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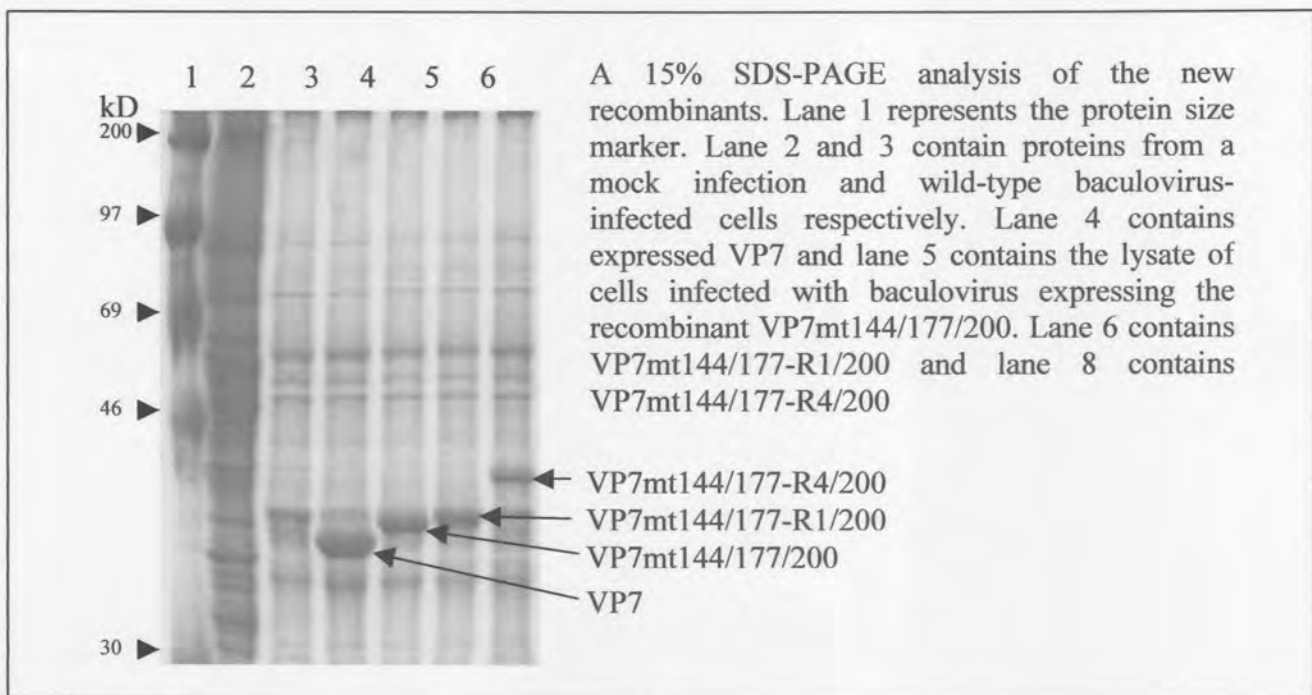
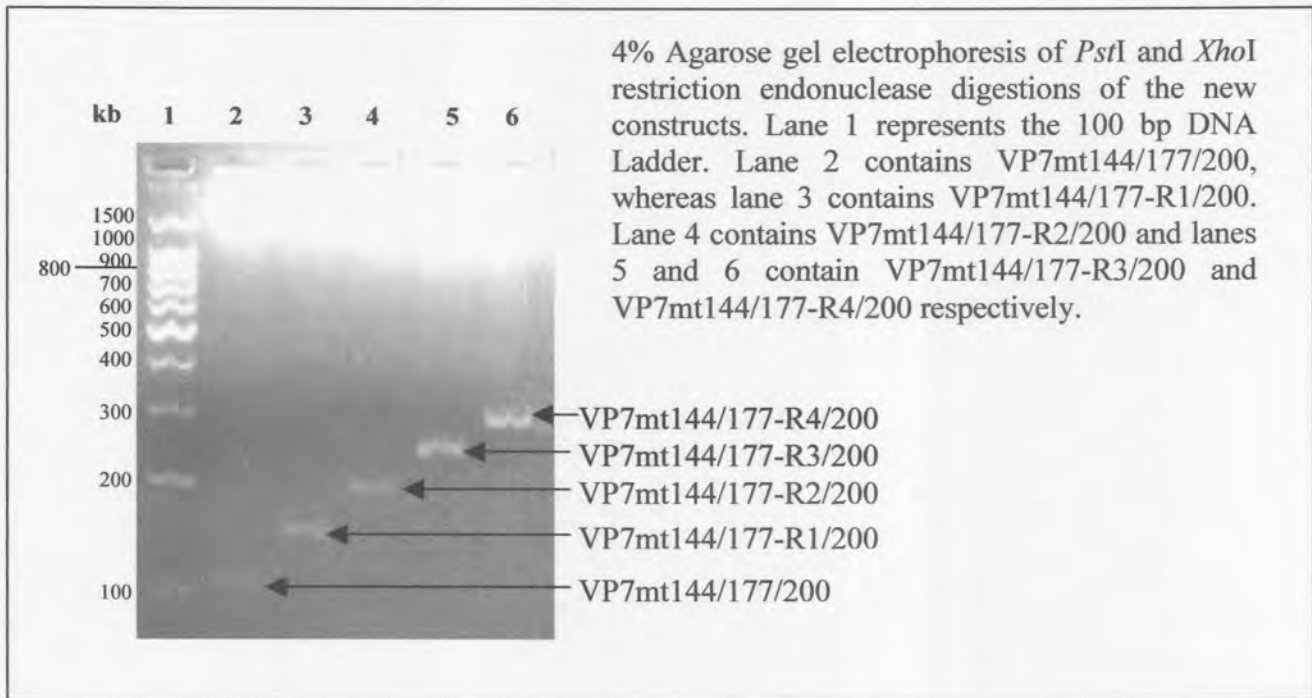
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Addendum

Oligonucleotides coding for the twelve amino acid RVLAIERYLKDL epitope of glycoprotein 120 of HIV subtype C was cloned into the 177 amino acid site of VP7mt144/177/200. A single epitope was inserted creating VP7mt144/177-R1/200. This new construct was subjected to subsequent insertions of the same peptide to create up to four copies of the epitope in the original VP7mt144/177/200 construct. The constructs containing one (VP7mt144/177-R1/200) and four (VP7mt144/177-R4/200) copies of the insert were expressed in Sf9 cells.



Nucleotide sequence of VP7mt144/177-R1/200 (1134 bp)

ATGGACGCGATACGAGCAAGAGCCTTGTCCGTTGTACGGGCATGTGTCACAGTGACAGATGCGAG
AGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGATTGCAATCAATAGGTATAATGGTTTAA
CAAATCATTCCGGTATCGATGAGGCCACAAACCCAAGCAGAACGAAATGAAATGTTTTTTATGTGT
ACTGATATGGTTTTAGCGGCGCTGAACGTCCAAATTGGGAATATTTACCAGATTATGATCAAGCG
TTGGCAACTGTGGGAGCTCTCGCAACGACTGAAATTCCATATAATGTTTCAGGCCATGAATGACATC
GTTAGAATAACGGGTCAGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGG
AGCGGTTGAGGTGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGT
CGAACGCGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGG
ACAGGTCAATGCGCTGCTAGCCCCAAGGCTGCATAGAGTCTTGGCTATAGAGAGATACCTAAAGGA
TCTGCAGGCGCGCAGGGGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTG
TGATCCTCAAGGTGCGAAGCTTTCTAGAGTCTGACTCACTTGAGAGCGCTCCAGGAACTTTTGTCA
CCGTTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATG
TTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTTATGGTATACGTCCTTGGATA
GATCGCTAGACACGGTTCGGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCA
CTTGGCACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTTT
TCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGC
GGCTTTGAGACCAGATTTTCAAGATGAATGGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCT
TGTGCTAGCAGCCTACCAC

Amino acid sequence of VP7mt144/177-R1/200 (378 amino acids)

MDAIRARALSVVRACVTVTDARVSLDPGVMETLGIAINRYNGLTNHSVSMR
PQTQAERNEMFFMCTDMVLAALNVQIGNISPDYDQALATV GALATTEI PYN
VQAMNDIVRITGQMOTFGPSKVQTGPYAGAVEVQQSGRYYPVPPGEFLEQGR
TRGGYINSNIAEVCMDAGAAGQVNALLAPRLHRVLAIERYLKDLQARRGDA
VMIYFVWRPLRIFCDPQGAKLSRVDSLESAPGTFVTVDGVNVAAGDVVAWN
TIAPVNVGNPGARRSILQFEVLWYTSLDRSLDTVPELAPTLTRCYAYVSPT
WHALRAVIFQQMNMQPINPPIFPPTERNEIVAYLLVASLADVYAALRPDFR
MNGVVAPVQGQINRALVLAAYH

Nucleotide sequence of VP7mt144/177-R4/200 (1251 bp)

ATGGACGCGATACGAGCAAGAGCCTTGTCCGTTGTACGGGCATGTGTCACAGTGACAGATGCGAG
AGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGATTGCAATCAATAGGTATAATGGTTTAA
CAAATCATTCCGGTATCGATGAGGCCACAAACCCAAGCAGAACGAAATGAAATGTTTTTTATGTGT
ACTGATATGGTTTTAGCGGCGCTGAACGTCCAAATTGGGAATATTTACCAGATTATGATCAAGCG
TTGGCAACTGTGGGAGCTCTCGCAACGACTGAAATTCCATATAATGTTTCAGGCCATGAATGACATC
GTTAGAATAACGGGTCAGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGG
AGCGGTTGAGGTGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGT
CGAACGCGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGG
ACAGGTCAATGCGCTGCTAGCCCCAAGGCTGCATAGAGTCTTGGCTATAGAGAGATACCTAAAGGA
TCTGCATAGAGTCTTGGCTATAGAGAGATACCTAAAGGATCTGCATAGAGTCTTGGCTATAGAGAGA
TACCTAAAGGATCTGCATAGAGTCTTGGCTATAGAGAGATACCTAAAGGATCTGCAGGCGCGCAGG
GGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCG
AAGCTTTCTAGAGTCTGACTCACTTGAGAGCGCTCCAGGAACTTTTGTACCAGTTGATGGAGTAAA
TGTTGCAGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGGC
ACGCAGATCAATTTTACAGTTTGAAGTGTTATGGTATACGTCCTTGGATAGATCGCTAGACACGGT

TCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTTGGCACGCATTACG
CGCTGTCATTTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTTTTCCACCGACTGAAAG
GAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGA
TTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTA
CCAC

Amino acid sequence of VP7mt144/177-R4/200 (417 amino acids)

MDAIRARALSVVVRACVTVTDARVSLDPGVMETLGLAINRYNGLTNHSVSMRPQTQAERNEMFFMCTD
MVLAAALNVQIGNISPDYDQALATVGALATTEIPYNVQAMNDIVRITGQMOTFGPSKVQTGPYAGAVE
VQSGRYYVPPGEFLEQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRLHRVLAIERYLKDLHRV
LAIERYLKDLHRVLAIERYLKDLHRVLAIERYLKDLQARRGDAVMYFVWRPLRIFCDPQGAKLSR
VDSLESAPGTFVTVDGVNVAAGDVVAWNTIAPVNVGNPGARRSILQFEVLWYTSLDRSLDTVPELAPT
LTRCYAYVSPTWHALRAVIFQMNMQPINPPIFPPTERNEIVAYLLVASLADVYAALRPDFRMNGVVA
PVGQINRALVLAAYH

Appendices

Appendix A. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7 with VP7mt144/177/200.

| | | |
|---------------|---|-----|
| VP7 | GTTTAAATTCGGTTAGGATGGACGCGATA CG AGCAAGAGCCTTGTCGGTTGTACGGGCA | 42 |
| | M D A I R A R A L S V V R A | 14 |
| mt144/177/200 | GTTTAAATTCGGTTAGGATGGACGCGATA GC AGCAAGAGCCTTGTCGGTTGTACGGGCA | 42 |
| | M D A I A A R A L S V V R A | 14 |
| | ***** | |
| VP7 | TGTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGG | 102 |
| | C V T V T D A R V S L D P G V M E T L G | 34 |
| mt144/177/200 | TGTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGG | 102 |
| | C V T V T D A R V S L D P G V M E T L G | 34 |
| | ***** | |
| VP7 | ATTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACC | 162 |
| | I A I N R Y N G L T N H S V S M R P Q T | 54 |
| mt144/177/200 | ATTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACC | 162 |
| | I A I N R Y N G L T N H S V S M R P Q T | 54 |
| | ***** | |
| VP7 | CAAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAAC | 222 |
| | Q A E R N E M F F M C T D M V L A A L N | 74 |
| mt144/177/200 | CAAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAAC | 222 |
| | Q A E R N E M F F M C T D M V L A A L N | 74 |
| | ***** | |
| VP7 | GTCCAAATTGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTC | 282 |
| | V Q I G N I S P D Y D Q A L A T V G A L | 94 |
| mt144/177/200 | GTCCAAATTGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTC | 282 |
| | V Q I G N I S P D Y D Q A L A T V G A L | 94 |
| | ***** | |
| VP7 | GCAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGT | 342 |
| | A T T E I P Y N V Q A M N D I V R I T G | 114 |
| mt144/177/200 | GCAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGT | 342 |
| | A T T E I P Y N V Q A M N D I V R I T G | 114 |
| | ***** | |
| VP7 | CAGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAG | 402 |
| | Q M Q T F G P S K V Q T G P Y A G A V E | 134 |
| mt144/177/200 | CAGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAG | 402 |
| | Q M Q T F G P S K V Q T G P Y A G A V E | 134 |
| | ***** | |
| VP7 | GTGCAACAATCTGGCAGATATTACGTACCG-----CAAGGTCGAACG | 444 |
| | V Q Q S G R Y Y V P Q G R T | 148 |
| mt144/177/200 | GTGCAACAATCTGGCAGATATTACGTACCG CCCGGGGAATTCCTCGAG CAAGGTCGAACG | 462 |
| | V Q Q S G R Y Y V P P G E F L E Q G R T | 154 |
| | ***** | |
| VP7 | CGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGA | 504 |
| | R G G Y I N S N I A E V C M D A G A A G | 168 |
| mt144/177/200 | CGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGA | 522 |
| | R G G Y I N S N I A E V C M D A G A A G | 174 |
| | ***** | |

| | | |
|---------------|---|-------|
| VP7 | CAGGTCAATGCGCTGCTAGCCCCAAGG-----AGGGGGGACGCAGTC | 556 |
| | Q V N A L L A P R R G D A V | 182 |
| mt144/177/200 | CAGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCTGCGCGCAGGGGGGACGCAGTC | 582 |
| | Q V N A L L A P R L Q R P A R R G D A V | 194 |
| | ***** | ***** |
| VP7 | ATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCG----- | 610 |
| | M I Y F V W R P L R I F C D P Q G A | 200 |
| mt144/177/200 | ATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTT | 642 |
| | M I Y F V W R P L R I F C D P Q G A K L | 214 |
| | ***** | ***** |
| VP7 | -----TCACTTGAGAGCGCTCCAGGAACCTTTTGTACCGTTGATGGAGTAAAT | 658 |
| | S L E S A P G T F V T V D G V N | 216 |
| mt144/177/200 | TCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTACCGTTGATGGAGTAAAT | 702 |
| | S R V D S L E S A P G T F V T V D G V N | 234 |
| | ***** | ***** |
| VP7 | GTTGCAGCTGGAGATGTCGTCGTCATGGAATACTATTGCACCGTGAATGTTGGAAATCCT | 718 |
| | V A A G D V V A W N T I A P V N V G N P | 236 |
| mt144/177/200 | GTTGCAGCTGGAGATGTCGTCGTCATGGAATACTATTGCACCGTGAATGTTGGAAATCCT | 762 |
| | V A A G D V V A W N T I A P V N V G N P | 254 |
| | ***** | ***** |
| VP7 | GGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCG | 778 |
| | G A R R S I L Q F E V L W Y T S L D R S | 256 |
| mt144/177/200 | GGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCG | 822 |
| | G A R R S I L Q F E V L W Y T S L D R S | 274 |
| | ***** | ***** |
| VP7 | CTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCC | 798 |
| | L D T V P E L A P T L T R C Y A Y V S P | 276 |
| mt144/177/200 | CTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCC | 882 |
| | L D T V P E L A P T L T R C Y A Y V S P | 294 |
| | ***** | ***** |
| VP7 | ACTTGGCACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGCAGCCTATTAATCCG | 858 |
| | T W H A L R A V I F Q Q M N M Q P I N P | 296 |
| mt144/177/200 | ACTTGGCACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGCAGCCTATTAATCCG | 942 |
| | T W H A L R A V I F Q Q M N M Q P I N P | 314 |
| | ***** | ***** |
| VP7 | CCGATTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTA | 918 |
| | P I F P P T E R N E I V A Y L L V A S L | 316 |
| mt144/177/200 | CCGATTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTA | 1002 |
| | P I F P P T E R N E I V A Y L L V A S L | 334 |
| | ***** | ***** |
| VP7 | GCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAAGATGAATGGTGTGTCGCGCCAGTA | 978 |
| | A D V Y A A L R P D F R M N G V V A P V | 336 |
| mt144/177/200 | GCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAAGATGAATGGTGTGTCGCGCCAGTA | 1062 |
| | A D V Y A A L R P D F R M N G V V A P V | 354 |
| | ***** | ***** |
| VP7 | GGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACG | 1020 |
| | G Q I N R A L V L A A Y H Stop | 349 |
| mt144/177/200 | GGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACG | 1104 |
| | G Q I N R A L V L A A Y H Stop | 367 |
| | ***** | ***** |

Appendix B-1. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VPmt144/177-A/200.

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mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT 43
                M D A I A A R A L S V V R A C 15
mt144/177-A/200 GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT 43
                M D A I A A R A L S V V R A C 15
                *****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA 103
                V T V T D A R V S L D P G V M E T L G I 35
mt144/177-A/200 GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA 103
                V T V T D A R V S L D P G V M E T L G I 35
                *****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC 163
                A I N R Y N G L T N H S V S M R P Q T Q 55
mt144/177-A/200 TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC 163
                A I N R Y N G L T N H S V S M R P Q T Q 55
                *****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTAAGTATGGTTTTAGCGGCGCTGAACG 223
                A E R N E M F F M C T D M V L A A L N V 75
mt144/177-A/200 AAGCAGAACGAAATGAAATGTTTTTTATGTGTAAGTATGGTTTTAGCGGCGCTGAACG 223
                A E R N E M F F M C T D M V L A A L N V 75
                *****

mt144/177/200  TCCAAATTGGGAATATTTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG 283
                Q I G N I S P D Y D Q A L A T V G A L A 95
mt144/177-A/200 TCCAAATTGGGAATATTTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG 283
                Q I G N I S P D Y D Q A L A T V G A L A 95
                *****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC 343
                T T E I P Y N V Q A M N D I V R I T G Q 115
mt144/177-A/200 CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC 343
                T T E I P Y N V Q A M N D I V R I T G Q 115
                *****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG 403
                M Q T F G P S K V Q T G P Y A G A V E V 135
mt144/177-A/200 AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG 403
                M Q T F G P S K V Q T G P Y A G A V E V 135
                *****

mt144/177/200  TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTGCAACGC 463
                Q Q S G R Y Y V P P G E F L E Q G R T R 155
mt144/177-A/200 TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTGCAACGC 463
                Q Q S G R Y Y V P P G E F L E Q G R T R 155
                *****

mt144/177/200  GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC 523
                G G Y I N S N I A E V C M D A G A A G Q 175
mt144/177-A/200 GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC 523
                G G Y I N S N I A E V C M D A G A A G Q 175
                *****

mt144/177/200  AGGTCAATGCGCTGCTAGCCCCAAGG----- 561
                V N A L L A P R 187

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mt144/177-A/200 AGGTCAATGCGCTGCTAGCCCCAAGGCTGCATAAGAAGAAAGAAGAGGGTGAGGATGATA 583
V N A L L A P R L H K K K E E G E D D T 195

mt144/177/200 -----CTGCAGGCGCGCAGGGGGGACGCAGTCATGA 592
L Q A R R G D A V M I 198

mt144/177-A/200 CTGCTCGACAGGAGATAAGAAAAGCATGGCTGCAGGCGCGCAGGGGGGACGCAGTCATGA 643
A R Q E I R K A W L Q A R R G D A V M I 215

mt144/177/200 TCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTA 612
Y F V W R P L R I F C D P Q G A K L S R 218

mt144/177-A/200 TCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTA 703
Y F V W R P L R I F C D P Q G A K L S R 235

mt144/177/200 GAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTGTCCCGTTGATGGAGTAAATGTTG 672
V D S L E S A P G T F V T V D G V N V A 238

mt144/177-A/200 GAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTGTCCCGTTGATGGAGTAAATGTTG 763
V D S L E S A P G T F V T V D G V N V A 255

mt144/177/200 CAGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGG 732
A G D V V A W N T I A P V N V G N P G A 258

mt144/177-A/200 CAGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGG 823
A G D V V A W N T I A P V N V G N P G A 275

mt144/177/200 CACGCAGATCAATTTTACAGTTTGAAGTGTTATGGTATACGTCCTTGGATAGATCGCTAG 792
R R S I L Q F E V L W Y T S L D R S L D 278

mt144/177-A/200 CACGCAGATCAATTTTACAGTTTGAAGTGTTATGGTATACGTCCTTGGATAGATCGCTAG 883
R R S I L Q F E V L W Y T S L D R S L D 295

mt144/177/200 ACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTT 852
T V P E L A P T L T R C Y A Y V S P T W 298

mt144/177-A/200 ACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTT 943
T V P E L A P T L T R C Y A Y V S P T W 315

mt144/177/200 GGCACGCATTACGCGCTGTCAATTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGA 912
H A L R A V I F Q Q M N M Q P I N P P I 318

mt144/177-A/200 GGCACGCATTACGCGCTGTCAATTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGA 1003
H A L R A V I F Q Q M N M Q P I N P P I 335

mt144/177/200 TTTTTCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTG 972
F P P T E R N E I V A Y L L V A S L A D 338

mt144/177-A/200 TTTTTCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTG 1063
F P P T E R N E I V A Y L L V A S L A D 355

mt144/177/200 ATGTGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCC 1032
V Y A A L R P D F R M N G V V A P V G Q 358

mt144/177-A/200 ATGTGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCC 1123
V Y A A L R P D F R M N G V V A P V G Q 375

mt144/177/200 AGATTAACAGAGCTCTTGTGCTAGCAGCCTACCCTAGTGGCTGCGGTGTTGCACGGTCA 1070
I N R A L V L A A Y H Stop 369

mt144/177-A/200 AGATTAACAGAGCTCTTGTGCTAGCAGCCTACCCTAGTGGCTGCGGTGTTGCACGGTCA 1161
I N R A L V L A A Y H Stop 386

Appendix B-2. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144-B/177/200.

```

mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCGGTTGTACGGGCAT 43
                M D A I A A R A L S V V R A C 15
mt144-B/177/200 GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCGGTTGTACGGGCAT 43
                M D A I A A R A L S V V R A C 15
                *****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA 103
                V T V T D A R V S L D P G V M E T L G I 35
mt144-B/177/200 GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA 103
                V T V T D A R V S L D P G V M E T L G I 35
                *****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC 163
                A I N R Y N G L T N H S V S M R P Q T Q 55
mt144-B/177/200 TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC 163
                A I N R Y N G L T N H S V S M R P Q T Q 55
                *****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG 223
                A E R N E M F F M C T D M V L A A L N V 75
mt144-B/177/200 AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG 223
                A E R N E M F F M C T D M V L A A L N V 75
                *****

mt144/177/200  TCCAAATTGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG 283
                Q I G N I S P D Y D Q A L A T V G A L A 95
mt144-B/177/200 TCCAAATTGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG 283
                Q I G N I S P D Y D Q A L A T V G A L A 95
                *****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC 343
                T T E I P Y N V Q A M N D I V R I T G Q 115
mt144-B/177/200 CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC 343
                T T E I P Y N V Q A M N D I V R I T G Q 115
                *****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG 403
                M Q T F G P S K V Q T G P Y A G A V E V 135
mt144-B/177/200 AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG 403
                M Q T F G P S K V Q T G P Y A G A V E V 135
                *****

mt144/177/200  TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAG----- 450
                Q Q S G R Y Y V P P G E F L E 150
mt144-B/177/200 TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGGTAGACGTTGATC 463
                Q Q S G R Y Y V P P G E F L E V D V D P 155
                *****

mt144/177/200  ----- 450
mt144-B/177/200 CAAATAAGGGTAAGTGAAAGAACATATAAAAAGAGGTAACCGAAAAATTATTGAAAGCGG 523
                N K G K W K E H I K E V T E K L L K A V 175

mt144/177/200  -----CAAGGTCGAACGCGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGG 505
                E Q G R T R G G Y I N S N I A E V C M D 170

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mt144-B/177/200 TCGAGCAAGGTCGAACGCGTGGTGGGTACATCAATTCAAATATTCAGAGAGTGTGTATGG 583
E Q G R T R G G Y I N S N I A E V C M D 195

mt144/177/200 ATGCAGGTGCTGCGGGACAGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCTGCGC 565
A G A A G Q V N A L L A P R L Q R P A R 190

mt144-B/177/200 ATGCAGGTGCTGCGGGACAGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCTGCGC 643
A G A A G Q V N A L L A P R L Q R P A R 215

mt144/177/200 GCAGGGGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATC 625
R G D A V M I Y F V W R P L R I F C D P 210

mt144-B/177/200 GCAGGGGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATC 703
R G D A V M I Y F V W R P L R I F C D P 235

mt144/177/200 CTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTCA 685
Q G A K L S R V D S L E S A P G T F V T 230

mt144-B/177/200 CTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTCA 763
Q G A K L S R V D S L E S A P G T F V T 255

mt144/177/200 CCGTTGATGGAGTAAATGTTGACGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAG 745
V D G V N V A A G D V V A W N T I A P V 250

mt144-B/177/200 CCGTTGATGGAGTAAATGTTGACGCTGGAGATGTCGTCGCATGGAATACTATTGCACCAG 823
V D G V N V A A G D V V A W N T I A P V 275

mt144/177/200 TGAATGTTGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATA 805
N V G N P G A R R S I L Q F E V L W Y T 270

mt144-B/177/200 TGAATGTTGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATA 883
N V G N P G A R R S I L Q F E V L W Y T 295

mt144/177/200 CGTCCCTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTT 865
S L D R S L D T V P E L A P T L T R C Y 290

mt144-B/177/200 CGTCCCTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTT 943
S L D R S L D T V P E L A P T L T R C Y 315

mt144/177/200 ATGCGTATGTCTCTCCCACTTGGCAGCATTACGCGCTGTCATTTTTTTCAGCAGATGAATA 925
A Y V S P T W H A L R A V I F Q Q M N M 310

mt144-B/177/200 ATGCGTATGTCTCTCCCACTTGGCAGCATTACGCGCTGTCATTTTTTTCAGCAGATGAATA 1003
A Y V S P T W H A L R A V I F Q Q M N M 335

mt144/177/200 TGCAGCCTATTAATCCGCGGATTTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATC 985
Q P I N P P I F P P T E R N E I V A Y L 330

mt144-B/177/200 TGCAGCCTATTAATCCGCGGATTTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATC 1063
Q P I N P P I F P P T E R N E I V A Y L 355

mt144/177/200 TATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTTCAGAAATGAATG 1045
L V A S L A D V Y A A L R P D F R M N G 350

mt144-B/177/200 TATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTTCAGAAATGAATG 1123
L V A S L A D V Y A A L R P D F R M N G 375

mt144/177/200 GTGTTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGT 1104
V V A P V G Q I N R A L V L A A Y H Stop 368

mt144-B/177/200 GTGTTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGT 1182
V V A P V G Q I N R A L V L A A Y H Stop 393

Appendix B-3. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144-B/177-A/200.

```

mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
mt144-B/177-A/ GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
                *****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
mt144-B/177-A/ GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
                *****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAATCATTCCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
mt144-B/177-A/ TTGCAATCAATAGGTATAATGGTTTAAACAATCATTCCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
                *****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
mt144-B/177-A/ AAGCAGAACGAAATGAAATGTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
                *****

mt144/177/200  TCCAAATGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
mt144-B/177-A/ TCCAAATGGGAATATTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
                *****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
mt144-B/177-A/ CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
                *****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                M Q T F G P S K V Q T G P Y A G A V E V  135
mt144-B/177-A/ AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                M Q T F G P S K V Q T G P Y A G A V E V  135
                *****

mt144/177/200  TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAG-----  450
                Q Q S G R Y Y V P P G E F L E  150
mt144-B/177-A/ TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGGTAGACGTTGATC  463
                Q Q S G R Y Y V P P G E F L E V D V D P  155
                *****

mt144/177/200  -----  450
                -----  150
mt144-B/177-A/ CAAATAAGGGTAAGTGAAAGAACATATAAAAGAGGTAACCGAAAATTATTGAAAGCGG  523
                N K G K W K E H I K E V T E K L L K A V  175

mt144/177/200  -----CAAGGTCGAACGCGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGG  505
                E Q G R T R G G Y I N S N I A E V C M D  170

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| | | |
|----------------|---|-------------|
| mt144-B/177-A/ | TCGAGCAAGGTCGAACGCGTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGG E Q G R T R G G Y I N S N I A E V C M D ***** | 583 195 |
| mt144/177/200 | ATGCAGGTGCTGCGGGACAGGTCAATGCGCTGCTAGCCCCAAGG----- A G A A G Q V N A L L A P R | 549 184 |
| mt144-B/177-A/ | ATGCAGGTGCTGCGGGACAGGTCAATGCGCTGCTAGCCCCAAGGCTGCATAAGAAGAAAG A G A A G Q V N A L L A P R L H K K K E ***** | 643 215 |
| mt144/177/200 | -----CTGCAGGCGCGCA L Q A R R | 562 189 |
| mt144-B/177-A/ | AAGAGGGTGAGGATGATACTGCTCGACAGGAGATAAGAAAAGCATGGCTGCAGGCGCGCA E G E D D T A R Q E I R K A W L Q A R R ***** | 703 235 |
| mt144/177/200 | GGGGGACGCAGTCATGATCTATTTTCGTTGGAGACCGTTGCGTATATTTTGTGATCCTC G D A V M I Y F V W R P L R I F C D P Q | 622 209 |
| mt144-B/177-A/ | GGGGGACGCAGTCATGATCTATTTTCGTTGGAGACCGTTGCGTATATTTTGTGATCCTC G D A V M I Y F V W R P L R I F C D P Q ***** | 763 255 |
| mt144/177/200 | AAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTACCG G A K L S R V D S L E S A P G T F V T V | 682 229 |
| mt144-B/177-A/ | AAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTACCG G A K L S R V D S L E S A P G T F V T V ***** | 823 275 |
| mt144/177/200 | TTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTGCGATGGAATACTATTGCACCAGTGA D G V N V A A G D V V A W N T I A P V N | 742 249 |
| mt144-B/177-A/ | TTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTGCGATGGAATACTATTGCACCAGTGA D G V N V A A G D V V A W N T I A P V N ***** | 883 295 |
| mt144/177/200 | ATGTTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGT V G N P G A R R S I L Q F E V L W Y T S | 802 269 |
| mt144-B/177-A/ | ATGTTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGT V G N P G A R R S I L Q F E V L W Y T S ***** | 943 315 |
| mt144/177/200 | CCTTGGATAGATCGCTAGACACGGTTCGGGAATTGGCTCCAACGCTCACAAGATGTTATG L D R S L D T V P E L A P T L T R C Y A | 862 289 |
| mt144-B/177-A/ | CCTTGGATAGATCGCTAGACACGGTTCGGGAATTGGCTCCAACGCTCACAAGATGTTATG L D R S L D T V P E L A P T L T R C Y A ***** | 1003 335 |
| mt144/177/200 | CGTATGTCTCTCCCACTTGGCACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGC Y V S P T W H A L R A V I F Q Q M N M Q | 922 309 |
| mt144-B/177-A/ | CGTATGTCTCTCCCACTTGGCACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGC Y V S P T W H A L R A V I F Q Q M N M Q ***** | 1063 355 |
| mt144/177/200 | AGCCTATTAATCCGCCGATTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTAT P I N P P I F P P T E R N E I V A Y L L | 982 329 |
| mt144-B/177-A/ | AGCCTATTAATCCGCCGATTTTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTAT P I N P P I F P P T E R N E I V A Y L L ***** | 1123 375 |
| mt144/177/200 | TAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTG V A S L A D V Y A A L R P D F R M N G V | 1042 349 |
| mt144-B/177-A/ | TAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTG V A S L A D V Y A A L R P D F R M N G V ***** | 1183 395 |



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mt144/177/200 TTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGC 1102
                V A P V G Q I N R A L V L A A Y H Stop 366
mt144-B/177-A/ TTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGC 1239
                V A P V G Q I N R A L V L A A Y H Stop 412
*****
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Appendix C-1. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144/177-100/200.

```

mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
mtVP7/VP2-100  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
*****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
mtVP7/VP2-100  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
*****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
mtVP7/VP2-100  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
*****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
mtVP7/VP2-100  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
*****

mt144/177/200  TCCAAATTGGGAATATTTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
mtVP7/VP2-100  TCCAAATTGGGAATATTTTACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
*****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
mtVP7/VP2-100  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
*****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403

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| | | |
|---------------|---|-----|
| | M Q T F G P S K V Q T G P Y A G A V E V | 135 |
| mtVP7/VP2-100 | AGATGCAAACATTTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG | 403 |
| | M Q T F G P S K V Q T G P Y A G A V E V | 135 |
| | ***** | |
| mt144/177/200 | TGCAACAATCTGGCAGATATTACGTACCG CCCCGGGAATTCCTCGAG CAAGGTCGAACGC | 463 |
| | Q Q S G R Y Y V P P G E F L E Q G R T R | 155 |
| mtVP7/VP2-100 | TGCAACAATCTGGCAGATATTACGTACCG CCCCGGGAATTCCTCGAG CAAGGTCGAACGC | 463 |
| | Q Q S G R Y Y V P P G E F L E Q G R T R | 155 |
| | ***** | |
| mt144/177/200 | GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC | 523 |
| | G G Y I N S N I A E V C M D A G A A G Q | 175 |
| mtVP7/VP2-100 | GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC | 523 |
| | G G Y I N S N I A E V C M D A G A A G Q | 175 |
| | ***** | |
| mt144/177/200 | AGGTCAATGCGCTGCTAGCCCCAAGG CTGCAGAGCCT ----- | 561 |
| | V N A L L A P R L Q R P | 187 |
| mtVP7/VP2-100 | AGGTCAATGCGCTGCTAGCCCCAAGG CTGCAG TTTTGATTTTTTGACAACATTCGTTTCATG | 583 |
| | V N A L L A P R L Q F D F L T T F V H A | 195 |
| | ***** | |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-100 | CGAAGAAGAAAGAAGAGGGGTGAGGATGATACTGCTCGACAGGAGATAAGAAAAGCATGGG | 643 |
| | K K K E E G E D D T A R Q E I R K A W V | 215 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-100 | TTAAGGGGATGCCTTATATGGATTTCTCAAACCATGAAAATCACGCGTGGATTCAACA | 703 |
| | K G M P Y M D F S K P M K I T R G F N R | 235 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-100 | GAAATATGCTTTTTCCTTGCGGCGCTCGATTTCATTTCAGAAAGAGGAACGGTGTAGATGTTG | 763 |
| | N M L F L A A L D S F R K R N G V D V D | 255 |
| mt144/177/200 | ----- | 561 |

| | | |
|---------------|---|------|
| | | 187 |
| mtVP7/VP2-100 | ATCCGAATAAGGGTAAGTGGAAAGAACATATAAAGGAGGTAACCGAAAAATTGAAGAAAG | 823 |
| | P N K G K W K E H I K E V T E K L K K A | 275 |
| mt144/177/200 | -----GCGCGCAGGGGGGACGCAGTCATGATCT | 589 |
| | A R R G D A V M I Y | 197 |
| mtVP7/VP2-100 | CGCAAACCGAAAATGGAGGACAACCATGCCAAGCGCGCAGGGGGGACGCAGTCATGATCT | 883 |
| | Q T E N G G Q P C Q A R R G D A V M I Y | 295 |
| | ***** | |
| mt144/177/200 | ATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTAGAG | 649 |
| | F V W R P L R I F C D P Q G A K L S R V | 117 |
| mtVP7/VP2-100 | ATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTAGAG | 943 |
| | F V W R P L R I F C D P Q G A K L S R V | 315 |
| | ***** | |
| mt144/177/200 | TCGACTCACTTGAGAGCGCTCCAGGAACCTTTGTCCCGTTGATGGAGTAAATGTTGCAG | 709 |
| | D S L E S A P G T F V T V D G V N V A A | 137 |
| mtVP7/VP2-100 | TCGACTCACTTGAGAGCGCTCCAGGAACCTTTGTCCCGTTGATGGAGTAAATGTTGCAG | 1003 |
| | D S L E S A P G T F V T V D G V N V A A | 335 |
| | ***** | |
| mt144/177/200 | CTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGGCAC | 769 |
| | G D V V A W N T I A P V N V G N P G A R | 157 |
| mtVP7/VP2-100 | CTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGGCAC | 1063 |
| | G D V V A W N T I A P V N V G N P G A R | 355 |
| | ***** | |
| mt144/177/200 | GCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCGCTAGACA | 829 |
| | R S I L Q F E V L W Y T S L D R S L D T | 177 |
| mtVP7/VP2-100 | GCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCGCTAGACA | 1123 |
| | R S I L Q F E V L W Y T S L D R S L D T | 375 |
| | ***** | |
| mt144/177/200 | CGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTTGGC | 889 |
| | V P E L A P T L T R C Y A Y V S P T W H | 197 |
| mtVP7/VP2-100 | CGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTTGGC | 1183 |
| | V P E L A P T L T R C Y A Y V S P T W H | 395 |
| | ***** | |
| mt144/177/200 | ACGCATTACGCGCTGTCATTTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTT | 949 |



| | | |
|---------------|---|------|
| | A L R A V I F Q Q M N M Q P I N P P I F | 217 |
| mtVP7/VP2-100 | ACGCATTACGCGCTGTCATTTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTT | 1243 |
| | A L R A V I F Q Q M N M Q P I N P P I F | 415 |
| | ***** | |
| mt144/177/200 | TTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATG | 1009 |
| | P P T E R N E I V A Y L L V A S L A D V | 237 |
| mtVP7/VP2-100 | TTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATG | 1303 |
| | P P T E R N E I V A Y L L V A S L A D V | 435 |
| | ***** | |
| mt144/177/200 | TGTATGCGGCTTTGAGACCAGATTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCCAGA | 1069 |
| | Y A A L R P D F R M N G V V A P V G Q I | 257 |
| mtVP7/VP2-100 | TGTATGCGGCTTTGAGACCAGATTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCCAGA | 1363 |
| | Y A A L R P D F R M N G V V A P V G Q I | 455 |
| | ***** | |
| mt144/177/200 | TTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACGGTCACCG | 1104 |
| | N R A L V L A A Y H Stop | 267 |
| mtVP7/VP2-100 | TTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACGGTCACCG | 1398 |
| | N R A L V L A A Y H Stop | 465 |
| | ***** | |

Appendix C-2. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144/177-150/200.

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mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
mtVP7/VP2-150  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
*****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
mtVP7/VP2-150  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
*****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
mtVP7/VP2-150  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
*****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
mtVP7/VP2-150  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
*****

mt144/177/200  TCCAAATTGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
mtVP7/VP2-150  TCCAAATTGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
*****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
mtVP7/VP2-150  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
*****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                M Q T F G P S K V Q T G P Y A G A V E V  135

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mtVP7/VP2-150  AGATGCAAACATTTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                 M Q T F G P S K V Q T G P Y A G A V E V  135
                 *****

mt144/177/200  TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTCGAACGC  463
                 Q Q S G R Y Y V P P G E F L E Q G R T R  155

mtVP7/VP2-150  TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTCGAACGC  463
                 Q Q S G R Y Y V P P G E F L E Q G R T R  155
                 *****

mt144/177/200  GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC  523
                 G G Y I N S N I A E V C M D A G A A G Q  175

mtVP7/VP2-150  GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC  523
                 G G Y I N S N I A E V C M D A G A A G Q  175
                 *****

mt144/177/200  AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCT-----  561
                 V N A L L A P R L Q R P  187

mtVP7/VP2-150  AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAAAGGTCCACTGAATGACTTACGAGTTA  583
                 D A K A S A M Y S G K G P L N D L R V K  195
                 *****

mt144/177/200  -----  561
                 187

mtVP7/VP2-150  AAATTGAGCGGGATGATTTATCTCGAGAGACAATTATTCAGATCATTGAGTACGGTAAGA  643
                 I E R D D L S R E T I I Q I I E Y G K K  215

mt144/177/200  -----  561
                 187

mtVP7/VP2-150  AATTTAATTCATCAGCAGGTGATAAGCAGGGGAACATTTCAATTGAAAAATTGGTAGAGT  703
                 F N S S A G D K Q G N I S I E K L V E Y  235

mt144/177/200  -----  561
                 187

mtVP7/VP2-150  ATTGTGATTTTTTGACAACATTCGTTTCATGCGAAGAAGAAGAAGAGGGTGAGGATGATA  763
                 C D F L T T F V H A K K K E E G E D D T  255
                 |

mt144/177/200  -----  561
                 187

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| | | |
|---------------|---|------|
| mtVP7/VP2-150 | CTGCTCGACAGGAGATAAGAAAAGCATGGGTAAAGGGGATGCCTTATATGGATTTCTCAA | 823 |
| | A R Q E I R K A W V K G M P Y M D F S K | 275 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-150 | AACCGATGAAAATCACGCGTGGATTCAACAGAAATATGCTTTTCCTTGCGGCGCTCGATT | 883 |
| | P M K I T R G F N R N M L F L A A L D S | 295 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-150 | CATTGAGAAAGAGGAACGGTGTAGATGTTGATCCGAATAAGGGTAAGTGGAAAGAACATA | 943 |
| | F R K R N G V D V D P N K G K W K E H I | 315 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-150 | TAAAGGAGGTAACCGAAAAATTGAAGAAAGCGCAAACCGAAAATGGAGGACAACCATGCC | 1003 |
| | K E V T E K L K K A Q T E N G G Q P C Q | 335 |
| mt144/177/200 | --GCGCGCAGGGGGGACGCAGTCATGATCTA†TTTCGTTTGGAGACCGTTGCGTATATTTT | 619 |
| | A R R G D A V M I Y F V W R P L R I F C | 207 |
| mtVP7/VP2-150 | AAGCGCGCAGGGGGGACGCAGTCATGATCTA†TTTCGTTTGGAGACCGTTGCGTATATTTT | 1063 |
| | A R R G D A V M I Y F V W R P L R I F C | 355 |
| | ***** | |
| mt144/177/200 | GTGATCCTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACTT | 679 |
| | D P Q G A K L S R V D S L E S A P G T F | 227 |
| mtVP7/VP2-150 | GTGATCCTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACTT | 1123 |
| | D P Q G A K L S R V D S L E S A P G T F | 375 |
| | ***** | |
| mt144/177/200 | TTGTCACCGTTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTCGCATGGAATACTATTG | 739 |
| | V T V D G V N V A A G D V V A W N T I A | 247 |
| mtVP7/VP2-150 | TTGTCACCGTTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTCGCATGGAATACTATTG | 1183 |
| | V T V D G V N V A A G D V V A W N T I A | 395 |
| | *!***** | |
| mt144/177/200 | CACCAGTGAATGTTGAAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTTAT | 799 |
| | P V N V G N P G A R R S I L Q F E V L W | 267 |

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mtVP7/VP2-150  CACCAGTGAATGTTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTTAT  1243
                P V N V G N P G A R R S I L Q F E V L W  415
                *****

mt144/177/200  GGTATACGTCCTTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAA  859
                Y T S L D R S L D T V P E L A P T L T R  287

mtVP7/VP2-150  GGTATACGTCCTTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAA  1303
                Y T S L D R S L D T V P E L A P T L T R  435
                *****

mt144/177/200  GATGTTATGCGTATGTCTCTCCCACTTGGCACGCATTACGCGCTGTCATTTTTTCAGCAGA  919
                C Y A Y V S P T W H A L R A V I F Q Q M  307

mtVP7/VP2-150  GATGTTATGCGTATGTCTCTCCCACTTGGCACGCATTACGCGCTGTCATTTTTTCAGCAGA  1363
                C Y A Y V S P T W H A L R A V I F Q Q M  455
                *****

mt144/177/200  TGAATATGCAGCCTATTAATCCGCCGATTTTTCCACCGACTGAAAGGAATGAAATTGTTG  979
                N M Q P I N P P I F P P T E R N E I V A  327

mtVP7/VP2-150  TGAATATGCAGCCTATTAATCCGCCGATTTTTCCACCGACTGAAAGGAATGAAATTGTTG  1423
                N M Q P I N P P I F P P T E R N E I V A  475
                *****

mt144/177/200  CGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAA  1039
                Y L L V A S L A D V Y A A L R P D F R M  347

mtVP7/VP2-150  CGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAA  1483
                Y L L V A S L A D V Y A A L R P D F R M  495
                *****

mt144/177/200  TGAATGGTGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACC  1099
                N G V V A P V G Q I N R A L V L A A Y H  367

mtVP7/VP2-150  TGAATGGTGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACC  1543
                N G V V A P V G Q I N R A L V L A A Y H  515
                *****

mt144/177/200  ACTAGTGGCTGCGGTGTTGCACGGTCACCGCTTTCATTAGTGTGCGGTCGGTTCTTATGC  1104
                Stop

mtVP7/VP2-150  ACTAGTGGCTGCGGTGTTGCACGGTCACCGCTTTCATTAGTGTGCGGTCGGTTCTTATGA  1548
                Stop
                *****

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Appendix C-3. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144/177-200/200.

```

mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15

mtVP7/VP2-200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
*****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35

mtVP7/VP2-200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
*****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55

mtVP7/VP2-200  TTGCAATCAATAGGTATAATGGTTTAAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
*****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTA CTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75

mtVP7/VP2-200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTA CTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
*****

mt144/177/200  TCCAAATTGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95

mtVP7/VP2-200  TCCAAATTGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
*****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115

mtVP7/VP2-200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
*****

mt144/177/200  AGATGCAAACATTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                M Q T F G P S K V Q T G P Y A G A V E V  135

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mtVP7/VP2-200 AGATGCAAACATTTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG 403
      M Q T F G P S K V Q T G P Y A G A V E V 135
      *****

mt144/177/200 TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTCGAACGC 463
      Q Q S G R Y Y V P P G E F L E Q G R T R 155

mtVP7/VP2-200 TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTCGAACGC 463
      Q Q S G R Y Y V P P G E F L E Q G R T R 155
      *****

mt144/177/200 GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC 523
      G G Y I N S N I A E V C M D A G A A G Q 175

mtVP7/VP2-200 GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC 523
      G G Y I N S N I A E V C M D A G A A G Q 175
      *****

mt144/177/200 AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCT----- 561
      V N A L L A P R L Q R P 187

mtVP7/VP2-200 AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAAGCTGAGATTTGGAATGATGTACCCAC 583
      V N A L L A P R L Q K L R F G M M Y P H 195
      *****

mt144/177/200 ----- 561
      187

mtVP7/VP2-200 ACTATTATGTTTTGCATAGTGATTACTGTATTGTACCAAATAAGGGGGAACTAGTATTG 643
      Y Y V L H S D Y C I V P N K G G T S I G 215

mt144/177/200 ----- 561
      187

mtVP7/VP2-200 GATCATGGCATATAAGAAAACGTA CTGAGGGTGATGCGAAAGCTTCTGCTATGTATTCTG 703
      S W H I R K R T E G D A K A S A M Y S G 235

mt144/177/200 ----- 561
      187

mtVP7/VP2-200 GAAAAGGTCCACTGAATGACTTACGAGTTAAAATTGAGCGGGATGATTTATCTCGAGAGA 763
      K G P L N D L R V K I E R D D L S R E T 255
      |

mt144/177/200 ----- 561
      187

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| | | |
|---------------|---|------|
| mtVP7/VP2-200 | CAATTATTCAGATCATTGAGTACGGTAAGAAATTTAATTCATCAGCAGGTGATAAGCAGG | 823 |
| | I I Q I I E Y G K K F N S S A G D K Q G | 275 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-200 | GGAACATTTCAATTGAAAAATTGGTAGAGTATTGTGATTTTTTGACAACATTCGTTTCATG | 883 |
| | N I S I E K L V E Y C D F L T T F V H A | 295 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-200 | CGAAGAAGAAAGAAGAGGGTGAGGATGATACTGCTCGACAGGAGATAAGAAAAGCATGGG | 943 |
| | K K K E E G E D D T A R Q E I R K A W V | 315 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-200 | TTAAGGGGATGCCTTATATGGATTTCTCAAACCGATGAAAATCACGCGTGGATTCAACA | 1003 |
| | K G M P Y M D F S K P M K I T R G F N R | 335 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-200 | GAAATATGCTTTTTCCTTGCGGCGCTCGATTCATTCAGAAAGAGGAACGGTGTAGATGTTG | 1063 |
| | N M L F L A A L D S F R K R N G V D V D | 355 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-200 | ATCCGAATAAGGGTAAGTGGAAAGAACATATAAAGGAGGTAACCGAAAAATTGAAGAAAG | 1123 |
| | P N K G K W K E H I K E V T E K L K K A | 375 |
| mt144/177/200 | -----GCGCGCAGGGGGGACGCAGTCATGATCT | 589 |
| | A R R G D A V M I Y | 197 |
| mtVP7/VP2-200 | CGCAAACCGAAAAATGGAGGACAACCATGCCAAGCGCGCAGGGGGGACGCAGTCATGATCT | 1183 |
| | Q T E N G G Q P C Q A R R G D A V M I Y | 395 |
| | ***** | |
| mt144/177/200 | ATTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTAGAG | 649 |
| | F V W R P L R I F C D P Q G A K L S R V | 217 |

| | | |
|---------------|---|------|
| mtVP7/VP2-200 | ATTTTCGTTTGGAGACCGTTGCGTATATTTTGTGATCCTCAAGGTGCGAAGCTTTCTAGAG | 1243 |
| | F V W R P L R I F C D P Q G A K L S R V | 415 |
| | ***** | |
| mt144/177/200 | TCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTCCCGTTGATGGAGTAAATGTTGCAG | 709 |
| | D S L E S A P G T F V T V D G V N V A A | 237 |
| mtVP7/VP2-200 | TCGACTCACTTGAGAGCGCTCCAGGAACCTTTTGTCCCGTTGATGGAGTAAATGTTGCAG | 1303 |
| | D S L E S A P G T F V T V D G V N V A A | 435 |
| | ***** | |
| mt144/177/200 | CTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGGCAC | 769 |
| | G D V V A W N T I A P V N V G N P G A R | 257 |
| mtVP7/VP2-200 | CTGGAGATGTCGTCGCATGGAATACTATTGCACCAGTGAATGTTGGAAATCCTGGGGCAC | 1363 |
| | G D V V A W N T I A P V N V G N P G A R | 455 |
| | ***** | |
| mt144/177/200 | GCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCGCTAGACA | 829 |
| | R S I L Q F E V L W Y T S L D R S L D T | 277 |
| mtVP7/VP2-200 | GCAGATCAATTTTACAGTTTGAAGTGTATGGTATACGTCCTTGGATAGATCGCTAGACA | 1423 |
| | R S I L Q F E V L W Y T S L D R S L D T | 475 |
| | ***** | |
| mt144/177/200 | CGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTTGGC | 889 |
| | V P E L A P T L T R C Y A Y V S P T W H | 297 |
| mtVP7/VP2-200 | CGGTTCCGGAATTGGCTCCAACGCTCACAAGATGTTATGCGTATGTCTCTCCCACTTGGC | 1483 |
| | V P E L A P T L T R C Y A Y V S P T W H | 495 |
| | ***** | |
| mt144/177/200 | ACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTT | 949 |
| | A L R A V I F Q Q M N M Q P I N P P I F | 317 |
| mtVP7/VP2-200 | ACGCATTACGCGCTGTCATTTTTCAGCAGATGAATATGCAGCCTATTAATCCGCCGATTT | 1543 |
| | A L R A V I F Q Q M N M Q P I N P P I F | 515 |
| | ***** | |
| mt144/177/200 | TTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATG | 1009 |
| | P P T E R N E I V A Y L L V A S L A D V | 337 |
| mtVP7/VP2-200 | TTCCACCGACTGAAAGGAATGAAATTGTTGCGTATCTATTAGTAGCTTCTTTAGCTGATG | 1603 |
| | P P T E R N E I V A Y L L V A S L A D V | 535 |
| | ***** | |
| mt144/177/200 | TGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTGTGTCGCGCCAGTAGGCCAGA | 1069 |
| | Y A A L R P D F R M N G V V A P V G Q I | 357 |



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mtVP7/VP2-200  TGTATGCGGCTTTGAGACCAGATTTTCAGAATGAATGGTGTTCGCGCCAGTAGGCCAGA  1663
                 Y A A L R P D F R M N G V V A P V G Q I  555
                 *****

mt144/177/200  TTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACGGTCACCG  1104
                 N R A L V L A A Y H Stop  367

mtVP7/VP2-200  TTAACAGAGCTCTTGTGCTAGCAGCCTACCACTAGTGGCTGCGGTGTTGCACGGTCACCG  1698
                 N R A L V L A A Y H Stop  565
                 *****
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Appendix C-4. CLUSTAL X Nucleotide and amino acid sequence alignment of VP7mt144/177/200 with VP7mt144/177-250/200.

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mt144/177/200  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15

mtVP7/VP2-250  GTTTAAATTCGGTTAGGATGGACGCGATAGCAGCAAGAGCCTTGTCCGTTGTACGGGCAT  43
                M D A I A A R A L S V V R A C  15
*****

mt144/177/200  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35

mtVP7/VP2-250  GTGTCACAGTGACAGATGCGAGAGTTAGTTTGGATCCAGGAGTGATGGAGACGTTAGGGA  103
                V T V T D A R V S L D P G V M E T L G I  35
*****

mt144/177/200  TTGCAATCAATAGGTATAATGGTTTAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55

mtVP7/VP2-250  TTGCAATCAATAGGTATAATGGTTTAACAAATCATTCGGTATCGATGAGGCCACAAACCC  163
                A I N R Y N G L T N H S V S M R P Q T Q  55
*****

mt144/177/200  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75

mtVP7/VP2-250  AAGCAGAACGAAATGAAATGTTTTTTATGTGTACTGATATGGTTTTAGCGGCGCTGAACG  223
                A E R N E M F F M C T D M V L A A L N V  75
*****

mt144/177/200  TCCAAATGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95

mtVP7/VP2-250  TCCAAATGGGAATATTTCCACCAGATTATGATCAAGCGTTGGCAACTGTGGGAGCTCTCG  283
                Q I G N I S P D Y D Q A L A T V G A L A  95
*****

mt144/177/200  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115

mtVP7/VP2-250  CAACGACTGAAATTCATATAATGTTTCAGGCCATGAATGACATCGTTAGAATAACGGGTC  343
                T T E I P Y N V Q A M N D I V R I T G Q  115
*****

mt144/177/200  AGATGCAAAACATTTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG  403
                M Q T F G P S K V Q T G P Y A G A V E V  135

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| | | |
|---------------|---|-----|
| mtVP7/VP2-250 | AGATGCAAACATTTCGGACCAAGCAAAGTGCAAACGGGGCCTTATGCAGGAGCGGTTGAGG | 403 |
| | M Q T F G P S K V Q T G P Y A G A V E V | 135 |
| | ***** | |
| mt144/177/200 | TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTGCAACGC | 463 |
| | Q Q S G R Y Y V P P G E F L E Q G R T R | 155 |
| mtVP7/VP2-250 | TGCAACAATCTGGCAGATATTACGTACCGCCCGGGGAATTCCTCGAGCAAGGTGCAACGC | 463 |
| | Q Q S G R Y Y V P P G E F L E Q G R T R | 155 |
| | ***** | |
| mt144/177/200 | GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC | 523 |
| | G G Y I N S N I A E V C M D A G A A G Q | 175 |
| mtVP7/VP2-250 | GTGGTGGGTACATCAATTCAAATATTGCAGAAGTGTGTATGGATGCAGGTGCTGCGGGAC | 523 |
| | G G Y I N S N I A E V C M D A G A A G Q | 175 |
| | ***** | |
| mt144/177/200 | AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGAGGCCT----- | 561 |
| | V N A L L A P R L Q R P | 187 |
| mtVP7/VP2-250 | AGGTCAATGCGCTGCTAGCCCCAAGGCTGCAGGAGAGTAAGAGAAAAGCAATCCTTGATC | 583 |
| | V N A L L A P R L Q E S K R K A I L D Q | 195 |
| | ***** | |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | AGAATAAGATGTCTAAGGTTGAACAATGGAGAGATGCGGTTAATGAAAGGATTGTGAGTA | 643 |
| | N K M S K V E Q W R D A V N E R I V S I | 215 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | TCGAACCAAAGCGAGGTGAGTGCTATGATCACGGAACCGACATTATCTACCAATTCATAA | 703 |
| | E P K R G E C Y D H G T D I I Y Q F I K | 235 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | AAAAGCTGAGATTGGAATGATGTACCCACACTATTATGTTTTGCATAGTGATTACTGTA | 763 |
| | K L R F G M M Y P H Y Y V L H S D Y C I | 255 |
| | | |
| mt144/177/200 | ----- | 561 |
| | | 187 |



| | | |
|---------------|--|------|
| mtVP7/VP2-250 | TTGTACCAAATAAGGGGGGAACTAGTATTGGATCATGGCATATAAGAAAACGTACTGAGG | 823 |
| | V P N K G G T S I G S W H I R K R T E G | 275 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | GTGATGCGAAAGCTTCTGCTATGTATTCTGGAAAAGGTCCACTGAATGACTTACGAGTTA | 883 |
| | D A K A S A M Y S G K G P L N D L R V K | 295 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | AAATTGAGCGGGATGATTTATCTCGAGAGACAATTATTCAGATCATTGAGTACGGTAAGA | 943 |
| | I E R D D L S R E T I I Q I I E Y G K K | 315 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | AATTTAATTCATCAGCAGGTGATAAGCAGGGGAACATTTCAATTGAAAAATTGGTAGAGT | 1003 |
| | F N S S A G D K Q G N I S I E K L V E Y | 335 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | ATTGTGATTTTTTGGACAACATTCGTTTCATGCCGAAGAAGAAGAGGGTGAGGATGATA | 1063 |
| | C D F L T T F V H A K K K E E G E D D T | 355 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | CTGCTCGACAGGAGATAAGAAAAGCATGGGTTAAGGGGATGCCTTATATGGATTTCTCAA | 1123 |
| | A R Q E I R K A W V K G M P Y M D F S K | 375 |
| mt144/177/200 | ----- | 561 |
| | | 187 |
| mtVP7/VP2-250 | AACCGATGAAAATCACGCGTGGATTCAACAGAAATATGCTTTTCCTTGCGGCGCTCGATT | 1183 |
| | P M K I T R G F N R N M L F L A A L D S | 395 |
| mt144/177/200 | ----- | 561 |
| | | 187 |

mtVP7/VP2-250 CATTGAGAAAGAGGAACGGTGTAGATGTTGATCCGAATAAGGGTAAGTGGAAAGAACATA 1243
F R K R N G V D V D P N K G K W K E H I 415

mt144/177/200 ----- 561
187

mtVP7/VP2-250 TAAAGGAGGTAACCGAAAAATTGAAGAAAGCGCAAACCGAAAAATGGAGGACAACCATGCC 1303
K E V T E K L K K A Q T E N G G Q P C Q 435

mt144/177/200 --GCGCGCAGGGGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTT 619
A R R G D A V M I Y F V W R P L R I F C 207

mtVP7/VP2-250 AAGCGCGCAGGGGGGACGCAGTCATGATCTATTTTCGTTTGGAGACCGTTGCGTATATTTT 1363
A R R G D A V M I Y F V W R P L R I F C 455

mt144/177/200 GTGATCCTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACTT 679
D P Q G A K L S R V D S L E S A P G T F 227

mtVP7/VP2-250 GTGATCCTCAAGGTGCGAAGCTTTCTAGAGTCGACTCACTTGAGAGCGCTCCAGGAACTT 1423
D P Q G A K L S R V D S L E S A P G T F 475

mt144/177/200 TTGTCACCGTTGATGGAGTAAATGTTGCAGC¹TGGAGATGTCGTCGCATGGAATACTATTG 739
V T V D G V N V A A G D V V A W N T I A 247

mtVP7/VP2-250 TTGTCACCGTTGATGGAGTAAATGTTGCAGCTGGAGATGTCGTCGCATGGAATACTATTG 1483
V T V D G V N V A A G D V V A W N T I A 495

mt144/177/200 CACCAGTGAATGTTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTTAT 799
P V N V G N P G A R R S I L Q F E V L W 267

mtVP7/VP2-250 CACCAGTGAATGTTGGAAATCCTGGGGCACGCAGATCAATTTTACAGTTTGAAGTGTTAT 1543
P V N V G N P G A R R S I L Q F E V L W 515

mt144/177/200 GGTATACGTCCTTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAA 859
Y T S L D R S L D T V P E L A P T L T R 287

mtVP7/VP2-250 GGTATACGTCCTTGGATAGATCGCTAGACACGGTTCCGGAATTGGCTCCAACGCTCACAA 1603
Y T S L D R S L D T V P E L A P T L T R 535

mt144/177/200 GATGTTATGCGTATGCTCTCTCCCACTTGGCAGCATTACGCGCTGTCATTTTTCAGCAGA 919
C Y A Y V S P T W H A L R A V I F Q Q M 307

mtVP7/VP2-250 GATGTTATGCGTATGTCTCTCCACTTGGCACGCATTACGCGCTGTCATTTTTTCAGCAGA 1663
 C Y A Y V S P T W H A L R A V I F Q Q M 555

mt144/177/200 TGAATATGCAGCCTATTAATCCGCCGATTTTTCCACCGACTGAAAGGAATGAAATTGTTG 979
 N M Q P I N P P I F P P T E R N E I V A 327

mtVP7/VP2-250 TGAATATGCAGCCTATTAATCCGCCGATTTTTCCACCGACTGAAAGGAATGAAATTGTTG 1723
 N M Q P I N P P I F P P T E R N E I V A 575

mt144/177/200 CGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAA 1039
 Y L L V A S L A D V Y A A L R P D F R M 347

mtVP7/VP2-250 CGTATCTATTAGTAGCTTCTTTAGCTGATGTGTATGCGGCTTTGAGACCAGATTTTCAGAA 1783
 Y L L V A S L A D V Y A A L R P D F R M 595

mt144/177/200 TGAATGGTGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACC 1099
 N G V V A P V G Q I N R A L V L A A Y H 367

mtVP7/VP2-250 TGAATGGTGTGTGTCGCGCCAGTAGGCCAGATTAACAGAGCTCTTGTGCTAGCAGCCTACC 1843
 N G V V A P V G Q I N R A L V L A A Y H 615

mt144/177/200 ACTAGTGGCTGCGGTGTTGCACGGTCACCGCTTTCATTAGTGTGCGGTCGGTTCTTATGC 1104
 Stop

mtVP7/VP2-250 ACTAGTGGCTGCGGTGTTGCACGGTCACCGCTTTCATTAGTGTGCGGTCGGTTCTTATGA 1845
 Stop
