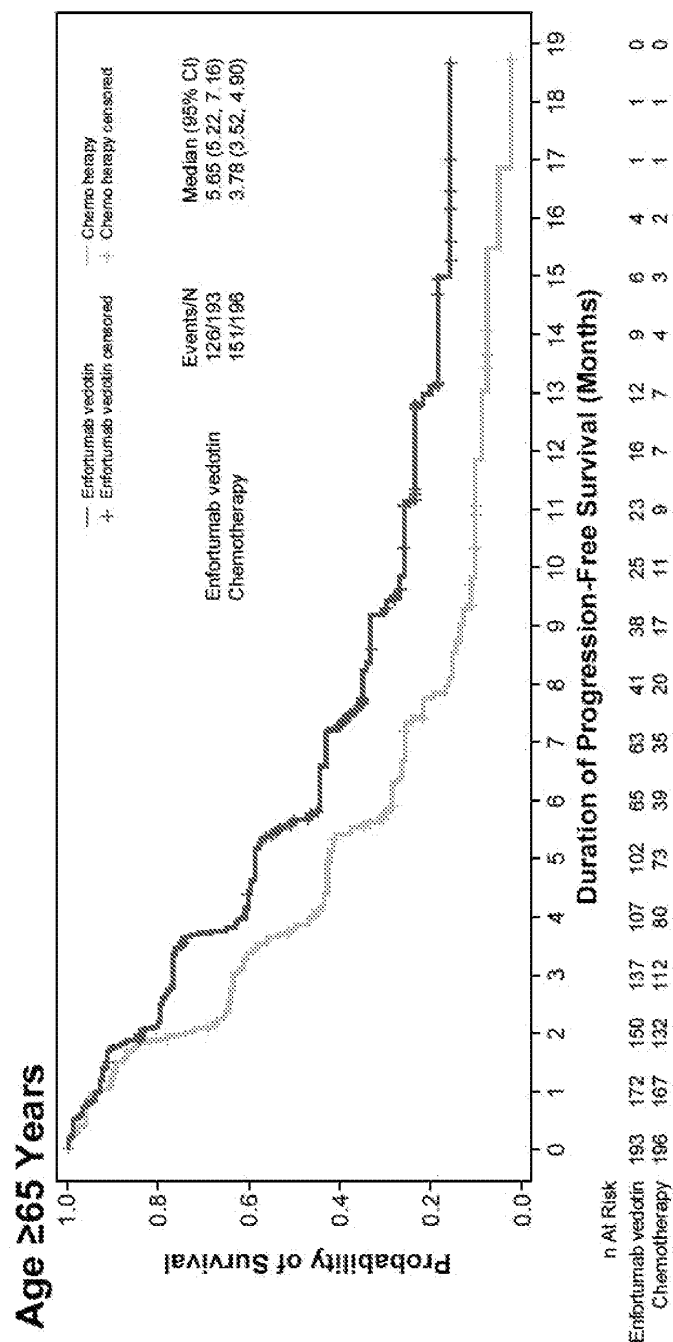


FIG. 11B

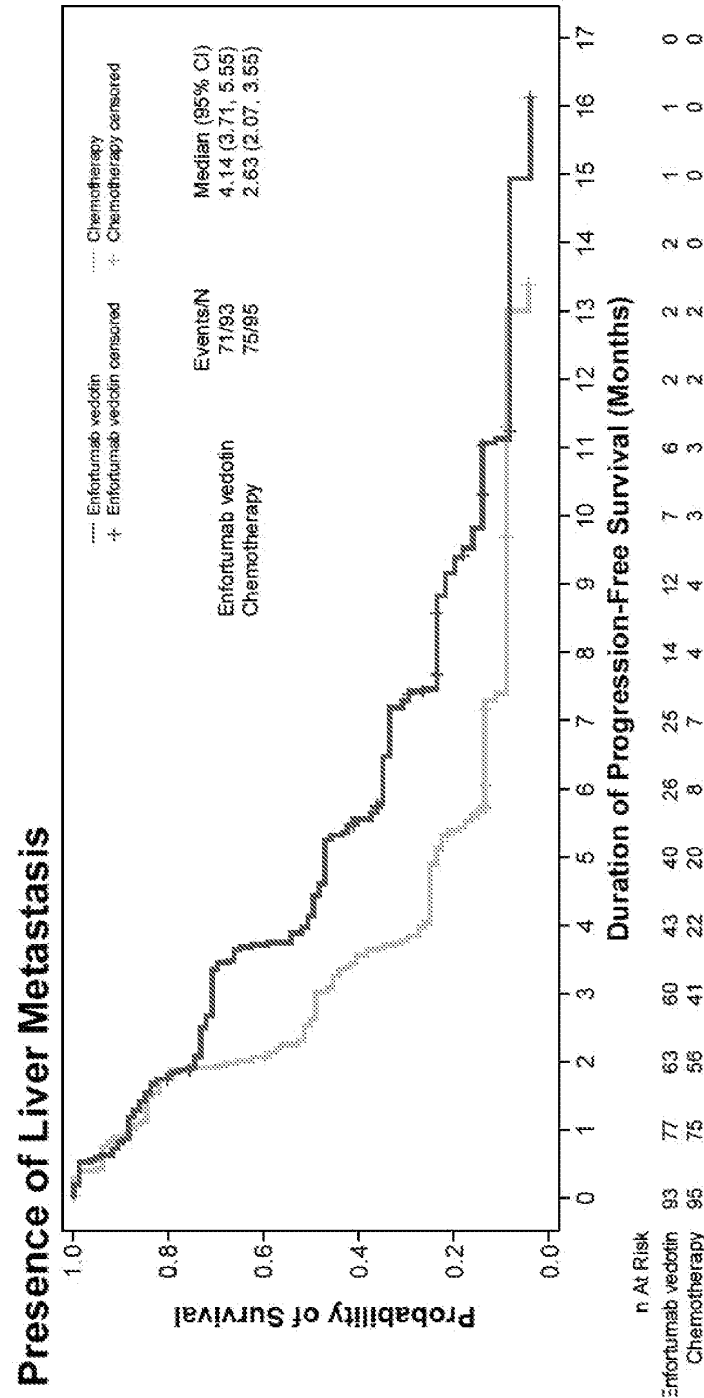


FIG. 11 C

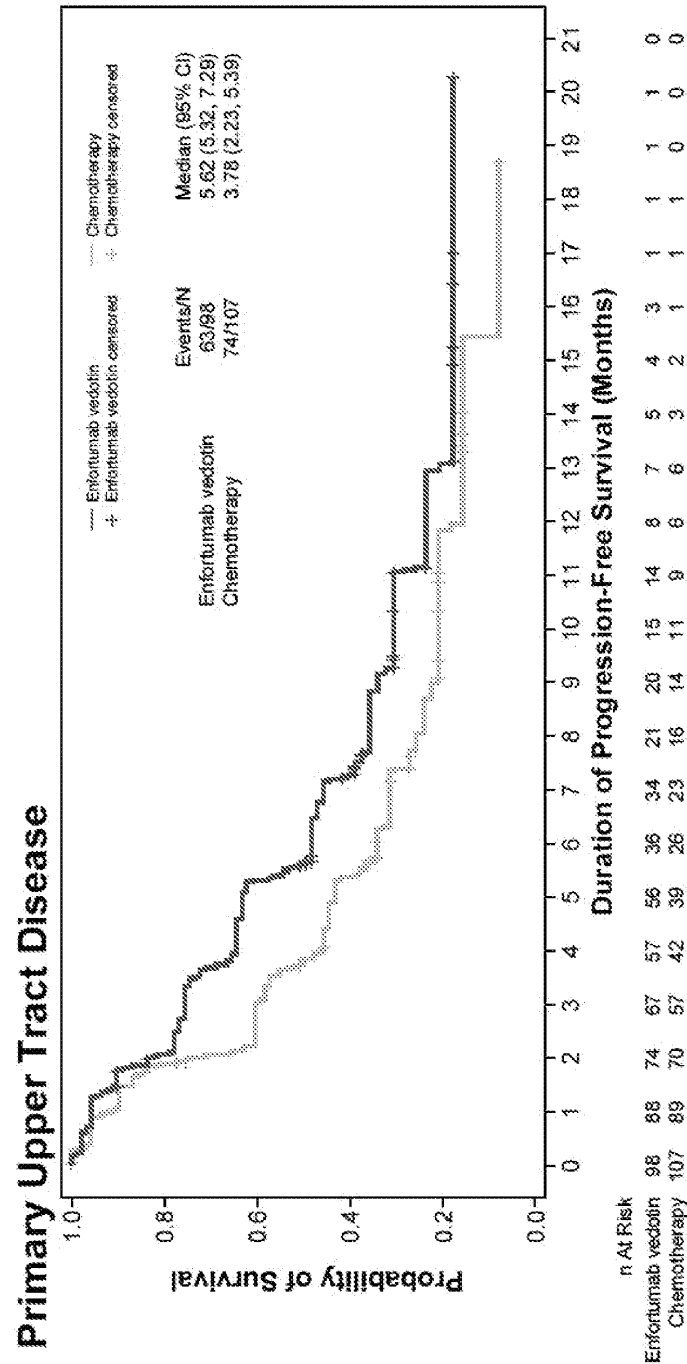


FIG. 11D

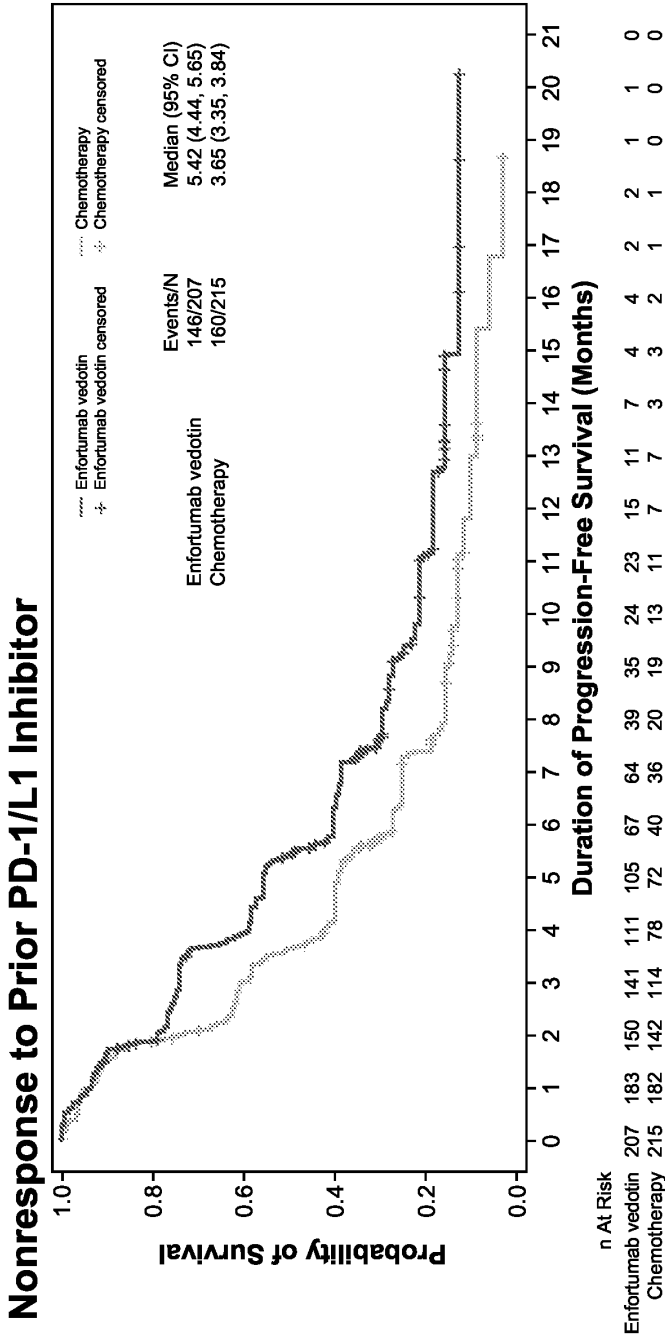
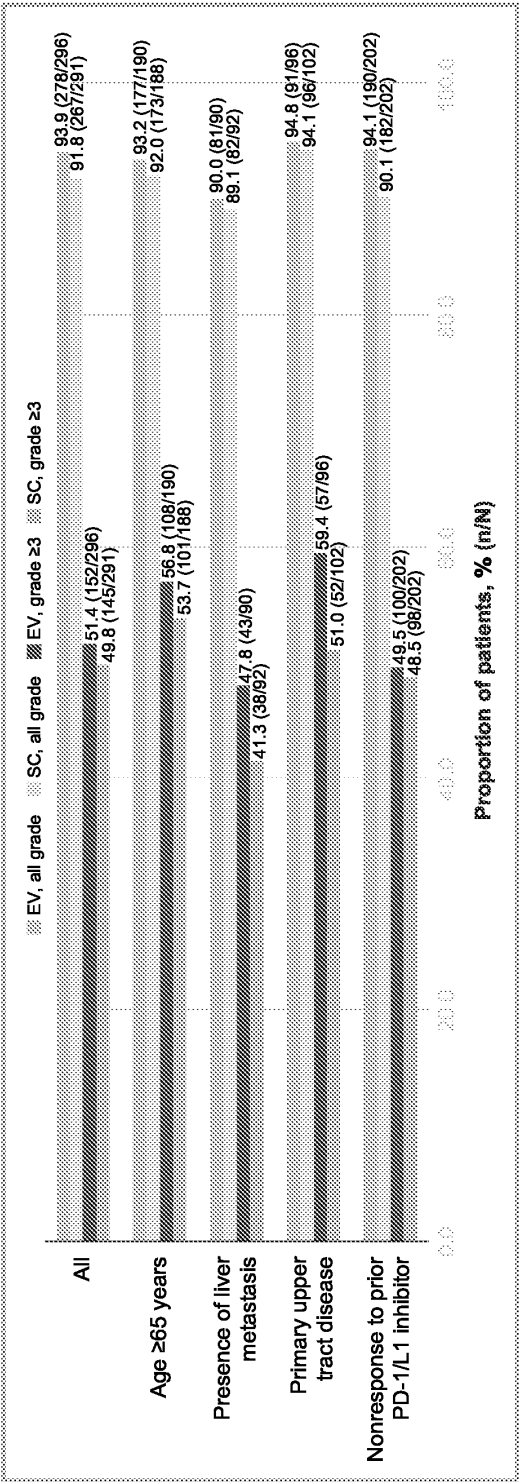
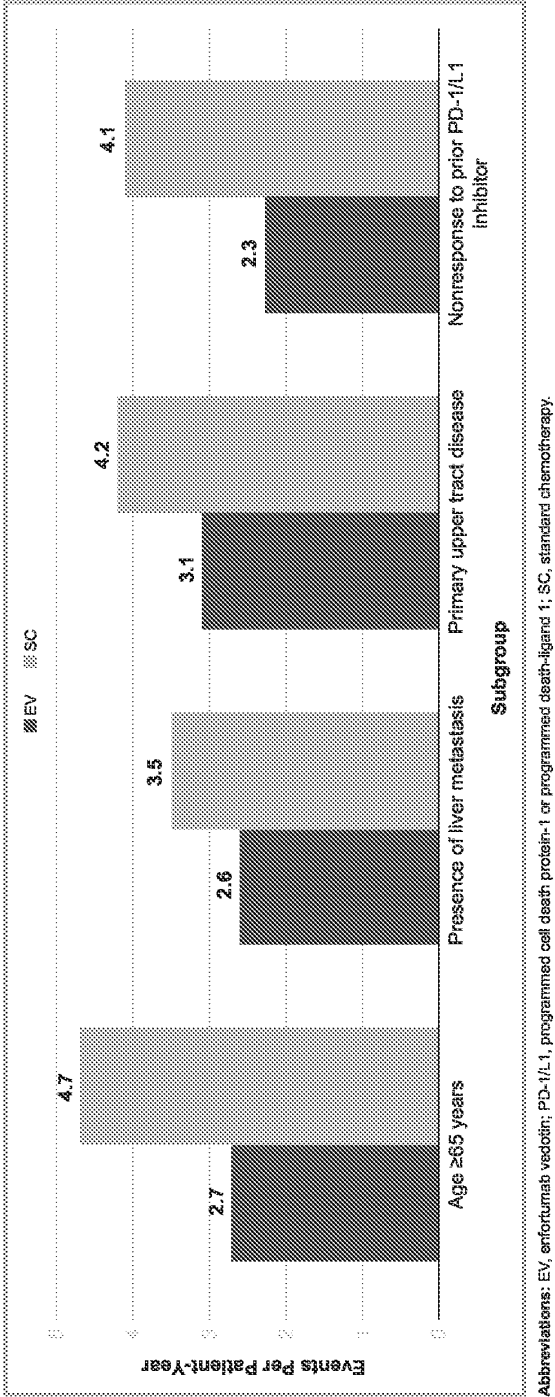


FIG. 12



Evaluated in all patients who received any amount of trial drug.  
Abbreviations: EV, enfortumab vedotin; PD-1/L1, programmed cell death protein-1 or programmed cell death ligand 1; SC, standard chemotherapy.

FIG. 13



Abbreviations: EV, enfortumab vedotin; PD-1/L1, programmed cell death protein-1 or programmed death-ligand 1; SC, standard chemotherapy.