

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  ggccgtcggttggtggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61  acggcttcttggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
121  tcccctagtgagaccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
181  cagttccttattcaagtctgcagccggctcccaggagatctcgggtggaacttcagaaac
1      M P L S L G A E M W G P E
241  gctgggcagctctgcctttcaaccATGCCCCCTGTCCCTGGGAGCCGAGATGTGGGGCCCTG
14   A W L L L L L L L A S F T G R C P A G E
301  AGGCCTGGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
34   L E T S D V V T V V L G Q D A K L P C F
361  AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAACTGCCCTGCT
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  GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94   Y E G R V E Q P P P P R N P L D G S V L
541  CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCACGCAACCCCTGGACGGCTCAGTGC
114  L R N A V Q A D E G E Y E C R V S T F P
601  TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTGAGCACCTTCC
134  A G S F Q A R L R L R V L V P P L P S L
661  CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCTCCCTGCCCTCAC
154  N P G P A L E E G Q G L T L A A S C T A
721  TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCTGGCAGCCTCCTGCACAG
174  E G S P A P S V T W D T E V K G T T S S
781  CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194  R S F K H S R S A A V T S E F H L V P S
841  GCCGTTCTTCAAGCACTCCCGCTCTGTGCGGTACCTCAGAGTTCCACTTGGTGCCTA
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  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 AAGGGCAGCCCCCTCCCTCATACAACCTGGACACGGCTGGATGGGCCTCTGCCAGTGGGG
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 ACGTCTGCCATGTGAGCAATGAGTTCTCCTCAAGGATTCTCAGGTCACTGTGGATGTTT
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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1261 TTGACCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTCTGCCTTCTGGTGGTGGTGGTGGTGCATGTCCC
374 Y H R R K A Q Q M T Q K Y 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 CCAGGGAGAACTCCATCCGAGGCTGCATTCCCATCACACGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAAGTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGACACCTGGTCTGAccca
1801 ggectgcctccctcccttaggctggtcctctctgttgacatgggagattttagctcatc
1861 ttgggggectccttaaacacccccatttcttgcggaagatgctccccatccactgactg
1921 cttgacctttacctccaacccctctgttcacatgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcagtgaaactgtggtgtatgtgccacgggatttgagtgggtgcgt
2161 gggcaacactgtcaggggttgccgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagacccagagcagtgattaatgatgcagaggttgaggagagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaaactgttacagaagccctctgccctctggtggcctc
2461 tgggctctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgagg
2521 aatactgctccgaatcacttttaatttttttttttttttttttcttgccctttccattagt
2581 tgtattttttattttatttttatttttttttttttttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaaactcctgggtcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagccttttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctactccaaggcactctt
2881 catgcaggcagcccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttgacctggtgacaagggtcctgttcaatagtgggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttgatcactaattcaaggctcttctggaatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggccacccagatacactc
3241 agccagaatacctagatttagtaccocaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaaggagaggtcccatccttcttccccagccagcctaggacttcgaatgtgga
3361 gctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcataattgtacat
3421 aaaaatgatattctgtttttaataaacagacaaaacttgaaaaa

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  GGTGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCCTTGTGCTATTTTAGA
   · 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  AGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGAGACTCTC
   · 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 CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATAACATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
   · 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 GTGGGTTTCATACATTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTACCATCTC
   · 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 TGGGAGAGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACACGGTCACCGTCTCCCTCAGCCTCCACCAA
   · 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 GGGGCCATCGGTCTTCCCGCTGGCACCCTCCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
   · 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 CAAGGACTACTTCCCGAACCCTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGCTGCACACCTTCCC
   · A V L Y S S G L Y S L S S V V T V P S S S L G T Q
601 GGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCA
   · 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 GACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGA
   · 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 CAAAACTCACACATGCCACCGTGGCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCCCTCTCCCCCAAA
   · 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 ACCCAAGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAGCTGAGGCCAGAGACCC
   · E V K F N W Y V D G E V H N A K T K P R E E Q Y
901 TGAGGTCAGTTCAGTCTGACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGACGTA
   · 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 CAACAGCACGTACCGTGTGGTCAGCGCTCTCACCGTCTGCACAGGACTGGCTGAATGCCAAGGAGTACAAGTG
   · 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 CAAGGTCTCCCAAAAGCCCTCCAGCCCCATCCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACC
   · 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 ACAGGTGTACACCCTGCCCCATCCCGGAGGAGATGACCAAGAACAGGTCAGCCTGACCTGGCTGGTCAAAGG
   · 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 CTTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACTACAGACACGCGCTCC
   · 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 CGTGCTGGACCTCCGACGGCTCTCTCTCTATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCGGGGAA
   · V F S C S V M H E A L H N H Y T Q K S L S L S F G
1351 CGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAGAGCTCTCCCTGTCCCGGG
   · 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  AGTCAGACCCAGTCAGGACACAGCAATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTC
   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  CCAGGTTCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTTGGAGACAGAGTCACC
   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 ATCACTTGTCCGGCGAGTCAGGGTATTAGCGGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAG
   F L I Y A A S T L Q S G V P S R F S G S G T D
226 TTCTGTATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAT
   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 CCCACITTTCCGGCGGAGGGACCAAGGTGGAGATCAAACGAACCTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCA
   S D E Q L K S G T A S V C L L N N F Y P R E A K
451 TCTGATGAGCAGTTGAAATCTGGAACCTGCTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGGCCAAA
   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 GTACAGTGGAAAGTGGATAACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
   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 AGCACTCAGAGCCTCAGCAGCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGCGAA
   V T H Q G L S S P V T K S F N R G E C *
676 GTCACCCATCAGGGCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

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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.

```

1  MELGLCWVFLVAILEGVOCEVOLVESGGGLVOPGGSLRLSCAASGFTFSS
51 YNMNVWRQAPGKGLEWVSYISSSSSTIYYADSVKGRFTISRDNAKNSLSL
101 QMNSLRDEDTAVYYCARAYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
151 SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS
201 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA
251 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
301 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNKEYKCKVSNKALPAP
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  MDMRVPAQLLGLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQG
51 ISGWLAWYQQKPGKAPKFLIYAASTLQSGVPSRFSGSGSGTDFTLTISSL
101 QPEDFATYYCQANSFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
151 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSST
201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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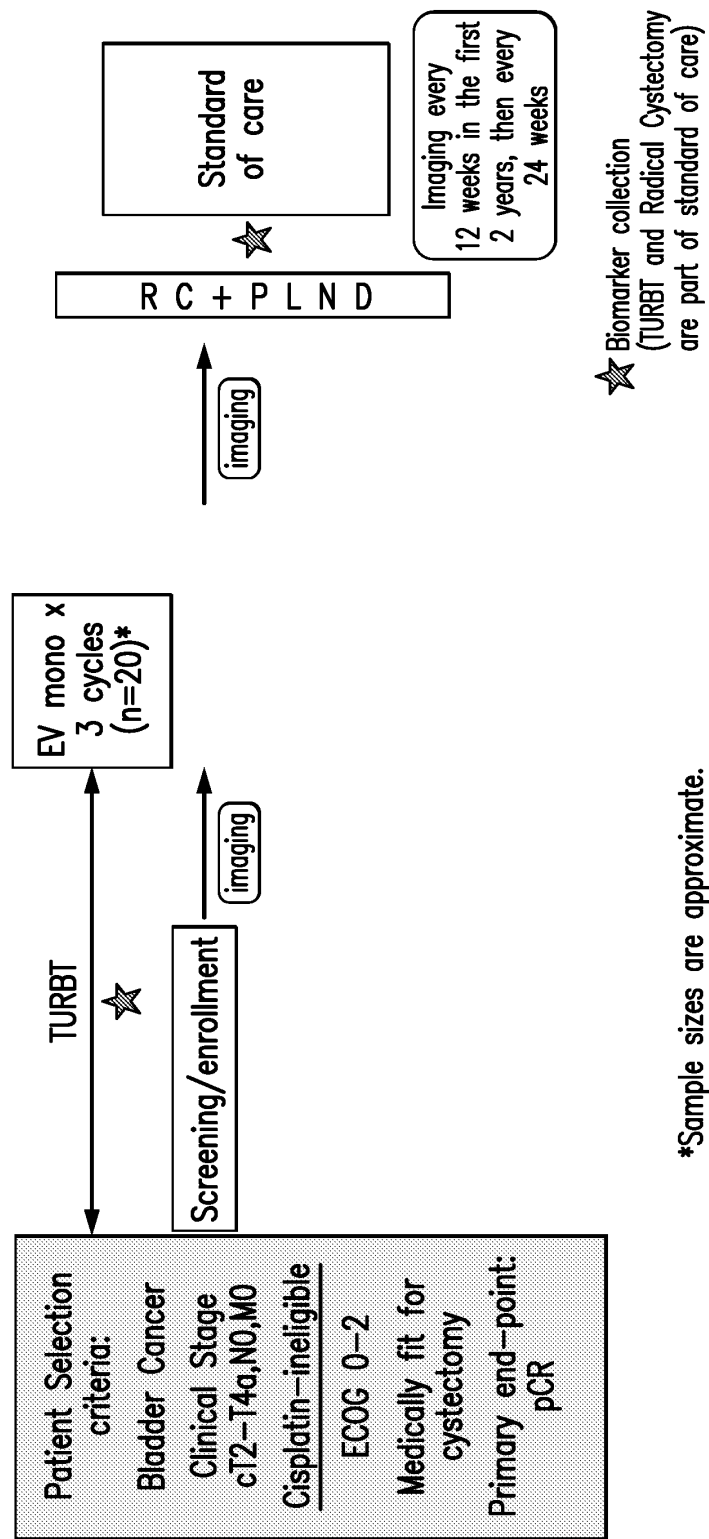


FIG. 2

EORTC-QLQ-C-30



EORTC QLQ-C30 (version 3)

We are interested in some things about you and your health. Please answer all of the questions yourself by circling the number that best applies to you. There are no "right" or "wrong" answers. The information that you provide will remain strictly confidential.

Please fill in your initials:

Your birthdate (Day, Month, Year):

Today's date (Day, Month, Year):

	Not at All	A Little	Quite a Bit	Very Much
1. Do you have any trouble doing strenuous <u>activities</u> , like carrying a heavy shopping bag or a suitcase?	1	2	3	4
2. Do you have any trouble taking a <u>long</u> walk?	1	2	3	4
3. Do you have any trouble taking a <u>short</u> walk outside of the house?	1	2	3	4
4. Do you need to stay in bed or a chair during the day?	1	2	3	4
5. Do you need help with eating, dressing, <u>washing</u> <u>yourself</u> or using the toilet?	1	2	3	4
During the past week:				
6. Were you limited in doing either your work or other daily activities?	1	2	3	4
7. Were you limited in pursuing your hobbies or <u>other</u> <u>leisure</u> time activities?	1	2	3	4
8. Were you short of breath?	1	2	3	4
9. Have you had pain?	1	2	3	4
10. Did you need to rest?	1	2	3	4
11. Have you had trouble sleeping?	1	2	3	4
12. Have you felt weak?	1	2	3	4
13. Have you lacked appetite?	1	2	3	4
14. Have you felt nauseated?	1	2	3	4
15. Have you vomited?	1	2	3	4
16. <u>Have you been constipated?</u>	1	2	3	4

Please go on to the next page

FIG. 3

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EQ-5D-5L

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

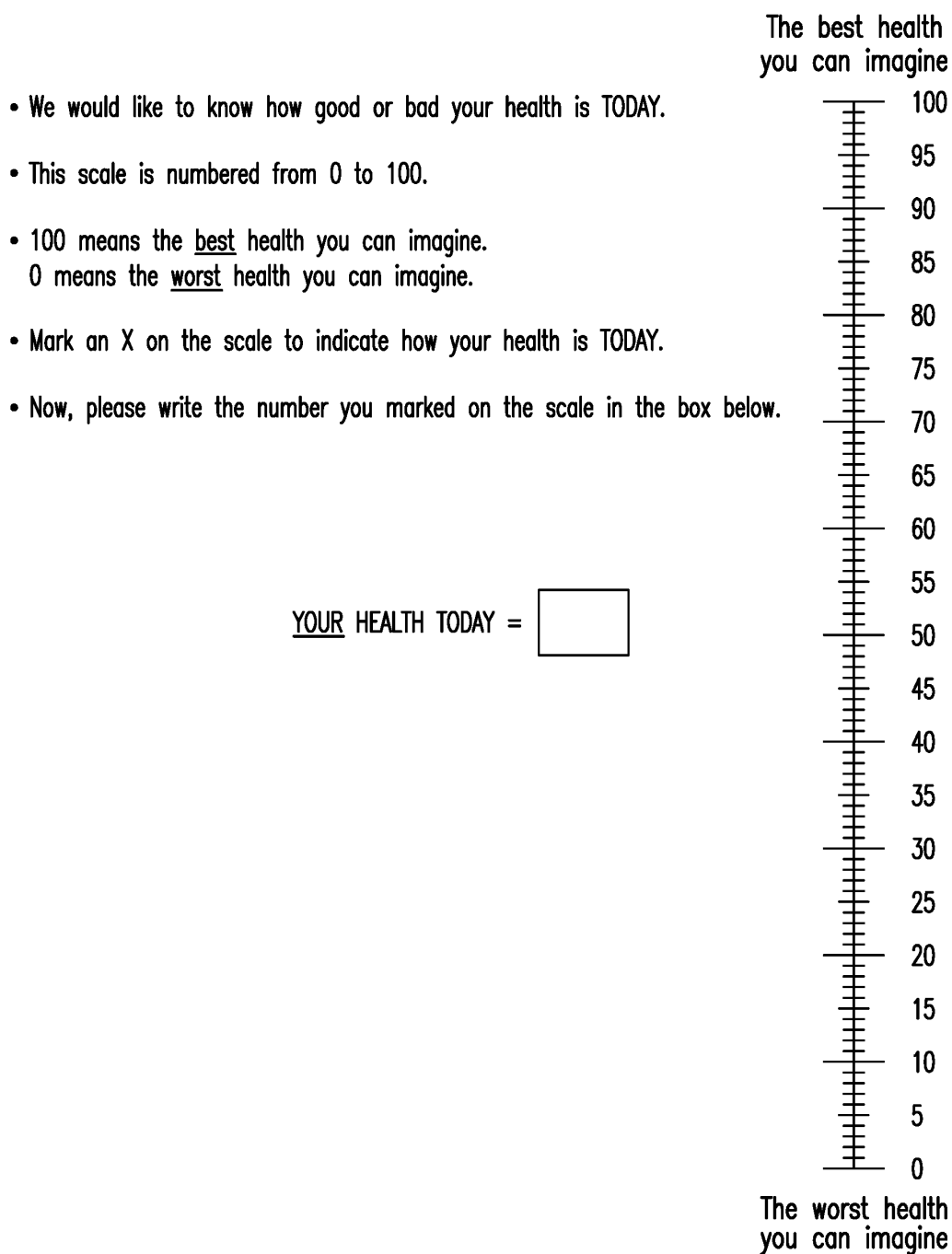
- I am not anxious or depressed ☐
- I am slightly anxious or depressed ☐
- I am moderately anxious or depressed ☐
- I am severely anxious or depressed ☐
- I am extremely anxious or depressed ☐

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FIG. 4

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FIG. 4 (Continued)

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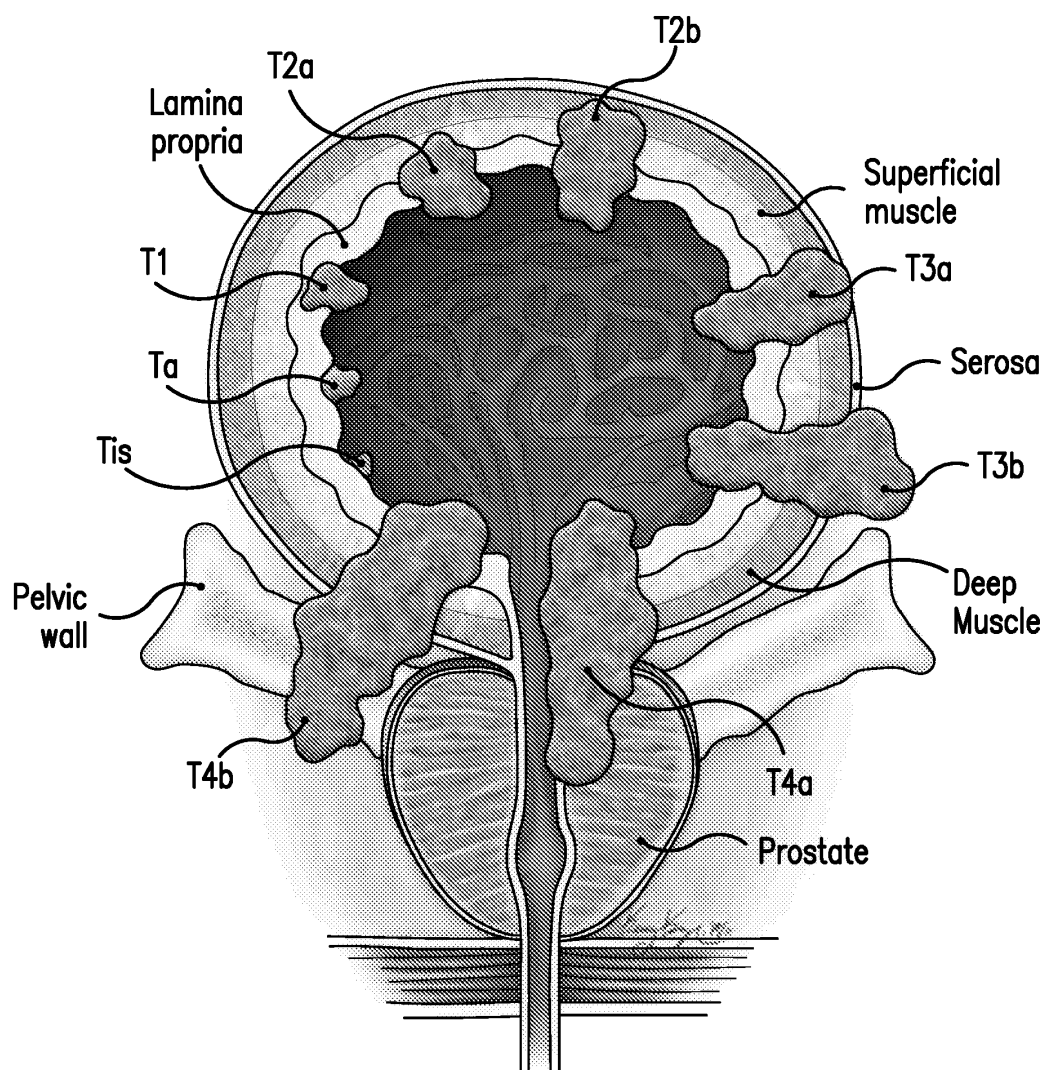


FIG. 5

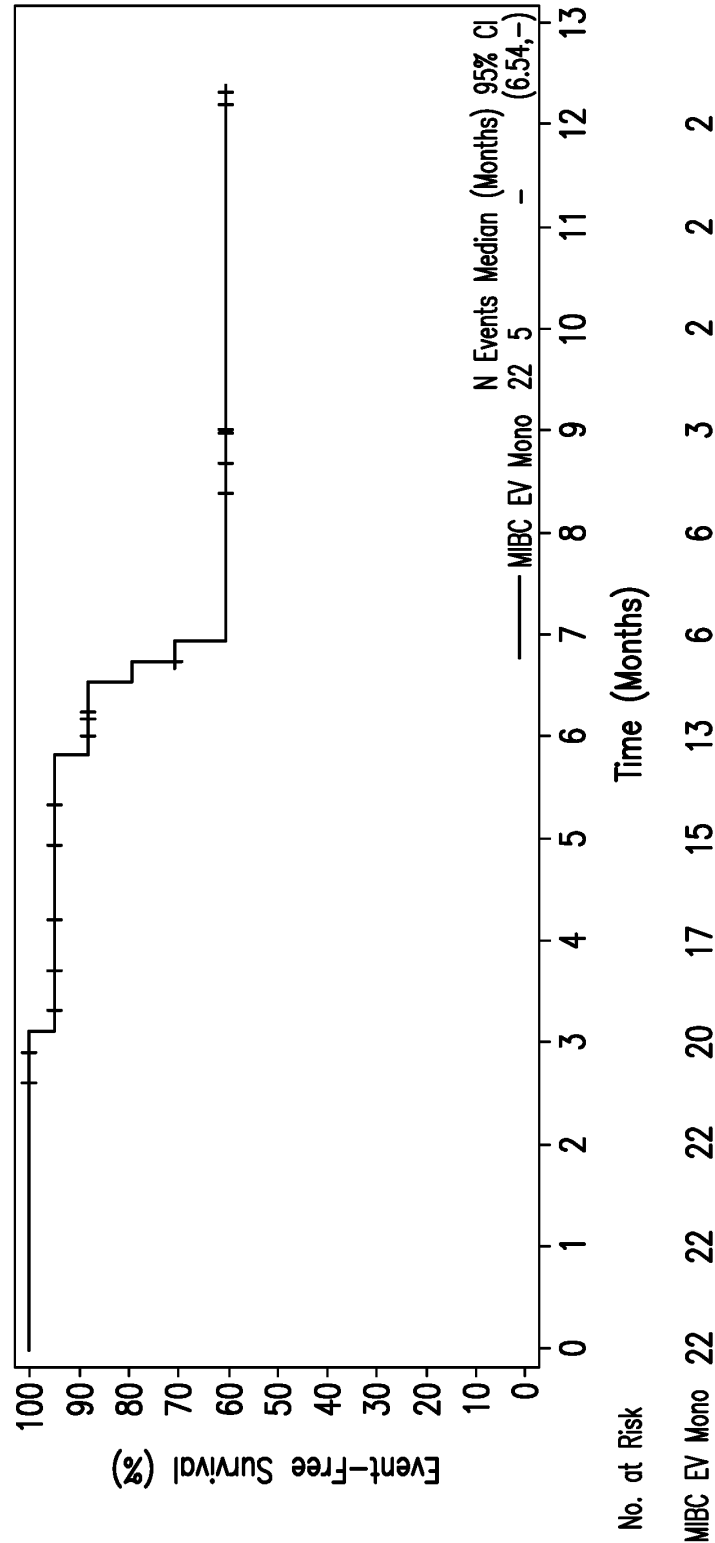


FIG. 6

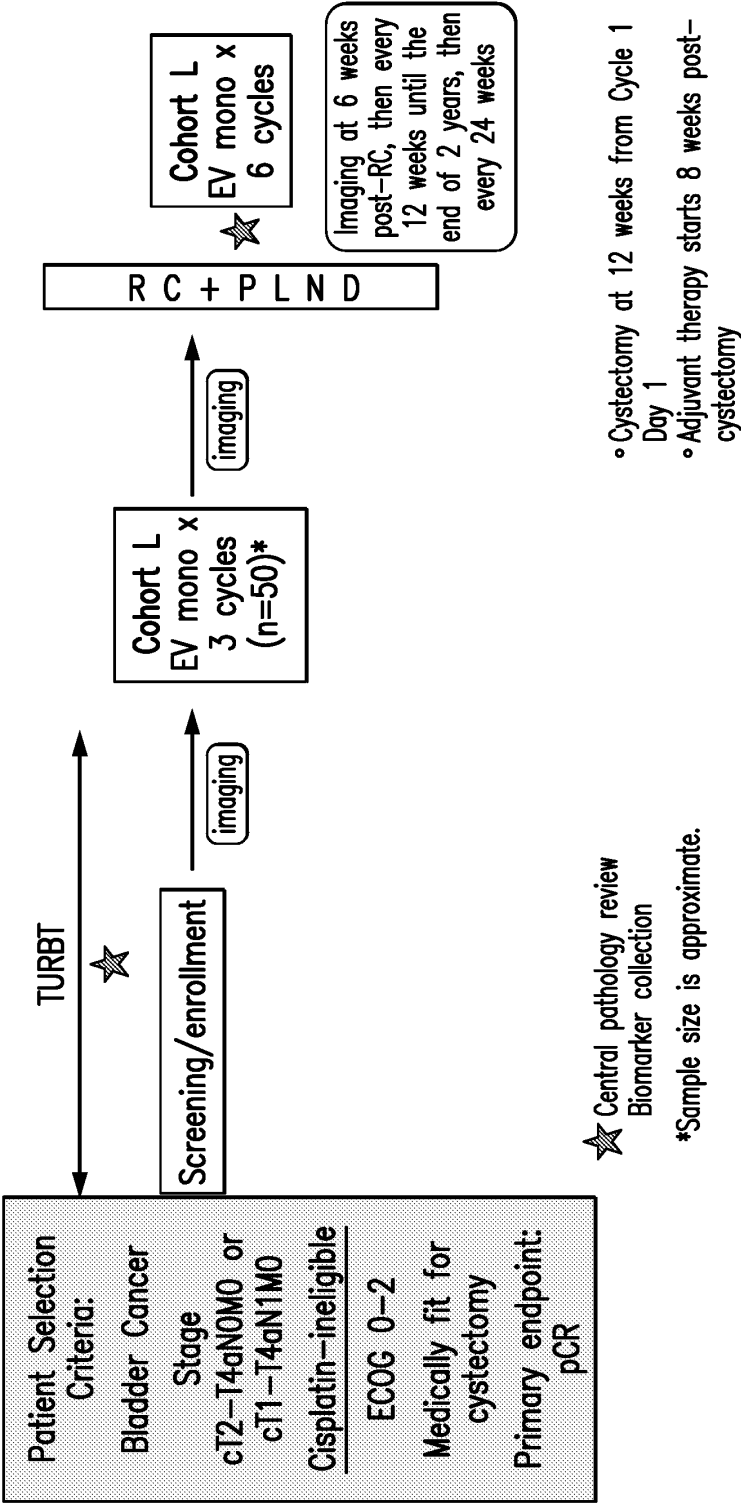


FIG. 7