

HGyV - CGGCGCGCG CGGCAGC- - - - - AGCCTG TACACAGAGA CGTCGCTCGG GTCCTCCGGA 52
 M55918 GAATTCCGAG TGGTTACTAT TCCATCACCA TTCTAGCCTG TACACAGAAA G- - - - TCAA GATGGACGAA 65
 Consensus GNNNNNCGNG NGGNNNCTAT TCCATCACCA TTCTAGCCTG TACACAGANA NGTCGCTCNN GNNNNNCGNA
 HGyV CCCTCGCTCC TCAACCTTTT CTTATTAATA TCATCACCCA GCGGACAAA CGCCACAAGG CGTGGTAACC 122
 M55918 TCGCTCGACT TCGCTCGCGA TTCGTGCAAG GCG- - - - - GGGGGCCGGA GGCCCC- - - - CGGTGGCC 123
 Consensus NCNNNNNNCN TCNNNCCNNN NTNNTNNAAN NCNTCACCCA GNGNGNCNNA NGCCNCNAGG CGNGGTNNCC
 HGyV AACGATATGT AAGTAAACTG AAGACTCATAC CGGTACAGGG GGGTACGTCA CCATGTACAG GGGGGTACGT 192
 M55918 CCCCTCCAAC GAGTGG- - - - - ACGTACAGGG GGGTACGTCA TC- CGTACAG GGGGGTACGT 181
 Consensus NNCNNNNNNN NAGTNNACTG AAGACTCATNC NNGTACAGGG GGGTACGTCA NCANGTACAG GGGGGTACGT
 HGyV CACCATGTAC AGGGGGGTAC GTCATCATGT ACAGGGGGGT ACGTACCAT GTACAGGGGG GTACGTACCC 262
 M55918 CATC- CGTAC AGGGGGGTAC GTCA- - - - - CAAAGAGGC GTTCC- - - - C GTACAGGGGG GTACGTAC- 238
 Consensus CANGANGTAC AGGGGGGTAC GTCATCATGT ACANNNGGN NNNNCACCAN GTACAGGGGG GTACGTACCC
 HGyV ATGTACAGGG GGGTACGTCA CAGCCAATCA GAATTGAGCA CGCC- CAGGA ACGCCCTGG GCGGGGAGAT 331
 M55918 GCGTACAGGG GGGTACGTCA CAGCCAATCA AAAGCTGCCA CGTTGCGAAA GTGACGTTTC GAAAATGGGC 308
 Consensus NNGTACAGGG GGGTACGTCA CAGCCAATCA NAANNNNCA CGNNGCENNA NNGNCNNTNN GNNNNNNGN
 VP2
 HGyV GCTATCAATT TAGGGATATA AGCAGAGCAC ATACCGGACG GCGGTAGGTA TGTCATCCGG CGGTCTCGGG 401
 M55918 GCGCAAGCC TCTCTATATA TTGAGCGCAC ATACCGGTCG GCAGTAGGTA TA- CGCAAGG CGGTCCGGGT 377
 Consensus GNNNNANNN TNNNATATA NNNAGNGCAC ATACCGGNCG GCNGTAGGTA TNCNNNGG CGGTCCNNGG
 VP2
 HGyV GATTGCA- - G CGCCTGTGAG AACCAGGCGG CTGGGGGCG TGAATTGCCG CTTAGGCAAG AGGGGCAACT 469
 M55918 GGATGCACGG GAACGGCGGA CAACCGGCGG CTGGGGGCG TGAATCGGCG CTTAGCCGAG AGGGGCAACC 447
 Consensus GNNTGCACGG NNNCNGNGNN NANCNGGCGG CTGGGGGCG TGAATNGNCG CTTAGNCNAG AGGGGCAACN
 VP2 Apoptin
 HGyV TGGGCCCAGC GGAGCCGGAT CCACGGGCAA GACACTAAAT GCAGACCCCC CGCTCTCGCC GACGAGCAAC 539
 M55918 TGGGCCCAGC GGAGCCGG- - CAGGGGCAA GTAATTCAA ATGAAC- - - - GCTCTCAA GAAGA- - - - 505
 Consensus TGGGCCCAGC GGAGCCGNNT CCANGGCAA GNNANTNNAN NNNNACCCCC CGCTCTCNNN GANGAGCAAC
 VP2 Apoptin
 HGyV AACTACTCAG TCAGAACTAT TAACGGCATA CGAGCATCCA ACAAGTTCGT CTCCGCCAGC AGAAACGACC 609
 M55918 - - - TACTCCA CCCGGACCAT CAACGGTGT CAGGCCACCA ACAAGTTCAC GGCCGTTGGA AACCCCTCAC 572
 Consensus AACTACTCNN NCNGNACNAT NAACGGNTN CNNGCNCNA ACAAGTTCNN NNCCGNNNGN ANNNCCNNN
 VP2 Apoptin
 HGyV TCGATAGAGA TCCAAATTGG TATCGGGTCA ACTATAATTA CTCTATCGCT ACCTGGCTAC GCCAGTGTGC 679
 M55918 TGCAGAGAGA TCCGGATTGG TATCGGTGGA ATTACAATCA CTCTATCGCT GTGTGGCTGC GCGAATGCTC 642
 Consensus TNNANAGAGA TCCNATTGG TATCGNNNA ANTANAATNA CTCTATCGCT NNNTGGCTNC GCNANTGNCC

VP2
Apoptin

HGyV CCGTTCTCAC GACGAGATCT GCACCTGCGG ACGATGGAGG AGTCACTGGT TCCAGGAGGC TAGTGGACTT 749
 M55918 GCGCTCCAC GCTAAGATCT GCAACTGCGG ACAATTCAGA AAGCACTGGT TTCAAGAATG TGCCGGACTT 712
 Consensus GCGNTCNAC GNNNAGATCT GCANCTGCGG ACNATNNAGN ANNCACTGGT TNCANGANNN TNNNGGACTT

VP2
Apoptin

HGyV GTCACACAGG AGACCCAGAC GGACCAGCTC GCCAGAGATC TACGTCGGCT TCGCGG- - CA AAGGAGAAGC 817
 M55918 GAGGACCGAT CAACCCAAGC - - - CTCCTC GAAGAAGCGA TCCTGCGACC CCTCCGAGTA CAGGGTAAGC 779
 Consensus GNNNNNCNNN NNACCCANN C GACNNNCTC GNNNNAGNN TNCNNCGNCN NCNCCGAGNA NAGGNNAAAGC

VP2
Apoptin

HGyV - AGCAAAAAG AAAACTTGAT TACCTTAAGG GAAAACGGAC CCC- - - CTAT AAAAAAGC- - - TAAGACTGT 880
 M55918 GAGCTAAAAG AAAGCTTGAT TACCACTACT CCCAGCCGAC CCCGAACCGC AAAAAGGCGT ATAAGACTGT 849
 Consensus GAGCNAAAAAG AAANCTTGAT TACCNNNANN NNNANCGAC CCCGAACNNN AAAAANGCGT ATAAGACTGT

VP2
Apoptin
VP1

HGyV AACATGGCAA GACTACGAAG AAGACGACCT CGCGGACGCT TTGGCTTCTA CCACAGAGGA CGATGGCACT 950
 M55918 AAGATGGCAA GAC- - - GAGC TCGCAGACCG AGAGGCCGAT TTTACTCCTT CAGAAGAGGA CGGTGGCACC 916
 Consensus AANATGGCAA GACTACGANN NNGNNGACCN NGNGGNCNT TTNCTNCTN CNNAGAGGA CGNTGGCACN

VP2
VP1

HGyV GGAGACACAG ACTGCGACGA AGACGCTATT CCCGGAGGGG TAAATTTCTA TATGCGCGTA GAAGATCCTT 1020
 M55918 ACCTCAAGCG ACTTCGACGA AGATA- - - - - TAAATTTCTA CATCGGAGGA GACAGCGGTA 971
 Consensus NNNNNNANNG ACTNCGACGA AGANNCTATT CCCGGAGGGG TAAATTTCTA NATNNGNGNA GANNNNNTN

VP2
VP1

HGyV TGATCGCCGC GTTAAGAGGA GGATCTT- - - CAACCCACAC CCGGCTCCT ATGTGGTAAG GCTACCGAAC 1087
 M55918 TCGTAGACGA GCTTTTAGGA AGGCCTTTCA CAACCCCGC CCCGGTACGT ATAGTGTGAG GCTGCCGAAC 1041
 Consensus TNNTNGNCGN GNTNNNAGGA NGNCTTTCA CAACCCNCC CNNGGNCNT ATNNGTNAG GCTNCCGAAC

VP1

HGyV CCTTACAATA AGCTTACCCT CTTTTTCCAA GGCATTGTAT TCATTCCGGA GGCTCAAGCT TTTGTTAAAA 1157
 M55918 CCCCAATCTA CTATGACTAT CCGCTTCCAA GGGGTCATCT TTCTCACGGA AGGACTCATT CTGCCTAAAA 1111
 Consensus CCNNANNNTA NNNTNACNNT CNNTTCCAA GGNTNTNT TNNTNCCGGA NGNCCNNNT NTNNNTAAAA

VP1

HGyV GCACCTA- - - - - - - - TAA AAAGACTAAC CTTACGGTTT GCCATGTAGC CTCCATAAAT GTTAACCTCC 1217
 M55918 ACAGCACAGC GGGGGGCTAT GCAGACCACA TGTACGGGGC GAGA- GTCGC CAAGATCTCT GTGAACCTGA 1180
 Consensus NCANCNAGC GGGGGGCTAN NNAGACNANN NNTACGGNNN GNNATGTNGC CNNNATNNNT GTNAACCTNN

VP1

HGyV GAGAATTTAT GCTTGCAACA ATGCCTTTAG ATGCAAAGAG CAAAATCGGA GGCCCTAACC CTTATCCTCA 1287
 M55918 AAGAGTTCTT GCTAGCTCA ATGAACCTGA CATACGTGAG CAAAATCGGA GGCCCATCG CCGGTGAGTT 1250
 Consensus NAGANTTNTT GCTNGCNCA ATGNNNTNN NNNNNNGAG CAAAATCGGA GGCCCNANCN CNNTNNNNN

VP1
 HGyV 1 340 1 360 1 380 1 400
 GCACCTTGCA GGGTGCCAAT GGTCAGCACA AACGACGCAG GAC - - GCATG GCCGTACGCA GCGGGCATGT 1355

M55918 GATTGCGGAC GGGTCTAAAT - - - - - CACA AGCCGCGGAC AATTGGCCTA ATTGCTGGCT GC - - - - CGC 1309
 Consensus GNNNNNGNAN GGGTNNNAAT GGTCAGCACA ANCNCCGNAN NANTGGCNTN NNNGNNNGCN GCGGGCANGN

VP1
 HGyV 1 420 1 440 1 460
 CAGAAACAAA AAGACCCAGC GTACCACCGA GTGAGTGGTG GCGCTGGGCT CTCCTGGTGA TGCACCCTAG 1425

M55918 TAGATAATAA CGTGCCCTCC GCTACACCAT CGGCATGGTG GAGATGGGCC TTAATGATGA TGCAGCCAC 1379
 Consensus NAGANANNA NNNNCCNNC GNNNCACNN NNGNNTGGTG GNGTGGGCN NTNNTGNTGA TGCANCCNAN

VP1
 HGyV 1 480 1 500 1 520 1 540
 AGCACCTGGC AGATTTTACA ATGCCCAAAA GCTAATGACT CTGGACGCTA TGGGAGACCT GTTAGGGGGC 1495

M55918 GGACTCTTGC CGGTTCTTTA ATCACC AAA GCAGATGACC CTGCAAGACA TGGGTCGCAT GTTTGGGGGC 1449
 Consensus NGNNNCTNGC NGNTTNTNNA ATNNCCAAA GCNNATGACN CTGNANGNNA TGGGNNNCNT GTTNGGGGGC

VP1
 HGyV 1 560 1 580 1 600
 TGGCAGCTAT TCAGGCATGT AAAAACCAAG TTCAGAGTGC TAGCGACTAT GGGACAAGGG GCTTTCTCAC 1565

M55918 TGGCACCTGT TCCGACACAT TGAACCCGC TTTCAGCTCC TTGCCACTAA GAATGAGGGA TCCTTCAGCC 1519
 Consensus TGGCANCTNT TCNGCANNT NAAACCNNT TTNNNNNTNC TNGCNACTAN GNNNNANGGN NCNTTCNNNC

VP1
 HGyV 1 620 1 640 1 660 1 680
 CAGTTGCAAG CCTACTTGTA CAAAATGACT ACTGGAGCAG GAGGCACTTA GAGGGCTTCC CAGTTAAAGG 1635

M55918 CCGTGGCGAG TCTTCTCTCC CAGGGAGAGT ACCTCA - - - - - CGCGTC GGGACGATGT TAAGTACAG- 1580
 Consensus CNGTNGCNAG NCTNCTNNNN CANNNGANT ACNNNAGCAG GAGGCNCNTN GNGNNNTNN NANNTANAGG

VP1
 HGyV 1 700 1 720 1 740
 TGCACCACCT ATGTGCACCA TGCAAAGAAA AACTCAGCAG TACGGCAACG TGGAGTCCAA TGCACCGGCA 1705

M55918 - - CAGCGATC ACCAGAACCG - GTGGCAAAA AGCGGACAAA C - CGATGACG GGGG - - CAT TGCTTATGCG 1644
 Consensus TGCANCNNN ANNGNACCN TGNNNNNAAA ANNNNNNCAN NACGNNNACG NGGNGTCCAN TGCNNNGCN

VP1
 HGyV 1 760 1 780 1 800 1 820
 GATGAGCAAT GGCTACCCGT AAATCCCCCA GACCCACCA GGTACCCAAA CCAGGGAGGA TGCTCCCAA 1775

M55918 ACCGGGAAAA TGAGACCCGA CGAGCAACAG TACCCTGCTA TGCCCCAGA CCCCCGATC ATCACCGCTA 1714
 Consensus NNNNGNAAAN NGNNACCCGN NNANCNCNN NACCCNCNN TGNNCCANA CCNNNNNNN NNCNCNNNA

VP1
 HGyV 1 840 1 860 1 880
 ACGTGGCTCC AGGCATATAC CGGCTTGCA GCTTAGAAGA CAGCAGCAGA TGCTTTTATT CAAAGGCTTG 1845

M55918 CTACAGCGCA AGGCACGCAA - - - - - GTCC GCTGCATGAA TAGCACGCAA GCTTGGTGGT CATGGGACAC 1778
 Consensus NNNNGCNCN AGGCANNAN CGGCTTGNNT GCTNNNNNA NAGCANNNA NNNTNTNTT CANNGGNNN

VP1
 HGyV 1 900 1 920 1 940 1 960
 TTTCCCAAGC TTTGCAGCGC TTTCTGCTAT GGGTGCACC TGGTCAATTC CTAGCACTCA AAAACCTATT 1915

M55918 ATATATGAGC TTTGCAACAC TCACAGCACT CGGTGCACAA TGGTCTTTTC CTCCAGGGCA ACGTTCAAGT 1848
 Consensus NTNNNNNAGC TTTGCANCNC TNNCNGCNT NGGTGCACNN TGGTCNTTC CTNNNNNCA ANNNNCNNT

VP1
 HGyV 1 980 2 000 2 020
 CAAAGAGGCT CATTTAACAA GCACTCCATC ACGGGGACAG GGGACCCCA GGGCCGACGG TGGTTAACAC 1985

M55918 TCTAGACGGT CCTTCAACCA CCACAAGGCG AGAGGAGCCG GGGACCCCA GGGCCAGAGA TGGCACACGC 1918
 Consensus NNNAGANGNT CNTTNACNA NCACNNNNN ANNGGNCNG GGGACCCNA GGGCCNNGN TGGNNACNC

VP1
 HGyV 2 040 2 060 2 080 2 100
 TTGTGCCTAA AGGAGTCGAG TGGATTACTG ACGACACCAT G - - - GAACCT ACGC - - - AAC TGGACACAGA 2049

M55918 TGGTGCCGCT CGGCACGGAG ACCATACCG ACAGCTACAT GTCAGCACCC GCATCAGAGC TGGACACTAA 1988
 Consensus TNGTGCCNN NGGNNNGAG NNNATNACNG ACNNCNCAT GTCAGNACCN NCNACAGAN TGGACACNNA

VP1

 HGyV **CATTGCAACA CTCTTCTTGG CTCAAGGCAG TCCAGTATGG GCACCCCTACA AATTCGGAAC TTTTCACAAA** 2119
 M55918 **TTTCTTTACG CTTTACGTAG CGCAAGGCAC AAATAAGTCG CAACAGTACA AGTTCGGCAC AGCTACATAC** 2058
 Consensus **NNTNNNNACN CTNTNCNTNG CNCAAGGCAN NNNNNNTNG NNCNNTACA ANTTCGGNAC NNNTNNNNAN**

VP1

 HGyV **GCGATGGCGC TAACAGCGAT GCAGACCACC CCTTGGTGCG TGGTGAAAGT CCGTTCCATC TGGCAGCTCG** 2189
 M55918 **GCGCTAAAGG AGCCGGTAAT GAAGAGCGAT GCATGGGCAG TGGTACGCGT CCAGTCGGTC TGGCAGCTGG** 2128
 Consensus **GCGNTNNNGN NNNCNGNNAT GNAGANCNNN NCNTGGNNNG TGGTNNNNGT CCNNTCNNTC TGGCAGCTNG**

VP1

 HGyV **GCAACCAAAG ACAGCCGTAC CCATGGCAAG TGAAGTGGTA CAACGAGCAC ACTGCAACGG ACAGATACAA** 2259
 M55918 **GTAACAGGCA GAGGCCATAC CCATGGGACG TCAACTGGGC GAAC- AGCAC CATGTACTGG G- GGACGCAG** 2196
 Consensus **GNAACNNNNN NNNGCCNTAC CCATGGNANG TNAACTGGNN NAACGAGCAC NNTGNANNGG NCNGANNAN**

VP1

 HGyV **CCC-----GC** 2264
 M55918 **CCCTGAAAAG GGGGGGGGGC TAAAGCCCC CCCCTTAAA CCCCCCCTG GGGGGGATTC CCCCCAGAC** 2266
 Consensus **CCCTGAAAAG GGGGGGGGGC TAAAGCCCC CCCCTTAAA CCCCCCCTG GGGGGGATTC CCCCCAGNC**

VP1

 HGyV **CCCCCGTCAA TAAATAATTA AATAAAC- - - AAATCGAA TTATTTATTT ATTTT** 2315
 M55918 **CCCCCCTTTA TATAGCACTC AATAAACGCA GAAAATAGAT TTATCGCACT ATC- -** 2319
 Consensus **CCCCNTNNA TANANNANTN AATAAACNCA GAAAATNGAN TTATNNNNNT ATNTT**