

Figure 1

Day of Necropsy	Organ	Control	APMV-2	APMV-4	APMV-6
2	Trachea	0/5	0/5	2/5	0/5
	Lung	0/5	0/5	1/5	2/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	1/5	2/5
4	Trachea	0/5	2/5	0/5	1/5
	Lung	0/5	2/5	0/5	1/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	1/5
7	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	2/5
	Gut	0/5	1/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	1/5
14	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	0/5
28	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	2/5	1/5	1/5

Figure 2

Day of Necropsy	Organ	Control	APMV serotype		
			2	4	6
2	Trachea – catarrhal Tracheitis	+	+	+	+
	Gut – mild enteritis	-	+	+	+
4	Trachea – focal ulceration of the respiratory epithelium, mild tracheitis	-	+	+	+
	Lung – focal BALT hyperplasia	-	-	+	-
	Pancreas – multifocal lymphocytic pancreatitis	-	-	+	+
7	Trachea – focal tracheal attenuation	-	+	-	-
	Lung – mild BALT hyperplasia	-	-	+	+
	Gut – cystic enteropathy, focal enteritis	-	-	-	+
	Pancreas – lymphocytic infiltrates in the pancreas	-	-	-	+
14	Trachea – tracheal attenuation, catarrhal tracheitis	-	+	+	+
	Lung – mild interstitial pneumonia, BALT hyperplasia	-	-	+	+
	Gut – GALT hyperplasia	-	-	+	+
28	Lung – lymphocytic bronchitis	-	+	+	+
	Gut – GALT hyperplasia	-	+	+	+
	Pancreas – lymphocytic pancreatitis	-	+	+	+

Figure 3

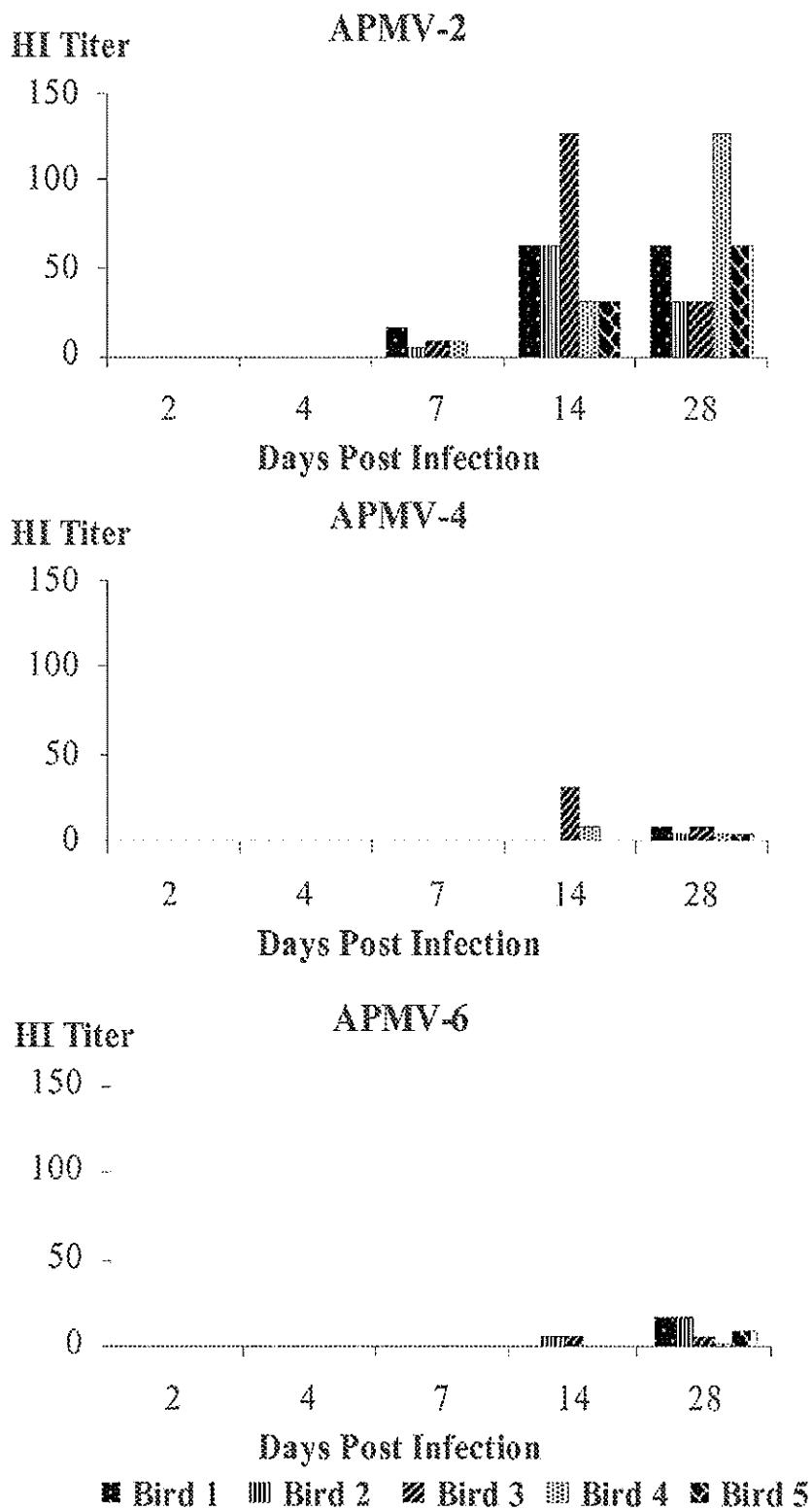


Figure 4

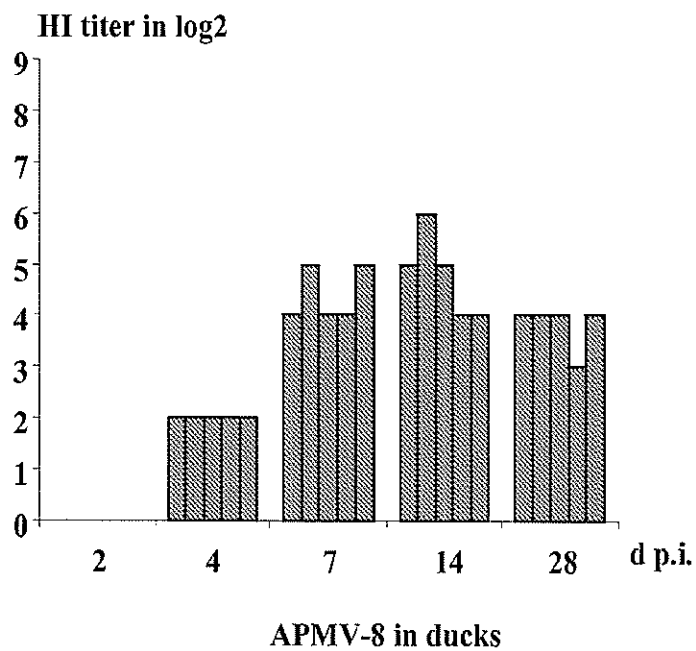
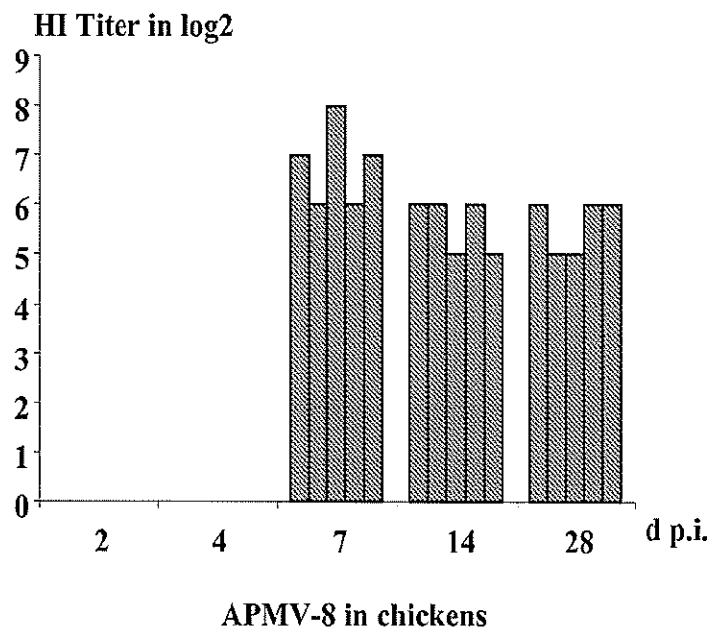


Figure 5

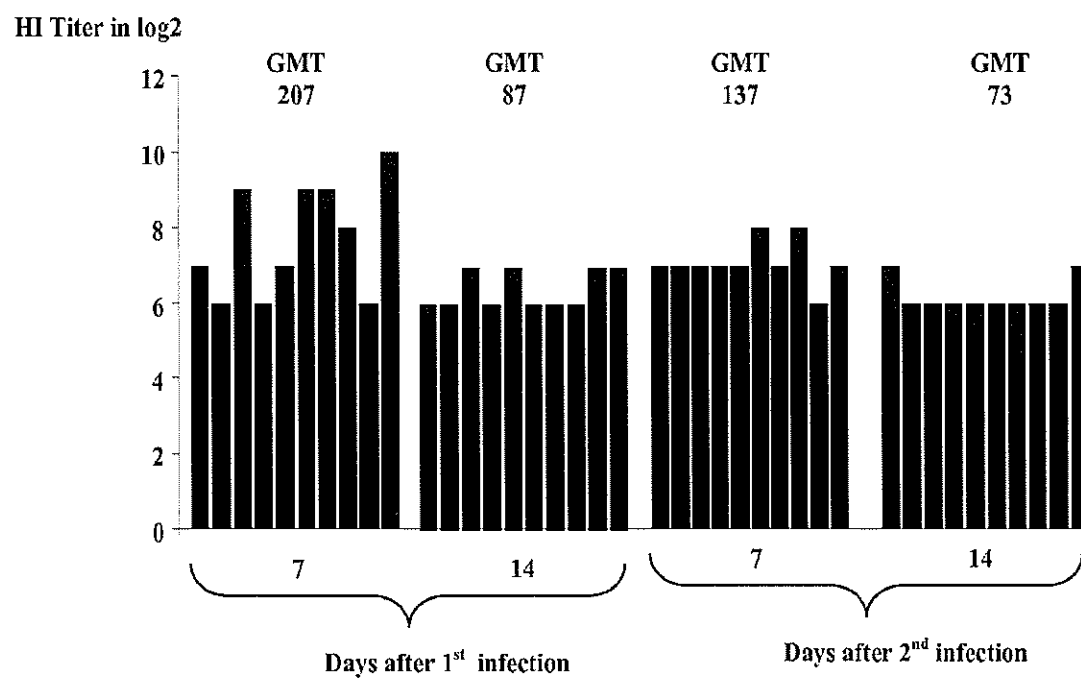


Figure 6

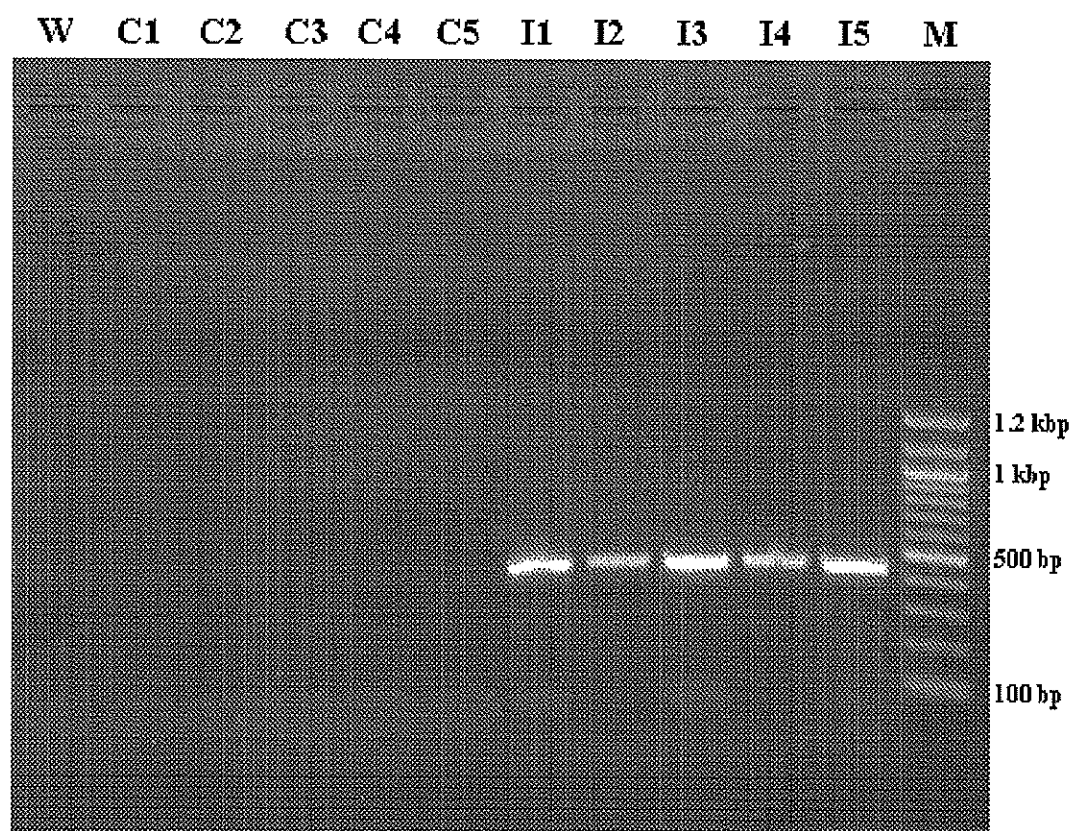


Figure 7					
Day p.i.	Organ	Chicken		Ducks	
		Control	APMV-8	Control	APMV-8
		Virus isolation ^a		RT-PCR	
2	Trachea	0/5 ^b	5/5	0/5	5/5
	Lung	0/5	3/5	0/5	3/5
	Gut	0/5	2/5	0/5	2/5
	Pancreas	0/5	0/5	0/5	0/5
4	Trachea	0/5	5/5	0/5	5/5
	Lung	0/5	1/5	0/5	1/5
	Gut	0/5	1/5	0/5	1/5
	Pancreas	0/5	1/5	0/5	1/5
7	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	2/5	0/5	2/5
14	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	0/5
28	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	1/5	0/5	1/5
	Pancreas	0/5	0/5	0/5	0/5

^a Method used for the detection of virus

^b Number of tissue samples tested positive/total number tested

Figure 8

Day p.i	Organ	Chicken		Duck	
		Control	APMV-8	Control	APMV-8
2	Trachea – catarrhal tracheitis	0/5 ^a	5/5	0/5	3/5
	Lung- interstitial pneumonia	0/5	0/5	0/5	1/5
	Gut – mild enteritis	0/5	0/5	0/5	1/5
4	Trachea - regeneration of respiratory epithelium, minimal tracheitis	0/5	1/5	0/5	5/5
	Pancreas - mild multifocal lymphocytic pancreatitis	0/5	1/5	0/5	0/5
7	Trachea – catarrhal tracheitis	0/5	5/5	0/5	2/5
	Lung - moderate to severe BALT	0/5	4/5	0/5	0/5
	Pancreas – multifocal lymphocytic pancreatitis	0/5	3/5	0/5	1/5
14	Trachea - catarrhal tracheitis	0/5	5/5	0/5	4/5
	Pancreas – lymphocytic pancreatitis	0/5	2/5	0/5	1/5
28	Trachea – catarrhal tracheitis	0/5	5/5	0/5	4/5
	Lung – BALT hyperplasia	0/5	2/5	0/5	2/5
	Gut – mild enteritis	0/5	3/5	0/5	0/5

^a number of tissues showing the histopathological changes/total number analyzed

Figure 9

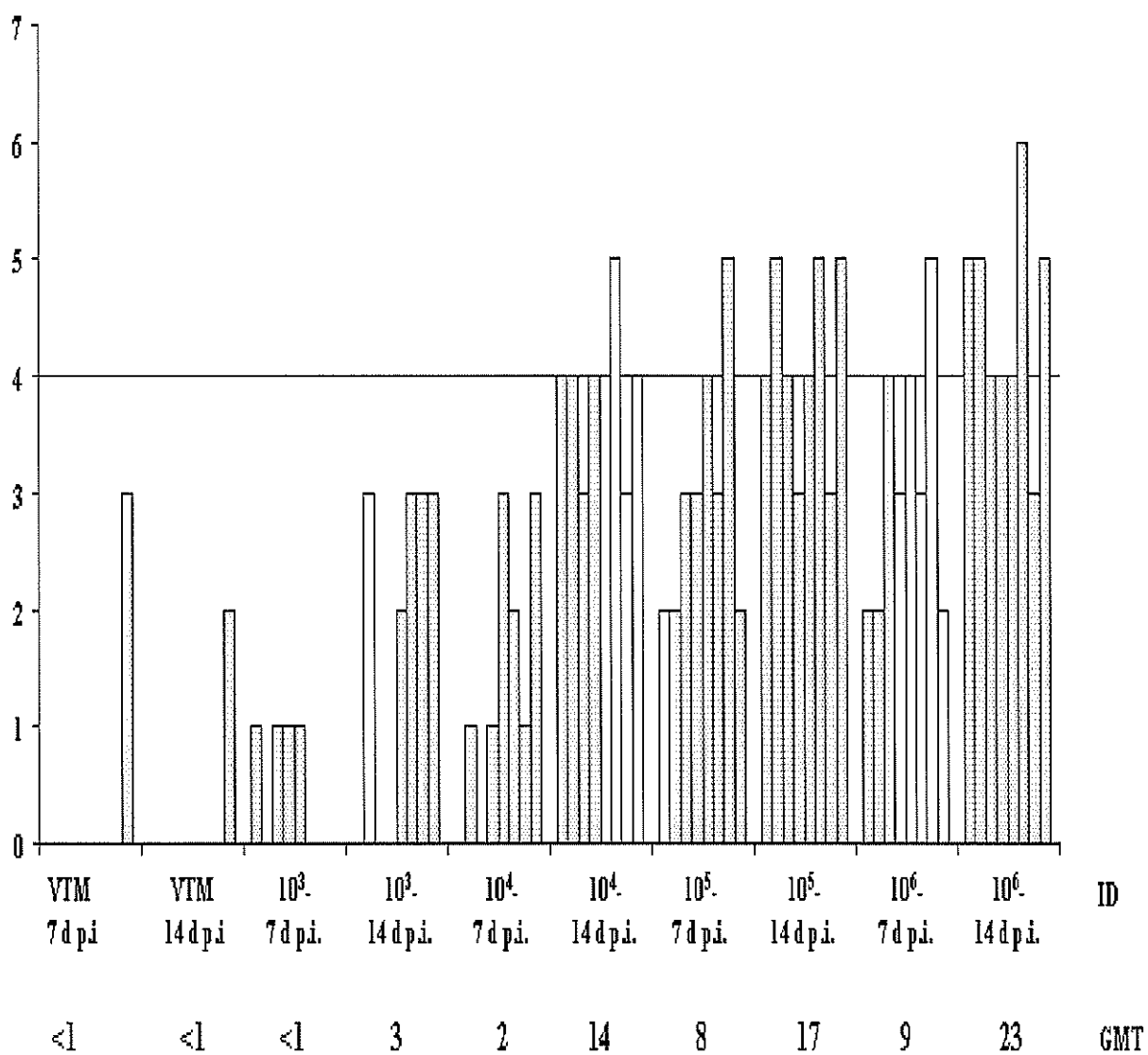
HI Titer in log₂

Figure 10

HI Titer in log₂

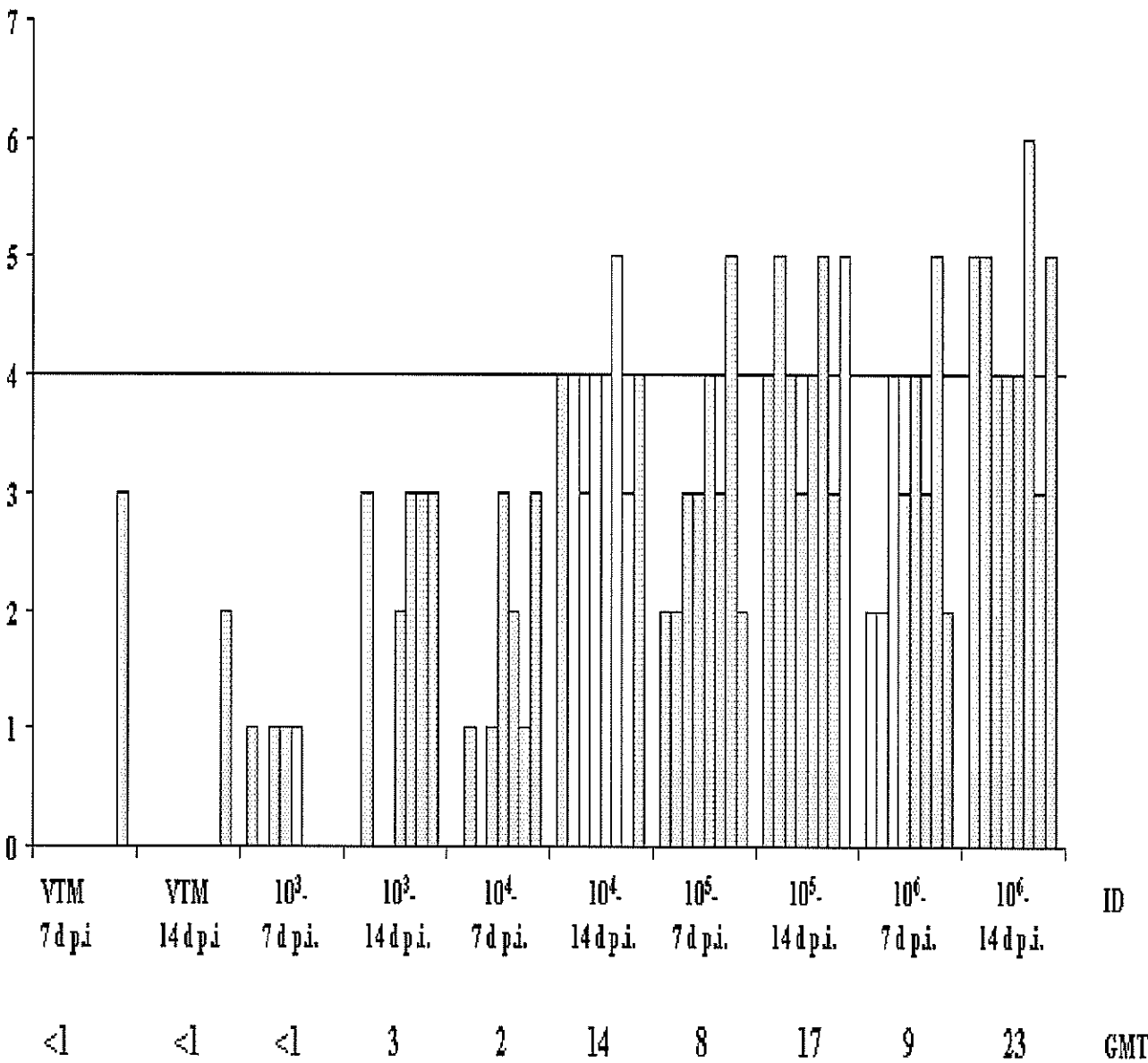


Figure 11 (1/3)

SEQ ID NO:	type	Gene name
1	DNA	APMV-8 genomic DNA
2	DNA	APMV-8 Nucleoprotein (NP) DNA
3	Protein	APMV-8 Nucleoprotein (NP) protein
4	DNA	APMV-8 phosphoprotein (P) DNA
5	Protein	APMV-8 phosphoprotein (P) protein
6	DNA	APMV-8 Matrixprotein (M) DNA
7	Protein	APMV-8 Matrixprotein (M) protein
8	DNA	APMV-8 Fusionprotein (F) DNA
9	Protein	APMV-8 Fusionprotein (F) protein
10	DNA	APMV-8 Hemagglutinin/neuraminidase (HN) DNA
11	Protein	APMV-8 Hemagglutinin/neuraminidase (HN) protein
12	DNA	APMV-8 Polymerase (L) DNA
13	Protein	APMV-8 Polymerase (L) protein 1
14	Protein	APMV-8 Polymerase (L) protein 2
15	DNA	APMV-1 genomic DNA (AF077761)
16	DNA	APMV-2 genomic DNA (EU338414)
17	DNA	APMV-3 genomic DNA (EU403085)
18	DNA	APMV-4 genomic DNA (FJ177514)
19	DNA	APMV-6 genomic DNA (EU622637)
20	DNA	APMV-7 genomic DNA Genbank No. FJ231524
21	oligo	APMV-PolyT (sense)
22	Oligo	8NPf1 (sense)
23	oligo	8NPr (antisense)
24	oligo	NP gene start sequence
25	oligo	P gene start sequence
26	oligo	M gene start sequence
27	oligo	F gene start sequence
28	oligo	HN gene start sequence
29	oligo	L gene start sequence
30	oligo	NP gene end sequence
31	oligo	P gene end sequence
32	oligo	M gene end sequence
33	oligo	F gene end sequence
34	oligo	HN gene end sequence
35	oligo	L gene (1) end sequence
36	oligo	L gene (2) end sequence
37	DNA	APMV-8 genomic DNA Genbank No. FJ215863.1
38	DNA	APMV-8 genomic DNA Genbank No. FJ215864.1
39	DNA	APMV-8 genomic DNA Genbank No. FJ619036
40	DNA	APMV-9 genomic DNA Genbank No. EU910942
41	Oligo	NP-FP-pc3 primer

Figure 11 (2/3)

42	Oligo	NP-RP-pc3 primer
43	Oligo	P-FP-pc3 primer
44	Oligo	P-RP-pc3 primer
45	Oligo	L-FP-pc3 primer
46	Oligo	L-RP-pc3 primer
47	DNA	5'-FLG of APMV-8 genome
48	DNA	3'-FLG of APMV-8 genome
49	DNA	Codon-optimized T7 polymerase (no EcoRI or NotI site)
50	oligo	EGFP-FP primer
51	oligo	EGFP-RP primer
52	DNA	APMV8 minigenome
53	DNA	NP gene of APMV-8 (FJ215863.1) Genbank FJ215863
54	Protein	NP protein of APMV-8 (FJ215863.1) Genbank ACO48297
55	DNA	P gene of APMV-8 (FJ215863.1) Genbank FJ215863
56	Protein	P protein of APMV-8 (FJ215863.1) Genbank ACO48298
57	DNA	M gene of APMV-8 (FJ215863.1) Genbank FJ215863
58	Protein	M protein of APMV-8 (FJ215863.1) Genbank ACO48299
59	DNA	F gene of APMV-8 (FJ215863.1) Genbank FJ215863
60	Protein	F protein of APMV-8 (FJ215863.1) Genbank ACO48300
61	DNA	HN gene of APMV-8 (FJ215863.1) Genbank FJ215863
62	Protein	HN protein of APMV-8 (FJ215863.1) Genbank ACO48301
63	DNA	L gene of APMV-8 (FJ215863.1) Genbank FJ215863
64	Protein	L protein of APMV-8 (FJ215863.1) Genbank ACO48302
65	DNA	NP gene of APMV-8 (FJ215864.1) Genbank FJ215864
66	Protein	NP protein of APMV-8 (FJ215864.1) Genbank ACO48303
67	DNA	P gene of APMV-8 (FJ215864.1) Genbank FJ215864
68	Protein	P protein of APMV-8 (FJ215864.1) Genbank ACO48304
69	DNA	M gene of APMV-8 (FJ215864.1) Genbank FJ215864
70	Protein	M protein of APMV-8 (FJ215864.1) Genbank ACO48305
71	DNA	F gene of APMV-8 (FJ215864.1) Genbank FJ215864
72	Protein	F protein of APMV-8 (FJ215864.1) Genbank ACO48306
73	DNA	HN gene of APMV-8 (FJ215864.1) Genbank FJ215864
74	Protein	HN protein of APMV-8 (FJ215864.1) Genbank ACO48307
75	DNA	L gene of APMV-8 (FJ215864.1) Genbank FJ215864
76	Protein	L protein of APMV-8 (FJ215864.1) Genbank ACO48308
77	DNA	NP gene of APMV-8 (FJ619036) Genbank FJ619036
78	Protein	NP protein of APMV-8 (FJ619036) Genbank ACN88139
79	DNA	P gene of APMV-8 (FJ619036) Genbank FJ619036
80	Protein	P protein of APMV-8 (FJ619036) Genbank ACN88140
81	DNA	M gene of APMV-8 (FJ619036) Genbank FJ619036
82	Protein	M protein of APMV-8 (FJ619036) Genbank ACN88143
83	DNA	F gene of APMV-8 (FJ619036) Genbank FJ619036
84	Protein	F protein of APMV-8 (FJ619036) Genbank ACN88144

Figure 11 (3/3)

85	DNA	HN gene of APMV-8 (FJ619036) Genbank FJ619036
86	Protein	HN protein of APMV-8 (FJ619036) Genbank ACN88145
87	DNA	L gene of APMV-8 (FJ619036) Genbank FJ619036
88	Protein	L protein of APMV-8 (FJ619036) Genbank ACN88146

Figure 12 (1/5)

SEQ ID NO:1 full length genome sequence of APMV-8

15342 BP DNA (antigenome, 5' to 3')

BASE COUNT 4850 A 3168 C 3159 G 4165 T

ORIGIN

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181 AACTTGTGAA GCCGGCTGTC AGGAGACCTG ATGTTGCCTC AACGGGTTTA CTCAGAGCGG
241 AAATACCTGT CTGTGTTACA TTATCTCAAG ACCCCGGTGA GAGATGGAGC CTTGCTTGCT
301 TGAATATTAG ATGGCTTGCG AGTGATTCAT CAACCACACC AATGAAGCAA GGAGCAATAT
361 TGTCACTGCT GAGTCTACAT TCAGACAATA TCGGAGCTCA CGCAACATTA GCAGCAAGGT
421 CTGCAGATGC TTCCTCACC ATACTTGAGG TAGATGAAGT AGATATTAGC AACTCACTAA
481 TCAAATTCAA CGCCAGAAGT GGTGTATCTG ACAAACGCTC AAATCAATTG CTTGCAATTG
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601 CCAGAGACCC GCTCGATCTA TCAGAGACTA TAGATCGCCT GCAGGGTATT GCAGCTCAGA
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721 AGAGGCTGGC CAAATATCAA CAACAAGGCC GACTGGTTAA GCAAGTACTC TTGCATTCTG
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Figure 12 (2/5)

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3481 CCACAATAGC CCCCTTCAT TGAGAACTGC AATAACTATC CGAGCAGGAG GTTTCATCTC
3541 GAATGCAGAC GAGAATATAA AATGTGCCAG CAAATTGACT GCAGGAGTGC AGTACATATT
3601 CCGCCCAATG TTTGTTTCAA TCACTAAATT ACACAATGGC AAATATATA GGGTGCCCAA
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4681 GGATAATATG ACTACCTGTC TTAAAGAAAC AATCACTACA TACAATAATA CTGTCAACAA
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5461 TGTGCGATCT TGTAAATTCA GCAGCAGCAC CCTATATTGC AGGCAGGTCA ACACAAGGGC
5521 ACTTCCCCCG CTAGTAGCTA GCTGTCTTCG AGGTAACATAT GATGATTGTC AATATACCAC
5581 AGAGATTGGA GCATTATCAT CCCGGTATAT AACACTAGAT GGGGGGGTCT TAGTTAATTG
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5761 CCAGCTGGAA GGGTCACTAT CATCAGTTTA TGCAAGAAAC ATCTCAATTG AGATCAGTCA
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5881 GAATCGTGTG GAGGATTTAA TTCACCAATC AGAGGAATGG CTGGCAAAGG TTAACCCACA
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6121 TAAGTTTGA TCATTCAAGC CAAAACAGAG GATCTAGGCT CAGGTTAATA ATAGTTCAAT
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6361 ATCTACCTTG TCTAAAGACA TCATGAGTAA CATTGCATCC AGTTTAGAAA ACATTGTAGA
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Figure 12 (3/5)

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6661 ATTGCAAGTG ACCAGTATCC AAAAAGACCT TGCAAGTCAA TTTAACATGT TGATAGATAG
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6781 GTATGCAGGA GGAATTGGAA ACCCTGTATT TACTGTCGAT GCTGGAGGTT CTATAGGATT
6841 CAAACAGTTT AGCTTAATAG AACATCCGAG CTTTATTGCT GGACCTACAA CGACCCGAGG
6901 CTGTACAAGA ATACCCACTT TTCACATGTC AGAAAGTCAT TGGTGCTACT CACACAACAT
6961 CATCGCTGCT GGCTGTCAAG ATGCCAGTGC ATCCAGTATG TATATCTCAA TGGGAGTTCT
7021 CCATGTGTCC TCATCTGGCA CTCCCATTFT TCTTACTACT GCAAGTGAGC TGATAGACGA
7081 TGGAGTTAAG CGTAAGTCAT GCAGCATTGT AGCAACCCAA TTTGGCTGTG ACATTTTGTG
7141 CAGTATTGTC ACAGAGAAGG AGGGAGATGA TTACTGGTCT GATACTCCGA CTCCAATGCG
7201 CCACGGCCGT TTTTCATTCA ATGGTAGTTT TGTAAGGCC GAACTACCAG TGTCAGTAT
7261 GTTCTCATCA TTCTCTGCCA ACTACCCTGC TGTGGGATCA GGCGAAATFG TAAAGATAG
7321 AATATTATTC CCAATTACG GAGGTATAAA GCAGACTTCA CCAGAGTTTA CCGAATTAGT
7381 GAAATACGGA CTCTTTGTAT CAACACCTAC AACTGTGTGC CAGAGTAGCT GGACTTATGA
7441 CCAGGTAAAA GCTGCGTATA GGCCAGATTA CATATCAGGC CGGTTCTGGG CACAAGTGAT
7501 ACTCAGCTGC GCTCTTGATG CAGTCGACTT ATCAAGTTGT ATTGTAAGA TTATGAATAG
7561 CAGCACAGTG ATGATGGCAG CGGAAGGAAG GATAATGAAG ATAGGGATTG ATTACTTTTA
7621 CTATCAGCGG TCATCTTCTT GGTGGCCATT GGCATTTGTC ACAAACTAG ACCCGCAAGA
7681 GTTGGCAGAC ACAAACTCAA TATGGCTGAC CAATTCCATA CCAATCCCGC AATCAAAGTT
7741 CCCTCGGCCCT TCATATTGAG AAAATTATTG CACAAAGCCA GCAGTTTGCC CTGCTACTTG
7801 TGTCACTGGT GTGTACTCTG ATATTTGGCC CCTGACCTCA TCTTCATCAC TCCCGAGCAT
7861 AATTTGGATC GGCCAGTACC TTGATGCTCC TGTTGGAAGG ACTTATCCTA GATTTGGAAT
7921 TGCAAAATCAG TCACACTGGT ACCTCCAAGA AGATATTCTA CCCACTTCCA CCGCAAGTGC
7981 GTATTCAACC ACTACATGTT TTAAGAATAC TGCCAGGAAT AGAGTGTTCT GCGTCACCAT
8041 TGCCGAATTT GCAGATGGGT TGTTGGAGA GTACAGGATA ACACCTCAGT TGTACGAATT
8101 AGTGAGAAAT AATTGAATAA CAATAATTTT GGGACTCATT TTGTCGCAA GTGAAATTGT
8161 CATCTTTAAA AATAATCAAT TCGATGATT TTATTGAACA TGATTAAGCA ATCATGTGGG
8221 AAATTTATTA TCTCATAAAT TCTAATAGTT GTAAATGATG AATTAAGAAA AAATGGAGGG
8281 CGACCTCTAC ACAACATGG ATATAAAACA AGTTGACCTG ATAATACAAC CCGAGGTTCA
8341 TCTCGATTCA CCCATCATAT TGAATAAACT GGCATATTA TGGCGCTTGA GTGGTTTACC
8401 CATGCCTGCA GACCTACGAG AAAAATCCGT AGTGATGCAC ATCCCGGACC ACATCTTAGA
8461 AAAATCAGAA TATCGGATCA AGCACCCTCT AGGGAAAATC AAGAGTGACA TAACACATTA
8521 CTGTCAGTAT TTTAATATTA ATTTGGCAA TATTGATCCG ATAACCCACC CCAAAGTTT
8581 GTATTGGTTA TCCAGACTAA CAATAGCTAG TGCTGGAAT TTAGGCATA TGAAAGATAG
8641 AATCTTGTGT ACAGTTGGCT CTGAATTTGG ACACAAAATT CAAGATTAT TTTCACTGCT
8701 GAGCCATAAA CTAGTAGGTA ACGGGGATTT ATTTAATCAA AGTCTCTCAG GTACACGTTT
8761 GACTGCAAGT CCGTTATCCC CTTTATGCAA TCAATTTGTC TCTGACATCA AGTCTGCAGT
8821 CAGCACACC TGCTCAGAAG CTGCTGGTCT TGGCTTCAT ATCAAACAAA CAATGAGATA
8881 TCTGATAAAA CAATCAGCA CTACAAATTC GGCTCATTTA ACAGAAATCA TAAAGAAGA
8941 ATGGGGTTTA GTAGGTATTA CTCCAGATCT TGTCATTCTT TTTGACAGAG TCAATAATAG
9001 TCTGACTGCA TTAACATTG AGATGGTTCT AATGTATTCA GATGTATTAG AATCCCGTGA
9061 CAATATTGTG TTAGTGGGCG GACTATCTAC CTTTCTACAG CCAGTAGTTA GTAGACTGGA
9121 GGTGTGTTT GATCTAGTAG ATTCATTGGC AAAAATCTTA GGTGACACAA TATATGAGAT
9181 TATTGCAGTG TTAGAGAGCT TGTCTTATGG GTCAGTTCAA CTACATGATG CAAGTCACTC
9241 TCATGCAGGG TCTTTTTTTT CATTTAACAT GAATGAACCT GATAACACAC TATCAAAGAG
9301 GGATAGATCCG AAACACAAGA AACTATAAT GAGCATTTATA AGACAATGCT TTTCTAATCT
9361 AGATGTTGAT CAAGCTGCAG AGATGCTATG CCTGATGAGA TTATTCGGAC ACCCAATGTT
9421 AACTGCACCG GATGCAGCAG CCAAAGTGAG GAAAGCAATG TGTGCTCCAA AACTGTTGA
9481 ACACGACACC ATCTTGAGA CATTATCTTT CTTCAAGGGG ATAATTATA ATGGGTACAG
9541 AAGATCACAC TCTGGCCTGT GGCCAATGT AGAGCCGTCT TCAATTTATG ATGATGATCT
9601 CAGACAGCTG TACTTAGAGT CAGCAGAGAT TTCCCATCAT TTTATGCTTA AAACTACAA
9661 GAGTTAAGC ATGATAGAAT TCAAGAAGAG CATAGACTAC GATCTTCATG ATGACCTAAG
9721 TACTTTCTTA AAGGATAGAG CAATTTGCCG CCCGAAATCC CAGTGGGATG TCATATTTCC
9781 TAAGTCTTTA CGCAGATCTC ATACGCAATC CCAGTATCTG GACGAAATTA AGAGCAACCG
9841 ATTGCTAATT GATTTTCTTG ATTCTGCTGA ATTTGACCTT GGAAAAGAAT TTGCATATGT
9901 AACCACAATG GATTATTTGC ACGATAATGA ATTTTGTGCT TCATATTCTC TAAAGGAAAA
9961 GGAGATCAAA ACTACTGGGA GGATATTTGC AAAAATGACA CGCAATATGA GAAGTTGCCA

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Figure 12 (4/5)

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10021 AGTAATACTT GAATCTTTGT TATCAAAGCA TATATGCAAG TTCTTCAAAG AGAATGGCGT
10081 TTCGATGGAG CAATTGTCTAT TGACCAAGAG TCTACTTGCA ATGTCTCAAC TCTCACCAAA
10141 AGTCTCGACT TTGCAGGACA CTGCATCAGC TCATGTAGGT AACTCAAAAT CTCAGATTGC
10201 AACCAGCAAC CCATCTCGGC ATCACTCGAC ACCCAATCAG ATGTCACTCT CAAATCGAAA
10261 AACGGTTGTA GCAACTTTCT TAACAACTGA CTTGGAAAAA TACTGCCTGC AGTGGCGATA
10321 TTCAACTATT AAATTGTTTG CACAAGCTCT AAATCAACTC TTTGGGATG ATCACGGATT
10381 TGAATGGATA CATTTAAGAC TTATGAACAG CACCTTATTT GTTGGCGATC CTTACTCGCC
10441 TCCTGAAGAT CCAACACTAG AAGATATAGA TAAAGCACCA AATGATGATA TCCTCATAGT
10501 TTCTCCAAGG GGAGGCATAG AGGGTTTATG TCAGAAAATG TGGACCATGA TATCAATTAG
10561 TGCTATACAC TGTGTAGCAG AGAAAATTGG TGCACGAGTG GCAGCAATGG TGCAGGGTGA
10621 TAATCAAGTA ATAGCTATCA CCAAAGAATT ATTCAGAGGA GAGAAAGCTT GTGATGTCAG
10681 AGATGAGTTA GACGAGCTTG GTCAAGTGTT TTTTGATGAG TTCAAGAGAC ACAATTATGC
10741 AATTGGACAC AATCTTAAGC TAAATGAGAC AATACAAAGC CAATCCTTTT TTGTATATTC
10801 CAAACGAATA TTCTTTGAAG GCGGATTGCT TAGTCAAGTC CTCAAAAATG CTGCCAAGTT
10861 ATGTATGGTT GCTGACCATC TAGGTGAAAA CACTGTATCT TCCTGTAGCA ACCTGAGCTC
10921 GACAATTGCC CGCTTAGTGG AAAATGGGTT TGAGAAGGAC ACTGCTTTTG TGTGAACCTT
10981 AGTCTACATC ATGACTCAGA TTCTTTTGA TGAGCATTAT TCGATTGTAT GCGATCACCA
11041 TAGTGTCAAA AGCTTGATTG GATCAAAAAA CCATCGGAAT TTATTGTATT CATCTCTAAT
11101 ACCAGGTCAG CTCGGCGGTT TCAACTTCCT CAATATAAGT CGGTTGTTCA CTAGGAATAT
11161 AGGTGACCCA GTAACATGTA GTCTGTCTGA TCTCAAATGC TTCATAGCCG CAGGTCTCCT
11221 TCCACCTAT GTCTTAAAA ATGTGGTTCT GCGTGAGCCT GGTCTGCGGA CATGGTTGAC
11281 GTTGTGCTCT GATCCTTACA CCCTTAACAT ACCATACACA CAGCTTCCAA CCACATATCT
11341 CAAAAGCAC ACCCAGCGAT CATTGCTTTC ACGTGCAGTA AATCCTTTAT TAGCCGGTGT
11401 ACAAGTGCCA AATCAGCATG AGGAAGAAGA GATGTTGGCT CGCTTTCTCC TTGATCGTGA
11461 ATATGTGATG CCCCGCGTTG CTCATGTAAT ACTAGAATCA TCAGTCCTTG GCAAACGGAA
11521 ACAAATCCAA GGCTTAATTG ATACAACTCC AACCATCATT AGAACATCTC TAGTTAATCT
11581 GCCAGTGCT AGAAAGAAAT GCGAAAAAAT AATCAATTAC TCTCTCAATT ATATTGCTGA
11641 GTGTCATGAC TCCTTACTTA GCCAGGTCTG CTTCACTGAT AATAAGGAAT ACTTGTGGTC
11701 AACCTCCTTA ATATCAGTTG AGACCTGTAG TGTGACAATT GCGGACTATC TGAGAGCTGT
11761 CAGCTGGTCT AATATATTAG GGGGAAGAAA CATATCCGGG GTGACTACAC CTGATACTAT
11821 TGAATTAATT CAAGGTTGTT TAATAGGTGA AAATCTAGT TGTACTCTTT GTGAATCGCA
11881 TGATGACGCA TTCACGTGGA TGCCTTGCC TGGCCACTT TACATCCCTG AACCACGGAT
11941 TACTAATCT AAAATGCGTG TGCCATATCT GGGTTCAAAA ACAGAGGAGC GGAAAAACAGC
12001 CTCAATGGCA GCAATAAAG GAATGTCACA TCACCTGCGT GCAGTCTTAA GAGGCACATC
12061 CGTATTTATT TGGGCATTG GGGATACAGA TATCAATTGG GATAATGCAT TGCAGATTGC
12121 CCAATCACGG TGTAACATCA CATTGGATCA AATGAGATTA CTTACACCAA TTCTTAGCAG
12181 TTCAATATT CAACATAGAC TCGATGACGG AATCAGCACG CAGAAATTTA CTCCTGCAAG
12241 CCTTGCTCGA ATCACATCCT TCGTTCACAT CTGTAATGAC AGCCAGAGGT TAGAGAAGGA
12301 TGGCTCATCT GTCGACTCAA ACTTGATTTA CCAGCAAATT ATGTTACTTG GACTCAGCAT
12361 CTTTGAAACA ATGTACTCAA TGGACCAAAA GTGGGTATT CATAACCATA CCTTGCATTT
12421 GCACACTGGA CACTCCTGTT GTCCAAGGGA ACTAGACATA AGTTTGGTGA ACCCGCCGAG
12481 ACATCAGACC CCGGAGCTGA CTAGCACAAC AACCACCCG TTCCTATATG ATCAGCTCCC
12541 ATTAAATCAA GAAAACCTGA CAACACTTGA GATTAAGACA TTAAATTTCA ATGAGCTCAA
12601 CATTGATGGT TTAGATTTTG GTGAAGGAAT ACAATTATTG AGTCGTTGTA CTGCAAGATT
12661 AATGGCAGAA TGTATTCTAG AGGAGGGAAT AGGCTCGTCA GTTAAAAATG AAGCAATTGT
12721 CAATTTTGAT AATTCACTCA ATTGGATTTT AGAGTGCCTA ATGTGTGATA TTCGCTCACT
12781 TTGTGTTAAT TTAGGTCAAG AGATACTATG TAGCCTGGCA TACCAATGT ATTACTTGCG
12841 AATCAGGGGT AGACGGGGCA TTCTTAATTA CTTGGACACA ACTTTGCAA GGATCCCTGT
12901 GATACAATTA GCCAACATTG CACTCACCAT TTCGCACCTT GAGATATTTT GCAGAATTGT
12961 CAACACCGGG ATCCATAACC AGATTAAGGG CCCATATGTG GCAACAACGG ATTTTCATAGC
13021 TGCAAGTAGA GATATCATAT TATCAGGTGC AAGGGAGTAT CTATCTTATT TAAGCAGTGG
13081 GCAGGAAGAC TGTACACAT TCTTCAACTG TCAAGATGGG GATCTTACTC CAAAAATGGA
13141 ACAGTATCTT GCAAGGAGGG CATGCCTTTT AACATTATTG TATAACTCTG GGCACCAGAT
13201 CCCCCTTATC CGATCACTGA CGCCAATAGA GAAGTGCAAG GTGCTCACAG AATACAATCA
13261 ACAAATFGAG TACGCAGATC AAGAGTTTAG CTCTGTACTA AAAGTGGTCA ATGCACTACT
13321 ACAAATCCTT AAGATAGATG CATTAGTTTC AAATCTCTAC TTCACCACCA GACGTGTTCT
13381 ATCAAACCTC AGATCATGTG ATAAGGCTAG ATCATATATT GAATATTTGT AACTGAGGA
13441 CTTGCGAGAG AAAGAGGATA CAGTACAATA TGACATCATG ACAACAAACG ATATCATACT

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Figure 12 (5/5)

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13501 TACTCATGGT CTATTCACAC AGATCGAAAT ATCTTATCAA GGAATAGTC TCCATAAGTT
13561 CCTTACTCCG GATAACGCGC CTGGATCTTT GATCCCATTC TCTATTTTAC CAAATTCAC
13621 TGCATGTGAC CCTCTTCATC ACTTGCTCAA GTCGGTCGGT ACATCAAGCA CAAAGTTGGTA
13681 CAAGTATGCA ATCGCCTATG CAGTGTCTGA AAAGAGGTCA GCTCGATTAG GAGGGAGCTT
13741 GTACATTGGT GAAGGGAGCG GAAGTGTGAT GACTTTACTC GAGTATCTTG AGCCATCTGT
13801 TGACATATTT TACAATTCAC TCTTCTCAA TGGTATGAAC CCACCACAAC GAAATTATGG
13861 GCTTATGCCA CTACAATTG TGAATTCGGT GGTTTATAAG AACTTAACGG CTAATCAGA
13921 ATGTAAGCTA GGGTTTGTC AGCAATTTAA ACCGTTGTGG AGAGACATAG ACATTGAGAC
13981 TAATGTTACA GATCCATCAT TTATCAATTT TGCATTGAAT GAAATCCCAA TGCAATCATT
14041 AAAACGAGTA AATTGTGATG TGGAAATTTGA CCGTGGTATG CCGATTGAAC GGGTTATTCA
14101 GGGTTACACC CATATCTTAC TTGTTGCCAC TTACGGATTA CAGCAAGATT CAATACTGTG
14161 GGTGAAGGTA TATAGGACAT CTGAAAAAGT ATTTCAATTC TTAAGTGTG CCATGATCAT
14221 GATCTTTGGT TATGTAAAAA TCCACAGGAA TGGTTATATG TCGACAAAGG ATGAAGAGTA
14281 CATATTGATG TCTGACTGCA AGGAACCTGT AAACATATCA GCTGTCCCTA ACATTCTTAC
14341 ACGTGTAAAGT GATTTAGTGT CGAAGAATCT GAGTCTTATC CATCCAGAAG ACCTCAGAAA
14401 AGTAAGGTGT GAAACAGATT CCCTGAATTT GAAGTGCAAT CATATTTATG AGAAAAATAT
14461 TGCCAGAAAA ATTCCATTAC AGGTATCATC AACTGACTCT TTGCTCCTCC AATTAGGCGG
14521 TGTATCAAC TCGGTGGGCT CAACTGATCC TAGAGAGGTT GCAACATTAT CTTCTATTGA
14581 GTGTATGGAC TATGTTGTCT CATCAATTGA TTTGGCTATA TTGGAGGCAA ATATTGTAAT
14641 CTCAGAGAGT GCTGGTCTTG ACCTCGCTTT AATGTTAGGC CCATTCAACT TAAATAAGCT
14701 TAAGAAAATT GACACAATCC TTAAGTCAAG CACCTATCAG CTAATCCCGT ACTGGTTGCG
14761 CTATGAGTAC TCTATTAATC CGAGATCTTT GTCATTTCTA ATCACTAAAT TACAACAATG
14821 CCGAATTTCA TGGTCAGATA TGATCACGAT TTCTGAATTT CGTAAGAAAT CCAAGCGGCC
14881 TATATTTATC AAACGAGTAA TAGGGAATCA ACAGCTAAAA TCATTCTTTA ATGAAAGCTC
14941 AAGTATTGTT TTGACTCGGG CTGAAGTTAA AGTCTGTATA AAGTTCCTCG GTGCAATCAT
15001 CAAGTTGAAA TAATTTCTGC GATTTTAAAG GGGTGTAAATG TTCTAATTG CACTTGAAGT
15061 AATATAGCTT GTAATCATTC GCTAGGGGAT AGGATAATTT CTCTAACCTC TGAATCTATA
15121 TTCCTAGAGT ATAACAAATA TATACATAAT AAAAATGATT TTAAGAAAAA ATCCGACACT
15181 CAAAGAAAAT TGGTGCCTGT AATATTCTTC TTGCCAAATG ATTGTGAAGT GTCTAGCCTA
15241 ACTTAAAACA ATCGTATTCG ATAGGGAAGA ATGATATATA AAATAACTAA TAAAAAATTG
15301 TATTAGTAAA AATTACCGTA TTCTCTGTAT TCCATTTCTG GT

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Figure 12

SEQ ID NO:2 DNA sequence encoding APMV-8 Nucleoprotein (NP)

1	ATG TCA TCT GTG TTC AAT GAG TAT CAG GCG CTT CAA GAA CAA CTT GTG	48
49	AAG CCG GCT GTC AGG AGA CCT GAT GTT GCC TCA ACG GGT TTA CTC AGA	96
97	GCG GAA ATA CCT GTC TGT GTT ACA TTA TCT CAA GAC CCC GGT GAG AGA	144
145	TGG AGC CTT GCT TGC TTG AAT ATT AGA TGG CTT GCG AGT GAT TCA TCA	192
193	ACC ACA CCA ATG AAG CAA GGA GCA ATA TTG TCA CTG CTG AGT CTA CAT	240
241	TCA GAC AAT ATG CGA GCT CAC GCA ACA TTA GCA GCA AGG TCT GCA GAT	288
289	GCT TCA CTC ACC ATA CTT GAG GTA GAT GAA GTA GAT ATT AGC AAC TCA	336
337	CTA ATC AAA TTC AAC GCC AGA AGT GGT GTA TCT GAC AAA CGC TCA AAT	384
385	CAA TTG CTT GCA ATT GCG GAT GAC ATC CCC AAA AGT TGC AGT AAT GGG	432
433	CAT CCA TTT CTT GAC ACA GAC ATT GAG ACC AGA GAC CCG CTC GAT CTA	480
481	TCA GAG ACT ATA GAT CGC CTG CAG GGT ATT GCA GCT CAG ATA TGG GTG	528
529	TCA GCC ATA AAG AGC ATG ACA GCG CCT GAC ACC GCA TCA GAG TCA GAA	576
577	AGT AAG AGG CTG GCC AAA TAT CAA CAA CAA GGC CGA CTG GTT AAG CAA	624
625	GTA CTC TTG CAT TCT GTA GTC AGG ACA GAA TTT ATG AGA GTT ATT CGG	672
673	GGC AGC TTG GTA CTG CGC CAG TTT ATG GTT AGC GAG TGC AAG AGG GCT	720
721	TCA GCC ATG GGC GGA GAC ACA TCT AGG TAC TAT GCT ATG GTG GGT GAC	768
769	ATC AGT CTT TAC ATC AAG AAT GCA GGA TTG ACT GCA TTT TTC CTC ACC	816
817	CTG AAG TTC GGA GTT GGT ACC CAG TAT CCA ACC TTA GCA ATG AGT GTT	864
865	TTC TCC AGT GAC CTT AAA AGG CTT GCT GCA CTC ATC AGG CTA TAC AAA	912
913	ACC AAG GGA GAC AAT GCA CCA TAC ATG GCA TTC CTG GAG GAC TCC GAT	960
961	ATG GGA AAT TTT GCT CCA GCA AAT TAT AGC ACA ATG TAC TCT TAT GCC	1008
1009	ATG GGC ATT GGG ACA ATT CTG GAA GCA TCT GTA TCT CGA TAC CAG TAT	1056
1057	GCC AGA GAC TTT ACC AGT GAG AAT TAT TTC CGT CTT GGA GTT GAG ACA	1104
1105	GCC CAA AGC CAG CAG GGA GCA TTT GAC GAG AGA ACA GCC CGA GAA ATG	1152
1153	GGC TTG ACT GAG GAA TCA AAA CAG CAG GTT AGA TCA CTG CTA ATG TCA	1200
1201	GTA GAC ATG GGT CCC AGT TCA ATT CAT GAG CCA TCT CGC CCT GCA TTT	1248
1249	ATC AGT CAA GAA GAA AAT AGG CAG CCT GCC CAG AAC TTG TCA GAT ACT	1296
1297	CAG GGT CAG ACC AAG CCA GTC CCG AAG CAG CCC GCA CCA AGG GCC GAC	1344
1345	TCA GAT GAC ATT GAT CCA TAC GAG AAC GGG CTA GAA TGG TAA	1386

SEQ ID NO:3 Protein sequence of APMV-8 Nucleoprotein (NP)

1	MSSVFNEYQALQEQLVKPAVRRPDVASTGLLRAEIPVCVTLSDPGER	48
49	WSLACLNIRWLASDSTTPMKQGAILSLLSLHSDNMRAHATLAARSAD	96
97	ASLTILEVDEVDISNSLIKFNARSGVSDKRSNQLLAIADDIPKSCSNG	144
145	HPFLDTDIETRDPLDLSETIDRLQGIAAQIIVWSAIKSMTAPDTASESE	192
193	SKRLAKYQQQGRVLVKQVLLHSVVRTEFMRVIRGSLVLRQFMVSECKRA	240
241	SAMGGDTSRYYAMVGDISLYIKNAGLTAFFLTLKFGVGTQYPTLAMSV	288
289	FSSDLKRLAALIRLYKTKGDNAPYMAFLESDMGNFAPANYSTMYSYA	336
337	MGIGTILEASVSRYQYARDFTSENYFRLGVETAQSQQGAFDERTAREM	384
385	GLTEESKQQVRSLLMSVDMGPSSIHEPSRPAFISQEENRQPAQNLSDT	432
433	QGQTKPVPKQPAPRADSDDDIDPYENGLEW*	462

Figure 13

SEQ ID NO:4 DNA sequence encoding APMV-8 Phosphoprotein (P)

1	ATG GAT TTC GCC AAT GAT GAA GAA ATT GCA GAA CTT TTG AAT CTC AGC	48
49	ACC AAT GTA ATC AAG GAG ATT CAG AAA TCC GAA CTC AAG CCT CCC CAA	96
97	ACC ACC GGA CGA CCA CCT GTC AGT CAA GGG AAC ACA AGA AAT CTA ACT	144
145	GAT CTA TGG GAA AAG GAG ACT GCA AGT CAG ACC AAG ACA CCG GCC CAA	192
193	TCT ACA CAA ACC ACA CAA GTT CAG TCT GAT GAA AAT GAG GAG GGA GAA	240
241	ATC AAG TCC GAG TCA ACT GAT GGC CAC ATC AGA GGA ACT GTT AAT CAA	288
289	TCA GAG CAA GTC CCA GAA CAA AAC CAG AGC AGA TCT TCA CCA GGT GAT	336
337	GAT CTC GAC AGA GCT CTC AAC AAG CTT GAA GGG AGA ATC AAT TTA ATC	384
385	AGC TCA ATG GAC AAA GAA ATT AAA AAG GGC CCT CGC ATC CAG AAT CTC	432
433	CCT GGG TCC CAG GCG GCA ACT CAA CAG GCG ACC CAC CCA TTG GCA GGG	480
481	GAC ACC CCG AAC ATG CAA GCA CAG ACA AAA GCC CTG GCG AAG CCA CAT	528
529	CAA GAG GCA ATC AAT CCT GGC AAC CAG GAC ACA GGA GAG AGT ATT CAT	576
577	TTA CCA CCT TCC ATG GCA CCA CCA GAG TCA TTA GTT GGT GCA ATC CGC	624
625	AAT GCA CCC CAA TTC GTG CCA GAC CAA TCT ATG ACG AAT GTA GAT GCG	672
673	GGG AGT GTC CAA CTA CAT GCA TCA TGT GCA GAG ATG ATA AGT AGA ATG	720
721	TTT GTA GAA GTT ATA TCC AAG CTT GAT AAA CTC GAG TCG AGA CTG AAT	768
769	GAT ATA GCA AAA GTT GTG AAC ACT ACC CCC CTT ATT AGG AAT GAT ATT	816
817	AAC CAA CTT AAG GCC ACA ACC GCA CTG ATG TCT AAC CAA ATT GCC TCC	864
865	ATA CAA ATT CTT GAC CCA GGG AAT GCA GGG GTG AGG TCC CTC TCT GAA	912
913	ATG AAA TCT GTG ACG AAG AAA GCT GCT GTT GTA ATT GCA GGG TTT GGA	960
961	GAC GAC CCA ACT CAA ATT ATT GAA GAA GGC ATT ATG GCC AAA GAT GCT	1008
1009	CTT GGA AAA CCT GTG CCT CCA ACA TCT GTT ATC TCA GCC AAA GCT CAG	1056
1057	ACT TCT TCC GGT GTG AGT AAG GGT GAA ATA GAA GGA TTG ATT GCA TTG	1104
1105	GTG GAA ACA TTA GTT GAC AAT GAC AAG AAG GCA GCA AAA CTG ATT AAA	1152
1153	ATG ATT GAT CAA GTT AAA TCC CAT GCC GAT TAC GCC CGA GTC AAG CAG	1200
1201	GCA ATA TAT AAT GCG TAA	1218

SEQ ID NO:5 Protein sequence of APMV-8 PhosphoProtein (P)

1	MDFANDEEIAELLNLSTNVIKEIQKSELKPPQTTGRPPVSQGNTRNLT	48
49	DLWEKETASQTKTPAQSTQTTQVQSDENEEGEIKSESTDGHIRGTVNQ	96
97	SEQVPEQNQSRSSPGDDLDRALNKLEGRINLISSMDKEIKKGPRIQNL	144
145	PGSQAATQQATHPLAGDTPNMQAQTKALAKPHQEAINPGNQDTGESIH	192
193	LPPSMAPPESLVGAIRNAPQFVPDQSMTNVDAGSVQLHASCAEMISRM	240
241	FVEVISKLDKLESRLNDIAKVVNTTPLIRNDINQLKATTALMSNQIAS	288
289	IQILDPGNAGVRSLSMKSVTKKAAVVIAGFGDDPTQIIIEEGIMAKDA	336
337	LGKVPPTSVISAKAQTSSGVSKGEIEGLIALVETLVDNDKKAALIK	384
385	MIDQVKSHADYARVKQAIYNA*	406

Figure 14

SEQ ID NO:6 DNA sequence encoding APMV-8 Matrixprotein (M)

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1  ATG GCA TAT ACA ACA TTG AAA CTG TGG GTG GAT GAG GGT GAC ATG TCG      48
49 TCT TCG CTC CTA TCA TTC CCG TTG GTA CTA AAA GAG ACA GAC AGA GGC      96
97 ACA AAG GAG CTT CAA CCA CAG GTA AGG GTA GAT TCA ATT GGC GAT GTG     144
145 CAG AAC GCC AAA GAG TCC TCG ATA TTC GTG ACT CTA TAT GGT TTC ATC     192
193 CAA GCA ATT AAG GAG AGT TCA GAT CGA TCG AAA TTC TTC CAT CCA AAA     240
241 GAT GAC TTC AAA CCT GAG ACA GTC ACT GCA GGA CTG GTA GTG GTA GGT     288
289 GCG ATC CGA ATG ATG GCT GAT GTT AAT ACC ATC TCT AAT GAC GCA CTA     336
337 GCG CTG GAG ATC ACT GTT AAG AAA TCT GCA ACT TCT CAA GAG AAA ATG     384
385 ACG GTG ATG TTC CAC AAT AGC CCC CCT TCA TTG AGA ACT GCA ATA ACT     432
433 ATC CGA GCA GGA GGT TTC ATC TCG AAT GCA GAC GAG AAT ATA AAA TGT     480
481 GCC AGC AAA TTG ACT GCA GGA GTG CAG TAC ATA TTC CGC CCA ATG TTT     528
529 GTT TCA ATC ACT AAA TTA CAC AAT GGC AAA CTA TAT AGG GTG CCC AAA     576
577 AGC ATC CAC AGC ATC TCA TCC ACT CTA CTG TAT AGT GTG ATG TTG GAG     624
625 GTA GGA TTC AAA GTG GAT ATT GGG AAG GAT CAT CCC CAG GCA AAG ATG     672
673 CTG AAG AAG GTC ACA ATC GGC GAT GCA GAC ACA TAC TGG GGG TTT GCA     720
721 TGG TTC CAC CTG TGC AAT TTC AAA AAG ACA TCC TCT AAG GGA AAG CCA     768
769 AGA ACG CTA GAC GAA CTA AAG ACA AAA GTC AAA AAT ATG GGG TTG AAA     816
817 TTG GAG TTA CAT GAC CTG TGG GGT CCG ACT ATT GTG GTC CAA ATC ACT     864
865 GGC AAG AGC AGC AAA TAT GCT CAA GGA TTT TTT TCC TCC AAT GGT ACT     912
913 TGT TGT CTC CCA ATC AGC AGA TCT GCA CCA GAG CTT GGG AAG CTT CTG     960
961 TGG TCT TGT TCA GCA ACT ATA GGT GAC GCA ACA GTT GTT ATC CAA TCA    1008
1009 AGC GAG AAA GGG GAA CTC CTA AGG TCT GAT GAC CTC GAG ATA CGA GGT    1056
1057 GCT GTG GCC TCC AAG AAA GGT AGA CTG GGC TCA TTT CAC CCC TTC AAA    1104
1105 AAA TGA                                                                1110

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SEQ ID NO:7 Protein sequence of APMV-8 Matrixprotein (M)

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1  MAYTTLKLWVDEGDMSSSLLSFPLVLKETDRGTELQPQVRVDSIGDV      48
49 QNAKESSIFVTLYGFIQAIKESSDRSKFFHPKDDFKPETVTAGLVVVG      96
97 AIRMMADVNTISNDALALEITVKKSATSQEKMTVMFHNSPPSLRTAIT     144
145 IRAGGFISNADENIKCASKLTAGVQYIFRPMFVSITKLHNGKLYRVPK     192
193 SIHSISSTLLYSVMLEVGFKVDIGKDHPPQAKMLKKVTIGDADTYWGFA     240
241 WFHLCNFKKTSSKGKPRTLDELKTKVKNMGLKLELHDLWGPTIVVQIT     288
289 GKSSKYAQGFFSSNGTCCLPISRSAPELGKLLWSCSATIGDATVVIQS     336
337 SEKGELLRSDDLEIRGAVASKKGRLGSEFHPFKK*                      370

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Figure 15

SEQ ID NO:8 DNA sequence encoding APMV-8 Fusionprotein (F)

1	ATG GGT CAA ATA TCA GTA TAT CTA ATT AAT AGC GTG CTA TTA TTG CTG	48
49	GTA TAT CCT GTG AAT TCG ATT GAC AAT ACA CTC ATT GCC CCA ATC GGA	96
97	GTT GCC AGC GCA AAT GAA TGG CAG CTT GCT GCA TAT ACA ACA TCA CTT	144
145	TCA GGG ACA ATT GCC GTG CGA TTC CTA CCT GTG CTC CCG GAT AAT ATG	192
193	ACT ACC TGT CTT AAA GAA ACA ATC ACT ACA TAC AAT AAT ACT GTC AAC	240
241	AAC ATC TTA GGC CCA CTC AAA TCC AAT CTG GAT GCA CTG CTC TCA TCT	288
289	GAG ACT TAT CCC CAG ACA AGA TTA ATT GGG GCA GTT ATA GGT TCA ATT	336
337	GCT CTC GGT GTT GCA ACA TCG GCT CAA ATC ACT GCT GCA GTT GCT CTC	384
385	AAG CAA GCG CAA GAC AAT GCA AGG AAC ATA CTA GCA CTC AAA GAA GCA	432
433	CTG TCC AAA ACC AAT GAG GCG GTC AAG GAG CTT AGT AGT GGG TTA CAA	480
481	CAA ACA GCT ATT GCA CTT GGT AAG ATA CAG AGT TTT GTG AAT GAG GAA	528
529	ATT CTG CCA TCT ATC AAC CAA CTG AGC TGC GAG GTG ACA GCC AAT AAA	576
577	CTT GGG GTG TAT TTA TCT CTG TAT CTC ACA GAA CTG ACC ACC ATA TTC	624
625	GGT GCA CAG CTG ACC AAC CCT GCA TTG ACT TCA TTA TCA TAT CAA GCA	672
673	CTG TAC AAC CTG TGT GGT GGC AAC ATG GCA ATG CTT ACT CAG AAG ATT	720
721	GGA ATT AAA CAG CAA GAC GTT AAT TCG CTA TAT GAA GCC GGA CTA ATC	768
769	ACA GGA CAA GTC ATT GGT TAT GAC TCT CAT TAC CAG CTG CTG GTC ATC	816
817	CAG GTC AAT TAT CCA AGC ATT TCT GAG GTC ACT GGT GTA CGT GCG ACA	864
865	GAA TTA GTC ACT GTT AGT GTA ACA ACA GAC AAG GGT GAA GGG AAA GCA	912
913	ATT GTA CCC CAA TTT GTA GCT GAA AGT CGG GTG ACT ATT GAA GAG CTT	960
961	GAT GTC GCA TCT TGT AAA TTC AGC AGC ACG ACC CTA TAT TGC AGG CAG	1008
1009	GTC AAC ACA AGG GCA CTT CCC CCG CTA GTA GCT AGC TGT CTT CGA GGT	1056
1057	AAC TAT GAT GAT TGT CAA TAT ACC ACA GAG ATT GGA GCA TTA TCA TCC	1104
1105	CGG TAT ATA ACA CTA GAT GGG GGG GTC TTA GTT AAT TGC AAG TCA ATT	1152
1153	GTT TGT AGG TGC CTT AAT CCA AGT AAG ATC ATC TCT CAA AAT ACA AAC	1200
1201	GCT GCA GTA ACA TAT GTT GAT GCC ACA ATC TGC AAA ACA ATT CAA TTG	1248
1249	GAT GAT ATA CAA CTC CAG CTG GAA GGG TCA CTA TCA TCA GTT TAT GCA	1296
1297	AGA AAC ATC TCA ATT GAG ATC AGT CAG GTG ACC ACA TCC GGG TCT TTA	1344
1345	GAT ATC AGC AGT GAG ATA GGA AAC ATC AAT AAT ACG GTG AAT CGT GTG	1392
1393	GAG GAT TTA ATT CAC CAA TCA GAG GAA TGG CTG GCA AAG GTT AAC CCA	1440
1441	CAC ATT GTT AAT AAT ACA CTA ATT GTA CTC TGT GTG TTA AGT GCG	1488
1489	CTT GCT GTG ATC TGG CTG GCA GTA TTA ACG GCT ATT ATA ATA TAC TTG	1536
1537	AGA ACA AAG TTG AAG ACT ATA TCG GCA TTA GCT GTA ACC AAT ACA ATA	1584
1585	CAG TCT AAC CCC TAT GTT AAC CAA ACG AAA CAT GAA TCT AAG TTT TGA	1632

SEQ ID NO:9 Protein sequence of APMV-8 Fusionprotein (F)

1	MGQISVYLINSVLLLLVYPVNSIDNTLIAPIGVASANEWQLAAYTTSL	48
49	SGTIAVRFLPVLDPNMTTCLKETITTYNNTVNNILGPLKSNLDALLSS	96
97	ETYPQTRLIGAVIGSIALGVATSAQITAVALKQAQDNARNILALKEA	144
145	LSKTNEAVKELSSGLQQTALALGKIQSFVNEEILPSINQLSCEVTANK	192
193	LGVYLSLYLTELTTIFGAQLTNPALTSLSYQALYNLCGGNMAMLTQKI	240
241	GIKQQDVNSLYEAGLITGQVIGYDSHYQLLVIQVNYPISIEVTGVRAT	288
289	ELVTVSVTTDKGEGKAIVPQFVAESRVTIEELDVASCKFSSTTLYCRQ	336
337	VNTRALPPLVASCLRGNYDDCQYTTEIGALSSRYITLDGGVLVNCKSI	384
385	VCRCLNPSKIIISQNTNAAVTYVDATICKTIQLDDIQLQLEGLSSVYA	432
433	RNISIEISQVTTSGSLDISSEIGNINNTVNRVEDLIHQSEEWLAKVNP	480
481	HIVNNTTLIVLCVLSALAVIWLAVLTAIIIYLRTKLKTISALAVTNTI	528
529	QSNPYVNQTKHESKF*	544

Figure 16

SEQ ID NO:10 DNA sequence encoding APMV-8 Hemagglutinin/neuraminidase (HN)

1	ATG AGT AAC ATT GCA TCC AGT TTA GAA AAC ATT GTA GAG CAG GAT AGT	48
49	CGA AAA ACA ACT TGG AGG GCC ATC TTT AGA TGG TCC GTT CTT CTT ATT	96
97	ACA ACA GGA TGC TTA GCC TTA TCC ATT GTT AGC ATA GTT CAA ATT GGA	144
145	AAT TTG AAA ATT CCT TCT GTA GGG GAT CTG GCT GAT GAA GTG GTG ACA	192
193	CCC TTG AAA ACC ACT CTG TCA GAT ACA CTC AGG AAT CCA ATT AAC CAG	240
241	ATA AAT GAT ATA TTT AGG ATT GTT GCC CTT GAT ATT CCA TTG CAA GTG	288
289	ACC AGT ATC CAA AAA GAC CTT GCA AGT CAA TTT AAC ATG TTG ATA GAT	336
337	AGT TTA AAT GCT ATC AAA TTA GGC AAC GGG ACC AAC CTT ATC ATA CCT	384
385	ACA TCA GAC AAG GAG TAT GCA GGA GGA ATT GGA AAC CCT GTA TTT ACT	432
433	GTC GAT GCT GGA GGT TCT ATA GGA TTC AAA CAG TTT AGC TTA ATA GAA	480
481	CAT CCG AGC TTT ATT GCT GGA CCT ACA ACG ACC CGA GGC TGT ACA AGA	528
529	ATA CCC ACT TTT CAC ATG TCA GAA AGT CAT TGG TGC TAC TCA CAC AAC	576
577	ATC ATC GCT GCT GGC TGT CAA GAT GCC AGT GCA TCC AGT ATG TAT ATC	624
625	TCA ATG GGA GTT CTC CAT GTG TCC TCA TCT GGC ACT CCC ATT TTT CTT	672
673	ACT ACT GCA AGT GAG CTG ATA GAC GAT GGA GTT AAC CGT AAG TCA TGC	720
721	AGC ATT GTA GCA ACC CAA TTT GGC TGT GAC ATT TTG TGC AGT ATT GTC	768
769	ACA GAG AAG GAG GGA GAT GAT TAC TGG TCT GAT ACT CCG ACT CCA ATG	816
817	CGC CAC GGC CGT TTT TCA TTC AAT GGT AGT TTT GTA GAA GCC GAA CTA	864
865	CCA GTG TCC AGT ATG TTC TCA TCA TTC TCT GCC AAC TAC CCT GCT GTG	912
913	GGA TCA GGC GAA ATT GTA AAA GAT AGA ATA TTA TTC CCA ATT TAC GGA	960
961	GGT ATA AAG CAG ACT TCA CCA GAG TTT ACC GAA TTA GTG AAA TAC GGA	1008
1009	CTC TTT GTA TCA ACA CCT ACA ACT GTG TGC CAG AGT AGC TGG ACT TAT	1056
1057	GAC CAG GTA AAA GCT GCG TAT AGG CCA GAT TAC ATA TCA GGC CGG TTC	1104
1105	TGG GCA CAA GTG ATA CTC AGC TGC GCT CTT GAT GCA GTC GAC TTA TCA	1152
1153	AGT TGT ATT GTA AAG ATT ATG AAT AGC AGC ACA GTG ATG ATG GCA GCG	1200
1201	GAA GGA AGG ATA ATG AAG ATA GGG ATT GAT TAC TTT TAC TAT CAG CGG	1248
1249	TCA TCT TCT TGG TGG CCA TTG GCA TTT GTC ACA AAA CTA GAC CCG CAA	1296
1297	GAG TTG GCA GAC ACA AAC TCA ATA TGG CTG ACC AAT TCC ATA CCA ATC	1344
1345	CCG CAA TCA AAG TTC CCT CGG CCT TCA TAT TCA GAA AAT TAT TGC ACA	1392
1393	AAG CCA GCA GGT TGC CCT GCT ACT TGT GTC ACT GGT GTG TAC TCT GAT	1440
1441	ATT TGG CCC CTG ACC TCA TCT TCA TCA CTC CCG AGC ATA ATT TGG ATC	1488
1489	GGC CAG TAC CTT GAT GCT CCT GTT GGA AGG ACT TAT CCT AGA TTT GGA	1536
1537	ATT GCA AAT CAG TCA CAC TGG TAC CTC CAA GAA GAT ATT CTA CCC ACT	1584
1585	TCC ACC GCA AGT GCG TAT TCA ACC ACT ACA TGT TTT AAG AAT ACT GCC	1632
1633	AGG AAT AGA GTG TTC TGC GTC ACC ATT GCC GAA TTT GCA GAT GGG TTG	1680
1681	TTT GGA GAG TAC AGG ATA ACA CCT CAG TTG TAC GAA TTA GTG AGA AAT	1728
1729	AAT TGA	1734

SEQ ID NO:11 Protein sequence of APMV-8 Hemagglutinin/neuraminidase (HN)

1	MSNIASSLENIVEQDSRKTWRAIFRWSVLLITTGCLALSIVSIVQIG	48
49	NLKIPSVGDLADEVVTPLKTTLSDTLRNPINQINDIFRIVALDIPLOV	96
97	TSIQKDIASQFNMLIDSLNAIKLNGTNLIIPTSDKEYAGGIGNPVFT	144
145	VDAGGSIGFKQFSLIEHPSFIAGPTTTRGCTRIPTFHMSHWCYSHN	192
193	IIAAGCQDASASSMYISMVGLHVSSSGTPIFLTASELIDGVRKSC	240
241	SIVATQFGCDILCSIVTEKEGDDYWSDTPTPMRHGRFSFNCSFVEAEL	288
289	PVSSMFSSFSANYPVAGSGEIVKDRILFPIYGGIKQTSPEFTELVKYG	336
337	LFVSTPTTVQCSSWTYDQVKAAYRPDIISGRFWAQVILSCALDAVDLS	384
385	SCIIVKIMNSSTVMMAAEGRIMKIGIDYFYQSSSWWPLAFVTKLDPQ	432
433	ELADTNSIWLNTNSIPIQSKFPRPSYSENYCTKPAVCPATCVTVGVYSD	480
481	IWPLTSSSSSLPSIIWIGQYLDAPVGRTPYPRFGIANQSHWYLQEDILPT	528
529	STASAYSTTTCFKNTARNRVFCVTIAEFADGLFGEYRITPQLYELVRN	576
577	N*	578

Figure 17 (1/4)

SEQ ID NO:12 DNA sequence encoding APMV-8 Polymerase (L)

1	ATG	GAG	GGC	GAC	CTC	TAC	ACA	AAC	ATG	GAT	ATA	AAA	CAA	GTT	GAC	CTG	48
49	ATA	ATA	CAA	CCC	GAG	GTT	CAT	CTC	GAT	TCA	CCC	ATC	ATA	TTG	AAT	AAA	96
97	CTG	GCA	CTA	TTA	TGG	CGC	TTG	AGT	GGT	TTA	CCC	ATG	CCT	GCA	GAC	CTA	144
145	CGA	CAA	AAA	TCC	GTA	GTG	ATG	CAC	ATC	CCG	GAC	CAC	ATC	TTA	GAA	AAA	192
193	TCA	GAA	TAT	CGG	ATC	AAG	CAC	CGT	CTA	GGG	AAA	ATC	AAG	AGT	GAC	ATA	240
241	ACA	CAT	TAC	TGT	CAG	TAT	TTT	AAT	ATT	AAT	TTG	GCA	AAT	ATT	GAT	CCG	288
289	ATA	ACC	CAC	CCC	AAA	AGT	TTG	TAT	TGG	TTA	TCC	AGA	CTA	ACA	ATA	GCT	336
337	AGT	GCT	GGA	ACT	TTT	AGG	CAT	ATG	AAA	GAT	AGA	ATC	TTG	TGT	ACA	GTT	384
385	GGC	TCT	GAA	TTT	GGA	CAC	AAA	ATT	CAA	GAT	TTA	TTT	TCA	CTG	CTG	AGC	432
433	CAT	AAA	CTA	GTA	GGT	AAC	GGG	GAT	TTA	TTT	AAT	CAA	AGT	CTC	TCA	GGT	480
481	ACA	CGT	TTG	ACT	GCA	AGT	CCG	TTA	TCC	CCT	TTA	TGC	AAT	CAA	TTT	GTC	528
529	TCT	GAC	ATC	AAG	TCT	GCA	GTC	ACG	ACA	CCC	TGG	TCA	GAA	GCT	CGT	TGG	576
577	TCT	TGG	CTT	CAT	ATC	AAA	CAA	ACA	ATG	AGA	TAT	CTG	ATA	AAA	CAA	TCA	624
625	CGC	ACT	ACA	AAT	TCG	GCT	CAT	TTA	ACA	GAA	ATC	ATA	AAA	GAA	GAA	TGG	672
673	GGT	TTA	GTA	GGT	ATT	ACT	CCA	GAT	CTT	GTC	ATT	CTT	TTT	GAC	AGA	GTC	720
721	AAT	AAT	AGT	CTG	ACT	GCA	TTA	ACA	TTT	GAG	ATG	GTT	CTA	ATG	TAT	TCA	768
769	GAT	GTA	TTA	GAA	TCC	CGT	GAC	AAT	ATT	GTG	TTA	GTG	GGG	CGA	CTA	TCT	816
817	ACC	TTT	CTA	CAG	CCA	GTA	GTT	AGT	AGA	CTG	GAG	GTG	TTG	TTT	GAT	CTA	864
865	GTA	GAT	TCA	TTG	GCA	AAA	ATC	TTA	GGT	GAC	ACA	ATA	TAT	GAG	ATT	ATT	912
913	GCA	GTG	TTA	GAG	AGC	TTG	TCT	TAT	GGG	TCA	GTT	CAA	CTA	CAT	GAT	GCA	960
961	AGT	CAC	TCT	CAT	GCA	GGG	TCT	TTT	TTT	TCA	TTT	AAC	ATG	AAT	GAA	CTT	1008
1009	GAT	AAC	ACA	CTA	TCA	AAG	AGG	GTA	GAT	CCG	AAA	CAC	AAG	AAC	ACT	ATA	1056
1057	ATG	AGC	ATT	ATA	AGA	CAA	TGC	TTT	TCT	AAT	CTA	GAT	GTT	GAT	CAA	GCT	1104
1105	GCA	GAG	ATG	CTA	TGC	CTG	ATG	AGA	TTA	TTC	GGA	CAC	CCA	ATG	TTA	ACT	1152
1153	GCA	CCG	GAT	GCA	GCA	GCC	AAA	GTG	AGG	AAA	GCA	ATG	TGT	GCT	CCA	AAA	1200
1201	CTT	GTT	GAA	CAC	GAC	ACC	ATC	TTG	CAG	ACA	TTA	TCT	TTC	TTC	AAG	GGG	1248
1249	ATA	ATT	ATA	AAT	GGG	TAC	AGA	AGA	TCA	CAC	TCT	GGC	CTG	TGG	CCC	AAT	1296
1297	GTA	GAG	CCG	TCT	TCA	ATT	TAT	GAT	GAT	GAT	CTC	AGA	CAG	CTG	TAC	TTA	1344
1345	GAG	TCA	GCA	GAG	ATT	TCC	CAT	CAT	TTT	ATG	CTT	AAA	AAC	TAC	AAG	AGT	1392
1393	TTA	AGC	ATG	ATA	GAA	TTC	AAG	AAG	AGC	ATA	GAC	TAC	GAT	CTT	CAT	GAT	1440
1441	GAC	CTA	AGT	ACT	TTC	TTA	AAG	GAT	AGA	GCA	ATT	TGC	CGG	CCG	AAA	TCC	1488
1489	CAG	TGG	GAT	GTG	ATA	TTT	CGT	AAG	TCT	TTA	CGC	AGA	TCT	CAT	ACG	CAG	1536
1537	TCC	CAG	TAT	CTG	GAC	GAA	ATT	AAG	AGC	AAC	CGA	TTG	CTA	ATT	GAT	TTT	1584
1585	CTT	GAT	TCT	GCT	GAA	TTT	GAC	CCT	GGA	AAA	GAA	TTT	GCA	TAT	GTA	ACC	1632
1633	ACA	ATG	GAT	TAT	TTG	CAC	GAT	AAT	GAA	TTT	TGT	GCT	TCA	TAT	TCT	CTA	1680
1681	AAG	GAA	AAG	GAG	ATC	AAA	ACT	ACT	GGG	AGG	ATA	TTT	GCA	AAA	ATG	ACA	1728
1729	CGC	AAT	ATG	AGA	AGT	TGC	CAA	GTA	ATA	CTT	GAA	TCT	TTG	TTA	TCA	AAG	1776
1777	CAT	ATA	TGC	AAG	TTC	TTA	AAA	GAG	AAT	GGC	GTT	TCG	ATG	GAG	CAA	TTG	1824
1825	TCA	TTG	ACC	AAG	AGT	CTA	CTT	GCA	ATG	TCT	CAA	CTC	TCA	CCA	AAA	GTC	1872
1873	TCG	ACT	TTG	CAG	GAC	ACT	GCA	TCA	CGT	CAT	GTA	GGT	AAC	TCA	AAA	TCT	1920
1921	CAG	ATT	GCA	ACC	AGC	AAC	CCA	TCT	CGG	CAT	CAC	TCG	ACA	CCC	AAT	CAG	1968
1969	ATG	TCA	CTC	TCA	AAT	CGA	AAA	ACG	GTT	GTA	GCA	ACT	TTC	TTA	ACA	ACT	2016
2017	GAC	TTG	GAA	AAA	TAC	TGC	CTG	CAG	TGG	CGA	TAT	TCA	ACT	ATT	AAA	TTG	2064
2065	TTT	GCA	CAA	GCT	CTA	AAT	CAA	CTC	TTT	GGG	ATT	GAT	CAC	GGG	TTT	GAA	2112
2113	TGG	ATA	CAT	TTA	AGA	CTT	ATG	AAC	AGC	ACC	TTA	TTT	GTT	GGC	GAT	CCT	2160
2161	TAC	TCG	CCT	CCT	GAA	GAT	CCA	ACA	CTA	GAA	GAT	ATA	GAT	AAA	GCA	CCA	2208
2209	AAT	GAT	GAT	ATC	TTC	ATA	GTT	TCT	CCA	AGG	GGA	GGC	ATA	GAG	GGT	TTA	2256
2257	TGT	CAG	AAA	ATG	TGG	ACC	ATG	ATA	TCA	ATT	AGT	GCT	ATA	CAC	TGT	GTA	2304
2305	GCA	GAG	AAA	ATT	GGT	GCA	CGA	GTG	GCA	GCA	ATG	GTG	CAG	GGT	GAT	AAT	2352
2353	CAA	GTA	ATA	GCT	ATC	ACC	AAA	GAA	TTA	TTC	AGA	GGA	GAG	AAA	GCT	TGT	2400
2401	GAT	GTC	AGA	GAT	GAG	TTA	GAC	GAG	CTT	GGT	CAA	GTG	TTT	TTT	GAT	GAG	2448
2449	TTC	AAG	AGA	CAC	AAT	TAT	GCA	ATT	GGA	CAC	AAT	CTT	AAG	CTA	AAT	GAG	2496
2497	ACA	ATA	CAA	AGC	CAA	TCC	TTT	TTT	GTA	TAT	TCC	AAA	CGA	ATA	TTC	TTT	2544
2545	GAA	GGG	CGA	TTG	CTT	AGT	CAA	GTC	CTC	AAA	AAT	GCT	GCC	AAG	TTA	TGT	2592
2593	ATG	GTT	GCT	GAC	CAT	CTA	GGT	GAA	AAC	ACT	GTA	TCT	TCC	TGT	AGC	AAC	2640

Figure 17 (2/4)

2641	CTG AGC TCG ACA ATT GCC CGC TTA GTG GAA AAT GGG TTT GAG AAG GAC	2688
2689	ACT GCT TTT GTG TTG AAC CTA GTC TAC ATC ATG ACT CAG ATT CTT TTT	2736
2737	GAT GAG CAT TAC TCG ATT GTA TGC GAT CAC CAT AGT GTC AAA AGC TTG	2784
2785	ATT GGA TCA AAA AAC CAT CGG AAT TTA TTG TAT TCA TCT CTA ATA CCA	2832
2833	GGT CAG CTC GGC GGT TTC AAC TTC CTC AAT ATA AGT CGG TTG TTC ACT	2880
2881	AGG AAT ATA GGT GAC CCA GTA ACA TGT AGT CTG TCT GAT CTC AAA TGC	2928
2929	TTC ATA GCC GCA GGT CTC CTT CCA CCC TAT GTC CTA AAA AAT GTG GTT	2976
2977	CTG CGT GAG CCT GGT CCT GGG ACA TGG TTG ACG TTG TGC TCT GAT CCT	3024
3025	TAC ACC CTT AAC ATA CCA TAC ACA CAG CTT CCA ACC ACA TAT CTC AAA	3072
3073	AAG CAC ACC CAG CGA TCA TTG CTT TCA CGT GCA GTA AAT CCT TTA TTA	3120
3121	GCC GGT GTA CAA GTG CCA AAT CAG CAT GAG GAA GAA GAG ATG TTG GCT	3168
3169	CGC TTT CTC CTT GAT CGT GAA TAT GTG ATG CCC CGC GTT GCT CAT GTA	3216
3217	ATA CTA GAA TCA TCA GTC CTT GGC AAA CGG AAA CAA ATC CAA GGC TTA	3264
3265	ATT GAT ACA ACT CCA ACC ATC ATT AGA ACA TCT CTA GTT AAT CTG CCA	3312
3313	GTG TCT AGA AAG AAA TGC GAA AAA ATA ATC AAT TAC TCT CTC AAT TAT	3360
3361	ATT GCT GAG TGT CAT GAC TCC TTA CTT AGC CAG GTC TGC TTC AGT GAT	3408
3409	AAT AAG GAA TAC TTG TGG TCA ACC TCC TTA ATA TCA GTT GAG ACC TGT	3456
3457	AGT GTG ACA ATT GCG GAC TAT CTG AGA GCT GTC AGC TGG TCT AAT ATA	3504
3505	TTA GGG GGA AGA AAC ATA TCC GGG GTG ACT ACA CCT GAT ACT ATT GAA	3552
3553	TTA ATT CAA GGT TGT TTA ATA GGT GAA AAT TCT AGT TGT ACT CTT TGT	3600
3601	GAA TCG CAT GAT GAC GCA TTC ACG TGG ATG CAC TTG CCT GGC CCA CTT	3648
3649	TAC ATC CCT GAA CCA TCA GTT ACT AAC TCT AAA ATG CGT GTG CCA TAT	3696
3697	CTG GGT TCA AAA ACA GAG GAG CGG AAA ACA GCC TCA ATG GCA GCA ATA	3744
3745	AAA GGA ATG TCA CAT CAC CTG CGT GCA GTC TTA AGA GGC ACA TCC GTA	3792
3793	TTT ATT TGG GCA TTT GGG GAT ACA GAT ATC AAT TGG GAT AAT GCA TTG	3840
3841	CAG ATT GCC CAA TCA CGG TGT AAC ATC ACA TTG GAT CAA ATG AGA TTA	3888
3889	CTT ACA CCA ATT CCT AGC AGT TCA AAT ATT CAA CAT AGA CTC GAT GAC	3936
3937	GGA ATC AGC ACG CAG AAA TTT ACT CCT GCA AGC CTT GCT CGA ATC ACA	3984
3985	TCC TTC GTT CAC ATC TGT AAT GAC AGC CAG AGG TTA GAG AAG GAT GGC	4032
4033	TCA TCT GTC GAC TCA AAC TTG ATT TAC CAG CAA ATT ATG TTA CTT GGA	4080
4081	CTC AGC ATC TTT GAA ACA ATG TAC TCA ATG GAC CAA AAG TGG GTA ATG	4128
4129	AAT AAC CAT ACC TTG CAT TTG CAC ACT GGA CAC TCC TGT TGT CCA AGG	4176
4177	GAA CTA GAC ATA AGT TTG GTG AAC CCG CCG AGA CAT CAG ACC CCG GAG	4224
4225	CTG ACT AGC ACA ACA ACC AAC CCG TTC CTA TAT GAT CAG CTC CCA TTA	4272
4273	AAT CAA GAA AAC TTG ACA ACA CTT GAG ATT AAG ACA TTT AAA TTC AAT	4320
4321	GAG CTC AAC ATT GAT GGT TTA GAT TTT GGT GAA GGA ATA CAA TTA TTG	4368
4369	AGT CGT TGT ACT GCA AGA TTA ATG GCA GAA TGT ATT CTA GAG GAG GGA	4416
4417	ATA GGC TCG TCA GTT AAA AAT GAA GCA ATT GTC AAT TTT GAT AAT TCA	4464
4465	GTC AAT TGG ATT TCA GAG TGC CTA ATG TGT GAT ATT CGC TCA CTT TGT	4512
4513	GTT AAT TTA GGT CAA GAG ATA CTA TGT AGC CTG GCA TAC CAA ATG TAT	4560
4561	TAC TTG CGA ATC AGG GGT AGA CGG GCC ATT CTT AAT TAC TTG GAC ACA	4608
4609	ACT TTG CAA AGG ATC CCT GTG ATA CAA TTA GCC AAC ATT GCA CTC ACC	4656
4657	ATT TCG CAC CCT GAG ATA TTT CGC AGA ATT GTC AAC ACC GGG ATC CAT	4704
4705	AAC CAG ATT AAG GGC CCA TAT GTG GCA ACA ACG GAT TTC ATA GCT GCA	4752
4753	AGT AGA GAT ATC ATA TTA TCA GGT GCA AGG GAG TAT CTA TCT TAT TTA	4800
4801	AGC AGT GGG CAG GAA GAC TGT TAC ACA TTC TTC AAC TGT CAA GAT GGG	4848
4849	GAT CTT ACT CCA AAA ATG GAA CAG TAT CTT GCA AGG AGG GCA TGC CTT	4896
4897	TTA ACA TTA TTG TAT AAT ACT GGG CAC CAG ATC CCC GTT ATC CGA TCA	4944
4945	CTG ACG CCA ATA GAG AAG TGC AAG GTG CTC ACA GAA TAC AAT CAA CAA	4992
4993	ATT GAG TAC GCA GAT CAA GAG TTT AGC TCT GTA CTA AAA GTG GTC AAT	5040
5041	GCA CTA CTA CAA AAT CCT AAG ATA GAT GCA TTA GTT TCA AAT CTC TAC	5088
5089	TTC ACC ACC AGA CGT GTT CTA TCA AAC CTC AGA TCA TGT GAT AAG GCT	5136
5137	AGA TCA TAT ATT GAA TAT TTG TAC ACT GAG GAC TTC GGA GAG AAA GAG	5184
5185	GAT ACA GTA CAA TAT GAC ATC ATG ACA AAC GAT ATC ATA CTT ACT	5232
5233	CAT GGT CTA TTC ACA CAG ATC GAA ATA TCT TAT CAA GGG AAT AGT CTC	5280
5281	CAT AAG TTC CTT ACT CCG GAT AAC GCG CCT GGA TCT TTG ATC CCA TTC	5328

Figure 17 (3/4)

5329	TCT ATT TCA CCA AAT TCA CTT GCA TGT GAC CCT CTT CAT CAC TTG CTC	5376
5377	AAG TCG GTC GGT ACA TCA AGC ACA AGT TGG TAC AAG TAT GCA ATC GCC	5424
5425	TAT GCA GTG TCT GAA AAG AGG TCA GCT CGA TTA GGA GGG AGC TTG TAC	5472
5473	ATT GGT GAA GGG AGC GGA AGT GTG ATG ACT TTA CTC GAG TAT CTT GAG	5520
5521	CCA TCT GTT GAC ATA TTT TAC AAT TCA CTC TTC TCA AAT GGT ATG AAC	5568
5569	CCA CCA CAA CGA AAT TAT GGG CTT ATG CCA CTA CAA TTT GTG AAT TCG	5616
5617	GTG GTT TAT AAG AAC TTA ACG GCT AAA TCA GAA TGT AAG CTA GGG TTT	5664
5665	GTC CAG CAA TTT AAA CCG TTG TGG AGA GAC ATA GAC ATT GAG ACT AAT	5712
5713	GTT ACA GAT CCA TCA TTT ATC AAT TTT GCA TTG AAT GAA ATC CCA ATG	5760
5761	CAA TCA TTA AAA CGA GTA AAT TGT GAT GTG GAA TTT GAC CGT GGT ATG	5808
5809	CCG ATT GAA CGG GTT ATT CAG GGT TAC ACC CAT ATC TTA CTT GTT GCC	5856
5857	ACT TAC GGA TTA CAG CAA GAT TCA ATA CTG TGG GTG AAG GTA TAT AGG	5904
5905	ACA TCT GAA AAA GTA TTT CAA TTC TTA CTG AGT GCC ATG ATC ATG ATC	5952
5953	TTT GGT TAT GTA AAA ATC CAC AGG AAT GGT TAT ATG TCG ACA AAG GAT	6000
6001	GAA GAG TAC ATA TTG ATG TCT GAC TGC AAG GAA CCT GTA AAC TAT ACA	6048
6049	GCT GTC CCT AAC ATT CTT ACA CGT GTA AGT GAT TTA GTG TCG AAG AAT	6096
6097	CTG AGT CTT ATC CAT CCA GAA GAC CTC AGA AAA GTA AGG TGT GAA ACA	6144
6145	GAT TCC CTG AAT TTG AAG TGC AAT CAT ATT TAT GAG AAA ATA ATT GCC	6192
6193	AGA AAA ATT CCA TTA CAG GTA TCA TCA ACT GAC TCT TTG CTC CTC CAA	6240
6241	TTA GGC GGT GTT ATC AAC TCG GTG GGC TCA ACT GAT CCT AGA GAG GTT	6288
6289	GCA ACA TTA TCT TCT ATT GAG TGT ATG GAC TAT GTT GTC TCA TCA ATT	6336
6337	GAT TTG GCT ATA TTG GAG GCA AAT ATT GTA ATC TCA GAG AGT GCT GGT	6384
6385	CTT GAC CTC GCT TTA ATG TTA GGC CCA TTC AAC TTA AAT AAG CTT AAG	6432
6433	AAA ATT GAC ACA ATC CTT AAG TCA AGC ACC TAT CAG CTA ATC CCG TAC	6480
6481	TGG TTG CGC TAT GAG TAC TCT ATT AAT CCG AGA TCT TTG TCA TTT CTA	6528
6529	ATC ACT AAA TTA CAA CAA TGC CGA ATT TCA TGG TCA GAT ATG ATC ACG	6576
6577	ATT TCT GAA TTT CGT AAG AAA TCC AAG CGG CCT ATA TTT ATC AAA CGA	6624
6625	GTA ATA GGG AAT CAA CAG CTA AAA TCA TTC TTT AAT GAA AGC TCA AGT	6672
6673	ATT GTT TTG ACT CGG GCT GAA GTT AAA GTC TGT ATA AAG TTC CTC GGT	6720
6721	GCA ATC ATC AAG TTG AAA TAA	6741

There are two **ATG** codons (bold and underline) that could be the start codon for APMV 8 Polymerase (L).

Figure 17 (4/4)

SEQ ID NO:13 Protein sequence (1) of APMV-8 Polymerase (L)

1	MEGDLYTNMDIKQVDLI IQPEVHLDSP IILNKLALLWRLSGLPMPADL	48
49	RQKSVVMH I PDHILEKSEYRIKHRLGKIKSDITHYCQYFNINLANIDP	96
97	ITHPKSLYWL SRLTIASAGTFRHMKDRILCTVGSEFGHKIQDLFSLLS	144
145	HKLVGNGDLFNQSLSGTRLTASPLSPLCNQFVSDIKSAVTPWSEARW	192
193	SWLHIKQTMRYLIKQSRRTNSAHLTEI I KEEWGLVGITPDLVILFDRV	240
241	NNSLTALT FEMVLMYSDVLESRDNI VLVGRLSTFLQPVVSRLEVLFDL	288
289	VDSLAKILGDTIYEI IAVLESLSYGSVQLHDASHSHAGSFFSFNMNEL	336
337	DNTLSKRVDPKHKNTIMSI I RQCFSNLDVDQAAEMLCLMRLFGHPMLT	384
385	APDAAAKVRKAMCAPKLV EHD TILQTL SFFKG I IINGYRRSHSGLWPN	432
433	VEPSSIYDDDLRQLYLESAE I SHHFMLKNYKSLSMIEFKSIDYDLHD	480
481	DLSTFLKDRAICRPKSQWDVIFR KSLRRSHTQSQYLDEIKSNRL LIDF	528
529	LDSAEFDPGKEFAYVT TMDYLHDNEFCASYSLKEKEIKTTGRIFAKMT	576
577	RNMRSQVILESLLSKHICKFFKENGVSMEQLSLTKSLLAMSQ LSPKV	624
625	STLQDTASRHVGNSKSIATSNPSRHHSTPNQMSLSNRKTVVATFLT T	672
673	DLEKYCLOWRYSTIKLFAQALNQLFGIDHGF EWIHLRLMNSTLFV GDP	720
721	YSPPEDPTLEDIDKAPND DIFIVSPRGGIEGLCQKMWTMISISAIHCV	768
769	AEKIGARVAAMVQGDNQVIAITKELFRGEKACDVRDELDELGOVFFDE	816
817	FKRHNYAIGHNLKLN ETIQSQSFFVYSKRIFFEGRLLSQVLKNAAKLC	864
865	MVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFVLNLVYIMTQILF	912
913	DEHYSIVCDHHSVKSLIGSKNHRNLLYSSLI PGQLGGFNFLNISRLFT	960
961	RNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREP GPGT WLTLCSDP	1008
1009	YTINIPYTQLPTTYLKKHTQ RSLLSRAVNPLLAGVQVPNQHEEEEMLA	1056
1057	RFLLDREYVMPRVAHVILESSVLGKRKQIQGLIDTPTTIIRTSLVNLP	1104
1105	VSRKKCEKIINYS LNYIAECHDSL S QVCFSDNKEYLWSTSLISVETC	1152
1153	SVTIADYLRAVSWSNILGGRNISGVTTPTDI ELIQGCLIGENSSCTL C	1200
1201	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAI	1248
1249	KGMSHHLRAVLRGTSVFIWAFGDTDINWDNALQIAQSRCNITLDQMRL	1296
1297	LTPIPSSSNIQHRLDDGISTQKFTPASLARITSFVHICNDSQRLEKDG	1344
1345	SSVDSNLIYQQIMLLGLSIFETMYSMDQKWVFNNHTLHLHTGHSCCPR	1392
1393	ELDISLVNPPRHQTPELTSTTTNPF LYDQLPLNQENLTLEIKTFKFN	1440
1441	ELNIDGLDFGEGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNS	1488
1489	VNWISECLMCDIRSLCVNLGQEILCSLAYQMYYLRI RGRRAILNYLDT	1536
1537	TLQRI PV IQLANIALTISHPEIFRRIVNTGIHNQIKGPYVATTD FIAA	1584
1585	SRDIILSGAREYLSYLSSGQEDCYTFFNCQDGD LTPKMEQYLARRACL	1632
1633	LTLLYNTGHQIPVIRSLTPIEKCKVLTEYNQQIEYADQEFSSVLKVVN	1680
1681	ALLQNPKIDALVS NLYFTTRRVLSNL RSCDKARSYIEYLYTEDFGEKE	1728
1729	DTVQYDIMTTNDIILTHGLFTQIEISYQGN SLHKFLTPDNAPGSLIPF	1776
1777	SISPNSLACDPLHLLKSVGTSSTSWYKYAIAYAVSEKRSARLGGS LY	1824
1825	IGEGSGSVMTLLEYLEPSVDIFYNSLFSNGMNPQRNYGLMPLQFVNS	1872
1873	VVYKNLTAKSECKLGFVQQFKPLWRDIDIETNVTDP SFINFALNEIPM	1920
1921	QSLKRVNCDVEFDRGMPIERVIQGYTHILLVATYGLQQDSILWVKVYR	1968
1969	TSEKVFQFLLSAMIMIFGYVKIHRNGYMSTKDEEYILMSDCKEPVNYT	2016
2017	AVPNILTRVSDLVSKNLSLIHPEDLRKVRCE TDSLNLKCNHIYEKIIA	2064
2065	RKIPLQVSS TDSL LLLQLGGVINSVGSTDPRE VATLSSIECMDYVVSSI	2112
2113	DLAILEANIVISESAGLDLALMLGPFNLNKLKKIDTILKSS TYQLIPY	2160
2161	WLRYEYSINPRSLSFLITKLQQCRISWSDMITISEFRKSKRP IFIKR	2208
2209	VIGNQQ LKSFFNESSSIVLTRA EVKVCIKFLGAI IKLK*	2247

Figure 18

SEQ ID NO:14 Protein sequence (2) of APMV-8 Polymerase (L)

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1   MDIKQVDLII QPEVHLDSP I LNKLALLWR LSGLPMPADL RQKSVVMHIP
51  DHILEKSEYR IKHRLGKIKS DITHYCQYFN INLANIDPIT HPKSLYWLSR
101 LTIASAGTFR HMKDRILCTV GSEFGHKIQD LFSLLSHKLV GNGDLFNQSL
151 SGTRLTASPL SPLCNQFVSD IKS AVTTPWS EARWSWLHIK QTMRYLIKQS
201 RTTNSAHLTE I IKEEWGLVG ITPDLVILFD RVNNSLTALT FEMVLMYSDV
251 LESRDNIVLV GRLSTFLQPV VSRLEVLFDL VDSLAKILGD TIYEIIAVLE
301 LSYGSVQLH DASHSHAGSF FSNMNELDN TSKRVDPKH KNTIMSIIRQ
351 CFSNLDVQA AEMLCMLRLF GHPMLTAPDA AAKVRKAMCA PKLVEHDTIL
401 QTLSFFKGII INGYRRSHSG LWPNVEPSSI YDDDLRQLYL ESAEISHHFM
451 LKNYKSLSMI EFKKSIDYDL HDDLSTFLKD RAICRPKSQW DVIFRKSLRR
501 SHTQSQYLDE IKS NRLLIDF LDSAEFDPGK EFAYVTMDY LHDNEFCASY
551 SLKEKEIKTT GRIFAKMTRN MRSCQVILES LLSKHICKFF KENGVSMEQL
601 SLTKSLLAMS QLSPKVSTLQ DTASRHVGNS KSQIATSNPS RHHSTPNQMS
651 LSNRKT VVAT FLTTDLEKYC LQWRYSTIKL FAQALNQLFG IDHGFWEIHL
701 RLMNSTLFVG DPYSPPEDPT LEDIDKAPND DIFIVSPRGG IEGLCQKMWT
751 MISISAIHCV AEKIGARVAA MVQGDNQVIA ITKELFRGEK ACDVRDELDE
801 LGQVFFDEFK RHNYAIGHNL KLN ETIQSQS FVYSKRIF EGRLLSQVLK
851 NAAKLCMVAD HLGENTVSSC SNLSSTIARL VENGFEKDTA FVLNLVYIMT
901 QILFDEHYSI VCDHHSVKSL IGSKNHRNLL YSSLIPGQLG GFNFLNISRL
951 FTRNIGDPVT CSLSDLKCFI AAGLPPYVL KNVVLREPGP GTWLTLCSDP
1001 YTLNIPYTQL PTTYLKHTQ RSLLSRAVNP LLAGVQVPNQ HEEEME LARF
1051 LLDREYVMPR VAHVILESSV LGKRKQIQGL IDTPTTIIRT SLVNLVPSRK
1101 KCEKIINYSL NYIAECHDSL LSQVCFSDNK EYLWSTSLIS VETCSVTIAD
1151 YLRAVSWSNI LGGRNISGVT TPD TIELIQG CLIGENSSCT LCESHDDAFT
1201 WMHLPGLYI PEP SVTNSKM RVPYLGSKTE ERKTASMAAI KGMSHHLRAV
1251 LRGT SVFIWA FGDTDINWDN ALQIAQSRCN ITLDQMRLLT PIPSSSNIQH
1301 RLDDGISTQK FTPASLARIT SFVHICNDSQ RLEKDGSSVD SNLIYQQIML
1351 LGLSIFETMY SMDQKWVFNN HTLHLHTGHS CCPRELDISL VNPPRHQTPE
1401 LTSTTNPFL YDQLPLNQEN LTLEIKTFK FNELNIDGLD FGEGIQLLSR
1451 CTARLMAECI LEEGIGSSVK NEAIVNFDNS VNWISECLMC DIRSLCVNLG
1501 QEILCSLAYQ MYYLRI RRR AILNYLDTTL QRIPVIQLAN IALTISHPEI
1551 FRRIVNTGIH NQIKGPYVAT TDFIAASRDI ILSGAREYLS YLSSGQEDCY
1601 TFFNCQDGL TPKMEQYLAR RACLLTLLYN TGHQIPVIRS LTPIEKCKVL
1651 TEYNQQIEYA DQEFSSVLKV VNALLQNPKI DALVSNLYFT TRRVLSNLSR
1701 CDKARSYIEY LYTEDFGEKE DTVQYDIMTT NDIILTHGLF TQIEISYQGN
1751 SLHKFLTPDN APGSLIPFSI SPNSLACDPL HHLLKSVGTS STSWYKYAIA
1801 YAVSEKRSAR LGGS LYIGEG SG SVMTLLEY LEPSVDIFYN SLFSNGMNPP
1851 QRNYGLMPLQ FVNSVVKYKNL TAKSECKLGF VQQFKPLWRD IDIATNVMDP
1901 SFINFALNEI PMQSLKRVNC DVEFDRGMPI ERVIQGYTHI LLVATYGLQQ
1951 DSILWVKVYR TSEKVFQFL SAMIMIFGYV KIHNRNGYMS KDEEYILMSD
2001 CKEPVNYTAV PNILTRVSDL VSKNLSLIHP EDLRKVRCE TDSLNLKCNHI
2051 YEKIIARKIP LQVSSTDSL LQLGGVINSV GSTDPREVAT LSSIECMDYV
2101 VSSIDLAI LE ANIVISESAG LDLALMLGPF NLNKLKKIDT ILKSSTYQLI
2151 PYWLRYEYSI NPRSL SFLIT KLQQCRISWS DMITISEFRK KSKRPIFIKR
2201 VIGNQQLKSF FNESSSIVLT RAEVKVCIKF LGAI IKL

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Figure 19A (1/2)

APMV-8 Reverse Genetics System

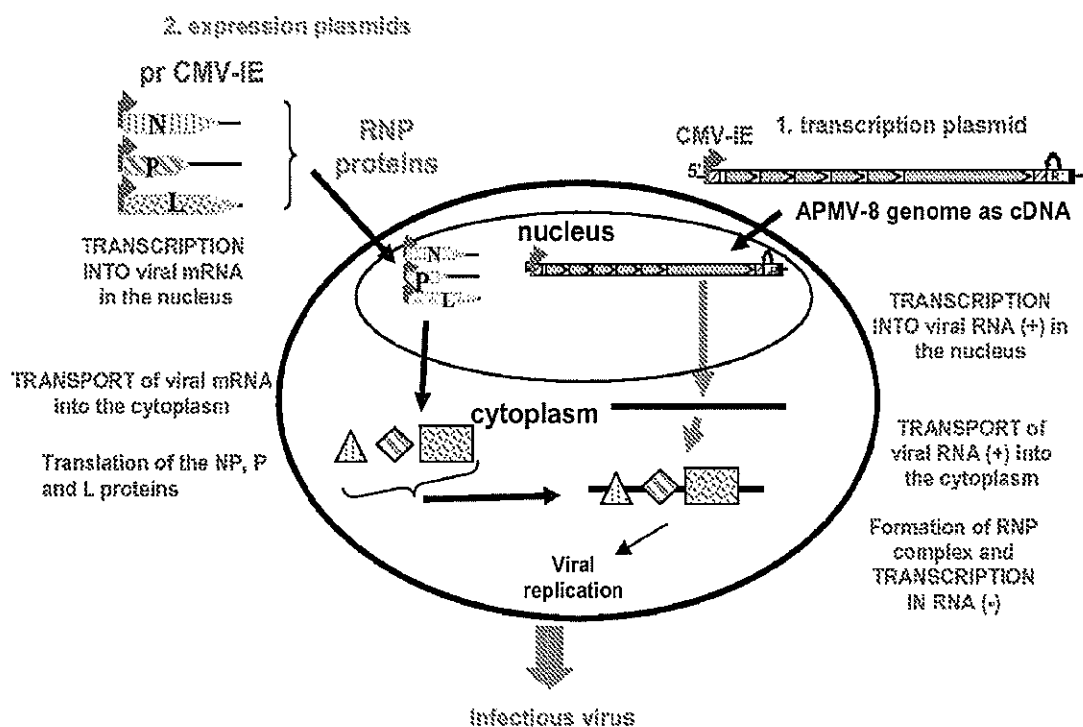


Figure 19B (2/2)

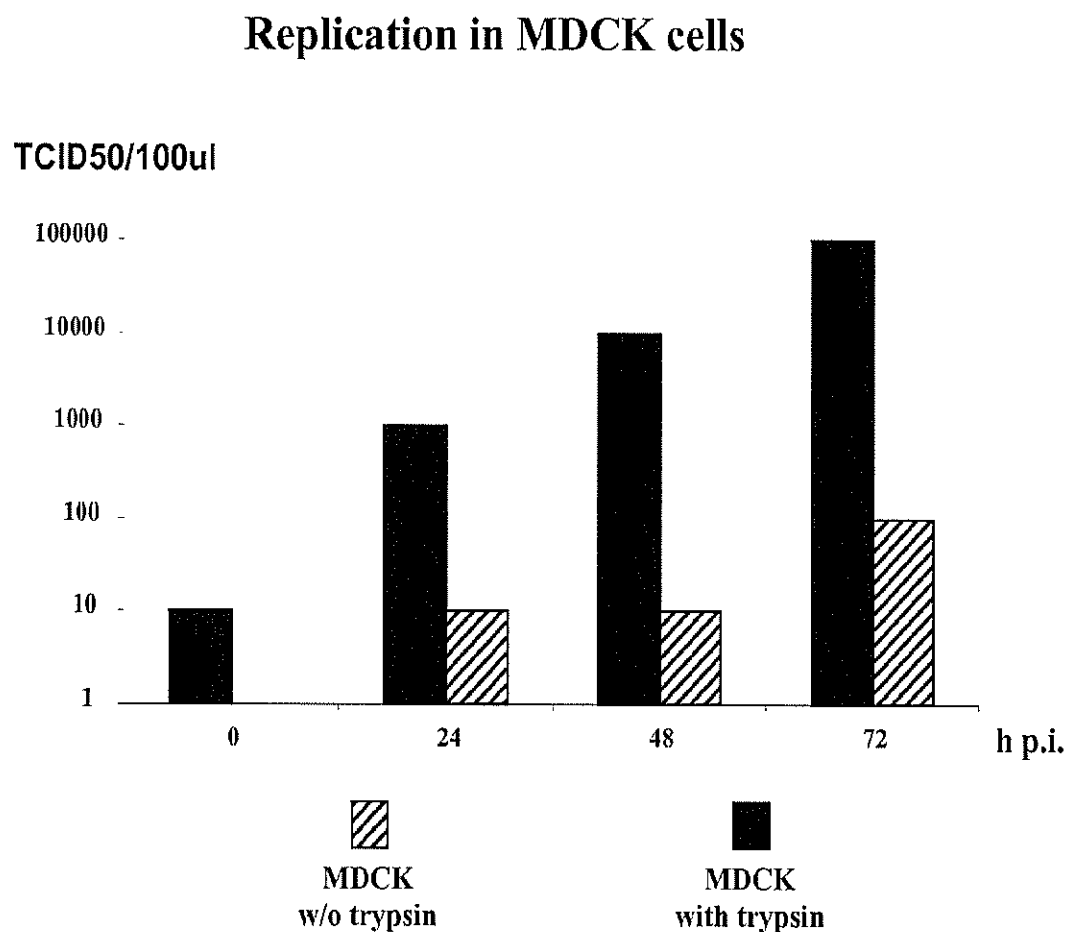


Figure 20

Commercial broiler 2 weeks after APMV-8 vaccination

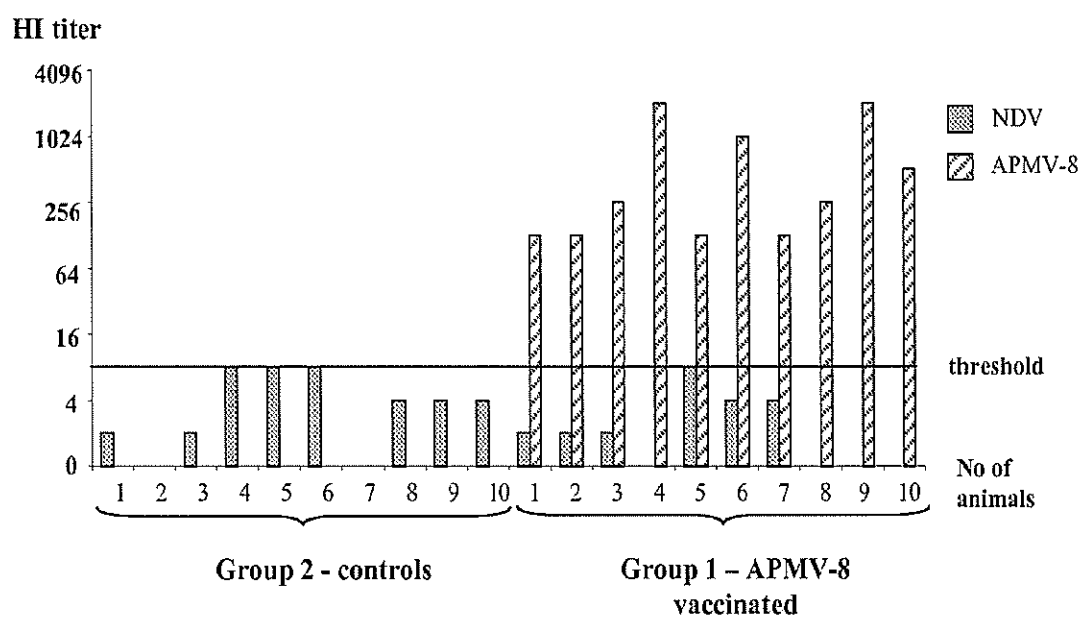


Figure 21

Commercial broiler 4 weeks after APMV-8 vaccination

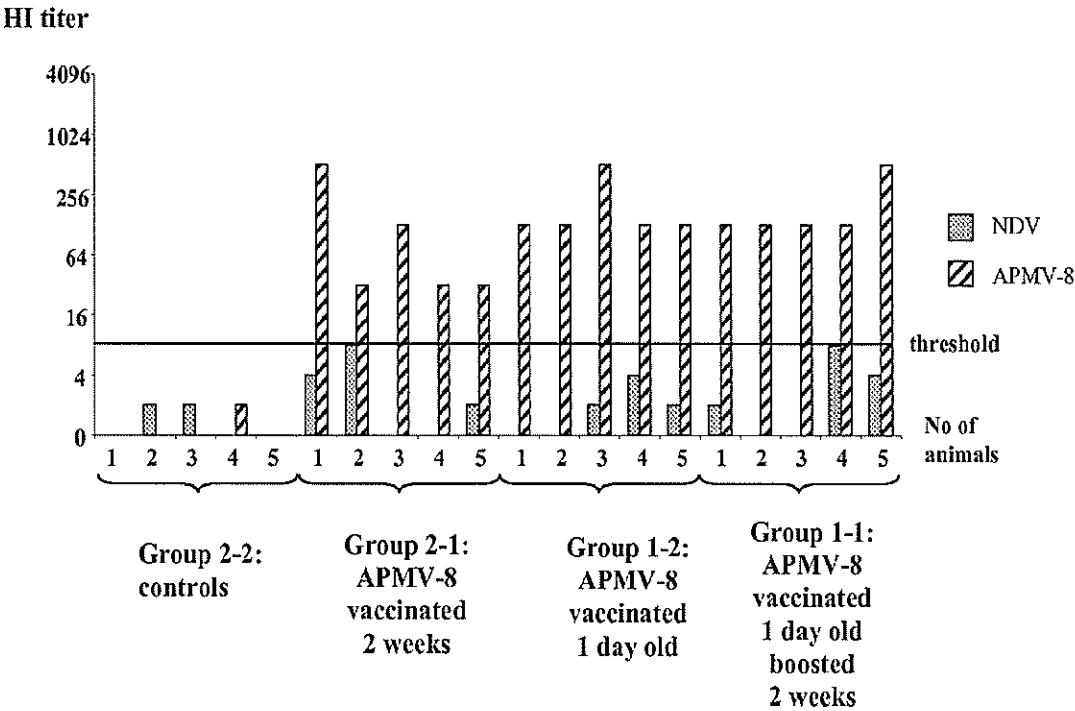


Figure 22

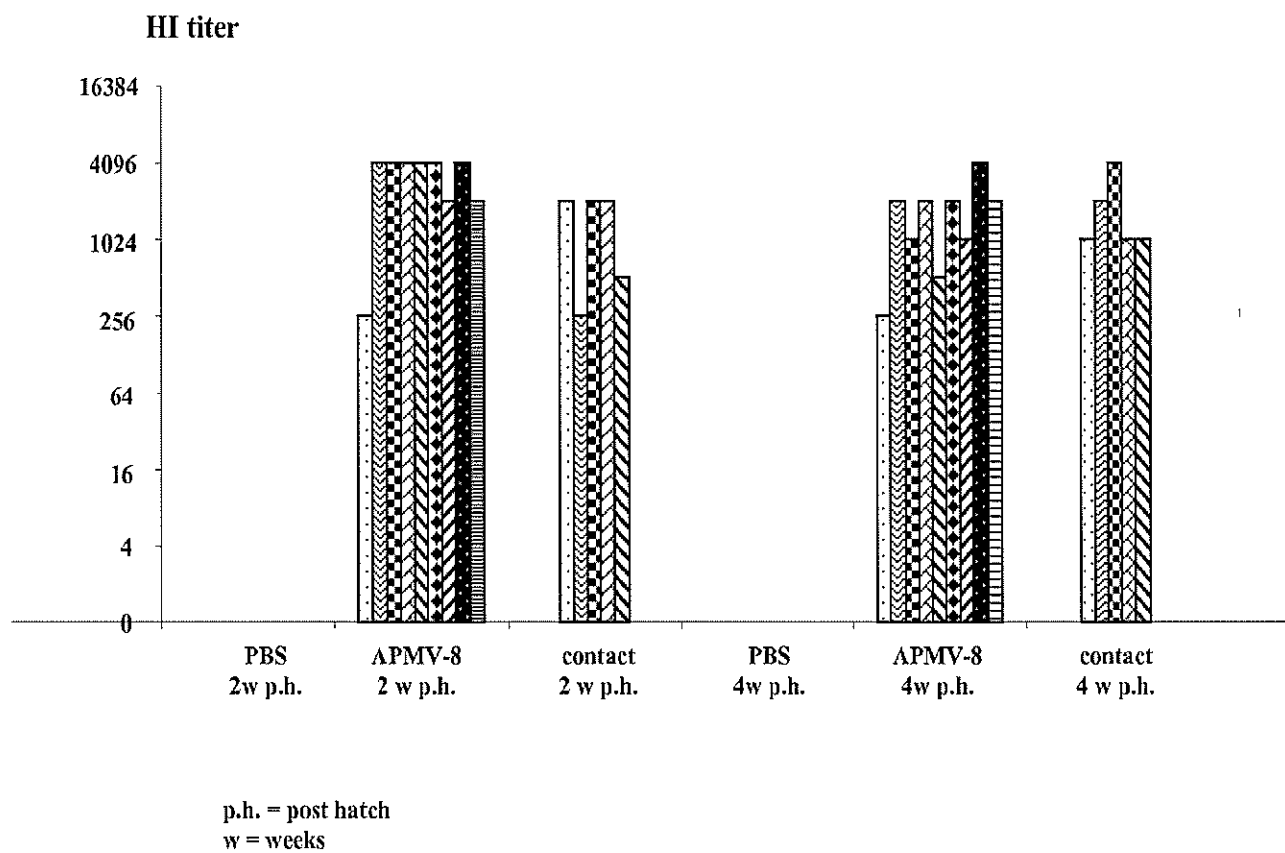
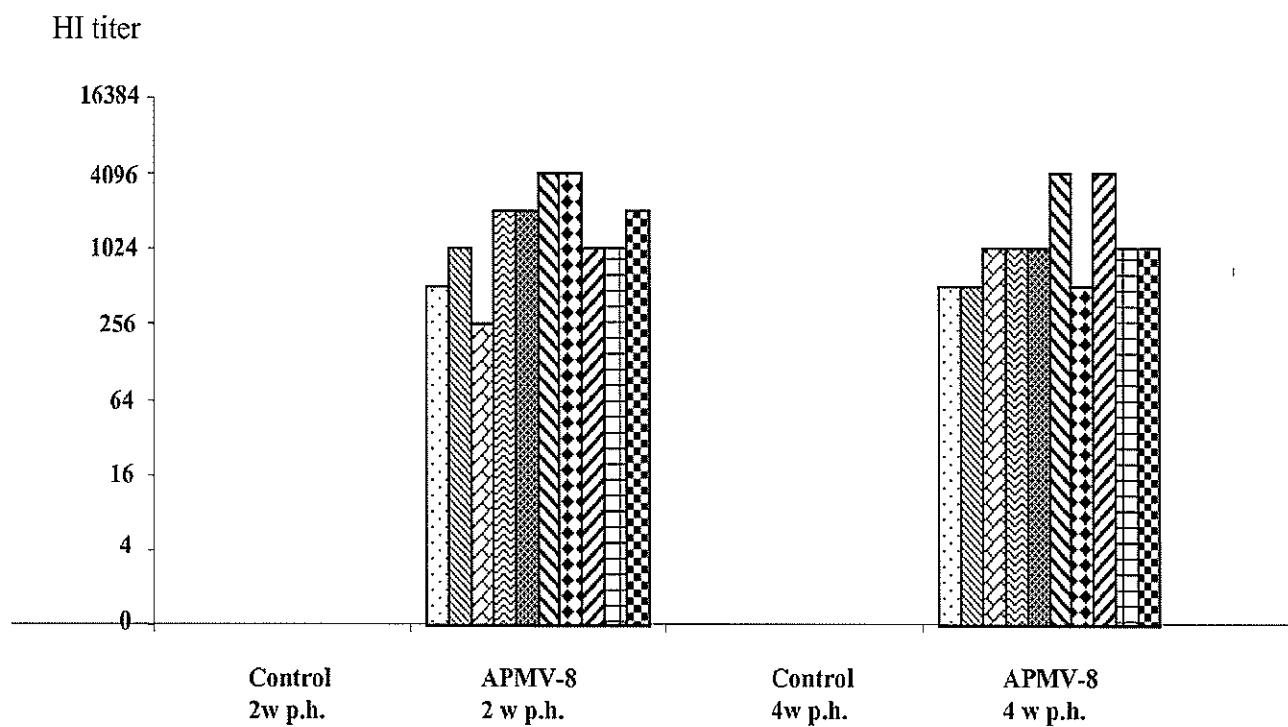
Study 1, *in ovo* vaccinated at day 18

Figure 23

Study 2: *in ovo* vaccinated at day 19

p.h. = post hatch
w = weeks

Figure 24

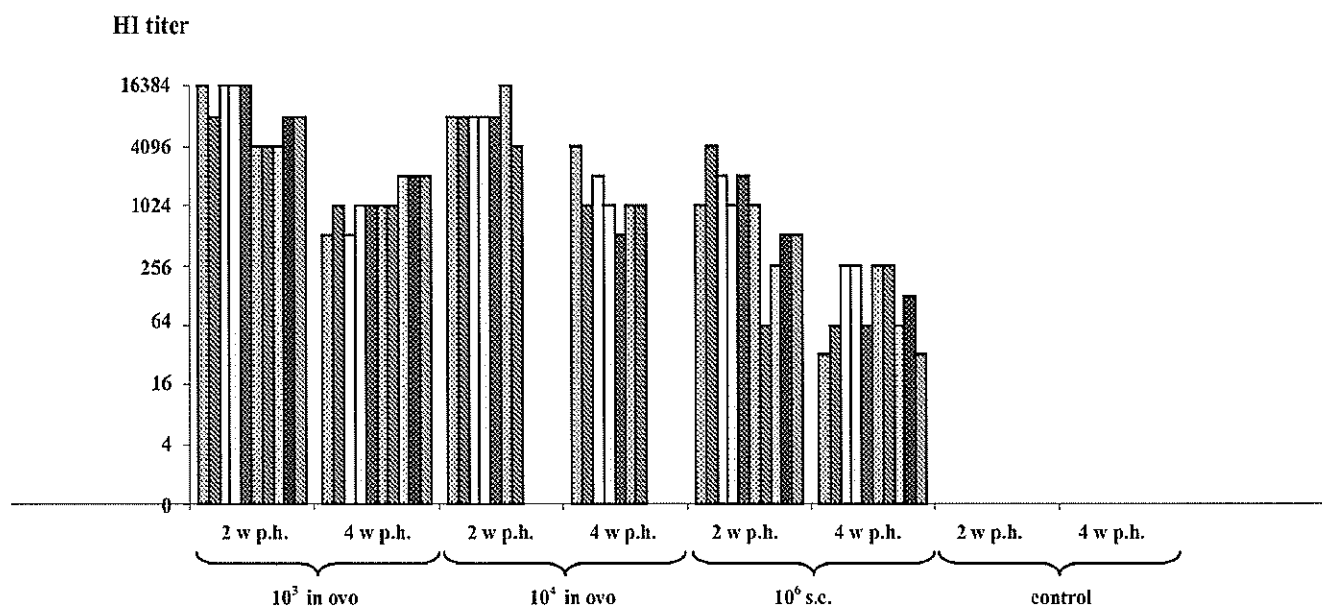
Study 3: *in ovo* vaccinated at day 18

Figure 25 (1/5)

5'-part, full length genome (5'-FLG) SEQ ID NO:47:

ggCGGCGCGGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATA
TGGAGTTCGCGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATGACGTCAAT
AATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAACTGCC
CACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGC
ATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGT
GATGCGGTTTTGGCAGTACATCAATGGCGGTGGATAGCGGTTTGAATCACGGGGATTTCAGTCTCCACCCCATGAC
GTCAATGGGAGTTTGTGGTGGCACCATAATCAACGGGACTTTCAGAAATGTCTGTAACAACCTCCGCCCCATTGACGCAA
TGGGCGGTAGGCGGTGACGGTGGGAGGTCTATATAAGCAGAGCTCCCGGGTgttaagcgtctgatgagtcggtgaggac
gaaactataggaaggaatttcctatagtcACCAACAAGGAATGCAAGACCAACGGGAACTTAAATAAAAACAATCGAA
TTATTGGGGCGCAAGCAAGTGGATCTCGAGCTCGAGGCCGAACCCCTGAATTTCACTGGAGGTTTTGAATAGGTCGCTA
TAGGACTCAATATGTCATCTGTGTTCAATGAGTATCAGGCGCTTCAAGAACAACTTGTGAAGCCGGCTGTCAGGAGACC
TGATGTTGCTCAACGGGTTTACTCAGACGGGAATACCTGTCTGTGTACATTATCTCAAGACCCCGGTGAGAGATGG
AGCCTTGCTTGTGTAATATTAGATGGCTTGGGAGTGATTCATCAACCACACCAATGAAGCAAGGAGCAATATTGTGAC
TGCTGAGTCTACATTGACACAATATGCGAGCTCAGCAACATTAGCAGCAAGGTCTGCAGATGCTTCACTCACCATACT
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CAATTGCTTGCAATTGCGGATGACATCCCAAAAGTTGCAGTAATGGGCATCCATTTCTTGACACAGACATTGAGACCA
GAGACCCGCTCGATCTATCAGAGACTATAGATCGCTGCAGGTATTGCAGCTCAGATATGGGTGTCAGCCATAAAGAG
CATGACAGCGCTGACACCGCATCAGAGTCAGAAAGTAAGAGGCTGGCCAAATATCAACAACAAGGCCGACTGGTTAAG
CAAGTACTCTTGCATTCTGTAGTCAGGACAGAATTTATGAGAGTTATTCGGGGCAGCTTGGTACTGCCCGAGTTTATGG
TTAGCGAGTGCAGAGGGCTTCAGCCATGGGCGGAGACACATCTAGGTACTATGCTATGGTGGGTGACATCAGTCTTTA
CATCAAGAATGCAGGATTGACTGCATTTTTCCTCACCCTGAAGTTCGGAGTTGGTACCCAGTATCCAACTTAGCAATG
AGTGTCTTCTCCAGTGACCTTAAAGGCTTGCTGCATCTCAGGCTATACAAAACCAAGGAGACAATGCACCATAACA
TGGCATTCCTGGAGGACTCCGATATGGGAAATTTGCTCCAGCAAATATAGCACAATGTACTCTTATGCCATGGGCAT
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AGCAGGTAGATCACTGCTAATGTGCTAGATGAGATGGGTCCAGTTCATTCATGAGCCATCTCGCCCTGCATTTATCAG
TCAAGAGAAGAAATAGGCAGCTTGCAGAACTTGTGATGATCAGGTCAGGTCAGACCAAGCCAGTCCCGAAGCAGCCCGCA
CCAAGGGCCGACTCAGATGACATTGATCCATACGAGAACGGGCTAGAATGGTAAATTCACCCACCCCGACACATCCACCT
ATACACCAATTCGCTGACATATTAACCAATCAACATTTCTATAAACTATAGTAGTCATTGATTTAAGAAAAATTTGGG
GGCGACCTCAATTTGTAACATACAGATCCGTCCACAACACCACTCAACAACCCACACACAATGGATTTCCGCAATGA
TGAAGAAATTGCAGAACTTTTGAATCTCAGCACCATGTAATCAAGGAGATTGAGAAATCCGAACTCAAGCCTCCCCAA
ACCACCGACGACCACTGTGATCAAGGGAACACAAGAAATCTAATGATCTATGGGAAAAGGAGACTGCAAGTCAGA
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TAGGTGCGATCCGAATGATGGCTGATGTTAATACCATCTCTAATGACGCACTAGCGCTGGAGATCACTGTTAAGAAATC
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GGAGGTTTCATCTCGAATGCAGACGAGAAATATAAATGTGCCAGCAAATGACTGCAGGAGTGCAGTACATATCCGCC
CAATGTTTGTTCATCACTAAATACACAATGGCAAATATATAGGGTGCCCAAAGCATCCACAGCATCTCATCCAC
TCTACTGTATAGTGTGATGTTGGAGGTAGGATTCAAAGTGGATATTGGGAAGGATCATCCCCAGGCAAGATGCTGAAG

Figure 25 (2/5)

AAGGTCACAATCGGCGATGCAGACACATACTGGGGGTTTGCATGGTTCACCTGTGCAATTTCAAAAAGACATCCTCTA
 AGGGAAAGCCAAGAACGCTAGACGAACATAAGACAAAAGTCAAAAATATGGGGTTGAAATTGGAGTTACATGACCTGTG
 GGGTCCGACTATTGTGGTCCAAATCACTGGCAAGAGCAGCAAAATATGCTCAAGGATTTTTCTCCTCAATGGTACTTGT
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 GGCAGGTCAACACAAGGGCACTTCCCCGCTAGTAGCTAGCTGTCTTCGAGGTAACATATGATGCCCGG

Restriction enzyme cleavage sites: upper case letter, bold and underlined

Human cytomegalovirus immediate early promoter: upper case letter, bold, italics

Hammerhead ribozyme sequence: lower case

Open reading frame for the viral proteins: upper case letter, bold

Non-coding sequences: upper case letter

Not I: **GCGGCCGC**

Bmt I: **GCTAGC**

Sac II: **CCGCGG**

3'-part, full length genome (3'-FLG) SEQ ID NO:48:

GCGGCCGCCAGGTCAACACAAGGGCACTTCCCCGCTAGTAGCTAGCTGTCTTCGAGGTAACATATGATGATTGTCAATA
 TACCACAGAGATTGGAGCATTATCATCCCGTATATAACACTAGTAGGGGGGCTTAGTTAATTGCAAGTCAATTGTT
 TGTAGGTGCCCTTAATCCAAGTAAGATCATCTCTCAAATAACAACGCTGCAGTAACATATGTTGATGCCACAATCTGCA
 AAACAATTCAATTGGATGATATACAACCTCCAGCTGGAAGGGTCACTATCATCAGTTTATGCAAGAAACATCTCAATTGA
 GATCAGTCAGGTGACCACATCCGGGTCTTTAGATATCAGCAGTGAGATAGGAAACATCAATAATACGGTGAATCGTGTG
 GAGGATTTAATTCAACCAATCAGAGGAATGGCTGGCAAAGGTTAACCACACATTGTTAATAATACAACACTAATTGTAC
 TCTGTGTGTTAAGTGCCTTGCTGTGATCTGGCTGGCAGTATTAAACGGCTATTATAATATACCTTGAGAACAAAGTTGAA
 GACTATATCGGCATTAGCTGTAACCAATACAATACAGTCTAACCCCTATGTTAACCAACGAAACATGAATCTAAGTTT
 TGATCATTCAAGCCAAAACAGAGGATCTAGGCTCAGGTTAATAATAGTTCAATCAATATTTGATTTATTAGGTTTTTTT
 CACTAATTATTAATATATACCTCGTGATTAGATGATAACGTTAAAGTCTTAGATATTTAATAAAAAATGTAACCTGGGGGC
 GACCCATTTATAGGTGAGTATATATTAGGAAGTCCTTATATTGCACTGTGATTTCAAACAATTATATTACCTCATATCT
 ACCTTGTCTAAAGACATCATGAGTAACATTGCATCCAGTTTAGAAAAATTGTAGAGCAGGATAGTCGAAAAACAACCTT
 GGAGGGCCATCTTTAGATGGTCCGTTCTTCTTATTACAACAGGATGCTTAGCCCTTATCCATTGTTAGCATAGTTCAAAT
 TGGAAATTTGAAATTCCTTCTGTAGGGGATCTGGCTGATGAAGTGGTGACCCCTTGAAACCACTCTGTGAGATACA
 CTCAGGAATCCAATTAACAGATAAATGATATATTTAGGATTGTTGCCCTTGATATTCCATTGCAAGTGACCGATATCC
 AAAAGACCTTGCAAGTCAATTTAACATGTTGATAGATAGTTTAAATGCTATCAAATTAGGCAACGGGACCAACCTTAT
 CATACCTACATCAGACAAGGAGTATGCAGGAGGAATTGAAACCTGTATTACTGTGATGCTGGAGGTTCTATAGGA
 TTCAAACAGTTTAAATAGAACATCCGAGCTTTATTGCTGGACCTACAACGACCGAGGCTGTACAAGAATACCCA
 CTTTTACATGTGCAAAAGTCATTGGTGCTACTCACACAACATCATCGCTGCTGGCTGTCAAGATGCCAGTGCATCCAG
 TATGTATATCTCAATGGGAGTTCTCCATGTGTCCTCATCTGGCACTCCCATTTTTCTTACTACTGCAAGTGAGCTGATA
 GACGATGGAGTTAACGTAAGTCATGCAGCATTGTAGCAACCAATTTGGCTGTGACATTTTGTGCAGTATTGTACAG

Figure 25 (3/5)

AGAAGGAGGGAGATGATTACTGGTCTGATACTCCGACTCCAATGCGCCACGGCCGCTTTTTCATTCAATGGTAGTTTGT
AGAAGCCGAACCTACCAGTGTCCAGTATGTTCTCATCTCTGCGCAACTACCCCTGCTGTGGGATCAGCGGAAATTGTA
AAAGATAGAATATTATTCCCAATTTACGAGGTATAAAGCAGACTTCACCAGAGTTTACCGAATTAGTGAAATACGGAC
TCTTTGTATCAACACCTACAACCTGTGTGCCAGAGTAGCTGGACTTATGACCAGGTAAAAGCTGCGTATAGGCCAGATTA
CATATCAGGCCGTTCTGGGCACAAGTGATACTCAGCTGCGCTCTTGATGCAGTCGACTTATCAAGTTGTATTGTAAAG
ATTATGAATAGCAGCACAGTGATGATGGCAGCGGAAGGATAATGAAGATAGGGATTGATTACTTTTACTATCAGC
GGTCATCTTCTTGGTGGCCATTGGCATTGTGTACAAAACCTAGACCCGCAAGAGTTGGCAGACACAACTCAATATGGCT
GACCAATTCATACCAATCCCGCAATCAAAGTTCCTCGGCCCTTCATATTAGAAAATTATTGCACAAAGCCAGCAGTT
TGCCCTGCTACTTGTGTCACTGGTGTGTAATCTGATATTGGCCCCGACCTCATCTTCATCACTCCCGAGCATAATTT
GGATCGGCCAGTACCTTGATGCTCCTGTTGGGAAGGACTTATCCTAGATTGGAATTGCAAAATCAGTCACACTGGTACCT
CCAAGAAGATATTCTACCCACTTCCACCGCAAGTGGTATTCAACCACTACATGTTTTAAGAATACTGCCAGGAATAGA
GTGTTCTGCGTCACCATTGGCGAATTTGCAGATGGGTGTTGTTGGAGAGTACAGGATAACACCTCAGTTGTACGAATTAG
TGAGAAATAATTGAATAACAATAATTTGGGACTCATTTTGTGCGCAAGTGAAATGTATCTTTAAAAATAATCAATT
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AATTAAGAAAAATGGAGGGCGACCTCTACACAAACATGGATATAAAACAAGTTGACCTGATAATACACCCGAGGTTT
ATCTCGATTACCCATCATATTGAATAAACTGGCACTATTATGGCGCTTGAGTGGTTTACCCATGCCTGCAGACCTACG
ACAAAAATCCGTAGTGTGATGCACATCCCGGACCACATCTTAGAAAAATCAGAATATCGGATCAAGCACCCTCTAGGGAAA
ATCAAGAGTGCATATAACACATTAATGTCACTATTTAATAATTTAATTTGGCAAAATTTGATCCGATAACCCACCCCAAAA
GTTTGTATTGGTTATCCAGACTAACAAATAGCTAGTGTGGAAGTCTTTAGGCATATGAAAGATAGAATCTTGTGTACAGT
TGGCTCTGAATTTGGACACAAAATTCAGATTTTATTTTCACTGCTGAGCCATAAACTAGTAGGTAAACGGGGATTTATTT
AATCAAGTCTCTCAGGTACACGTTTGTGCTGCAAGTCCGTTATCCCTTTATGCAATCAATTTGTCTGTGACATCAAGT
CTGCAGTCACGACACCCTGGTCAGAAGCTCGTTGGTCTTGGCTTCATATCAAAACAAAATGAGATATCTGATAAAACA
ATCACGCACTACAAATTCGGCTCATTTAACAGAAATCATAAAGAAGAATGGGGTTAGTAGGTATTACTCCAGATCTT
GTCATCTTTTGTACAGAGTCAATAATAGTCTGACTGCATTAACTTTGAGATGGTTCTAATGTATTAGATGTATTAG
AATCCCGTGACAATATTGTGTAGTGGGCGGACTATCTACCTTTCTACAGCCAGTAGTTAGTAGACTGGAGGTGTGTT
TGATCTAGTAGATTTCATTGGCAAAAATCTTAGGTGACACAATATATGAGATTATTGCAGTGTAGAGAGCTTGTCTTAT
GGGTCACTTCACTACATGATGCAAGTCACTCTCATGCAGGTCTTTTTTTTCAATTAACATGAATGAAGTTGATAACA
CACTATCAAAGAGGGTAGATCCGAAACACAAGAACTATAATGAGCATTATAAGACAATGCTTTTCTAATCTAGATGT
TGATCAAGCTGCAGAGATGCTATGCCTGATGAGATTATTCGGACACCCCAATGTTAACTGCACCGGATGCAGCAGCCAAA
GTGAGGAAAGCAATGTGTGCTCCAAAACCTGTTGAACACGACACCATCTTGACAGACATTATCTTTCTCAAGGGGATAA
TTATAAATGGGTACAGAAGATCACACTCTGGCCTGTGGCCCAATGTAGAGCCGCTCTCAATTTATGATGATGATCTCAG
ACAGCTGACTTAGAGTCAGCAGAGATTTCCCATCATTTTATGCTTAAAACTACAAGAGTTTAAAGCATAGATAAATC
AAGAAGACATAGATACGATCTTCATGATGACCTAAGTACTTTCTTAAAGGATAGAGCAATTTGCGCGCGGAAATCCC
AGTGGGATGTATATTTCTGTAAGTCTTTACGAGATCTCATACGAGTCCAGTATCTGGACGAAATTAAGAGCAACCG
ATTGCTAATGATTTTCTTGATTCTGCTGAATTTGACCCTGGAAAAGAATTTGCATATGTAACCACAATGGATTATTTG
CAGGATAATGAATTTTGTGCTTCATATTTCTTAAAGGAAAAGGAGATCAAACTACTGGGAGGATATTTGCAAAAATGA
CAGCAATATGAGAGTTGCAAGTAATCTTGAATCTTTGTTATCAAGCATATATGCAAGTTCTTCAAGAGAAATGG
CGTTTCGATGGAGCAATGTGCTATGACCAAGAGTCTACTTGAATGTCTCAACTCTACCAAAAGTCTCGACTTTGCAG
GACACTGCATCAGTCACTAGGTAACTCAAAATCTCAGATTGCAACCAGCAACCCATCTCGGCATCACTCGACACCCA
ATCAGATGCTAGATCTCAAAATCGAAAAACGGTTGTAGTAACTTCTTAAACAAGTCACTTGGAAAAATGCTGCTGCACTG
GCGATATTCAACTATTAAATTTGTTGCAAGCTCTAAATCAACTCTTTGGGATTGATCAGCGAATTTGAATGGATACAT
TTAAGACTTATGAACAGCACCTTATTTGTTGGCGATCCTTACTCGCTCTGAAGATCCAACACTAGAAGATATAGATA
AAGCACCAAATGATGATATCTTCATAGTTTCTCCAAGGGGAGGCATAGAGGGTTTATGTCAGAAAATGTGGACCATGAT
ATCAATTAGTGCTATACACTGTGTAGCAGAGAAAATTTGGTGCAGAGTGGCAGCAATGGTGCAGGGTGATAATCAAGTA
ATAGCTATCACCAAGAATTTATCAGAGGAGAGAAAGCTTGTGATGTGAGAGATGAGTTAGACGAGCTTGGTCAAGTGT
TTTTTGATGAGTTCAAGAGACACAATTTGCAATTTGGACACAATCTTAAGCTAAATGAGACAAATACAAGCCAAATCCTT
TTTTGTATATTCAAACGAATATTCTTTGAAGGGCGATTGCTTAGTCAAGTCTCAAAAATGCTGCGCAAGTTATGTATG
GTTGCTGACCATCTAGGTGAAACCACTGTATCTTCTGTAGCAACCTGAGCTCGACAATTTGCCGCTTAGTGGAAAATG
GGTTTGAGAAGGACACTGCTTTTGTGTTGAACCTAGTCTACATCATGACTCAGATTCTTTTTTGATGAGCATTACTCGAT
TGTATGCGATCACCATAGTGTCAAAGCTTGATTGGATCAAAAAACCATCGGAATTTATTGTATTATCTCTAATACCA
GGTCAGCTCGGCGGTTTCAACTTCTCAATATAAGTCGGTTGTTCACTAGGAATATAGGTGACCCAGTAACATGTAGTC
TGTCTGATCTCAAAATGCTTCTAGCCGAGGTCTCCTTCCACCTATGTCTTAAAAATGTGGTTCTGCGTGAGCTGG
TCTGGGACATGGTTGACGTTGTGCTCTGATCCTTACACCTTAACATACCATACACAGCTTCCAACCATATCTC
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AGGAAGAGAGATGTTGGCTCGCTTCTCCTTGATCGTGAATATGTGATGCCCGCGTTGCTCATGTAATACTAGAATC
ATCAGTCTTGGCAACGGAACCAATCCAAGGCTTAATTGATACAACTCCAACCATCATTAGAACATCTCTAGTTAAT
CTGCCAGTGTCTAGAAAGAAATGCGAAAAAATAATCAATTACTCTCTCAATTATATTGCTGAGTGTGATGACTCCTTAC
TTAGCCAGGTCTGCTCAGTGATAATAAGGAATACTTGTGGTCAACCTCCTTAATATCAGTTGAGACCTGTAGTGTGAC
AATTGCGGACTATCTGAGAGTGTGAGTGGTCTAATATATTAGGGGGAAGAAACATATCCGGGGTACTACACCTGAT

Figure 25 (4/5)

ACTATTGAATTAATCAAGGTGTTTAAATAGGTGAAAATCTAGTTGTAATCGCATGATGACGCATTCA
 CGTGGATGCACCTTGCTGGCCCACTTTACATCCCTGAACCATCAGTTACTAATCTAAAATGCGTGTGCCATATCTGGG
 TTCAAAAACAGAGGAGCGGAAAACAGCCTCAATGGCAGCAATAAAGGAATGTCACATCACCTGCGTGCAGTCTTAAGA
 GGCACATCCGTATTTATTTGGGCATTTGGGGATACAGATATCAATTGGGATAATGCATTGCAGATTGCCAATCACGGT
 GTAACATCACATTGGATCAATGAGATTACTTACACCAATTCCTAGCAGTTCAAATATTCAACATAGACTCGATGACGG
 AATCAGCAGCAGAAATTTACTCTGCAAGCCTTGCTCGAATCACATCCTTCGTTTCAATCTGTAATGACAGCCAGAGG
 TTAGAGAAGGATGGCTCATCTGTCGACTCAAACCTTGATTTACCAGCAAATTTATGTTACTTGGACTCAGCATCTTTGAAA
 CAATGTACTCAATGGACCAAAAGTGGGTATTCAATAACCATACCTTGCAATTTGCACACTGGACACTCCTGTTGTCCAAAG
 GGAACATAGACATAAGTTTGGTGAACCCGCGAGACATCAGACCCCGGAGCTGACTAGCACAAACCAACCCGTTCTTA
 TATGATCAGCTCCCATTAATCAAGAAAACCTTGACAACACTTGAGATTAAAGACATTTAAATCAATGAGCTCAACATTG
 ATGGTTTAGATTTTGGTGAAGGAATACAATTATTGAGTCTGTACTGCAAGATTAATGGCAGAATGTATTCTAGAGGA
 GGAATAGGCTCGTCAGTTAAAATGAAGCAATTGTCAATTTTGATAATTCAGTCAATTGGATTTCAGAGTGCCTAATG
 TGTGATATTCGCTCACTTTGTGTTAATTTAGGTCAAGAGATATATGTAGCCTGGCATACCAATGTATTACTTTCGAA
 TCAGGGGTAGACGGGCCATTCTTAATTACTTTGGACACAACCTTGCAAGGATCCCTGTGATACAATTAGCCAACATTGC
 ACTCAACATTTGCGACCCCTGAGATATTTGCGAGAATTGTCAACACCGGGATCCATAACAGATTAAGGGCCCATATGTG
 GCAACAACGGATTTTCATAGCTGCAAGTAGAGATATCATATTTCAGGTGCAAGGGAGTATCTATCTTATTTAAGCAGTG
 GGCAGGAAGACTGTTTACACATTTCTCAACTGTCAAGATGGGGATCTTACTCCAAAATGGAACAGTATCTTGCAAGGAG
 GGCATGCCCTTTAACATTATTGTATAATACTGGGCACCAGATCCCCGTTATCCGATCACTGACGCCAATAGAGAAGTGC
 AAGGTGCTCACAGAATAACAATAAATGAGTACGCAGATCAAGAGTTTAGCTCTGTACTAAAAGTGGTCAATGCAC
 TACTACAAAATCCTAAGATAGATGCATTAGTTTCAAATCTCTACTTCACCACCAGACGTGTTCTATCAAACCTCAGATC
 ATGTGATAAGGCTAGATCATATATTGAATATTTGTACACTGAGGACTTCGGAGAGAAAGAGGATACAGTACAATATGAC
 ATCATGACAACAAACGATATCATACTTACTCATGTTCTATTCAACAGATCGAAATATCTTATCAAGGGAATAGTCTCC
 ATAAGTTCCTTACTCCGGATAACGCGCCTGGATCTTTGATCCCATTTCTTATTTCAACAAATCACTTGCATGTGACCC
 TCTTCATCACTTGCTCAAGTCGGTGGTACATCAAGCACAAGTTGGTACAAGTATGCAATCGCCTATGCAGTGTCTGAA
 AAGAGGTGAGTCAAGTATAGGAGGAGCTTGTACATTTGGTGAAGGAGCGAAGTGTGATGACTTTTACTCGAGTATCTTG
 AGCCATCTGTTGACATATTTTACAATCACTCTTCTCAAATGGTATGAACCCACCACAACGAAATATGGGCTTATGCC
 ACTACAATTTGTGAATTCGGTGGTTTATAAGAACTTAACGGCTAAATCAGAATGTAAGCTAGGGTTTGTCCAGCAATTT
 AAACCGTTTGGAGAGACATAGACATTGAGACTAATGTTACAGATCCATCATTTATCAATTTTGCATTGAATGAAATCC
 CAATGCAATCATTAACAGAGTAAATTTGTATGTGGAATTTGACCGTGGTATGCCGATTGAACGGGTATTTCAGGGTTA
 CACCCATATCTTACTTGTGGCACTTACGGATTACAGCAAGATTCAATACTGTGGGTGAAGGTATATAGGACATCTGAA
 AAAGTATTTCAATCTTACTGAGTGCCATGATCATGATCTTTGGTTATGTAATAATCCACAGGAATGGTTATATGTGCA
 CAAAGGTGAGAGATCATATTGATGTCTGACTGCAAGGAACCTGTAAACTATACAGCTGTCCCTAACATTTCTTACACG
 TGTAAGTGATTTAGTGTGCAAGAATCTGAGTCTTATCCATCCAGAAGACCTCAGAAAAGTAAGGTGTGAAACAGATTCC
 CTGAATTTGAAGTGCAATCATATTTATGAGAAAATAATTGCCAGAAAATTCATTACAGGTATCATCAACTGACTCTT
 TGCTCCTCAATTAGGCGGTGTTATCAACTCGGTGGGCTCAACTGATCCTAGAGAGGTTGCAACATTATCTTCTATTGA
 GTGATAGGACTATGTTGTCTCATCAATTGATTTGGCTATATTGGAGGCAATATTGTAATCTCAGAGAGTGCTGGTCTT
 GACCTCGCTTTAATGTTAGGCCATTCAACTTAAATAAGCTTAAGAAAATTGACACAATCCTTAAGTCAAGCACCTATC
 AGCTAATCCCGTACTGGTTGCGCTATGAGTACTCTATTAATCCGAGATCTTTGTCAATTTCTAATCACTAAATTACAACA
 ATGCCGAATTTCAAGTGCAGATATGATCAGATTTCTGAATTTTCGTAAGAAATCCAGCGGCTATATTTATCAACGA
 GTAATAGGGAATCAACAGCTAAAATCATCTTTAATGAAAGCTCAAGTATTGTTTGGACTCGGGCTGAAGTTAAAGTCT
 GTATAAAGTTCCTCGGTGCAATCATCAAGTTGAAATAATTTCTGCGATTTTAAAGGGGTGTAATGTTCTAATTTGCACT
 TGAAGTAATATAGCTTGTAAATCATTCGCTAGGGGATAGGATAATTTCTTAACCTCTGAATCTATATTCCTAGAGTATA
 ACAATATATACATAATAAATGATTTTAAAGAAAATCCGACACTCAAGAAAATTTGGTGCCTGTAATATTCTTCTT
 GCCAAATGATGTGAAGTGTCTAGCCTAACTTAAACAATCGTATTCGATAGGGAAGATGATATATAAATAACTAAT
 AAAAAATTGTATTAGTAAAAATTACCGTATTTCTGTATTCCATTTCTGGTgggtcggcacgcatctccacctctcg
 cgtccgacgtggcatccgaaggaggacgcacgtccactcggtggctaagggagggcgctagagctcgctgatcagc
 ctcgactgtgcctcttagttgcccagccatctgttggcttggccctcccccggtgccttccttgacctggaaggtgcccact
 cccactgtcctttcctaataaaatgaggaattgcatcgcatgtctgagtaggtgtcattctattctggggggtgggg
 tggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtctgggtagcgggtgggctctatgCCGCGG

Restriction enzyme cleavage sites: upper case letter, bold and underlined

Human cytomegalovirus immediate early promoter: upper case letter, bold, italics

Hepatitis delta ribozyme sequence: lower case

Open reading frame for the viral proteins: upper case letter, bold typed

Non-coding sequences: upper case letter

Bovine growth hormone poly A sequence: lower case letter, underlined

Not I: **GCGGCCGC**

Bmt I: **GCTAGC**

Sac II: **CCGCGG**

Figure 26

Plasmid encoding the proteins which are part of the
riboprotein complex of APMV-8

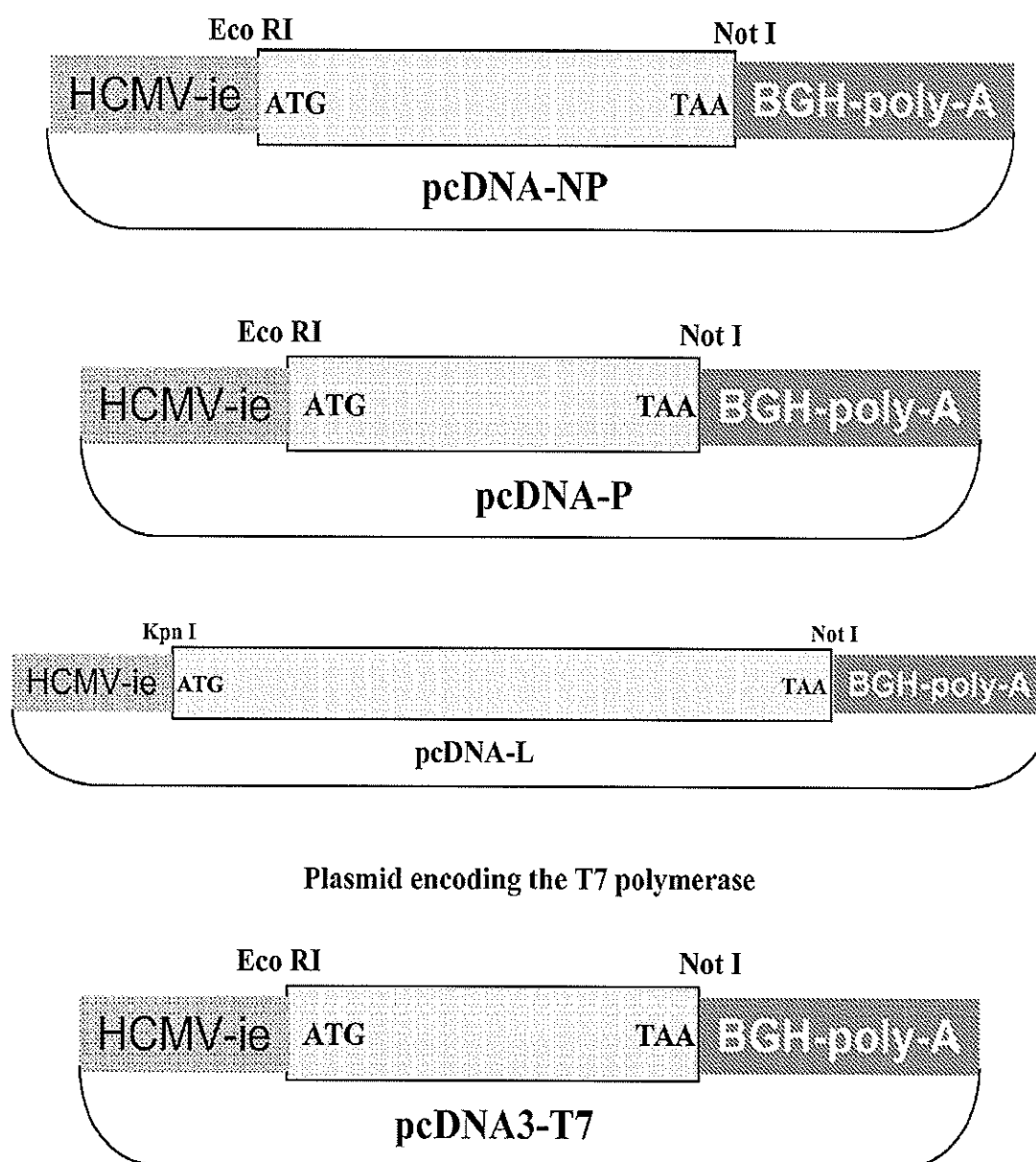
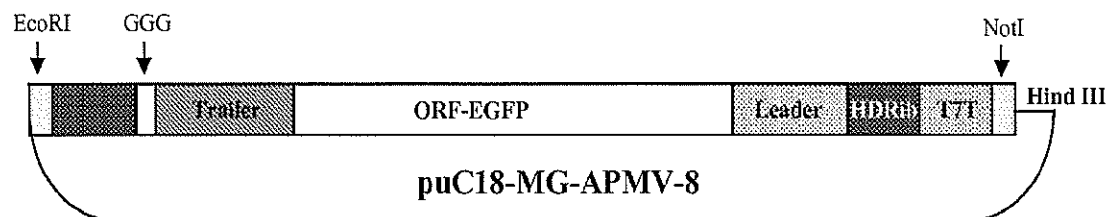
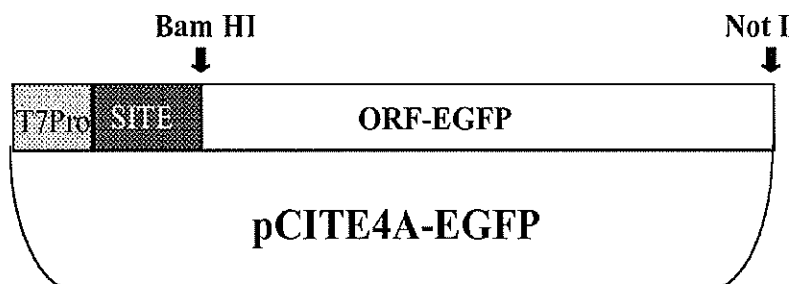


Figure 27

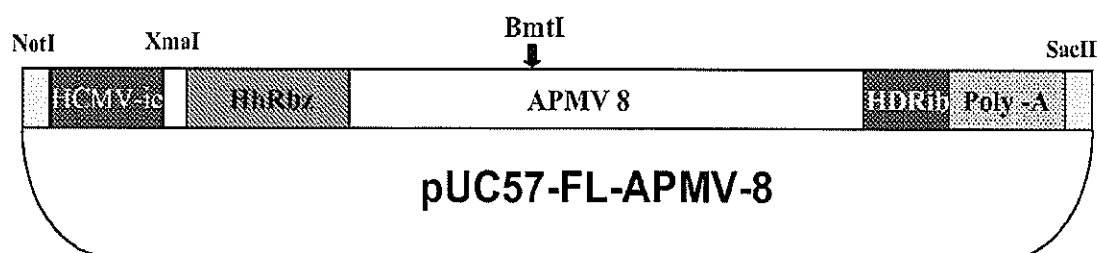
Plasmid containing a minigenome for APMV-8

T7Pro: T7 promoter
GGG: base triplet consisting of three G
Trailer: complete sequence of the trailer sequence of the APMV-8 virus
Leader: complete sequence of the leader sequence of the APMV-8 virus
ORF-EGFP: open reading frame of the enhanced green fluorescent protein
HDRib: hepatitis delta ribozyme sequence
T7T: T7 terminator
Restriction enzyme cleavage sites: EcoRI, NotI, HindIII

Plasmid encoding the EGFP under the control of the SITE promoter

T7Pro: T7 promoter
Site: internal ribosome entry site
ORF-EGFP: open reading frame of the enhanced green fluorescent protein
Restriction enzyme cleavage sites: BamHI, NotI

Figure 28

Plasmid containing the full length sequence of APMV-8

HCMV-ie: human cytomegalovirus immediate early promoter
 APMV 8: full length sequence of APMV 8 in antigenomic orientation
 HhRbz: hammerhead ribozyme sequence
 HDRib: hepatitis delta ribozyme sequence
 Poly A: bovine growth hormone polyadenylation signal sequence
 Restriction enzyme cleavage sites: Not I, XmaI, BmtI, SacII

Figure 29

Construction of the minigenome**Eco RI**

GAATTCTAATACGACTCACTATAGGGaccagaaatggaatacaggaaatacggtaatttttactaatacaattttttat
tagttattttatatatacattcttccctatcgaatacgaattgttttaagttaggctagacacttcacaatcatttggcaa
gaagaatattacaggcaccaattttctttgagtgctggattttttcttaaaatcatttttattatgtatatatttgtaa
tactctaggaatatagattcagaggttagagaaattatcctatcccctagcgaatgattacaagctataattacttcaag
tgcaaattagaacattacacccctttaaaatcgcaaaa**TACAAGCTATATTACTTCAAGTGCAAATTAGAACATTAC**
ACCCCTTTAAAAATCGCAGAAATTACTTGTACAGCTCGTCCATGCCGAGAGTGATCCCGGCGGCGGTACGAACCTCCAGC
AGGACCATGTGATCGCGCTTCTCGTTGGGGTCTTTGCTCAGGGCGGACTGGGTGCTCAGGTAGTGGTTGTCGGGCAGCA
GCACGGGGCCGTCGCCGATGGGGGTGTTCTGCTGGTAGTGGTCGGCGAGCTGCACGCTGCCGTCTCGATGTTGTGGCG
GATCTTGAAGTTCACCTTGATGCCGTTCTTCTGCTTGTCGGCCATGATATAGACGTTGTGGCTGTTGTAGTTGTACTCC
AGCTTGTGCCCCAGGATGTTGCCGTCCTCCTTGAAGTCGATGCCCTTCAGCTCGATGCGGTTACACAGGGTGTCCGCTT
CGAAGCTTCACTCGGGCGGGTCTTGTAGTTGCCGTCGTCCTTGAAGAAGATGGTGGCTCCTGGACGTAGCCTTCGGG
CATGGCGGACTTGAAGAAGTCGTGCTGCTTCATGTGGTCGGGGTAGCGGCTGAAGCACTGCACGCCGTAGGTACAGGGTG
GTCACGAGGGTGGGCCAGGGCACGGGCAGCTTGCCGGTGGTGCAGATGAAGTTCAGGGTCAGCTTGCCGTAGGTGGCAT
CGCCCTCGCCCTCGCCGACACGCTGAAGTGTGGCCGTTTACGTCGCCGTCAGCTCGACCAGGATGGGCACCACCCC
GGTGAACAGCTCCTCGCCCTTGCTCACCATattgagtcctatagcgacctattcaaaacctccagtgaatttcagggtt
tcggcctcgagctcgagatccacttgcttcgcccccaataattcgattgtttatttaaagtcccgttggtcttgcac
tccttggttggtgggtcgccatggcatctccacctcctcgcggtcccgacctgggcatccgaaggaggacgcacgtccac
tcggatggcctaagggagggcgTAGCATAACCCCTTGGGGCTCTAAACGGGTCTTGAGGGGTTTTTGGCGGCCGC

Not I

Restriction enzymes: italics and underlined

T7 polymerase promoter: upper case letter, bold and underlined

Additional three G nucleotides: upper case letter and underlined

Trailer sequence with genomic sequence: lower case letter

Sequence of the open reading frame of the enhanced green fluorescent protein in antisense orientation: upper case letter, bold

Leader sequence with genomic sequence: lower case letter and underlined

Hepatitis delta ribozyme sequence: lower case letter, underlined, and bold

T7 terminator sequence: upper case letter

Figure 30

NP protein alignment

		1	50
SEQ ID NO:3 (NP)	(1)	MSEVFNEYQALQEQLVKPAVERPPDVASTGLLRAEIPVCVTLSQDPGERWS	
SEQ ID NO:54 (NP)	(1)	MSEVFNEYQALQEQLVKENVRRPPDVASTGLLRAEIPVCVTLSQDPGERWS	
SEQ ID NO:66 (NP)	(1)	MSEVFNEYQALQEQLVKPAVERPPDVASTGLLRAEIPVCVTLSQDPGERWS	
SEQ ID NO:78 (NP)	(1)	MSEVFNEYQALQEQLVKPAVERPPDVASTGLLRAEIPVCVTLSQDPGERWS	
		51	100
SEQ ID NO:3 (NP)	(51)	LACLNIIRNLASDSSTTPMKQGAISLLSLHSDNMRRAHATLAASADASLT	
SEQ ID NO:54 (NP)	(51)	LACLNIIRNLASDSSTTPMKQGAISLLSLHSDNMRRAHATLAASADASLT	
SEQ ID NO:66 (NP)	(51)	LACLNIIRNLASDSSTTPMKQGAISLLSLHSDNMRRAHATLAASADASLT	
SEQ ID NO:78 (NP)	(51)	LACLNIIRNLASDSSTTPMKQGAISLLSLHSDNMRRAHATLAASADASLT	
		101	150
SEQ ID NO:3 (NP)	(101)	ILEVDEVDIENGLIKFNARGVSVSKRSNQLLAIADDPKSCSNGHPFLDT	
SEQ ID NO:54 (NP)	(101)	ILEVDEVDIENGLIKFNARGVSVSKRSNQLLAIADDPKSCSNGHPFLDT	
SEQ ID NO:66 (NP)	(101)	ILEVDEVDIENGLIKFNARGVSVSKRSNQLLAIADDPKSCSNGHPFLDT	
SEQ ID NO:78 (NP)	(101)	ILEVDEVDIENGLIKFNARGVSVSKRSNQLLAIADDPKSCSNGHPFLDT	
		151	200
SEQ ID NO:3 (NP)	(151)	DIETRDPLDLEETIDRLQGIAGIIVWSAINKMTAPDTASESHSKRLAKYQ	
SEQ ID NO:54 (NP)	(151)	DIETRDPLDLEETIDRLQGIAGIIVWSAINKMTAPDTASESHSKRLAKYQ	
SEQ ID NO:66 (NP)	(151)	DIETRDPLDLEETIDRLQGIAGIIVWSAINKMTAPDTASESHSKRLAKYQ	
SEQ ID NO:78 (NP)	(151)	DIETRDPLDLEETIDRLQGIAGIIVWSAINKMTAPDTASESHSKRLAKYQ	
		201	250
SEQ ID NO:3 (NP)	(201)	QQGRLVKQVLLHSVYVTEFPMVIRGSLVLAQFMVSECKRASAMGGDTSEY	
SEQ ID NO:54 (NP)	(201)	QQGRLVKQVLLHSVYVTEFPMVIRGSLVLAQFMVSECKRASAMGGDTSEY	
SEQ ID NO:66 (NP)	(201)	QQGRLVKQVLLHSVYVTEFPMVIRGSLVLAQFMVSECKRASAMGGDTSEY	
SEQ ID NO:78 (NP)	(201)	QQGRLVKQVLLHSVYVTEFPMVIRGSLVLAQFMVSECKRASAMGGDTSEY	
		251	300
SEQ ID NO:3 (NP)	(251)	YAMVGDISLYIKHAGLTAFPLTLKFGVGTQYPTLAMSVPFSDLERLAALI	
SEQ ID NO:54 (NP)	(251)	YAMVGDISLYIKHAGLTAFPLTLKFGVGTQYPTLAMSVPFSDLERLAALI	
SEQ ID NO:66 (NP)	(251)	YAMVGDISLYIKHAGLTAFPLTLKFGVGTQYPTLAMSVPFSDLERLAALI	
SEQ ID NO:78 (NP)	(251)	YAMVGDISLYIKHAGLTAFPLTLKFGVGTQYPTLAMSVPFSDLERLAALI	
		301	350
SEQ ID NO:3 (NP)	(301)	RLYKTKGDNAPYMAFLEDSDMGNFAPANYSTMYSYANGIGTILEASVERY	
SEQ ID NO:54 (NP)	(301)	RLYKTKGDNAPYMAFLEDSDMGNFAPANYSTMYSYANGIGTILEASVERY	
SEQ ID NO:66 (NP)	(301)	RLYKTKGDNAPYMAFLEDSDMGNFAPANYSTMYSYANGIGTILEASVERY	
SEQ ID NO:78 (NP)	(301)	RLYKTKGDNAPYMAFLEDSDMGNFAPANYSTMYSYANGIGTILEASVERY	
		351	400
SEQ ID NO:3 (NP)	(351)	QYARDPTSENYFRLGVETAQSQQGAFDERTAREMGLTEESKQVRLIMS	
SEQ ID NO:54 (NP)	(351)	QYARDPTSENYFRLGVETAQSQQGAFDERTAREMGLTEESKQVRLIMS	
SEQ ID NO:66 (NP)	(351)	QYARDPTSENYFRLGVETAQSQQGAFDERTAREMGLTEESKQVRLIMS	
SEQ ID NO:78 (NP)	(351)	QYARDPTSENYFRLGVETAQSQQGAFDERTAREMGLTEESKQVRLIMS	
		401	450
SEQ ID NO:3 (NP)	(401)	VDMGPSSEVHEPSRPAPISQENRQPAQNSLTQCGTKPVPHQAPRADPD	
SEQ ID NO:54 (NP)	(401)	VDMGPSSEVHEPSRPAPISQENRQPAQNSLTQCGTKPVPHQAPRADPD	
SEQ ID NO:66 (NP)	(401)	VDMGPSSEVHEPSRPAPISQENRQPAQNSLTQCGTKPVPHQAPRADPD	
SEQ ID NO:78 (NP)	(401)	VDMGPSSEVHEPSRPAPISQENRQPAQNSLTQCGTKPVPHQAPRADPD	
		451	462
SEQ ID NO:3 (NP)	(451)	DIDPYENGLEW-	
SEQ ID NO:54 (NP)	(451)	DIDPYENGLEW-	
SEQ ID NO:66 (NP)	(451)	DIDPYENGLEW-	
SEQ ID NO:78 (NP)	(451)	DIDPYENGLEW-	

Protein sequence identity:

SEQ ID NO:3 v. SEQ ID NO:54: 99% sequence identity
 SEQ ID NO:3 v. SEQ ID NO:66: 93% sequence identity
 SEQ ID NO:3 v. SEQ ID NO:78: 93% sequence identity

DNA sequence identity:

SEQ ID NO:2 v. SEQ ID NO:53: 99% sequence identity
 SEQ ID NO:2 v. SEQ ID NO:65: 97% sequence identity
 SEQ ID NO:2 v. SEQ ID NO:77: 97% sequence identity

Figure 31

P protein alignment

		1	50
SEQ ID NO:5 (P)	(1)	MDFANDEEIAELLNLSTNYIKIQKSELKPPQTTGRPPVSGGNTNRNLTDL	
SEQ ID NO:56 (P)	(1)	MDFANDEEIAELLNLSTNYIKIQKSELKPPQTTGRPPVSGGNTNRNLTDL	
SEQ ID NO:68 (P)	(1)	MDFANDEEIAELLNLSTNYIKIQKSELKPPQTTGRPPVSGGNTNRNLTDL	
SEQ ID NO:80 (P)	(1)	MDFANDEEIAELLNLSTNYIKIQKSELKPPQTTGRPPVSGGNTNRNLTDL	
		51	100
SEQ ID NO:5 (P)	(51)	WEKETASQNTTPAQSTQTTQVQSDNEEEIKSESIDGHIKGTVNLQGV	
SEQ ID NO:56 (P)	(51)	WEKETASQNTTPAQSTQTTQVQSDNEEEIKSESIDGHIKGTVNLQGV	
SEQ ID NO:68 (P)	(51)	WEKETASQNTTPAQSTQTTQVQSDNEEEIKSESIDGHIKGTVNLQGV	
SEQ ID NO:80 (P)	(51)	WEKETASQNTTPAQSTQTTQVQSDNEEEIKSESIDGHIKGTVNLQGV	
		101	150
SEQ ID NO:5 (P)	(101)	PEQNQSRSSPGDLDLALNKLKGRINLSSMCKEIKGPRIGLPGSQAA	
SEQ ID NO:56 (P)	(101)	PEQNQSRSSPGDLDLALNKLKGRINLSSMCKEIKGPRIGLPGSQAA	
SEQ ID NO:68 (P)	(101)	PEQNQSRSSPGDLDLALNKLKGRINLSSMCKEIKGPRIGLPGSQAA	
SEQ ID NO:80 (P)	(101)	PEQNQSRSSPGDLDLALNKLKGRINLSSMCKEIKGPRIGLPGSQAA	
		151	200
SEQ ID NO:5 (P)	(151)	TQQATHPLAGDTPNMQATKALAKPHQEAINEFGNQDTGNIHLPPSMAPP	
SEQ ID NO:56 (P)	(151)	TQQATHPLAGDTPNMQATKALAKPHQEAINEFGNQDTGNIHLPPSMAPP	
SEQ ID NO:68 (P)	(151)	TQQATHPLAGDTPNMQATKALAKPHQEAINEFGNQDTGNIHLPPSMAPP	
SEQ ID NO:80 (P)	(151)	TQQATHPLAGDTPNMQATKALAKPHQEAINEFGNQDTGNIHLPPSMAPP	
		201	250
SEQ ID NO:5 (P)	(201)	ESLYGAIKNAPQFVFDQSMNVDAAGSVQLHSCAEMISRMVEVEVISKLEK	
SEQ ID NO:56 (P)	(201)	ESLYGAIKNAPQFVFDQSMNVDAAGSVQLHSCAEMISRMVEVEVISKLEK	
SEQ ID NO:68 (P)	(201)	ESLYGAIKNAPQFVFDQSMNVDAAGSVQLHSCAEMISRMVEVEVISKLEK	
SEQ ID NO:80 (P)	(201)	ESLYGAIKNAPQFVFDQSMNVDAAGSVQLHSCAEMISRMVEVEVISKLEK	
		251	300
SEQ ID NO:5 (P)	(251)	LESRLNDIAKVVTFTPLIRNDINQLKATTALMENQIASIQILDPGNAGVR	
SEQ ID NO:56 (P)	(251)	LESRLNDIAKVVTFTPLIRNDINQLKATTALMENQIASIQILDPGNAGVR	
SEQ ID NO:68 (P)	(251)	LESRLNDIAKVVTFTPLIRNDINQLKATTALMENQIASIQILDPGNAGVR	
SEQ ID NO:80 (P)	(251)	LESRLNDIAKVVTFTPLIRNDINQLKATTALMENQIASIQILDPGNAGVR	
		301	350
SEQ ID NO:5 (P)	(301)	SLSEMKSVTKKAAYVIAGFGDDPTQIIIEGIMAKDALGKPVVPTSVIAAK	
SEQ ID NO:56 (P)	(301)	SLSEMKSVTKKAAYVIAGFGDDPTQIIIEGIMAKDALGKPVVPTSVIAAK	
SEQ ID NO:68 (P)	(301)	SLSEMKSVTKKAAYVIAGFGDDPTQIIIEGIMAKDALGKPVVPTSVIAAK	
SEQ ID NO:80 (P)	(301)	SLSEMKSVTKKAAYVIAGFGDDPTQIIIEGIMAKDALGKPVVPTSVIAAK	
		351	400
SEQ ID NO:5 (P)	(351)	AQTSSGVSEGEIEGLIALVETLVNDKKAANKLIKIMIDQVKSHADYARVKQ	
SEQ ID NO:56 (P)	(351)	AQTSSGVSEGEIEGLIALVETLVNDKKAANKLIKIMIDQVKSHADYARVKQ	
SEQ ID NO:68 (P)	(351)	AQTSSGVSEGEIEGLIALVETLVNDKKAANKLIKIMIDQVKSHADYARVKQ	
SEQ ID NO:80 (P)	(351)	AQTSSGVSEGEIEGLIALVETLVNDKKAANKLIKIMIDQVKSHADYARVKQ	
		401	
SEQ ID NO:5 (P)	(401)	AIYNA-	
SEQ ID NO:56 (P)	(401)	AIYNA-	
SEQ ID NO:68 (P)	(401)	AIYNA-	
SEQ ID NO:80 (P)	(401)	AIYNA-	

Protein sequence identity:

SEQ ID NO:5 v. SEQ ID NO:56: 99% sequence identity
 SEQ ID NO:5 v. SEQ ID NO:68: 96% sequence identity
 SEQ ID NO:5 v. SEQ ID NO:80: 95% sequence identity

DNA sequence identity:

SEQ ID NO:4 v. SEQ ID NO:55: 99% sequence identity
 SEQ ID NO:4 v. SEQ ID NO:67: 96% sequence identity
 SEQ ID NO:4 v. SEQ ID NO:79: 96% sequence identity

Figure 32

M protein alignment

		1	50
SEQ ID NO: 58 (M)	(1)	MAYTTFLKLVDEGDMSSLLSPFVLKRTDRTGKELQPOVRVDSIGDVQN	
SEQ ID NO: 7 (M)	(1)	MAYTTFLKLVDEGDMSSLLSPFVLKRTDRTGKELQPOVRVDSIGDVQN	
SEQ ID NO: 70 (M)	(1)	MAYTTFLKLVDEGDMSSLLSPFVLKRTDRTGKELQPOVRVDSIGDVQN	
SEQ ID NO: 82 (M)	(1)	MAYTTFLKLVDEGDMSSLLSPFVLKRTDRTGKELQPOVRVDSIGDVQN	
		51	100
SEQ ID NO: 58 (M)	(51)	AKESSEIFVTLGGFIQAIKESDGRSKFFHPKIDFPETVTAGLVVVGAIRM	
SEQ ID NO: 7 (M)	(51)	AKESSEIFVTLGGFIQAIKESDGRSKFFHPKIDFPETVTAGLVVVGAIRM	
SEQ ID NO: 70 (M)	(51)	AKESSEIFVTLGGFIQAIKESDGRSKFFHPKIDFPETVTAGLVVVGAIRM	
SEQ ID NO: 82 (M)	(51)	AKESSEIFVTLGGFIQAIKESDGRSKFFHPKIDFPETVTAGLVVVGAIRM	
		101	150
SEQ ID NO: 58 (M)	(101)	MADVNTIISNDALALEITVKKSATSQEKMTVMFHNSPPELRATITIRAGGF	
SEQ ID NO: 7 (M)	(101)	MADVNTIISNDALALEITVKKSATSQEKMTVMFHNSPPELRATITIRAGGF	
SEQ ID NO: 70 (M)	(101)	MADVNTIISNDALALEITVKKSATSQEKMTVMFHNSPPELRATITIRAGGF	
SEQ ID NO: 82 (M)	(101)	MADVNTIISNDALALEITVKKSATSQEKMTVMFHNSPPELRATITIRAGGF	
		151	200
SEQ ID NO: 58 (M)	(151)	ISNADENIKCASKLTAGVQYIFPMPFVSITKLHNGKLYRVPKSIHSISST	
SEQ ID NO: 7 (M)	(151)	ISNADENIKCASKLTAGVQYIFPMPFVSITKLHNGKLYRVPKSIHSISST	
SEQ ID NO: 70 (M)	(151)	ISNADENIKCASKLTAGVQYIFPMPFVSITKLHNGKLYRVPKSIHSISST	
SEQ ID NO: 82 (M)	(151)	ISNADENIKCASKLTAGVQYIFPMPFVSITKLHNGKLYRVPKSIHSISST	
		201	250
SEQ ID NO: 58 (M)	(201)	LLYSVMLEVGFKVDIGKDHFPQAMLKIVTIGDADTYWGFARFHLGNPKKT	
SEQ ID NO: 7 (M)	(201)	LLYSVMLEVGFKVDIGKDHFPQAMLKIVTIGDADTYWGFARFHLGNPKKT	
SEQ ID NO: 70 (M)	(201)	LLYSVMLEVGFKVDIGKDHFPQAMLKIVTIGDADTYWGFARFHLGNPKKT	
SEQ ID NO: 82 (M)	(201)	LLYSVMLEVGFKVDIGKDHFPQAMLKIVTIGDADTYWGFARFHLGNPKKT	
		251	300
SEQ ID NO: 58 (M)	(251)	SSKCKPRTLDELKTVKXNMGKLELEDLWGPTIIVVQITCKSSKYAQGFPS	
SEQ ID NO: 7 (M)	(251)	SSKCKPRTLDELKTVKXNMGKLELEDLWGPTIIVVQITCKSSKYAQGFPS	
SEQ ID NO: 70 (M)	(251)	SSKCKPRTLDELKTVKXNMGKLELEDLWGPTIIVVQITCKSSKYAQGFPS	
SEQ ID NO: 82 (M)	(251)	SSKCKPRTLDELKTVKXNMGKLELEDLWGPTIIVVQITCKSSKYAQGFPS	
		301	350
SEQ ID NO: 58 (M)	(301)	SNGTCCLPISRSAPFLGKLLWSCSATIGDATVVIQSSKGEELRESDDLEI	
SEQ ID NO: 7 (M)	(301)	SNGTCCLPISRSAPFLGKLLWSCSATIGDATVVIQSSKGEELRESDDLEI	
SEQ ID NO: 70 (M)	(301)	SNGTCCLPISRSAPFLGKLLWSCSATIGDATVVIQSSKGEELRESDDLEI	
SEQ ID NO: 82 (M)	(301)	SNGTCCLPISRSAPFLGKLLWSCSATIGDATVVIQSSKGEELRESDDLEI	
		351	370
SEQ ID NO: 58 (M)	(351)	RGAVASKKRGLSSFPFKK-	
SEQ ID NO: 7 (M)	(351)	RGAVASKKRGLSSFPFKK-	
SEQ ID NO: 70 (M)	(351)	RGAVASKKRGLSSFPFKK-	
SEQ ID NO: 82 (M)	(351)	RGAVASKKRGLSSFPFKK-	

Protein sequence identity:

SEQ ID NO: 7 v. SEQ ID NO: 58:	99% sequence identity
SEQ ID NO: 7 v. SEQ ID NO: 70:	98% sequence identity
SEQ ID NO: 7 v. SEQ ID NO: 82:	98% sequence identity

DNA sequence identity:

SEQ ID NO: 6 v. SEQ ID NO: 57:	99% sequence identity
SEQ ID NO: 6 v. SEQ ID NO: 69:	97% sequence identity
SEQ ID NO: 6 v. SEQ ID NO: 81:	97% sequence identity

Figure 33

F protein alignment

		1	50
SEQ ID NO: 60 (F)	(1)	MGKISVYLINSVLLLVYPVNSIDNTLAPIGVASANEWQLAAYTTLSG	
SEQ ID NO: 72 (F)	(1)	MGKISVYLINSVLLLVYPVNSIDNTLAPIGVASANEWQLAAYTTLSG	
SEQ ID NO: 84 (F)	(1)	MGKISVYLINSVLLLVYPVNSIDNTLAPIGVASANEWQLAAYTTLSG	
SEQ ID NO: 9 (F)	(1)	MGKISVYLINSVLLLVYPVNSIDNTLAPIGVASANEWQLAAYTTLSG	
		51	100
SEQ ID NO: 60 (F)	(51)	TIAVRFLPVLFDNMTTCLEETITTYNTVNNILGFLKGNLDALLSSETYP	
SEQ ID NO: 72 (F)	(51)	TIAVRFLPVLFDNMTTCLEETITTYNTVNNILGFLKGNLDALLSSETYP	
SEQ ID NO: 84 (F)	(51)	TIAVRFLPVLFDNMTTCLEETITTYNTVNNILGFLKGNLDALLSSETYP	
SEQ ID NO: 9 (F)	(51)	TIAVRFLPVLFDNMTTCLEETITTYNTVNNILGFLKGNLDALLSSETYP	
		101	150
SEQ ID NO: 60 (F)	(101)	QTRLGAVIGSIALGVATSAQITAAVALKQACUNARNILALKEALSKTNE	
SEQ ID NO: 72 (F)	(101)	QTRLGAVIGSIALGVATSAQITAAVALKQACUNARNILALKEALSKTNE	
SEQ ID NO: 84 (F)	(101)	QTRLGAVIGSIALGVATSAQITAAVALKQACUNARNILALKEALSKTNE	
SEQ ID NO: 9 (F)	(101)	QTRLGAVIGSIALGVATSAQITAAVALKQACUNARNILALKEALSKTNE	
		151	200
SEQ ID NO: 60 (F)	(151)	AVKELSSGLQQTALALGKIQSFVNEEILPSINQLSCEVTANKLGVLISLY	
SEQ ID NO: 72 (F)	(151)	AVKELSSGLQQTALALGKIQSFVNEEILPSINQLSCEVTANKLGVLISLY	
SEQ ID NO: 84 (F)	(151)	AVKELSSGLQQTALALGKIQSFVNEEILPSINQLSCEVTANKLGVLISLY	
SEQ ID NO: 9 (F)	(151)	AVKELSSGLQQTALALGKIQSFVNEEILPSINQLSCEVTANKLGVLISLY	
		201	250
SEQ ID NO: 60 (F)	(201)	LEELTFTEGAGLTNPALTSLSYQALYNLCGNNHMLTQKIGIKQDVNSEL	
SEQ ID NO: 72 (F)	(201)	LEELTFTEGAGLTNPALTSLSYQALYNLCGNNHMLTQKIGIKQDVNSEL	
SEQ ID NO: 84 (F)	(201)	LEELTFTEGAGLTNPALTSLSYQALYNLCGNNHMLTQKIGIKQDVNSEL	
SEQ ID NO: 9 (F)	(201)	LEELTFTEGAGLTNPALTSLSYQALYNLCGNNHMLTQKIGIKQDVNSEL	
		251	300
SEQ ID NO: 60 (F)	(251)	YEAGLITQGVICGYDEQYQLNVIQVNPISIEVTGVATELVTVSVTTDKG	
SEQ ID NO: 72 (F)	(251)	YEAGLITQGVICGYDEQYQLNVIQVNPISIEVTGVATELVTVSVTTDKG	
SEQ ID NO: 84 (F)	(251)	YEAGLITQGVICGYDEQYQLNVIQVNPISIEVTGVATELVTVSVTTDKG	
SEQ ID NO: 9 (F)	(251)	YEAGLITQGVICGYDEQYQLNVIQVNPISIEVTGVATELVTVSVTTDKG	
		301	350
SEQ ID NO: 60 (F)	(301)	ECKAIVPQFVAESVETIERLDVASCKPSTTLYCRQVNTALPLVASCL	
SEQ ID NO: 72 (F)	(301)	ECKAIVPQFVAESVETIERLDVASCKPSTTLYCRQVNTALPLVASCL	
SEQ ID NO: 84 (F)	(301)	ECKAIVPQFVAESVETIERLDVASCKPSTTLYCRQVNTALPLVASCL	
SEQ ID NO: 9 (F)	(301)	ECKAIVPQFVAESVETIERLDVASCKPSTTLYCRQVNTALPLVASCL	
		351	400
SEQ ID NO: 60 (F)	(351)	RGNYDDCQYTFEIGALSSRYITLDGGVLVNCISIVCRCLNPSKILSQNTN	
SEQ ID NO: 72 (F)	(351)	RGNYDDCQYTFEIGALSSRYITLDGGVLVNCISIVCRCLNPSKILSQNTN	
SEQ ID NO: 84 (F)	(351)	RGNYDDCQYTFEIGALSSRYITLDGGVLVNCISIVCRCLNPSKILSQNTN	
SEQ ID NO: 9 (F)	(351)	RGNYDDCQYTFEIGALSSRYITLDGGVLVNCISIVCRCLNPSKILSQNTN	
		401	450
SEQ ID NO: 60 (F)	(401)	AAVTVVDATICKTIQLDDIQLQLEGSLSSVYARNISIEISQVTTSGSLDI	
SEQ ID NO: 72 (F)	(401)	AAVTVVDATICKTIQLDDIQLQLEGSLSSVYARNISIEISQVTTSGSLDI	
SEQ ID NO: 84 (F)	(401)	AAVTVVDATICKTIQLDDIQLQLEGSLSSVYARNISIEISQVTTSGSLDI	
SEQ ID NO: 9 (F)	(401)	AAVTVVDATICKTIQLDDIQLQLEGSLSSVYARNISIEISQVTTSGSLDI	
		451	500
SEQ ID NO: 60 (F)	(451)	ESSEIGNINNTVNRVEDLIHQSEEWLAKVNPPIVNTTLIVLCVLSALAVI	
SEQ ID NO: 72 (F)	(451)	ESSEIGNINNTVNRVEDLIHQSEEWLAKVNPPIVNTTLIVLCVLSALAVI	
SEQ ID NO: 84 (F)	(451)	ESSEIGNINNTVNRVEDLIHQSEEWLAKVNPPIVNTTLIVLCVLSALAVI	
SEQ ID NO: 9 (F)	(451)	ESSEIGNINNTVNRVEDLIHQSEEWLAKVNPPIVNTTLIVLCVLSALAVI	
		501	544
SEQ ID NO: 60 (F)	(501)	WLAVLTATIIYLRTEKLTISALAVNTTIQSNFYVNGTKHESKF-	
SEQ ID NO: 72 (F)	(501)	WLAVLTATIIYLRTEKLTISALAVNTTIQSNFYVNGTKHESKF-	
SEQ ID NO: 84 (F)	(501)	WLAVLTATIIYLRTEKLTISALAVNTTIQSNFYVNGTKHESKF-	
SEQ ID NO: 9 (F)	(501)	WLAVLTATIIYLRTEKLTISALAVNTTIQSNFYVNGTKHESKF-	

Protein sequence identity:

SEQ ID NO: 9 v. SEQ ID NO: 60: 99% sequence identity
 SEQ ID NO: 9 v. SEQ ID NO: 72: 98% sequence identity
 SEQ ID NO: 9 v. SEQ ID NO: 84: 98% sequence identity

DNA sequence identity:

SEQ ID NO: 8 v. SEQ ID NO: 59: 99% sequence identity
 SEQ ID NO: 8 v. SEQ ID NO: 71: 97% sequence identity
 SEQ ID NO: 8 v. SEQ ID NO: 83: 97% sequence identity

Figure 34 (1/2)

HN protein alignment

		1	50
SEQ ID NO: 11 (HN)	(1)	MSNIASSLENIVEQDSKNTTWRAI FWSVLLI ITTCLALSISIVQIGNL	
SEQ ID NO: 62 (HN)	(1)	MSNIASSLENIVEQDSKNTTWRAI FWSVLLI ITTCLALSISIVQIGNL	
SEQ ID NO: 74 (HN)	(1)	MSNIASSLENIVEQDSKNTTWRAI FWSVLLI ITTCLALSISIVQIGNL	
SEQ ID NO: 86 (HN)	(1)	MSNIASSLENIVEQDSKNTTWRAI FWSVLLI ITTCLALSISIVQIGNL	
		51	100
SEQ ID NO: 11 (HN)	(51)	KIPSVGDLADEVVTPLKTTLEDTLRKPIQINDIFRIVALDIPLQVTSIQ	
SEQ ID NO: 62 (HN)	(51)	KIPSVGDLADEVVTPLKTTLEDTLRKPIQINDIFRIVALDIPLQVTSIQ	
SEQ ID NO: 74 (HN)	(51)	KIPSVGDLADEVVTPLKTTLEDTLRKPIQINDIFRIVALDIPLQVTSIQ	
SEQ ID NO: 86 (HN)	(51)	KIPSVGDLADEVVTPLKTTLEDTLRKPIQINDIFRIVALDIPLQVTSIQ	
		101	150
SEQ ID NO: 11 (HN)	(101)	KDLASQFPMELIDSLNAIKLNGCTNLI IPTSDKEYAGGIGNPVFTVDAGGS	
SEQ ID NO: 62 (HN)	(101)	KDLASQFPMELIDSLNAIKLNGCTNLI IPTSDKEYAGGIGNPVFTVDAGGS	
SEQ ID NO: 74 (HN)	(101)	KDLASQFPMELIDSLNAIKLNGCTNLI IPTSDKEYAGGIGNPVFTVDAGGS	
SEQ ID NO: 86 (HN)	(101)	KDLASQFPMELIDSLNAIKLNGCTNLI IPTSDKEYAGGIGNPVFTVDAGGS	
		151	200
SEQ ID NO: 11 (HN)	(151)	IGFKQFSLIENPFIAGPTTTTGCTRIPTFMSESHWCYSHNIIAAGCCQD	
SEQ ID NO: 62 (HN)	(151)	IGFKQFSLIENPFIAGPTTTTGCTRIPTFMSESHWCYSHNIIAAGCCQD	
SEQ ID NO: 74 (HN)	(151)	IGFKQFSLIENPFIAGPTTTTGCTRIPTFMSESHWCYSHNIIAAGCCQD	
SEQ ID NO: 86 (HN)	(151)	IGFKQFSLIENPFIAGPTTTTGCTRIPTFMSESHWCYSHNIIAAGCCQD	
		201	250
SEQ ID NO: 11 (HN)	(201)	ASASSMYISMGVLVHVSSEGTPIFLTASELIDGYNKKSCEIVATQFGCD	
SEQ ID NO: 62 (HN)	(201)	ASASSMYISMGVLVHVSSEGTPIFLTASELIDGYNKKSCEIVATQFGCD	
SEQ ID NO: 74 (HN)	(201)	ASASSMYISMGVLVHVSSEGTPIFLTASELIDGYNKKSCEIVATQFGCD	
SEQ ID NO: 86 (HN)	(201)	ASASSMYISMGVLVHVSSEGTPIFLTASELIDGYNKKSCEIVATQFGCD	
		251	300
SEQ ID NO: 11 (HN)	(251)	ILCSIVTEKEGDDYWSNTPTPMHGRFSPNGSFVEAEIPVGSMSFSEFAN	
SEQ ID NO: 62 (HN)	(251)	ILCSIVTEKEGDDYWSNTPTPMHGRFSPNGSFVEAEIPVGSMSFSEFAN	
SEQ ID NO: 74 (HN)	(251)	ILCSIVTEKEGDDYWSNTPTPMHGRFSPNGSFVEAEIPVGSMSFSEFAN	
SEQ ID NO: 86 (HN)	(251)	ILCSIVTEKEGDDYWSNTPTPMHGRFSPNGSFVEAEIPVGSMSFSEFAN	
		301	350
SEQ ID NO: 11 (HN)	(301)	YPAVGSSEIVKDRILFPIYGNIGQTSPEFTLVKYGLEFVSTPTTVQSSW	
SEQ ID NO: 62 (HN)	(301)	YPAVGSSEIVKDRILFPIYGNIGQTSPEFTLVKYGLEFVSTPTTVQSSW	
SEQ ID NO: 74 (HN)	(301)	YPAVGSSEIVKDRILFPIYGNIGQTSPEFTLVKYGLEFVSTPTTVQSSW	
SEQ ID NO: 86 (HN)	(301)	YPAVGSSEIVKDRILFPIYGNIGQTSPEFTLVKYGLEFVSTPTTVQSSW	
		351	400
SEQ ID NO: 11 (HN)	(351)	TYDQVKAAAYRDPYISGRFWAQVILSCALDAVDLSSCIVKIMNSSTVMMAA	
SEQ ID NO: 62 (HN)	(351)	TYDQVKAAAYRDPYISGRFWAQVILSCALDAVDLSSCIVKIMNSSTVMMAA	
SEQ ID NO: 74 (HN)	(351)	TYDQVKAAAYRDPYISGRFWAQVILSCALDAVDLSSCIVKIMNSSTVMMAA	
SEQ ID NO: 86 (HN)	(351)	TYDQVKAAAYRDPYISGRFWAQVILSCALDAVDLSSCIVKIMNSSTVMMAA	
		401	450
SEQ ID NO: 11 (HN)	(401)	EGRIKIKIGIDYFYQSSSNWPLAFVTKLPQELADTNSIWLNSIPIPIQ	
SEQ ID NO: 62 (HN)	(401)	EGRIKIKIGIDYFYQSSSNWPLAFVTKLPQELADTNSIWLNSIPIPIQ	
SEQ ID NO: 74 (HN)	(401)	EGRIKIKIGIDYFYQSSSNWPLAFVTKLPQELADTNSIWLNSIPIPIQ	
SEQ ID NO: 86 (HN)	(401)	EGRIKIKIGIDYFYQSSSNWPLAFVTKLPQELADTNSIWLNSIPIPIQ	
		451	500
SEQ ID NO: 11 (HN)	(451)	SKFPRPSYSENYCTKPAVCATCVTCVYSIDIWPLTSSSSLPSTIWIQGYL	
SEQ ID NO: 62 (HN)	(451)	SKFPRPSYSENYCTKPAVCATCVTCVYSIDIWPLTSSSSLPSTIWIQGYL	
SEQ ID NO: 74 (HN)	(451)	SKFPRPSYSENYCTKPAVCATCVTCVYSIDIWPLTSSSSLPSTIWIQGYL	
SEQ ID NO: 86 (HN)	(451)	SKFPRPSYSENYCTKPAVCATCVTCVYSIDIWPLTSSSSLPSTIWIQGYL	
		501	550
SEQ ID NO: 11 (HN)	(501)	DAPVGRITYPRFGIANQSHWYLQEDILPTSTASAYSTTTCFKNTARNRVFC	
SEQ ID NO: 62 (HN)	(501)	DAPVGRITYPRFGIANQSHWYLQEDILPTSTASAYSTTTCFKNTARNRVFC	
SEQ ID NO: 74 (HN)	(501)	DAPVGRITYPRFGIANQSHWYLQEDILPTSTASAYSTTTCFKNTARNRVFC	
SEQ ID NO: 86 (HN)	(501)	DAPVGRITYPRFGIANQSHWYLQEDILPTSTASAYSTTTCFKNTARNRVFC	
		551	578
SEQ ID NO: 11 (HN)	(551)	VTIAEFADGLFGYRIITPQLXELVRN-	
SEQ ID NO: 62 (HN)	(551)	VTIAEFADGLFGYRIITPQLXELVRN-	
SEQ ID NO: 74 (HN)	(551)	VTIAEFADGLFGYRIITPQLXELVRN-	
SEQ ID NO: 86 (HN)	(551)	VTIAEFADGLFGYRIITPQLXELVRN-	

Figure 34 (2/2)

Protein sequence identity:

SEQ ID NO:11	v. SEQ ID NO:62:	99% sequence identity
SEQ ID NO:11	v. SEQ ID NO:74:	99% sequence identity
SEQ ID NO:11	v. SEQ ID NO:86:	99% sequence identity

DNA sequence identity:

SEQ ID NO:10	v. SEQ ID NO:61:	99% sequence identity
SEQ ID NO:10	v. SEQ ID NO:73:	97% sequence identity
SEQ ID NO:10	v. SEQ ID NO:85:	97% sequence identity

Figure 35 (1/5)

L protein alignment

	1	50
SEQ ID NO:13 (L1)	(1) MEGDLYTNMIRKQVDLI IQPEVHLDSPFI INKIAL LNWRLSGLEMPADLRQ	
SEQ ID NO:14 (L2)	(1) -----MDIKQVDLI IQPEVHLDSPFI INKIAL LNWRLSGLEMPADLRQ	
SEQ ID NO:64 (L)	(1) -----MDIKQVDLI IQPEVHLDSPFI INKIAL LNWRLSGLEMPADLRQ	
SEQ ID NO:76 (L)	(1) -----MUKQVDLI IQPEVHLDSPFI INKIAL LNWRLSGLEMPADLRQ	
SEQ ID NO:88 (L)	(1) -----MUKQVDLI IQPEVHLDSPFI INKIAL LNWRLSGLEMPADLRQ	
	51	100
SEQ ID NO:13 (L1)	(51) KSVVMHI PDHILEKSEYRIKHRLGFIKSDITHYCOYFNINLANIDPITTF	
SEQ ID NO:14 (L2)	(43) KSVVMHI PDHILEKSEYRIKHRLGFIKSDITHYCOYFNINLANIDPITTF	
SEQ ID NO:64 (L)	(43) KSVVMHI PDHILEKSEYRIKHRLGFIKSDITHYCOYFNINLANIDPITTF	
SEQ ID NO:76 (L)	(43) KSVVMHI PDHILEKSEYRIKHRLGFIKSDITHYCOYFNINLANIDPITTF	
SEQ ID NO:88 (L)	(43) KSVVMHI PDHILEKSEYRIKHRLGFIKSDITHYCOYFNINLANIDPITTF	
	101	150
SEQ ID NO:13 (L1)	(101) KSLYWLGRLTIASAGTFPRMKDRILCTVGSERFGHKIQDLFSLLSHKLGVN	
SEQ ID NO:14 (L2)	(93) KSLYWLGRLTIASAGTFPRMKDRILCTVGSERFGHKIQDLFSLLSHKLGVN	
SEQ ID NO:64 (L)	(93) KSLYWLGRLTIASAGTFPRMKDRILCTVGSERFGHKIQDLFSLLSHKLGVN	
SEQ ID NO:76 (L)	(93) KSLYWLGRLTIASAGTFPRMKDRILCTVGSERFGHKIQDLFSLLSHKLGVN	
SEQ ID NO:88 (L)	(93) KSLYWLGRLTIASAGTFPRMKDRILCTVGSERFGHKIQDLFSLLSHKLGVN	
	151	200
SEQ ID NO:13 (L1)	(151) GDLFWQSLSGTTLTASPLSPICQFVSDIKSAVTTFWSEARWSEWLIKQY	
SEQ ID NO:14 (L2)	(143) GDLFWQSLSGTTLTASPLSPICQFVSDIKSAVTTFWSEARWSEWLIKQY	
SEQ ID NO:64 (L)	(143) GDLFWQSLSGTTLTASPLSPICQFVSDIKSAVTTFWSEARWSEWLIKQY	
SEQ ID NO:76 (L)	(143) GDLFWQSLSGTTLTASPLSPICQFVSDIKSAVTTFWSEARWSEWLIKQY	
SEQ ID NO:88 (L)	(143) GDLFWQSLSGTTLTASPLSPICQFVSDIKSAVTTFWSEARWSEWLIKQY	
	201	250
SEQ ID NO:13 (L1)	(201) MRYLIKQSEITTSNANLREIIRKEWGLVGI TPDVLVLPDRVNSLALTFE	
SEQ ID NO:14 (L2)	(193) MRYLIKQSEITTSNANLREIIRKEWGLVGI TPDVLVLPDRVNSLALTFE	
SEQ ID NO:64 (L)	(193) MRYLIKQSEITTSNANLREIIRKEWGLVGI TPDVLVLPDRVNSLALTFE	
SEQ ID NO:76 (L)	(193) MRYLIKQSEITTSNANLREIIRKEWGLVGI TPDVLVLPDRVNSLALTFE	
SEQ ID NO:88 (L)	(193) MRYLIKQSEITTSNANLREIIRKEWGLVGI TPDVLVLPDRVNSLALTFE	
	251	300
SEQ ID NO:13 (L1)	(251) MVLMTSDVLESRDNIIVLGRISTFLQPVVSRLEVLFDLVDSLAKLGLDTI	
SEQ ID NO:14 (L2)	(243) MVLMTSDVLESRDNIIVLGRISTFLQPVVSRLEVLFDLVDSLAKLGLDTI	
SEQ ID NO:64 (L)	(243) MVLMTSDVLESRDNIIVLGRISTFLQPVVSRLEVLFDLVDSLAKLGLDTI	
SEQ ID NO:76 (L)	(243) MVLMTSDVLESRDNIIVLGRISTFLQPVVSRLEVLFDLVDSLAKLGLDTI	
SEQ ID NO:88 (L)	(243) MVLMTSDVLESRDNIIVLGRISTFLQPVVSRLEVLFDLVDSLAKLGLDTI	
	301	350
SEQ ID NO:13 (L1)	(301) YEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMELDNTLSKRVDPKHKY	
SEQ ID NO:14 (L2)	(293) YEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMELDNTLSKRVDPKHKY	
SEQ ID NO:64 (L)	(293) YEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMELDNTLSKRVDPKHKY	
SEQ ID NO:76 (L)	(293) YEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMELDNTLSKRVDPKHKY	
SEQ ID NO:88 (L)	(293) YEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMELDNTLSKRVDPKHKY	
	351	400
SEQ ID NO:13 (L1)	(351) TIMSIIRQCFSNLDVQAEMLCMLRFGHPMLTAPDAAAKVKKAMCAPK	
SEQ ID NO:14 (L2)	(343) TIMSIIRQCFSNLDVQAEMLCMLRFGHPMLTAPDAAAKVKKAMCAPK	
SEQ ID NO:64 (L)	(343) TIMSIIRQCFSNLDVQAEMLCMLRFGHPMLTAPDAAAKVKKAMCAPK	
SEQ ID NO:76 (L)	(343) TIMSIIRQCFSNLDVQAEMLCMLRFGHPMLTAPDAAAKVKKAMCAPK	
SEQ ID NO:88 (L)	(343) TIMSIIRQCFSNLDVQAEMLCMLRFGHPMLTAPDAAAKVKKAMCAPK	
	401	450
SEQ ID NO:13 (L1)	(401) LVRHDTILQTLSEFFKGI INCYRSHSGLWPNVPEPSIYDDDLRQLYLE	
SEQ ID NO:14 (L2)	(393) LVRHDTILQTLSEFFKGI INCYRSHSGLWPNVPEPSIYDDDLRQLYLE	
SEQ ID NO:64 (L)	(393) LVRHDTILQTLSEFFKGI INCYRSHSGLWPNVPEPSIYDDDLRQLYLE	
SEQ ID NO:76 (L)	(393) LVRHDTILQTLSEFFKGI INCYRSHSGLWPNVPEPSIYDDDLRQLYLE	
SEQ ID NO:88 (L)	(393) LVRHDTILQTLSEFFKGI INCYRSHSGLWPNVPEPSIYDDDLRQLYLE	
	451	500
SEQ ID NO:13 (L1)	(451) ARISHHFMLKNYKSLMIEPKRSIDYDLHDDLSTFLKDRATCRPKSQWDV	
SEQ ID NO:14 (L2)	(443) ARISHHFMLKNYKSLMIEPKRSIDYDLHDDLSTFLKDRATCRPKSQWDV	
SEQ ID NO:64 (L)	(443) ARISHHFMLKNYKSLMIEPKRSIDYDLHDDLSTFLKDRATCRPKSQWDV	
SEQ ID NO:76 (L)	(443) ARISHHFMLKNYKSLMIEPKRSIDYDLHDDLSTFLKDRATCRPKSQWDV	
SEQ ID NO:88 (L)	(443) ARISHHFMLKNYKSLMIEPKRSIDYDLHDDLSTFLKDRATCRPKSQWDV	

Figure 35 (2/5)

	501	550
SEQ ID NO:13 (L1)	(501) IFKSLKRSNTQSYMDRIKSNRLIDFLDSAEFDPEKEFAYVTMDYLK	
SEQ ID NO:14 (L2)	(493) IFKSLKRSNTQSYMDRIKSNRLIDFLDSAEFDPEKEFAYVTMDYLK	
SEQ ID NO:64 (L)	(493) IFKSLKRSNTQSYMDRIKSNRLIDFLDSAEFDPEKEFAYVTMDYLK	
SEQ ID NO:76 (L)	(493) IFKSLKRSNTQSYMDRIKSNRLIDFLDSAEFDPEKEFAYVTMDYLK	
SEQ ID NO:88 (L)	(493) IFKSLKRSNTQSYMDRIKSNRLIDFLDSAEFDPEKEFAYVTMDYLK	
	551	600
SEQ ID NO:13 (L1)	(551) DNEPCASYSLKKEIKTTCRIFAKMTFNMRSQVILESLSKHICKFFKE	
SEQ ID NO:14 (L2)	(543) DNEPCASYSLKKEIKTTCRIFAKMTFNMRSQVILESLSKHICKFFKE	
SEQ ID NO:64 (L)	(543) DNEPCASYSLKKEIKTTCRIFAKMTFNMRSQVILESLSKHICKFFKE	
SEQ ID NO:76 (L)	(543) DNEPCASYSLKKEIKTTCRIFAKMTFNMRSQVILESLSKHICKFFKE	
SEQ ID NO:88 (L)	(543) DNEPCASYSLKKEIKTTCRIFAKMTFNMRSQVILESLSKHICKFFKE	
	601	650
SEQ ID NO:13 (L1)	(601) NGVSEQLSLTKELLAMSQLSPKVTTLQDTASRNVGNSQSQTATNPSEK	
SEQ ID NO:14 (L2)	(593) NGVSEQLSLTKELLAMSQLSPKVTTLQDTASRNVGNSQSQTATNPSEK	
SEQ ID NO:64 (L)	(593) NGVSEQLSLTKELLAMSQLSPKVTTLQDTASRNVGNSQSQTATNPSEK	
SEQ ID NO:76 (L)	(593) NGVSEQLSLTKELLAMSQLSPKVTTLQDTASRNVGNSQSQTATNPSEK	
SEQ ID NO:88 (L)	(593) NGVSEQLSLTKELLAMSQLSPKVTTLQDTASRNVGNSQSQTATNPSEK	
	651	700
SEQ ID NO:13 (L1)	(651) HSTPNQMSLENKTVVATFLTTDLKCYCQWRYSTIKLFAQALNQLFGID	
SEQ ID NO:14 (L2)	(643) HSTPNQMSLENKTVVATFLTTDLKCYCQWRYSTIKLFAQALNQLFGID	
SEQ ID NO:64 (L)	(643) HSTPNQMSLENKTVVATFLTTDLKCYCQWRYSTIKLFAQALNQLFGID	
SEQ ID NO:76 (L)	(643) HSTPNQMSLENKTVVATFLTTDLKCYCQWRYSTIKLFAQALNQLFGID	
SEQ ID NO:88 (L)	(643) HSTPNQMSLENKTVVATFLTTDLKCYCQWRYSTIKLFAQALNQLFGID	
	701	750
SEQ ID NO:13 (L1)	(701) HGFENIHLKLMNSTLFGDPYSPPEDPTLEDIDKAPNDIFIVSPGGIE	
SEQ ID NO:14 (L2)	(693) HGFENIHLKLMNSTLFGDPYSPPEDPTLEDIDKAPNDIFIVSPGGIE	
SEQ ID NO:64 (L)	(693) HGFENIHLKLMNSTLFGDPYSPPEDPTLEDIDKAPNDIFIVSPGGIE	
SEQ ID NO:76 (L)	(693) HGFENIHLKLMNSTLFGDPYSPPEDPTLEDIDKAPNDIFIVSPGGIE	
SEQ ID NO:88 (L)	(693) HGFENIHLKLMNSTLFGDPYSPPEDPTLEDIDKAPNDIFIVSPGGIE	
	751	800
SEQ ID NO:13 (L1)	(751) GLCQKMTMISISAIHCVAEKIGARVAMVQGNQVIAITKELFGEKAC	
SEQ ID NO:14 (L2)	(743) GLCQKMTMISISAIHCVAEKIGARVAMVQGNQVIAITKELFGEKAC	
SEQ ID NO:64 (L)	(743) GLCQKMTMISISAIHCVAEKIGARVAMVQGNQVIAITKELFGEKAC	
SEQ ID NO:76 (L)	(743) GLCQKMTMISISAIHCVAEKIGARVAMVQGNQVIAITKELFGEKAC	
SEQ ID NO:88 (L)	(743) GLCQKMTMISISAIHCVAEKIGARVAMVQGNQVIAITKELFGEKAC	
	801	850
SEQ ID NO:13 (L1)	(801) DVRDELDELQGVFFDEFKRNVAIGHNLKINETIQSQSFVYSKRIFTEG	
SEQ ID NO:14 (L2)	(793) DVRDELDELQGVFFDEFKRNVAIGHNLKINETIQSQSFVYSKRIFTEG	
SEQ ID NO:64 (L)	(793) DVRDELDELQGVFFDEFKRNVAIGHNLKINETIQSQSFVYSKRIFTEG	
SEQ ID NO:76 (L)	(793) DVRDELDELQGVFFDEFKRNVAIGHNLKINETIQSQSFVYSKRIFTEG	
SEQ ID NO:88 (L)	(793) DVRDELDELQGVFFDEFKRNVAIGHNLKINETIQSQSFVYSKRIFTEG	
	851	900
SEQ ID NO:13 (L1)	(851) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV	
SEQ ID NO:14 (L2)	(843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV	
SEQ ID NO:64 (L)	(843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV	
SEQ ID NO:76 (L)	(843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV	
SEQ ID NO:88 (L)	(843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV	
	901	950
SEQ ID NO:13 (L1)	(901) LNLVYIMTQILFDEHYSTVCDHHSVKSLIGSKNHNLLYSGLIPGQLGGF	
SEQ ID NO:14 (L2)	(893) LNLVYIMTQILFDEHYSTVCDHHSVKSLIGSKNHNLLYSGLIPGQLGGF	
SEQ ID NO:64 (L)	(893) LNLVYIMTQILFDEHYSTVCDHHSVKSLIGSKNHNLLYSGLIPGQLGGF	
SEQ ID NO:76 (L)	(893) LNLVYIMTQILFDEHYSTVCDHHSVKSLIGSKNHNLLYSGLIPGQLGGF	
SEQ ID NO:88 (L)	(893) LNLVYIMTQILFDEHYSTVCDHHSVKSLIGSKNHNLLYSGLIPGQLGGF	
	951	1000
SEQ ID NO:13 (L1)	(951) NPLNISKLFTRNIGDPVTCSLSDLKCFIAGLLPPYVLKNVVLREPGGT	
SEQ ID NO:14 (L2)	(943) NPLNISKLFTRNIGDPVTCSLSDLKCFIAGLLPPYVLKNVVLREPGGT	
SEQ ID NO:64 (L)	(943) NPLNISKLFTRNIGDPVTCSLSDLKCFIAGLLPPYVLKNVVLREPGGT	
SEQ ID NO:76 (L)	(943) NPLNISKLFTRNIGDPVTCSLSDLKCFIAGLLPPYVLKNVVLREPGGT	
SEQ ID NO:88 (L)	(943) NPLNISKLFTRNIGDPVTCSLSDLKCFIAGLLPPYVLKNVVLREPGGT	
	1001	1050
SEQ ID NO:13 (L1)	(1001) WLFLCSDPYTLNIPYTQLPTTYLKKEHQRSLLSRVNPPLAGVQVPQKE	
SEQ ID NO:14 (L2)	(993) WLFLCSDPYTLNIPYTQLPTTYLKKEHQRSLLSRVNPPLAGVQVPQKE	
SEQ ID NO:64 (L)	(993) WLFLCSDPYTLNIPYTQLPTTYLKKEHQRSLLSRVNPPLAGVQVPQKE	
SEQ ID NO:76 (L)	(993) WLFLCSDPYTLNIPYTQLPTTYLKKEHQRSLLSRVNPPLAGVQVPQKE	
SEQ ID NO:88 (L)	(993) WLFLCSDPYTLNIPYTQLPTTYLKKEHQRSLLSRVNPPLAGVQVPQKE	

Figure 35 (3/5)

		1051		1100
SEQ ID NO:13 (L1)	(1051)	EEEMLARFLDREYVMPVAVHVLSEVLGKKKQIQGLIDTPTTIIRTEL		
SEQ ID NO:14 (L2)	(1043)	EEEMLARFLDREYVMPVAVHVLSEVLGKKKQIQGLIDTPTTIIRTEL		
SEQ ID NO:64 (L)	(1043)	EEEMLARFLDREYVMPVAVHVLSEVLGKKKQIQGLIDTPTTIIRTEL		
SEQ ID NO:76 (L)	(1043)	EEEMLARFLDREYVMPVAVHVLSEVLGKKKQIQGLIDTPTTIIRTEL		
SEQ ID NO:88 (L)	(1043)	EEEMLARFLDREYVMPVAVHVLSEVLGKKKQIQGLIDTPTTIIRTEL		
		1101		1150
SEQ ID NO:13 (L1)	(1101)	VNLFVSRKKCEKIINYSLNIAECHDSLLSQVCFSDNKEYLWSTSLISVE		
SEQ ID NO:14 (L2)	(1093)	VNLFVSRKKCEKIINYSLNIAECHDSLLSQVCFSDNKEYLWSTSLISVE		
SEQ ID NO:64 (L)	(1093)	VNLFVSRKKCEKIINYSLNIAECHDSLLSQVCFSDNKEYLWSTSLISVE		
SEQ ID NO:76 (L)	(1093)	VNLFVSRKKCEKIINYSLNIAECHDSLLSQVCFSDNKEYLWSTSLISVE		
SEQ ID NO:88 (L)	(1093)	VNLFVSRKKCEKIINYSLNIAECHDSLLSQVCFSDNKEYLWSTSLISVE		
		1151		1200
SEQ ID NO:13 (L1)	(1151)	TCSVTIADYLRAVSWENILGCRNIGSVTFPTDTELIQICLIGENSSCTLC		
SEQ ID NO:14 (L2)	(1143)	TCSVTIADYLRAVSWENILGCRNIGSVTFPTDTELIQICLIGENSSCTLC		
SEQ ID NO:64 (L)	(1143)	TCSVTIADYLRAVSWENILGCRNIGSVTFPTDTELIQICLIGENSSCTLC		
SEQ ID NO:76 (L)	(1143)	TCSVTIADYLRAVSWENILGCRNIGSVTFPTDTELIQICLIGENSSCTLC		
SEQ ID NO:88 (L)	(1143)	TCSVTIADYLRAVSWENILGCRNIGSVTFPTDTELIQICLIGENSSCTLC		
		1201		1250
SEQ ID NO:13 (L1)	(1201)	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSETEERTASMAAING		
SEQ ID NO:14 (L2)	(1193)	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSETEERTASMAAING		
SEQ ID NO:64 (L)	(1193)	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSETEERTASMAAING		
SEQ ID NO:76 (L)	(1193)	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSETEERTASMAAING		
SEQ ID NO:88 (L)	(1193)	ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSETEERTASMAAING		
		1251		1300
SEQ ID NO:13 (L1)	(1251)	MSHHLRAVLGTSVFIWAGDGDIDWDNALQIAGSRCHITLDQMLLTPI		
SEQ ID NO:14 (L2)	(1243)	MSHHLRAVLGTSVFIWAGDGDIDWDNALQIAGSRCHITLDQMLLTPI		
SEQ ID NO:64 (L)	(1243)	MSHHLRAVLGTSVFIWAGDGDIDWDNALQIAGSRCHITLDQMLLTPI		
SEQ ID NO:76 (L)	(1243)	MSHHLRAVLGTSVFIWAGDGDIDWDNALQIAGSRCHITLDQMLLTPI		
SEQ ID NO:88 (L)	(1243)	MSHHLRAVLGTSVFIWAGDGDIDWDNALQIAGSRCHITLDQMLLTPI		
		1301		1350
SEQ ID NO:13 (L1)	(1301)	PSSSNIQRLDGIISTQKFTPASLARITSEVHICNDGQRLKDGSEVDEN		
SEQ ID NO:14 (L2)	(1293)	PSSSNIQRLDGIISTQKFTPASLARITSEVHICNDGQRLKDGSEVDEN		
SEQ ID NO:64 (L)	(1293)	PSSSNIQRLDGIISTQKFTPASLARITSEVHICNDGQRLKDGSEVDEN		
SEQ ID NO:76 (L)	(1293)	PSSSNIQRLDGIISTQKFTPASLARITSEVHICNDGQRLKDGSEVDEN		
SEQ ID NO:88 (L)	(1293)	PSSSNIQRLDGIISTQKFTPASLARITSEVHICNDGQRLKDGSEVDEN		
		1351		1400
SEQ ID NO:13 (L1)	(1351)	LIYQQIMLLGLSIFETMYSMQKXVFNHHTLELTGHSCCPRELDISLVN		
SEQ ID NO:14 (L2)	(1343)	LIYQQIMLLGLSIFETMYSMQKXVFNHHTLELTGHSCCPRELDISLVN		
SEQ ID NO:64 (L)	(1343)	LIYQQIMLLGLSIFETMYSMQKXVFNHHTLELTGHSCCPRELDISLVN		
SEQ ID NO:76 (L)	(1343)	LIYQQIMLLGLSIFETMYSMQKXVFNHHTLELTGHSCCPRELDISLVN		
SEQ ID NO:88 (L)	(1343)	LIYQQIMLLGLSIFETMYSMQKXVFNHHTLELTGHSCCPRELDISLVN		
		1401		1450
SEQ ID NO:13 (L1)	(1401)	PPRHQTPPELTSTTTNPFLYDQLPLNQENLTLEIKTFEFNELNIDGLDFG		
SEQ ID NO:14 (L2)	(1393)	PPRHQTPPELTSTTTNPFLYDQLPLNQENLTLEIKTFEFNELNIDGLDFG		
SEQ ID NO:64 (L)	(1393)	PPRHQTPPELTSTTTNPFLYDQLPLNQENLTLEIKTFEFNELNIDGLDFG		
SEQ ID NO:76 (L)	(1393)	PPRHQTPPELTSTTTNPFLYDQLPLNQENLTLEIKTFEFNELNIDGLDFG		
SEQ ID NO:88 (L)	(1393)	PPRHQTPPELTSTTTNPFLYDQLPLNQENLTLEIKTFEFNELNIDGLDFG		
		1451		1500
SEQ ID NO:13 (L1)	(1451)	EGIQLLSCTARIMAECTILEGIGSSVKNEAIVNFDNSVNWISECLMCDI		
SEQ ID NO:14 (L2)	(1443)	EGIQLLSCTARIMAECTILEGIGSSVKNEAIVNFDNSVNWISECLMCDI		
SEQ ID NO:64 (L)	(1443)	EGIQLLSCTARIMAECTILEGIGSSVKNEAIVNFDNSVNWISECLMCDI		
SEQ ID NO:76 (L)	(1443)	EGIQLLSCTARIMAECTILEGIGSSVKNEAIVNFDNSVNWISECLMCDI		
SEQ ID NO:88 (L)	(1443)	EGIQLLSCTARIMAECTILEGIGSSVKNEAIVNFDNSVNWISECLMCDI		
		1501		1550
SEQ ID NO:13 (L1)	(1501)	RSLCVNLQGEILCSLAYQMYLRIKGRRAILNYLDTTLQRIPIVIGLANIA		
SEQ ID NO:14 (L2)	(1493)	RSLCVNLQGEILCSLAYQMYLRIKGRRAILNYLDTTLQRIPIVIGLANIA		
SEQ ID NO:64 (L)	(1493)	RSLCVNLQGEILCSLAYQMYLRIKGRRAILNYLDTTLQRIPIVIGLANIA		
SEQ ID NO:76 (L)	(1493)	RSLCVNLQGEILCSLAYQMYLRIKGRRAILNYLDTTLQRIPIVIGLANIA		
SEQ ID NO:88 (L)	(1493)	RSLCVNLQGEILCSLAYQMYLRIKGRRAILNYLDTTLQRIPIVIGLANIA		
		1551		1600
SEQ ID NO:13 (L1)	(1551)	LTISHPFEIFRIVNTGHNQIKGPVATTFIAASRDIIISGAREYLSYL		
SEQ ID NO:14 (L2)	(1543)	LTISHPFEIFRIVNTGHNQIKGPVATTFIAASRDIIISGAREYLSYL		
SEQ ID NO:64 (L)	(1543)	LTISHPFEIFRIVNTGHNQIKGPVATTFIAASRDIIISGAREYLSYL		
SEQ ID NO:76 (L)	(1543)	LTISHPFEIFRIVNTGHNQIKGPVATTFIAASRDIIISGAREYLSYL		
SEQ ID NO:88 (L)	(1543)	LTISHPFEIFRIVNTGHNQIKGPVATTFIAASRDIIISGAREYLSYL		

Figure 35 (4/5)

	1601	1650
SEQ ID NO:13 (L1)	(1601) ESQEDCYTFFNCGDGLTPKMEQYLARRACILTLTYNTHQIPIVIRSLT	
SEQ ID NO:14 (L2)	(1593) SSGQEDCYTFFNCGDGLTPKMEQYLARRACILTLTYNTHQIPIVIRSLT	
SEQ ID NO:64 (L)	(1593) SSGQEDCYTFFNCGDGLTPKMEQYLARRACILTLTYNTHQIPIVIRSLT	
SEQ ID NO:76 (L)	(1593) SSGQEDCYTFFNCGDGLTPKMEQYLARRACILTLTYNTHQIPIVIRSLT	
SEQ ID NO:88 (L)	(1593) SSGQEDCYTFFNCGDGLTPKMEQYLARRACILTLTYNTHQIPIVIRSLT	
	1651	1700
SEQ ID NO:13 (L1)	(1651) PIRKCKVLTEYNQOIEYADQEFSSVLKVVNALLQNPIDALVSNLYFTTR	
SEQ ID NO:14 (L2)	(1643) PIRKCKVLTEYNQOIEYADQEFSSVLKVVNALLQNPIDALVSNLYFTTR	
SEQ ID NO:64 (L)	(1643) PIRKCKVLTEYNQOIEYADQEFSSVLKVVNALLQNPIDALVSNLYFTTR	
SEQ ID NO:76 (L)	(1643) PIRKCKVLTEYNQOIEYADQEFSSVLKVVNALLQNPIDALVSNLYFTTR	
SEQ ID NO:88 (L)	(1643) PIRKCKVLTEYNQOIEYADQEFSSVLKVVNALLQNPIDALVSNLYFTTR	
	1701	1750
SEQ ID NO:13 (L1)	(1701) RVLSNLRSCDKRAISYIEVLYTEDFGKEDTVQYDINTNDIILTHGLFTQ	
SEQ ID NO:14 (L2)	(1693) RVLSNLRSCDKRAISYIEVLYTEDFGKEDTVQYDINTNDIILTHGLFTQ	
SEQ ID NO:64 (L)	(1693) RVLSNLRSCDKRAISYIEVLYTEDFGKEDTVQYDINTNDIILTHGLFTQ	
SEQ ID NO:76 (L)	(1693) RVLSNLRSCDKRAISYIEVLYTEDFGKEDTVQYDINTNDIILTHGLFTQ	
SEQ ID NO:88 (L)	(1693) RVLSNLRSCDKRAISYIEVLYTEDFGKEDTVQYDINTNDIILTHGLFTQ	
	1751	1800
SEQ ID NO:13 (L1)	(1751) IEISYQGSLSLHKFLTPDNAPGSLIPFSISPNGLACDPLHLLKSVGTST	
SEQ ID NO:14 (L2)	(1743) IEISYQGSLSLHKFLTPDNAPGSLIPFSISPNGLACDPLHLLKSVGTST	
SEQ ID NO:64 (L)	(1743) IEISYQGSLSLHKFLTPDNAPGSLIPFSISPNGLACDPLHLLKSVGTST	
SEQ ID NO:76 (L)	(1743) IEISYQGSLSLHKFLTPDNAPGSLIPFSISPNGLACDPLHLLKSVGTST	
SEQ ID NO:88 (L)	(1743) IEISYQGSLSLHKFLTPDNAPGSLIPFSISPNGLACDPLHLLKSVGTST	
	1801	1850
SEQ ID NO:13 (L1)	(1801) SWYKYAIAYAVSEKRSARLGSSLYICGSGGSVMTLLEYLPSVDIFPNSL	
SEQ ID NO:14 (L2)	(1793) SWYKYAIAYAVSEKRSARLGSSLYICGSGGSVMTLLEYLPSVDIFPNSL	
SEQ ID NO:64 (L)	(1793) SWYKYAIAYAVSEKRSARLGSSLYICGSGGSVMTLLEYLPSVDIFPNSL	
SEQ ID NO:76 (L)	(1793) SWYKYAIAYAVSEKRSARLGSSLYICGSGGSVMTLLEYLPSVDIFPNSL	
SEQ ID NO:88 (L)	(1793) SWYKYAIAYAVSEKRSARLGSSLYICGSGGSVMTLLEYLPSVDIFPNSL	
	1851	1900
SEQ ID NO:13 (L1)	(1851) FSNCGMPPQRNYGLMPLQFVNSVVTNLTAKSECKLGFVQQKPLWRDID	
SEQ ID NO:14 (L2)	(1843) FSNCGMPPQRNYGLMPLQFVNSVVTNLTAKSECKLGFVQQKPLWRDID	
SEQ ID NO:64 (L)	(1843) FSNCGMPPQRNYGLMPLQFVNSVVTNLTAKSECKLGFVQQKPLWRDID	
SEQ ID NO:76 (L)	(1843) FSNCGMPPQRNYGLMPLQFVNSVVTNLTAKSECKLGFVQQKPLWRDID	
SEQ ID NO:88 (L)	(1843) FSNCGMPPQRNYGLMPLQFVNSVVTNLTAKSECKLGFVQQKPLWRDID	
	1901	1950
SEQ ID NO:13 (L1)	(1901) IETNVTDPSPFNFALNEIFMQSLKRVNCDVEFDRCMPIERVIGQYTHILL	
SEQ ID NO:14 (L2)	(1893) IETNVTDPSPFNFALNEIFMQSLKRVNCDVEFDRCMPIERVIGQYTHILL	
SEQ ID NO:64 (L)	(1893) IETNVTDPSPFNFALNEIFMQSLKRVNCDVEFDRCMPIERVIGQYTHILL	
SEQ ID NO:76 (L)	(1893) IETNVTDPSPFNFALNEIFMQSLKRVNCDVEFDRCMPIERVIGQYTHILL	
SEQ ID NO:88 (L)	(1893) IETNVTDPSPFNFALNEIFMQSLKRVNCDVEFDRCMPIERVIGQYTHILL	
	1951	2000
SEQ ID NO:13 (L1)	(1951) VATYGLQDSDILWYVYVYTSSEKVPQFLSAMIMIFGYVKIHNNGYMSAKD	
SEQ ID NO:14 (L2)	(1943) VATYGLQDSDILWYVYVYTSSEKVPQFLSAMIMIFGYVKIHNNGYMSAKD	
SEQ ID NO:64 (L)	(1943) VATYGLQDSDILWYVYVYTSSEKVPQFLSAMIMIFGYVKIHNNGYMSAKD	
SEQ ID NO:76 (L)	(1943) VATYGLQDSDILWYVYVYTSSEKVPQFLSAMIMIFGYVKIHNNGYMSAKD	
SEQ ID NO:88 (L)	(1943) VATYGLQDSDILWYVYVYTSSEKVPQFLSAMIMIFGYVKIHNNGYMSAKD	
	2001	2050
SEQ ID NO:13 (L1)	(2001) EHYILMSDCKEPVNYTAVPNILTRVSDLVSEKLSLHPEDLKRVCEETS	
SEQ ID NO:14 (L2)	(1993) EHYILMSDCKEPVNYTAVPNILTRVSDLVSEKLSLHPEDLKRVCEETS	
SEQ ID NO:64 (L)	(1993) EHYILMSDCKEPVNYTAVPNILTRVSDLVSEKLSLHPEDLKRVCEETS	
SEQ ID NO:76 (L)	(1993) EHYILMSDCKEPVNYTAVPNILTRVSDLVSEKLSLHPEDLKRVCEETS	
SEQ ID NO:88 (L)	(1993) EHYILMSDCKEPVNYTAVPNILTRVSDLVSEKLSLHPEDLKRVCEETS	
	2051	2100
SEQ ID NO:13 (L1)	(2051) LNLKCNHIEYKIIARKIPIQVSTDSLLLQLGCVINSVGSTDPREVATLS	
SEQ ID NO:14 (L2)	(2043) LNLKCNHIEYKIIARKIPIQVSTDSLLLQLGCVINSVGSTDPREVATLS	
SEQ ID NO:64 (L)	(2043) LNLKCNHIEYKIIARKIPIQVSTDSLLLQLGCVINSVGSTDPREVATLS	
SEQ ID NO:76 (L)	(2043) LNLKCNHIEYKIIARKIPIQVSTDSLLLQLGCVINSVGSTDPREVATLS	
SEQ ID NO:88 (L)	(2043) LNLKCNHIEYKIIARKIPIQVSTDSLLLQLGCVINSVGSTDPREVATLS	
	2101	2150
SEQ ID NO:13 (L1)	(2101) STECMYVVSIDLAILEANIVISESAGLDLALMLGPFNLKLNKIDTIL	
SEQ ID NO:14 (L2)	(2093) STECMYVVSIDLAILEANIVISESAGLDLALMLGPFNLKLNKIDTIL	
SEQ ID NO:64 (L)	(2093) STECMYVVSIDLAILEANIVISESAGLDLALMLGPFNLKLNKIDTIL	
SEQ ID NO:76 (L)	(2093) STECMYVVSIDLAILEANIVISESAGLDLALMLGPFNLKLNKIDTIL	
SEQ ID NO:88 (L)	(2093) STECMYVVSIDLAILEANIVISESAGLDLALMLGPFNLKLNKIDTIL	

Figure 35 (5/5)

		2151		2200
SEQ ID NO:13 (L1)	(2151)	KSSTYQLIPYWLRYEYSINPRSLSPFLITKLQOCRIWSDMITISEFHKKS		
SEQ ID NO:14 (L2)	(2143)	KSSTYQLIPYWLRYEYSINPRSLSPFLITKLQOCRIWSDMITISEFHKKS		
SEQ ID NO:64 (L)	(2143)	KSSTYQLIPYWLRYEYSINPRSLSPFLITKLQOCRIWSDMITISEFHKKS		
SEQ ID NO:76 (L)	(2143)	KSSTYQLIPYWLRYEYSINPRSLSPFLITKLQOCRIWSDMITISEFHKKS		
SEQ ID NO:88 (L)	(2143)	KSSTYQLIPYWLRYEYSINPRSLSPFLITKLQOCRIWSDMITISEFHKKS		
		2201		2247
SEQ ID NO:13 (L1)	(2201)	KRPPIKRVIGNQLKSPFNSSSIVLTRAEVKVCIKFLGAIILK-		
SEQ ID NO:14 (L2)	(2193)	KRPPIKRVIGNQLKSPFNSSSIVLTRAEVKVCIKFLGAIILK-		
SEQ ID NO:64 (L)	(2193)	KRPPIKRVIGNQLKSPFNSSSIVLTRAEVKVCIKFLGAIILK-		
SEQ ID NO:76 (L)	(2193)	KRPPIKRVIGNQLKSPFNSSSIVLTRAEVKVCIKFLGAIILK-		
SEQ ID NO:88 (L)	(2193)	KRPPIKRVIGNQLKSPFNSSSIVLTRAEVKVCIKFLGAIILK-		

Protein sequence identity:

SEQ ID NO:14	v. SEQ ID NO:64:	99% sequence identity
SEQ ID NO:14	v. SEQ ID NO:76:	99% sequence identity
SEQ ID NO:14	v. SEQ ID NO:88:	98% sequence identity

DNA sequence identity:

SEQ ID NO:12	v. SEQ ID NO:63:	99% sequence identity
SEQ ID NO:12	v. SEQ ID NO:75:	97% sequence identity
SEQ ID NO:12	v. SEQ ID NO:87:	97% sequence identity