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APPENDIX A

Nucleotide sequence alignments of reassortant virus genome segments

VP2 gene (Segment 2)

```
                                 1                                                50
AHSV-3                     (1)   TGTGCAATGATTTCACGGAATG-AGACGCGAGAGAGCACGCTCAAGGGAT
AHSV-4                     (1)   TATATGAGG-TTATACGATGTGCAGACAAGGGAGCAGGCACTAAATACCT
R4-2_{4,5,7,10}            (1)   TATATGAGG-TTATACGATGTGCAGACAAGGGAGCAGGCACTAAATACCT
R4-2_{7,10}                (1)   TATATGAGG-TTATACGATGTGCAGACAAGGGAGCAGGCACTAAATACCT
R4-2_{10}                  (1)   TATATGAGG-TTATACGATGTGCAGACAAGGGAGCAGGCACTAAATACCT
R3-2_{5,10}                (1)   TGTGCAATGATTTCACGGAATG-AGACGCGAGAGAGCACGCTCAAGGGAT
R3-2_{3,5}                 (1)   TGTGCAATGATTTCACGGAATG-AGACGCGAGAGAGCACGCTCAAGGGAT
                                 51                                              100
AHSV-3                    (50)   TTA-GTATGTTTACTGCAATTGTTAAAAGTGAGAGACTGATAGATACCCT
AHSV-4                    (50)   TCACGGATTTTCACAGGTGT-GTTGAGTCGGAACTGCTTTTACCGACACT
R4-2_{4,5,7,10}           (50)   TCACGGATTTTCACAGGTGT-GTTGAGTCGGAACTGCTTTTACCGACACT
R4-2_{7,10}               (50)   TCACGGATTTTCACAGGTGT-GTTGAGTCGGAACTGCTTTTACCGACACT
R4-2_{10}                 (50)   TCACGGATTTTCACAGGTGT-GTTGAGTCGGAACTGCTTTTACCGACACT
R3-2_{5,10}               (50)   TTA-GTATGTTTACTGCAATTGTTAAAAGTGAGAGACTGATAGATACCCT
R3-2_{3,5}                (50)   TTA-GTATGTTTACTGCAATTGTTAAAAGTGAGAGACTGATAGATACCCT
                                 101                                             150
AHSV-3                    (99)   GTTCTTGAATTTCTTGTTATGGATTGTCTTTGAAATGGAGAATGTTGATG
AHSV-4                    (99)   TAAACTTAACTTTCTGCTGTGGATTGTCTTTGAAATGGAAAACGTTGAAG
R4-2_{4,5,7,10}           (99)   TAAACTTAACTTTCTGCTGTGGATTGTCTTTGAAATGGAAAACGTTGAAG
R4-2_{7,10}               (99)   TAAACTTAACTTTCTGCTGTGGATTGTCTTTGAAATGGAAAACGTTGAAG
R4-2_{10}                 (99)   TAAACTTAACTTTCTGCTGTGGATTGTCTTTGAAATGGAAAACGTTGAAG
R3-2_{5,10}               (99)   GTTCTTGAATTTCTTGTTATGGATTGTCTTTGAAATGGAGAATGTTGATG
R3-2_{3,5}                (99)   GTTCTTGAATTTCTTGTTATGGATTGTCTTTGAAATGGAGAATGTTGATG
                                 151                                             200
AHSV-3                   (149)   TGAGCGCTGCTAATAAGAGACATCCATTATTAATATCGCATGAAAAAGGA
AHSV-4                   (149)   TGAACGCGGCGTACAAGCGTCATCCGCTTTTAATCTCAACTGCCAAAGGG
R4-2_{4,5,7,10}          (149)   TGAACGCGGCGTACAAGCGTCATCCGCTTTTAATCTCAACTGCCAAAGGG
R4-2_{7,10}              (149)   TGAACGCGGCGTACAAGCGTCATCCGCTTTTAATCTCAACTGCCAAAGGG
R4-2_{10}                (149)   TGAACGCGGCGTACAAGCGTCATCCGCTTTTAATCTCAACTGCCAAAGGG
R3-2_{5,10}              (149)   TGAGCGCTGCTAATAAGAGACATCCATTATTAATATCGCATGAAAAAGGA
R3-2_{3,5}               (149)   TGAGCGCTGCTAATAAGAGACATCCATTATTAATATCGCATGAAAAAGGA
                                 201                                             250
AHSV-3                   (199)   TTACGTTTAATTGGCGTAGATTTGTTTAATGGCGCGCTTTCGATTTCCAC
AHSV-4                   (199)   TTAAGGGTTATCGGCGTTGATATTTTCAACTCACAGCTTTCGATATCAAT
R4-2_{4,5,7,10}          (199)   TTAAGGGTTATCGGCGTTGATATTTTCAACTCACAGCTTTCGATATCAAT
R4-2_{7,10}              (199)   TTAAGGGTTATCGGCGTTGATATTTTCAACTCACAGCTTTCGATATCAAT
R4-2_{10}                (199)   TTAAGGGTTATCGGCGTTGATATTTTCAACTCACAGCTTTCGATATCAAT
R3-2_{5,10}              (199)   TTACGTTTAATTGGCGTAGATTTGTTTAATGGCGCGCTTTCGATTTCCAC
R3-2_{3,5}               (199)   TTACGTTTAATTGGCGTAGATTTGTTTAATGGCGCGCTTTCGATTTCCAC
                                 251                                             300
AHSV-3                   (249)   GGGGGGGTGGATTCCGTATCTAGAGAGGATATGTTCAGAGGAGAAAGCTC
AHSV-4                   (249)   GAGCGGATGGATTCCGTATGTCGAACGGATGTGCGCGGAGAGTAAAGTTC
R4-2_{4,5,7,10}          (249)   GAGCGGATGGATTCCGTATGTCGAACGGATGTGCGCGGAGAGTAAAGTTC
R4-2_{7,10}              (249)   GAGCGGATGGATTCCGTATGTCGAACGGATGTGCGCGGAGAGTAAAGTTC
R4-2_{10}                (249)   GAGCGGATGGATTCCGTATGTCGAACGGATGTGCGCGGAGAGTAAAGTTC
R3-2_{5,10}              (249)   GGGGGGGTGGATTCCGTATCTAGAGAGGATATGTTCAGAGGAGAAAGCTC
R3-2_{3,5}               (249)   GGGGGGGTGGATTCCGTATCTAGAGAGGATATGTTCAGAGGAGAAAGCTC
                                 301
AHSV-3                   (299)   AGA-GAAGG
AHSV-4                   (299)   AAACGAAGT
R4-2_{4,5,7,10}          (299)   AAACGAAGT
R4-2_{7,10}              (299)   AAACGAAGT
R4-2_{10}                (299)   AAACGAAGT
R3-2_{5,10}              (299)   AGA-GAAGG
R3-2_{3,5}               (299)   AGA-GAAGG
```

VP3 gene (Segment 3)

```
                        1                                                50
AHSV-2              (1) ATTTAAAAGCAACCATTCTCACTCCATCCCTCTCCTCTTCTGTGTACACA
AHSV-3              (1) ATTTAAAAGCGACCATCCTCACTCCATCCCTCTCCTCCTCCGTGTACACA
AHSV-4              (1) ATTTAAAAGCGACCATTCTCACTCCATCCCTCTCCTCCTCTGTGTACACA
R4-2_{4,5,7,10}     (1) ATTTAAAAGCGACCATTCTCACTCCATCCCTCTCCTCCTCTGTGTACACA
R4-2_{7,10}         (1) ATTTAAAAGCGACCATTCTCACTCCATCCCTCTCCTCCTCTGTGTACACA
R4-2_{10}           (1) ATTTAAAAGCGACCATTCTCACTCCATCCCTCTCCTCCTCTGTGTACACA
R3-2_{5,10}         (1) ATTTAAAAGCGACCATCCTCACTCCATCCCTCTCCTCCTCCGTGTACACA
R3-2_{3,5}          (1) ATTTAAAAGCAACCATTCTCACTCCATCCCTCTCCTCTTCTGTGTACACA
                        51                                              100
AHSV-2             (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAGAATTT
AHSV-3             (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGCGAATCAAAAAATTT
AHSV-4             (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAAAATTT
R4-2_{4,5,7,10}    (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAAAATTT
R4-2_{7,10}        (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAAAATTT
R4-2_{10}          (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAAAATTT
R3-2_{5,10}        (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGCGAATCAAAAAATTT
R3-2_{3,5}         (51) TAAGGCATTGCCGTCAGTATCTCGTCGGGCGGCCGTGAATCAAAAAATTT
                        101                      127
AHSV-2            (101) AATCTTGATGTTCCGTAACATACCACC
AHSV-3            (101) AATCTTGATATTCCGTAACATACCACC
AHSV-4            (101) AATCTTGATATTCCGTAACATACCGCC
R4-2_{4,5,7,10}   (101) AATCTTGATATTCCGTAACATACCGCC
R4-2_{7,10}       (101) AATCTTGATATTCCGTAACATACCGCC
R4-2_{10}         (101) AATCTTGATATTCCGTAACATACCGCC
R3-2_{5,10}       (101) AATCTTGATATTCCGTAACATACCACC
R3-2_{3,5}        (101) AATCTTGATGTTCCGTAACATACCACC
```

NS1 gene (segment 5)

		1 50
AHSV-2	(1)	CCAGTGGTTGATTCAAAAATTGCTGAACTAACGGGAGGCACAGATGTATT
AHSV-3	(1)	CCAGTGGTTGATTCAAAAATTGCTGAACTAACAGGAGGCATAGATGTATT
AHSV-4	(1)	CCAGTGGTTGATTCAAAAATCGCTGAACTAACAGGAGGCACGGATGTATT
$R4\text{-}2_{4,5,7,10}$	(1)	CCAGTGGTTGATTCAAAAATTGCTGAACTAACGGGAGGCACAGATGTATT
$R4\text{-}2_{7,10}$	(1)	CCAGTGGTTGATTCAAAAATCGCTGAACTAACAGGAGGCACGGATGTATT
$R4\text{-}2_{10}$	(1)	CCAGTGGTTGATTCAAAAATCGCTGAACTAACAGGAGGCACGGATGTATT
$R3\text{-}2_{5,10}$	(1)	CCAGTGGTTGATTCAAAAATTGCTGAACTAACGGGAGGCACAGATGTATT
$R3\text{-}2_{3,5}$	(1)	CCAGTGGTTGATTCAAAAATTGCTGAACTAACGGGAGGCACAGATGTATT
		51 100
AHSV-2	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGCGCCAAATGTCA
AHSV-3	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGTGCCAAATGTCA
AHSV-4	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGTGCCAAATGTCA
$R4\text{-}2_{4,5,7,10}$	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGCGCCAAATGTCA
$R4\text{-}2_{7,10}$	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGTGCCAAATGTCA
$R4\text{-}2_{10}$	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGTGCCAAATGTCA
$R3\text{-}2_{5,10}$	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGCGCCAAATGTCA
$R3\text{-}2_{3,5}$	(51)	TTATACACGTGCGTATGTACATGCGGACAATCACAAAGCGCCAAATGTCA
		101 150
AHSV-2	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
AHSV-3	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATCGATGATCATTGGGTG
AHSV-4	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
$R4\text{-}2_{4,5,7,10}$	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
$R4\text{-}2_{7,10}$	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
$R4\text{-}2_{10}$	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
$R3\text{-}2_{5,10}$	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
$R3\text{-}2_{3,5}$	(101)	GAGATTTGATGATGAATGAAGTCTTCAGGAAGATTGATGATCATTGGGTG
		151 200
AHSV-2	(151)	ATTCAGAAGTGTCATACAACGAAGGAAGCGATTACCGTAACTGCAATTCA
AHSV-3	(151)	ATTCAGAAGTGTCATACAACGAAGGAAGCGATTACCGTAACTGCAATTCA
AHSV-4	(151)	ATTCAGAAGTGTCATACCACGAAGGAAGCGATTACTGTAACTGCAATTCA
$R4\text{-}2_{4,5,7,10}$	(151)	ATTCAGAAGTGTCATACAACGAAGGAAGCGATTACCGTAACTGCAATTCA
$R4\text{-}2_{7,10}$	(151)	ATTCAGAAGTGTCATACCACGAAGGAAGCGATTACTGTAACTGCAATTCA
$R4\text{-}2_{10}$	(151)	ATTCAGAAGTGTCATACCACGAAGGAAGCGATTACTGTAACTGCAATTCA
$R3\text{-}2_{5,10}$	(151)	ATTCAGAAGTGTCATACAACGAAGGAAGCGATTACCGTAACTGCAATTCA
$R3\text{-}2_{3,5}$	(151)	ATTCAGAAGTGTCATACAACGAAGGAAGCGATTACCGTAACTGCAATTCA
		201 250
AHSV-2	(201)	AATCCAGAGGTCGATCAGAGGTGATGGACAGTGGGATACTCCGATGTTTC
AHSV-3	(201)	GATCCAGAGGTCGATCAGAGGTGATGGGCAGTGGGATACTCCGATGTTTC
AHSV-4	(201)	GATTCAGAGGTCGATCAGAGGTGATGGGCAGTGGGATACTCCGATGTTTC
$R4\text{-}2_{4,5,7,10}$	(201)	AATCCAGAGGTCGATCAGAGGTGATGGACAGTGGGATACTCCGATGTTTC
$R4\text{-}2_{7,10}$	(201)	GATTCAGAGGTCGATCAGAGGTGATGGGCAGTGGGATACTCCGATGTTTC
$R4\text{-}2_{10}$	(201)	GATTCAGAGGTCGATCAGAGGTGATGGGCAGTGGGATACTCCGATGTTTC
$R3\text{-}2_{5,10}$	(201)	AATCCAGAGGTCGATCAGAGGTGATGGACAGTGGGATACTCCGATGTTTC
$R3\text{-}2_{3,5}$	(201)	AATCCAGAGGTCGATCAGAGGTGATGGACAGTGGGATACTCCGATGTTTC
		251 300
AHSV-2	(251)	ACCAATCAATGGCTCTGTTGACACGATTGATTGTTTATTGGTTAACGGAT
AHSV-3	(251)	ACCAATCAATGGCTCTGTTAACACGATTGATTGTTTATTGGTTAACGGAT
AHSV-4	(251)	ACCAATCAATGGCTCTGTTAACACGATTGATTGTTTATTGGTTAACGGAT
$R4\text{-}2_{4,5,7,10}$	(251)	ACCAATCAATGGCTCTGTTGACACGATTGATTGTTTATTGGTTAACGGAT
$R4\text{-}2_{7,10}$	(251)	ACCAATCAATGGCTCTGTTAACACGATTGATTGTTTATTGGTTAACGGAT
$R4\text{-}2_{10}$	(251)	ACCAATCAATGGCTCTGTTAACACGATTGATTGTTTATTGGTTAACGGAT
$R3\text{-}2_{5,10}$	(251)	ACCAATCAATGGCTCTGTTGACACGATTGATTGTTTATTGGTTAACGGAT
$R3\text{-}2_{3,5}$	(251)	ACCAATCAATGGCTCTGTTGACACGATTGATTGTTTATTGGTTAACGGAT

		301 … 350
AHSV-2	(301)	GTGACTGAGAGAAGCGCTATCTTTCGGCTGACTTGTTTCGCAATCTTCGG
AHSV-3	(301)	GTGACTGAGAGAAGCGCTATCTTTCGGCTGACTTGTTTCGCAATCTTCGG
AHSV-4	(301)	GTGACTGAGAGAAGTGCTATCTTTCGGCTGACTTGTTTCGCGATCTTCGG
R4-2$_{4,5,7,10}$	(301)	GTGACTGAGAGAAGCGCTATCTTTCGGCTGACTTGTTTCGCAATCTTCGG
R4-2$_{7,10}$	(301)	GTGACTGAGAGAAGTGCTATCTTTCGGCTGACTTGTTTCGCGATCTTCGG
R4-2$_{10}$	(301)	GTGACTGAGAGAAGTGCTATCTTTCGGCTGACTTGTTTCGCGATCTTCGG
R3-2$_{5,10}$	(301)	GTGACTGAGAGAAGCGCTATCTTTCGGCTGACTTGTTTCGCAATCTTCGG
R3-2$_{3,5}$	(301)	GTGACTGAGAGAAGCGCTATCTTTCGGCTGACTTGTTTCGCAATCTTCGG
		351 … 399
AHSV-2	(351)	ATGTAAGCCAACAGCTCGAGGTAGATATATTGATTGGGACGATCTTGGA
AHSV-3	(351)	ATGTAAGCCAACAGCTCGAGGTAGATATATTGACTGGGATGATCTTGGA
AHSV-4	(351)	ATGTAAGCCGACGGCTCGAGGTAGATATATTGATTGGGATGATCTTGGA
R4-2$_{4,5,7,10}$	(351)	ATGTAAGCCAACAGCTCGAGGTAGATATATTGATTGGGACGATCTTGGA
R4-2$_{7,10}$	(351)	ATGTAAGCCGACGGCTCGAGGTAGATATATTGATTGGGATGATCTTGGA
R4-2$_{10}$	(351)	ATGTAAGCCGACGGCTCGAGGTAGATATATTGATTGGGATGATCTTGGA
R3-2$_{5,10}$	(351)	ATGTAAGCCAACAGCTCGAGGTAGATATATTGATTGGGACGATCTTGGA
R3-2$_{3,5}$	(351)	ATGTAAGCCAACAGCTCGAGGTAGATATATTGATTGGGACGATCTTGGA

VP5 gene (Segment 6)

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                             1                                                50
AHSV-3                  (1)  TGAAGAAGCTGTGCAGGAGATGTTGGATTTAAGTGCCGAGGTCATCGAAA
AHSV-4                  (1)  TGATGAAGCGATTCAGGAGATGCTCGACTTAAGCGCAGAAGTGATTGAGA
R4-2_{4,5,7,10}         (1)  TGATGAAGCGATTCAGGAGATGCTCGACTTAAGCGCAGAAGTGATTGAGA
R4-2_{7,10}             (1)  TGATGAAGCGATTCAGGAGATGCTCGACTTAAGCGCAGAAGTGATTGAGA
R4-2_{10}               (1)  TGATGAAGCGATTCAGGAGATGCTCGACTTAAGCGCAGAAGTGATTGAGA
R3-2_{5,10}             (1)  TGAAGAAGCTGTGCAGGAGATGTTGGATTTAAGTGCCGAGGTCATCGAAA
R3-2_{3,5}              (1)  TGAAGAAGCTGTGCAGGAGATGTTGGATTTAAGTGCCGAGGTCATCGAAA
                             51                                              100
AHSV-3                 (51)  CGGCGGCTGAGGAGGTGCCAATCTTTGGCGCAGGCGCAGCAAATGTTGTT
AHSV-4                 (51)  CTGCGTCGGAGGAGGTACCAATTTTTGGCGCTGGGGCGGCGAACGTTATC
R4-2_{4,5,7,10}        (51)  CTGCGTCGGAGGAGGTACCAATTTTTGGCGCTGGGGCGGCGAACGTTATC
R4-2_{7,10}            (51)  CTGCGTCGGAGGAGGTACCAATTTTTGGCGCTGGGGCGGCGAACGTTATC
R4-2_{10}              (51)  CTGCGTCGGAGGAGGTACCAATTTTTGGCGCTGGGGCGGCGAACGTTATC
R3-2_{5,10}            (51)  CGGCGGCTGAGGAGGTGCCAATCTTTGGCGCAGGCGCAGCAAATGTTGTT
R3-2_{3,5}             (51)  CGGCGGCTGAGGAGGTGCCAATCTTTGGCGCAGGCGCAGCAAATGTTGTT
                             101                                             150
AHSV-3                (101)  GCGACGACACGCGCAATCCAAGGGGGTCTAAAGTTGAAGGAGATAATAGA
AHSV-4                (101)  GCCACAACCCGAGCAATACAGGGGGGGTTAAAACTAAAGGAAATTGTTGA
R4-2_{4,5,7,10}       (101)  GCCACAACCCGAGCAATACAGGGGGGGTTAAAACTAAAGGAAATTGTTGA
R4-2_{7,10}           (101)  GCCACAACCCGAGCAATACAGGGGGGGTTAAAACTAAAGGAAATTGTTGA
R4-2_{10}             (101)  GCCACAACCCGAGCAATACAGGGGGGGTTAAAACTAAAGGAAATTGTTGA
R3-2_{5,10}           (101)  GCGACGACACGCGCAATCCAAGGGGGTCTAAAGTTGAAGGAGATAATAGA
R3-2_{3,5}            (101)  GCGACGACACGCGCAATCCAAGGGGGTCTAAAGTTGAAGGAGATAATAGA
                             151                              185
AHSV-3                (151)  TAAACTCACAGGGATTGATCTCTCTCATTTGAAAG
AHSV-4                (151)  TAAGCTTACGGGAATAGACTTGAGTCATTTGAAGG
R4-2_{4,5,7,10}       (151)  TAAGCTTACGGGAATAGACTTGAGTCATTTGAAGG
R4-2_{7,10}           (151)  TAAGCTTACGGGAATAGACTTGAGTCATTTGAAGG
R4-2_{10}             (151)  TAAGCTTACGGGAATAGACTTGAGTCATTTGAAGG
R3-2_{5,10}           (151)  TAAACTCACAGGGATTGATCTCTCTCATTTGAAAG
R3-2_{3,5}            (151)  TAAACTCACAGGGATTGATCTCTCTCATTTGAAAG
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VP7 gene (Segment 7)

```
                           1                                                50
AHSV-2               (1)   GGACCAAGTAAAGTGCAGACGGGACCTTATGCAGGAGCGGCTGAGGTGCA
AHSV-3               (1)   GGACCAAGCAAAGTACAGACGGGACCTTATGCAGGAGCAGTTGAGGTGCA
AHSV-4               (1)   GGACCAAGCAAAGTGCAAACGGGACCTTATGCAGGAGCGGTAGAGGTGCA
R4-2_{4,5,7,10}      (1)   GGACCAAGTAAAGTGCAGACGGGACCTTATGCAGGAGCGGCTGAGGTGCA
R3-2_{5,10}          (1)   GGACCAAGCAAAGTACAGACGGGACCTTATGCAGGAGCAGTTGAGGTGCA
R3-2_{3,5}           (1)   GGACCAAGCAAAGTACAGACGGGACCTTATGCAGGAGCAGTTGAGGTGCA
                           51                                              100
AHSV-2              (51)   ACAGTCTGGCAGATATTATGTACCGCAAGGTCGAACACGTGGTGGGTACA
AHSV-3              (51)   ACAATCTGGCAGATATTACGTACCGCAAGGTCGAACACGTGGTGGGTACA
AHSV-4              (51)   ACAATCTGGCAGATATTACGTACCGCAAGGTCGAACACGTGGTGGGTACA
R4-2_{4,5,7,10}     (51)   ACAGTCTGGCAGATATTATGTACCGCAAGGTCGAACACGTGGTGGGTACA
R3-2_{5,10}         (51)   ACAATCTGGCAGATATTACGTACCGCAAGGTCGAACACGTGGTGGGTACA
R3-2_{3,5}          (51)   ACAATCTGGCAGATATTACGTACCGCAAGGTCGAACACGTGGTGGGTACA
                           101                                             150
AHSV-2             (101)   TCAATTCAAATATTGCTGAAGTGTGTATGGATGCGGGTGCTGCGGGACAG
AHSV-3             (101)   TTAATTCAAATATTGCTGAAGTGTGTATGGATGCAGGCGCTGCGGGACAG
AHSV-4             (101)   TCAATTCAAATATTGCTGAGGTGTGTATGGATGCAGGTGCTGCGGGACAG
R4-2_{4,5,7,10}    (101)   TCAATTCAAATATTGCTGAAGTGTGTATGGATGCGGGTGCTGCGGGACAG
R3-2_{5,10}        (101)   TTAATTCAAATATTGCTGAAGTGTGTATGGATGCAGGCGCTGCGGGACAG
R3-2_{3,5}         (101)   TTAATTCAAATATTGCTGAAGTGTGTATGGATGCAGGCGCTGCGGGACAG
                           151                                             200
AHSV-2             (151)   GTCAATGCGCTGCTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
AHSV-3             (151)   GTCAATGCGCTGCTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
AHSV-4             (151)   GTCAATGCGCTGTTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
R4-2_{4,5,7,10}    (151)   GTCAATGCGCTGCTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
R3-2_{5,10}        (151)   GTCAATGCGCTGCTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
R3-2_{3,5}         (151)   GTCAATGCGCTGCTAGCCCCAAGGAGGGGGGACGCAGTCATGATCTATTT
                           201                                             250
AHSV-2             (201)   CGTTTGGAGACCGCTGCGTATATTCTGTGATCCTCAAGGTGCATCACTCG
AHSV-3             (201)   TGTTTGGAGACCATTGCGTATATTTTGTGATCCTCAAGGTGCGTCACTTG
AHSV-4             (201)   CGTTTGGAGGCCGTTGCGTATATTTTGTGATCCTCAGGGTGCGTCACTTG
R4-2_{4,5,7,10}    (201)   CGTTTGGAGACCGCTGCGTATATTCTGTGATCCTCAAGGTGCATCACTCG
R3-2_{5,10}        (201)   TGTTTGGAGACCATTGCGTATATTTTGTGATCCTCAAGGTGCGTCACTTG
R3-2_{3,5}         (201)   TGTTTGGAGACCATTGCGTATATTTTGTGATCCTCAAGGTGCGTCACTTG
                           251
AHSV-2             (251)   AGAGCGCTCC
AHSV-3             (251)   AAAGCGCTCC
AHSV-4             (251)   AGAGCGCTCC
R4-2_{4,5,7,10}    (251)   AGAGCGCTCC
R3-2_{5,10}        (251)   AAAGCGCTCC
R3-2_{3,5}         (251)   AAAGCGCTCC
```

NS2 gene (Segment 8)

		1 50
AHSV-2	(1)	AGCTTAATGATTACTGAGAGTGGAATTGAGGTAACGCAAAACCGATGGGA
AHSV-3	(1)	AGTTTAATGATTACTGAGAGTGGAATTGAGGTAACGCAAAACCGATGGGA
AHSV-4	(1)	AGTTTAATGATTACTGAAAGTGGAATTGAGGTGACGCAAAACCGATGGGA
$R4\text{-}2_{4,5,7,10}$	(1)	AGTTTAATGATTACTGAAAGTGGAATTGAGGTGACGCAAAACCGATGGGA
$R4\text{-}2_{7,10}$	(1)	AGTTTAATGATTACTGAAAGTGGAATTGAGGTGACGCAAAACCGATGGGA
$R4\text{-}2_{10}$	(1)	AGTTTAATGATTACTGAAAGTGGAATTGAGGTGACGCAAAACCGATGGGA
$R3\text{-}2_{5,10}$	(1)	AGTTTAATGATTACTGAGAGTGGAATTGAGGTAACGCAAAACCGATGGGA
$R3\text{-}2_{3,5}$	(1)	AGTTTAATGATTACTGAGAGTGGAATTGAGGTAACGCAAAACCGATGGGA
		51 100
AHSV-2	(51)	GGAGTGGAGCTTTGAGGCGTTAACACCAGTACCGATGGCTGTGGCGGTGA
AHSV-3	(51)	GGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCAGTGGCGGTGA
AHSV-4	(51)	AGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCTGTGGCGGTCA
$R4\text{-}2_{4,5,7,10}$	(51)	AGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCTGTGGCGGTCA
$R4\text{-}2_{7,10}$	(51)	AGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCTGTGGCGGTCA
$R4\text{-}2_{10}$	(51)	AGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCTGTGGCGGTCA
$R3\text{-}2_{5,10}$	(51)	GGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCAGTGGCGGTGA
$R3\text{-}2_{3,5}$	(51)	GGAGTGGAGTTTTGAAGCGTTAACACCAGTACCAATGGCAGTGGCGGTGA
		101 150
AHSV-2	(101)	ATGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
AHSV-3	(101)	ATGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
AHSV-4	(101)	ACGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
$R4\text{-}2_{4,5,7,10}$	(101)	ACGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
$R4\text{-}2_{7,10}$	(101)	ACGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
$R4\text{-}2_{10}$	(101)	ACGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
$R3\text{-}2_{5,10}$	(101)	ATGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
$R3\text{-}2_{3,5}$	(101)	ATGTAGGGAGAGGCTCGTTTGACACTGAGATTAAATATGTGAGAGGAAGC
		151 200
AHSV-2	(151)	GGTGCAGTTCCACCTTATACGAAGAATGGAATGGATCGAAGAGCGATGCC
AHSV-3	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGATCGAAGAGCGATGCC
AHSV-4	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGACCGAAGAGCGATGCC
$R4\text{-}2_{4,5,7,10}$	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGACCGAAGAGCGATGCC
$R4\text{-}2_{7,10}$	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGACCGAAGAGCGATGCC
$R4\text{-}2_{10}$	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGACCGAAGAGCGATGCC
$R3\text{-}2_{5,10}$	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGATCGAAGAGCGATGCC
$R3\text{-}2_{3,5}$	(151)	GGTGCGGTTCCACCTTATACGAAGAATGGAATGGATCGAAGAGCGATGCC
		201 250
AHSV-2	(201)	TTCTTTACCAGGAATAACGACTTTGGATGTTGGAGTTAGAGATTTGCGTT
AHSV-3	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
AHSV-4	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
$R4\text{-}2_{4,5,7,10}$	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
$R4\text{-}2_{7,10}$	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
$R4\text{-}2_{10}$	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
$R3\text{-}2_{5,10}$	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
$R3\text{-}2_{3,5}$	(201)	TTCTTTACCAGGAATAACAACTTTGGATGTTGGAGTTAGAGATTTGCGTT
		251 300
AHSV-2	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
AHSV-3	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
AHSV-4	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
$R4\text{-}2_{4,5,7,10}$	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
$R4\text{-}2_{7,10}$	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
$R4\text{-}2_{10}$	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
$R3\text{-}2_{5,10}$	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC
$R3\text{-}2_{3,5}$	(251)	TAAAGATGAAGGAGAACAGGGAGGCAGAAAGGGAGAAGATGGAACGAGCC

301 350
AHSV-2 (301) CTAAGTGGTGGGCTCGATATGGGAAGCTGTAGAATGTATGGGGGAGGAAG
AHSV-3 (301) CTGAGTGGTGGGCTCGATATGGGAAGCTGTAGAATGTATGGGGGAGGAAG
AHSV-4 (301) CTAAGTGGTGGGCTCGATATGGGGAGCTGTAGAATGTATGGAGGAGGAAG
R4-$2_{4,5,7,10}$ (301) CTAAGTGGTGGGCTCGATATGGGGAGCTGTAGAATGTATGGAGGAGGAAG
R4-$2_{7,10}$ (301) CTAAGTGGTGGGCTCGATATGGGGAGCTGTAGAATGTATGGAGGAGGAAG
R4-2_{10} (301) CTAAGTGGTGGGCTCGATATGGGGAGCTGTAGAATGTATGGAGGAGGAAG
R3-$2_{5,10}$ (301) CTGAGTGGTGGGCTCGATATGGGAAGCTGTAGAATGTATGGGGGAGGAAG
R3-$2_{3,5}$ (301) CTGAGTGGTGGGCTCGATATGGGAAGCTGTAGAATGTATGGGGGAGGAAG
351 400
AHSV-2 (351) AAATGACGTGCGTGAGATTACCTTGGATGAGGCCGGACCATCACGTACGC
AHSV-3 (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCTGGACCATCGCGTACAC
AHSV-4 (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCCGGACCATCACGTACAC
R4-$2_{4,5,7,10}$ (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCCGGACCATCACGTACAC
R4-$2_{7,10}$ (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCCGGACCATCACGTACAC
R4-2_{10} (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCCGGACCATCACGTACAC
R3-$2_{5,10}$ (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCTGGACCATCGCGTACAC
R3-$2_{3,5}$ (351) AAATGATGTGCGTGAGATCACCTTGGATGAGGCTGGACCATCGCGTACAC
401 450
AHSV-2 (401) CAAGGAGACTTTCTGTTCAGAGCAATGAAAGCCGTTCAGATGATGTGGCG
AHSV-3 (401) CAAGGAAACTTTCTGTTCAGAGCAATGAAAGTCGTTCAGATGATGTGGCA
AHSV-4 (401) CGAGGAAACTTTCTGTTCAGAGTAATGAAAGTCGTTCAGACGATGTGGCA
R4-$2_{4,5,7,10}$ (401) CGAGGAAACTTTCTGTTCAGAGTAATGAAAGTCGTTCAGACGATGTGGCA
R4-$2_{7,10}$ (401) CGAGGAAACTTTCTGTTCAGAGTAATGAAAGTCGTTCAGACGATGTGGCA
R4-2_{10} (401) CGAGGAAACTTTCTGTTCAGAGTAATGAAAGTCGTTCAGACGATGTGGCA
R3-$2_{5,10}$ (401) CAAGGAAACTTTCTGTTCAGAGCAATGAAAGTCGTTCAGATGATGTGGCA
R3-$2_{3,5}$ (401) CAAGGAAACTTTCTGTTCAGAGCAATGAAAGTCGTTCAGATGATGTGGCA
451 500
AHSV-2 (451) CGAAGACATGCTGAGTTGGTAGAGATGGAGCGATTAAGAATGATGAAGAA
AHSV-3 (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGATTAAGAATGATGAAGAA
AHSV-4 (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGACTAAGAATGATGAAGAA
R4-$2_{4,5,7,10}$ (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGACTAAGAATGATGAAGAA
R4-$2_{7,10}$ (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGACTAAGAATGATGAAGAA
R4-2_{10} (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGACTAAGAATGATGAAGAA
R3-$2_{5,10}$ (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGATTAAGAATGATGAAGAA
R3-$2_{3,5}$ (451) CGAAGACATGCTGAGTTGGTGGAGATGGAGCGATTAAGAATGATGAAGAA
501 550
AHSV-2 (501) CGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGATAGTGATGATC
AHSV-3 (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGATAGTGATGATC
AHSV-4 (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGAAAGTGATGATC
R4-$2_{4,5,7,10}$ (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGAAAGTGATGATC
R4-$2_{7,10}$ (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGAAAGTGATGATC
R4-2_{10} (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGAAAGTGATGATC
R3-$2_{5,10}$ (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGATAGTGATGATC
R3-$2_{3,5}$ (501) TGAACCAGTACGTACAGAGAGTATGTGGTGTCAAAGTGATAGTGATGATC
551 584
AHSV-2 (551) AATCTGATGAGGATCACGAGATTGGGAGTACAGA
AHSV-3 (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
AHSV-4 (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
R4-$2_{4,5,7,10}$ (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
R4-$2_{7,10}$ (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
R4-2_{10} (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
R3-$2_{5,10}$ (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA
R3-$2_{3,5}$ (551) AATCTGATGAGGATCACGAGGTTGGGAGTACAGA

VP6 gene (Segment 9)

		113 162
AHSV-2	(113)	GATAGGACAGGCGGCCGCAGCGGAGATTCAAAAACTGAGGGAGAGGAGGC
AHSV-3	(113)	GATAGGATTGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
AHSV-4	(113)	GATAGGACAGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
R4-$2_{4,5,7,10}$	(113)	GATAGGACAGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
R4-$2_{7,10}$	(113)	GATAGGACAGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
R4-2_{10}	(113)	GATAGGACAGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
R3-$2_{5,10}$	(113)	GATAGGATTGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
R3-$2_{3,5}$	(113)	GATAGGATTGGCGGCTGCAGCGGAAATTCAAAAACTGAGGGAGAGGAGGC
		163 212
AHSV-2	(163)	AAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCGACGCAGGAGA
AHSV-3	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
AHSV-4	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
R4-$2_{4,5,7,10}$	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
R4-$2_{7,10}$	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
R4-2_{10}	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
R3-$2_{5,10}$	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
R3-$2_{3,5}$	(163)	GAAGGCTGGAGGGGGCGATAGACGGATTGGAGGATTAGCAACGCAGGAGA
		213 262
AHSV-2	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTCTCT
AHSV-3	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
AHSV-4	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
R4-$2_{4,5,7,10}$	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
R4-$2_{7,10}$	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
R4-2_{10}	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
R3-$2_{5,10}$	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
R3-$2_{3,5}$	(213)	TTGCAGACTTTGTGAAGAAGAAGATCGGAGTTGAAGTTCAGGTGTTTTCT
		263 312
AHSV-2	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
AHSV-3	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
AHSV-4	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
R4-$2_{4,5,7,10}$	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
R4-$2_{7,10}$	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
R4-2_{10}	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
R3-$2_{5,10}$	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
R3-$2_{3,5}$	(263)	AAAGGAATGAGCAACTTATTTACTGTAGATAAGTCATTGCTTGAGCGGGG
		313
AHSV-2	(313)	TGGGTTAGGG
AHSV-3	(313)	TGGGTTAGGG
AHSV-4	(313)	TGGGTTAGGA
R4-$2_{4,5,7,10}$	(313)	TGGGTTAGGA
R4-$2_{7,10}$	(313)	TGGGTTAGGA
R4-2_{10}	(313)	TGGGTTAGGA
R3-$2_{5,10}$	(313)	TGGGTTAGGG
R3-$2_{3,5}$	(313)	TGGGTTAGGG

NS3 gene (Segment 10)

		351 400
AHSV-2	(165)	TATGTTTATTTGCGCGAACGTAACTATGGCTACTTCTCTAGTTGGAGGTA
AHSV-3	(165)	GATCTTTATGAGCGGGTGCGTAACGATGGCTACCTCGATGGCGGGCGGGT
AHSV-4	(351)	GATCTTTATTAGCGGATGTGTGACGTTGGCAACATCGATGGTTGGAGGGT
$\text{R4-2}_{4,5,7,10}$	(165)	TATGTTTATTTGCGCGAACGTAACTATGGCTACTTCTCTAGTTGGAGGTA
$\text{R4-2}_{7,10}$	(165)	TATGTTTATTTGCGCGAACGTAACTATGGCTACTTCTCTAGTTGGAGGTA
R4-2_{10}	(165)	TATGTTTATTTGCGCGAACGTAACTATGGCTACTTCTCTAGTTGGAGGTA
$\text{R3-2}_{5,10}$	(165)	TATGTTTATTTGCGCGAACGTAACTATGGCTACTTCTCTAGTTGGAGGTA
		401 450
AHSV-2	(215)	TGTCAATCGTTGATGAGGATATTGCTAAGCATTTGGCGTTTAATGGAAAA
AHSV-3	(215)	TAACGATTATTGATAATGAAATATATGAAGACCT------TAGTGGAGAT
AHSV-4	(401)	TAAGTATTGTCGATAGCGAAATATTTGAAGATTA------TAAGGAGAAC
$\text{R4-2}_{4,5,7,10}$	(215)	TGTCAATCGTTGATGAGGATATTGCTAAGCATTTGGCGTTTAATGGAAAA
$\text{R4-2}_{7,10}$	(215)	TGTCAATCGTTGATGAGGATATTGCTAAGCATTTGGCGTTTAATGGAAAA
R4-2_{10}	(215)	TGTCAATCGTTGATGAGGATATTGCTAAGCATTTGGCGTTTAATGGAAAA
$\text{R3-2}_{5,10}$	(215)	TGTCAATCGTTGATGAGGATATTGCTAAGCATTTGGCGTTTAATGGAAAA
		451 500
AHSV-2	(265)	GAGGATTGGGTGTCAAAAACGGTCCATGGTTTAAATTTGTTATGTACTAC
AHSV-3	(259)	---GGTTGGCTGTCGAAGACGATTCACGGTTTGAATTTGCTGTGTACCAC
AHSV-4	(445)	---GATTGGTTAGTGAAAACGATACATGGGCTGAATTTGTTATGTACCAC
$\text{R4-2}_{4,5,7,10}$	(265)	GAGGATTGGGTGTCAAAAACGGTCCATGGTTTAAATTTGTTATGTACTAC
$\text{R4-2}_{7,10}$	(265)	GAGGATTGGGTGTCAAAAACGGTCCATGGTTTAAATTTGTTATGTACTAC
R4-2_{10}	(265)	GAGGATTGGGTGTCAAAAACGGTCCATGGTTTAAATTTGTTATGTACTAC
$\text{R3-2}_{5,10}$	(265)	GAGGATTGGGTGTCAAAAACGGTCCATGGTTTAAATTTGTTATGTACTAC
		501 550
AHSV-2	(315)	GATGCTACTGGCAGCGAATAAAATATCGGAAAAGGTGAGAGAAGAGATTG
AHSV-3	(306)	TATGTTGTTAGCGGCTGGAAAAATATCAGATAAAATACAGGAGGAGATCT
AHSV-4	(492)	AGTTTTGTTGGCGGCGGGTAAGATTTCTGATAAAATACAAGAGGAGATTT
$\text{R4-2}_{4,5,7,10}$	(315)	GATGCTACTGGCAGCGAATAAAATATCGGAAAAGGTGAGAGAAGAGATTG
$\text{R4-2}_{7,10}$	(315)	GATGCTACTGGCAGCGAATAAAATATCGGAAAAGGTGAGAGAAGAGATTG
R4-2_{10}	(315)	GATGCTACTGGCAGCGAATAAAATATCGGAAAAGGTGAGAGAAGAGATTG
$\text{R3-2}_{5,10}$	(315)	GATGCTACTGGCAGCGAATAAAATATCGGAAAAGGTGAGAGAAGAGATTG
		551 600
AHSV-2	(365)	CGAGGACAAAAAGAGACATCGCGAAAAGACGATCGTACGTATCAGCTGCG
AHSV-3	(356)	CACGCACAAAGCGGGATATAGCGAAGAGAGAATCATATGTTTCCGCGGCT
AHSV-4	(542)	CACAGACAAAGCGTGATATTGCGAAAAGAGAGTCTTACGTATCTGCGGCG
$\text{R4-2}_{4,5,7,10}$	(365)	CGAGGACAAAAAGAGACATCGCGAAAAGACGATCGTACGTATCAGCTGCG
$\text{R4-2}_{7,10}$	(365)	CGAGGACAAAAAGAGACATCGCGAAAAGACGATCGTACGTATCAGCTGCG
R4-2_{10}	(365)	CGAGGACAAAAAGAGACATCGCGAAAAGACGATCGTACGTATCAGCTGCG
$\text{R3-2}_{5,10}$	(365)	CGAGGACAAAAAGAGACATCGCGAAAAGACGATCGTACGTATCAGCTGCG
		601 650
AHSV-2	(415)	ACGATGTCTTGGGATGGCGATAGCGTAACTCTATTACGAGATGTAAAAAA
AHSV-3	(406)	AGTATGTCTTGGAGTGGGGATACGAGCGTTCTATTAAAAGAGGTAAAATA
AHSV-4	(592)	AGTATGTCATGGAATGGAGATACTGAAGTATTATTACAGGCAATTAAGTA
$\text{R4-2}_{4,5,7,10}$	(415)	ACGATGTCTTGGGATGGCGATAGCGTAACTCTATTACGAGATGTAAAAAA
$\text{R4-2}_{7,10}$	(415)	ACGATGTCTTGGGATGGCGATAGCGTAACTCTATTACGAGATGTAAAAAA
R4-2_{10}	(415)	ACGATGTCTTGGGATGGCGATAGCGTAACTCTATTACGAGATGTAAAAAA
$\text{R3-2}_{5,10}$	(415)	ACGATGTCTTGGGATGGCGATAGCGTAACTCTATTACGAGATGTAAAAAA
		651
AHSV-2	(465)	TGGAGACTAGCGG
AHSV-3	(456)	TGGCGACAGCTAG
AHSV-4	(642)	TGGCGATAGCTAG
$\text{R4-2}_{4,5,7,10}$	(465)	TGGAGACTAGCGG
$\text{R4-2}_{7,10}$	(465)	TGGAGACTAGCGG
R4-2_{10}	(465)	TGGAGACTAGCGG
$\text{R3-2}_{5,10}$	(465)	TGGAGACTAGCGG

APPENDIX B

Amino acid sequence alignment of NS3 of AHSV-2, AHSV-3 and AHSV-4. Dots indicate identity to AHSV-2 82/61 NS3.

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                    1                                               50
AHSV-2 82/61        MNLASISQSYMSHNENERSIVPYIPPPY-HPTAPALAVSASQMETMSLGI
AHSV-3 M322/97      .S..T.AEN..M..G.Q.A....V....AYAN..TLGGQ.GE..S.....
AHSV-4 HS39/97      ....T.AKN.SM..GESGA....V....NFAS..TFSQRT....SV....
                    51                                             100
AHSV-2 82/61        LNQAMSSSAGASGALKDEKAAFGAVAEALRDPEPIRKIKRRVGIQTLKTL
AHSV-3 M322/97      .......TT...R...........M...........Q..KH..LR...H.
AHSV-4 HS39/97      .......TT...............M...........Q..KQ...R...N.
                    101                                            150
AHSV-2 82/61        KVELSGMRRKKLILKIIMFICANVTMATSLVGGMSIVDEDIAKHLAFDGK
AHSV-3 M322/97      .I..AS...RYA..RVVI.MSGC......MA..LT.I.NE.YED.SG..-
AHSV-4 HS39/97      .M..AT.....SA...MI..SGC..L...M...L....DE.LRDYKNND-
                    151                                            200
AHSV-2 82/61        GDWVSKTVHGLNLLCTTMLLAANKISEKVREEIARTKRDIAKRQSYVSAA
AHSV-3 M322/97      --.L...I..............G...D.IQ...S.........E......
AHSV-4 HS39/97      --.LM..I.........V....G...D.MQ...S.........E......
                    201              220
AHSV-2 82/61        TMSWDGDSVTLLRDVKYGD-
AHSV-3 M322/97      S...S..TSV..KE.....S
AHSV-4 HS39/97      S...S..TEM..QGI...ES
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