

Structure of capsid-modified PyCS-GFP adenoviruses

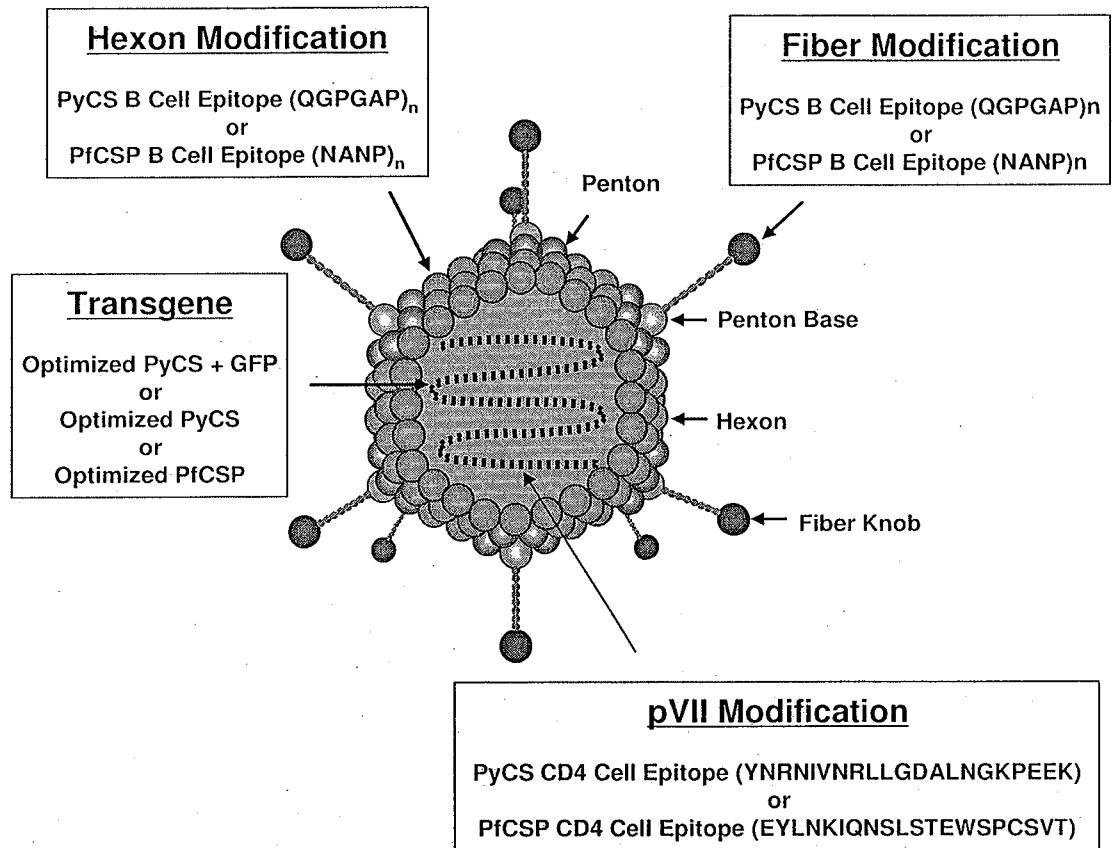


Fig. 1

Construction of HVR1-modified adenovirus vector

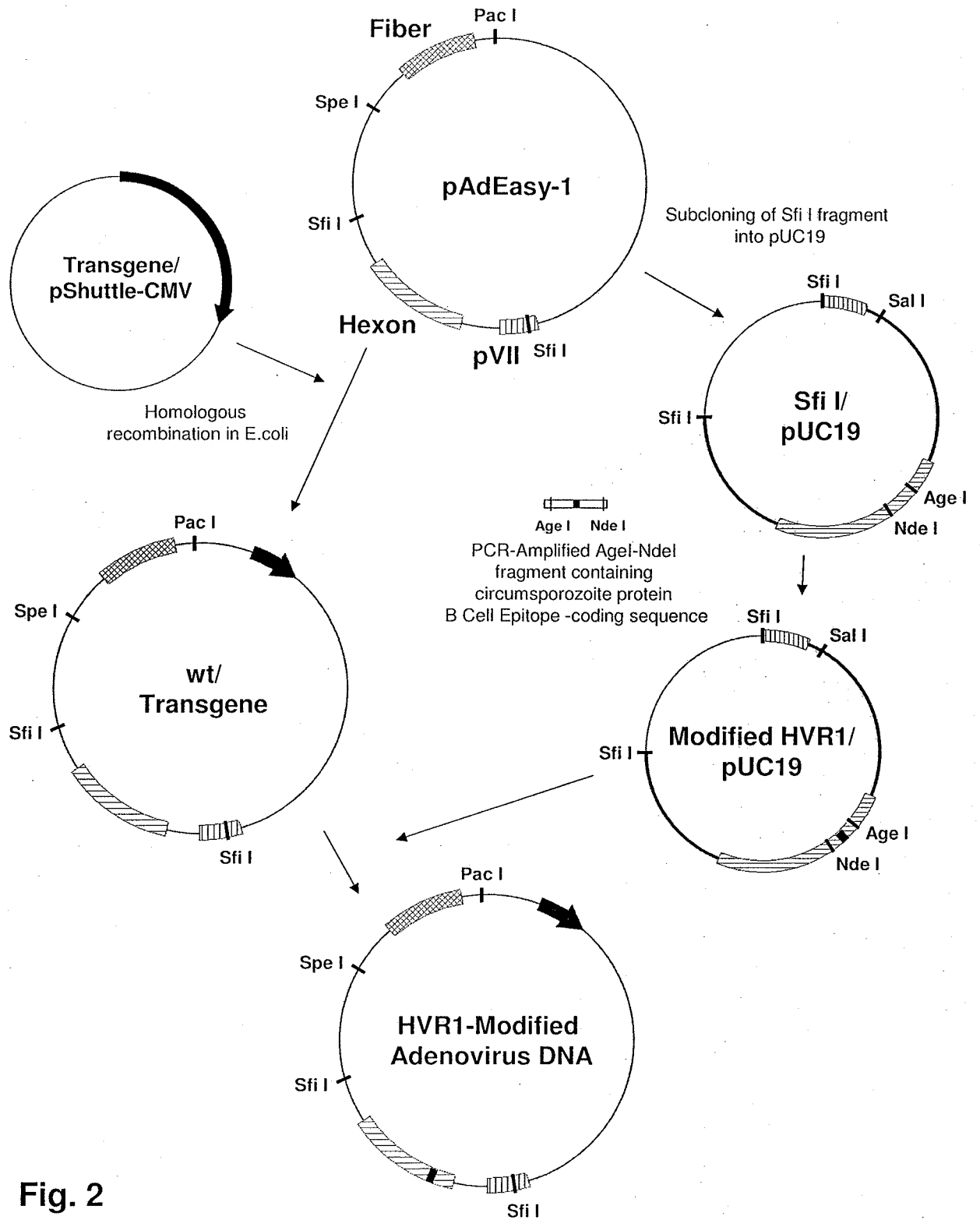


Fig. 2

Construction of HVR5-Modified adenovirus vector

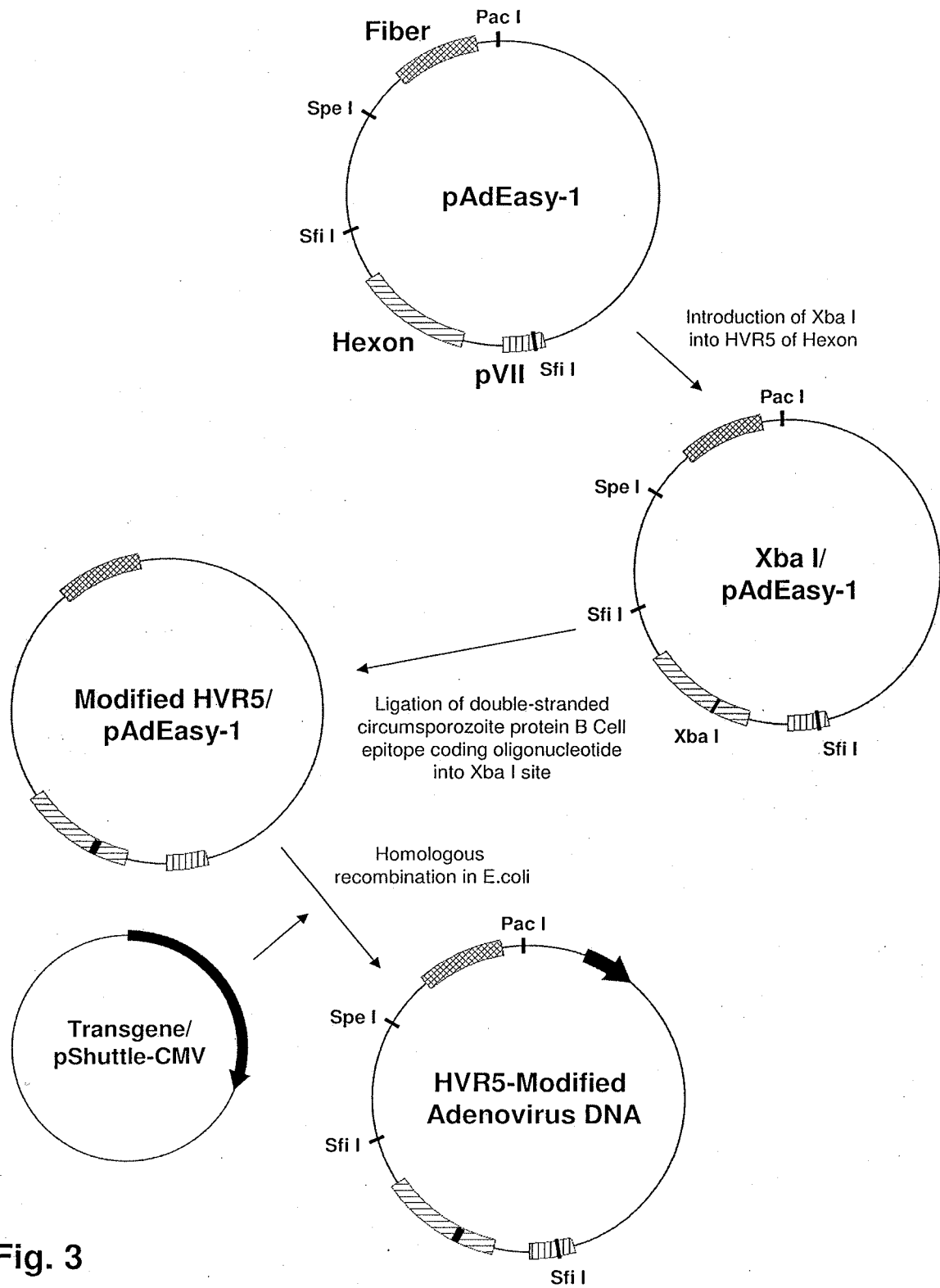


Fig. 3

Construction of Fiber-modified adenovirus vector

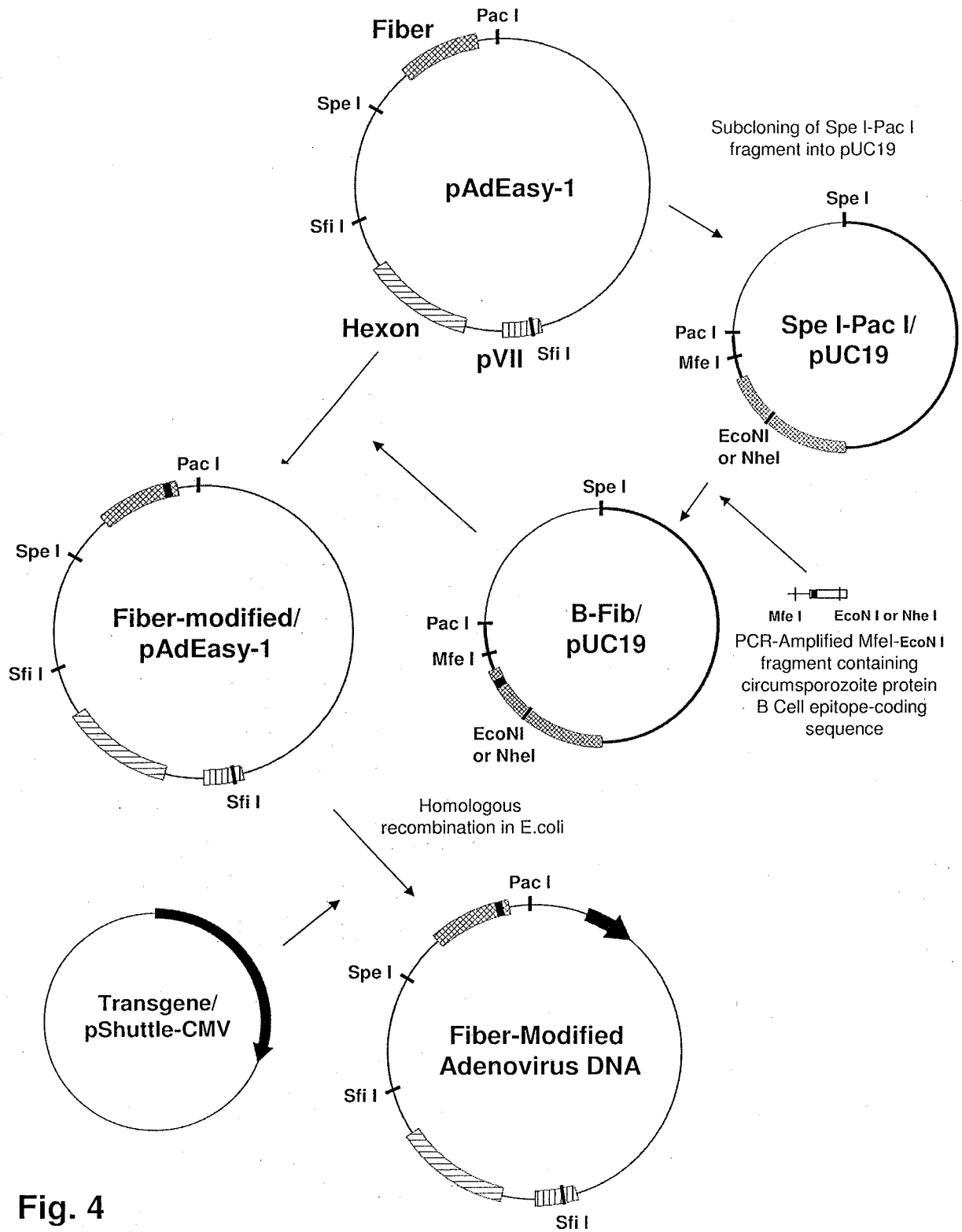


Fig. 4

Construction of HVR1 and Fiber-modified adenovirus vector

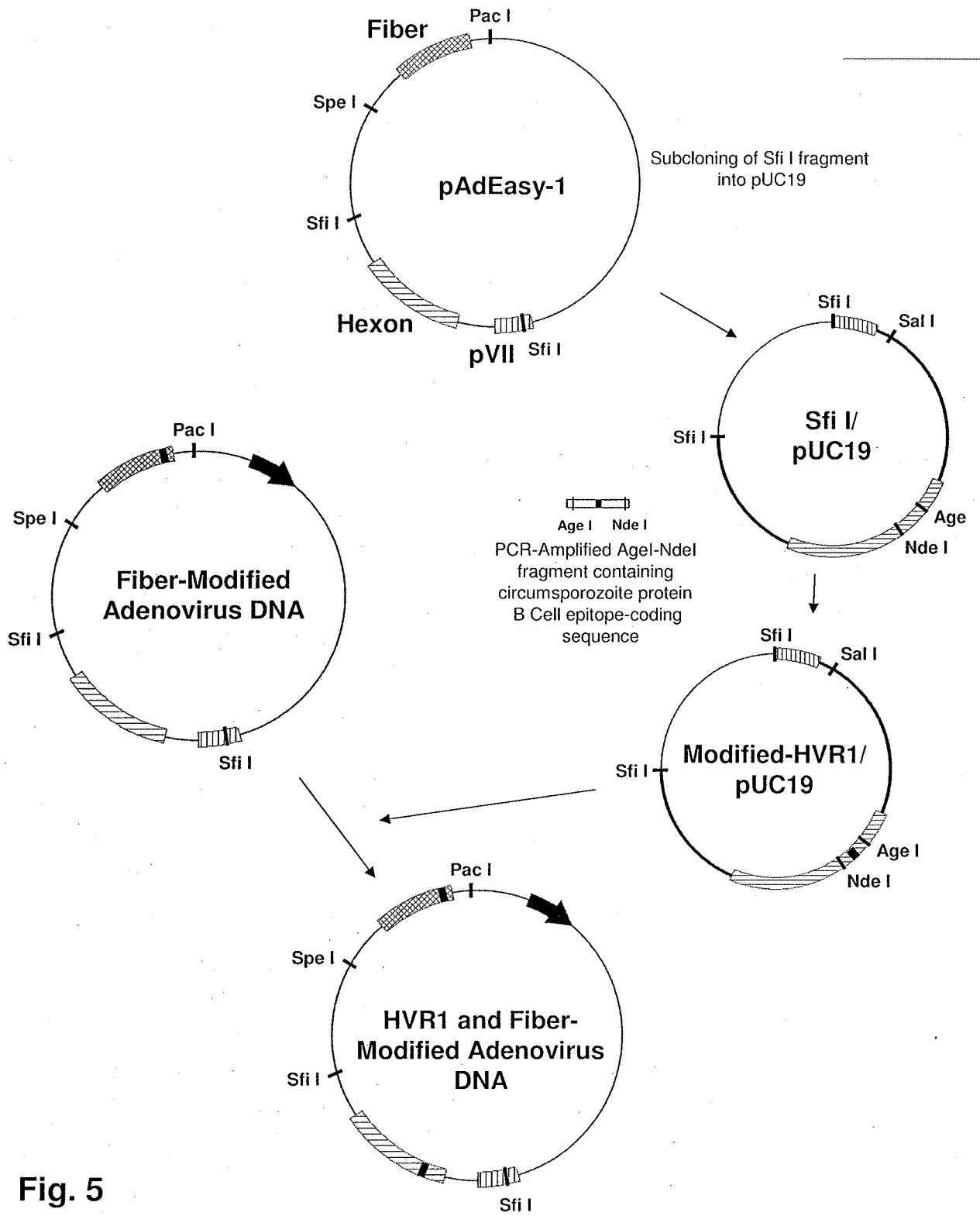


Fig. 5

Construction of Fiber and pVII-modified adenovirus vector

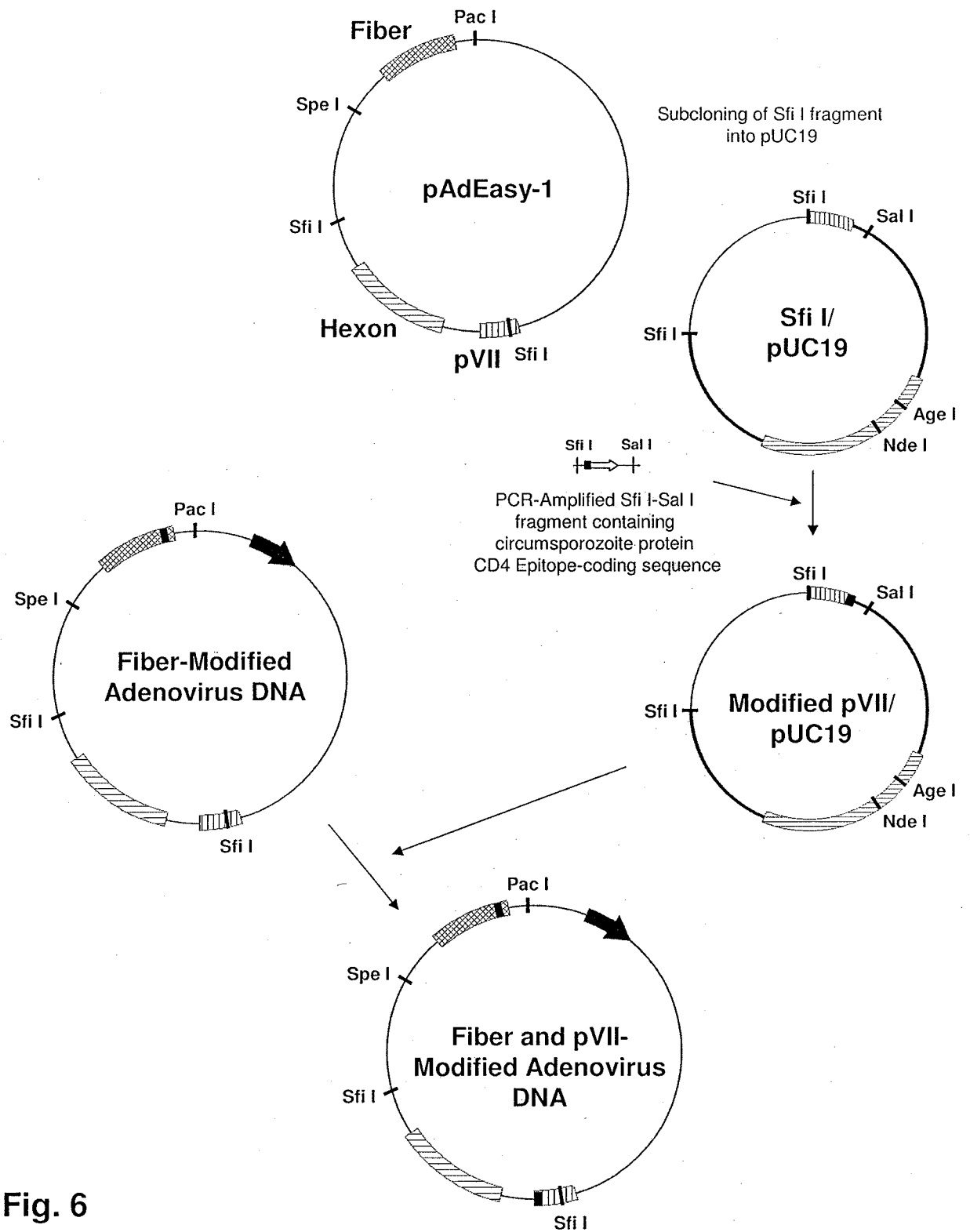


Fig. 6

Construction of HVR1 and pVII-modified adenovirus vector

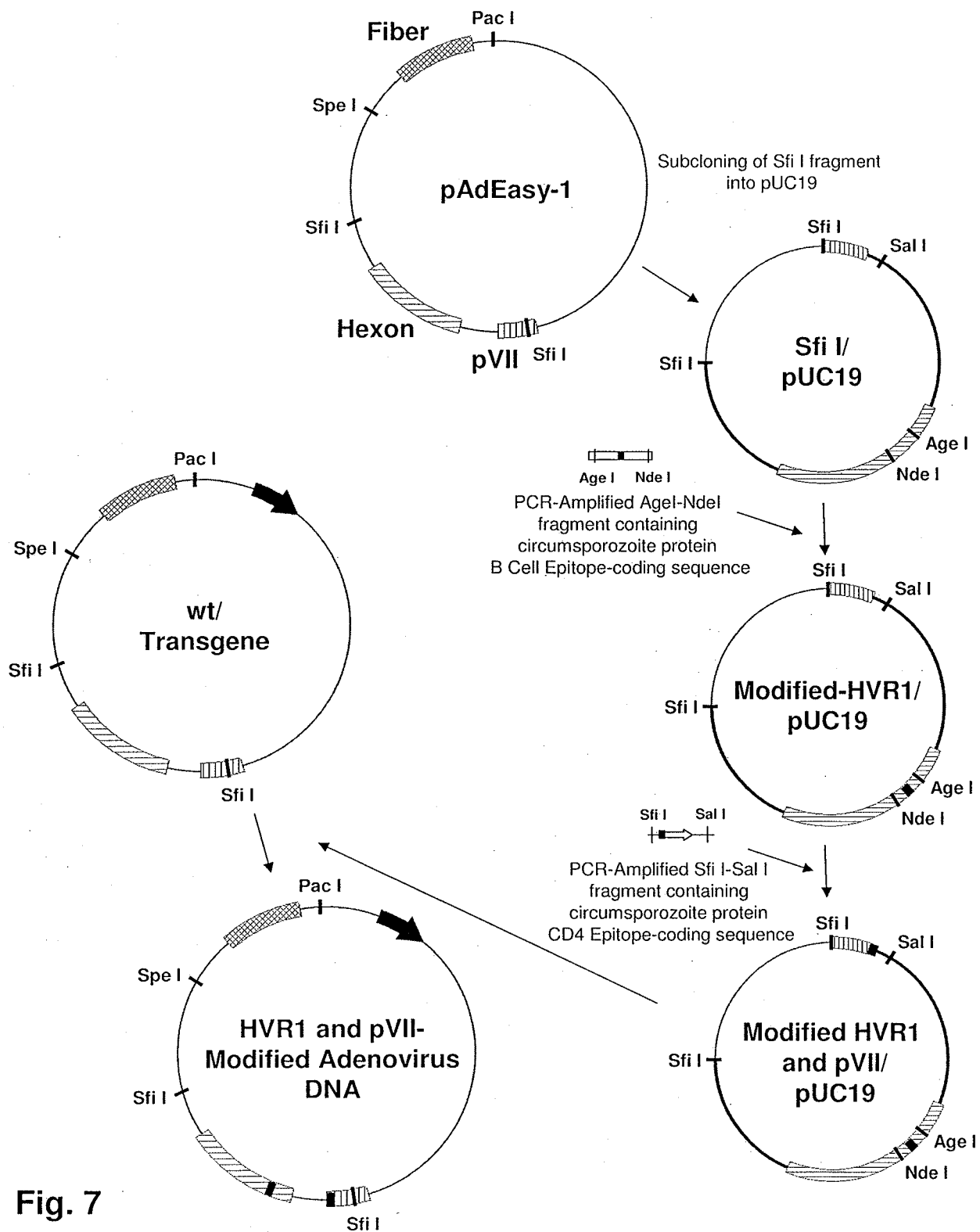


Fig. 7

Construction of HVR1, Fiber and pVII-Modified adenovirus vector

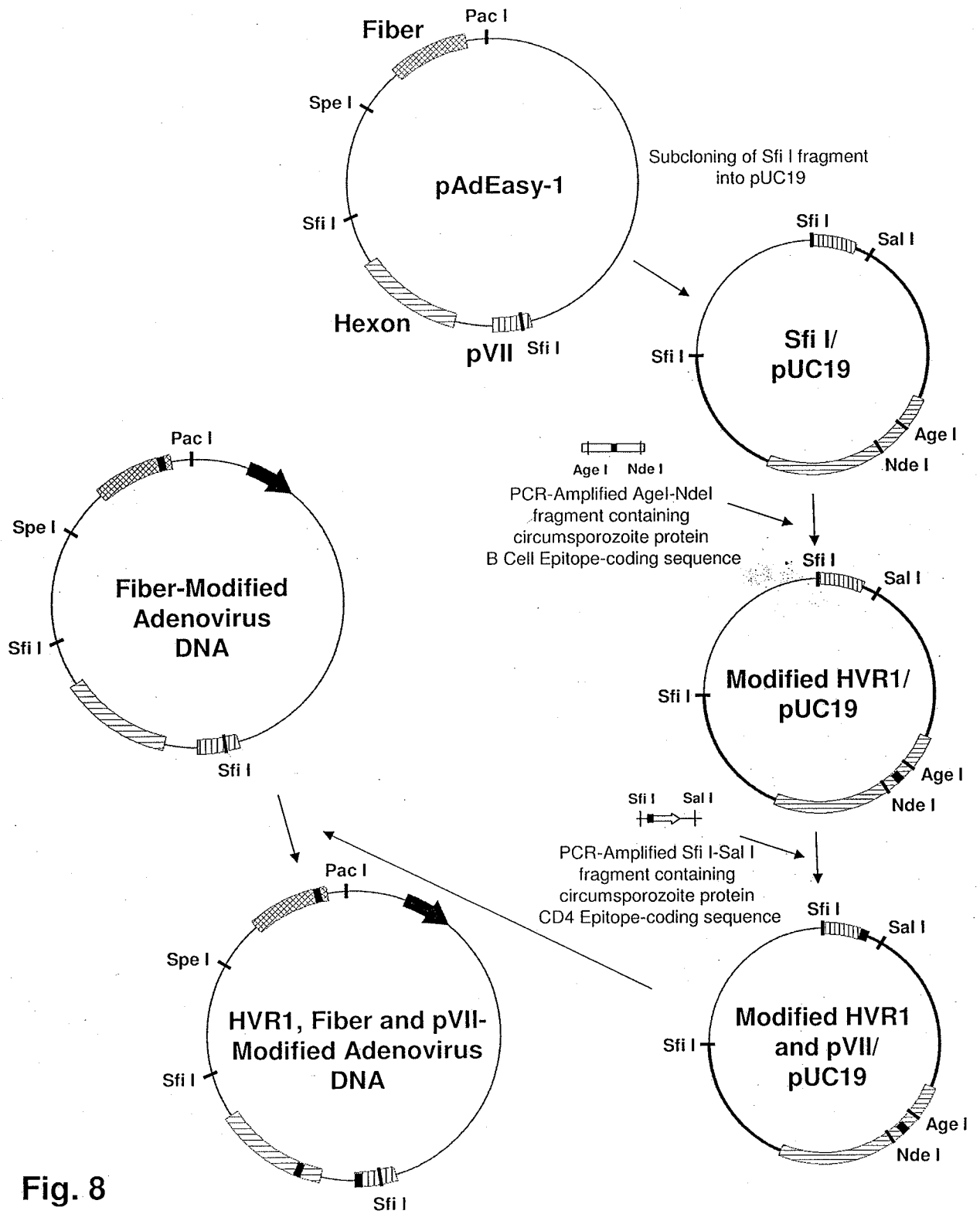


Fig. 8

Codon-optimized *Plasmodium yoelii* circumsporozoite protein sequence SEQ IDNO : 1 and 30

```

1           M K K C T I L V V A S L L L V D
1  GGTACCGCCACCATGAAGAAGTGACCATCCTGGTGGTGGCCAGCCTGCTGCTGGTGGAC

17  S L L P G Y G Q N K S V Q A Q R N L N E
61  AGCCTGCTGCCCGGCTACGGCCAGAACAGAGCGTGCAGGCCAGAGAACCTGAACGAG

37  L C Y N E E N D N K L Y H V L N S K N G
121 CTGTGCTACAACGAGGAGAACGACAACAAGCTGTACCACGTGCTGAACAGCAAGAACGGC

57  K I Y N R N I V N R L L G D A L N G K P
181 AAGATCTACAACAGGAACATCGTGAACAGGCTGCTGGGCGACGCCCTGAACGGCAAGCCC

77  E E K K D D P P K D D N K D D L P K E E
241 GAGGAGAAGAAGGACGACCCCCCAAGGACGACAACAAGGACGACCTGCCAAGGAGGAG

97  K K D D L P K E E K K D D P P K D P K K
301 AAGAAGGACGACCTGCCCAAGGAGGAGAAGAAGGACGACCCCCCAAGGACCCCAAGAAG

117 D D P P K E A Q N K L N Q P V V A D E N
361 GACGACCCCCCAAGGAGGCCAGAACAAAGCTGAACGACCCGCTAGTGGCAGATGAAAT

137 V D Q G P G A P Q G P G A P Q G P G A P
421 GTAGATCAAGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACA

157 Q G P G A P Q G P G A P Q G P G A P Q G
481 CAGGGGCCAGGAGCACCACAGGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACAAGGA

177 P G A P Q G P G A P Q G P G A P Q G P G
541 CCAGGAGCACCACAAGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACAAGGGCCAGGA

197 A P Q G P G A P Q G P G A P Q G P G A P
601 GCACCGCAGGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACAAGGACGAGGAGCACCACA

217 Q G P G A P Q G P G A P Q G P G A P Q G
661 CAGGGTCCAGGAGCACCACAAGGACCAGGAGCACCACAAGGACCAGGAGCACCACAAGGT

237 P G A P Q G P G A P Q G P G A P Q E P P
721 CCAGGAGCACCACAGGGGCCAGGAGCACCACAAGGGCCAGGAGCACCACAAGAACCACC

257 Q Q P P Q Q P P Q Q P P Q Q P P Q Q P P
781 CAACAACCCCAACAAGCCACCACAAGCCACCACAAGCCACCACAAGCCACCA

277 Q Q P N N N N N N N N G N N N E D S Y V P
841 CAACAACCAACAACAACAACAACAACGGCAACAACAAGGAGACGCTACGTGCC

297 S A E Q I L E F V K Q I S S Q L T E E W
901 AGGCCGAGCAGATCCTGGAGTTCGTGAAGCAGATCAGCAGCCAGCTGACCGAGGAGTGG

317 S Q C S V T C G S G V R V R K R K N V N
961 AGCCAGTGCAGCGTGACCTGCGGCAGCGCGTGAGGGTGAGGAAGAGGAAGAAGCTGAAC

337 K Q P E N L T L E D I D T E I C K M D K
1021 AAGCAGCCCGAGAACCTGACCTGGAGGACATCGACACCGAGATCTGCAAGATGGACAAG

357 C S S I F N I V S N S L G
1081 TGCAGCAGCATCTTCAACATCGTGAGCAACAGCCTGGGCTAAAGCTT

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Fig. 9

Codon-optimized *Plasmodium falciparum* circumsporozoite protein sequence SEQ IDNOS : 2 and 43

```

1           M M R K L A I L S V S S F L F V
1  GGTACCGCCACCATGATGCGCAAGCTCGCCATACTGTCTGTTAGTAGCTTTCTCTTTGTA

17  E A L F Q E Y Q C Y G S S S N T R V L N
61  GAGGCCCTGTTTCAGGAATACCAGTGCTATGGCAGCAGCAGCAACACTCGTGTGCTGAAC

37  E L N Y D N A G T N L Y N E L E M N Y Y
121 GAACCTTAACATGATAATGCAGGAACAAATTTATATAACGAACTGGAGATGAATTACTAT

57  G K Q E N W Y S L K K N S R S L G E N D
181 GGTAAGCAGGAAAATTGGTACTCTCTGAAAAAGAACTCTAGATCTCTGGGCGAGAACGAC

77  D G N N E D N E K L R K P K H K K L K Q
241 GACGGCAATAATGAAGACAATGAAAAGCTGAGGAAGCCAAAGCACAAAAAACTAAAGCAG

97  P A D G N P D P N A N P N V D P N A N P
301 CCCGACAGCGCAATCCAGACCCCAATGCTAACCCAAACGTGGACCCCAATGCTAATCCA

117 N V D P N A N P N V D P N A N P N A N P
361 AACGTGGATCCTAACGCTAACCGAATGTGGACCTAACGCCAATCCAAATGCGAATCCC

137 N A N P N A N P N A N P N A N P N A N P
421 AACGCTAATCCTAAGCAAACCGAATGCTAACCTAACGCAAACCCCAACGCTAACCCC

157 N A N P N A N P N A N P N A N P N A N P
481 AACGCGAACCCCAATGCCAACCCCAACGCCAACCCGAACGCCAATCCAAACGCTAACCC

177 N A N P N A N P N A N P N A N P N A N P
541 AATGCCAATCCTAATGCCAATCCGAACGCCAATCCAAATGCCAATCCAAATGCTAATCCC

197 N V D P N A N P N A N P N A N P N A N P
601 AACGTGGACCCCAACGCGAACCCCTAATGCCAACCCCAACGCTAATCCAAATGCGAACCC

217 N A N P N A N P N A N P N A N P N A N P
661 AACGCCAACCCGAATGCTAATCCCAATGCCAACCCCAATGCTAATCCCAATGCCAACCC

237 N A N P N A N P N A N P N A N P N A N P
721 AATGCCAATCCCAACGCCAACCCCAACGCAAACCCCTAATGCTAACCCGAACGCCAATCCG

257 N A N P N A N P N A N P N A N P N A N P N K N N
781 AACGCAAATCCTAATGCTAATCCTAACGCTAACCCCAACGCCAATCCAAATAAGAACAA

277 Q G N G Q G H N M P N D P N R N V D E N
841 CAAGGCAACGGGCAGGGGCACAATATGCCAATGACCCTAACCGGAATGTCGACGAGAAT

297 A N A N S A V K N N N N E E P S D K H I
901 GCAAATGCCAATAGCGCCGTGAAAAATAATAACGAGGAGCCAAAGTGACAAACACATT

317 K E Y L N K I O N S L S T E W S P C S V
961 AAGGAATATTGAACAAGATTCAAACCTCCTCAACAGAATGGTCTCCTTGCAGCGTG

337 T C G N G I Q V R I K P G S A N K P K D
1021 ACTTGTGGAATGGCATCCAGGTTCTGATTAACAGGTAGTGCCAACAAGCCCAAGGAT

357 E L D Y A N D I E K K I C K M E K C -
1081 GAACTAGACTATGCGAATGATATAGAGAAAAAATCTGTAAGATGGAGAAATGCTAGCTT

1141 CTAGA

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Fig. 10

Hexon sequence of (QGPGAP)₃-HVR1 adenovirus SEQ IDNOS : 3 and 31

```

1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTACCACAGACCCG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGCGTGTGCTGGACAGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAAACTCCTTGCGAATGGGATGAACAGGGCCCT

141 G A P Q G P G A P Q G P G A P K T H V F
421 GGAGCTCCACAGGGACCAAGGTGCACCTCAAGGGCCTGGAGCCCTAAAACCTACGATTTT

161 G Q A P Y S G I N I T K E G I Q I G V E
481 GGGCAGGCGCCTTATTCTGGTATAAATATTACAAAGGAGGGTATTCAAATAGGTGTGCA

181 G Q T P K Y A D K T F Q P E P Q I G E S
541 GGTCAAACACCTAAATATGCCGATAAAACATTCAACCTGAACCTCAAATAGGAGAATCT

201 Q W Y E T E I N H A A G R V L K K T T P
601 CAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCTAAAAAAGACTACCCCA

221 M K P C Y G S Y A K P T N E N G G Q G I
661 ATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATT

241 L V K Q Q N G K L E S Q V E M Q F F S T
721 CTTGTAAAGCAACAAAATGGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACT

261 T E A A A G N G D N L T P K V V L Y S E
781 ACTGAGGCAGCCGACGGCAATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAA

281 D V D I E T P D T H I S Y M P T I K E G
841 GATGTAGATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAAGGAAGGT

301 N S R E L M G Q Q S M P N R P N Y I A F
901 AACTCAGGAGAACTAATGGGCCAACAACTATGCCCAACAGGCCTAATTACATTGCTTTT

321 R D N F I G L M Y Y N S T G N M G V L A
961 AGGGACAATTTTATTGGTCTAATGTATTACAACAGCACGGGTAATATGGGTGTTCTGGCG

341 G Q A S Q L N A V V D L Q D R N T E L S
1021 GGCCAAGCATCGCAGTTGAATGCTGTTGTAGATTTGCAAGACAGAAACACAGAGCTTTCA

361 Y Q L L L D S I G D R T R Y F S M W N Q
1081 TACCAGCTTTTGCTTGATTCCATTGGTGATAGAACCAGGTACTTTTCTATGTGGAATCAG

381 A V D S Y D P D V R I I E N H G T E D E
1141 GCTGTTGACAGCTATGATCCAGATGTTAGAATTATTGAAAATCATGGAAGTGAAGATGAA

```

Fig. 11

401 L P N Y C F P L G G V I N T E T L T K V
 1201 CTTCCAAATTACTGCTTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTA

 421 K P K T G Q E N G W E K D A T E F S D K
 1261 AAACCTAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAA

 441 N E I R V G N N F A M E I N L N A N L W
 1321 AATGAAATAAGAGTTGGAAATAATTTTCCCATGGAAATCAATCTAAATGCCAACCTGTGG

 461 R N F L Y S N I A L Y L P D K L K Y S P
 1381 AGAAATTTCTGTACTCCAACATAGCGCTGTATTTGCCCGACAAGCTAAAGTACAGTCT

 481 S N V K I S D N P N T Y D Y M N K R V V
 1441 TCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCGAGTGGT

 501 A P G L V D C Y I N L G A R W S L D Y M
 1501 GCTCCCGGGCTAGTGGACTGCTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATG

 521 D N V N P F N H H R N A G L R Y R S M L
 1561 GACAACGTCAACCCATTTAACCACCACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTG

 541 L G N G R Y V P F H I Q V P Q K F F A I
 1621 CTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCTCAGAAGTTCTTTGCCATT

 561 K N L L L L P G S Y T Y E W N F R K D V
 1681 AAAAACCTCCTTCTCCTGCCGGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTT

 581 N M V L Q S S L G N D L R V D G A S I K
 1741 AACATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAA

 601 F D S I C L Y A T F F P M A H N T A S T
 1801 TTTGATAGCATTTGCCTTTACGCCACCTTCTTCCCATGGCCACAACACCGCTCCACG

 621 L E A M L R N D T N D Q S F N D Y L S A
 1861 CTTGAGGCCATGCTTAGAAACGACACCAACGACCACTCTTTAACGACTATCTCTCCGCC

 641 A N M L Y P I P A N A T N V P I S I P S
 1921 GCCAACATGCTCTACCTATACCCGCCAACGCTACCAACGTGCCCATATCCATCCCTCC

 661 R N W A A F R G W A F T R L K T K E T P
 1981 CGCAACTGGGCGGCTTTCCGCGGCTGGGCTTACGCGGCTTAAGACTAAGGAAACCCCA

 681 S L G S G Y D P Y Y T Y S G S I P Y L D
 2041 TCACTGGGCTCGGGCTACGACCCTTATTACACCTACTCTGGCTCTATACCTACCTAGAT

 701 G T F Y L N H T F K K V A I T F D S S V
 2101 GGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGCT

 721 S W P G N D R L L T P N E F E I K R S V
 2161 AGCTGGCCTGGCAATGACCGCTGCTTACCCCAACGAGTTTGAATTAAGCGCTCAGTT

 741 D G E G Y N V A Q C N M T K D W F L V Q
 2221 GACGGGGAGGGTTACAACGTTGCCAGTGTAAATGACCAAGACTGGTTCCTGGTACAA

 761 M L A N Y N I G Y Q G F Y I P E S Y K D
 2281 ATGCTAGCTAACTATAACATTGGCTACCAGGGCTTCTATATCCAGAGAGCTACAAGGAC

 781 R M Y S F F R N F Q P M S R Q V V D D T
 2341 CGCATGTACTCCTTCTTTAGAACTTCCAGCCCATGAGCGTCAGGTGGTGGATGATACT

Fig. 11

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801 K Y K D Y Q Q V G I L H Q H N N S G F V
2401 AAATACAAGGACTACCAACAGGTGGGCATCCTACACCAACACAACAACTCTGGATTTGTT

821 G Y L A P T M R E G Q A Y P A N F P Y P
2461 GGCTACCTTGCCCCACCATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCG

841 L I G K T A V D S I T Q K K F L C D R T
2521 CTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACC

861 L W R I P F S S N F M S M G A L T D L G
2581 CTTTGGCGCATCCATTCTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGC

881 Q N L L Y A N S A H A L D M T F E V D P
2641 CAAAACCTTCTCTACGCCAACTCGGCCACGGCTAGACATGACTTTTGAGGTGGATCCC

901 M D E P T L L Y V L F E V F D V V R V H
2701 ATGGACGAGCCACCCTTCTTTATGTTTTGTTTGAAGTCTTTGACGTGGTCCGTGTGCAC

921 Q P H R G V I E T V Y L R T P F S A G N
2761 CAGCCGCACCGCGCGTCATCGAAACCGTGTACCTGCGCACGCCCTTCTCGGCCGGCAAC

941 A T T -
2821 GCCACAACATAA

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Fig. 11

Hexon sequence of (QGPGAP)₄-HVR1 adenovirus SEQ IDNO : 4 and 32

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCACTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCACTTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCGAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAATCCTTGCAATGGGATGAACAGGGACCA

141 G A P Q G P G A P Q G P G A P Q G P G A
421 GGAGCACACAGGGACAGGAGCACACAGGGACAGGAGCACCGCAAGGTCTGTGGTGT

161 P K T H V F G Q A P Y S G I N I T K E G
481 CCTAAAATCAGCTATTTGGGCAAGCGCCTTATTCTGGTATAAATATTACAAAGGAGGGT

181 I Q I G V E G Q T P K Y A D K T F Q P E
541 ATTCAAATAGGTGTCGAAGGTCAAACACCTAAATATGCCGATAAAACATTTCAACCTGAA

201 P Q I G E S Q W Y E T E I N H A A G R V
601 CCTCAAATAGGAGATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTC

221 L K K T T P M K P C Y G S Y A K P T N E
661 CTA AAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAA

241 N G G Q G I L V K Q Q N G K L E S Q V E
721 AATGGAGGGCAAGGCATTCTTGTAAGCAACAAAATGGAAAGCTAGAAAGTCAAGTGGAA

261 M Q F F S T T E A A A G N G D N L T P K
781 ATGCAATTTTCTCACTACTGAGGCAGCCGAGGCAATGGTGATACTTGACTCCTAAA

281 V V L Y S E D V D I E T P D T H I S Y M
841 GTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCTTACATG

301 P T I K E G N S R E L M G Q Q S M P N R
901 CCCACTATTAAGGAAGGTAACCTACGAGAACTAATGGGCCAACAATCTATGCCCAACAGG

321 P N Y I A F R D N F I G L M Y Y N S T G
961 CCTAATTACATTGCTTTTAGGGACAATTTTATTGGTCTAATGTATTACAACAGCACGGGT

341 N M G V L A G Q A S Q L N A V V D L Q D
1021 AATATGGGTGTTCTGGCGGGCAAGCATCGCAGTTGAATGCTGTTGTAGATTGCAAGAC

361 R N T E L S Y Q L L L D S I G D R T R Y
1081 AGAAACACAGAGCTTTCATACAGCTTTTGCTTGATTCCATTGGTGATAGAACCAGGTAC

381 F S M W N Q L P N Y C F P L G G V I N T
1141 TTTTCTATGTGAATCAGCTTCCAAATTACTGCTTTCCACTGGGAGGTGTGATTAATACA
    
```

Fig. 12

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401 E T L T K V K P K T G Q E N G W E K D A
1201 GAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCT

421 T E F S D K N E I R V G N N F A M E I N
1261 ACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAAATAATTTTGCCATGGAAATCAAT

441 L N A N L W R N F L Y S N I A L Y L P D
1321 CTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTTGCCCGAC

461 K L K Y S P S N V K I S D N P N T Y D Y
1381 AAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTAC

481 M N K R V V A P G L V D C Y I N L G A R
1441 ATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACTTGGAGCACGC

501 W S L D Y M D N V N P F N H H R N A G L
1501 TGGTCCCTTGACTATATGGACAACGTCAACCCATTAAACCCACCCGCAATGCTGGCCGTG

521 R Y R S M L L G N G R Y V P F H I Q V P
1561 CGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCT

541 Q K F F A I K N L L L L P G S Y T Y E W
1621 CAGAAGTTCTTTGCCATTAAAACTCCTTCTCCTGCCGGGCTCATACACTACGAGTGG

561 N F R K D V N M V L Q S S L G N D L R V
1681 AACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTT

581 D G A S I K F D S I C L Y A T F F P M A
1741 GACGGAGCCAGCATTAAAGTTTGATAGCATTGCTTTACGCCACCTTCTTCCCATGGCG

601 H N T A S T L E A M L R N D T N D Q S F
1801 CACAACACCGCCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAACGACCGATCCTTT

621 N D Y L S A A N M L Y P I P A N A T N V
1861 AACGACTATCTCTCGCCGCCAACATGCTCTACCCATATACCCGCCAACGCTACCAACGTG

641 P I S I P S R N W A A F R G W A F T R L
1921 CCCATATCCATCCCCTCCGCAACTGGGCGGCTTTCCGCGGCTGGGCCTTACGCGCCCTT

661 K T K E T P S L G S G Y D P Y Y T Y S G
1981 AAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCCCTATTACACCTACTCTGGC

681 S I P Y L D G T F Y L N H T F K K V A I
2041 TCTATACCCATACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATT

701 T F D S S V S W P G N D R L L T P N E F
2101 ACCTTTGACTCTTCTGTCAGCTGGCCTGGCAATGACCGCCTGCTTACCCCAACGAGTTT

721 E I K R S V D G E G Y N V A Q C N M T K
2161 GAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAA

741 D W F L V Q M L A N Y N I G Y Q G F Y I
2221 GACTGGTTCCTGGTACAATGCTAGCTAACTATAACATTGGCTACCAGGGCTTCTATATC

761 P E S Y K D R M Y S F F R N F Q P M S R
2281 CCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGCCCATGAGCCGT

781 Q V V D D T K Y K D Y Q Q V G I L H Q H
2341 CAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATCCTACCAACAC

801 N N S G F V G Y L A P T M R E G Q A Y P
2401 AACAACTCTGGATTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCCTACCTT

```

Fig. 12

821 A N F P Y P L I G K T A V D S I T Q K K
2461 GCTAACTTCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAG

841 F L C D R T L W R I P F S S N F M S M G
2521 TTTCTTTGGGATCGCACCCCTTTGGCGCATCCATTCTCCAGTAACCTTATGTCCATGGGC

861 A L T D L G Q N L L Y A N S A H A L D M
2581 GCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCCGCCACGGCTAGACATG

881 T F E V D P M D E P T L L Y V L F E V F
2641 ACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTATGTTTTGTTGAAGTCTT

901 D V V R V H Q P H R G V I E T V Y L R T
2701 GACGTGGTCCGTGTGCACCGCCGACCGCGGCGTCATCGAAACCGTGACCTGCGCAG

921 P F S A G N A T T -
2761 CCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 12

Hexon sequence of (QGPGAP)₅-HVR1 adenovirus SEQ IDNOS : 5 and 33

```

1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121  CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181  TCCGAGCGTTTGACGCTCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241  AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCACGTAC

101  F D I R G V L D R G P T F K P Y S G T A
301  TTTGACATCCGCGCGTGTGTCGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGGC

121  Y N A L A P K G A P N P C E W D E Q G P
361  TACAAGCCCTGGCTCCCAAGGGTCCCCAAATCCTTGCAATGGGATGAACAGGGACCA

141  G A P Q G P G A P Q G P G A P Q G P G A
421  GGAGCACACAGGACCGAGGACCAAGGACCGAGGACCGCAAGGTCTGGTGCT

161  P Q G P G A P K T H V F G Q A P Y S G I
481  CCTCAGGACCGAGGACCAAAAACTCAGTATTGGGCGAGGCGCCTTATTCTGGTATA

181  N I T K E G I Q I G V E G Q T P K Y A D
541  AATATTACAAAGGAGGTATTCAAATAGGTGTGAAAGGTCAAACACCTAAATATGCCGAT

201  K T F Q P E P Q I G E S Q W Y E T E I N
601  AAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAAT

221  H A A G R V L K K T T P M K P C Y G S Y
661  CATCGAGCTGGGAGAGTCCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATAT

241  A K P T N E N G G Q G I L V K Q Q N G K
721  GCAAAACCCACAAATGAAATGGAGGGCAAGGCATTCTGTAAAGCAACAAATGGAAG

261  L E S Q V E M Q F F S T T E A A A G N G
781  CTAGAAAGTCAAGTGGAATGCAATTTTCTCAACTACTGAGGCAGCCGAGGCAATGGT

281  D N L T P K V V L Y S E D V D I E T P D
841  GATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGAC

301  T H I S Y M P T I K E G N S R E L M G Q
901  ACTCATATTTCTTACATGCCCACTATTAAGGAAGTAACACGAGAACTAATGGGCCAA

321  Q S M P N R P N Y I A F R D N F I G L M
961  CAATCTATGCCCAACAGGCTAATTACATTGCTTTTAGGGACAATTTATTGGTCTAATG

341  Y Y N S T G N M G V L A G Q A S Q L N A
1021  TATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTGAATGCT

361  V V D L Q D R N T E L S Y Q L L L D S I
1081  GTTGTAGATTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCCTTGATTCCATT

381  G D R T R Y F S M W N Q L P N Y C F P L
1141  GGTGATAGAACCAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTTCCACTG

```

Fig. 13

401 G G V I N T E T L T K V K P K T G Q E N
 1201 GGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTGAGGAAAAAT

 421 G W E K D A T E F S D K N E I R V G N N
 1261 GGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAAATAAT

 441 F A M E I N L N A N L W R N F L Y S N I
 1321 TTTGCCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATA

 461 A L Y L P D K L K Y S P S N V K I S D N
 1381 GCGCTGTATTTGCCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAAC

 481 P N T Y D Y M N K R V V A P G L V D C Y
 1441 CCAAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGAGCTGCTAC

 501 I N L G A R W S L D Y M D N V N P F N H
 1501 ATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTTAACCCAG

 521 H R N A G L R Y R S M L L G N G R Y V P
 1561 CACCGCAATGCTGGCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCC

 541 F H I Q V P Q K F F A I K N L L L L P G
 1621 TTCCACATCCAGGTGCTCAGAAGTTCTTTGCCATTAAAACTCCTTCTCCTGCCGGGG

 561 S Y T Y E W N F R K D V N M V L Q S S L
 1681 TCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTA

 581 G N D L R V D G A S I K F D S I C L Y A
 1741 GGAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATTGCTTTACGCC

 601 T F F P M A H N T A S T L E A M L R N D
 1801 ACCTTCTTCCCATGGCCCAACACCGCCTCCAGCTTGAGGCCATGCTTAGAAACGAC

 621 T N D Q S F N D Y L S A A N M L Y P I P
 1861 ACCAACGACCACTCTTAACGACTATCTCTCGCCGCAACATGCTCTACCCATATACCC

 641 A N A T N V P I S I P S R N W A A F R G
 1921 GCCAACGCTACCAACGTGCCATATCCATCCCTCCGCAACTGGCGGGCTTTCCGCGG

 661 W A F T R L K T K E T P S L G S G Y D P
 1981 TGGGCTTACGCGCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCT

 681 Y Y T Y S G S I P Y L D G T F Y L N H T
 2041 TATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTACCTCAACACACC

 701 F K K V A I T F D S S V S W P G N D R L
 2101 TTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTGAGCTGGCCTGGCAATGACCGCCTG

 721 L T P N E F E I K R S V D G E G Y N V A
 2161 CTTACCCCAACGAGTTTGAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCC

 741 Q C N M T K D W F L V O M L A N Y N I G
 2221 CAGTGTAACATGACCAAAGACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGC

 761 Y Q G F Y I P E S Y K D R M Y S F F R N
 2281 TACCAGGGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAAAC

 781 F Q P M S R Q V V D D T K Y K D Y Q Q V
 2341 TTCCAGCCCATGAGCCGTGAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTG

 801 G I L H Q H N N S G F V G Y L A P T M R
 2401 GGCATCCTACCAACACAACAACCTCTGGATTGTTGGCTACCTTGGCCCCACCATGCGG

Fig. 13

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821  E G Q A Y P A N F P Y P L I G K T A V D
2461 GAAGGACAGGCCTACCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGAC

841  S I T Q K K F L C D R T L W R I P F S S
2521 AGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTCCTCAGT

861  N F M S M G A L T D L G Q N L L Y A N S
2581 AACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCC

881  A H A L D M T F E V D P M D E P T L L Y
2641 GCCCAGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTTAT

901  V L F E V F D V V R V H Q P H R G V I E
2701 GTTTTGTGTTGAAGTCTTTGACGTGGTCCGTGTGCACAGCCGCACCGCGCGTCATCGAA

921  T V Y L R T P F S A G N A T T -
2761 ACCGTGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

```

Fig. 13

Hexon sequence of (QGPGAP)₆-HVR1 adenovirus SEQ IDNOS : 6 and 34

1 M A T P S M M P Q W S Y M H I S G Q D A
1 ATGGCTACCCCTTCGATGATGCCGCAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21 S E Y L S P G L V Q F A R A T E T Y F S
61 TCGGAGTACCTGAGCCCCGGGCTGGTGCAATTTGCCCGCGCCACCGAGACGTACTTCAGC

41 L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61 S Q R L T L R F I P V D R E D T A Y S Y
181 TCCACGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTCGGTACTCGTAC

81 K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTCCACCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGCGGTGCTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCCAAATCCTTGCGAATGGGATGAACAGGGACCA

141 G A P Q G P G A P Q G P G A P Q G P G A
421 GGAGCACACAGGGACAGGAGCACACAGGGACAGGAGCACCGCAAGGTCCTGGTGCT

161 P Q G P G A P Q G P G A P K T H V F G Q
481 CCTCAGGGACAGGAGCACACAGGGACAGGAGCACCAAAAACCTCACGTAATTTGGGACG

181 A P Y S G I N I T K E G I Q I G V E G Q
541 GCGCCTTATTCTGGTATAAATATTACAAGGAGGGTATTCAAATAGGTGTCAAGGTCAA

201 T P K Y A D K T F Q P E P Q I G E S Q W
601 ACACCTAAATATGCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGG

221 Y E T E I N H A A G R V L K K T T P M K
661 TACGAACACGAAATTAATCATGCACTGGGAGAGTCTCAAAAAAGACTACCCCAATGAAA

241 P C Y G S Y A K P T N E N G G Q G I L V
721 CCATGTTACGGTTCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATTCTTGTA

261 K Q Q N G K L E S Q V E M Q F F S T T E
781 AAGCAACAAAAATGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACTACTGAG

281 A A A G N G D N L T P K V V L Y S E D V
841 GCAGCCGACGGCAATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTA

301 D I E T P D T H I S Y M P T I K E G N S
901 GATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAAGGAAGTAACTCA

321 R E L M G Q Q S M P N R P N Y I A F R D
961 CGAGAATAATGGGCCAACATCTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGAC

341 N F I G L M Y Y N S T G N M G V L A G Q
1021 AATTTTATTGGTCTAATGTATTACAACAGCAGCGGTAATATGGGTGTTCTGGCGGGCCAA

361 A S Q L N A V V D L Q D R N T E L S Y Q
1081 GCATCGCAGTTGAATGCTGTGTAGATTGCAAGACAGAAACACAGAGCTTTCATACCGAG

381 L L L D S I G D R T R Y F S M W N Q L P
1141 CTTTTGCTTGATTCATTGGTGATAGAACCAGGTACTTTTCTATGTGGAATCAGCTTCCA

Fig. 14

401 N Y C F P L G G V I N T E T L T K V K P
 1201 AATTACTGCTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAAACCT

 421 K T G Q E N G W E K D A T E F S D K N E
 1261 AAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAATGAA

 441 I R V G N N F A M E I N L N A N L W R N
 1321 ATAAGAGTTGGAATAATTTTGCCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAAT

 461 F L Y S N I A L Y L P D K L K Y S P S N
 1381 TTCCTGTACTCCAACATAGCGCTGTATTTGCCGACAAGCTAAAGTACAGTCCTTCCAAC

 481 V K I S D N P N T Y D Y M N K R V V A P
 1441 GTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCAGTGGTGGCTCC

 501 G L V D C Y I N L G A R W S L D Y M D N
 1501 GGGCTAGTGGACTGCTACATTAACCTTGGAGCACGCTGGTCCCTTGACTATATGGACAAC

 521 V N P F N H H R N A G L R Y R S M L L G
 1561 GTCAACCCATTTAACCAACACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGG

 541 N G R Y V P F H I Q V P Q K F F A I K N
 1621 AATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCTCAGAAGTTCTTTGCCATAAAAAC

 561 L L L L P G S Y T Y E W N F R K D V N M
 1681 CTCCTTCTCCTGCCGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATG

 581 V L Q S S L G N D L R V D G A S I K F D
 1741 GTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGAT

 601 S I C L Y A T F F P M A H N T A S T L E
 1801 AGCATTTGCTTTACGCCACCTTCTTCCCATGGCCACAACACCGCTCCACGCTTGAG

 621 A M L R N D T N D Q S F N D Y L S A A N
 1861 GCCATGCTTAGAAACGACACCAACGACGAGTCCTTTAAGGACTATCTCTCCGCCGCCAAC

 641 M L Y P I P A N A T N V P I S I P S R N
 1921 ATGCTCTACCTATACCCGCCAAGCTACCAAGTGCCATATCCATCCCTCCCGCAAC

 661 W A A F R G W A F T R L K T K E T P S L
 1981 TGGGCGGCTTTCCGGGCTGGGCTTACGCGCTTAAGACTAAGGAAACCCATCACTG

 681 G S G Y D P Y Y T Y S G S I P Y L D G T
 2041 GGCTCGGGCTACGACCTTATTACACCTACTCTGGCTCTATACCTACCTAGATGGAAC

 701 F Y L N H T F K K V A I T F D S S V S W
 2101 TTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTGAGCTGG

 721 P G N D R L L T P N E F E I K R S V D G
 2161 CCTGGCAATGACCGCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGG

 741 E G Y N V A Q C N M T K D W F L V Q M L
 2221 GAGGGTTACAACGTTGCCAGTGTAAATGACCAAAGACTGGTTCCTGGTACAATGCTA

 761 A N Y N I G Y Q G F Y I P E S Y K D R M
 2281 GCTAACTATAACATTGGCTACCGGGCTTCTATATCCAGAGAGCTACAAGGACCGCATG

 781 Y S F F R N F Q P M S R Q V V D D T K Y
 2341 TACTCCTTCTTTAGAACTTCCAGCCATGAGCCGTCAGGTGGTGGATGATAAATAC

 801 K D Y Q Q V G I L H Q H N N S G F V G Y
 2401 AAGGACTACCAACAGGTGGGCATCCTACACCAACACAACAACTCTGGATTTGTTGGCTAC

Fig. 14

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821  L A P T M R E G Q A Y P A N F P Y P L I
2461 CTTGCCCCACCATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATA

841  G K T A V D S I T Q K K F L C D R T L W
2521 GGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGG

861  R I P F S S N F M S M G A L T D L G Q N
2581 CGCATCCATTCTCCAGTAACCTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAAC

881  L L Y A N S A H A L D M T F E V D P M D
2641 CTTCTCTACGCCAACTCCGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGAC

901  E P T L L Y V L F E V F D V V R V H Q P
2701 GAGCCACCCCTTCTTTATGTTTGTGTTGAAGTCTTTGACGTGGTCCGTGTGCACCAAGCCG

921  H R G V I E T V Y L R T P F S A G N A T
2761 CACCGGGGCGTCATCGAAACCGGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACA

941  T -
2821 ACATAA

```

Fig. 14

Hexon sequence of (QGPGAP)₇-HVR1 adenovirus SEQ IDNOS : 7 and 35

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1  M A T P S M M P O W S Y M H I S G O D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCGGGCTGGTGCAGTTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAAAATCCTTGCGAATGGGATGAACAGGGACCA

141 G A P Q G P G A P Q G P G A P Q G P G A
421 GGAGCACACAGGGACAGGAGCACACAGGGACAGGAGCACACAGGGACAGGAGCA

161 P Q G P G A P Q G P G A P Q G P G A P K
481 CCACAGGGACAGGAGCACACAGGGACAGGAGCACCGCAAGGTCTGGTGTCTCTAAA

181 T H V F G Q A P Y S G I N I T K E G I Q
541 ACTCACGTATTTGGGACGGCGCCTTATTCTGGTATAAATATTACAAAGGAGGGTATTCAA

201 I G V E G Q T P K Y A D K T F Q P E P Q
601 ATAGGTGTGCAAGGTCAAACACCTAAATATGCCGATAAAACATTTCAACCTGAACCTCAA

221 I G E S Q W Y E T E I N H A A G R V L K
661 ATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCCTAAAA

241 K T T P M K P C Y G S Y A K P T N E N G
721 AAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAAATGGA

261 G Q G I L V K Q Q N G K L E S Q V E M Q
781 GGGCAAGGCATTCTGTAAAGCAACAAATGGAAGCTAGAAAGTCAAGTGGAATGCAA

281 F F S T T E A A A G N G D N L T P K V V
841 TTTTCTCAACTACTGAGGCAGCCGAGGCAATGGTGATACTTGACTCCTAAAGTGGA

301 L Y S E D V D I E T P D T H I S Y M P T
901 TTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCTTACATGCCCACT

321 I K E G N S R E L M G Q Q S M P N R P N
961 ATTAAGGAAGGTAACACAGAGAACTAATGGGCCAACAATCTATGCCCAACAGGCCTAAT

341 Y I A F R D N F I G L M Y Y N S T G N M
1021 TACATTGCTTTTAGGACAAATTTATTGGTCTAATGTATTACAACAGCACGGGTAATATG

361 G V L A G Q A S Q L N A V V D L Q D R N
1081 GGTGTTCTGGCGGCCAAGCATCGCAGTTGAATGCTGTGTAGATTGCAAGACAGAAAC

381 T E L S Y Q L L L D S I G D R T R Y F S
1141 ACAGAGCTTTCATACCAAGCTTTGCTTGATTCCATTGGTGATAGAACCAGGTACTTTTCT

```

Fig. 15

401 M W N Q L P N Y C F P L G G V I N T E T
 1201 ATGTGGAATCAGCTTCCAAATTACTGCTTCCACTGGGAGGTGTGATTAATACAGAGACT

 421 L T K V K P K T G Q E N G W E K D A T E
 1261 CTTACCAAGGTAAAACCTAAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAA

 441 F S D K N E I R V G N N F A M E I N L N
 1321 TTTTCAGATAAAAATGAAATAAGAGTTGGAAATAATTTGCCATGGAAATCAATCTAAAT

 461 A N L W R N F L Y S N I A L Y L P D K L
 1381 GCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTGCCCCACAAGCTA

 481 K Y S P S N V K I S D N P N T Y D Y M N
 1441 AAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAAC

 501 K R V V A P G L V D C Y I N L G A R W S
 1501 AAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACCTGGAGCACGCTGGTCC

 521 L D Y M D N V N P F N H H R N A G L R Y
 1561 CTTGACTATATGGACAACGTCAACCCATTTAACCAACACCGCAATGCTGGCCTGCGCTAC

 541 R S M L L G N G R Y V P F H I Q V P Q K
 1621 CGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCTCAGAA

 561 F F A I K N L L L L P G S Y T Y E W N F
 1681 TTCTTTGCCATTA AAAACCTCCTTCTCTGCGGGGCTCATACACCTACGAGTGGAACTTC

 581 R K D V N M V L Q S S L G N D L R V D G
 1741 AGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGA

 601 A S I K F D S I C L Y A T F F P M A H N
 1801 GCCAGCATTAAAGTTTGATAGCATTTCGCTTTACGCCACCTTCTTCCCATGGCCACAAC

 621 T A S T L E A M L R N D T N D Q S F N D
 1861 ACCGCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAACGACGAGTCCTTTAACGAC

 641 Y L S A A N M L Y P I P A N A T N V P I
 1921 TATCTCTCCGCCGCCAACATGCTCTACCTATACCCGCCAACGCTACCAACGTGCCATTA

 661 S I P S R N W A A F R G W A F T R L K T
 1981 TCCATCCCTCCCGCAACTGGGCGGCTTCCGCGGCTGGGCTTACGCGCCTTAAGACT

 681 K E T P S L G S G Y D P Y Y T Y S G S I
 2041 AAGGAAACCCATCACTGGGCTCGGGCTACGACCCCTATTACACCTACTCTGGCTCTATA

 701 P Y L D G T F Y L N H T F K K V A I T F
 2101 CCCTACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTT

 721 D S S V S W P G N D R L L T P N E F E I
 2161 GACTCTTCTGTGAGCTGGCCTGGCAATGACCGCTGCTTACCCCAACGAGTTTGAATTT

 741 K R S V D G E G Y N V A Q C N M T K D W
 2221 AAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAAAGACTGG

 761 F L V Q M L A N Y N I G Y Q G F Y I P E
 2281 TTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACGAGGCTTCTATATCCAGAG

 781 S Y K D R M Y S F F R N F O P M S R O V
 2341 AGCTACAAGGACGCATGTACTCTTCTTTAGAACTCCAGCCCATGAGCCGTGAGGTG

 801 V D D T K Y K D Y Q Q V G I L H Q H N N
 2401 GTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATCTACCAACACACAACAC

Fig. 15

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821  S G F V G Y L A P T M R E G O A Y P A N
2461 TCTGGATTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCCTACCTGCTAAC

841  F P Y P L I G K T A V D S I T Q K K F L
2521 TTCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTT

861  C D R T L W R I P F S S N F M S M G A L
2581 TCGGATCGCACCCCTTTGGCGCATCCATTCTCCAGTAAC TTATGTCCATGGGCGCACTC

881  T D L G Q N L L Y A N S A H A L D M T F
2641 ACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCCGCCACGCGCTAGACATGACTTTT

901  E V D P M D E P T L L Y V L F E V F D V
2701 GAGGTGGATCCCATGGACGAGCCACCCCTTCTTTATGTTTTGTTGAAGTCTTTGACGTG

921  V R V H Q P H R G V I E T V Y L R T P F
2761 GTCCGTGTGCACGACGCGCACCGCGCGTCATCGAAACCGTGTACCTGCGCACGCCCTTC

941  S A G N A T T -
2821 TCGGCCGGCAACGCCACAACATAA

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Fig. 15

Hexon sequence of (QGPGAP)₈-HVR1 adenovirus SEQ IDNOs : 8 and 36

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTCCCCGCGCCACCGAGACGTACTTCAGG

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAG

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGCGTGTGACAGGGGCCCTACTTTTAAGCCCTACTCTGGACATGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTCCCCAAATCCTTGCGAATGGGATGAACAGGGACCA

141  G A P Q G P G A P Q G P G A P Q G P G A
421  GGAGCACCACAGGGACAGGAGCACCACAGGGACAGGAGCACCACAGGGACAGGAGCA

161  P Q G P G A P Q G P G A P Q G P G A P Q
481  CCACAGGGACAGGAGCACCACAGGGACAGGAGCACCACAGGTCCTGGTGTCTCATG

181  G P G A P K T H V F G Q A P Y S G I N I
541  GGACCAGGAGCACCACAACTACAGTATTTGGGAGGCGCCTTATTCTGGTATAAATAT

201 T K E G I Q I G V E G Q T P K Y A D K T
601 ACAAAGGAGGGTATTCAAATAGGTGTGCAAGGTCAAACACCTAAATATGCCGATAAAACA

221 F Q P E P Q I G E S Q W Y E T E I N H A
661 TTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCA

241 A G R V L K K T T P M K P C Y G S Y A K
721 GCTGGGAGAGTCCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAA

261 P T N E N G G Q G I L V K Q Q N G K L E
781 CCCACAAATGAAAATGGAGGGCAAGGCATTCTTGTAAGCAACAAATGGAAGCTAGAA

281 S Q V E M Q F F S T T E A A A G N G D N
841 AGTCAAGTGGAATGCAATTTTCTCACTACTGAGGCAGCCGAGGCAATGGTGATAAC

301 L T P K V V L Y S E D V D I E T P D T H
901 TTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCAT

321 I S Y M P T I K E G N S R E L M G Q Q S
961 ATTTCTTACATGCCACTATTAAGGAAGGTAACACAGAGAACTAATGGGCCAACAACTCT

341 M P N R P N Y I A F R D N F I G L M Y Y
1021 ATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTATTGGTCTAATGTATTAC

361 N S T G N M G V L A G Q A S O L N A V V
1081 AACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTA

381 D L Q D R N T E L S Y Q L L L D S I G D
1141 GATTTGCAAGACAGAAACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATTGGTGAT

```

Fig. 16

401 R T R Y F S M W N Q L P N Y C F P L G G
 1201 AGAACCGAGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTCCACTGGGAGGT

 421 V I N T E T L T K V K P K T G Q E N G W
 1261 GTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAAATGGATGG

 441 E K D A T E F S D K N E I R V G N N F A
 1321 GAAAAAGATGCTACAGAATTTTCAGATAAAAATGAAATAAGAGTTGGAAAATAATTTTGCC

 461 M E I N L N A N L W R N F L Y S N I A L
 1381 ATGGAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTG

 481 Y L P D K L K Y S P S N V K I S D N P N
 1441 TATTTGCCCGACAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAAC

 501 T Y D Y M N K R V V A P G L V D C Y I N
 1501 ACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAAAC

 521 L G A R W S L D Y M D N V N P F N H H R
 1561 CTTGGAGCACGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTAAACCAACCCGCG

 541 N A G L R Y R S M L L G N G R Y V P F H
 1621 AATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCAG

 561 I Q V P Q K F F A I K N L L L L P G S Y
 1681 ATCCAGGTGCCTCAGAAGTCTTTGCCATTAAAAACCTCCTTCTCCTGCCGGGCTCATAC

 581 T Y E W N F R K D V N M V L Q S S L G N
 1741 ACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTAGGAAAT

 601 D L R V D G A S I K F D S I C L Y A T F
 1801 GACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATTTCCTTTACGCCACCTTC

 621 F P M A H N T A S T L E A M L R N D T N
 1861 TTCCCATGGCCACAACACCGCTCCAGGCTTGAGGCCATGCTTAGAAACGACACCAAC

 641 D Q S F N D Y L S A A N M L Y P I P A N
 1921 GACCAGTCCTTTACGACTATCTCTCCGCCGCAACATGCTCTACCTATACCCGCAAC

 661 A T N V P I S I P S R N W A A F R G W A
 1981 GCTACCAACGTGCCATATCCATCCCTCCGCAACTGGGCGGCTTCCGCGGCTGGGCG

 681 F T R L K T K E T P S L G S G Y D P Y Y
 2041 TTCACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCCCTATTAC

 701 T Y S G S I P Y L D G T F Y L N H T F K
 2101 ACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTACCTCAACACACCTTTAAG

 721 K V A I T F D S S V S W P G N D R L L T
 2161 AAGGTGGCCATTACCTTTGACTCTTGTGTAGCTGGCTGGCAATGACCGCTGCTTAC

 741 P N E F E I K R S V D G E G Y N V A Q C
 2221 CCCAACGAGTTTGAATAAGCGCTCAGTTGACGGGAGGGTTACAACTGTGCCAGTGT

 761 N M T K D W F L V Q M L A N Y N I G Y O
 2281 AACATGACCAAGACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACCG

 781 G F Y I P E S Y K D R M Y S F F R N F Q
 2341 GGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAG

 801 P M S R Q V V D D T K Y K D Y Q Q V G I
 2401 CCCATGAGCCGTCAGGTGGTGGATGATACTAAATAAGGACTACCAACAGGTGGGCATC

Fig. 16

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821  L H Q H N N S G F V G Y L A P T M R E G
2461 CTACACCAACACAACAACTCTGGATTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGA

841  Q A Y P A N F P Y P L I G K T A V D S I
2521 CAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATT

861  T O K K F L C D R T L W R I P F S S N F
2581 ACCCAGAAAAAGTTTCTTTGGGATCGCACCCCTTTGGCGCATCCCATTCCTCCAGTAACTTT

881  M S M G A L T D L G Q N L L Y A N S A H
2641 ATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCCGCCAC

901  A L D M T F E V D P M D E P T L L Y V L
2701 GCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCCACCCTTCTTTATGTTTG

921  F E V F D V V R V H Q P H R G V I E T V
2761 TTTGAAGTCTTTGACGTGGTCCGTGTGCACCAGCCGACCCGCGCGTCATCGAAACCGTG

941  Y L R T P F S A G N A T T -
2821 TACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

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Fig. 16

Hexon sequence of (QGPGAP)₉-HVR1 adenovirus SEQ IDNOS : 9 and 37

```

1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGAGCTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCGACGTTTGACGCTGCGGTTTCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTGACATCCGCGGCGTGTGGACAGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAAACTCTTGCGAATGGGATGAACAGGAGCCA

141 G A P Q G P G A P Q G P G A P Q G P G A
421 GGAGCACCACAGGACCAGGAGCACCACAGGAGCACCACAGGAGCACCACAGGAGCAGGAGCA

161 P Q G P G A P Q G P G A P Q G P G A P Q
481 CCACAGGAGCAGGAGCACCACAGGAGCACCAGGAGCACCAGGAGCACCAGGAGCAGGAGCA

181 G P G A P Q G P G A P K T H V F G Q A P
541 GGACCAGGAGCACCACAGGAGCACCAGGAGCACCAGGAGCACCAGGAGCACCAGGAGCAGGAGCA

201 Y S G I N I T K E G I Q I G V E G Q T P
601 TATTCTGGTATAAATATTACAAAGGAGGGTATTCAAATAGGTGTGCAAGGTCAAACACCT

221 K Y A D K T F Q P E P Q I G E S Q W Y E
661 AAATATGCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAA

241 T E I N H A A G R V L K K T T P M K P C
721 ACAGAAATTAATCATGCAGCTGGGAGAGTCCTAAAAAGACTACCCCAATGAAACCATGT

261 Y G S Y A K P T N E N G G Q G I L V K Q
781 TACGGTTCATATGCAAAACCCACAAATGAAAATGGAGGGCAAGGCATTCTTGTAAGCAA

281 Q N G K L E S Q V E M Q F F S T T E A A
841 CAAAATGGAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACTACTGAGGCAGCC

301 A G N G D N L T P K V V L Y S E D V D I
901 GCAGGCAATGGTGATAACTTGACTCTAAAGTGGTATTGTACAGTGAAGATGTAGATATA

321 E T P D T H I S Y M P T I K E G N S R E
961 GAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACACAGAGAA

341 L M G Q Q S M P N R P N Y I A F R D N F
1021 CTAATGGGCCAACAACTCTATGCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTT

361 I G L M Y Y N S T G N M G V L A G Q A S
1081 ATTGGTCTAATGTATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAGCATCG

381 Q L N A V V D L Q D R N T E L S Y Q L L
1141 CAGTTGAATGCTGTTGTAGATTGCAAGACAGAAACAGAGCTTTCATACCAGCTTTTG

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Fig. 17

401 L D S I G D R T R Y F S M W N Q L P N Y
 1201 CTTGATTCCATTGGTGATAGAACAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTAC

 421 C F P L G G V I N T E T L T K V K P K T
 1261 TGCTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAAACCTAAAAACA

 441 G O E N G W E K D A T E F S D K N E I R
 1321 GGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAATGAAATAAGA

 461 V G N N F A M E I N L N A N L W R N F L
 1381 GTTGGAAATAATTTTGGCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTCTG

 481 Y S N I A L Y L P D K L K Y S P S N V K
 1441 TACTCCAACATAGCGCTGTATTGCCCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAA

 501 I S D N P N T Y D Y M N K R V V A P G L
 1501 ATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCAGTGGTGGCTCCCGGGCTA

 521 V D C Y I N L G A R W S L D Y M D N V N
 1561 GTGGAAGTGTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAAC

 541 P F N H H R N A G L R Y R S M L L G N G
 1621 CCATTTAACCACCACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGT

 561 R Y V P F H I Q V P Q K F F A I K N L L
 1681 CGCTATGTGCCCTTCCACATCCAGGTGCCTCAGAAGTCTTTGCCATTAACCAACCTCCTT

 581 L L P G S Y T Y E W N F R K D V N M V L
 1741 CTCCTGCCGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTCTCTG

 601 Q S S L G N D L R V D G A S I K F D S I
 1801 CAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATT

 621 C L Y A T F F P M A H N T A S T L E A M
 1861 TGCTTTACGCCACCTTCTTCCCATGGCCCAACACCCGCTCCACGCTTGAGGCCATG

 641 L R N D T N D Q S F N D Y L S A A N M L
 1921 CTTAGAAACGACACCAACGACAGTCCTTTAAGCACTATCTCTCGCCGCCAACATGCTC

 661 Y P I P A N A T N V P I S I P S R N W A
 1981 TACCTATACCCGCCAACGCTACCAACGTGCCATATCCATCCCCTCCCGCAACTGGGCG

 681 A F R G W A F T R L K T K E T P S L G S
 2041 GCTTTCGCGGCTGGGCCCTTACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCG

 701 G Y D P Y Y T Y S G S I P Y L D G T F Y
 2101 GGCTACGACCTTATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTAC

 721 L N H T F K K V A I T F D S S V S W P G
 2161 CTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTGAGCTGGCCTGGC

 741 N D R L L T P N E F E I K R S V D G E G
 2221 AATGACCGCCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGT

 761 Y N V A O C N M T K D W F L V O M L A N
 2281 TACAACGTTGCCAGTGTAACATGACCAAAGACTGGTTCTGGTACAAATGCTAGCTAAC

 781 Y N I G Y Q G F Y I P E S Y K D R M Y S
 2341 TATAACATTGGCTACCAAGGCTTCTATATCCCAGAGAGCTACAAGGACCGCATGTAAGTCC

 801 F F R N F Q P M S R Q V V D D T K Y K D
 2401 TTCITTAGAAACTTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGAC

Fig. 17

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821 Y Q Q V G I L H Q H N N S G F V G Y L A
2461 TACCAACAGGTGGGCATCCTACACCAACACAACAACTCTGGATTGTTGGCTACCTTGCC

841 P T M R E G Q A Y P A N F P Y P L I G K
2521 CCCACCATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATAGGCAAG

861 T A V D S I T Q K K F L C D R T L W R I
2581 ACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATC

881 P F S S N F M S M G A L T D L G Q N L L
2641 CCATTCTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTC

901 Y A N S A H A L D M T F E V D P M D E P
2701 TACGCCAACTCGGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCC

921 T L L Y V L F E V F D V V R V H Q P H R
2761 ACCCTTCTTTATGTTTGTGTTGAAGTCTTTGACGTGGTCCGTGTGCACGACCGCACCGC

941 G V I E T V Y L R T P F S A G N A T T -
2821 GCGGTCATCGAAACCGGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACACATAA

```

Fig. 17

Hexon sequence of (QGPGAP)₁₁-HVR1 adenovirus SEQ IDNOS : 10 and 38

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121  CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181  TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241  AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGGCTTCACGTAC

101  F D I R G V L D R G P T F K P Y S G T A
301  TTTGACATCCGCGGCGTGGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121  Y N A L A P K G A P N P C E W D E Q G P
361  TACAACGCCCTGGCTCCCAAGGGTGCCCAAAATCCTTGCGAATGGGATGAACAGGGACCA

141  G A P Q G P G A P Q G P G A P Q G P G A
421  GGAGCACCACAGGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCA

161  P Q G P G A P Q G P G A P Q G P G A P Q
481  CCACAGGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCA

181  G P G A P Q G P G A P Q G P G A P Q G P
541  GGACCAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGACCA

201  G A P K T H V F G Q A P Y S G I N I T K
601  GGAGCACCAAAAACTACGTATTTGGGCAGGCGCCTTATTCTGGTATAAATATTACAAAG

221  E G I Q I G V E G Q T P K Y A D K T F Q
661  GAGGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATATGCCGATAAAACATTTCAA

241  P E P Q I G E S Q W Y E T E I N H A A G
721  CCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGGTGGG

261  R V L K K T T P M K P C Y G S Y A K P T
781  AGAGTCCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACA

281  N E N G G Q G I L V K Q Q N G K L E S Q
841  AATGAAAATGGAGGCAAGGCATTCTTGTAAGCAACAAAATGGAAAGCTAGAAAGTCAA

301  V E M Q F F S T T E A A A G N G D N L T
901  GTGGAATGCAATTTTCTCACTACTGAGGCAGCCGAGGCAATGGTGATAACTTGACT

321  P K V V L Y S E D V D I E T P D T H I S
961  CCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCT

341  Y M P T I K E G N S R E L M G Q Q S M P
1021  TACATGCCCACTATTAAGGAAGGTAACACGAGAACTAATGGGCAACAATCTATGCC

361  N R P N Y I A F R D N F I G L M Y Y N S
1081  AACAGGCCTAATTACATTGCTTTTAGGGACAATTTTATTGGTCTAATGTATTACAACAGC

381  T G N M G V L A G Q A S Q L N A V V D L
1141  ACGGGTAATATGGGTGTTCTGGCGGGCAAGCATCGCAGTTGAATGCTGTGTAGATTGG

```

Fig. 18

401 Q D R N T E L S Y Q L L L D S I G D R T
 1201 CAAGACAGAAACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATTGGTGATAGAACC

 421 R Y F S M W N Q L P N Y C F P L G G V I
 1261 AGGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTTCCACTGGGAGGTGTGATT

 441 N T E T L T K V K P K T G O E N G W E K
 1321 AATACAGAGACTCTTACCAAGGTAAACCTAAACACAGGTCAGGAAATGGATGGGAAAAA

 461 D A T E F S D K N E I R V G N N F A M E
 1381 GATGCTACAGAATTTTCAGATAAAAAATGAAATAAGAGTTGGAAATAATTTTGCCATGGAA

 481 I N L N A N L W R N F L Y S N I A L Y L
 1441 ATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTTG

 501 P D K L K Y S P S N V K I S D N P N T Y
 1501 CCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTAC

 521 D Y M N K R V V A P G L V D C Y I N L G
 1561 GACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACTTGGAA

 541 A R W S L D Y M D N V N P F N H H R N A
 1621 GCACGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTTAACGACCCCGCAATGCT

 561 G L R Y R S M L L G N G R Y V P F H I Q
 1681 GGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTGGCTATGTGCCCTTCCACATCCAG

 581 V P Q K F F A I K N L L L L P G S Y T Y
 1741 GTGCCTCAGAAGTTCTTTGCCATTAACCTCCTTCTCCTGCCGGGCTCATACACCTAC

 601 E W N F R K D V N M V L Q S S L G N D L
 1801 GAGTGAACCTTCAGGAAGGATGTTAATCATGGTTCTGCAGAGCTCCCTAGGAAATGACCTA

 621 R V D G A S I K F D S I C L Y A T F F P
 1861 AGGGTTGACGGAGCCAGCATTAAGTTTGATAGCATTGCGCTTACGCCACCTTCTTCCCC

 641 M A H N T A S T L E A M L R N D T N D Q
 1921 ATGGCCACACACCGCCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAACGACCATG

 661 S F N D Y L S A A N M L Y P I P A N A T
 1981 TCCTTTAAGCACTATCTCTCGCCGCGCAACATGCTCTACCTATACCGGCAACGCTACC

 681 N V P I S I P S R N W A A F R G W A F T
 2041 AACGTGCCATATCCATCCCCTCCGCAACTGGGCGGCTTTCCGCGGCTGGGCTTCACG

 701 R L K T K E T P S L G S G Y D P Y Y T Y
 2101 CGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCTTATTACACCTAC

 721 S G S I P Y L D G T F Y L N H T F K K V
 2161 TCTGGCTCTATACCTACCTAGATGGAACCTTTACCTCAACCACACCTTTAAGAAGGTG

 741 A I T F D S S V S W P G N D R L L T P N
 2221 GCCATTACCTTTGACTCTTCTGTGCTAGCTGGCCTGGCAATGACCGCCTGCTTACCCCAAC

 761 E F E I K R S V D G E G Y N V A Q C N M
 2281 GAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATG

 781 T K D W F L V Q M L A N Y N I G Y Q G F
 2341 ACCAAAGACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACCGGGCTTC

 801 Y I P E S Y K D R M Y S F F R N F O P M
 2401 TATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGCCCATG

Fig. 18

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821  S R Q V V D D T K Y K D Y Q Q V G I L H
2461 AGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATCCTACAC

841  Q H N N S G F V G Y L A P T M R E G Q A
2521 CAACACAACAACCTCTGGATTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCC

861  Y P A N F P Y P L I G K T A V D S I T Q
2581 TACCCTGCTAACTTCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAG

881  K K F L C D R T L W R I P F S S N F M S
2641 AAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTCTCCAGTAACTTTATGTCC

901  M G A L T D L G Q N L L Y A N S A H A L
2701 ATGGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCGGCCACGCGCTA

921  D M T F E V D P M D E P T L L Y V L F E
2761 GACATGACTTTTGAGGTGGATCCCATGGACGAGCCCACCTTCTTTATGTTTTGTTTGAA

941  V F D V V R V H Q P H R G V I E T V Y L
2821 GTCTTTGACGTGGTCCGTGTGCACCAGCCGACCGGGCGTCATCGAAACCGTGTACCTG

961  R T P F S A G N A T T -
2881 CGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

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Fig. 18

Hexon sequence of (QGPGAP)₁₂-HVR1 adenovirus SEQ IDNOs : 11 and 39

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGAGCTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGC

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAG

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121  Y N A L A P K G A P N P C E W D E Q G P
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAATCCTTGCGAATGGGATGAACAGGGACCA

141  G A P Q G P G A P Q G P G A P Q G P G A
421 GGAGCACCACAGGGACAGGAGCACCACAGGGACAGGAGCACCACAGGGACAGGAGCA

161  P Q G P G A P Q G P G A P Q G P G A P Q
481 CCACAGGGACAGGAGCACCACAGGGACAGGAGCACCACAGGGACAGGAGCACCACAG

181  G P G A P Q G P G A P Q G P G A P Q G P
541 GGACAGGAGCACCAGGTCCTGGTGCTCCTCAGGGACAGGAGCACCACAGGACCA

201  G A P Q G P G A P K T H V F G Q A P Y S
601 GGAGCACCACAGGGACAGGAGCACCACAACTACGATTTTGGGAGGCGCTTATTCT

221  G I N I T K E G I Q I G V E G Q T P K Y
661 GGTATAAATTACAAAGGAGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATAT

241  A D K T F Q P E P Q I G E S Q W Y E T E
721 GCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGATCTCAGTGGTACGAAACAGAA

261  I N H A A G R V L K K T T P M K P C Y G
781 ATTAATCATGCAGCTGGGAGAGTCCTAAAAAGACTACCCCAATGAAACCATGTTACGGT

281  S Y A K P T N E N G G Q G I L V K Q Q N
841 TCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATTCTGTAAAGCAACAAAT

301  G K L E S Q V E M Q F F S T T E A A A G
901 GGAAAGCTAGAAAGTCAAGTGGAATGCAATTTTCTCACTACTGAGGAGCCGACGGC

321  N G D N L T P K V V L Y S E D V D I E T
961 AATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACC

341  P D T H I S Y M P T I K E G N S R E L M
1021 CCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACACAGAGAACTAATG

361  G Q Q S M P N R P N Y I A F R D N F I G
1081 GGCCAACAATCTATGCCCAACAGGCTAATTACATTGCTTTAGGGACAATTTTATTGGT

381  L M Y Y N S T G N M G V L A G Q A S Q L
1141 CTAATGTATTACAACAGCAGGGTAATATGGGTGTTCTGGCGGGCAAGCATGCGAGTTG

```

Fig. 19

401 N A V V D L Q D R N T E L S Y Q L L L D
 1201 AATGCTGTTGTAGATTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGAT

 421 S I G D R T R Y F S M W N Q L P N Y C F
 1261 TCCATTGGTGATAGAACCAGGTACTTTTCTATGTGAATCAGCTTCCAAATTACTGCTT

 441 P L G G V I N T E T L T K V K P K T G Q
 1321 CCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAG

 461 E N G W E K D A T E F S D K N E I R V G
 1381 GAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAAATGAAATAAGAGTTGGA

 481 N N F A M E I N L N A N L W R N F L Y S
 1441 AATAATTTTGCCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCC

 501 N I A L Y L P D K L K Y S P S N V K I S
 1501 AACATAGCGCTGATTGCCCCAGACAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCT

 521 D N P N T Y D Y M N K R V V A P G L V D
 1561 GATAACCCAAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGCTAGTGGAC

 541 C Y I N L G A R W S L D Y M D N V N P F
 1621 TGCTACATTAACTTGGAGCAGCTGGTCCCTTGACTATATGGACAAGTCAACCCATT

 561 N H H R N A G L R Y R S M L L G N G R Y
 1681 AACCACCACCGCAATGCTGGCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTGGCTAT

 581 V P F H I Q V P Q K F F A I K N L L L L
 1741 GTGCCCTTCCACATCCAGGTGCCTCAGAAGTTCTTTGCCATTAACCACTCCTCTCCTG

 601 P G S Y T Y E W N F R K D V N M V L Q S
 1801 CCGGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGC

 621 S L G N D L R V D G A S I K F D S I C L
 1861 TCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTGATAGCATTGCTT

 641 Y A T F F P M A H N T A S T L E A M L R
 1921 TACGCCACCTTCTTCCCATGGCCACACACCGCCTCCACGCTTGAGGCCATGCTTAGA

 661 N D T N D Q S F N D Y L S A A N M L Y P
 1981 AACGACACCAACGACAGTCCTTTAACGACTATCTCTCCGCCCAACATGCTCTACCTT

 681 I P A N A T N V P I S I P S R N W A A F
 2041 ATACCCGCCAACGCTACCAACGTGCCATATCCATCCCCTCCCGCAACTGGGCGGCTTTC

 701 R G W A F T R L K T K E T P S L G S G Y
 2101 CGCGGCTGGGCTTACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTAC

 721 D P Y Y T Y S G S I P Y L D G T F Y L N
 2161 GACCCTTATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTACCTCAAC

 741 H T F K K V A I T F D S S V S W P G N D
 2221 CACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTGAGCTGGCCTGGCAATGAC

 761 R L L T P N E F E I K R S V D G E G Y N
 2281 CGCCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAAC

 781 V A Q C N M T K D W F L V Q M L A N Y N
 2341 GTTGCCAGTGTAACATGACCAAGACTGGTTCTGGTACAAATGCTAGCTAACTATAAC

 801 I G Y Q G F Y I P E S Y K D R M Y S F F
 2401 ATGGCTACCAAGGCTTCTATATCCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTT

Fig. 19

821 R N F Q P M S R Q V V D D T K Y K D Y Q
 2461 AGAAACTTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAA

 841 Q V G I L H Q H N N S G F V G Y L A P T
 2521 CAGGTGGGCATCCTACACCAACACAACAACTCTGGATTTGTTGGCTACCTTGCCCCCACC

 861 M R E G Q A Y P A N F P Y P L I G K T A
 2581 ATGCGCGAAGGACAGGCCTACCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCA

 881 V D S I T Q K K F L C D R T L W R I P F
 2641 GTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTC

 901 S S N F M S M G A L T D L G Q N L L Y A
 2701 TCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCC

 921 N S A H A L D M T F E V D P M D E P T L
 2761 AACTCCGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTT

 941 L Y V L F E V F D V V R V H Q P H R G V
 2821 CTTTATGTTTTGTTTGAAGTCTTTGACGTGGTCCGTGTGCACCAAGCCGACCGCGGCGTC

 961 I E T V Y L R T P F S A G N A T T -
 2881 ATCGAAACCGTGTAACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 19

Hexon sequence of (NANP)₄-HVR1 adenovirus SEQ IDNOS : 12 and 44

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1  M A T P S M M P O W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCAAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAATCCTTGCGAATGGGATGAAACGCTAAT

141 P N A N P N A N P N A N P K T H V F G Q
421 CCCAACGCTAACCCAAATGCAAATCCTAATGCCAACCCAAAACCTCACGTAATTTGGGCA

161 A P Y S G I N I T K E G I Q I G V E G Q
481 GCGCCTTATCTGTATATAATATTACAAAGGAGGGTATTCAAATAGGTGTGGAAGGTCAA

181 T P K Y A D K T F Q P E P Q I G E S Q W
541 ACACCTAAATATGCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGG

201 Y E T E I N H A A G R V L K K T T P M K
601 TACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCCTAAAAAGACTACCCCAATGAAA

221 P C Y G S Y A K P T N E N G G Q G I L V
661 CCATGTTACGGTTCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATTCTTGTA

241 K Q Q N G K L E S Q V E M Q F F S T T E
721 AAGCAACAAATGGAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCACTACTGAG

261 A A A G N G D N L T P K V V L Y S E D V
781 GCAGCCGACGCAATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTA

281 D I E T P D T H I S Y M P T I K E G N S
841 GATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACCA

301 R E L M G Q Q S M P N R P N Y I A F R D
901 CGAGAACTAATGGGCCAACAACTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGAC

321 N F I G L M Y Y N S T G N M G V L A G Q
961 AATTTTATTGGTCTAATGTATTACAACAGCACGGTAATATGGGTGTTCTGGCGGGCCAA

341 A S Q L N A V V D L Q D R N T E L S Y Q
1021 GCATCGCAGTTGAATGCTGTTGTAGATTTGCAAGACAGAAACACAGAGCTTTCATACCAG

361 L L L D S I G D R T R Y F S M W N Q A V
1081 CTTTGTCTTGATTCCATTGGTGATAGAACCAGGTACTTTCTATGTGGAATCAGGCTGTT

381 D S Y D P D V R I I E N H G T E D E L P
1141 GACAGCTATGATCCAGATGTTAGAATTATTGAAAATCATGGAACCTGAAGATGAACITCCA

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Fig. 20

401 N Y C F P L G G V I N T E T L T K V K P
 1201 AATTACTGCTTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCT

 421 K T G Q E N G W E K D A T E F S D K N E
 1261 AAAACAGGTGAGGAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAAATGAA

 441 I R V G N N F A M E I N L N A N L W R N
 1321 ATAAGAGTTGGAAATAATTTTGGCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAAT

 461 F L Y S N I A L Y L P D K L K Y S P S N
 1381 TTCCTGTACTCCAACATAGCGCTGTATTTGCCGACAAGCTAAAGTACAGTCCTTCCAAC

 481 V K I S D N P N T Y D Y M N K R V V A P
 1441 GTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCC

 501 G L V D C Y I N L G A R W S L D Y M D N
 1501 GGGCTAGTGGACTGCTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAAC

 521 V N P F N H H R N A G L R Y R S M L L G
 1561 GTCAACCCATTTAACCAACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGC

 541 N G R Y V P F H I Q V P Q K F F A I K N
 1621 AATGGTGGCTATGTGCCCTCCACATCCAGGTGCCTCAGAAGTCTTTGCCATAAAAAC

 561 L L L L P G S Y T Y E W N F R K D V N M
 1681 CTCCTTCTCCTGCCGGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATG

 581 V L Q S S L G N D L R V D G A S I K F D
 1741 GTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTGAT

 601 S I C L Y A T F F P M A H N T A S T L E
 1801 AGCATTTGCTTTACGCCACCTTCTTCCCATGGCCACAACACCGCTCCACGGCTTGA

 621 A M L R N D T N D Q S F N D Y L S A A N
 1861 GCCATGCTTAGAAACGACACCAACGACAGTCCTTTAACGACTATCTCTCCGCGCCAAC

 641 M L Y P I P A N A T N V P I S I P S R N
 1921 ATGCTCTACCTATACCGCCAACGCTACCAACGTGCCATATCCATCCCCTCCGCAAC

 661 W A A F R G W A F T R L K T K E T P S L
 1981 TGGGCGGCTTTCCGCGGCTGGGCCTTCACGCGCCTTAAGACTAAGGAAACCCATCACTG
 681 G S G Y D P Y Y T Y S G S I P Y L D G T
 2041 GGCTCGGGCTACGACCCCTTATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACC

 701 F Y L N H T F K K V A I T F D S S V S W
 2101 TTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTACGCTGG

 721 P G N D R L L T P N E F E I K R S V D G
 2161 CCTGGCAATGACCGCCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGG

 741 E G Y N V A Q C N M T K D W F L V Q M L
 2221 GAGGGTTACAACGTTGCCAGTGTAACATGACCAAAGACTGGTTCCTGGTACAAATGCTA

 761 A N Y N I G Y Q G F Y I P E S Y K D R M
 2281 GCTAACTATAACATTGGCTACCAGGGCTTCTATATCCCAGAGAGCTACAAGGACCGCATG

 781 Y S F F R N F Q P M S R Q V V D D T K Y
 2341 TACTCCTTCTTTAGAAACTTCCAGCCCATGAGCCGTGAGGTGGTGGATGATACTAAATAC

 801 K D Y Q Q V G I L H Q H N N S G F V G Y
 2401 AAGGACTACCAACAGGTGGGCATCCTACCAACACAACAACCTCTGGATTGTTGGCTAC

Fig. 20

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821  L A P T M R E G Q A Y P A N F P Y P L I
2461 CTTGCCCCACCATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATA

841  G K T A V D S I T Q K K F L C D R T L W
2521 GGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCITTGG

861  R I P F S S N F M S M G A L T D L G Q N
2581 CGCATCCCATTCTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAAAC

881  L L Y A N S A H A L D M T F E V D P M D
2641 CTTCTCTACGCCAACTCCGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGAC

901  E P T L L Y V L F E V F D V V R V H Q P
2701 GAGCCACCCCTTCTTTATGTTTTGTTTGAAGTCTTTGACGTGGTCCGTGTGCACACGCGG

921  H R G V I E T V Y L R T P F S A G N A T
2761 CACCGCGGGGTGCATCGAAACCGGTGTACCTGCGCAGGCCCTTCTCGGCCGGCAACGCCACA

941  T -
2821 ACATAA

```

Fig. 20

Hexon sequence of (NANP)₆-HVR1 adenovirus SEQ IDNOS : 13 and 45

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTCCCCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGTCCCAAGGGTCCCCAAATCCTTGCGAATGGGATGAAATGCAAAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAACGCGAACCCGAATGCTAAT

161 P K T H V F G Q A P Y S G I N I T K E G
481 CCTAAAACACAGTATTTGGGCAGGCGCCTTATTCTGGTATAAATATTACAAAGGAGGGT

181 I Q I G V E G Q T P K Y A D K T F Q P E
541 ATTCAAATAGGTGTCGAAGGTCAAACACCTAAATATGCCGATAAAACATTTCAACCTGAA

201 P Q I G E S Q W Y E T E I N H A A G R V
601 CCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTG

221 L K K T T P M K P C Y G S Y A K P T N E
661 CTA AAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAA

241 N G G Q G I L V K Q Q N G K L E S Q V E
721 AATGGAGGGCAAGGCATTCTTGTAAGCAACAAATGGAAAGCTAGAAAGTCAAGTGGAA

261 M Q F F S T T E A A A G N G D N L T P K
781 ATGCAATTTTCTCAACTACTGAGGCAGCCGAGGCAATGGTGATAACTTGACTCCTAAA

281 V V L Y S E D V D I E T P D T H I S Y M
841 GTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCTTACATG

301 P T I K E G N S R E L M G Q Q S M P N R
901 CCCACTATTAAGGAAGGTAACCTACGAGAACTAATGGGCCAACAACTATGCCCAACAGG

321 P N Y I A F R D N F I G L M Y Y N S T G
961 CCTAATTACATTGCTTTTAGGGACAATTTTATTGGTCTAATGTATTACAACAGCAGGGGT

341 N M G V L A G Q A S Q L N A V V D L Q D
1021 AATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTAGATTTGCAAGAC

361 R N T E L S Y Q L L L D S I G D R T R Y
1081 AGAAACACAGAGCTTTCATACGAGCTTTTGCTTGATTCCATTGGTGATAGAACCAGGTAC

381 F S M W N Q L P N Y C F P L G G V I N T
1141 TTTTCTATGTGAATCAGCTTCCAAATTACTGCTTCCACTGGGAGGTGTGATTAATACA

```

Fig. 21

401 E T L T K V K P K T G Q E N G W E K D A
 1201 GAGACTCTTACCAAGGTAAACCTAAAAACAGGTCAGGAAAATGGATGGGAAAAAGATGG

 421 T E F S D K N E I R V G N N F A M E I N
 1261 ACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAAATAATTTGCCATGGAAATCAAT

 441 L N A N L W R N F L Y S N I A L Y L P D
 1321 CTAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTGCCCGAC

 461 K L K Y S P S N V K I S D N P N T Y D Y
 1381 AAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTAC

 481 M N K R V V A P G L V D C Y I N L G A R
 1441 ATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACCTTGGAGCAGCG

 501 W S L D Y M D N V N P F N H H R N A G L
 1501 TGGTCCCTTGACTATATGGACAAGTCAACCCATTTAACCACCACCGCAATGCTGGCGCT

 521 R Y R S M L L G N G R Y V P F H I Q V P
 1561 CGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCT

 541 Q K F F A I K N L L L L P G S Y T Y E W
 1621 CAGAAGTTCTTTGCCATTAACCACTCTCTCTGCGGGGCTCATACACCTACGAGTGG

 561 N F R K D V N M V L Q S S L G N D L R V
 1681 AACTTCAGGAAGGATGTTAACATGGTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGT

 581 D G A S I K F D S I C L Y A T F F P M A
 1741 GACGGAGCCAGCATTAAAGTTTGATAGCATTGCTTTACGCCACCTTCTTCCCATGGCC

 601 H N T A S T L E A M L R N D T N D Q S F
 1801 CACAACACCGCCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAACGACCAGTCCTTT

 621 N D Y L S A A N M L Y P I P A N A T N V
 1861 AACGACTATCTCTCCGCCGCCAACATGCTCTACCTATACCCGCCAACGCTACCAACGTG

 641 P I S I P S R N W A A F R G W A F T R L
 1921 CCCATATCCATCCCCTCCGCAACTGGCGGCTTCCGCGGCTGGGCTTACGCGGCTT

 661 K T K E T P S L G S G Y D P Y Y T Y S G
 1981 AAGACTAAGGAAACCCCATCACTGGGCTCGGGCTACGACCCTTATTACACCTACTCTGGC

 681 S I P Y L D G T F Y L N H T F K K V A I
 2041 TCTATACCTACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATT

 701 T F D S S V S W P G N D R L L T P N E F
 2101 ACCTTTGACTCTTCTGTGAGCTGGCCTGGCAATGACCGCTGCTTACCCCAACGAGTTT

 721 E I K R S V D G E G Y N V A Q C N M T K
 2161 GAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAA

 741 D W F L V Q M L A N Y N I G Y Q G F Y I
 2221 GACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACCAGGGCTTCTATATC

 761 P E S Y K D R M Y S F F R N F Q P M S R
 2281 CCAGAGAGCTACAAGGACCGCATGTACTCTTCTTTAGAACTTCCAGCCCATGAGCCGT

 781 Q V V D D T K Y K D Y Q Q V G I L H Q H
 2341 CAGGTGGTGGATGATACTAAATAACAAGGACTACCAACAGGTGGGCATCCTACACCAACAC

 801 N N S G F V G Y L A P T M R E G Q A Y P
 2401 AACAACTCTGGATTTGTTGGCTACCTTGGCCCCACCATGCGCGAAGGACAGGCTACCTC

Fig. 21

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821  A N F P Y P L I G K T A V D S I T Q K K
2461 GCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAG

841  F L C D R T L W R I P F S S N F M S M G
2521 TTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTCAGTAACCTTTATGTCCATGGGC

861  A L T D L G Q N L L Y A N S A H A L D M
2581 GCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCCGCCACGCGCTAGACATG

881  T F E V D P M D E P T L L Y V L F E V F
2641 ACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTTATGTTTTGTTGAAGTCTTT

901  D V V R V H Q P H R G V I E T V Y L R T
2701 GACGTGGTCCGTGTGCACCGCCGACCGCGGCGTCATCGAAACCGTGTACCTGCGCAGG

921  P F S A G N A T T -
2761 CCCTTCTCGGCCGGCAACGCCACAACATAA

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Fig. 21

Hexon sequence of (NANP)₈-HVR1 adenovirus SEQ IDNOS : 14 and 46

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1  M A T P S M M P Q W S Y M H I S G O D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGGC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCGAGCGTTTGACGCTGCGGTTTATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101  F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121  Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGCCCCAAATCCTTGCGAATGGGATGAAATGCAAAI

141  P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAACGCCGAACCGGAATGCTAAT

161  P N A N P N A N P K T H V F G Q A P Y S
481 CCTAATGCAAAATCCAAATGCAAAATCCAAAACACTACGTATTTGGGCAGGCGCTTATTCT

181  G I N I T K E G I O I G V E G O T P K Y
541 GGTATAAATATTACAAAGGAGGGTATTCAAATAGGTGTGCAAGGTCAAACACCTAAATAT

201  A D K T F Q P E P Q I G E S Q W Y E T E
601 GCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAA

221  I N H A A G R V L K K T T P M K P C Y G
661 ATTAATCATGAGCTGGGAGAGTCTAAAAAGACTACCCCAATGAAACCATGTTACGGT

241  S Y A K P T N E N G G Q G I L V K Q Q N
721 TCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATCTTGTAAGCAACAAAAT

261  G K L E S Q V E M Q F F S T T E A A A G
781 GGAAAGCTAGAAAGTCAAGTGAAATGCAATTTTCTCAACTACTGAGGCAGCCGACGGC

281  N G D N L T P K V V L Y S E D V D I E T
841 AATGGTGATAACTTGACTCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACC

301  P D T H I S Y M P T I K E G N S R E L M
901 CCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACCTACGAGAACTAATG

321  G Q Q S M P N R P N Y I A F R D N F I G
961 GGCCAACAATCTATGCCCAACAGGCTAATTACATTGCTTTTAGGGACAATTTTATTGGT

341  L M Y Y N S T G N M G V L A G O A S O L
1021 CTAATGTATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTG

361  N A V V D L Q D R N T E L S Y Q L L L D
1081 AATGCTGTGTAGATTTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGAT

381  S I G D R T R Y F S M W N Q L P N Y C F
1141 TCCATTGGTGATAGAACAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTT

```

Fig. 22

401 P L G G V I N T E T L T K V K P K T G Q
 1201 CCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAAACCTAAAACAGGTCAG

 421 E N G W E K D A T E F S D K N E I R V G
 1261 GAAAATGGATGGGAAAAAGATGCTACAGAAATTTTCAGATAAAAATGAAATAAGAGTTGGA

 441 N N F A M E I N L N A N L W R N F L Y S
 1321 AATAATTTTGCCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCC

 461 N I A L Y L P D K L K Y S P S N V K I S
 1381 AACATAGCGCTGTATTTGCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCT

 481 D N P N T Y D Y M N K R V V A P G L V D
 1441 GATAACCCAAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGAG

 501 C Y I N L G A R W S L D Y M D N V N P F
 1501 TGCTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATT

 521 N H H R N A G L R Y R S M L L G N G R Y
 1561 AACCAACACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTCGTAT

 541 V P F H I Q V P Q K F F A I K N L L L L
 1621 GTGCCCTTCCACATCCAGGTGCTCAGAAGTTCTTTGCCATTAAAAACCTCCTTCTCCTG

 561 P G S Y T Y E W N F R K D V N M V L Q S
 1681 CCGGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGC

 581 S L G N D L R V D G A S I K F D S I C L
 1741 TCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATTTCCTT

 601 Y A T F F P M A H N T A S T L E A M L R
 1801 TACGCCACCTTCTTCCCATGGCCACAACACCGCCTCCACGCTTGAGGGCATGCTTAGA

 621 N D T N D Q S F N D Y L S A A N M L Y P
 1861 AACGACACCAACGACAGTCCTTTAAGACTATCTCTCCGCCGCAACATGCTCTACCTT

 641 I P A N A T N V P I S I P S R N W A A F
 1921 ATACCCGCCAACGCTACCAACGTGCCATATCCATCCCCTCCGCAACTGGGGGGTTTC

 661 R G W A F T R L K T K E T P S L G S G Y
 1981 CGCGGCTGGGCCTTACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTAC

 681 D P Y Y T Y S G S I P Y L D G T F Y L N
 2041 GACCCTTATTACACCTACTCTGGCTCTATACCTACCTAGATGGAACCTTTTACCTCAAC

 701 H T F K K V A I T F D S S V S W P G N D
 2101 CACACCTTTAAGAAGGTGCCATTACCTTTGACTCTTCTGTCAGCTGGCCTGGCAATGAC

 721 R L L T P N E F E I K R S V D G E G Y N
 2161 CGCCTGCTTACCCCAACGAGTTTGAATAAAGCGCTCAGTTGACGGGGAGGGTTACAAC

 741 V A Q C N M T K D W F L V Q M L A N Y N
 2221 GTTGCCCAAGTGAACATGACCAAGACTGGTTCTGGTACAAATGCTAGCTAACTATAAC

 761 I G Y Q G F Y I P E S Y K D R M Y S F F
 2281 ATTGGCTACCAAGGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTT

 781 R N F Q P M S R Q V V D D T K Y K D Y Q
 2341 AGAAACTTCCAGCCCATGAGCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAA

 801 Q V G I L H Q H N N S G F V G Y L A P T
 2401 CAGGTGGGCATCCTACACCAACACAACAACCTCTGGATTGTTGGCTACCTTGGCCCCACC

Fig. 22

821 M R E G Q A Y P A N F P Y P L I G K T A
 2461 ATGCGCGAAGGACAGGCCTACCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCA

 841 V D S I T Q K K F L C D R T L W R I P F
 2521 GTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTC

 861 S S N F M S M G A L T D L G O N L L Y A
 2581 TCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCC

 881 N S A H A L D M T F E V D P M D E P T L
 2641 AACTCCGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTT

 901 L Y V L F E V F D V V R V H O P H R G V
 2701 CTTTATGTTTTGTTGAAGTCTTTGACGTGGTCCGTGTGCACCAGCCGACCCGGCGGTC

 921 I E T V Y L R T P F S A G N A T T -
 2761 ATCGAAACCGGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 22

Hexon sequence of (NANP)₁₀-HVR1 adenovirus SEQ IDNOS : 15 and 47

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCGAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAAGCCCTGGCTCCCAAGGGTGCCCAATCCTTGCGAATGGGATGAAATGCAAAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAACGCGAACCGGAATGCTAAT

161 P N A N P N A N P N A N P N A N P K T H
481 CCTAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATCTCAC

181 V F G Q A P Y S G I N I T K E G I Q I G
541 GTATTGGGCGAGGCGCTTATTCTGGTATAAATATTACAAAGGAGGGTATTCAAATAGGT

201 V E G Q T P K Y A D K T F Q P E P Q I G
601 GTCGAAGGTCAAACACCTAAATATGCCGATAAAACATTCAACCTGAACCTCAAATAGGA

221 E S Q W Y E T E I N H A A G R V L K K T
661 GAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCTAAAAAGACT

241 T P M K P C Y G S Y A K P T N E N G G Q
721 ACCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAAATGGAGGGCAA

261 G I L V K Q Q N G K L E S Q V E M Q F F
781 GGCATTCTGTAAAGCAACAAATGGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTTC

281 S T T E A A A G N G D N L T P K V V L Y
841 TCACTACTGAGGCGAGCGCAGGCAATGGTGATACTTGACTCTAAAGTGGTATTGTAC

301 S E D V D I E T P D T H I S Y M P T I K
901 AGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAAG

321 E G N S R E L M G Q Q S M P N R P N Y I
961 GAAGGTAACCTACGAGAACTAATGGGCCAACAATCTATGCCCAACAGGCCTAATTACATT

341 A F R D N F I G L M Y Y N S T G N M G V
1021 GCTTTTAGGGACAATTTTATTGGTCTAATGTATTACAACAGCACGGGTAATATGGGTGTT

361 L A G Q A S Q L N A V V D L Q D R N T E
1081 CTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTAGATTGCAAGACAGAAACACAGAG

381 L S Y Q L L L D S I G D R T R Y F S M W
1141 CTTTCATACCAGCTTTTGTGTTGATTCCATTGGTGATAGAACCAGGTACTTTTCTATGTGG

```

Fig. 23

401 N Q L P N Y C F P L G G V I N T E T L T
 1201 AATCAGCTTCCAAATTACTGCTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACC

 421 K V K P K T G O E N G W E K D A T E F S
 1261 AAGGTAAACCTAAACAGGTCAGGAAATGGATGGGAAAAAGATGCTACAGAATTTTCA

 441 D K N E I R V G N N F A M E I N L N A N
 1321 GATAAAATGAAATAAGAGTTGGAAATAATTTGCCATGGAAATCAATCTAAATGCCAAC

 461 L W R N F L Y S N I A L Y L P D K L K Y
 1381 CTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTTGCCGACAAGCTAAAGTAC

 481 S P S N V K I S D N P N T Y D Y M N K R
 1441 AGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCGA

 501 V V A P G L V D C Y I N L G A R W S L D
 1501 GTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACTTGGAGCACGCTGGTCCCTTGAC

 521 Y M D N V N P F N H H R N A G L R Y R S
 1561 TATATGGACAACGTCAACCCATTTAACCACCACCGCAATGCTGGCCTGCGCTACCGCTCA

 541 M L L G N G R Y V P F H I Q V P Q K F F
 1621 ATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCTCAGAGTTCTTT

 561 A I K N L L L L P G S Y T Y E W N F R K
 1681 GCCATTAACCTCCTTCTCCTGCGGGCTCATACACCTACGAGTGGAACTTCAGGAAG

 581 D V N M V L Q S S L G N D L R V D G A S
 1741 GATGTTAACATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGC

 601 I K F D S I C L Y A T F F P M A H N T A
 1801 ATTAAGTTGATAGCATTTGCCTTTACGCCACCTTCTTCCCATGGCCACAACACCGGC

 621 S T L E A M L R N D T N D Q S F N D Y L
 1861 TCCAGCCTTGAGGCCATGCTTAGAAACGACACCAACGACCACTTAAAGACTATCTC

 641 S A A N M L Y P I P A N A T N V P I S I
 1921 TCCGCCGCCAACATGCTCTACCTATACCCGCCAACGCTACCAACGTGCCATATCCATC

 661 P S R N W A A F R G W A F T R L K T K E
 1981 CCCTCCGCAACTGGGCGGCTTTCCGCGGCTGGGCTTACGCGCCTTAAGACTAAGGAA

 681 T P S L G S G Y D P Y Y T Y S G S I P Y
 2041 ACCCATCACTGGGCTCGGGCTACGACCTTATTACACCTACTCTGGCTCTATACCCTAC

 701 L D G T F Y L N H T F K K V A I T F D S
 2101 CTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCT

 721 S V S W P G N D R L L T P N E F E I K R
 2161 TCTGTCAGCTGGCCTGGCAATGACCGCTGCTTACCCCCAACGAGTTTGAATTAAGCGC

 741 S V D G E G Y N V A Q C N M T K D W F L
 2221 TCAGTTGACGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAAGACTGGTTCCTG

 761 V Q M L A N Y N I G Y Q G F Y I P E S Y
 2281 GTACAAATGCTAGCTAACTATAACATTGGCTACCGGGCTTCTATATCCAGAGAGCTAC

 781 K D R M Y S F F R N F Q P M S R Q V V D
 2341 AAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGCCCATGAGCCGTGAGGTGGTGGAT

 801 D T K Y K D Y Q Q V G I L H Q H N N S G
 2401 GATACTAAATACAAGGACTACCAACAGGTGGGCATCCTACACCAACACAACCTCTGGA

Fig. 23

821 F V G Y L A P T M R E G Q A Y P A N F P
2461 TTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCTACCTGCTAACTTCCC
841 Y P L I G K T A V D S I T Q K K F L C D
2521 TATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGGGAT
861 R T L W R I P F S S N F M S M G A L T D
2581 CGCACCCCTTTGGCGCATCCATTCTCCAGTAACTTTATGTCCATGGGCGCACTCACAGAC
881 L G Q N L L Y A N S A H A L D M T F E V
2641 CTGGGCCAAAACCTTCTCTACGCCAACTCGGCCACGCGCTAGACATGACTTTTGAGGTG
901 D P M D E P T L L Y V L F E V F D V V R
2701 GATCCCATGGACGAGCCACCCCTTCTTTATGTTTTGTTTGAAGTCTTTGACGTGGTCCGT
921 V H Q P H R G V I E T V Y L R T P F S A
2761 GTGCACCAGCCGACCGCGGCGTCATCGAAACCGTGTACCTGCGCACGCCCTTCTCGGCC
941 G N A T T -
2821 GGCAACGCCACAACATAA

Fig. 23

Hexon sequence of (NANP)₁₂-HVR1 adenovirus SEQ IDNOS : 16 and 48

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCGGGCTGGTGCAGTTTGCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTGACATCCGCGCGTGTGACAGGGGCCCTACTTTAAGCCCTACTCTGGCAGTGGC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAAGCCCTGGCTCCCAAGGGTGGCCCAATCCTTGCGAATGGGATGAAATGCAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAATGCAATCCAAATGCAATCCAAATGCAATCCAAATGCAATCCAAATGCAAT

161 P N A N P N A N P N A N P N A N P N A N
481 CCAATGCAATCCAAATGCAATCCAAACGCGAACCAGTGAATCCTAATGCAAT

181 P N A N P K T H V F G Q A P Y S G I N I
541 CCAATGCAATCCAAAACTCAGTATTTGGGCGGGCCTATTCTGGTATAAATAT

201 T K E G I Q I G V E G Q T P K Y A D K T
601 ACAAAGGAGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATATGCCGATAAAAC

221 F Q P E P Q I G E S Q W Y E T E I N H A
661 TTCAACCTGAACCTCAAATAGGAGAACTCAGTGGTACGAAACAGAAATTAATCATGCA

241 A G R V L K K T T P M K P C Y G S Y A K
721 GCTGGGAGAGTCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAA

261 P T N E N G G Q G I L V K Q Q N G K L E
781 CCCACAAATGAAATGGAGGGCAAGGCATTCTGTAAAGCAACAAATGGAAAGCTAGAA

281 S Q V E M Q F F S T T E A A A G N G D N
841 AGTCAAGTGGAATGCAATTTTCTCAACTACTGAGGCAGCCGAGGCAATGGTGATAAC

301 L T P K V V L Y S E D V D I E T P D T H
901 TTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCAT

321 I S Y M P T I K E G N S R E L M G Q Q S
961 ATTTCTTACATGCCACTATTAAGGAAGGTAACACAGAGAACTAATGGGCCAACAACTCT

341 M P N R P N Y I A F R D N F I G L M Y Y
1021 ATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTATTGGTCTAATGTATTAC

361 N S T G N M G V L A G Q A S Q L N A V V
1081 AACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTA

381 D L Q D R N T E L S Y Q L L L D S I G D
1141 GATTTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATTGGTGAT

```

Fig. 24

401 R T R Y F S M W N Q L P N Y C F P L G G
 1201 AGAACCAGGTACTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTTCCACTGGGAGGT

 421 V I N T E T L T K V K P K T G Q E N G W
 1261 GTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAATGGATGG

 441 E K D A T E F S D K N E I R V G N N F A
 1321 GAAAAAGATGCTACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAAATAATTTTGCC

 461 M E I N L N A N L W R N F L Y S N I A L
 1381 ATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTG

 481 Y L P D K L K Y S P S N V K I S D N P N
 1441 TATTTGCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAAC

 501 T Y D Y M N K R V V A P G L V D C Y I N
 1501 ACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAAC

 521 L G A R W S L D Y M D N V N P F N H H R
 1561 CTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTTAACCACCCACCGC

 541 N A G L R Y R S M L L G N G R Y V P F H
 1621 AATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCGAC

 561 I Q V P Q K F F A I K N L L L L P G S Y
 1681 ATCCAGGTGCCTCAGAAGTTCTTTGCCATTAACCTCCTTCTCCTGCCGGGCTCATAC

 581 T Y E W N F R K D V N M V L Q S S L G N
 1741 ACCTACGAGTGGAACTTCAGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTAGGAAAT

 601 D L R V D G A S I K F D S I C L Y A T F
 1801 GACCTAAGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATTGCTTTACGCCACCTTC

 621 F P M A H N T A S T L E A M L R N D T N
 1861 TTCCCATGGCCACACACCGCCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAAC

 641 D Q S F N D Y L S A A N M L Y P I P A N
 1921 GACCAGTCCTTTAACGACTATCTCTCGCCGCCAACATGCTCTACCTATACCCGCCAAC

 661 A T N V P I S I P S R N W A A F R G W A
 1981 GCTACCAACGTGCCATATCCATCCCTCCCGCAACTGGCGGGCTTCCGCGGCTGGGCG

 681 F T R L K T K E T P S L G S G Y D P Y Y
 2041 TTCACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCCTTATTAC

 701 T Y S G S I P Y L D G T F Y L N H T F K
 2101 ACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAG

 721 K V A I T F D S S V S W P G N D R L L T
 2161 AAGGTGGCATTACCTTTGACTCTTCTGTGAGCTGGCTGGCAATGACCGCCTGCTTACC

 741 P N E F E I K R S V D G E G Y N V A Q C
 2221 CCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGT

 761 N M T K D W F L V Q M L A N Y N I G Y Q
 2281 AACATGACCAAAGACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACCAG

 781 G F Y I P E S Y K D R M Y S F F R N F Q
 2341 GGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAG

 801 P M S R O V V D D T K Y K D Y Q Q V G I
 2401 CCCATGAGCCGTGAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATC

Fig. 24

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821 L H Q H N N S G F V G Y L A P T M R E G
2461 CTACACCAACACAACAACTCTGGATTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGA

841 Q A Y P A N F P Y P L I G K T A V D S I
2521 CAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATT

861 T Q K K F L C D R T L W R I P F S S N F
2581 ACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTTCTCCAGTAACTTT

881 M S M G A L T D L G Q N L L Y A N S A H
2641 ATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTAGGCCAACTCCGCCAC

901 A L D M T F E V D P M D E P T L L Y V L
2701 GCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTTATGTTTGG

921 F E V F D V V R V H Q P H R G V I E T V
2761 TTTGAAGTCTTTGACGTGGTCCGTGTGCACCGCCGACCGGGCGGTGCATCGAAAACCGTG

941 Y L R T P F S A G N A T T -
2821 TACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

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Fig. 24

Hexon sequence of (NANP)₁₄-HVR1 adenovirus SEQ IDNOS : 17 and 49

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTCCCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCTGCTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGCCCCAAATCCTTGCGAATGGGATGAAAATGCAAAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

161 P N A N P N A N P N A N P N A N P N A N
481 CCAAATGCAAAATCCAAATGCAAAATCCAAACGCGAAGCCGAATGCTAATCCTAATGCAAAAT

181 P N A N P N A N P N A N P N A N P K T H V F G Q
541 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATGCAAAATGCAAAATGCAAAAT

201 A P Y S G I N I T K E G I Q I G V E G Q
601 GCGCCTTATTCTGGTATAAATATTACAAAGGAGGGTATTCAAATAGGTGTCGAAGGTCAA

221 T P K Y A D K T F Q P E P Q I G E S Q W
661 ACACCTAAATATGCCGATAAAACATTTCACCTGAACCTCAAATAGGAGAATCTCAGTGG

241 Y E T E I N H A A G R V L K K T T P M K
721 TACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCTAAAAAAGACTACCCCAATGAAA

261 P C Y G S Y A K P T N E N G G Q G I L V
781 CCATGTTACGGTTCATATGCAAAACCCACAAATGAAAATGGAGGGCAAGGCATTCTTGTA

281 K Q Q N G K L E S Q V E M Q F F S T T E
841 AAGCAACAAAATGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACTACTGAG

301 A A A G N G D N L T P K V V L Y S E D V
901 GCAGCCGCAGGCAATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTA

321 D I E T P D T H I S Y M P T I K E G N S
961 GATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAAGTCA

341 R E L M G Q Q S M P N R P N Y I A F R D
1021 CGAGAACTAATGGGCCAACAAATCTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGAC

361 N F I G L M Y Y N S T G N M G V L A G Q
1081 AATTTTATTGGTCTAATGTATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAA

381 A S Q L N A V V D L Q D R N T E L S Y Q
1141 GCATCGCAGTTGAATGCTGTTGTAGATTGCAAGACAGAAACAGAGCTTTCATACCGA

```

Fig. 25

401 L L L D S I G D R T R Y F S M W N Q L P
 1201 CTTTGGCTTGATTCCATTGGTGATAGAACAGGTACTTTTCTATGTGGAATCAGCTTCCA

 421 N Y C F P L G G V I N T E T L T K V K P
 1261 AATTACTGCTTTCCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCT

 441 K T G Q E N G W E K D A T E F S D K N E
 1321 AAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAAATGAA

 461 I R V G N N F A M E I N L N A N L W R N
 1381 ATAAGAGTTGGAAATAATTTTGGCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAAT

 481 F L Y S N I A L Y L P D K L K Y S P S N
 1441 TTCTGTACTCCAACATAGCGCTGTATTGCCCCGACAAGCTAAAGTACAGTCCTTCCAAC

 501 V K I S D N P N T Y D Y M N K R V V A P
 1501 GTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCAGTGGTGGCTCC

 521 G L V D C Y I N L G A R W S L D Y M D N
 1561 GGGCTAGTGGACTGCTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAAC

 541 V N P F N H H R N A G L R Y R S M L L G
 1621 GTCAACCCATTTAACCACCACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGG

 561 N G R Y V P F H I Q V P Q K F F A I K N
 1681 AATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCTCAGAAGTTCTTTGCCATTAACAA

 581 L L L L P G S Y T Y E W N F R K D V N M
 1741 CTCCTTCTCCTGCCGGCTCATACACCTACGAGTGGAACTTCAGGAAGGATGTTAACATG

 601 V L Q S S L G N D L R V D G A S I K F D
 1801 GTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGT

 621 S I C L Y A T F F P M A H N T A S T L E
 1861 AGCATTTGCCTTTACGCCACCTTCTTCCCATGGCCACAACACCGCCTCCACGGCTTGA

 641 A M L R N D T N D Q S F N D Y L S A A N
 1921 GCCATGCTTAGAAACGACACCAACGACAGTCCTTTAACGACTATCTCTCGCCGCCAAC

 661 M L Y P I P A N A T N V P I S I P S R N
 1981 ATGCTCTACCTATACCCGCCAACGCTACCAACGTGCCATATCCATCCCTCCCGCAAC

 681 W A A F R G W A F T R L K T K E T P S L
 2041 TGGGCGGCTTCCGCGGCTGGGCTTACGCGCTTAAGACTAAGGAAACCCATCACTG

 701 G S G Y D P Y Y T Y S G S I P Y L D G T
 2101 GGCTCGGGCTACGACCCTTATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAAC

 721 F Y L N H T F K K V A I T F D S S V S W
 2161 TTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTACGCTG

 741 P G N D R L L T P N E F E I K R S V D G
 2221 CCTGGCAATGACCGCTGCTTACCCCAACGAGTTTGAATTAAGCGCTCAGTTGACGGG

 761 E G Y N V A Q C N M T K D W F L V Q M L
 2281 GAGGGTTACAACGTTGCCAGTGTAACATGACCAAAGACTGGTTCTGGTACAAATGCTA

 781 A N Y N I G Y Q G F Y I P E S Y K D R M
 2341 GCTAACTATAACATTGGCTACCAGGGCTTCTATATCCAGAGAGCTACAAGGACCGCATG

 801 Y S F F R N F Q P M S R Q V V D D T K Y
 2401 TACTCCTTCTTTAGAACTTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATAC

Fig. 25

821 K D Y Q Q V G I L H Q H N N S G F V G Y
2461 AAGGACTACCAACAGGTGGGCATCCTACACCAACACAACAACCTGGATTGTGGGTAC

841 L A P T M R E G Q A Y P A N F P Y P L I
2521 CTTGCCCCCACCATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATA

861 G K T A V D S I T Q K K F L C D R T L W
2581 GGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTGG

881 R I P F S S N F M S M G A L T D L G Q N
2641 CGCATCCCATTCTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAAC

901 L L Y A N S A H A L D M T F E V D P M D
2701 CTTCTCTACGCCAACTCCGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGAC

921 E P T L L Y V L F E V F D V V R V H Q P
2761 GAGCCCAACCCTCTTTATGTTTTGTTGAAGTCTTTGACGTGGTCCGTGTGCACACGCCG

941 H R G V I E T V Y L R T P F S A G N A T
2821 CACCGCGGCGTCATCGAAACCGTGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACA

961 T -
2881 ACATAA

Fig. 25

Hexon sequence of (NANP)₁₆-HVR1 adenovirus SEQ IDNOS : 18 and 50

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121  CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181  TCCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241  AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101  F D I R G V L D R G P T F K P Y S G T A
301  TTTGACATCCGCGGCTGCTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121  Y N A L A P K G A P N P C E W D E N A N
361  TACAACGCCCTGGCTCCCAAGGGTGCCTCAATCTTGCATGGGATGAAATGCAAAAT

141  P N A N P N A N P N A N P N A N P N A N
421  CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

161  P N A N P N A N P N A N P N A N P N A N
481  CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

181  P N A N P N A N P N A N P N A N P N A N
541  CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

201  P K T H V F G Q A P Y S G I N I T K E G
601  CCAAAAACACAGTATTTGGGCGGCGCTTATTCTGGTATAAATATTACAAAGGAGGGT

221  I Q I G V E G Q T P K Y A D K T F Q P E
661  ATTCAAATAGGTGCGAAGGTCAAACACCTAAATATGCCGATAAAACATTTCACCTGAA

241  P Q I G E S Q W Y E T E I N H A A G R V
721  CCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTC

261  L K K T T P M K P C Y G S Y A K P T N E
781  CTAAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAA

281  N G G Q G I L V K Q Q N G K L E S Q V E
841  AATGGAGGGCAAGGCATTCTTGTAAGCAACAAATGGAAAGCTAGAAAGTCAAGTGGAA

301  M Q F F S T T E A A A G N G D N L T P K
901  ATGCAATTTTCTCAACTACTGAGGCGCGCAGGCAATGGTGATAACTTGACTCCTAAA

321  V V L Y S E D V D I E T P D T H I S Y M
961  GTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACACTCATATTCTTACATG

341  P T I K E G N S R E L M G Q Q S M P N R
1021  CCCACTATTAAGGAAGGTAACACAGAGAACTAATGGGCAACAACTATGCCAACAGG

361  P N Y I A F R D N F I G L M Y Y N S T G
1081  CCTAATTACATTGCTTTTAGGGACAATTTATTGGTCTAATGTATTACAACAGCAGGGT

381  N M G V L A G Q A S Q L N A V V D L Q D
1141  AATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTAGATTGCAAGAC

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Fig. 26

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401 R N T E L S Y O L L L D S I G D R T R Y
1201 AGAAACACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATTGGTGATAGAACCAGGTAG

421 F S M W N O L P N Y C F P L G G V I N T
1261 TTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTCCACTGGGAGGTGTGATTAATACA

441 E T L T K V K P K T G Q E N G W E K D A
1321 GAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAATGGATGGGAAAAGATGCT

461 T E F S D K N E I R V G N N F A M E I N
1381 ACAGAATTTTCAGATAAAAAATGAAATAAGAGTTGGAAATAATTTGCCATGGAAATCAAT

481 L N A N L W R N F L Y S N I A L Y L P D
1441 CTAAATGCCAACCTGTGGAGAAATTCCTGTACTCCAACATAGCGCTGTATTTGCCCGAC

501 K L K Y S P S N V K I S D N P N T Y D Y
1501 AAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTGTGATAACCCAAACACCTACGACTAC

521 M N K R V V A P G L V D C Y I N L G A R
1561 ATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACTTGGAGCACGC

541 W S L D Y M D N V N P F N H H R N A G L
1621 TGGTCCCTTGACTATATGGACAACGTCAACCCATTAAACCACCCGCAATGCTGGCCTG

561 R Y R S M L L G N G R Y V P F H I Q V P
1681 CGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCT

581 Q K F F A I K N L L L L P G S Y T Y E W
1741 CAGAAGTCTTTGCCATTAACCTCCTTCTCCTGCCGGGCTCATACCTACGAGTGG

601 N F R K D V N M V L Q S S L G N D L R V
1801 AACTTCAGGAAGGATGTTACATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTT

621 D G A S I K F D S I C L Y A T F F P M A
1861 GACGGAGCCAGCATTAAGTTTGATAGCATTTGCCCTTACGCCACCTTCTCCCATGGCC

641 H N T A S T L E A M L R N D T N D Q S F
1921 CACAACACCGCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAACGACAGTCTTT

661 N D Y L S A A N M L Y P I P A N A T N V
1981 AACGACTATCTCTCGCCGCCAACATGCTCTACCCTATACCGCCAACGCTACCAACGTG

681 P I S I P S R N W A A F R G W A F T R L
2041 CCCATATCCATCCCCTCCGCAACTGGGCGGCTTTCCGCGGCTGGGCTTCACGCGCCTT

701 K T K E T P S L G S G Y D P Y Y T Y S G
2101 AAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCCTTATTACACCTACTCTGGC

721 S I P Y L D G T F Y L N H T F K K V A I
2161 TCTATACCCTACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATT

741 T F D S S V S W P G N D R L L T P N E F
2221 ACCTTTGACTCTTCTGTGAGCTGGCCTGGCAATGACCGCCTGCTTACCCCAACGAGTTT

761 E I K R S V D G E G Y N V A Q C N M T K
2281 GAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAA

781 D W F L V Q M L A N Y N I G Y Q G F Y I
2341 GACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACGAGGCTTCTATATC

801 P E S Y K D R M Y S F F R N F O P M S R
2401 CCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGCCCATGAGCCGT

```

Fig. 26

821 Q V V D D T K Y K D Y Q Q V G I L H Q H
 2461 CAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATCCTACACCAACAC

 841 N N S G F V G Y L A P T M R E G Q A Y P
 2521 AACAACTCTGGATTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCCTACCGT

 861 A N F P Y P L I G K T A V D S I T Q K K
 2581 GCTAACTTCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAG

 881 F L C D R T L W R I P F S S N F M S M G
 2641 TTTCTTTGCGATCGCACCCCTTTGGCGCATCCATTCTCCAGTAACTTTATGTCCATGGGC

 901 A L T D L G Q N L L Y A N S A H A L D M
 2701 GCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCCGCCACGCGCTAGACATG

 921 T F E V D P M D E P T L L Y V L F E V F
 2761 ACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTTATGTTTGTGTTGAAGTCTTT

 941 D V V R V H Q P H R G V I E T V Y L R T
 2821 GACGTGGTCCGTGTGCACCAGCCGACCGGGCGTCATCGAAACCGTGTACCTGCGCAG

 961 P F S A G N A T T -
 2881 CCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 26

Hexon sequence of (NANP)₁₈-HVR1 adenovirus SEQ IDNOS : 19 and 51

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGGCCGGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGGGTTCACCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGGCCCAATCCTTGCGAATGGGATGAAAATGCAAAAT

141  P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAAT

161  P N A N P N A N P N A N P N A N P N A N
481 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAAT

181  P N A N P N A N P N A N P N A N P N A N
541 CCAAATGCAAATCCAAACGCAACCGAATGCTAATCCTAATGCAAATCCAAATGCAAAT

201  P N A N P N A N P K T H V F G Q A P Y S
601 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATGCAAATGCAAATGCAAATGCAAAT

221 G I N I T K E G I Q I G V E G Q T P K Y
661 GGTATAAATATTACAAAGGAGGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATAT

241 A D K T F Q P E P Q I G E S Q W Y E T E
721 GCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAA

261 I N H A A G R V L K K T T P M K P C Y G
781 ATTAATCATGCAGCTGGGAGAGTCCTAAAAAAGACTACCCCAATGAAACCATGTTACGGT

281 S Y A K P T N E N G G Q G I L V K Q Q N
841 TCATATGCAAAACCCACAAATGAAAATGGAGGGCAAGGCATTCTTGTAAGCAACAAAAT

301 G K L E S Q V E M Q F F S T T E A A A G
901 GGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACTACTGAGGCAGCCGAGGG

321 N G D N L T P K V V L Y S E D V D I E T
961 AATGGTGATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAAC

341 P D T H I S Y M P T I K E G N S R E L M
1021 CCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACACGAGAACTAATG

361 G Q Q S M P N R P N Y I A F R D N F I G
1081 GGCCAACAATCTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTTATTGGT

381 L M Y Y N S T G N M G V L A G Q A S Q L
1141 CTAATGTATTACAACAGCAGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTG

```

Fig. 27

401 N A V V D L Q D R N T E L S Y Q L L L D
 1201 AATGCTGTGTAGATTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGT

 421 S I G D R T R Y F S M W N Q L P N Y C F
 1261 TCCATTGGTGATAGAACCAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTT

 441 P L G G V I N T E T L T K V K P K T G Q
 1321 CCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAG

 461 E N G W E K D A T E F S D K N E I R V G
 1381 GAAAATGGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAAAAGAAATAGAGTTGGA

 481 N N F A M E I N L N A N L W R N F L Y S
 1441 AATAATTTTGCCATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTCCTGTACTCC

 501 N I A L Y L P D K L K Y S P S N V K I S
 1501 AACATAGCGTGTATTTGCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCT

 521 D N P N T Y D Y M N K R V V A P G L V D
 1561 GATAACCCAAACCTACGACTACATGAACAAGCAGTGGTGGCTCCCGGCTAGTGGAG

 541 C Y I N L G A R W S L D Y M D N V N P F
 1621 TGCTACATTAACTTGGAGCAGCTGGTCCCTTGACTATATGGACAAGTCAACCCATT

 561 N H H R N A G L R Y R S M L L G N G R Y
 1681 AACCACCACCGCAATGCTGGCTGCGCTACCGCTCAATGTTGCTGGGAATGGTCGCTAT

 581 V P F H I Q V P Q K F F A I K N L L L L
 1741 GTGCCCTTCCACATCCAGTGCCTCAGAAGTTCTTTGCCATTAACCTCCTCTCCTG

 601 P G S Y T Y E W N F R K D V N M V L Q S
 1801 CCGGGCTCATACCTACGAGTGGAACTTCAAGGAAGGATGTTAATAGTTCTGCAGAG

 621 S L G N D L R V D G A S I K F D S I C L
 1861 TCCCTAGGAAATGACCTAAGGTTGACGGAGCCAGCATTAAAGTTGATAGCATTGCTT

 641 Y A T F F P M A H N T A S T L E A M L R
 1921 TACGCCACCTTCTTCCCATGGCCACAACACCGCTCCACGCTTGAGGCCATGCTTAGA

 661 N D T N D Q S F N D Y L S A A N M L Y P
 1981 AACGACCAACGACGAGTCTTAAAGACTATCTCTCCGCGCCAACATGCTGTACCT

 681 I P A N A T N V P I S I P S R N W A A F
 2041 ATACCGCCAACGCTACCAACGTGCCATATCCATCCCCTCCGCAACTGGGCGGCTTTC

 701 R G W A F T R L K T K E T P S L G S G Y
 2101 CGCGGCTGGGCTTACGCGCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTAG

 721 D P Y Y T Y S G S I P Y L D G T F Y L N
 2161 GACCCTTATTACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTACCTCAAC

 741 H T F K K V A I T F D S S V S W P G N D
 2221 CACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTAGCTGGCCTGGCAATGAC

 761 R L L T P N E F E I K R S V D G E G Y N
 2281 CGCCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGTTACAAC

 781 V A Q C N M T K D W F L V Q M L A N Y N
 2341 GTTGCCAGTGTAACATGACCAAGACTGGTTCTGGTACAAATGCTAGCTAACTATAAC

 801 I G Y Q G F Y I P E S Y K D R M Y S F F
 2401 ATTGGCTACCAGGGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTT

Fig. 27

821 R N F Q P M S R Q V V D D T K Y K D Y Q
 2461 AGAAACTTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAA

 841 Q V G I L H Q H N N S G F V G Y L A P T
 2521 CAGGTGGGCATCCTACACCAACACAACAACTCTGGATTGTGGCTACCTTGCCCCCACC

 861 M R E G Q A Y P A N F P Y P L I G K T A
 2581 ATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCTATCCGCTTATAGGCAAGACCGCA

 881 V D S I T Q K K F L C D R T L W R I P F
 2641 GTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCTTTGGCGCATCCCATTG

 901 S S N F M S M G A L T D L G Q N L L Y A
 2701 TCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCC

 921 N S A H A L D M T F E V D P M D E P T L
 2761 AACTCGGCCACGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGGCCACCCTT

 941 L Y V L F E V F D V V R V H Q P H R G V
 2821 CTTTATGTTTGTGGAAGTCTTTGACGTGGTCCGTGTGCACCAGCCGACCGCGCGCTC

 961 I E T V Y L R T P F S A G N A T T -
 2881 ATCGAAACCGTGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 27

Hexon sequence of (NANP)₂₀-HVR1 adenovirus SEQ IDNOS : 20 and 52

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGTGGTGCAGTTTGGCCGCGCCACGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCAGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCGAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATAGTGGTACTCGTAT

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTCCACCTAGCTGTGGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAT

101 F D I R G V L D R G P T F K P Y S G T A
301 TTGACATCCGCGCGGTGCTGGACAGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGGCCCAAATCCTTGCGAATGGGATGAAAAATGCAAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAAT

161 P N A N P N A N P N A N P N A N P N A N
481 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAAT

181 P N A N P N A N P N A N P N A N P N A N
541 CCAAATGCAAATCCAAACGCGAACCAGTAATGCTAATCCTAATGCAAATCCAAATGCAAAT

201 P N A N P N A N P N A N P N A N P N A N P K T H
601 CCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAATGCAAATCCAAAACTCAG

221 V F G Q A P Y S G I N I T K E G I Q I G
661 GTATTTGGGCGAGCGCCTTATTCTGGTATAAATATTACAAAGGAGGGTATTCAATAGGT

241 V E G Q T P K Y A D K T F Q P E P Q I G
721 GTCGAAGGTCAAACACCTAAATATGCCGATAAAACATTTCAACCTGAACCTCAAATAGGA

261 E S Q W Y E T E I N H A A G R V L K K T
781 GAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCTGGGAGAGTCTAAAAAGAGT

281 T P M K P C Y G S Y A K P T N E N G G Q
841 ACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCCACAAATGAAAATGGAGGGCAA

301 G I L V K Q Q N G K L E S Q V E M Q F F
901 GGCATTCTTGTAAGCAACAAAATGAAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTTT

321 S T T E A A A G N G D N L T P K V V L Y
961 TCAACTACTGAGGCGAGCGCAGGCAATGGTGATAACTTGACTCCTAAAGTGGTATTGTAT

341 S E D V D I E T P D T H I S Y M P T I K
1021 AGTGAAGATGTAGATATAGAAACCCAGACACTCATATTTCTTACATGCCCACTATTAAG

361 E G N S R E L M G Q Q S M P N R P N Y I
1081 GAAGGTAACTCAGGAGAACTAATGGGCCAACAATCTATGCCCAACAGGCCTAATTACATT

381 A F R D N F I G L M Y Y N S T G N M G V
1141 GCTTTTAGGGACAATTTTATTGGTCTAATGTATTACAACAGCACGGGTAATATGGGTGTT

```

Fig. 28

401 L A G Q A S Q L N A V V D L Q D R N T E
 1201 CTGGCGGGCCAAGCATCGCAGTTGAATGCTGTTGTAGATTTGCAAGACAGAAACACAGAG

 421 L S Y O L L L D S I G D R T R Y F S M W
 1261 CTTTCATACCAGCTTTTGCTTGATTCCATTGGTGATAGAACCAGGTACTTTTCTATGTGG

 441 N O L P N Y C F P L G G V I N T E T L T
 1321 AATCAGCTTCCAAATTACTGCTTTCACCTGGGAGGTGTGATTAATACAGAGACTCTTACC

 461 K V K P K T G Q E N G W E K D A T E F S
 1381 AAGGTAAACCTAAACAGGTCAGGAAAATGGATGGGAAAAAGATGCTACAGAATTTTCA

 481 D K N E I R V G N N F A M E I N L N A N
 1441 GATAAAAATGAAATAAGAGTTGGAATAATTTGCCATGGAAATCAATCTAAATGCCAAC

 501 L W R N F L Y S N I A L Y L P D K L K Y
 1501 CTGTGGAGAAATTTCTGTACTCCAACATAGCGCTGTATTTGCCCGACAAGCTAAAGTAC

 521 S P S N V K I S D N P N T Y D Y M N K R
 1561 AGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATGAACAAGCGA

 541 V V A P G L V D C Y I N L G A R W S L D
 1621 GTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAACTTGGAGCAGCTGGTCCCTTGAC

 561 Y M D N V N P F N H H R N A G L R Y R S
 1681 TATATGGACAACGTCAACCATTTAACCACACCGCAATGCTGGCCTGCCCTACCGCTCA

 581 M L L G N G R Y V P F H I Q V P Q K F F
 1741 ATGTTGCTGGCAATGGTCGCTATGTGCCCTTCCACATCCAGGTGCCTCAGAAGTCTTT

 601 A I K N L L L L P G S Y T Y E W N F R K
 1801 GCCATTAAAAACCTCCTTCTCCTGCCGGGCTCATACACCTACGAGTGGAACCTCAGGAAG

 621 D V N M V L Q S S L G N D L R V D G A S
 1861 GATGTTAATCATGGTTCTGCAGAGCTCCCTAGGAAATGACCTAAGGGTGGAGGAGCCAGC

 641 I K F D S I C L Y A T F F P M A H N T A
 1921 ATTAAGTTTGATAGCATTGCTTTACGCCACCTTCTTCCCATGGCCACACACCGCC

 661 S T L E A M L R N D T N D Q S F N D Y L
 1981 TCCAGCCTTGAGGCCATGCTTAGAAACGACACCAACGACCAGTCTTTAACGACTATCTC

 681 S A A N M L Y P I P A N A T N V P I S I
 2041 TCCGCCGCCAACATGCTCTACCTATACCCGCCAACGCTACCAACGTGCCCATATCCATC

 701 P S R N W A A F R G W A F T R L K T K E
 2101 CCCTCCCGCAACTGGGCGGCTTCCGCGGCTGGGCTTACGCGCCTTAAGACTAAGGAA

 721 T P S L G S G Y D P Y Y T Y S G S I P Y
 2161 ACCCCATCACTGGGCTCGGGCTACGACCTTATTACACCTACTCTGGCTCTATACCTAC

 741 L D G T F Y L N H T F K K V A I T F D S
 2221 CTAGATGGAACCTTTTACCTCAACCACACCTTTAAGAAGGTGGCCATTACCTTTGACTCT

 761 S V S W P G N D R L L T P N E F E I K R
 2281 TCTGTCAGCTGGCCTGGCAATGACCGCTGCTTACCCCAACGAGTTTGAATTAAGCGC

 781 S V D G E G Y N V A O C N M T K D W F L
 2341 TCAGTTGACGGGGAGGGTTACAACGTTGCCAGTGTAACATGACCAAGAGCTGGTTCCTG

 801 V O M L A N Y N I G Y Q G F Y I P E S Y
 2401 GTACAAATGCTAGCTAACTATAACATTGGCTACCAGGGCTTCTATATCCAGAGAGCTAC

Fig. 28

821 K D R M Y S F F R N F Q P M S R Q V V D
 2461 AAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGCCCATGAGCCGTCAGGTGGTGGAT

 841 D T K Y K D Y Q Q V G I L H Q H N N S G
 2521 GATACTAAATACAAGGACTACCAACAGGTGGGCATCCTACCAACACAACAACCTCTGGA

 861 F V G Y L A P T M R E G Q A Y P A N F P
 2581 TTTGTTGGCTACCTTGCCCCACCATGCGCGAAGGACAGGCCTACCTGCTAACTTCCCC

 881 Y P L I G K T A V D S I T Q K K F L C D
 2641 TATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGAT

 901 R T L W R I P F S S N F M S M G A L T D
 2701 CGCACCCCTTTGGCGCATCCATTCTCCAGTAACCTTATGTCCATGGGCGCACTCACAGAC

 921 L G Q N L L Y A N S A H A L D M T F E V
 2761 CTGGGCCAAAACCTTCTCTACGCCAACTCCGCCACGCGCTAGACATGACTTTTGAGGTG

 941 D P M D E P T L L Y V L F E V F D V V R
 2821 GATCCCATGGACGAGCCACCCTTCTTTATGTTTTGTTGAAGTCTTTGACGTGGTCCGT

 961 V H Q P H R G V I E T V Y L R T P F S A
 2881 GTGCACGAGCCGACCGCGGCGTCATCGAAACCGTGTACCTGCGCACGCCCTTCTCGGCC

 981 G N A T T -
 2941 GGCAACGCCACAACATAA

Fig. 28

Hexon sequence of (NANP)₂₂-HVR1 adenovirus SEQ IDNOS : 21 and 53

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGGTGATAACCGTGTGTGGACATGGCTTCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGGCGTGTGGACAGGGGCCCTACTTTAAGCCCTACTCTGGCACTGCC

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAACGCCCTGGCTCCCAAGGGTGCCCAATCCTTGCGAATGGGATGAAATGCAAAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

161 P N A N P N A N P N A N P N A N P N A N
481 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

181 P N A N P N A N P N A N P N A N P N A N
541 CCAAATGCAAAATCCAAACGCGAACCAGGATGCTAATCCTAATGCAAAATCCAAATGCAAAAT

201 P N A N P N A N P N A N P N A N P N A N
601 CCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAATCCAAATGCAAAAT

221 P N A N P K T H V F G Q A P Y S G I N I
661 CCAAATGCAAAATCCAAACTCAGTATTTGGGAGGCGCCTTATTCTGGTATAAAATATT

241 T K E G I Q I G V E G Q T P K Y A D K T
721 ACAAGGAGGGTATTCAAATAGGTGTGAAGGTCAACACCTAAATATGCCGATAAAACA

261 F Q P E P Q I G E S Q W Y E T E I N H A
781 TTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCA

281 A G R V L K K T T P M K P C Y G S Y A K
841 GCTGGGAGAGTCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAA

301 P T N E N G G Q G I L V K Q Q N G K L E
901 CCCACAAATGAAATGGAGGGCAAGGCATTCTTGTAAGCAACAAATGGAAAGCTAGAA

321 S Q V E M Q F F S T T E A A A G N G D N
961 AGTCAAGTGGAATGCAATTTTCTCAACTACTGAGGCAGCCGAGGCAATGGTGATAAC

341 L T P K V V L Y S E D V D I E T P D T H
1021 TTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGACATCAT

361 I S Y M P T I K E G N S R E L M G Q Q S
1081 ATTTCTTACATGCCCACTATTAAGGAAGGTAACACGAGAACTAATGGGCAACAATCT

381 M P N R P N Y I A F R D N F I G L M Y Y
1141 ATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTTATTGGTCTAATGTATTAC

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Fig. 29

401 N S T G N M G V L A G Q A S Q L N A V V
 1201 AACAGCACGGGTAATATGGGTGTTCTGGCGGCCAAGCATCGCAGTTGAATGCTGTTGTA

 421 D L Q D R N T E L S Y Q L L L D S I G D
 1261 GATTTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATTGGTGAT

 441 R T R Y F S M W N O L P N Y C F P L G G
 1321 AGAACCAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTAAGTCTTCCACTGGGAGGT

 461 V I N T E T L T K V K P K T G Q E N G W
 1381 GTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAATGGATGG

 481 E K D A T E F S D K N E I R V G N N F A
 1441 GAAAAAGATGCTACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAATAATTTTGCC

 501 M E I N L N A N L W R N F L Y S N I A L
 1501 ATGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATAGCGCTG

 521 Y L P D K L K Y S P S N V K I S D N P N
 1561 TATTTGCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAAC

 541 T Y D Y M N K R V V A P G L V D C Y I N
 1621 ACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTACATTAAC

 561 L G A R W S L D Y M D N V N P F N H H R
 1681 CTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTAAACCACCACCGC

 581 N A G L R Y R S M L L G N G R Y V P F H
 1741 AATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTCGCTATGTGCCCTTCCAC

 601 I Q V P Q K F F A I K N L L L L P G S Y
 1801 ATCCAGGTGCCTCAGAAGTTCTTTGCCATTAAAAACCTCCTTCTCCTGCCGGCTCATAC

 621 T Y E W N F R K D V N M V L Q S S L G N
 1861 ACCTACGAGTGGAACCTCAGGAAGGATGTTAACATGGTCTGCAGAGCTCCCTAGGAAAT

 641 D L R V D G A S I K F D S I C L Y A T F
 1921 GACCTAAGGGTTGACGGAGCCAGCATTAAAGTTTGATAGCATTTCCTTTACGCCACCTTC

 661 F P M A H N T A S T L E A M L R N D T N
 1981 TTCCCATGGCCACAAACCGCCTCCACGCTTGAGGCCATGCTTAGAAACGACACCAAC

 681 D Q S F N D Y L S A A N M L Y P I P A N
 2041 GACCAGTCCTTTAAGACTATCTCTCCGCCCAACATGCTCTACCTATACCCGCCAAC

 701 A T N V P I S I P S R N W A A F R G W A
 2101 GCTACCAACGTGCCATATCCATCCCCTCCGCAACTGGCGGGCTTTCCGCGCTGGGCG

 721 F T R L K T K E T P S L G S G Y D P Y Y
 2161 TTCAGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCTTATTAC

 741 T Y S G S I P Y L D G T F Y L N H T F K
 2221 ACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTACCTCAACCACACCTTTAAG

 761 K V A I T F D S S V S W P G N D R L L T
 2281 AAGGTGGCATTACCTTTGACTCTTCTGTCAGCTGGCCTGGCAATGACCGCTGCTTACC

 781 P N E F E I K R S V D G E G Y N V A Q C
 2341 CCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACTGTGCCAGTGT

 801 N M T K D W F L V Q M L A N Y N I G Y Q
 2401 AACATGACCAAGACTGGTTCCTGGTACAAATGCTAGCTAACTATAACATTGGCTACCAAG

Fig. 29

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821  G F Y I P E S Y K D R M Y S F F R N F Q
2461 GGCTTCTATATCCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAAACTTCCAG

841  P M S R Q V V D D T K Y K D Y Q Q V G I
2521 CCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTGGGCATC

861  L H Q H N N S G F V G Y L A P T M R E G
2581 CTACACCAACACAACAACCTCTGGATTTGTTGGCTACCTTGCCCCCACCATGCGCGAAGGA

881  Q A Y P A N F P Y P L I G K T A V D S I
2641 CAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATT

901  T Q K K F L C D R T L W R I P F S S N F
2701 ACCCAGAAAAAGTTTCTTTGCGATCGCACCTTTGGCGCATCCCATTCTCCAGTAACTTT

921  M S M G A L T D L G Q N L L Y A N S A H
2761 ATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCGGCCAC

941  A L D M T F E V D P M D E P T L L Y V L
2821 GCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCCTTCTTTATGTTTTG

961  F E V F D V V R V H Q P H R G V I E T V
2881 TTTGAAGTCTTTGACGTGGTCCGTGTGCACCAGCCGACCGCGGCGTCATCGAAACCGTG

981  Y L R T P F S A G N A T T -
2941 TACCTGCGCACGCCCTTCTCGGCCGCAACGCCACAACATAA

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Fig. 29

Hexon sequence of (NANP)₂₈-HVR1 adenovirus SEQ IDNOS : 22 and 54

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGAGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAAGTTTCCCCCGCCACCGAGACGTAAGTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCCAGCGTTTGACGCTGCGGTTTCATCCCTGTGGACCGTGAAGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101 F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGCGGTGCTGGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCAGTCCG

121 Y N A L A P K G A P N P C E W D E N A N
361 TACAAAGCCCTGGTCCCAAGGTGCCCAAATCCTTGCGAATGGGATGAAACGCCCAAT

141 P N A N P N A N P N A N P N A N P N A N
421 CCAAATGCGAATCCCAACGCTAATCCTAACGCAACCGCAATGCTAACCTAACGCAAC

161 P N A N P N A N P N A N P N A N P N A N
481 CCAAACGCTAACCCCAACGCAACCCCAATGCCAACCCCAACGCAACCCCAACGCAAC

181 P N A N P N A N P N A N P N A N P N A N
541 CCAAACGCTAACCTAATGCCAATCCTAATGCCAATCCGAACGCAATCCAAATGCCAAT

201 P N A N P N V D P N A N P N A N P N A N
601 CCAAATGCTAATCCCAACGTGGACCCCAACGCAACCCCAATGCCAACCCCAACGCTAAT

221 P N A N P N A N P N A N P N A N P N A N
661 CCAAATGCGAACCCCTAACGCCAACCCGAATGCTAATCCCAATGCCAACCCCAATGCTAAT

241 P N A N P N A N P K T H V F G Q A P Y S
721 CCAAATGCGAACCCCTAATGCCAATCCCAAACTCACGTATTGGGAGGGCGCTATTCT

261 G I N I T K E G I Q I G V E G Q T P K Y
781 GGTATAAATATTACAAAGGAGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATAT

281 A D K T F Q P E P Q I G E S Q W Y E T E
841 GCCGATAAAACATTTCAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAA

301 I N H A A G R V L K K T T P M K P C Y G
901 ATTAATCATGCAGCTGGGAGAGTCCTAAAAAAGACTACCCCAATGAAACCATGTTACGGT

321 S Y A K P T N E N G G Q G I L V K Q Q N
961 TCATATGCAAAACCCACAAATGAAATGGAGGGCAAGGCATTCTTGTAAGCAACAAAT

341 G K L E S Q V E M Q F F S T T E A A A G
1021 GGAAAGCTAGAAAGTCAAGTGGAAATGCAATTTTCTCAACTACTGAGGCAGCCGACGGC

361 N G D N L T P K V V L Y S E D V D I E T
1081 AATGGTGATACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACC

381 P D T H I S Y M P T I K E G N S R E L M
1141 CCAGACACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACACGAGAATAATG

```

Fig. 30

401 G Q Q S M P N R P N Y I A F R D N F I G
 1201 GGCCAACAATCTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTATTGGT
 421 L M Y Y N S T G N M G V L A G Q A S Q L
 1261 CTAATGTATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCCAAGCATCGCAGTTG
 441 N A V V D L Q D R N T E L S Y Q L L L D
 1321 AATGCTGTTGTAGATTTGCAAGACAGAAACACAGAGCTTTCATACCAGCTTTTGCTTGAT
 461 S I G D R T R Y F S M W N Q L P N Y C F
 1381 TCCATTGGTGATAGAACCAGGTACTTTTCTATGTGGAATCAGCTTCCAAATTACTGCTTT
 481 P L G G V I N T E T L T K V K P K T G Q
 1441 CCACTGGGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAG
 501 E N G W E K D A T E F S D K N E I R V G
 1501 GAAAATGGATGGGAAAAAGATGCTACAGAATTTTCCAGATAAAAATGAAATAAGAGTTGGA
 521 N N F A M E I N L N A N L W R N F L Y S
 1561 AATAATTTTGCCTGGAAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCC
 541 N I A L Y L P D K L K Y S P S N V K I S
 1621 AACATAGCGCTGTATTTGCCCGACAAGCTAAAGTACAGTCCTTCCAACGTAAAAATTTCT
 561 D N P N T Y D Y M N K R V V A P G L V D
 1681 GATAACCCAAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGAC
 581 C Y I N L G A R W S L D Y M D N V N P F
 1741 TGCTACATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATT
 601 N H H R N A G L R Y R S M L L G N G R Y
 1801 AACCACCACCGCAATGCTGGCCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTGGCTAT
 621 V P F H I Q V P Q K F F A I K N L L L L
 1861 GTGCCCTTCCACATCCAGGTGCCTCAGAAGTTCTTTGCCATTAACCACTCTCTCCTG
 641 P G S Y T Y E W N F R K D V N M V L Q S
 1921 CCGGGCTCATACCTACGAGTGAACCTCAGGAAGGATGTTAACATGGTTCTGCGAGAG
 661 S L G N D L R V D G A S I K F D S I C L
 1981 TCCCTAGGAATGACCTAAGGGTTGACGGAGCCAGCATTAAGTTTGATAGCATTTGCCCT
 681 Y A T F F P M A H N T A S T L E A M L R
 2041 TACGCCACCTTCTTCCCATGGCCACAACACCGCTCCACGCTTGAGGCCATGCTTAGA
 701 N D T N D Q S F N D Y L S A A N M L Y P
 2101 AACGACACCAACGACGAGTCCTTTAAGGACTATCTCTCCGCCGCCAATGCTCTACCT
 721 I P A N A T N V P I S I P S R N W A A F
 2161 ATACCCGCCAACGCTACCAACGTGCCATATCCATCCCTCCCGCAACTGGGCGGCTTTG
 741 R G W A F T R L K T K E T P S L G S G Y
 2221 CGCGGCTGGGCTTACGCGCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTAC
 761 D P Y Y T Y S G S I P Y L D G T F Y L N
 2281 GACCTTATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTTACCTCAAC
 781 H T F K K V A I T F D S S V S W P G N D
 2341 CACACCTTTAAGAAGGTGGCCATTACCTTTGACTCTTCTGTCAGCTGGCCTGGCAATGAC
 801 R L L T P N E F E I K R S V D G E G Y N
 2401 CGCCTGCTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAAC

Fig. 30

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821 V A Q C N M T K D W F L V Q M L A N Y N
2461 GTTGCCCAAGTGAACATGACCAAAGACTGGTTCCCTGGTACAAATGCTAGCTAACTATAAC

841 I G Y Q G F Y I P E S Y K D R M Y S F F
2521 ATTGGCTACCAGGGCTTCTATATCCAGAGAGCTACAAGGACCGCATGTA CTCTCTTT

861 R N F Q P M S R Q V V D D T K Y K D Y Q
2581 AGAAACTTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAA

881 Q V G I L H Q H N N S G F V G Y L A P T
2641 CAGGTGGGCATCCTACACCAACACAACAACCTCTGGATTTGTTGGCTACCTTGCCCCACC

901 M R E G Q A Y P A N F P Y P L I G K T A
2701 ATGCGCGAAGGACAGGCCTACCCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCA

921 V D S I T Q K K F L C D R T L W R I P F
2761 GTTGACAGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCTTTGGCGCATCCCATT

941 S S N F M S M G A L T D L G Q N L L Y A
2821 TCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCC

961 N S A H A L D M T F E V D P M D E P T L
2881 AACTCCGCCCACGGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCTT

981 L Y V L F E V F D V V R V H Q P H R G V
2941 CTTTATGTTTTGTTGAAGTCTTTGACGTGGTCCGTGTGCACGACCGCACCGCGCGTC

1001 I E T V Y L R T P F S A G N A T T -
3001 ATCGAAACCGGTACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACATAA

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Fig. 30

Hexon sequence of (QGPGAP)₃-HVR5 adenovirus SEQ IDNOS : 23 and 40

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1  M A T P S M M P Q W S Y M H I S G Q D A
1  ATGGCTACCCCTTCGATGATGCCGCGTGGTCTTACATGCACATCTCGGGCCAGGACGCC

21  S E Y L S P G L V Q F A R A T E T Y F S
61  TCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTTGCCCGCGCCACCGAGACGTACTTCAGC

41  L N N K F R N P T V A P T H D V T T D R
121 CTGAATAACAAGTTTAGAAACCCACGGTGGCGCCTACGCACGACGTGACCACAGACCGG

61  S Q R L T L R F I P V D R E D T A Y S Y
181 TCCCAGCGTTTGACGCTGCGGTTCCCTGTGGACCGTAGGATACTGCGTACTCGTAC

81  K A R F T L A V G D N R V L D M A S T Y
241 AAGGCGCGGTTACCCCTAGCTGTGGTGATAACCGTGTGCTGGACATGGCTTCCACGTAC

101  F D I R G V L D R G P T F K P Y S G T A
301 TTTGACATCCGCGCGTGTGCGACAGGGGCCCTACTTTTAAGCCCTACTCTGGCACTGCC

121  Y N A L A P K G A P N P C E W D E A A T
361 TACAACGCCCTGGTCCCAAGGGTGCCCAATCCTTGCGAATGGGATGAAGCTGCTACT

141  A L E I N L E E E D D D N E D E V D E Q
421 GCTCTTGAATAAACCTAGAAGAAGAGGACGATGACAACGAAGACGAAGTAGACGAGCAA

161  A E Q Q K T H V F G Q A P Y S G I N I T
481 GCTGAGCAGCAAAAACTCACGTATTTGGGCAGGCGCCTTATTCTGGTATAAATATTACA

181  K E G I Q I G V E G Q T P K Y A D K T F
541 AAGGAGGGTATTCAAATAGGTGTCGAAGGTCAAACACCTAAATATGCCGATAAAACATT

201  Q P E P Q I G E S Q W Y E T E I N H A A
601 CAACCTGAACCTCAAATAGGAGAATCTCAGTGGTACGAAACAGAAATTAATCATGCAGCT

221  G R V L K K T T P M K P C Y G S Y A K P
661 GGGAGAGTCCTAAAAAGACTACCCCAATGAAACCATGTTACGGTTCATATGCAAAACCC

241  T N E N G G Q G I L V K Q Q N G K L E S
721 ACAAATGAAATGGAGGGCAAGGCATTCTTGTAAGCAACAAATGGAAAGCTAGAAAGT

261  Q V E M Q F F S A S Q G P G A P Q G P G
781 CAAGTGAAATGCAATTTTCTCAGCTAGCCAGGGCCCTGGAGCTCCACAGGGACCGGT

281  A P Q G P G A P G T S T T E A A A G N G
841 GCACCTCAAGGGCCTGGAGCCCTGGCACTAGCACTACTGAGGCAGCCGCGAGGCAATGGT

301  D N L T P K V V L Y S E D V D I E T P D
901 GATAACTTGACTCCTAAAGTGGTATTGTACAGTGAAGATGTAGATATAGAAACCCAGAC

321  T H I S Y M P T I K E G N S R E L M G Q
961 ACTCATATTTCTTACATGCCCACTATTAAGGAAGGTAACACGAGAACTAATGGGCCAA

341  Q S M P N R P N Y I A F R D N F I G L M
1021 CAATCTATGCCCAACAGGCCTAATTACATTGCTTTTAGGGACAATTTATTGGTCTAATG

361  Y Y N S T G N M G V L A G Q A S Q L N A
1081 TATTACAACAGCACGGGTAATATGGGTGTTCTGGCGGGCAAGCATCGCAGTTGAATGCT

381  V V D L Q D R N T E L S Y Q L L L D S I
1141 GTTGTAGATTGCAAGACAGAAACAGAGCTTTCATACCAGCTTTTGCTTGATTCCATT

```

Fig. 31

401 G D R T R Y F S M W N Q A V D S Y D P D
 1201 GGTGATAGAACCAGGTACTTTTCTATGTGGAATCAGGCTGTTGACAGCTATGATCCAGAT

 421 V R I I E N H G T E D E L P N Y C F P L
 1261 GTTAGAATTATTGAAATCATGGAACGAAGATGAACCTCCAATTTACTGCTTTCCACTG

 441 G G V I N T E T L T K V K P K T G Q E N
 1321 GGAGGTGTGATTAATACAGAGACTCTTACCAAGGTAAACCTAAACAGGTCAGGAAAT

 461 G W E K D A T E F S D K N E I R V G N N
 1381 GGATGGGAAAAAGATGCTACAGAATTTTCAGATAAAATGAAATAAGAGTTGGAATAAT

 481 F A M E I N L N A N L W R N F L Y S N I
 1441 TTTGCCATGGAATCAATCTAAATGCCAACCTGTGGAGAAATTTCTGTACTCCAACATA

 501 A L Y L P D K L K Y S P S N V K I S D N
 1501 GCGCTGTATTTGCCGACAAGCTAAAGTACAGTCCTCCAACGTAAAAATTTCTGATAAC

 521 P N T Y D Y M N K R V V A P G L V D C Y
 1561 CCAACACCTACGACTACATGAACAAGCGAGTGGTGGCTCCCGGGCTAGTGGACTGCTAC

 541 I N L G A R W S L D Y M D N V N P F N H
 1621 ATTAACCTTGGAGCAGCTGGTCCCTTGACTATATGGACAACGTCAACCCATTTAACCAC

 561 H R N A G L R Y R S M L L G N G R Y V P
 1681 CACCGCAATGCTGGCTGCGCTACCGCTCAATGTTGCTGGGCAATGGTGGCTATGTGCC

 581 F H I Q V P Q K F F A I K N L L L L P G
 1741 TTCCACATCCAGGTGCTCAGAAAGTTCTTTGCCATTAACCTCCTTCTCCTGCCGGG

 601 S Y T Y E W N F R K D V N M V L Q S S L
 1801 TCATACACCTACGAGTGAACCTCAGGAAGGATGTTAACATGGTTCTGCAGAGCTCCCTA

 621 G N D L R V D G A S I K F D S I C L Y A
 1861 GGAAATGACCTAAGGGTTGACGGAGCCAGCATTAGTTTGATAGCATTGCTTTACGCC

 641 T F F P M A H N T A S T L E A M L R N D
 1921 ACCTTCTTCCCATGCCCCACACCCGCTCCACGCTTGAGGCCATGCTTAGAAAGCAG

 661 T N D Q S F N D Y L S A A N M L Y P I P
 1981 ACCAAGCAGCAGCTTTTAACGACTATCTCTCCGCCGCAACATGCTTACCCTATACCC

 681 A N A T N V P I S I P S R N W A A F R G
 2041 GCCAACGCTACCAACGTGCCATATCCATCCCTCCCGCAACTGGGCGGCTTTCCGCCG

 701 W A F T R L K T K E T P S L G S G Y D P
 2101 TGGGCCTTACGCGCCTTAAGACTAAGGAAACCCATCACTGGGCTCGGGCTACGACCT

 721 Y Y T Y S G S I P Y L D G T F Y L N H T
 2161 TATTACACCTACTCTGGCTCTATACCCTACCTAGATGGAACCTTTACCTCAACCACACC

 741 F K K V A I T F D S S V S W P G N D R L
 2221 TTTAAGAAGGTGGCCATTACCTTTGACTCTCTGTGAGCTGGCCTGGCAATGACCGCTG

 761 L T P N E F E I K R S V D G E G Y N V A
 2281 CTTACCCCAACGAGTTTGAAATTAAGCGCTCAGTTGACGGGGAGGGTTACAACGTTGCC

 781 Q C N M T K D W F L V Q M L A N Y N I G
 2341 CAGTGTAACATGACCAAGACTGGTTCCTGGTACAATGCTAGCTAACTATAACATTGGC

Fig. 31

801 Y Q G F Y I P E S Y K D R M Y S F F R N
 2401 TACCAGGGCTTCTATATCCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAAAC

 821 F Q P M S R Q V V D D T K Y K D Y Q Q V
 2461 TTCCAGCCCATGAGCCGTCAGGTGGTGGATGATACTAAATACAAGGACTACCAACAGGTG

 841 G I L H Q H N N S G F V G Y L A P T M R
 2521 GGCATCCTACCAACACAACAACCTCTGGATTTGTTGGCTACCTTGCCCCCACCATGCGC

 861 E G Q A Y P A N F P Y P L I G K T A V D
 2581 GAAGGACAGGCCTACCTGCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGAC

 881 S I T Q K K F L C D R T L W R I P F S S
 2641 AGCATTACCCAGAAAAAGTTTCTTTGCGATCGCACCCCTTTGGCGCATCCCATTCTCCAGT

 901 N F M S M G A L T D L G Q N L L Y A N S
 2701 AACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTCTCTACGCCAACTCC

 921 A H A L D M T F E V D P M D E P T L L Y
 2761 GCCCAGCGCTAGACATGACTTTTGAGGTGGATCCCATGGACGAGCCACCCTTCTTTAT

 941 V L F E V F D V V R V H Q P H R G V I E
 2821 GTTTTGTTTGAAGTCTTTGACGTGGTCCGTGTGCACGACCGCACCGCGGCGTCATCGAA

 961 T V Y L R T P F S A G N A T T -
 2881 ACCGTGTACCTGCGCAGGCCCTTCTCGGCCGGCAACGCCACAACATAA

Fig. 31

Fiber sequence of (QGPGAP)₃-Fib adenovirus SEQ IDNOS : 24 and 41

```

1  M K R A R P S E D T F N P V Y P Y D T E
1  ATGAAGCGCGCAAGACCGTCTGAAGATACCTTCAACCCCGTGTATCCATATGACACGGAA

21  T G P P T V P F L T P P F V S P N G F Q
61  ACCGGTCTCCAACGTGCGCTTTTCTTACTCCTCCCTTTGTATCCCCAATGGGTTTCAA

41  E S P P G V L S L R L S E P L V T S N G
121  GAGAGTCCCCCTGGGGTACTCTCTTTGCGCCTATCCGAACCTCTAGTTACCTCCAATGGC

61  M L A L K M G N G L S L D E A G N L T S
181  ATGCTTGCCTCAAAATGGGCAACGGCCTCTCTCTGGACGAGGCCGGCAACCTTACCTCC

81  Q N V T T V S P P L K K T K S N I N L E
241  CAAAATGTAACCACTGTGAGCCACCTCTCAAAAAACCAAGTCAAAACATAAACCTGGAA

101  I S A P L T V T S E A L T V A A A A P L
301  ATATCTGCACCCCTCAGGTTACCTCAGAAGCCCTAACTGTGGCTGCCGCCGCACCTCTA

121  M V A G N T L T M Q S Q A P L T V H D S
361  ATGGTCGCGGGCAACACACTCACCATGCAATCAGGCCCGCTAACCGTGCACGACTCC

141  K L S I A T Q G P L T V S E G K L A L Q
421  AAACCTAGCATTGCCACCAAGGACCCCTCAGGTGTCAGAAGGAAAGCTAGCCCTGCAA

161  T S G P L T T T D S S T L T I T A S P P
481  ACATCAGGCCCCCTCACCACCACCGATAGCAGTACCCTTACTATCACTGCCTCACCCTCT

181  L T T A T G S L G I D L K E P I Y T Q N
541  CTAACACTGCCACTGGTAGCTTGGGCATTGACTTGAAAGAGCCATTATACACAAAT

201  G K L G L K Y G A P L H V T D D L N T L
601  GGAAACTAGGACTAAAGTACGGGGCTCCTTGCATGTAACAGACGACCTAAACACTTTG

221  T V A T G P G V T I N N T S L Q T K V T
661  ACCGTAGCAACTGGTCCAGGTGTGACTATTAATAACTTCTTGCAAACTAAAGTTACT

241  G A L G F D S Q G N M Q L N V A G G L R
721  GGAGCCTTGGGTTTTGATTCACAAGGCAATATGCAACTTAATGTAGCAGGAGGACTAAGG

261  I D S Q N R R L I L D V S Y P F D A Q N
781  ATTGATTCTCAAAACAGACGCCCTTATACTTGATGTTAGTTATCCGTTTGATGCTCAAAAC

281  Q L N L R L G Q G P L F I N S A H N L D
841  CAACTAAATCTAAGACTAGGACAGGGCCCTCTTTTATAAACTCAGCCCACTTGGAT

301  I N Y N K G L Y L F T A S N N S K K L E
901  ATTAACACAAAGGCTTTACTTGTTTACAGCTTCAACAATTCCAAAAAGCTTGAG

321  V N L S T A K G L M F D A T A I A I N A
961  GTTAACCTAAGCACTGCCAAGGGTTGATGTTTGACGCTACAGCCATAGCCATTAATGCA

341  G D G L E F G S P N A P N T N P L K T K
1021  GGAGATGGGCTTGAATTTGGTTACCTAATGCACCAACACAAATCCCTCAAAACAAA

361  I G H G L E F D S N K A M V P K L G T G
1081  ATTGGCCATGGCCTAGAATTTGATTCAAACAAGGCTATGGTTCCTAACTAGGAACTGGC

381  L S F D S T G A I T V G N K N N D K L T
1141  CTTAGTTTGTACAGCACAGGTGCCATTACAGTAGGAAACAAAAATAATGATAAGCTAACT

```

Fig. 32

401 L W T T P A P S P N C R L N A E K D A K
 1201 TTGTGGACCACACCAGCTCCATCTCCTAACTGTAGACTAAATGCAGAGAAAGATGCTAAA

 421 L T L V L T K C G S Q I L A T V S V L A
 1261 CTCACCTTTGGTCTTAACAAAATGTGGCAGTCAAATACTTGCTACAGTTTCAGTTTGGCT

 441 V K G S L A P I S G T V Q S A H L I I R
 1321 GTTAAAGGCAGTTTGGCTCCAATATCTGGAACAGTTCAAAGTGCTCATCTTATTATAAGA

 461 F D E N G V L L N N S F L D P E Y W N F
 1381 TTTGACGAAAATGGAGTGCTACTAAACAATTCTTCCTGGACCCAGAATATTGGAACTTT

 481 R N G D L T E G T A Y T N A V G F M P N
 1441 AGAAATGGAGATCTTACTGAAGGCACAGCCTATACAAACGCTGTTGGATTTATGCCATAAC

 501 L S A Y P K S H G K T A K S N I V S Q V
 1501 CTATCAGCTTATCCAAAATCTCACGGTAAACTGCCAAAAGTAACATTGTCAGTCAAGTT

 521 Y L N G D K T K P V T L T I T L N G T Q
 1561 TACTTAAACGGAGACAAAAGTAAACCTGTAACACTAACCATTACACTAAACGGTACACAG

 541 E T G Q G P G A P Q G P G A P Q G P G A
 1621 GAAACAGGACAGGGCCCTGGAGCTCCACAGGGACCAGGTGCACCTCAAGGGCCCTGGAGCC

 561 P D T T P S A Y S M S F S W D W S G H N
 1681 CCTGACACAACCTCAAGTGCATACTCTATGTCATTTTCATGGGACTGGTCTGGCCACAAC

 581 Y I N E I F A T S S Y T F S Y I A Q E -
 1741 TACATTAATGAAATATTTGCCACATCCTCTTACACTTTTTCATACATTGCCCAAGAATAA

Fig. 32

Fiber sequence of (NANP)₄-Fib adenovirus SEQ IDNOs : 25 and 55

```

1  M K R A R P S E D T F N P V Y P Y D T E
1  ATGAAGCGCGCAAGACCGTCTGAAGATACCTTCAACCCCGTGTATCCATATGACACGGAA

21  T G P P T V P F L T P P F V S P N G F Q
61  ACCGGTCTCCAACTGTGCCTTTTCTTACTCCTCCCTTTGTATCCCCAATGGGTTTCAA

41  E S P P G V L S L R L S E P L V T S N G
121 GAGAGTCCCCCTGGGGTACTCTCTTTGCGCCTATCCGAACCTCTAGTTACCTCCAATGGC

61  M L A L K M G N G L S L D E A G N L T S
181 ATGCTTGCCTCAAAATGGGCAACGGCCTCTCTGTGACGAGGCCGGCAACCTTACCTCC

81  Q N V T T V S P P L K K T K S N I N L E
241 CAAAATGTAACCACTGTGAGCCACCTCTCAAAAAACCAAGTCAACATAAACCTGGAA

101 I S A P L T V T S E A L T V A A A A P L
301 ATATCTGCACCCCTCACAGTTACCTCAGAAGCCCTAACTGTGGTGCCGCGCACCTCTA

121 M V A G N T L T M Q S Q A P L T V H D S
361 ATGGTCGCGGGCAACACACTCACCATGCAATCACAGGCCCGCTAACCGTGCACGACTCC

141 K L S I A T Q G P L T V S E G K L A L Q
421 AAACCTAGCATTGCCACCAAGGACCCCTCACAGTGTGAGAAAGGAGTACCCCTGCAA

161 T S G P L T T T D S S T L T I T A S P P
481 ACATCAGGCCCCCTCACCACCACCGATAGCAGTACCTTACTATCACTGCTCAGCCCTC

181 L T T A T G S L G I D L K E P I Y T Q N
541 CTAACCTAGCCACTGGTAGCTTGGGATTGACTTGAAGAGCCCATTTATACAAAAAT

201 G K L G L K Y G A P L H V T D D L N T L
601 GGAACCTAGGACTAAAGTACGGGGCTCCTTTGCATGTAACAGACGACCTAAACACTTTG

221 T V A T G P G V T I N N T S L Q T K V T
661 ACCGTAGCAACTGGTCCAGGTGTGACTATTAATAACTTCTCCTGCAAACTAAAGTTACT

241 G A L G F D S Q G N M Q L N V A G G L R
721 GGAGCCTTGGGTTTGTTCACAAGGCAATATGCAACTTAATGTAGCAGGAGGACTAAGG

261 I D S Q N R R L I L D V S Y P F D A Q N
781 ATTGATTCTAAAACAGACGCCTTATACCTTGATGTTAGTTATCCGTTTGATGCTCAAAAC

281 Q L N L R L G Q G P L F I N S A H N L D
841 CAACTAAATCTAAGACTAGGACAGGGCCCTCTTTTATAAACTCAGCCACAACCTGGAT

301 I N Y N K G L Y L F T A S N N S K K L E
901 ATTAACCTACAACAAAGGCCTTTACTTGTTCAGCTTCAACAATCCAAAAAGCTTGAG

321 V N L S T A K G L M F D A T A I A I N A
961 GTTAACCTAAGCACTGCCAAGGGTTGATGTTGACGCTACAGCCATAGCCATTAATGCA

341 G D G L E F G S P N A P N T N P L K T K
1021 GGAGATGGGCTTGAATTTGGTTACCTAATGCACCAACACAAATCCCTCAAAACAAA

361 I G H G L E F D S N K A M V P K L G T G
1081 ATTGGCCATGGCCTAGAATTTGATTCAAACAAGGCTATGGTTCCTAACTAGGAAGTGGC

381 L S F D S T G A I T V G N K N N D K L T
1141 CTTAGTTTGTACAGCACAGGTGCCATTACAGTAGGAAACAAAATAATGATAAGCTAACT

```

Fig. 33

401 L W T T P A P S P N C R L N A E K D A K
 1201 TTGTGGACCACACAGCTCCATCTCCTAACTGTAGACTAAATGCAGAGAAAGATGCTAAA

 421 L T L V L T K C G S Q I L A T V S V L A
 1261 CTCACCTTTGGTCTTAACAAAATGTGGCAGTCAAATACTTGCTACAGTTTCAGTTTGGCT

 441 V K G S L A P I S G T V Q S A H L I I R
 1321 GTTAAAGGCAGTTTGGCTCCAATATCTGGAACAGTCAAAGTGCTCATCTTATTATAAGA

 461 F D E N G V L L N N S F L D P E Y W N F
 1381 TTTGACGAAAATGGAGTGCTACTAAACAATTCCTTCCTGGACCCAGAATATTGGAACCTT

 481 R N G D L T E G T A Y T N A V G F M P N
 1441 AGAAATGGAGATCTTACTGAAGGCACAGCCTATACAAACGCTGTTGGATTTATGCCTAAC

 501 L S A Y P K S H G K T A K S N I V S Q V
 1501 CTATCAGCTTATCCAAAATCTCACGGTAAAAGTGCCTAAAGTAAACATTGTCAGTCAAGT

 521 Y L N G D K T K P V T L T I T L N G T Q
 1561 TACTTAAACGGAGACAAAATAACCTGTAACACTAACCATTACACTAAACGGTACACAG

 541 E T G N A N P N A N P N A N P N A N P D
 1621 GAAACAGGAAACGCTAATCCCAACGCTAACCCAAATGCAATCCTAATGCCAACCCCGAC

 561 T T P S A Y S M S F S W D W S G H N Y I
 1681 ACAACTCCAAGTGCATACTCTATGTATTTTCATGGGACTGGTCTGGCCACAACCTACATT

 581 N E I F A T S S Y T F S Y I A Q E -
 1741 AATGAAATATTTGCCACATCCTCTTACACTTTTTTCATACATTGCCCAAGAATAA

Fig. 33

pVII sequence of PyCSCD4-pVII adenovirus SEQ IDNOS : 26 and 42

```

1  M S I L I S P S N N T G W G L R F P S K
1  ATGTCCATCCTTATATCGCCAGCAATAACACAGGCTGGGGCCTGCGCTTCCCAAGCAAG

21  M F G G A K K R S D Q H P V R V R G H Y
61  ATGTTTGGCGGGGCAAGAAGCGCTCCGACCAACACCCAGTGCAGTGCAGGGGCACTAG

41  R A P W G A H K R G R T G R T T V D D A
121 CGCGCGCCCTGGGGCGCGCACAACGCGGCCGCACTGGGCGCACACCGTCGATGACGCG

61  I D A V V E E A R N Y T P T P P P V S T
181 ATCGACGCGGTGGTGGAGGAGGCGCAACTACAGCCACGCGCCACCCAGTGTCCACA

81  V D A A I Q T V V R G A R R Y A K M K R
241 GTGGACGCGGCATTGACACCGTGGTGGCGGAGCCCGCGCTATGCTAAATGAAGAGA

101 R R R R V A R R H R R R P G T A A Q R A
301 CGCGCGAGGCGGTAGCACGTGCCACCGCCGCGACCCGCACTGCCGCCAACGCGCG

121 A A A L L N R A R R T G R R A A M R A A
361 GCGGCGGCCCTGCTTAACCGCGCACGTGCGACCGCGCGACGGGCGGCCATGCGGGCCGCT

141 R R L A A G I V T V P P R S R R R A A A
421 CGAAGGCTGGCCGCGGTATTGTCAGTGTGCCCCAGGTCCAGGCGACGAGCGGCGCGC

161 A A A A A I S A M T Q G R R G N V Y W V
481 GCAGCAGCCGCGGCCATTAGTGCTATGACTCAGGGTGCAGGGGCAACGTGTATTGGGTG

181 R D S V S G L R V P V R T R P P R N V R
541 CGCGACTCGGTAGCGGCCTGCGCGTGCCCGTGCGCACCCGCCCCCGCGCAACGTGCGC

201 T R P P R N Y N R N I V N R L L G D A L
601 ACCGCCCCCGCGCAACTACAACAGGAACATCGTGAACAGGCTGCTGGGCGACGCCCTG

221 N G K P E E K -
661 AACGGCAAGCCGAGGAGAAGTAG

```

Fig. 34

pVII sequence of PfCSPCD4-pVII-1 adenovirus SEQ IDNOS : 27 and 56

```

1  M S I L I S P S N N T G W G L R F P S K
1  ATGTCCATCCTTATATCGCCAGCAATAACACAGGCTGGGGCTGCGCTTCCCAAGCAAG

21  M F G G A K K R S D Q H P V R V R G H Y
61  ATGTTTGGCGGGCCAAGAAGCGCTCCGACCAACACCCAGTGCGCGTGCGCGGGCACTAG

41  R A P W G A H K R G R T G R T T V D D A
121 CGCGCGCCCTGGGGCGCGCACAAACGCGCCGCACTGGGCGCACACCGTCGATGACGCG

61  I D A V V E E A R N Y T P T P P P V S T
181 ATCGACGCGGTGGTGGAGGAGGCGCAACTACAGCCACGCCGCCACCGAGTGCCACA

81  V D A A I Q T V V R G A R R Y A K M K R
241 GTGGACGCGCCATTGACACGCGGTGGTGGCGGAGCCCGCGCTATGCTAAATGAAGAGA

101 R R R R V A R R H R R R P G T A A Q R A
301 CGGCGGAGGCGCGTAGCACGTCGCCACCGCCGCCGACCCGCACTGCGGCCAACGCGCG

121 A A A L L N R A R R T G R R A A M R A A
361 GCGGCGGCCCTGCTTAACCGCGCACGTGCGACCGGCCGACGGCGGCCATGCGGGCCGCT

141 R R L A A G I V T V P P R S R R R A A A
421 CGAAGGCTGGCGCGGGTATTGTCAGTGTGCCCCCAGGTCCAGGCGACGAGCGGGCCGCG

161 A A A A A I S A M T Q G R R G N V Y W V
481 GCAGCAGCCGCGGCCATTAGTGCTATGACTCAGGGTCGCAGGGGCAACGTGTATTGGGTG

181 R D S V S G L R V P V R T R P P R N E Y
541 CGCGACTCGGTTAGCGGCCTGCGCGTGCCCGTGCGCACCGCCCCCGCGCAACGAATAG

201 L N K I Q N S L S T E W S P C S V T -
601 TTGAACAAGATTCAAAACTCCCTCTCAACAGAATGGTCTCCTTGCAGCGTGACTTAG

```

Fig. 35

pVII sequence of PfCSPCD4-pVII-2 adenovirus SEQ IDNOS : 28 and 57

```

1  M S I L I S P S N N T G W G L R F P S K
1  ATGTCCATCCTTATATCGCCAGCAATAACACAGGCTGGGGCCTGCGCTTCCCAAGCAAG

21  M F G G A K K R S D Q H P V R V R G H Y
61  ATGTTTGGCGGGCCAAGAAGCGCTCCGACCAACACCCAGTGCGCGTGCGCGGGCACTAC

41  R A P W G A H K R G R T G R T T V D D A
121  CGCGCGCCCTGGGGCGCGCACAACGCGGCGCACTGGGCGCACCACCGTCGATGACGCG

61  I D A V V E E A R N Y T P T P P P V S T
181  ATCGACGCGGTGGTGGAGGAGCGCGCACTACACGCCACGCGCCACCAAGTGCCACA

81  V D A A I Q T V V R G A E Y L N K I Q N
241  GTGGACGCGGCATTGAGACGCGGTGCGCGGAGCCGAATATTGAACAAGATTCAAAAC

101  S L S T E W S P C S V T R R Y A K M K R
301  TCCTCTCAACAGAATGGTCTCCTTGCAAGCGTGACTCGGCGCTATGCTAAAATGAAGAGA

121  R R R R V A R R H R R R P G T A A Q R A
361  CGCGGAGGCGCGTAGCACGTGCGCACCGCGCGGACCGGCGACTGCCGCCAACGCGCG

141  A A A L L N R A R R T G R R A A M R A A
421  GCGGCGCCCTGCTTAACGCGCACGTGCGACCGCGGACGCGGCGGCATGCGGGCGGCT

161  R R L A A G I V T V P P R S R R R A A A
481  CGAAGGCTGGCGCGGGTATTGTCACTGTGCCCCCAGGTCCAGGCGACGAGCGGCGCG

181  A A A A A I S A M T Q G R R G N V Y W V
541  GCAGCAGCGCGGCCATTAGTGCTATGACTCAGGGTCGCGAGGGGCAACGTGTATTGGGTG

201  R D S V S G L R V P V R T R P P R N V R
601  CGCGACTCGGTTAGCGGCCTGCGCGTGCCCGTGCGCACCGGCCCCCGCGCAACGTGCGC

221  T R P P R N Y N R N I V N R L L G D A L
661  ACCCGCCCCCGCGCAACTACAACAGGAACATCGTGAACAGGCTGCTGGGCGACGCCCTG

241  T R P P R N -
721  ACCCGCCCCCGCGCAACTAG

```

Fig. 36

pVII sequence of PfcSPCD4-pVII-3 adenovirus SEQ IDNOS : 29 and 58

```

1  M S I L I S P S N N T G W G L R F P S K
1  ATGTCCATCCTTATATCGCCAGCAATAACACAGGCTGGGGCTGCGCTTCCAAGCAAG

21  M F G G A K K R S D Q H P V R V R G H Y
61  ATGTTTGGCGGGCCAAAGAAGCGCTCCGACCAACACCCAGTGGCGTGGCGGGGCACTAC

41  R A P W G A H K R G R T G R T T V D D A
121 CGCGCGCCCTGGGGCGCGCACAACGCGGCCGCACTGGGCGCACCACCGTCGATGACGCC

61  I D A V V E E A R N Y T P T P P P V S T
181 ATCGACGCGGTGGTGGAGGAGCGCAACTACGCCCACGCCGCCACCACTGTCACA

81  V D A A I Q T V V R G A R R Y A K M K R
241 GTGGACGCGCCATTAGACCGTGGTGGCGGAGCCGCGCTATGCTAAATGAAGAGA

101 R R R R V A R R H R R R P G T A A Q R A
301 CGCGGAGGCGCGTAGCACGTCGCCACCGCCGCCGACCCGCGCACTGCCGCCAACGCGCG

121 A A A L L N R A R R T G R R A A M R A A
361 GCGGCGGCCCTGCTTAACCGCGCACGTCGCACCGCCGACGGCGGCCATCGGGCCGCT

141 E Y L N K I Q N S L S T E W S P C S V I
421 GAATATTTGAACAAGATTCAAAGTCCCTCTCAACAGAATGGTCTCCTTGCAAGCGTGACT

161 R R L A A G I V T V P P R S R R R A A A
481 CGAAGGCTGGCCGCGGTATTGTCACTGTGCCCCCAGGTCCAGGCGACGAGCGCGCGC

181 A A A A A I S A M T Q G R R G N V Y W V
541 GCAGCAGCCGCGCCATTAGTGCTATGACTCAGGGTCGCAGGGGCAACGTGATTGGGTG

201 R D S V S G L R V P V R T R P P R N V R
601 CGCGACTCGGTAGCGGCCTGCGCGTGCCGTCGCGACCCGCCCCCGCGCAACGTGCGC

221 T R P P R N -
661 ACCCGCCCCCGGCAACTAG

```

Fig. 37

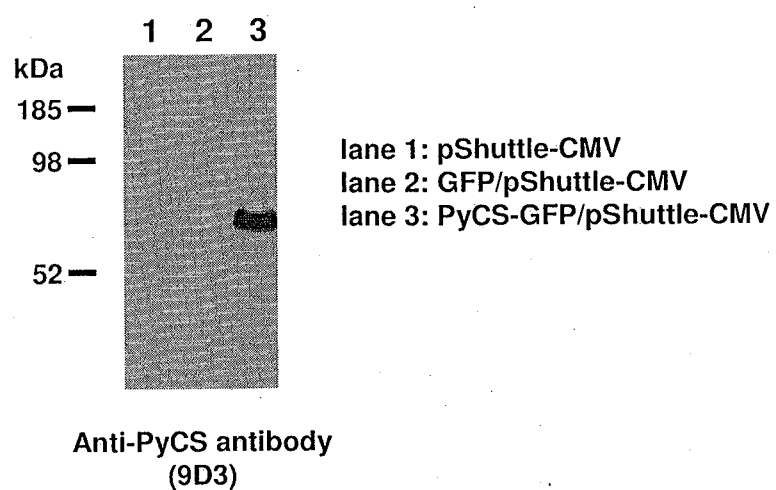


Fig. 38

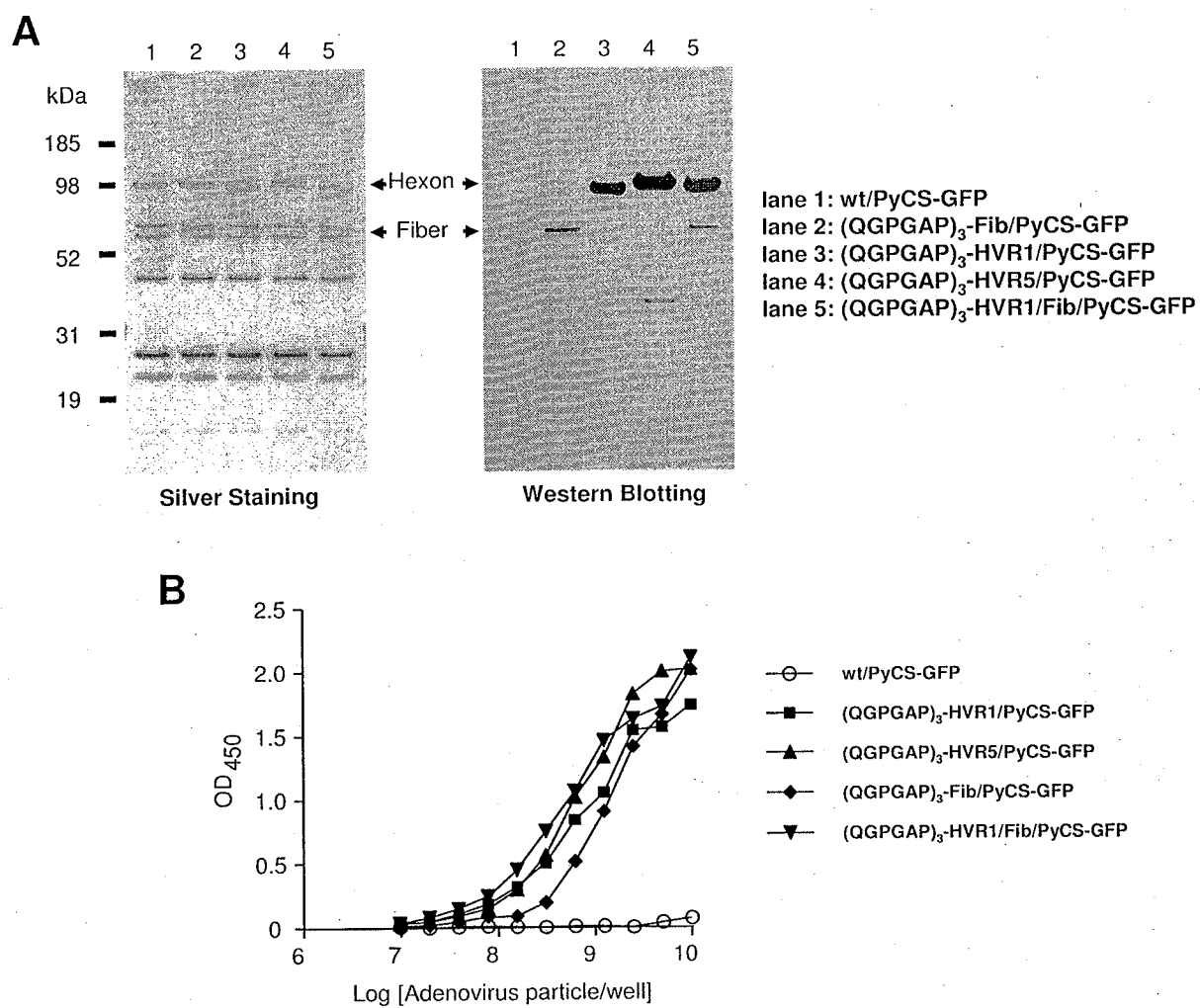


Fig. 39

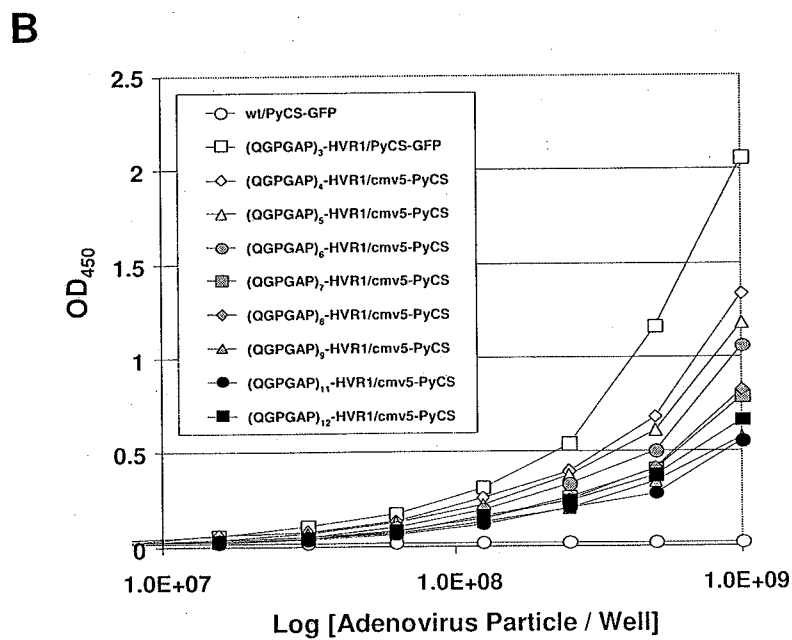
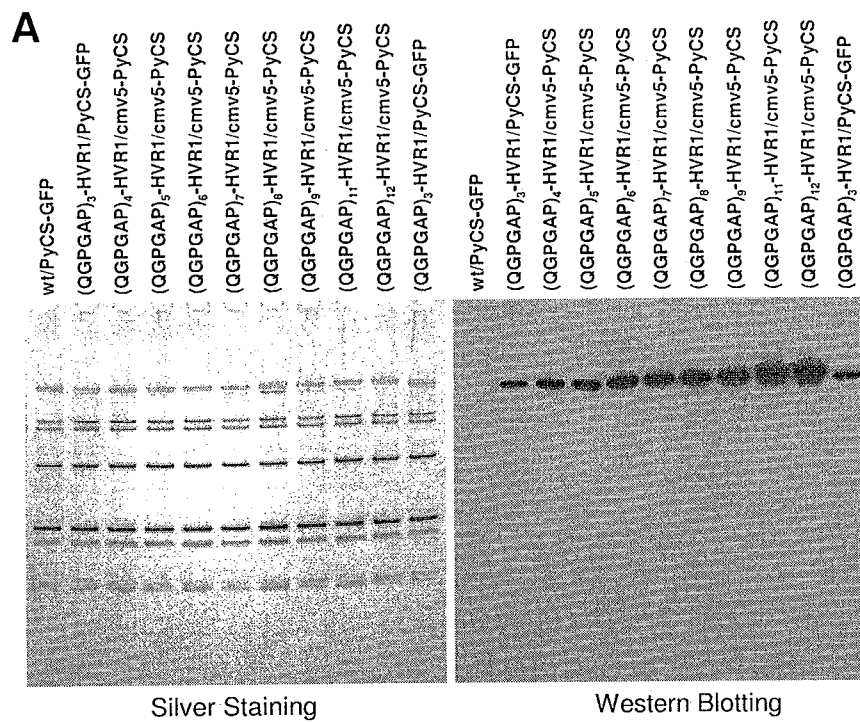


Fig. 40

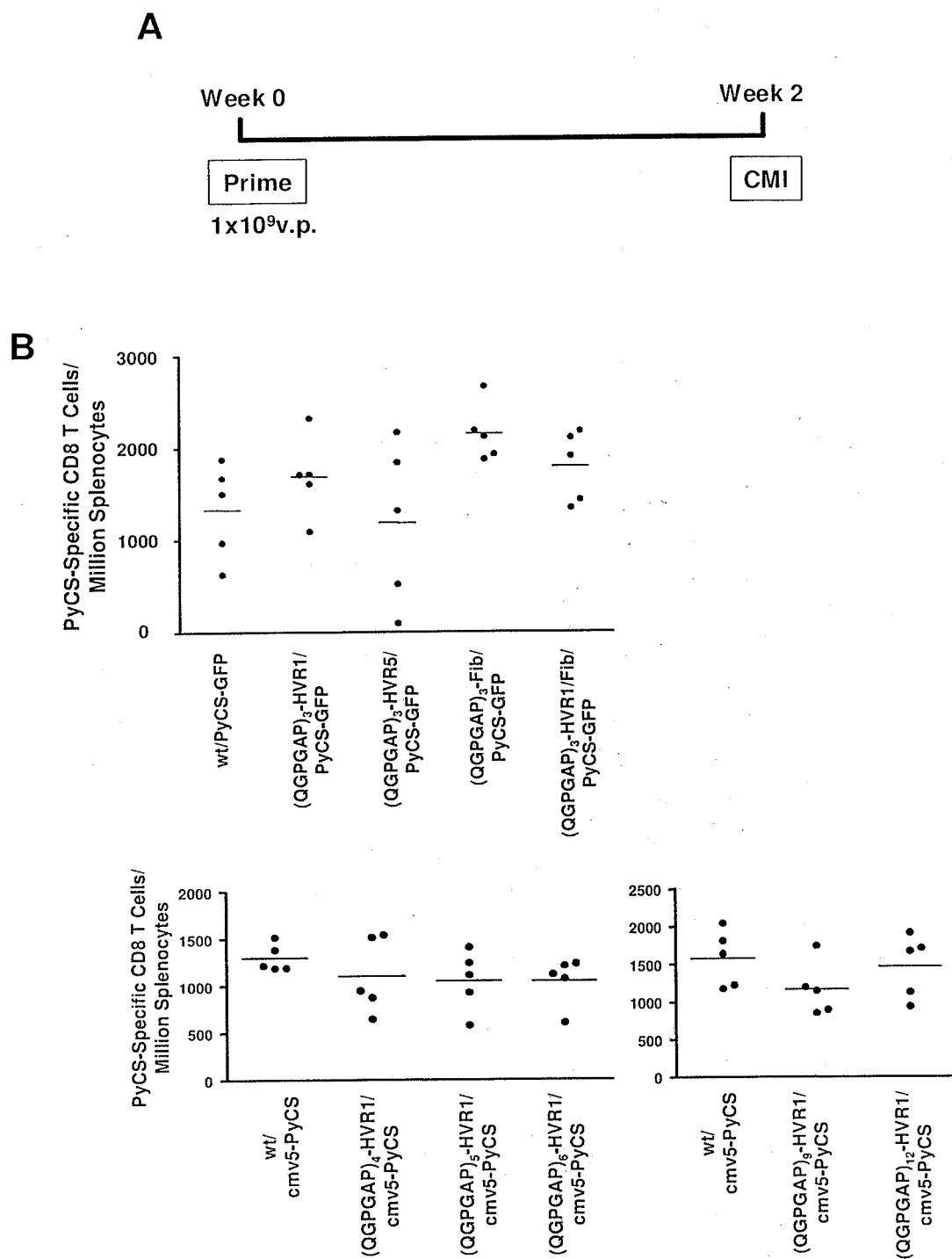


Fig. 41

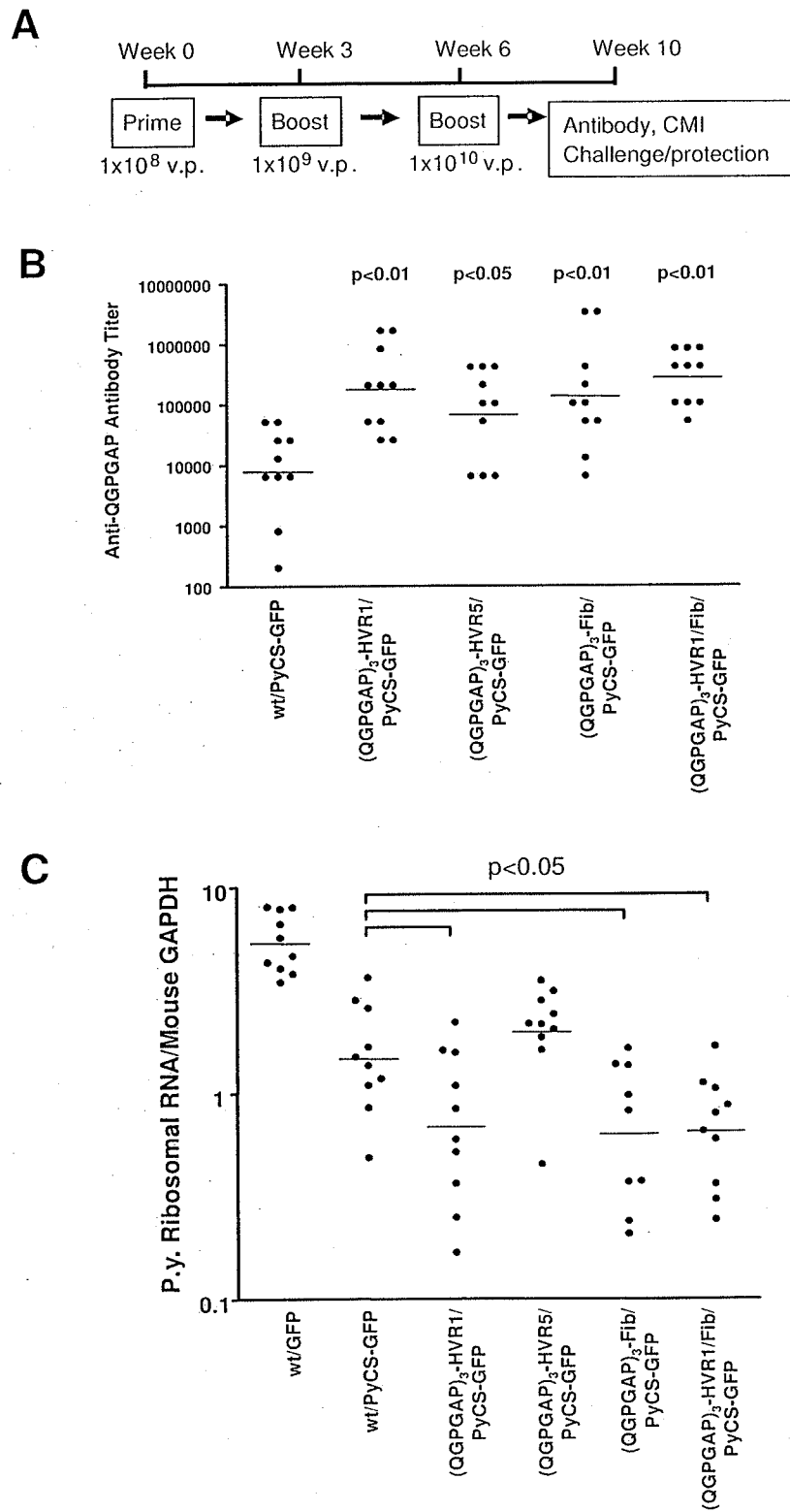


Fig. 42

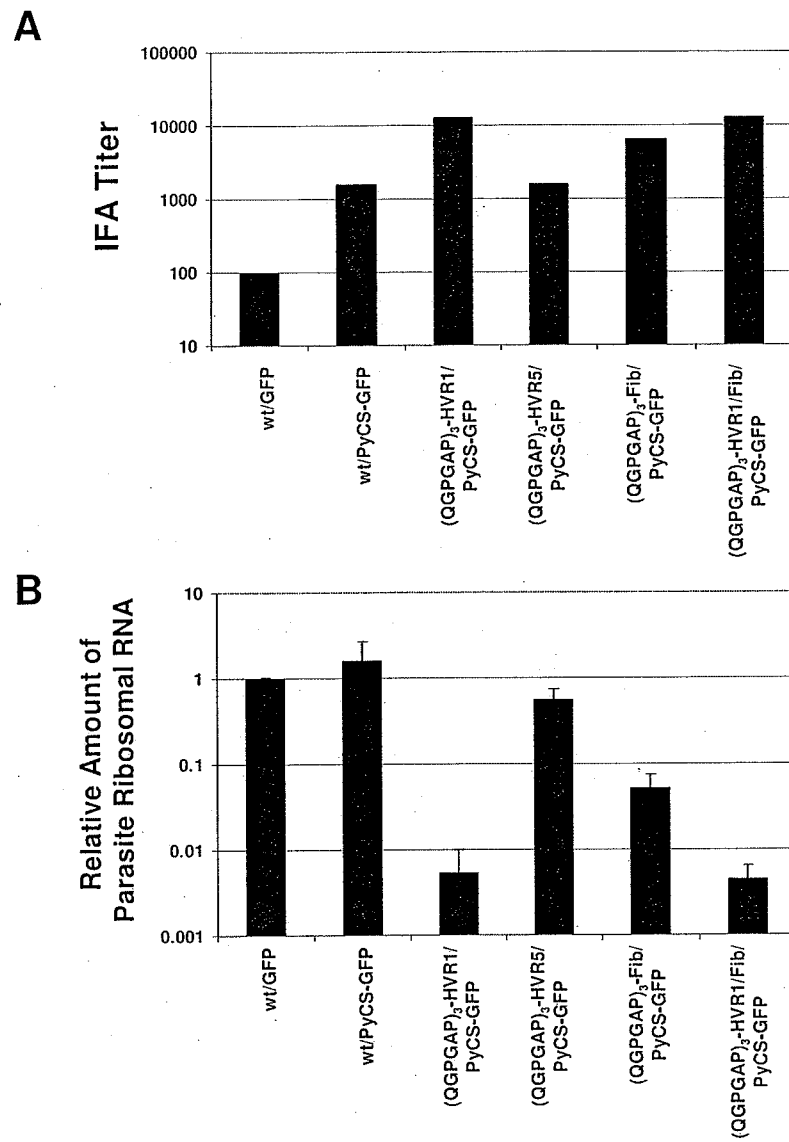


Fig. 43

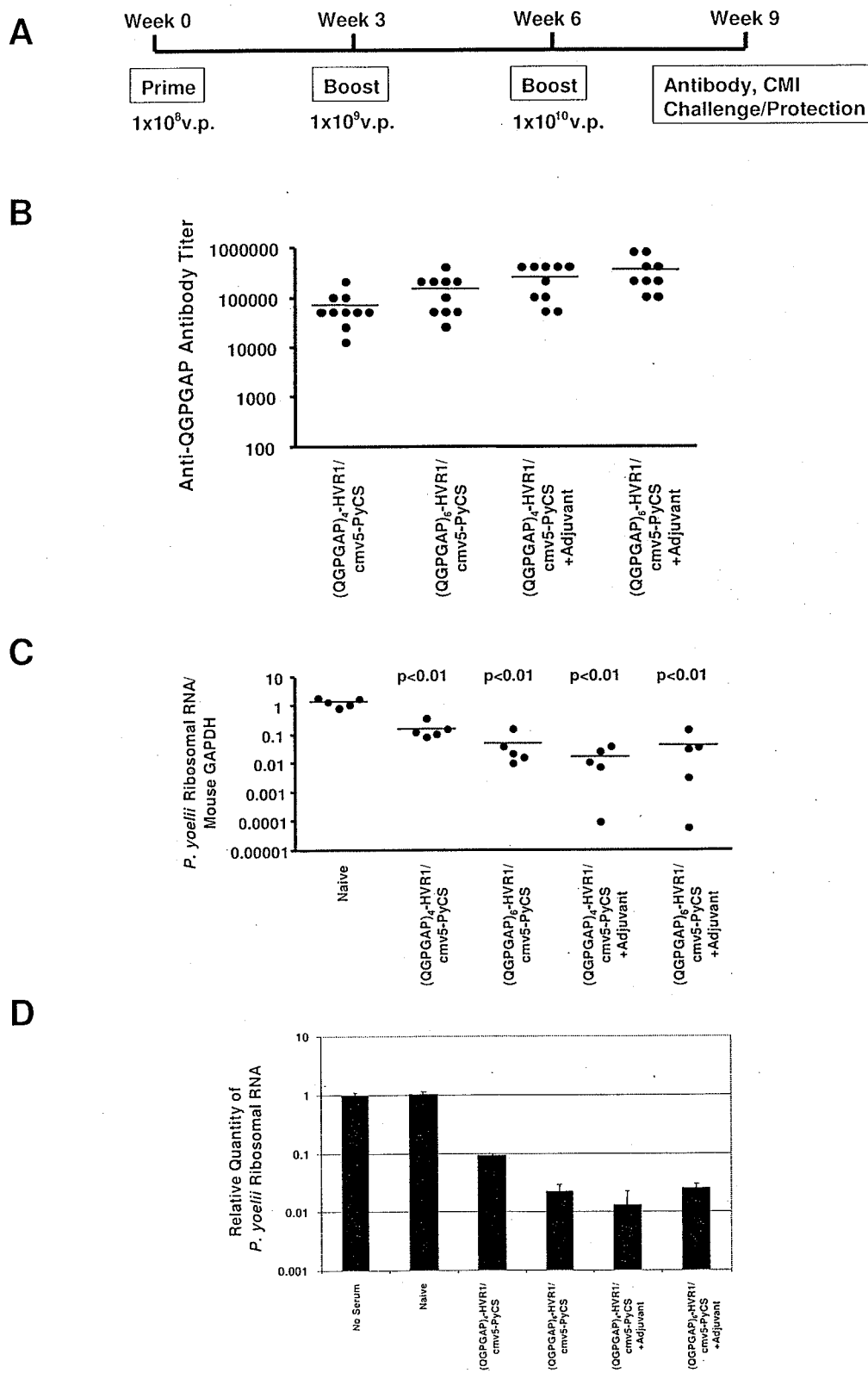


Fig. 44

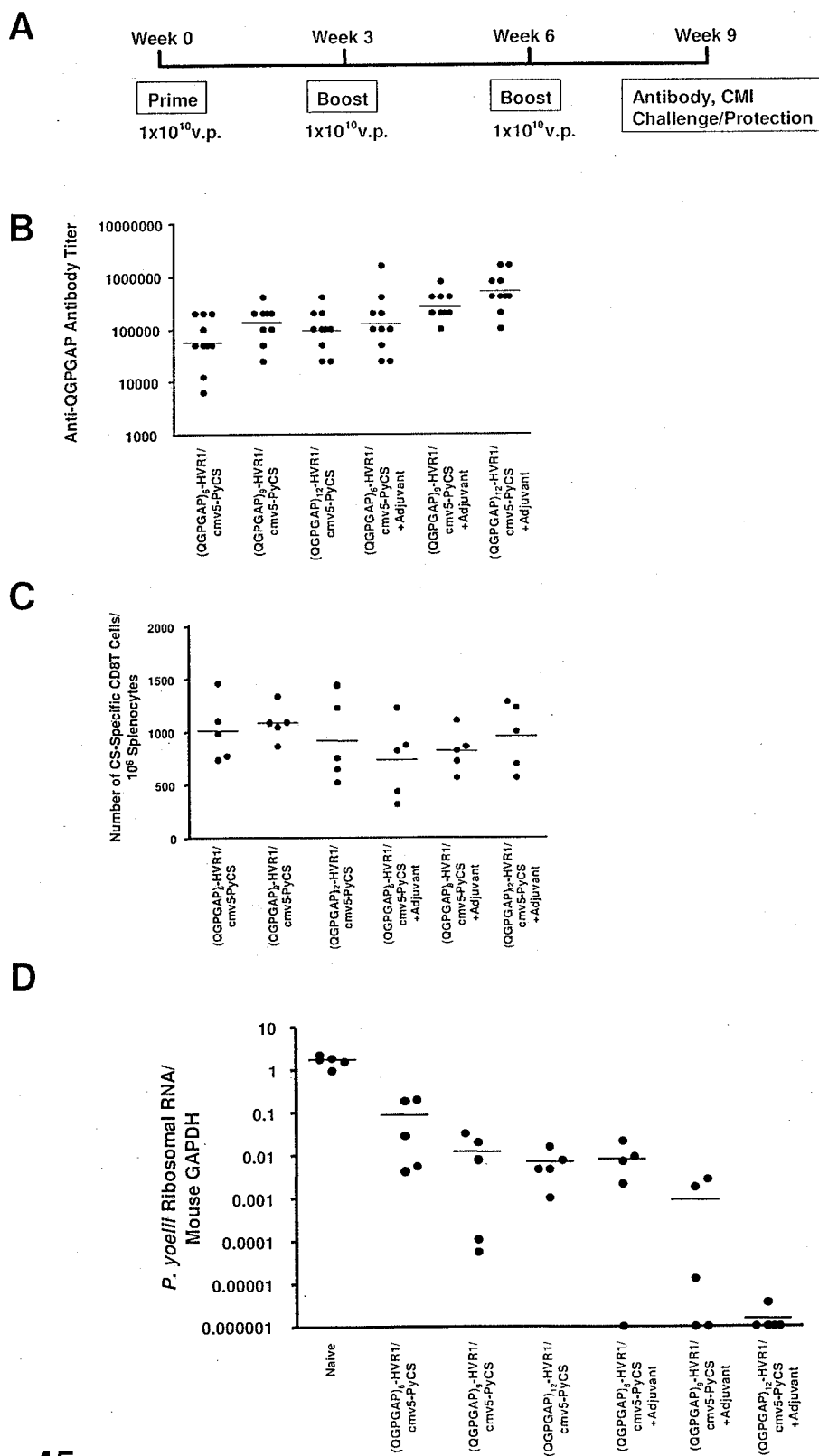


Fig. 45

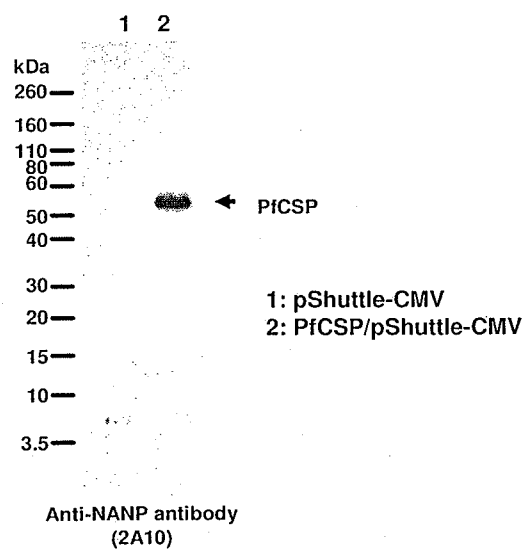
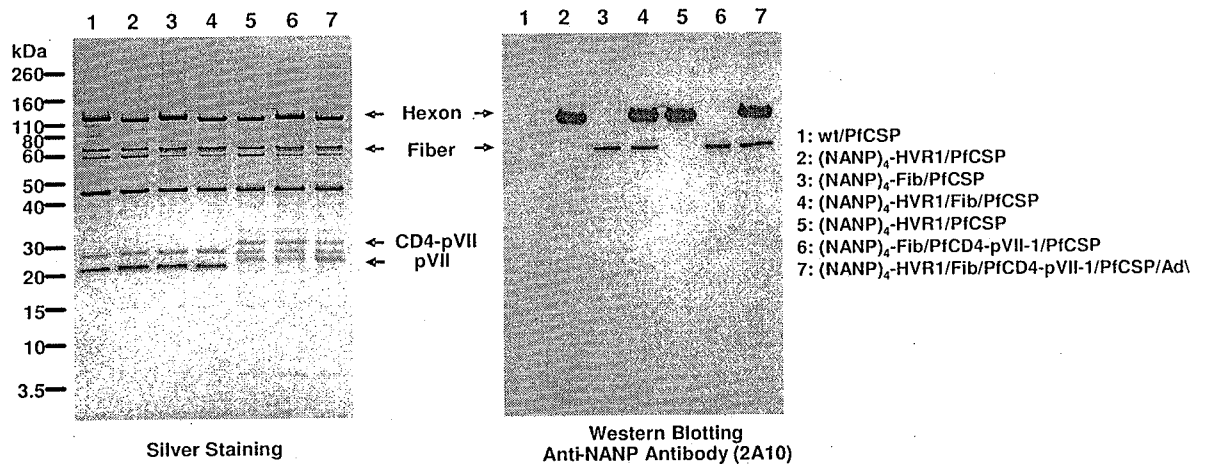


Fig. 46

A



B

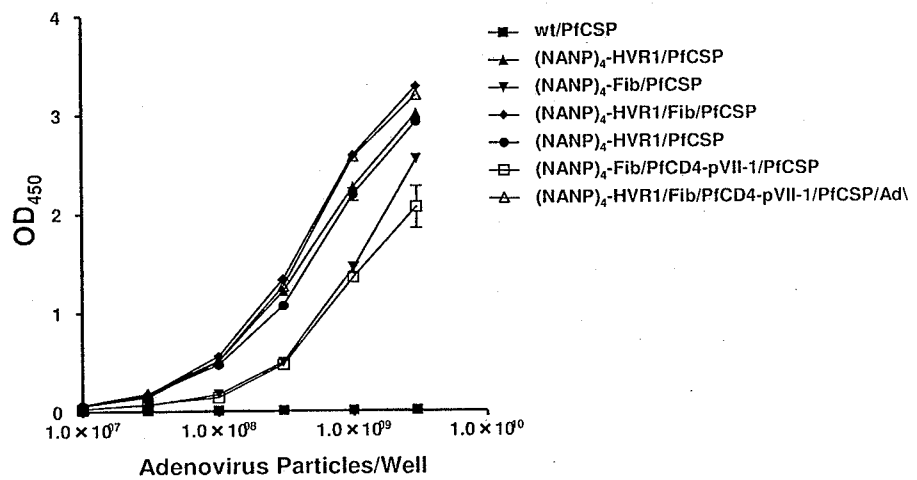
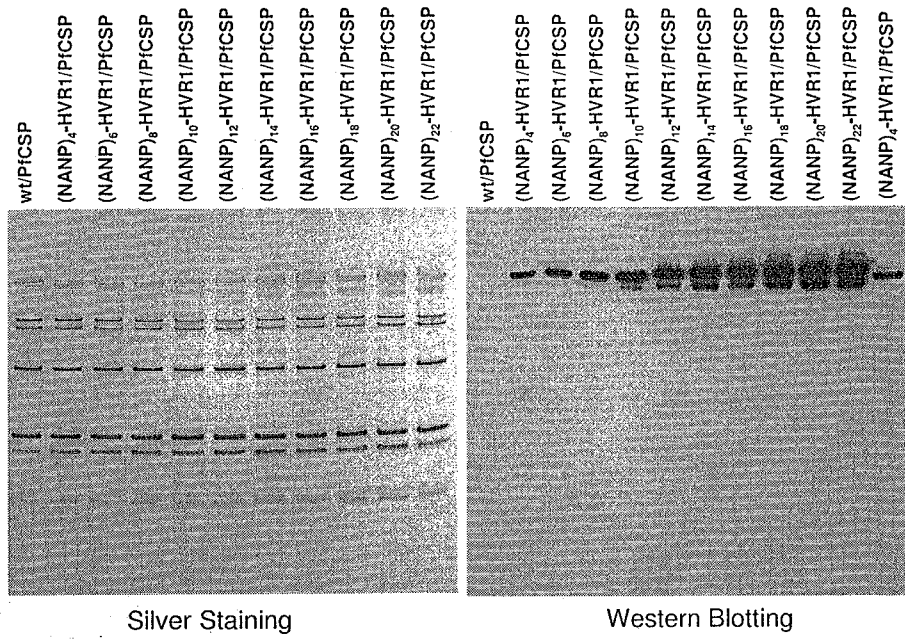


Fig. 47

A



B

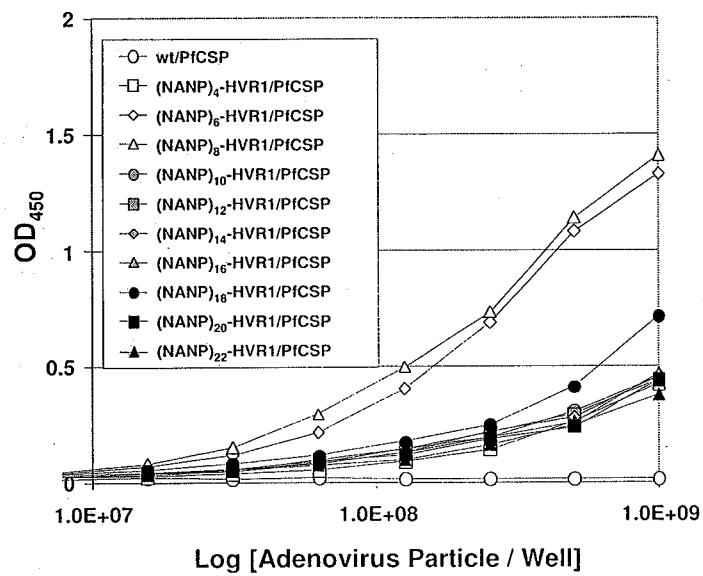


Fig. 48

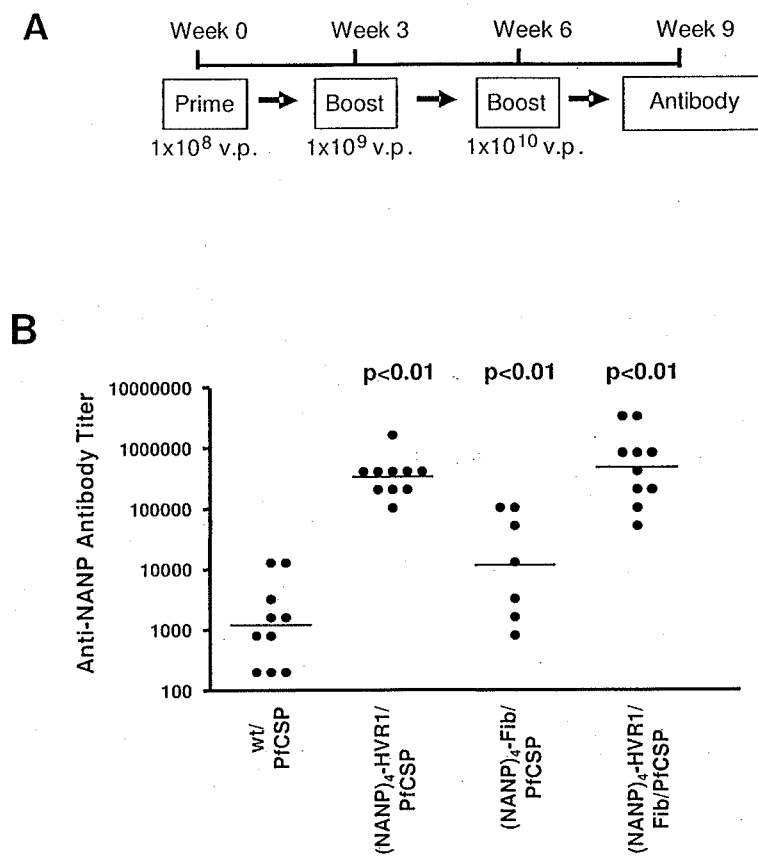
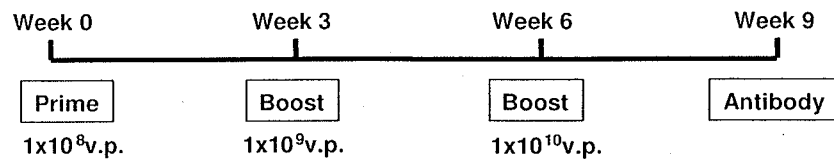


Fig. 49

A



B

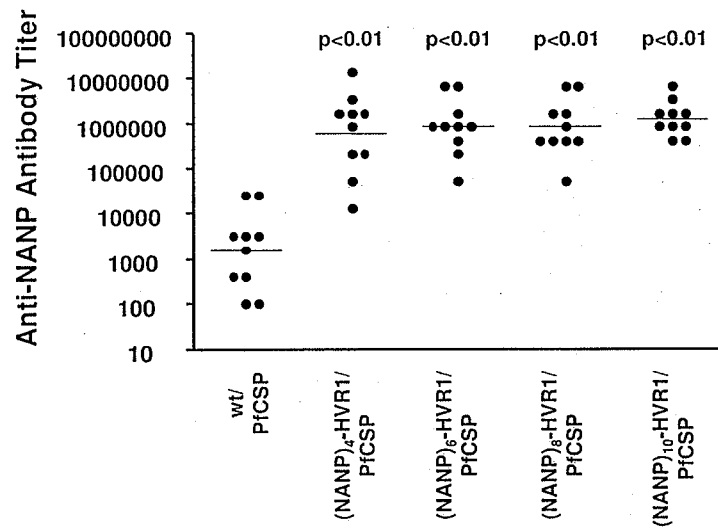


Fig. 50

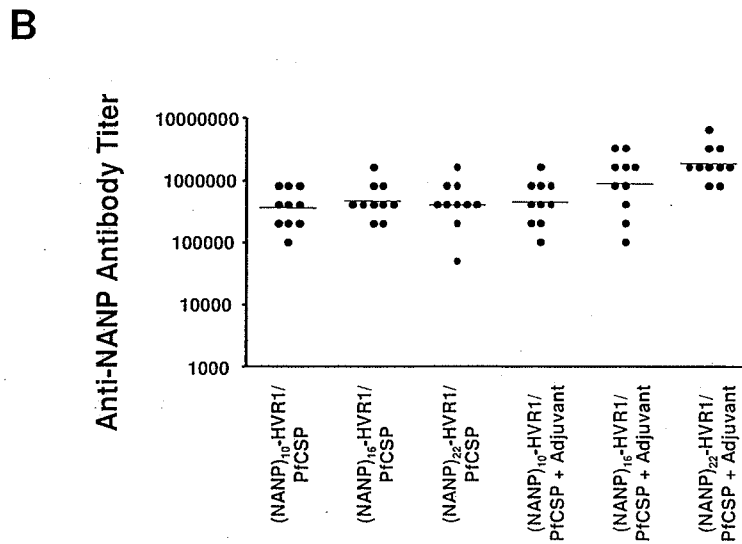
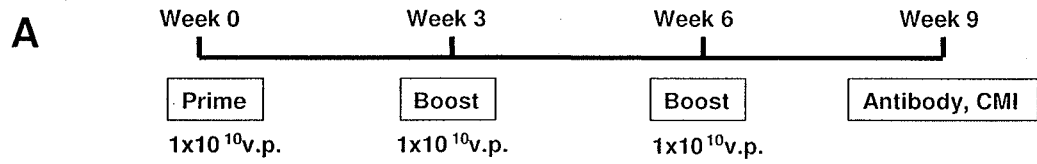


Fig. 51

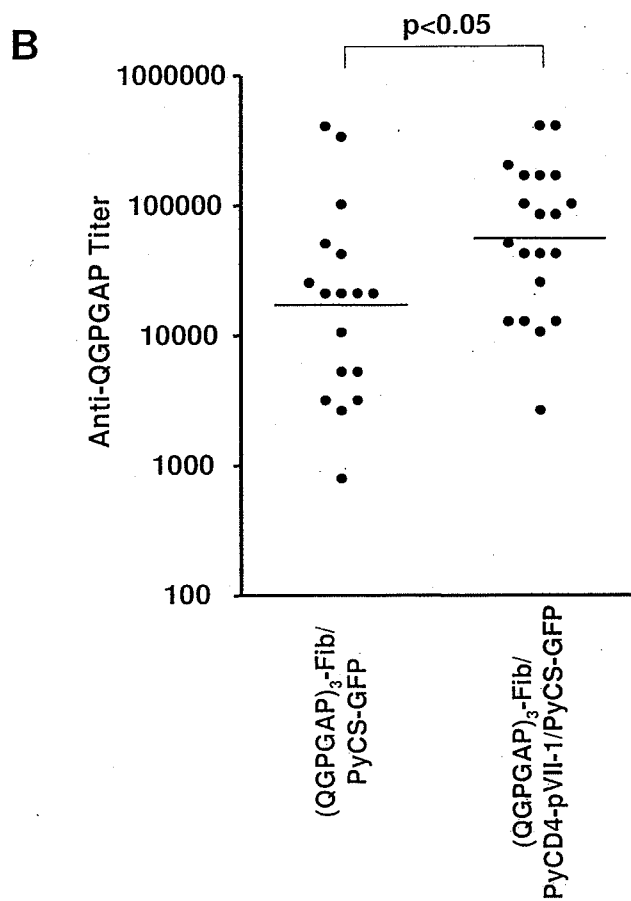
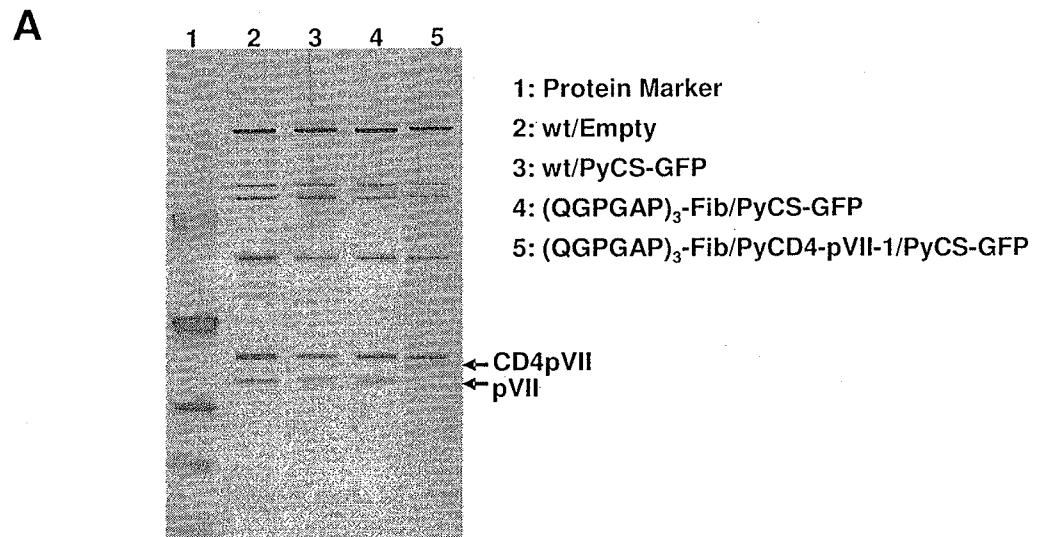


Fig. 52

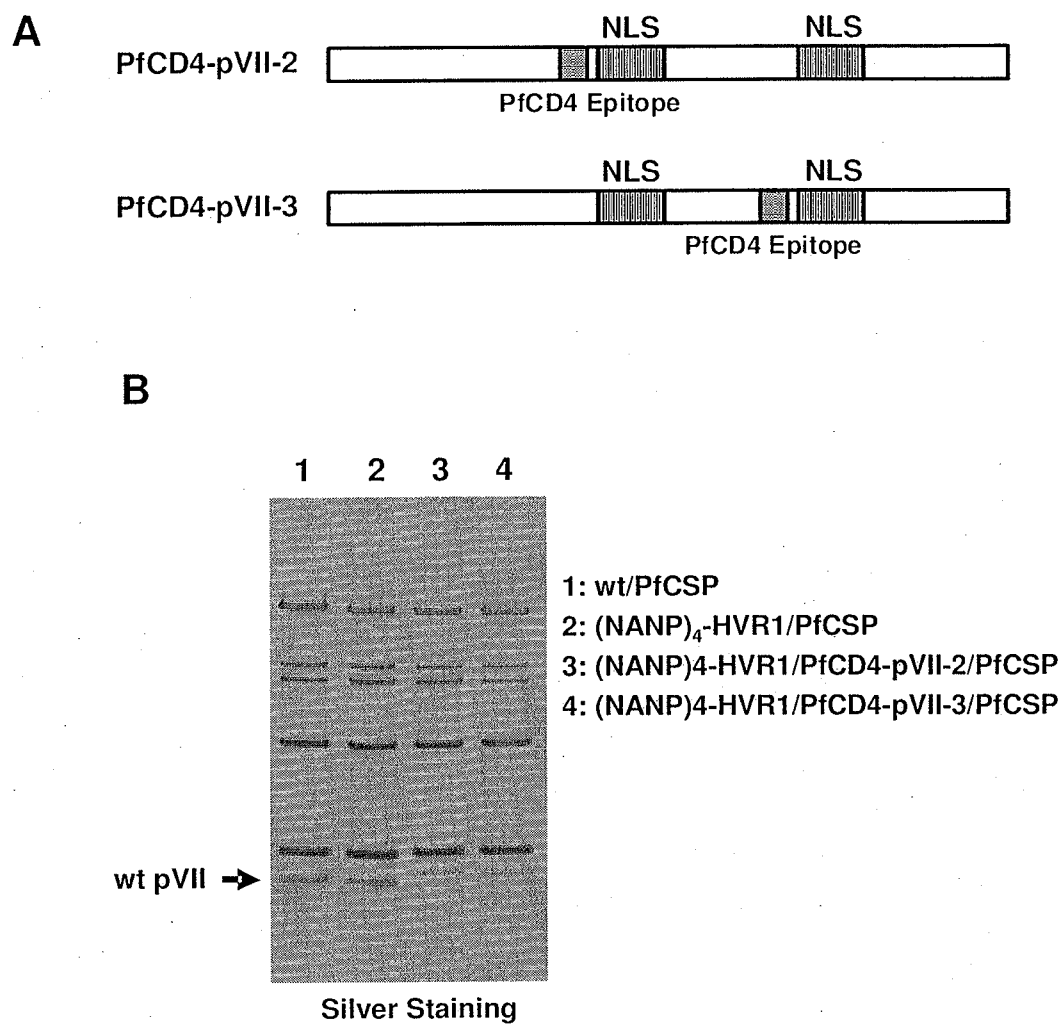


Fig. 53

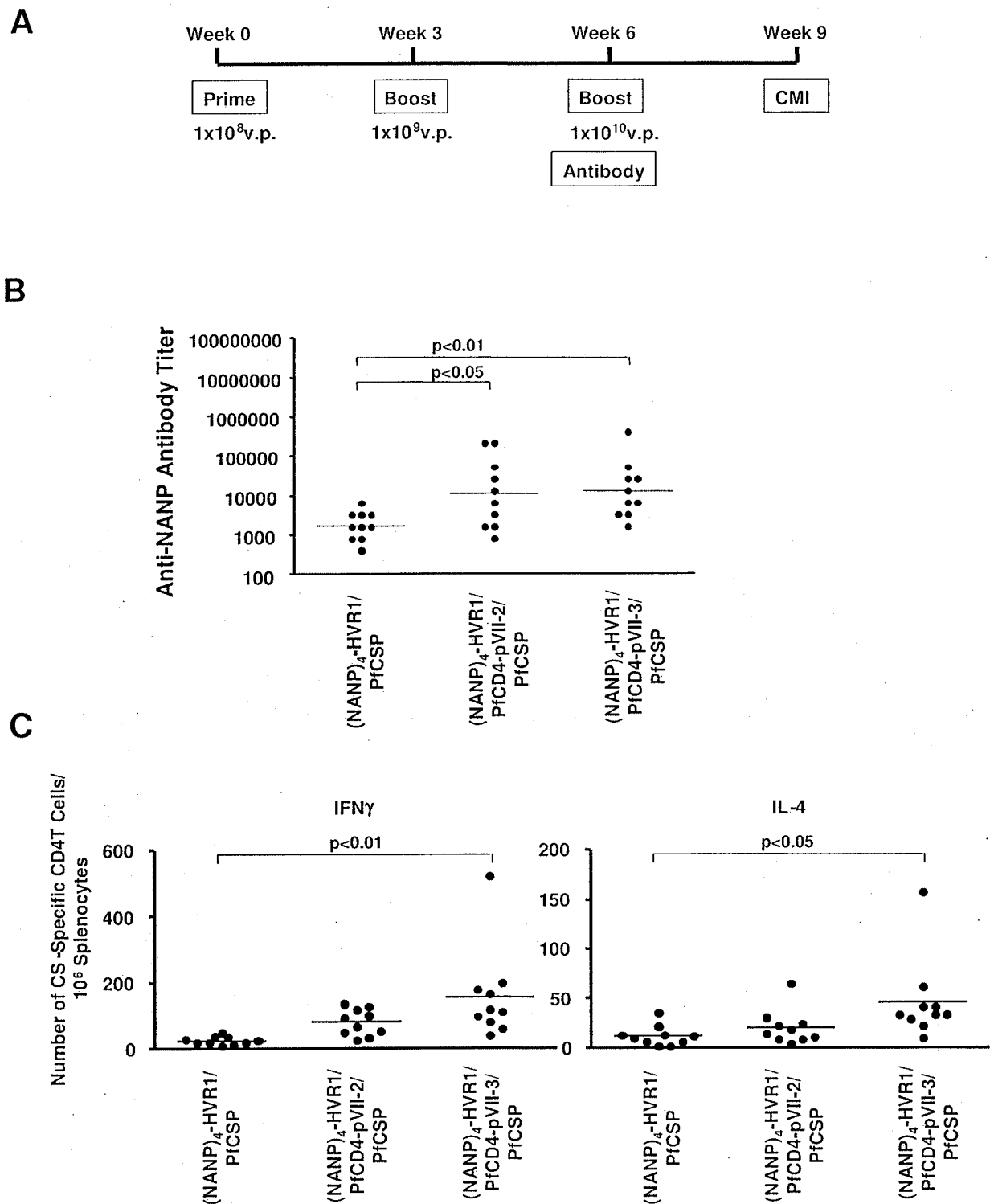


Fig. 54

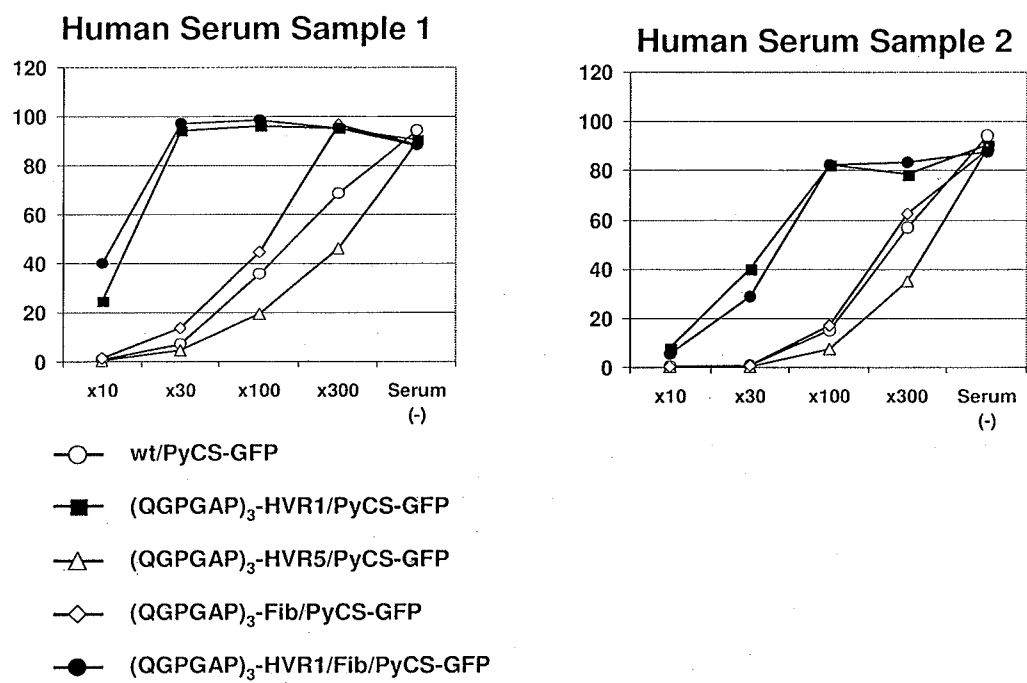


Fig. 55

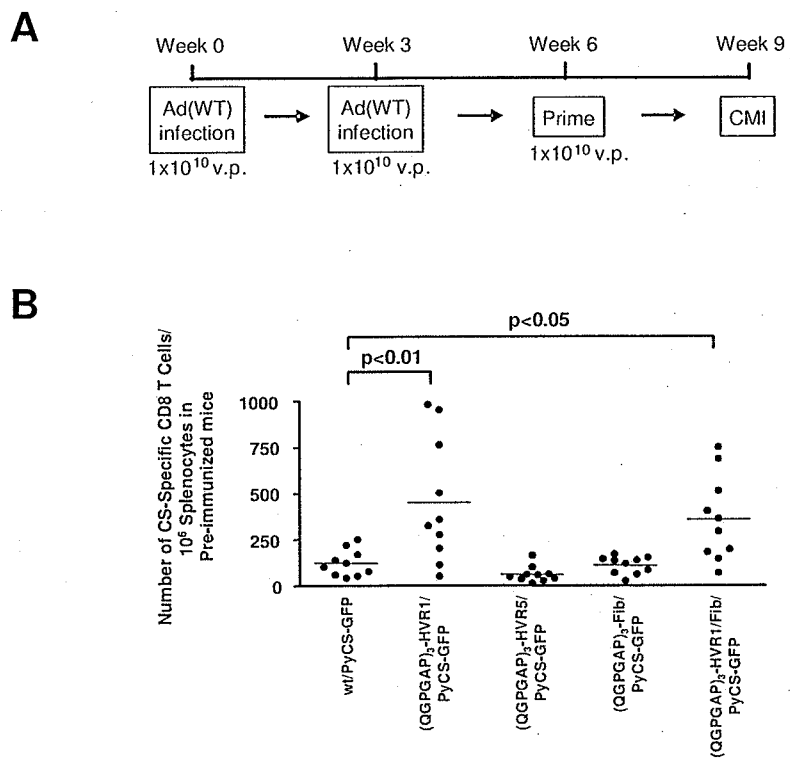
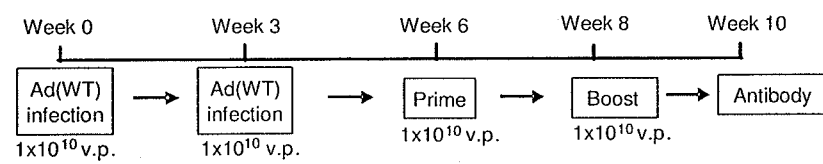


Fig. 56

A



B

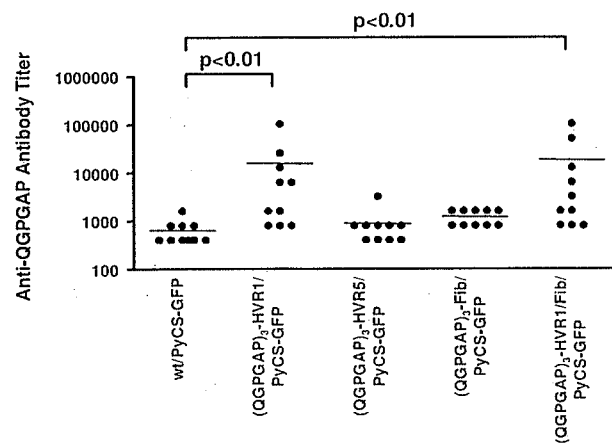


Fig. 57