

Figure 1

SEQ ID NO:	type	Gene Description
1	DNA	EHV-1 DNA polymerase (Pol) gene (AY464052) from EHV-1 V592 strain
2	Protein	EHV-1 DNA polymerase (pol) protein (AAS45914.1) encoded by AY464052 from EHV-1 V592 strain
3	DNA	EHV-1 DNA polymerase (Pol) (AY665713) from EHV-1 Ab4 strain
4	Protein	EHV-1 DNA polymerase (pol) protein (AAT67287.1) encoded by AY665713 from EHV-1 Ab4 strain
5	DNA	EHV-1 DNA polymerase (Pol) (NC_001491) from EHV-1
6	Protein	EHV-1 DNA polymerase (pol) protein (YP_053075.1) encoded by NC_001491
7	DNA	EHV-1 glycoprotein (gC) gene (AY464052) from EHV-1 V592 strain
8	Protein	EHV-1 glycoprotein (gC) protein (AAS45900.1) encoded by AY464052 from EHV-1 V592 strain
9	DNA	EHV-1 glycoprotein (gC) gene (AY665713) from EHV-1 Ab4 strain
10	Protein	EHV-1 glycoprotein (gC) protein (AAT67273.1) encoded by AY665713 from EHV-1 Ab4 strain
11	DNA	EHV-1 glycoprotein (gC) gene (NC_001491) from EHV-1
12	Protein	EHV-1 glycoprotein (gC) protein (YP_053061.1) encoded by NC_001491
13	Protein	EHV-1 RacL DNA polymerase partial sequence
14	Protein	EHV-1 RacL DNA polymerase partial sequence comprising N at 752 of full length EHV-1 DNA polymerase
15	Protein	EHV-1 RacL DNA polymerase partial sequence with amino acid deletion at 752 of full length EHV-1 DNA polymerase
16	Primer	Primer PN1
17	Primer	Primer PN2
18	Primer	Primer P1
19	Primer	Primer P2
20	Primer	Primer P3
21	Primer	Primer P4
22	Primer	Primer P5
23	Primer	Primer P6
24	Primer	Primer P7

Figure 1 (continued)		
25	Primer	Primer P8
26	Primer	Primer P9
27	Primer	Primer P10
28	Primer	Primer gC-1
29	Primer	Primer gC-2
30	Primer	Primer Δ gC-1
31	Primer	Primer Δ gC-2
32	Primer	Primer Poly1
33	Primer	Primer Poly2
34	DNA	EHV-1 glycoprotein (gC) gene from EHV-1 RacL11 strain
35	Protein	EHV-1 glycoprotein (gC) protein from EHV-1 RacL11 strain
36	DNA	EHV-1 DNA polymerase (Pol) from EHV-1 NY03 strain
37	Protein	EHV-1 DNA polymerase (pol) protein from EHV-1 NY03 strain

Figure 2 (1/3)

Cloning scheme

Fig. 2A

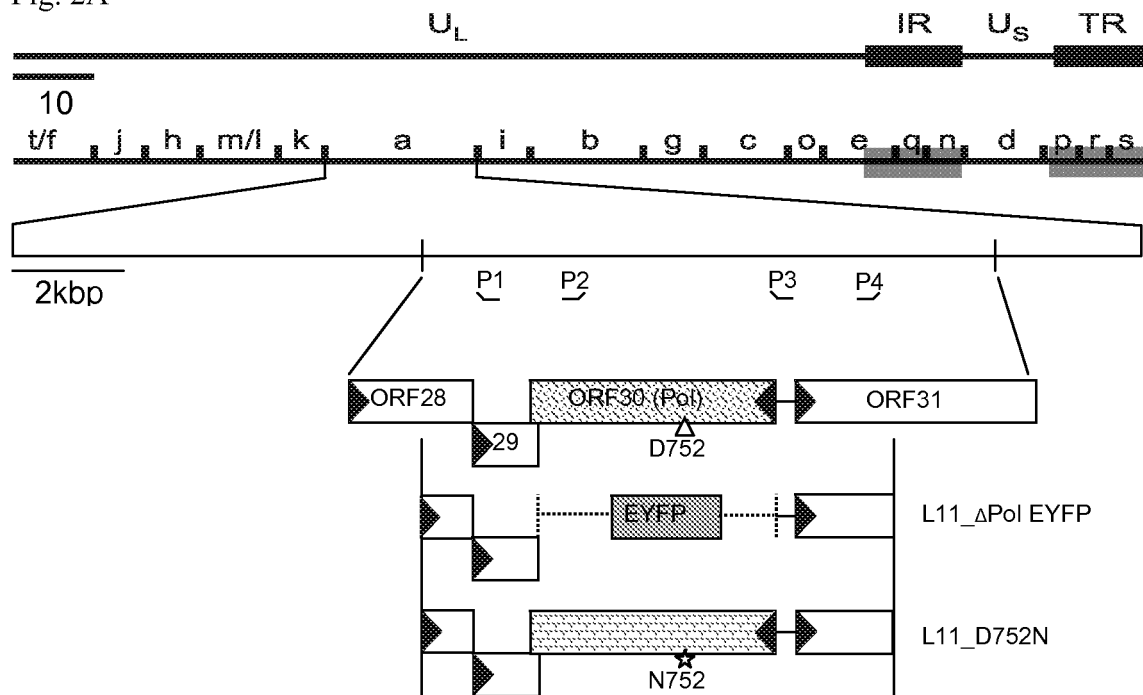


FIG. 2B

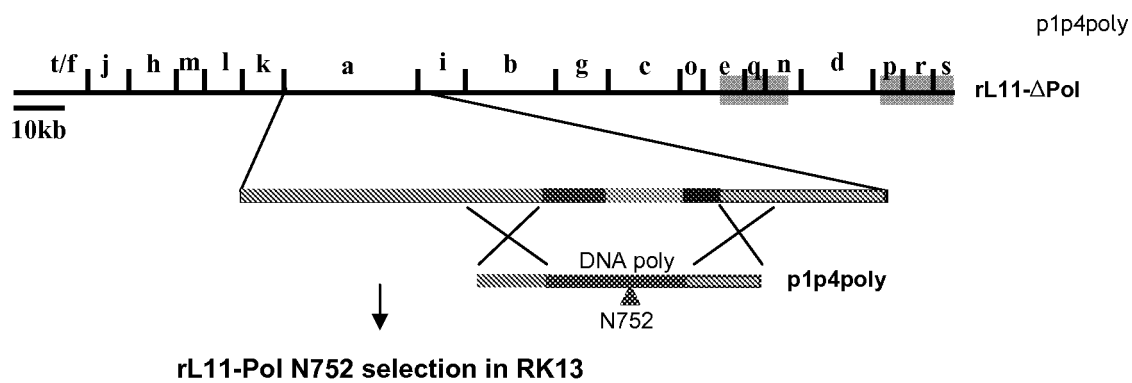


Figure 2 (2/3)

Fig. 2C

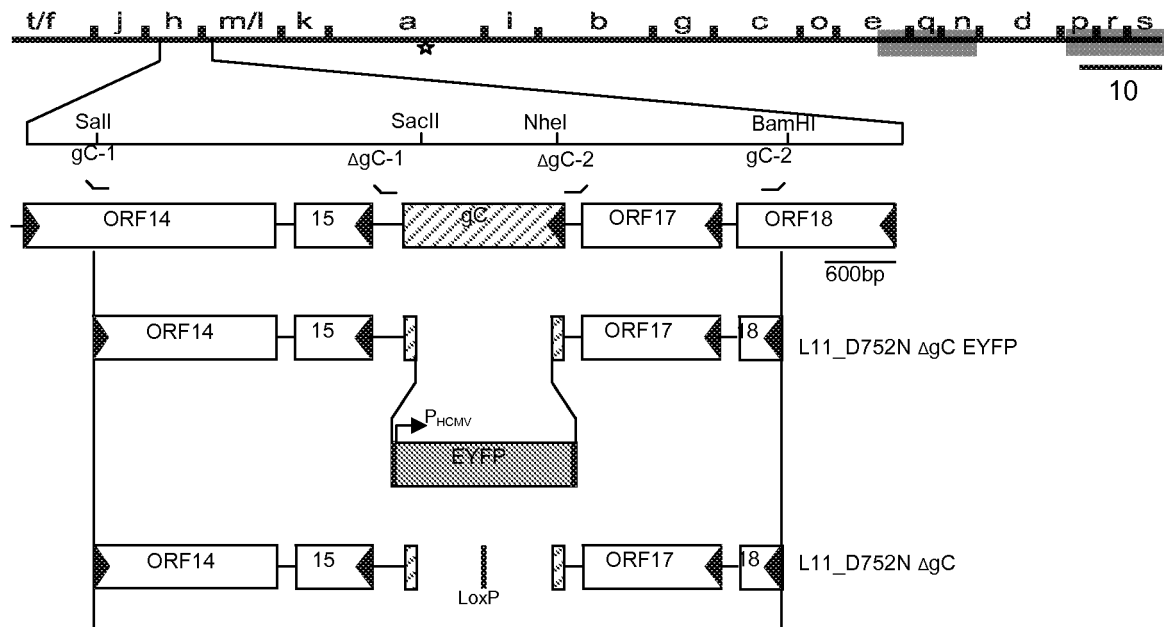


Figure 2 (3/3)

Fig. 2D

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F D S Q A D A A S E T S E L A M D S Q S H A F D S T D E P D RacL11
F D S Q A D A A S E T S E L A M D S Q S H A F D S T D E P D rRacL11-poly N752
F D S Q A D A A S E T S E L A M D S Q S H A F D S T D E P D pRacL11-delta AA752

G V D G T P D A A G S G A T S E N G G G K P G V G R A V G Y RacL11
G V D G T P D A A G S G A T S E N G G G K P G V G R A V G Y rRacL11-poly N752
G V D G T P D A A G S G A T S E N G G G K P G V G R A V G Y pRacL11-delta AA752

Q G A K V L D P V S G F H V D P V V V F D F A S L Y P S I I RacL11
Q G A K V L D P V S G F H V D P V V V F D F A S L Y P S I I rRacL11-poly N752
Q G A K V L D P V S G F H V D P V V V F D F A S L Y P S I I pRacL11-delta AA752

Q A H N L C F T T L A L D E V D L A G L Q P S V D Y S T F E RacL11
Q A H N L C F T T L A L D E V D L A G L Q P S V N Y S T F E rRacL11-poly N752
Q A H N L C F T T L A L D E V D L A G L Q P S V - Y S T F E pRacL11-delta AA752

V G D Q K L F F V H A H I R E S L L G I L L R D W L A M R K RacL11
V G D Q K L F F V H A H I R E S L L G I L L R D W L A M R K rRacL11-poly N752
V G D Q K L F F V H A H I R E S L L G I L L R D W L A M R K pRacL11-delta AA752

A V R A R I P T S T P E E A V L L D K Q Q S A I K V I C N S RacL11
A V R A R I P T S T P E E A V L L D K Q Q S A I K V I C N S rRacL11-poly N752
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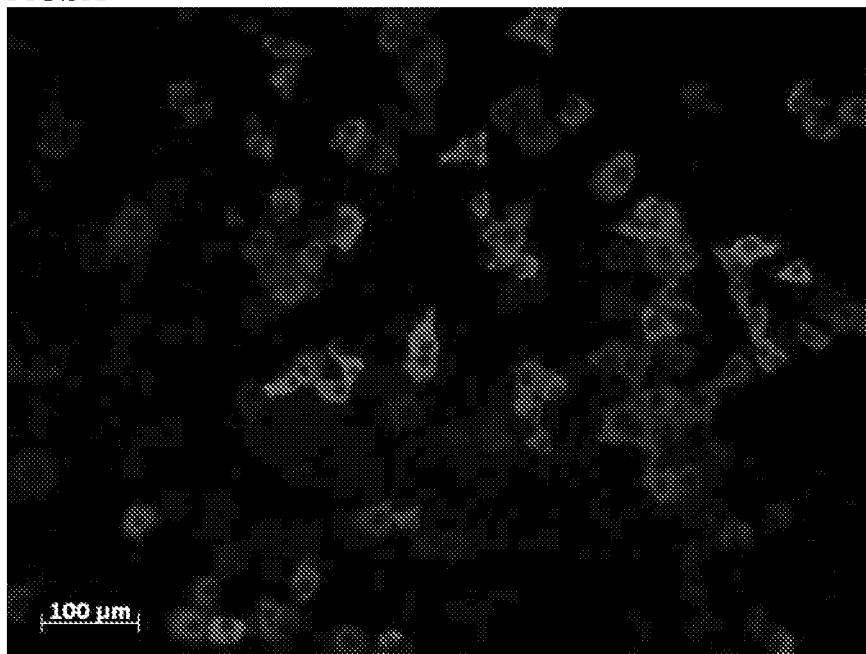
V Y G F T G V A N G L L P C L RacL11
V Y G F T G V A N G L L P C L rRacL11-poly N752
V Y G F T G V A N G L L P C L pRacL11-delta AA752

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RacL11:	SEQ ID NO:13
rRacL11-poly N752:	SEQ ID NO:14
pRacL11-delta AA752:	SEQ ID NO:15

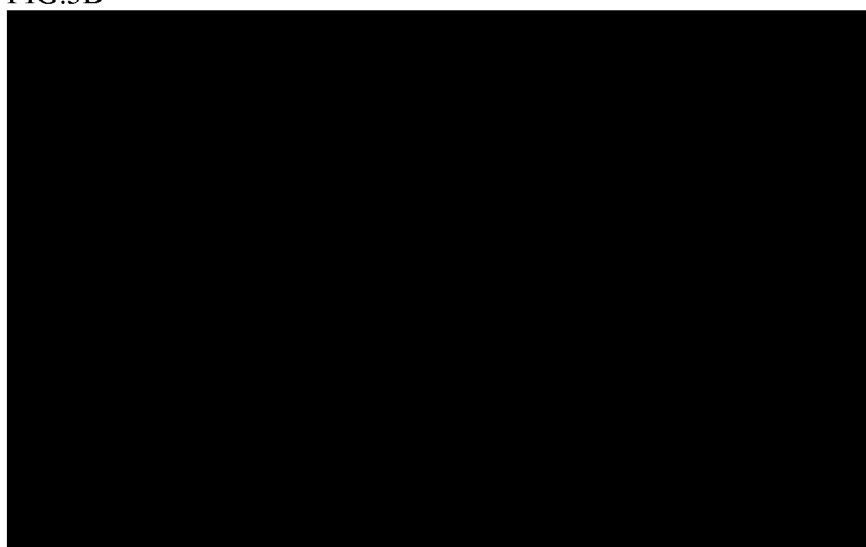
Figure 3

FIG.3A



RK13-Pol

FIG.3B



RK13

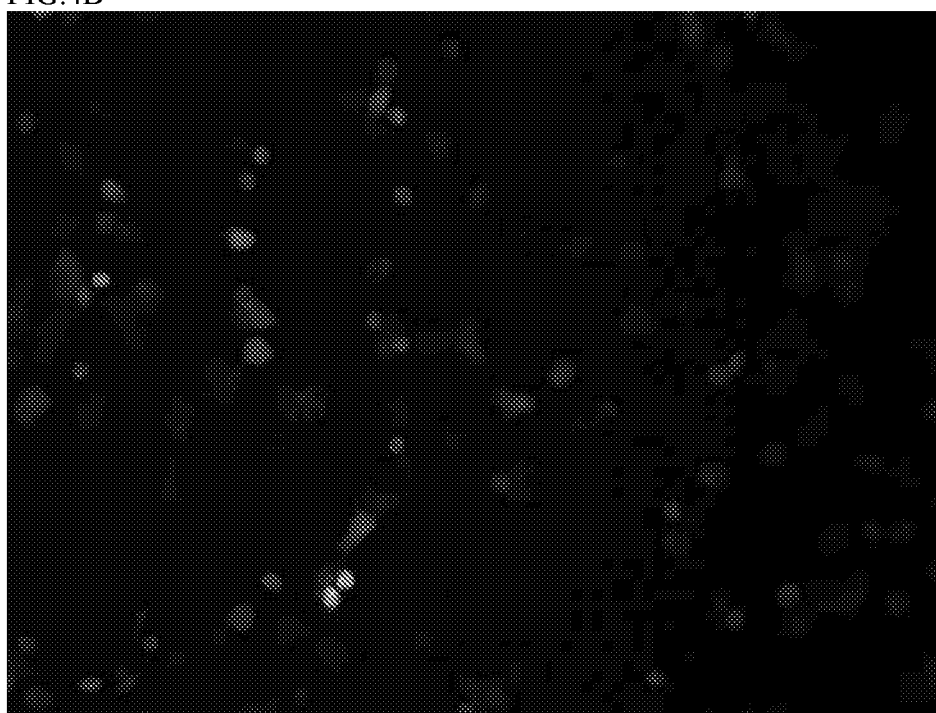
Figure 4

FIG.4A



**L11- Δ Pol EYFP
in RK13-Pol**

FIG.4B



**L11- Δ Pol
EYFP in RK13**

Figure 5

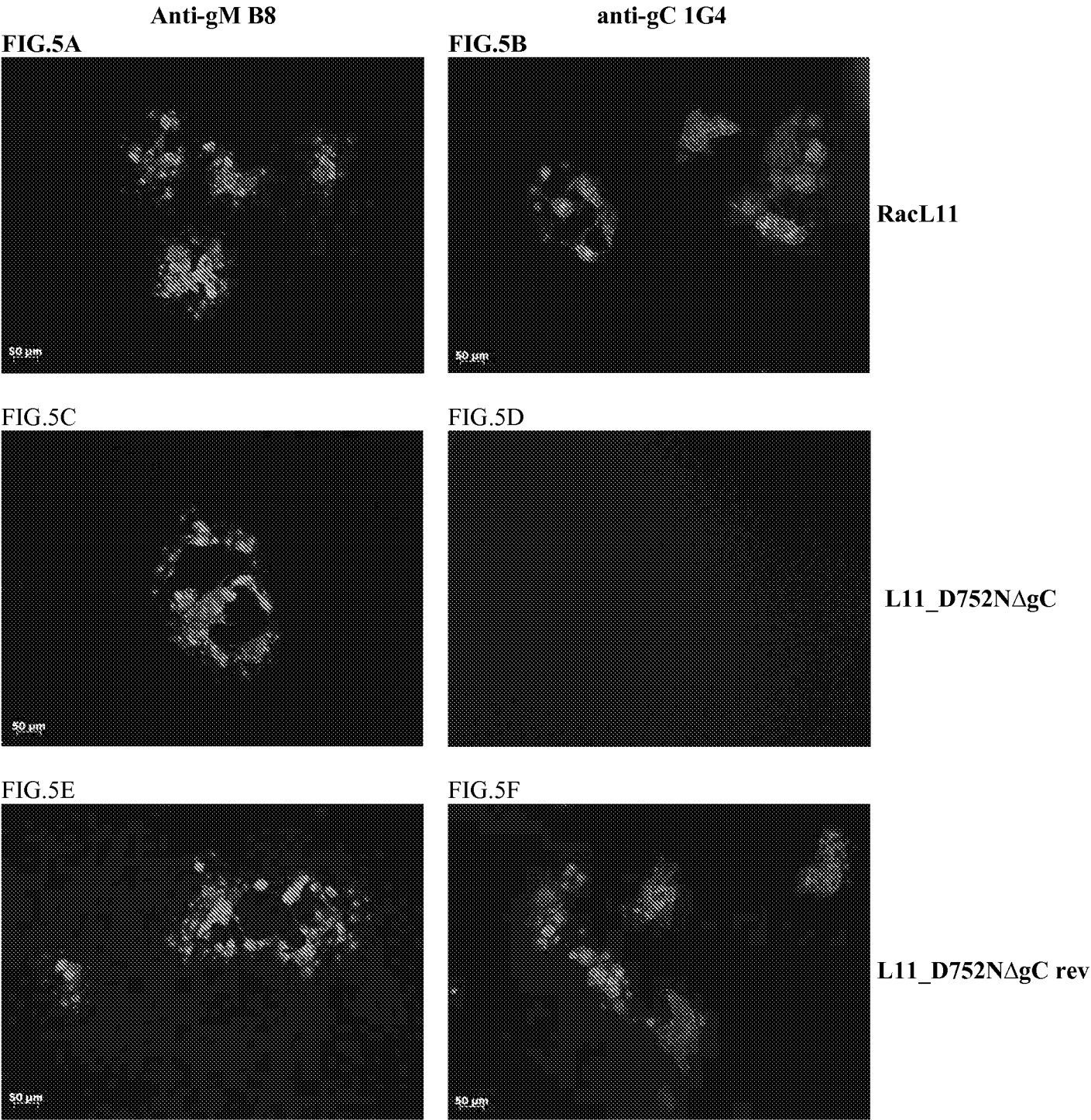


Figure 6

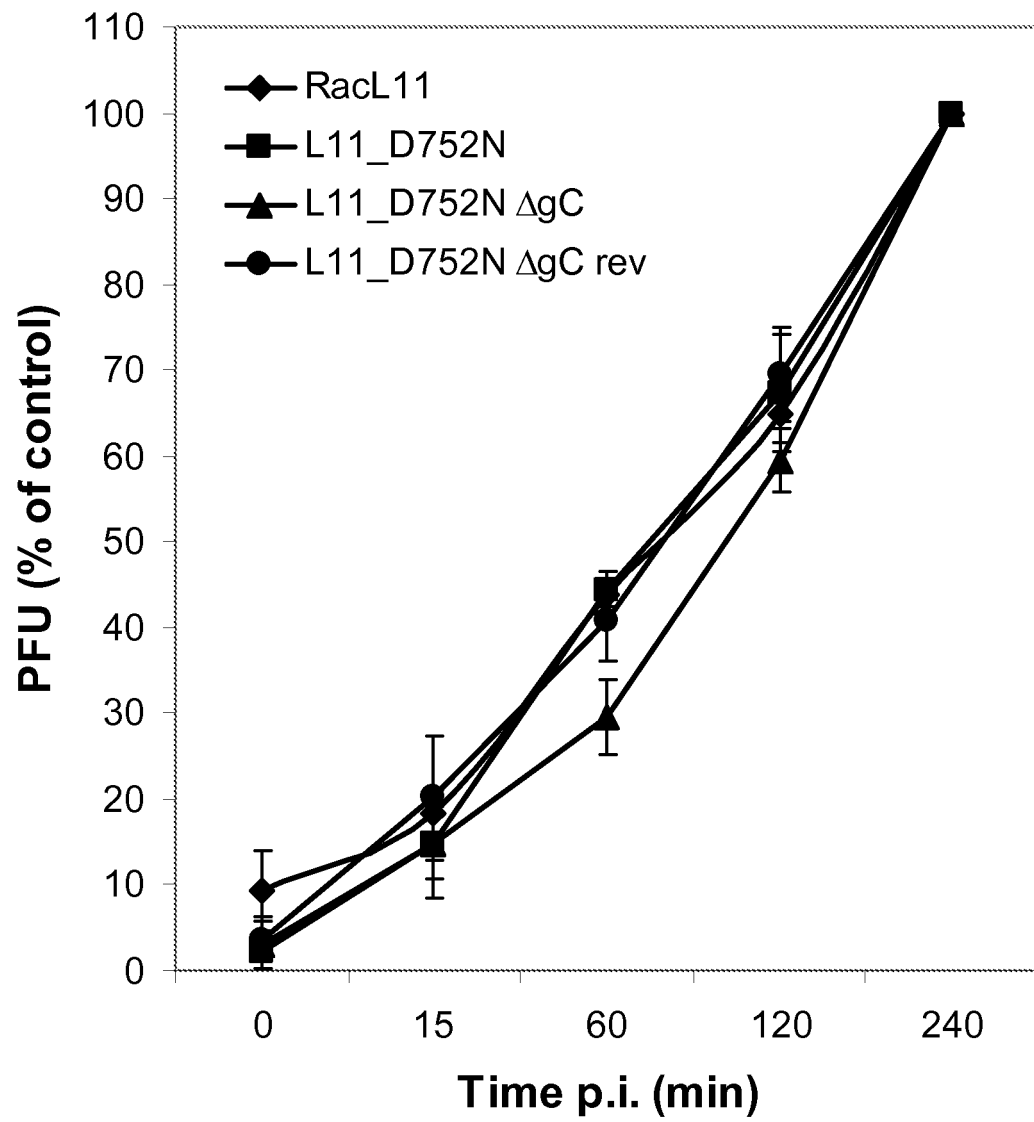


Figure 7

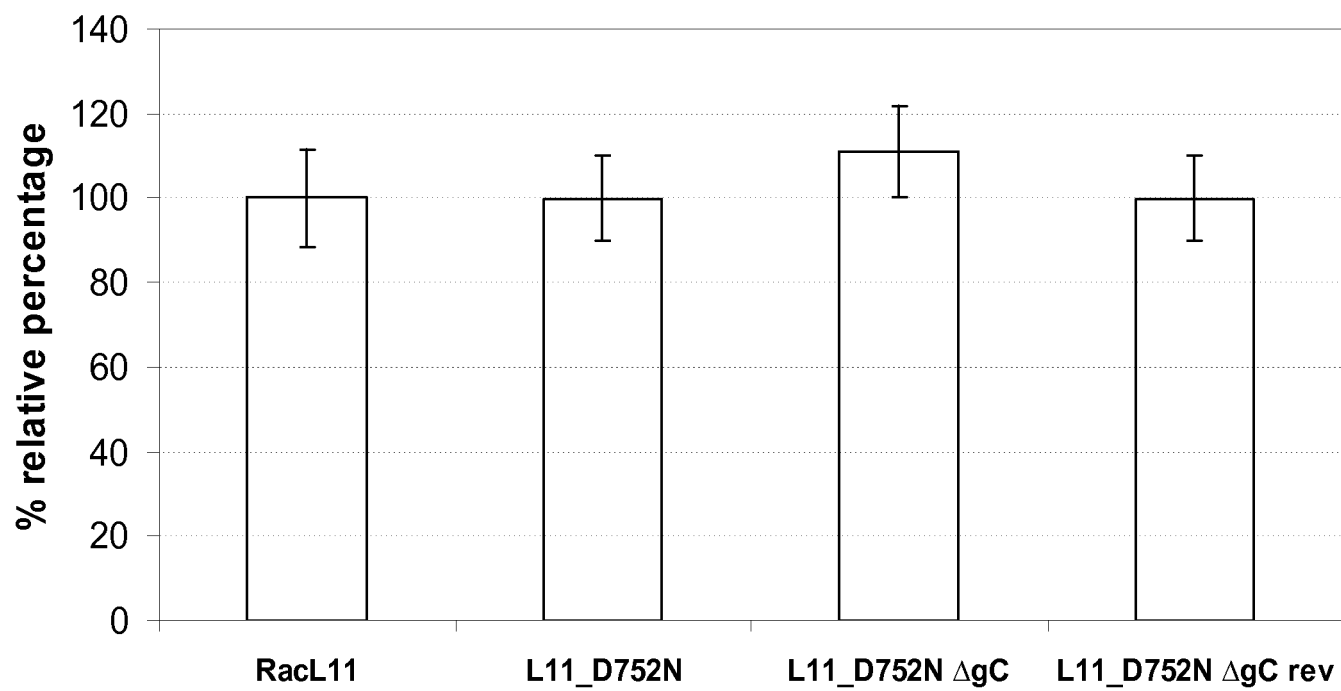


Figure 8

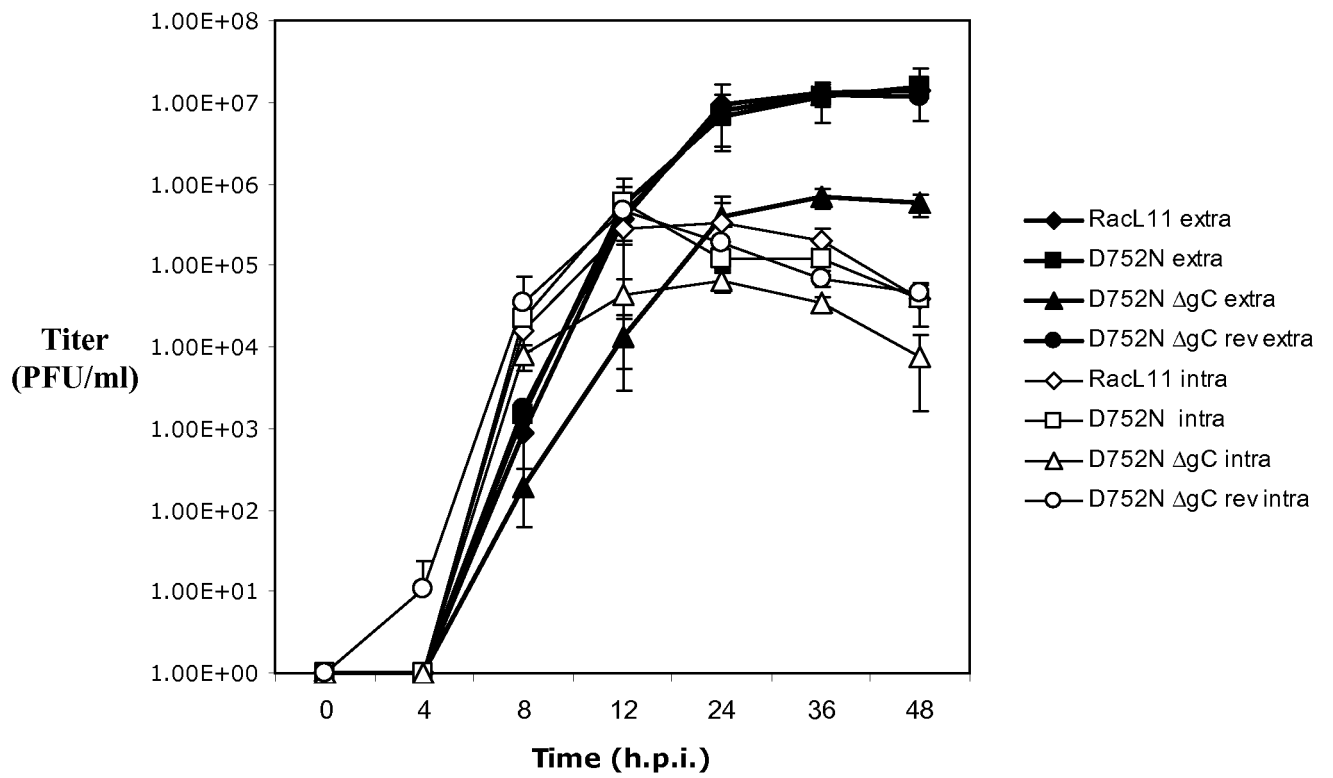


Figure 9 (1/2)

FIG. 9A

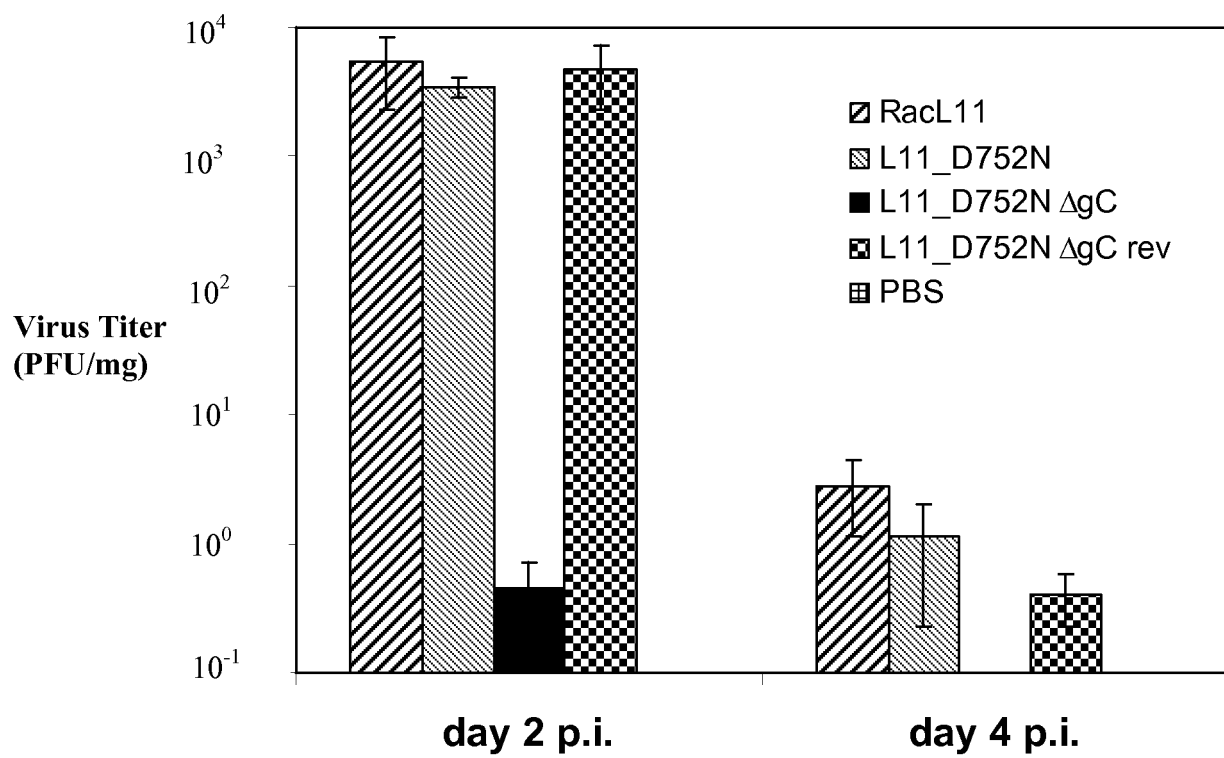


Figure 9 (2/2)

FIG. 9B

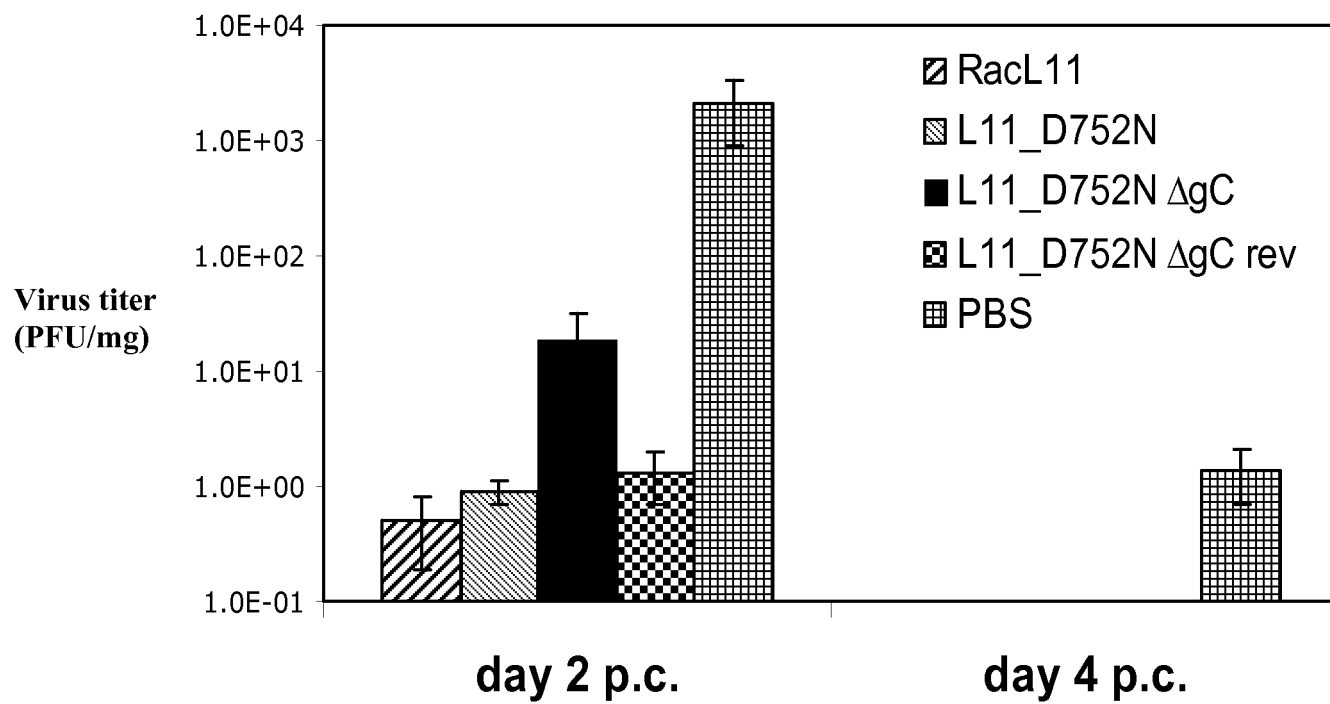


Figure 10

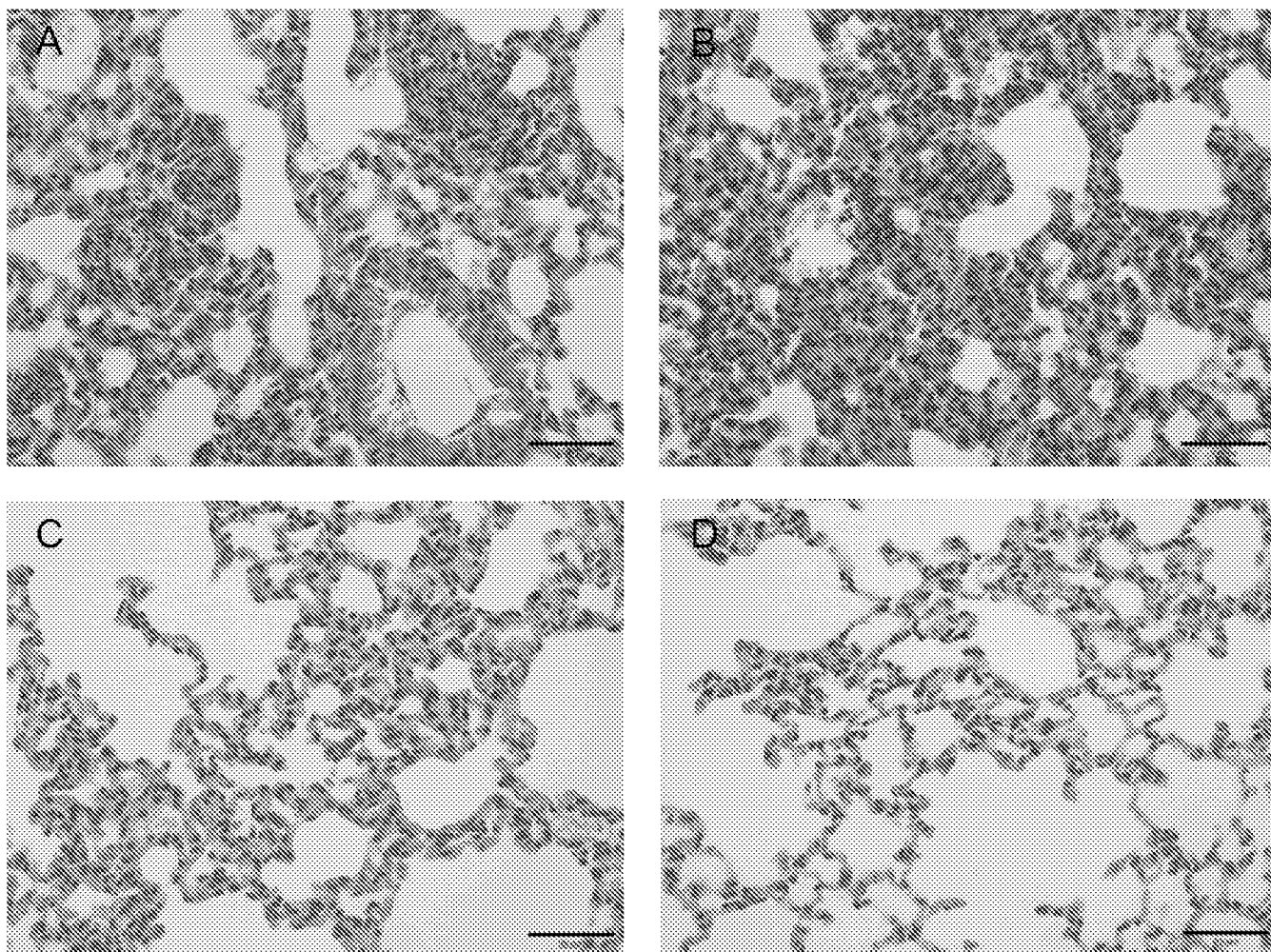


Figure 11 (1/2)

FIG. 11A

CF test

Group	Horse	Day -1	Day 7	Day 13	Day 27	Day 41	Day 49	Day 56
A	68378	<5	20	20	10	40	20	40
A	68473	<5	5	10	10	40	20	20
A	68504	<5	10	20	10	20	10	40
A	68685	<5	10	10	10	20	20	10
A	68703	<5	20	40	20	80	40	160
A	68716	<5	80	80	40	160	40	20
A	68837	<5	20	40	40	40	40	20
A	68871	<5	40	40	20	20	20	40
A	Mean	<5.0	25.6	32.5	20.0	52.5	26.3	43.8
B	68460	<5	<5	5	20	40	20	80
B	68551	<5	<5	<5	20	80	40	20
B	68564	<5	<5	20	20	160	80	160
B	68581	<5	<5	<5	40	160	40	80
B	68594	<5	80	40	40	40	20	20
B	68638	<5	<5	<5	20	80	40	40
B	68642	<5	<5	10	20	80	40	80
B	68655	<5	<5	<5	5	80	40	40
B	Mean	<5.0	<14.4	<11.9	23.1	90.0	40.0	65.0
C	68430	<5	<5	<5	<5	<5	<5	160
C	68443	<5	<5	<5	<5	<5	<5	80
C	68577	<5	<5	<5	<5	<5	<5	40
C	68625	<5	<5	<5	<5	<5	<5	80
C	68672	<5	<5	<5	<5	<5	<5	80
C	68698	<5	<5	<5	<5	<5	<5	160
C	68841	<5	<5	<5	<5	<5	<5	160
C	68988	<5	<5	<5	<5	<5	<5	160
C	Mean	<5.0	<5.0	<5.0	<5.0	<5.0	<5.0	115.0

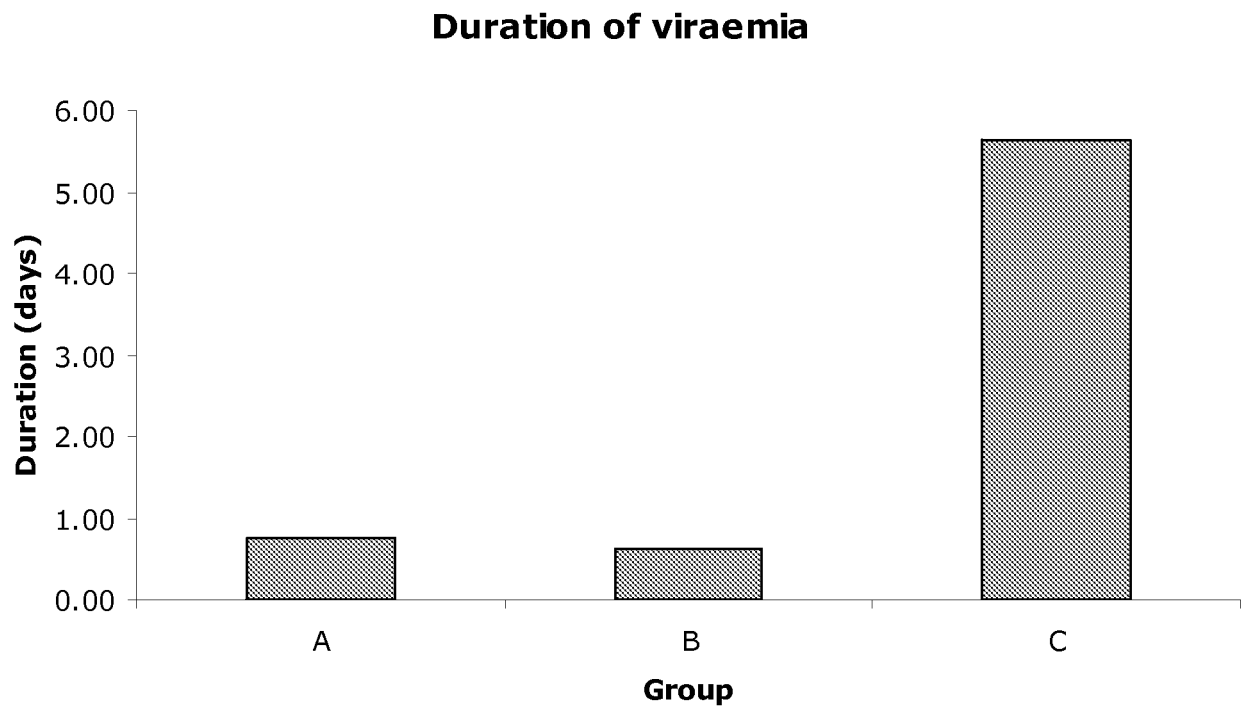
Figure 11 (2/2)

FIG. 11B

VN test

Group	Horse	Day -1	Day 7	Day 13	Day 27	Day 41	Day 49	Day 56
A	68378	<5	<5	5	5	20	40	40
A	68473	<5	<5	5	5	20	40	20
A	68504	<5	<5	10	5	20	40	20
A	68685	<5	<5	5	5	20	40	20
A	68703	<5	<5	10	5	20	20	20
A	68716	<5	<5	<5	<5	10	20	20
A	68837	<5	<5	<5	<5	20	40	20
A	68871	<5	<5	10	10	20	40	80
A	Mean	<5.0	<5.0	<6.9	<5.6	18.8	35.0	30.0
B	68460	<5	<5	<5	<5	5	10	80
B	68551	<5	<5	<5	5	10	20	20
B	68564	<5	<5	<5	<5	10	20	80
B	68581	<5	<5	<5	<5	10	20	40
B	68594	<5	<5	20	20	40	40	40
B	68638	<5	<5	<5	<5	10	10	10
B	68642	<5	<5	<5	5	5	20	80
B	68655	<5	<5	<5	<5	10	10	20
B	Mean	<5.0	<5.0	<6.9	<6.9	12.5	18.8	46.3
C	68430	<5	<5	<5	<5	<5	<5	<5
C	68443	<5	<5	<5	<5	<5	<5	<5
C	68577	<5	<5	<5	<5	<5	<5	<5
C	68625	<5	<5	<5	<5	<5	<5	<5
C	68672	<5	<5	<5	<5	<5	<5	<5
C	68698	<5	<5	<5	<5	<5	<5	5
C	68841	<5	<5	<5	<5	<5	<5	<5
C	68988	<5	<5	<5	<5	<5	<5	<5
C	Mean	<5.0	<5.0	<5.0	<5.0	<5.0	<5.0	~5.0

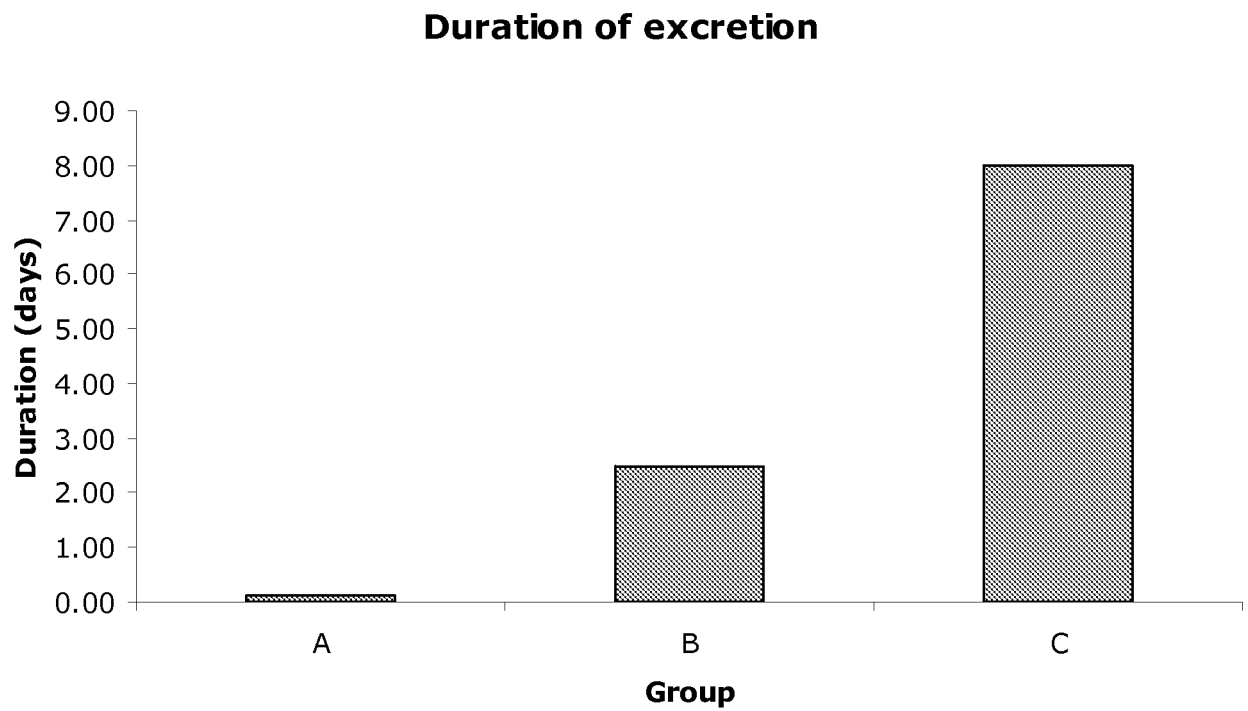
Figure 12



Group	Nb of viremic horses
A	3
B	3
C	8

Figure 13

Excretion in Nasal Swabs



Group	Nb of horses shedding virus
A	1
B	6
C	8

Figure 14
FIG. 14A EHV-1 DNA Polymerase polynucleotide sequence alignment

		1	50
AY464052 (Pol)	(1)	TCAGCTTTGATGGGGAGCTGCTTCTAGAGTACAAAAAACTGTATGCAGTA	
AY665713 (Pol)	(1)	TCAGCTTTGATGGGGAGCTGCTTCTAGAGTACAAAAAACTGTATGCAGTA	
NC_001491 (Pol)	(1)	TCAGCTTTGATGGGGAGCTGCTTCTAGAGTACAAAAAACTGTATGCAGTA	
		51	100
AY464052 (Pol)	(51)	TTGACGACTTTCTTCTCCGGTGTAAGGGCGTCAGCTTTTCAAAGCCG	
AY665713 (Pol)	(51)	TTGACGACTTTCTTCTCCGGTGTAAGGGCGTCAGCTTTTCAAAGCCG	
NC_001491 (Pol)	(51)	TTGACGACTTTCTTCTCCGGTGTAAGGGCGTCAGCTTTTCAAAGCCG	
		101	150
AY464052 (Pol)	(101)	GCGCGCTCAAGCAGTGCCCTGGGTTTTCTGGGGGCTTGTGGGGGTTTC	
AY665713 (Pol)	(101)	GCGCGCTCAAGCAGTGCCCTGGGTTTTCTGGGGGCTTGTGGGGGTTTC	
NC_001491 (Pol)	(101)	GCGCGCTCAAGCAGTGCCCTGGGTTTTCTGGGGGCTTGTGGGGGTTTC	
		151	200
AY464052 (Pol)	(151)	CGGAATAAACCGCTTTAAAGATTTTCTGTTGTTCTCACATCAFTTCCGA	
AY665713 (Pol)	(151)	CGGAATAAACCGCTTTAAAGATTTTCTGTTGTTCTCACATCAFTTCCGA	
NC_001491 (Pol)	(151)	CGGAATAAACCGCTTTAAAGATTTTCTGTTGTTCTCACATCAFTTCCGA	
		201	250
AY464052 (Pol)	(201)	ATAGAGCCTTAAAGGTCACGCTTATGGTACCCAACAGGTGGGAGAAATAG	
AY665713 (Pol)	(201)	ATAGAGCCTTAAAGGTCACGCTTATGGTACCCAACAGGTGGGAGAAATAG	
NC_001491 (Pol)	(201)	ATAGAGCCTTAAAGGTCACGCTTATGGTACCCAACAGGTGGGAGAAATAG	
		251	300
AY464052 (Pol)	(251)	TAGTCTGTGTTTACGGGTACGTCATTCTCGGAAACATAGGTCGGGTCTTC	
AY665713 (Pol)	(251)	TAGTCTGTGTTTACGGGTACGTCATTCTCGGAAACATAGGTCGGGTCTTC	
NC_001491 (Pol)	(251)	TAGTCTGTGTTTACGGGTACGTCATTCTCGGAAACATAGGTCGGGTCTTC	
		301	350
AY464052 (Pol)	(301)	GGCGAGGTCGGAAACAGCAGTTTGCCTTTAGGTTGGGGGCGTGCGGTCT	
AY665713 (Pol)	(301)	GGCGAGGTCGGAAACAGCAGTTTGCCTTTAGGTTGGGGGCGTGCGGTCT	
NC_001491 (Pol)	(301)	GGCGAGGTCGGAAACAGCAGTTTGCCTTTAGGTTGGGGGCGTGCGGTCT	
		351	400
AY464052 (Pol)	(351)	TGGTTACCACGGGGTTTTGGGCGGTACCGCGCATTTAGTTTACTACACCC	
AY665713 (Pol)	(351)	TGGTTACCACGGGGTTTTGGGCGGTACCGCGCATTTAGTTTACTACACCC	
NC_001491 (Pol)	(351)	TGGTTACCACGGGGTTTTGGGCGGTACCGCGCATTTAGTTTACTACACCC	
		401	450
AY464052 (Pol)	(401)	GCTTCGCGTTCGCGGGCTCGGTCTGCGCAACTATCACATACGGAATTCT	
AY665713 (Pol)	(401)	GCTTCGCGTTCGCGGGCTCGGTCTGCGCAACTATCACATACGGAATTCT	
NC_001491 (Pol)	(401)	GCTTCGCGTTCGCGGGCTCGGTCTGCGCAACTATCACATACGGAATTCT	
		451	500
AY464052 (Pol)	(451)	CTCTTTTACGCTGGGCAGTTCTTCATTCTCTATGGCGAGCTTAAAGTAGA	
AY665713 (Pol)	(451)	CTCTTTTACGCTGGGCAGTTCTTCATTCTCTATGGCGAGCTTAAAGTAGA	
NC_001491 (Pol)	(451)	CTCTTTTACGCTGGGCAGTTCTTCATTCTCTATGGCGAGCTTAAAGTAGA	
		501	550
AY464052 (Pol)	(501)	CGGTGAGGTGCGGCAGGCGCTTGTGGTATACGATTGGGTGAGCGGCTC	
AY665713 (Pol)	(501)	CGGTGAGGTGCGGCAGGCGCTTGTGGTATACGATTGGGTGAGCGGCTC	
NC_001491 (Pol)	(501)	CGGTGAGGTGCGGCAGGCGCTTGTGGTATACGATTGGGTGAGCGGCTC	

Figure 14 (continued)

		551	600
AY464052 (Pol)	(551)	AGCTCAGCAGTCATAACGAAC	TCGCGCACGTCCAAGTTGGGGG
AY665713 (Pol)	(551)	AGCTCAGCAGTCATAACGAAC	TCGCGCACGTCCAAGTTGGGGG
NC_001491 (Pol)	(551)	AGCTCAGCAGTCATAACGAAC	TCGCGCACGTCCAAGTTGGGGG
		601	650
AY464052 (Pol)	(601)	ACGGTTGTACGCCTCTACCA	GCACTCGCCCAAACCTTGTC
AY665713 (Pol)	(601)	ACGGTTGTACGCCTCTACCA	GCACTCGCCCAAACCTTGTC
NC_001491 (Pol)	(601)	ACGGTTGTACGCCTCTACCA	GCACTCGCCCAAACCTTGTC
		651	700
AY464052 (Pol)	(651)	GTAGCGGGCGCCCCACCCAT	TTCTGCGGGAGGCACGTCTGT
AY665713 (Pol)	(651)	GTAGCGGGCGCCCCACCCAT	TTCTGCGGGAGGCACGTCTGT
NC_001491 (Pol)	(651)	GTAGCGGGCGCCCCACCCAT	TTCTGCGGGAGGCACGTCTGT
		701	750
AY464052 (Pol)	(701)	GCCGCCGTGGCCACATCCTCG	TGTAACAACAAAAGATCTACC
AY665713 (Pol)	(701)	GCCGCCGTGGCCACATCCTCG	TGTAACAACAAAAGATCTACC
NC_001491 (Pol)	(701)	GCCGCCGTGGCCACATCCTCG	TGTAACAACAAAAGATCTACC
		751	800
AY464052 (Pol)	(751)	CGCGTACAAGTTTATGAAAG	AGCAGTTATTTTTCGGGACC
AY665713 (Pol)	(751)	CGCGTACAAGTTTATGAAAG	AGCAGTTATTTTTCGGGACC
NC_001491 (Pol)	(751)	CGCGTACAAGTTTATGAAAG	AGCAGTTATTTTTCGGGACC
		801	850
AY464052 (Pol)	(801)	CCTTCATGAGCATCTTCCCC	CGTTTATGACACCTATGTACT
AY665713 (Pol)	(801)	CCTTCATGAGCATCTTCCCC	CGTTTATGACACCTATGTACT
NC_001491 (Pol)	(801)	CCTTCATGAGCATCTTCCCC	CGTTTATGACACCTATGTACT
		851	900
AY464052 (Pol)	(851)	GTGATCAGCAGCAGTCGCTG	AAAGGTCTTCTCACACTCCAG
AY665713 (Pol)	(851)	GTGATCAGCAGCAGTCGCTG	AAAGGTCTTCTCACACTCCAG
NC_001491 (Pol)	(851)	GTGATCAGCAGCAGTCGCTG	AAAGGTCTTCTCACACTCCAG
		901	950
AY464052 (Pol)	(901)	CGCTCTAAAGAGGTCCGCTG	AAATCTGACGCGACATAGCAT
AY665713 (Pol)	(901)	CGCTCTAAAGAGGTCCGCTG	AAATCTGACGCGACATAGCAT
NC_001491 (Pol)	(901)	CGCTCTAAAGAGGTCCGCTG	AAATCTGACGCGACATAGCAT
		951	1000
AY464052 (Pol)	(951)	CCGATACCCCTCGTACGTC	AGGCCACAAACTTGATAAAAC
AY665713 (Pol)	(951)	CCGATACCCCTCGTACGTC	AGGCCACAAACTTGATAAAAC
NC_001491 (Pol)	(951)	CCGATACCCCTCGTACGTC	AGGCCACAAACTTGATAAAAC
		1001	1050
AY464052 (Pol)	(1001)	GTGTCTCCGTAGATAAACCT	GGACGGAGTAAGGCTTGTGG
AY665713 (Pol)	(1001)	GTGTCTCCGTAGATAAACCT	GGACGGAGTAAGGCTTGTGG
NC_001491 (Pol)	(1001)	GTGTCTCCGTAGATAAACCT	GGACGGAGTAAGGCTTGTGG
		1051	1100
AY464052 (Pol)	(1051)	TATAGCCCTTGGAAATTTG	TCTCCAGCAGCTCGCGCGT
AY665713 (Pol)	(1051)	TATAGCCCTTGGAAATTTG	TCTCCAGCAGCTCGCGCGT
NC_001491 (Pol)	(1051)	TATAGCCCTTGGAAATTTG	TCTCCAGCAGCTCGCGCGT
		1101	1150
AY464052 (Pol)	(1101)	AGTGAACGTAATCTCGGGT	CTTGAGGAGCATGTGCGCT
AY665713 (Pol)	(1101)	AGTGAACGTAATCTCGGGT	CTTGAGGAGCATGTGCGCT
NC_001491 (Pol)	(1101)	AGTGAACGTAATCTCGGGT	CTTGAGGAGCATGTGCGCT

Figure 14 (continued)

			1151	1200
AY464052 (Po1)	(1151)		ACGGTAGCCGCTATCCTCAGACACGGCAACAGGCCGTTTGCCACCCCCGT	
AY665713 (Po1)	(1151)		ACGGTAGCCGCTATCCTCAGACACGGCAACAGGCCGTTTGCCACCCCCGT	
NC_001491 (Po1)	(1151)		ACGGTAGCCGCTATCCTCAGACACGGCAACAGGCCGTTTGCCACCCCCGT	
			1201	1250
AY464052 (Po1)	(1201)		GAATCCGTAAACCGAGTTGCATATCACCTTAATCGCAGACTGCTGCTTAT	
AY665713 (Po1)	(1201)		GAATCCGTAAACCGAGTTGCATATCACCTTAATCGCAGACTGCTGCTTAT	
NC_001491 (Po1)	(1201)		GAATCCGTAAACCGAGTTGCATATCACCTTAATCGCAGACTGCTGCTTAT	
			1251	1300
AY464052 (Po1)	(1251)		CTAGTAAAACTGCCTCCTCGGGGGTGCTGGTGGGGATTGCGGCCCTCACC	
AY665713 (Po1)	(1251)		CTAGTAAAACTGCCTCCTCGGGGGTGCTGGTGGGGATTGCGGCCCTCACC	
NC_001491 (Po1)	(1251)		CTAGTAAAACTGCCTCCTCGGGGGTGCTGGTGGGGATTGCGGCCCTCACC	
			1301	1350
AY464052 (Po1)	(1301)		GCCTTTTCGCATGGCCAGCCAGTCGCGCAGCAAGATGCCAAGCAGGCTTTC	
AY665713 (Po1)	(1301)		GCCTTTTCGCATGGCCAGCCAGTCGCGCAGCAAGATGCCAAGCAGGCTTTC	
NC_001491 (Po1)	(1301)		GCCTTTTCGCATGGCCAGCCAGTCGCGCAGCAAGATGCCAAGCAGGCTTTC	
			1351	1400
AY464052 (Po1)	(1351)		GCGAATATGGGCGTGGACAAAAATAAATTTTGGTCACCCACCTCGAAGC	
AY665713 (Po1)	(1351)		GCGAATATGGGCGTGGACAAAAATAAATTTTGGTCACCCACCTCGAAGC	
NC_001491 (Po1)	(1351)		GCGAATATGGGCGTGGACAAAAATAAATTTTGGTCACCCACCTCGAAGC	
			1401	1450
AY464052 (Po1)	(1401)		TCGAGTAGTGTGACGGATGGTTGAAGCCCGGCCAGATCCACTTCATCGAGC	
AY665713 (Po1)	(1401)		TCGAGTAGTGTGACGGATGGTTGAAGCCCGGCCAGATCCACTTCATCGAGC	
NC_001491 (Po1)	(1401)		TCGAGTAGTGTGACGGATGGTTGAAGCCCGGCCAGATCCACTTCATCGAGC	
			1451	1500
AY464052 (Po1)	(1451)		GCCAGGGTGGTGAAACAGAGGTTATGGGCCTGGATAATGCTTGGGTATAA	
AY665713 (Po1)	(1451)		GCCAGGGTGGTGAAACAGAGGTTATGGGCCTGGATAATGCTTGGGTATAA	
NC_001491 (Po1)	(1451)		GCCAGGGTGGTGAAACAGAGGTTATGGGCCTGGATAATGCTTGGGTATAA	
			1501	1550
AY464052 (Po1)	(1501)		GCTAGCGAAGTCAAACACAACCACGGGGTCCACATGAAAGCCGGATACGG	
AY665713 (Po1)	(1501)		GCTAGCGAAGTCAAACACAACCACGGGGTCCACATGAAAGCCGGATACGG	
NC_001491 (Po1)	(1501)		GCTAGCGAAGTCAAACACAACCACGGGGTCCACATGAAAGCCGGATACGG	
			1551	1600
AY464052 (Po1)	(1551)		GGTCTAGAACCCTTTGCTCCCTGGTAGCCACACGGCCCTCCCGACGCCGGGC	
AY665713 (Po1)	(1551)		GGTCTAGAACCCTTTGCTCCCTGGTAGCCACACGGCCCTCCCGACGCCGGGC	
NC_001491 (Po1)	(1551)		GGTCTAGAACCCTTTGCTCCCTGGTAGCCACACGGCCCTCCCGACGCCGGGC	
			1601	1650
AY464052 (Po1)	(1601)		TTCCCGCCTCCGTTTTCAGAAGTAGCGCCAGATCCTGCGGCGTCCGGGGT	
AY665713 (Po1)	(1601)		TTCCCGCCTCCGTTTTCAGAAGTAGCGCCAGATCCTGCGGCGTCCGGGGT	
NC_001491 (Po1)	(1601)		TTCCCGCCTCCGTTTTCAGAAGTAGCGCCAGATCCTGCGGCGTCCGGGGT	
			1651	1700
AY464052 (Po1)	(1651)		ACCGTCCACACCGTCGGGTTCTGTCTGTACTGTGGAAGGCGTGGCTTTGGC	
AY665713 (Po1)	(1651)		ACCGTCCACACCGTCGGGTTCTGTCTGTACTGTGGAAGGCGTGGCTTTGGC	
NC_001491 (Po1)	(1651)		ACCGTCCACACCGTCGGGTTCTGTCTGTACTGTGGAAGGCGTGGCTTTGGC	
			1701	1750
AY464052 (Po1)	(1701)		TATCCATAGCCAACTCCGAAGTCTCTGACGCGGCGTCTGCCTGACTGTCA	
AY665713 (Po1)	(1701)		TATCCATAGCCAACTCCGAAGTCTCTGACGCGGCGTCTGCCTGACTGTCA	
NC_001491 (Po1)	(1701)		TATCCATAGCCAACTCCGAAGTCTCTGACGCGGCGTCTGCCTGACTGTCA	

Figure 14 (continued)

		1751	1800
AY464052 (Pol)	(1751)	AACCGGCGTCTGTTGTCTGGCAAAATGAAATTTCTCTCGGGGCGAGTTT	
AY665713 (Pol)	(1751)	AACCGGCGTCTGTTGTCTGGCAAAATGAAATTTCTCTCGGGGCGAGTTT	
NC_001491 (Pol)	(1751)	AACCGGCGTCTGTTGTCTGGCAAAATGAAATTTCTCTCGGGGCGAGTTT	
		1801	1850
AY464052 (Pol)	(1801)	CAGCAAGCACGTGTACACGCGAATTTGCTGACCGTCAAAAATTACCCGCG	
AY665713 (Pol)	(1801)	CAGCAAGCACGTGTACACGCGAATTTGCTGACCGTCAAAAATTACCCGCG	
NC_001491 (Pol)	(1801)	CAGCAAGCACGTGTACACGCGAATTTGCTGACCGTCAAAAATTACCCGCG	
		1851	1900
AY464052 (Pol)	(1851)	TTAGGGTGATACGGGCGAGTTTGGCCACCGCCGATAGTTCCAGATGGGGG	
AY665713 (Pol)	(1851)	TTAGGGTGATACGGGCGAGTTTGGCCACCGCCGATAGTTCCAGATGGGGG	
NC_001491 (Pol)	(1851)	TTAGGGTGATACGGGCGAGTTTGGCCACCGCCGATAGTTCCAGATGGGGG	
		1901	1950
AY464052 (Pol)	(1901)	AGGTACTTAAAAACAGCTTGCCACCAGCCTAGAGTCCTGGATACAATA	
AY665713 (Pol)	(1901)	AGGTACTTAAAAACAGCTTGCCACCAGCCTAGAGTCCTGGATACAATA	
NC_001491 (Pol)	(1901)	AGGTACTTAAAAACAGCTTGCCACCAGCCTAGAGTCCTGGATACAATA	
		1951	2000
AY464052 (Pol)	(1951)	CTCTCCTATTACGCCCTCCGGTCAGGCCCTCCCGCGTAATAGGAGGGTA	
AY665713 (Pol)	(1951)	CTCTCCTATTACGCCCTCCGGTCAGGCCCTCCCGCGTAATAGGAGGGTA	
NC_001491 (Pol)	(1951)	CTCTCCTATTACGCCCTCCGGTCAGGCCCTCCCGCGTAATAGGAGGGTA	
		2001	2050
AY464052 (Pol)	(2001)	TTTCTTTATAGGGAAGGTCTATCTTATGCTCGCCGAGGACGTCCTCCACG	
AY665713 (Pol)	(2001)	TTTCTTTATAGGGAAGGTCTATCTTATGCTCGCCGAGGACGTCCTCCACG	
NC_001491 (Pol)	(2001)	TTTCTTTATAGGGAAGGTCTATCTTATGCTCGCCGAGGACGTCCTCCACG	
		2051	2100
AY464052 (Pol)	(2051)	ACCGCGTCGAGTTTGTAGCTGGGTAGCTTTAGCTTTTCCGTCGCCACAGA	
AY665713 (Pol)	(2051)	ACCGCGTCGAGTTTGTAGCTGGGTAGCTTTAGCTTTTCCGTCGCCACAGA	
NC_001491 (Pol)	(2051)	ACCGCGTCGAGTTTGTAGCTGGGTAGCTTTAGCTTTTCCGTCGCCACAGA	
		2101	2150
AY464052 (Pol)	(2101)	ATACATGTCTAGAGATATCAGGCCATTGATTTTACCTTGCTCTTCTTCT	
AY665713 (Pol)	(2101)	ATACATGTCTAGAGATATCAGGCCATTGATTTTACCTTGCTCTTCTTCT	
NC_001491 (Pol)	(2101)	ATACATGTCTAGAGATATCAGGCCATTGATTTTACCTTGCTCTTCTTCT	
		2151	2200
AY464052 (Pol)	(2151)	GAAATGGTTCGTGGCGATGTCCACACCTTAAACAGCCCCCTTTGTTG	
AY665713 (Pol)	(2151)	GAAATGGTTCGTGGCGATGTCCACACCTTAAACAGCCCCCTTTGTTG	
NC_001491 (Pol)	(2151)	GAAATGGTTCGTGGCGATGTCCACACCTTAAACAGCCCCCTTTGTTG	
		2201	2250
AY464052 (Pol)	(2201)	AACTTGCCGTACCCGTCCAGCTTGATGTTATACACCGACGTTACCTTGTT	
AY665713 (Pol)	(2201)	AACTTGCCGTACCCGTCCAGCTTGATGTTATACACCGACGTTACCTTGTT	
NC_001491 (Pol)	(2201)	AACTTGCCGTACCCGTCCAGCTTGATGTTATACACCGACGTTACCTTGTT	
		2251	2300
AY464052 (Pol)	(2251)	AACTATGTACGCCAGTCAAAATTAACGATGTTGTAGCCGGTGGCGAACT	
AY665713 (Pol)	(2251)	AACTATGTACGCCAGTCAAAATTAACGATGTTGTAGCCGGTGGCGAACT	
NC_001491 (Pol)	(2251)	AACTATGTACGCCAGTCAAAATTAACGATGTTGTAGCCGGTGGCGAACT	
		2301	2350
AY464052 (Pol)	(2301)	CGGGAGAGTACTGCTTGAGAAAGGTGAGGAAGGCAACCAGCAGCTCGTAC	
AY665713 (Pol)	(2301)	CGGGAGAGTACTGCTTGAGAAAGGTGAGGAAGGCAACCAGCAGCTCGTAC	
NC_001491 (Pol)	(2301)	CGGGAGAGTACTGCTTGAGAAAGGTGAGGAAGGCAACCAGCAGCTCGTAC	

Figure 14 (continued)

			2351	2400
AY464052 (Pol)	(2351)		TCGCTGTCAAACCTCCAAAACCGTCGGTCTGGGCTCGCCGCGCTGGACGCA	
AY665713 (Pol)	(2351)		TCGCTGTCAAACCTCCAAAACCGTCGGTCTGGGCTCGCCGCGCTGGACGCA	
NC_001491 (Pol)	(2351)		TCGCTGTCAAACCTCCAAAACCGTCGGTCTGGGCTCGCCGCGCTGGACGCA	
			2401	2450
AY464052 (Pol)	(2401)		TGCAAAACGAGTATTCTCTCAGAGATATCGCATGACCCGAGGGAAAACAGCA	
AY665713 (Pol)	(2401)		TGCAAAACGAGTATTCTCTCAGAGATATCGCATGACCCGAGGGAAAACAGCA	
NC_001491 (Pol)	(2401)		TGCAAAACGAGTATTCTCTCAGAGATATCGCATGACCCGAGGGAAAACAGCA	
			2451	2500
AY464052 (Pol)	(2451)		GGGTGTGTTCTGGTTCTGAGTAGCAAGCGAGTACAGCAGACAGGAGATC	
AY665713 (Pol)	(2451)		GGGTGTGTTCTGGTTCTGAGTAGCAAGCGAGTACAGCAGACAGGAGATC	
NC_001491 (Pol)	(2451)		GGGTGTGTTCTGGTTCTGAGTAGCAAGCGAGTACAGCAGACAGGAGATC	
			2501	2550
AY464052 (Pol)	(2501)		TGGATGACCAGGTCTCTTGGTTAGTTGCCACTGGGAACGCCATTTTCGTT	
AY665713 (Pol)	(2501)		TGGATGACCAGGTCTCTTGGTTAGTTGCCACTGGGAACGCCATTTTCGTT	
NC_001491 (Pol)	(2501)		TGGATGACCAGGTCTCTTGGTTAGTTGCCACTGGGAACGCCATTTTCGTT	
			2551	2600
AY464052 (Pol)	(2551)		ACCCGTTCCAGCTTTACACTCTATATCAAAGCACATGAGCTTATAGTCGG	
AY665713 (Pol)	(2551)		ACCCGTTCCAGCTTTACACTCTATATCAAAGCACATGAGCTTATAGTCGG	
NC_001491 (Pol)	(2551)		ACCCGTTCCAGCTTTACACTCTATATCAAAGCACATGAGCTTATAGTCGG	
			2601	2650
AY464052 (Pol)	(2601)		GCCAGGCAGCCTCGTCTGGTATCGGCTCCAGGTTATCGGGAGTACAGTTA	
AY665713 (Pol)	(2601)		GCCAGGCAGCCTCGTCTGGTATCGGCTCCAGGTTATCGGGAGTACAGTTA	
NC_001491 (Pol)	(2601)		GCCAGGCAGCCTCGTCTGGTATCGGCTCCAGGTTATCGGGAGTACAGTTA	
			2651	2700
AY464052 (Pol)	(2651)		ATCTCCACGTGCTTGAGGTGACGTGTGCTCAACGGGGCGAAGTTGAAC	
AY665713 (Pol)	(2651)		ATCTCCACGTGCTTGAGGTGACGTGTGCTCAACGGGGCGAAGTTGAAC	
NC_001491 (Pol)	(2651)		ATCTCCACGTGCTTGAGGTGACGTGTGCTCAACGGGGCGAAGTTGAAC	
			2701	2750
AY464052 (Pol)	(2701)		ACGCTCTCCGTGGGTGCCGGGTGCGAGGCGGTACCAACCCAAAACCTGGTAA	
AY665713 (Pol)	(2701)		ACGCTCTCCGTGGGTGCCGGGTGCGAGGCGGTACCAACCCAAAACCTGGTAA	
NC_001491 (Pol)	(2701)		ACGCTCTCCGTGGGTGCCGGGTGCGAGGCGGTACCAACCCAAAACCTGGTAA	
			2751	2800
AY464052 (Pol)	(2751)		AATTTTCATTGTCCAACAACAGCCGCGTGGTCACGTCCACGCTCCCTTCG	
AY665713 (Pol)	(2751)		AATTTTCATTGTCCAACAACAGCCGCGTGGTCACGTCCACGCTCCCTTCG	
NC_001491 (Pol)	(2751)		AATTTTCATTGTCCAACAACAGCCGCGTGGTCACGTCCACGCTCCCTTCG	
			2801	2850
AY464052 (Pol)	(2801)		AATTTTGTAATCTCCGGGTGAAAGTTGTGCGCAGATGAACCTCCAGGCG	
AY665713 (Pol)	(2801)		AATTTTGTAATCTCCGGGTGAAAGTTGTGCGCAGATGAACCTCCAGGCG	
NC_001491 (Pol)	(2801)		AATTTTGTAATCTCCGGGTGAAAGTTGTGCGCAGATGAACCTCCAGGCG	
			2851	2900
AY464052 (Pol)	(2851)		GCTGCTGGAGGCAGATACTCTATAGTAGAGAGCTGGCTTAGATCCAAAGT	
AY665713 (Pol)	(2851)		GCTGCTGGAGGCAGATACTCTATAGTAGAGAGCTGGCTTAGATCCAAAGT	
NC_001491 (Pol)	(2851)		GCTGCTGGAGGCAGATACTCTATAGTAGAGAGCTGGCTTAGATCCAAAGT	
			2901	2950
AY464052 (Pol)	(2901)		AGTACAGCGTCGTGTGGCACACGGTCTCCACTTTGAAGCAGTCCGCAGAC	
AY665713 (Pol)	(2901)		AGTACAGCGTCGTGTGGCACACGGTCTCCACTTTGAAGCAGTCCGCAGAC	
NC_001491 (Pol)	(2901)		AGTACAGCGTCGTGTGGCACACGGTCTCCACTTTGAAGCAGTCCGCAGAC	

Figure 14 (continued)

			2951	3000
AY464052 (Pol)	(2951)		ACGTGCTTTCGCCCCCACCATCCCCCGCCGCTGCGCGCGCTCTGTTTGCC	
AY665713 (Pol)	(2951)		ACGTGCTTTCGCCCCCACCATCCCCCGCCGCTGCGCGCGCTCTGTTTGCC	
NC_001491 (Pol)	(2951)		ACGTGCTTTCGCCCCCACCATCCCCCGCCGCTGCGCGCGCTCTGTTTGCC	
			3001	3050
AY464052 (Pol)	(3001)		GCCGTTGCCATTTCCAGGGCCGCGCTCAAAGCCGAGCTGTGCGCGCAGT	
AY665713 (Pol)	(3001)		GCCGTTGCCATTTCCAGGGCCGCGCTCAAAGCCGAGCTGTGCGCGCAGT	
NC_001491 (Pol)	(3001)		GCCGTTGCCATTTCCAGGGCCGCGCTCAAAGCCGAGCTGTGCGCGCAGT	
			3051	3100
AY464052 (Pol)	(3051)		CCACCATTGCGCGCACGAGTTCTGCCTCGGTGGTTATTCCACAAGCGCTA	
AY665713 (Pol)	(3051)		CCACCATTGCGCGCACGAGTTCTGCCTCGGTGGTTATTCCACAAGCGCTA	
NC_001491 (Pol)	(3051)		CCACCATTGCGCGCACGAGTTCTGCCTCGGTGGTTATTCCACAAGCGCTA	
			3101	3150
AY464052 (Pol)	(3101)		TCCACCTCCGCCTTTGCCATGTAAAAATAATGGCGCACACCATAGACGTG	
AY665713 (Pol)	(3101)		TCCACCTCCGCCTTTGCCATGTAAAAATAATGGCGCACACCATAGACGTG	
NC_001491 (Pol)	(3101)		TCCACCTCCGCCTTTGCCATGTAAAAATAATGGCGCACACCATAGACGTG	
			3151	3200
AY464052 (Pol)	(3151)		AACCGCGACTCGCTTTCCACACTCGCTCATTTCCAGCAGTGTTACCACAG	
AY665713 (Pol)	(3151)		AACCGCGACTCGCTTTCCACACTCGCTCATTTCCAGCAGTGTTACCACAG	
NC_001491 (Pol)	(3151)		AACCGCGACTCGCTTTCCACACTCGCTCATTTCCAGCAGTGTTACCACAG	
			3201	3250
AY464052 (Pol)	(3201)		ACCCGCTTGGGCGGGATAGCTCAGCAAACCTGGATGGGTTCATCGTGTGAG	
AY665713 (Pol)	(3201)		ACCCGCTTGGGCGGGATAGCTCAGCAAACCTGGATGGGTTCATCGTGTGAG	
NC_001491 (Pol)	(3201)		ACCCGCTTGGGCGGGATAGCTCAGCAAACCTGGATGGGTTCATCGTGTGAG	
			3251	3300
AY464052 (Pol)	(3251)		GCGCTCTCCGAAGTCTCTACTATGTGCTACACGTGAAATCTCTCAAATCT	
AY665713 (Pol)	(3251)		GCGCTCTCCGAAGTCTCTACTATGTGCTACACGTGAAATCTCTCAAATCT	
NC_001491 (Pol)	(3251)		GCGCTCTCCGAAGTCTCTACTATGTGCTACACGTGAAATCTCTCAAATCT	
			3301	3350
AY464052 (Pol)	(3301)		GGGGTTGAATCCATCGCCCCGAAAATCCTGGCCGTTCCAAACCCGAATCC	
AY665713 (Pol)	(3301)		GGGGTTGAATCCATCGCCCCGAAAATCCTGGCCGTTCCAAACCCGAATCC	
NC_001491 (Pol)	(3301)		GGGGTTGAATCCATCGCCCCGAAAATCCTGGCCGTTCCAAACCCGAATCC	
			3351	3400
AY464052 (Pol)	(3351)		TGCGAGGCCAGCAACCTCCGGAGGCCAAAGTTCAGCACGTGTACTCTGAG	
AY665713 (Pol)	(3351)		TGCGAGGCCAGCAACCTCCGGAGGCCAAAGTTCAGCACGTGTACTCTGAG	
NC_001491 (Pol)	(3351)		TGCGAGGCCAGCAACCTCCGGAGGCCAAAGTTCAGCACGTGTACTCTGAG	
			3401	3450
AY464052 (Pol)	(3401)		CCATCGCAGTACACTTTGGGTGGGCGCTCCAAGGTGCCCACGTGTACACC	
AY665713 (Pol)	(3401)		CCATCGCAGTACACTTTGGGTGGGCGCTCCAAGGTGCCCACGTGTACACC	
NC_001491 (Pol)	(3401)		CCATCGCAGTACACTTTGGGTGGGCGCTCCAAGGTGCCCACGTGTACACC	
			3451	3500
AY464052 (Pol)	(3451)		GCGTCGCTGGTGGCGGGGGCTTCTTCATCGAGGCATCTTGGAGCTATAA	
AY665713 (Pol)	(3451)		GCGTCGCTGGTGGCGGGGGCTTCTTCATCGAGGCATCTTGGAGCTATAA	
NC_001491 (Pol)	(3451)		GCGTCGCTGGTGGCGGGGGCTTCTTCATCGAGGCATCTTGGAGCTATAA	
			3501	3550
AY464052 (Pol)	(3501)		ACTTAAAGCTACCCACCTCTGTGCAGTACGAGTGTGGGGGGGCTTGGG	
AY665713 (Pol)	(3501)		ACTTAAAGCTACCCACCTCTGTGCAGTACGAGTGTGGGGGGGCTTGGG	
NC_001491 (Pol)	(3501)		ACTTAAAGCTACCCACCTCTGTGCAGTACGAGTGTGGGGGGGCTTGGG	

Figure 14 (continued)

			3551		3600
AY464052	(Pol)	(3551)	CGCTCTGTCTCCGCGGTCTGCCCGCTTCCCGGCTGAAAAATGGGCTCTT		
AY665713	(Pol)	(3551)	CGCTCTGTCTCCGCGGTCTGCCCGCTTCCCGGCTGAAAAATGGGCTCTT		
NC_001491	(Pol)	(3551)	CGCTCTGTCTCCGCGGTCTGCCCGCTTCCCGGCTGAAAAATGGGCTCTT		
			3601		3650
AY464052	(Pol)	(3601)	GCCAATAAACGGATTAAAAAACCCGCTCCTGCGAACGGAGTTGGCCTGTT		
AY665713	(Pol)	(3601)	GCCAATAAACGGATTAAAAAACCCGCTCCTGCGAACGGAGTTGGCCTGTT		
NC_001491	(Pol)	(3601)	GCCAATAAACGGATTAAAAAACCCGCTCCTGCGAACGGAGTTGGCCTGTT		
			3651	3663	
AY464052	(Pol)	(3651)	CGCGCGCCGCCAT		
AY665713	(Pol)	(3651)	CGCGCGCCGCCAT		
NC_001491	(Pol)	(3651)	CGCGCGCCGCCAT		

Sequence identity percentage:

AY464052 (SEQ ID NO:1) v. AY665713 (SEQ ID NO:3): 99.9%
 AY464052 (SEQ ID NO:1) v. NC_001491 (SEQ ID NO:5): 99.9%
 AY665713 (SEQ ID NO:3) v. NC_001491 (SEQ ID NO:5): 100%

Figure 14 (continued)

FIG. 14B EHV-1 DNA Polymerase full length protein sequence alignment

	1	50
EHV-1 Pol (SEQ2)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV
EHV-1 Pol (SEQ37)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV
EHV-1 Pol (SEQ4)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV
EHV-1 Pol (SEQ6)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV
	51	100
EHV-1 Pol (SEQ2)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNFAASGG
EHV-1 Pol (SEQ37)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNFAASGG
EHV-1 Pol (SEQ4)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNFAASGG
EHV-1 Pol (SEQ6)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNFAASGG
	101	150
EHV-1 Pol (SEQ2)	(101)	CWPRRIKRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS
EHV-1 Pol (SEQ37)	(101)	CWPRRIKRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS
EHV-1 Pol (SEQ4)	(101)	CWPRRIKRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS
EHV-1 Pol (SEQ6)	(101)	CWPRRIKRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS
	151	200
EHV-1 Pol (SEQ2)	(151)	RPSGSVVTLLGMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV
EHV-1 Pol (SEQ37)	(151)	RPSGSVVTLLGMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV
EHV-1 Pol (SEQ4)	(151)	RPSGSVVTLLGMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV
EHV-1 Pol (SEQ6)	(151)	RPSGSVVTLLGMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV
	201	250
EHV-1 Pol (SEQ2)	(201)	RAMVDCAHSSALSAAALGNNGGCKQSGGSGGGWGGKHVSADCFEVETVCH
EHV-1 Pol (SEQ37)	(201)	RAMVDCAHSSALSAAALGNNGGCKQSGGSGGGWGGKHVSADCFEVETVCH
EHV-1 Pol (SEQ4)	(201)	RAMVDCAHSSALSAAALGNNGGCKQSGGSGGGWGGKHVSADCFEVETVCH
EHV-1 Pol (SEQ6)	(201)	RAMVDCAHSSALSAAALGNNGGCKQSGGSGGGWGGKHVSADCFEVETVCH
	251	300
EHV-1 Pol (SEQ2)	(251)	TTLYYFGSKPALYYRVSASSSRLLGGFICDNFHPFITKFEQSVDTVTRLLL
EHV-1 Pol (SEQ37)	(251)	TTLYYFGSKPALYYRVSASSSRLLGGFICDNFHPFITKFEQSVDTVTRLLL
EHV-1 Pol (SEQ4)	(251)	TTLYYFGSKPALYYRVSASSSRLLGGFICDNFHPFITKFEQSVDTVTRLLL
EHV-1 Pol (SEQ6)	(251)	TTLYYFGSKPALYYRVSASSSRLLGGFICDNFHPFITKFEQSVDTVTRLLL
	301	350
EHV-1 Pol (SEQ2)	(301)	DNENFTSFGWYRLRPGTHGERVQLRPFVERHVTSSDVEINCTFDNLEPIFD
EHV-1 Pol (SEQ37)	(301)	DNENFTSFGWYRLRPGTHGERVQLRPFVERHVTSSDVEINCTFDNLEPIFD
EHV-1 Pol (SEQ4)	(301)	DNENFTSFGWYRLRPGTHGERVQLRPFVERHVTSSDVEINCTFDNLEPIFD
EHV-1 Pol (SEQ6)	(301)	DNENFTSFGWYRLRPGTHGERVQLRPFVERHVTSSDVEINCTFDNLEPIFD
	351	400
EHV-1 Pol (SEQ2)	(351)	EAAWFDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN
EHV-1 Pol (SEQ37)	(351)	EAAWFDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN
EHV-1 Pol (SEQ4)	(351)	EAAWFDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN
EHV-1 Pol (SEQ6)	(351)	EAAWFDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN
	401	450
EHV-1 Pol (SEQ2)	(401)	HEHTLLFSLGSCDISSEYSFACVQRGEPRPTVLEFDSEYELIVAFITFLK
EHV-1 Pol (SEQ37)	(401)	HEHTLLFSLGSCDISSEYSFACVQRGEPRPTVLEFDSEYELIVAFITFLK
EHV-1 Pol (SEQ4)	(401)	HEHTLLFSLGSCDISSEYSFACVQRGEPRPTVLEFDSEYELIVAFITFLK
EHV-1 Pol (SEQ6)	(401)	HEHTLLFSLGSCDISSEYSFACVQRGEPRPTVLEFDSEYELIVAFITFLK

Figure 14 (continued)

	451	500
EHV-1 Pol (SEQ2)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNEGGGLFKVWDIA
EHV-1 Pol (SEQ37)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNEGGGLFKVWDIA
EHV-1 Pol (SEQ4)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNEGGGLFKVWDIA
EHV-1 Pol (SEQ6)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNEGGGLFKVWDIA
	501	550
EHV-1 Pol (SEQ2)	(501)	TNHFQKRSKVKINGLISLDMYSVATEKLLKLP SYKLD AVVG DV LG EHKIDL
EHV-1 Pol (SEQ37)	(501)	TNHFQKRSKVKINGLISLDMYSVATEKLLKLP SYKLD AVVG DV LG EHKIDL
EHV-1 Pol (SEQ4)	(501)	TNHFQKRSKVKINGLISLDMYSVATEKLLKLP SYKLD AVVG DV LG EHKIDL
EHV-1 Pol (SEQ6)	(501)	TNHFQKRSKVKINGLISLDMYSVATEKLLKLP SYKLD AVVG DV LG EHKIDL
	551	600
EHV-1 Pol (SEQ2)	(551)	PYKEIPSYIAGGPDRRGVIGEYCIQDSRLVGKLF FFKYLP HLELS AVAKLA
EHV-1 Pol (SEQ37)	(551)	PYKEIPSYIAGGPDRRGVIGEYCIQDSRLVGKLF FFKYLP HLELS AVAKLA
EHV-1 Pol (SEQ4)	(551)	PYKEIPSYIAGGPDRRGVIGEYCIQDSRLVGKLF FFKYLP HLELS AVAKLA
EHV-1 Pol (SEQ6)	(551)	PYKEIPSYIAGGPDRRGVIGEYCIQDSRLVGKLF FFKYLP HLELS AVAKLA
	601	650
EHV-1 Pol (SEQ2)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFD SQADAASETSE
EHV-1 Pol (SEQ37)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFD SQADAASETSE
EHV-1 Pol (SEQ4)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFD SQADAASETSE
EHV-1 Pol (SEQ6)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFD SQADAASETSE
	651	700
EHV-1 Pol (SEQ2)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ37)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ4)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ6)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
	701	750
EHV-1 Pol (SEQ2)	(701)	KVLDPVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ37)	(701)	KVLDPVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ4)	(701)	KVLDPVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ6)	(701)	KVLDPVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
	751	800
EHV-1 Pol (SEQ2)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ37)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ4)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ6)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
	801	850
EHV-1 Pol (SEQ2)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ37)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ4)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ6)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
	851	900
EHV-1 Pol (SEQ2)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ37)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ4)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ6)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
	901	950
EHV-1 Pol (SEQ2)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGK
EHV-1 Pol (SEQ37)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGK
EHV-1 Pol (SEQ4)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGK
EHV-1 Pol (SEQ6)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGK

Figure 14 (continued)

		951	1000
EHV-1 Pol (SEQ2)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAKVTDVFFPAEWV	
EHV-1 Pol (SEQ37)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAKVTDVFFPAEWV	
EHV-1 Pol (SEQ4)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAKVTDVFFPAEWV	
EHV-1 Pol (SEQ6)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAKVTDVFFPAEWV	
		1001	1050
EHV-1 Pol (SEQ2)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	
EHV-1 Pol (SEQ37)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	
EHV-1 Pol (SEQ4)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	
EHV-1 Pol (SEQ6)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	
		1051	1100
EHV-1 Pol (SEQ2)	(1051)	PHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVVNSMRGTAQN	
EHV-1 Pol (SEQ37)	(1051)	PHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVVNSMRGTAQN	
EHV-1 Pol (SEQ4)	(1051)	PHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVVNSMRGTAQN	
EHV-1 Pol (SEQ6)	(1051)	PHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVVNSMRGTAQN	
		1101	1150
EHV-1 Pol (SEQ2)	(1101)	FVVTKTARPQPKRKLLVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	
EHV-1 Pol (SEQ37)	(1101)	FVVTKTARPQPKRKLLVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	
EHV-1 Pol (SEQ4)	(1101)	FVVTKTARPQPKRKLLVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	
EHV-1 Pol (SEQ6)	(1101)	FVVTKTARPQPKRKLLVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	
		1151	1200
EHV-1 Pol (SEQ2)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTPTFTFEE	
EHV-1 Pol (SEQ37)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTPTFTFEE	
EHV-1 Pol (SEQ4)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTPTFTFEE	
EHV-1 Pol (SEQ6)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTPTFTFEE	
		1201	1220
EHV-1 Pol (SEQ2)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ37)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ4)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ6)	(1201)	ESRRILHTVFCTLEAAPHQ	

Sequence identity percentage:

AAS45914.1 (SEQ ID NO :2) v. AAT67287.1 (SEQ ID NO :4): 99.8%

AAS45914.1 (SEQ ID NO :2) v. YP_053075.1 (SEQ ID NO:6): 99.8%

AAT67287.1 (SEQ ID NO :4) v. YP_053075.1 (SEQ ID NO:6): 100%

AAS45914.1 (SEQ ID NO :2) v. SEQ ID NO:37: 99.8%

AAT67287.1 (SEQ ID NO :4) v. SEQ ID NO:37: 99.8%

YP_053075.1 (SEQ ID NO:6) v. SEQ ID NO:37: 99.8%

Figure 14 (continued)

FIG. 14C EHV-1 DNA Polymerase protein sequence alignment (full-length and partial)

		1	50
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV	
EHV-1 Pol (SEQ37)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(1)	MAAREQANSVRRSGFFNPFFIGKRPFFRPGSGQTAETERPRPPQHSYCTEV	
		51	100
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLEPPKVVYCDGSEYDVLPASGG	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLEPPKVVYCDGSEYDVLPASGG	
EHV-1 Pol (SEQ37)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLEPPKVVYCDGSEYDVLPASGG	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(51)	GSFKFIAPRCLDEEAPADQRRGVHVGTLEPPKVVYCDGSEYDVLPASGG	
		101	150
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(101)	CWPRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(101)	CWPRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS	
EHV-1 Pol (SEQ37)	(101)	CWPRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(101)	CWPRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELS	
		151	200
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(151)	RPSGSVVTLTLCMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(151)	RPSGSVVTLTLCMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV	
EHV-1 Pol (SEQ37)	(151)	RPSGSVVTLTLCMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(151)	RPSGSVVTLTLCMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELV	
		201	250
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(201)	RAMVDCAHSSALSAAALGNNGCKQSGGSGGGWGGKHVSADCFKVVETVCH	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(201)	RAMVDCAHSSALSAAALGNNGCKQSGGSGGGWGGKHVSADCFKVVETVCH	
EHV-1 Pol (SEQ37)	(201)	RAMVDCAHSSALSAAALGNNGCKQSGGSGGGWGGKHVSADCFKVVETVCH	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(201)	RAMVDCAHSSALSAAALGNNGCKQSGGSGGGWGGKHVSADCFKVVETVCH	
		251	300
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(251)	TTLYYFGSKPALYYRVSAASSRLGGFICDNFHPFITKFEQSVDTTTRLLI	
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(251)	TTLYYFGSKPALYYRVSAASSRLGGFICDNFHPFITKFEQSVDTTTRLLI	
EHV-1 Pol (SEQ37)	(251)	TTLYYFGSKPALYYRVSAASSRLGGFICDNFHPFITKFEQSVDTTTRLLI	
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(251)	TTLYYFGSKPALYYRVSAASSRLGGFICDNFHPFITKFEQSVDTTTRLLI	

Figure 14 (continued)

		301	350
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(301)	DNENFTSFCWYRLRPGTHGERVQLRPVERHVTSSDVEINCTPDNLEPIPD	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(301)	DNENFTSFCWYRLRPGTHGERVQLRPVERHVTSSDVEINCTPDNLEPIPD	-----
EHV-1 Pol (SEQ37)	(301)	DNENFTSFCWYRLRPGTHGERVQLRPVERHVTSSDVEINCTPDNLEPIPD	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(301)	DNENFTSFCWYRLRPGTHGERVQLRPVERHVTSSDVEINCTPDNLEPIPD	-----
		351	400
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(351)	EAAWPDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(351)	EAAWPDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN	-----
EHV-1 Pol (SEQ37)	(351)	EAAWPDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(351)	EAAWPDYKLMCFDIECKAGTGNEMAFFVATNQEDLVIQISCLLYSLATQN	-----
		401	450
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(401)	HEHTLLFSLGSCDISEEYSFACVQGEPRPTVLEFDSEYELLVAFLTFLK	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(401)	HEHTLLFSLGSCDISEEYSFACVQGEPRPTVLEFDSEYELLVAFLTFLK	-----
EHV-1 Pol (SEQ37)	(401)	HEHTLLFSLGSCDISEEYSFACVQGEPRPTVLEFDSEYELLVAFLTFLK	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(401)	HEHTLLFSLGSCDISEEYSFACVQGEPRPTVLEFDSEYELLVAFLTFLK	-----
		451	500
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIRKLDGYGKFNKGGLFKVWDIA	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIRKLDGYGKFNKGGLFKVWDIA	-----
EHV-1 Pol (SEQ37)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIRKLDGYGKFNKGGLFKVWDIA	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(451)	QYSPEFATGYNIVNFDWAYIVNKVTSVYNIRKLDGYGKFNKGGLFKVWDIA	-----
		501	550
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(501)	TNHFQKSKVKINGLISLDMYSVATEKLELPSYKLDVAVGDLGEHKIDL	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(501)	TNHFQKSKVKINGLISLDMYSVATEKLELPSYKLDVAVGDLGEHKIDL	-----
EHV-1 Pol (SEQ37)	(501)	TNHFQKSKVKINGLISLDMYSVATEKLELPSYKLDVAVGDLGEHKIDL	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(501)	TNHFQKSKVKINGLISLDMYSVATEKLELPSYKLDVAVGDLGEHKIDL	-----
		551	600
EHV-1 Pol (SEQ13)	(1)	-----	-----
EHV-1 Pol (SEQ4)	(551)	PYKEIPSYYAGGPDRRGVIGEYCIQDSRLVGKLFKKYLPHELSAVAKLA	-----
EHV-1 Pol (SEQ14)	(1)	-----	-----
EHV-1 Pol (SEQ2)	(551)	PYKEIPSYYAGGPDRRGVIGEYCIQDSRLVGKLFKKYLPHELSAVAKLA	-----
EHV-1 Pol (SEQ37)	(551)	PYKEIPSYYAGGPDRRGVIGEYCIQDSRLVGKLFKKYLPHELSAVAKLA	-----
EHV-1 Pol (SEQ15)	(1)	-----	-----
EHV-1 Pol (SEQ6)	(551)	PYKEIPSYYAGGPDRRGVIGEYCIQDSRLVGKLFKKYLPHELSAVAKLA	-----

Figure 14 (continued)

	601	650
EHV-1 Pol (SEQ13)	(1)	-----FDSQADAASETSE
EHV-1 Pol (SEQ4)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFDSQADAASETSE
EHV-1 Pol (SEQ14)	(1)	-----FDSQADAASETSE
EHV-1 Pol (SEQ2)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFDSQADAASETSE
EHV-1 Pol (SEQ37)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFDSQADAASETSE
EHV-1 Pol (SEQ15)	(1)	-----FDSQADAASETSE
EHV-1 Pol (SEQ6)	(601)	RITLTRVIFDGGQIRVYTCLLKLARERNFILPDNRRRFDSQADAASETSE
	651	700
EHV-1 Pol (SEQ13)	(14)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ4)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ14)	(14)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ2)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ37)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ15)	(14)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
EHV-1 Pol (SEQ6)	(651)	LAMDSQSHAFDSTDEPDGVDGTFDAAGSGATSENGGGKPGVGRAVGYQGA
	701	750
EHV-1 Pol (SEQ13)	(64)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ4)	(701)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ14)	(64)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ2)	(701)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ37)	(701)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ15)	(64)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
EHV-1 Pol (SEQ6)	(701)	KVLDFVSGFHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPS
	751	800
EHV-1 Pol (SEQ13)	(114)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ4)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ14)	(114)	VNYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ2)	(751)	VNYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ37)	(751)	VNYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ15)	(114)	VYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
EHV-1 Pol (SEQ6)	(751)	VDYSTFEVGDQKLFVVAHIRESLGILLRDWLAMRKAVRARIPTSTPEE
	801	850
EHV-1 Pol (SEQ13)	(164)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCL-----
EHV-1 Pol (SEQ4)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ14)	(164)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCL-----
EHV-1 Pol (SEQ2)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ37)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
EHV-1 Pol (SEQ15)	(163)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCL-----
EHV-1 Pol (SEQ6)	(801)	AVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTR
	851	900
EHV-1 Pol (SEQ13)	(196)	-----
EHV-1 Pol (SEQ4)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ14)	(196)	-----
EHV-1 Pol (SEQ2)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ37)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY
EHV-1 Pol (SEQ15)	(195)	-----
EHV-1 Pol (SEQ6)	(851)	DYVHSRWATRELLEDNFPGAIGFRNHKPYSVRVYIGDTSVFIFKVGGLTY

Figure 14 (continued)

		901	950
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRIILLITKKKYIGVINGGK	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRIILLITKKKYIGVINGGK	-----
EHV-1 Pol (SEQ37)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRIILLITKKKYIGVINGGK	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(901)	EGVSELGDAMSRQISADLFRAPIKLECEKTFQRIILLITKKKYIGVINGGK	-----
		951	1000
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAEYTDVPPAEWV	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAEYTDVPPAEWV	-----
EHV-1 Pol (SEQ37)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAEYTDVPPAEWV	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(951)	MLMKGVDLVRKNNCSFINLYARHLVDLLLYDEDVATAAAEYTDVPPAEWV	-----
		1001	1050
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	-----
EHV-1 Pol (SEQ37)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(1001)	GRPLPSGFDKFGKRVLVEAYNRITAPNLDVREFVMTAELSRSPESYTNKRL	-----
		1051	1100
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(1051)	PHLTVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVNSMRGTAQN	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(1051)	PHLTVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVNSMRGTAQN	-----
EHV-1 Pol (SEQ37)	(1051)	PHLTVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVNSMRGTAQN	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(1051)	PHLTVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREAGVNSMRGTAQN	-----
		1101	1150
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(1101)	PVVTKTARPQPKRKLIVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(1101)	PVVTKTARPQPKRKLIVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	-----
EHV-1 Pol (SEQ37)	(1101)	PVVTKTARPQPKRKLIVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(1101)	PVVTKTARPQPKRKLIVSDLAEDPTYVSENDVPLNTDYYFSHLLGTISVT	-----
		1151	1200
EHV-1 Pol (SEQ13)	(196)	-----	-----
EHV-1 Pol (SEQ4)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTFFTPPEE	-----
EHV-1 Pol (SEQ14)	(196)	-----	-----
EHV-1 Pol (SEQ2)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTFFTPPEE	-----
EHV-1 Pol (SEQ37)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTFFTPPEE	-----
EHV-1 Pol (SEQ15)	(195)	-----	-----
EHV-1 Pol (SEQ6)	(1151)	FKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTFFTPPEE	-----

Figure 14 (continued)

		1201	1220
EHV-1 Pol (SEQ13)	(196)	-----	
EHV-1 Pol (SEQ4)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ14)	(196)	-----	
EHV-1 Pol (SEQ2)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ37)	(1201)	ESRRILHTVFCTLEAAPHQ	
EHV-1 Pol (SEQ15)	(195)	-----	
EHV-1 Pol (SEQ6)	(1201)	ESRRILHTVFCTLEAAPHQ	

Figure 15

FIG. 15A EHV-1 glycoprotein C polynucleotide sequence alignment

		1	50
AY464052 (gC)	(1)	ATGTGGTTGCCTAATCTCGTGAGATTTGTGGCGGTGCGGTATCTAATCTG	
AY665713 (gC)	(1)	ATGTGGTTGCCTAATCTCGTGAGATTTGTGGCGGTGCGGTATCTAATCTG	
gC of RacL11	(1)	ATGTGGTTGCCTAATCTCGTGAGATTTGTGGCGGTGCGGTATCTAATCTG	
NC_001491 (gC)	(1)	ATGTGGTTGCCTAATCTCGTGAGATTTGTGGCGGTGCGGTATCTAATCTG	
		51	100
AY464052 (gC)	(51)	TGCCGGGGCGATATTAACCTTATGCCTCTGGAGCTAGTGCTAGCTCCAGCC	
AY665713 (gC)	(51)	TGCCGGGGCGATATTAACCTTATGCCTCTGGAGCTAGTGCTAGCTCCAGCC	
gC of RacL11	(51)	TGCCGGGGCGATATTAACCTTATGCCTCTGGAGCTAGTGCTAGCTCCAGCC	
NC_001491 (gC)	(51)	TGCCGGGGCGATATTAACCTTATGCCTCTGGAGCTAGTGCTAGCTCCAGCC	
		101	150
AY464052 (gC)	(101)	AGAGTACGCCCCTACACCAACTCACACAACCTCCGAATCTAACTACCGCA	
AY665713 (gC)	(101)	AGAGTACGCCCCTACACCAACTCACACAACCTCCGAATCTAACTACCGCA	
gC of RacL11	(101)	AGAGTACGCCCCTACACCAACTCACACAACCTCCGAATCTAACTACCGCA	
NC_001491 (gC)	(101)	AGAGTACGCCCCTACACCAACTCACACAACCTCCGAATCTAACTACCGCA	
		151	
200			
AY464052 (gC)	(151)	CACGGCGCGGGCTCTGACAACACAACCTAACGCAAACGGTACAGAATCTAC	
AY665713 (gC)	(151)	CACGGCGCGGGCTCTGACAACACAACCTAACGCAAACGGTACAGAATCTAC	
gC of RacL11	(151)	CACGGCGCGGGCTCTGACAACACAACCTAACGCAAACGGTACAGAATCTAC	
NC_001491 (gC)	(151)	CACGGCGCGGGCTCTGACAACACAACCTAACGCAAACGGTACAGAATCTAC	
		201	250
AY464052 (gC)	(201)	ACACTCCCATGAAACCACAATCACCTGCACCAAGAGTCTCATATCTGTGC	
AY665713 (gC)	(201)	ACACTCCCATGAAACCACAATCACCTGCACCAAGAGTCTCATATCTGTGC	
gC of RacL11	(201)	ACACTCCCATGAAACCACAATCACCTGCACCAAGAGTCTCATATCTGTGC	
NC_001491 (gC)	(201)	ACACTCCCATGAAACCACAATCACCTGCACCAAGAGTCTCATATCTGTGC	
		251	300
AY464052 (gC)	(251)	CCTACTACAAATCTGTGATATGAACTGTACAACGTCGGTAGGCGTAAAT	
AY665713 (gC)	(251)	CCTACTACAAATCTGTGATATGAACTGTACAACGTCGGTAGGCGTAAAT	
gC of RacL11	(251)	CCTACTACAAATCTGTGATATGAACTGTACAACGTCGGTAGGCGTAAAT	
NC_001491 (gC)	(251)	CCTACTACAAATCTGTGATATGAACTGTACAACGTCGGTAGGCGTAAAT	
		301	350
AY464052 (gC)	(301)	TATAGCGAGTACCGCCTCGAGATTTACTTGAACCAGCGCACCCCATTTTC	
AY665713 (gC)	(301)	TATAGCGAGTACCGCCTCGAGATTTACTTGAACCAGCGCACCCCATTTTC	
gC of RacL11	(301)	TATAGCGAGTACCGCCTCGAGATTTACTTGAACCAGCGCACCCCATTTTC	
NC_001491 (gC)	(301)	TATAGCGAGTACCGCCTCGAGATTTACTTGAACCAGCGCACCCCATTTTC	
		351	400
AY464052 (gC)	(351)	GGGTACGCCCCCGGGCGACGAAGAAAACCTACATCAACCATAACGCCACCA	
AY665713 (gC)	(351)	GGGTACGCCCCCGGGCGACGAAGAAAACCTACATCAACCATAACGCCACCA	
gC of RacL11	(351)	GGGTACGCCCCCGGGCGACGAAGAAAACCTACATCAACCATAACGCCACCA	
NC_001491 (gC)	(351)	GGGTACGCCCCCGGGCGACGAAGAAAACCTACATCAACCATAACGCCACCA	

Figure 15 (Continued)

		401	450
AY464052 (gC)	(401)	AGGATCAGACTCTGCTGTTATTCTCAACGGCAGAGAGGAAAAAATCTCGA	
AY665713 (gC)	(401)	AGGATCAGACTCTGCTGTTATTCTCAACGGCAGAGAGGAAAAAATCTCGA	
gC of RacL11	(401)	AGGATCAGACTCTGCTGTTATTCTCAACGGCAAGAGGAAAAAATCTCGA	
NC_001491 (gC)	(401)	AGGATCAGACTCTGCTGTTATTCTCAACGGCAGAGAGGAAAAAATCTCGA	
		451	500
AY464052 (gC)	(451)	AGGGGTGGCCAGCTGGGAGTTATCCCAGACAGGCTACCAAAGCGCAGCT	
AY665713 (gC)	(451)	AGGGGTGGCCAGCTGGGAGTTATCCCAGACAGGCTACCAAAGCGCAGCT	
gC of RacL11	(451)	AGGGGTGGCCAGCTGGGAGTTATCCCAGACAGGCTACCAAAGCGCAAGCT	
NC_001491 (gC)	(451)	AGGGGTGGCCAGCTGGGAGTTATCCCAGACAGGCTACCAAAGCGCAGCT	
		501	550
AY464052 (gC)	(501)	GTTTAACCTTCCCCTCCACACGGAAGGTGGTACAAAGTTTCCACTGACCA	
AY665713 (gC)	(501)	GTTTAACCTTCCCCTCCACACGGAAGGTGGTACAAAGTTTCCACTGACCA	
gC of RacL11	(501)	GTTTAACCTTCCCCTCCACACGGAAGGTGGTACAAAGTTTCCACTGACCA	
NC_001491 (gC)	(501)	GTTTAACCTTCCCCTCCACACGGAAGGTGGTACAAAGTTTCCACTGACCA	
		551	600
AY464052 (gC)	(551)	TCAAATCTGTAGATTGGCGGACGGCCGGCATTACGTGTGGTCCTTGAT	
AY665713 (gC)	(551)	TCAAATCTGTAGATTGGCGGACGGCCGGCATTACGTGTGGTCCTTGAT	
gC of RacL11	(551)	TCAAATCTGTAGATTGGCGGACGGCCGGCATTACGTGTGGTCCTTGAT	
NC_001491 (gC)	(551)	TCAAATCTGTAGATTGGCGGACGGCCGGCATTACGTGTGGTCCTTGAT	
		601	650
AY464052 (gC)	(601)	GCCAAAAATGGCACGCTCGTTAACAGTACCAGCGTTACCGTCTCAACCTA	
AY665713 (gC)	(601)	GCCAAAAATGGCACGCTCGTTAACAGTACCAGCGTTACCGTCTCAACCTA	
gC of RacL11	(601)	GCCAAAAATGGCACGCTCGTTAACAGTACCAGCGTTACCGTCTCAACCTA	
NC_001491 (gC)	(601)	GCCAAAAATGGCACGCTCGTTAACAGTACCAGCGTTACCGTCTCAACCTA	
		651	700
AY464052 (gC)	(651)	CAACGCACCGTTGCTGGACCTTTCCGTTACCCGAGCCTGAAGGGGGAAA	
AY665713 (gC)	(651)	CAACGCACCGTTGCTGGACCTTTCCGTTACCCGAGCCTGAAGGGGGAAA	
gC of RacL11	(651)	CAACGCACCGTTGCTGGACCTTTCCGTTACCCGAGCCTGAAGGGGGAAA	
NC_001491 (gC)	(651)	CAACGCACCGTTGCTGGACCTTTCCGTTACCCGAGCCTGAAGGGGGAAA	
		701	750
AY464052 (gC)	(701)	ACTACAGGGCCACGTGCGTCGTCGCAAGCTACTTTCCACACAGCTCCGTC	
AY665713 (gC)	(701)	ACTACAGGGCCACGTGCGTCGTCGCAAGCTACTTTCCACACAGCTCCGTC	
gC of RacL11	(701)	ACTACAGGGCCACGTGCGTCGTCGCAAGCTACTTTCCACACAGCTCCGTC	
NC_001491 (gC)	(701)	ACTACAGGGCCACGTGCGTCGTCGCAAGCTACTTTCCACACAGCTCCGTC	
		751	800
AY464052 (gC)	(751)	AAGCTGCGGTGGTACAAAAATGCCCGCGAGGTGGACTTTACAAAGTACGT	
AY665713 (gC)	(751)	AAGCTGCGGTGGTACAAAAATGCCCGCGAGGTGGACTTTACAAAGTACGT	
gC of RacL11	(751)	AAGCTGCGGTGGTACAAAAATGCCCGCGAGGTGGACTTTACAAAGTACGT	
NC_001491 (gC)	(751)	AAGCTGCGGTGGTACAAAAATGCCCGCGAGGTGGACTTTACAAAGTACGT	
		801	850
AY464052 (gC)	(801)	TACGAACGCCTCAAGCGTGTGGGTAGACGGGCTAATCAGCGAATCTCTA	
AY665713 (gC)	(801)	TACGAACGCCTCAAGCGTGTGGGTAGACGGGCTAATCAGCGAATCTCTA	
gC of RacL11	(801)	TACGAACGCCTCAAGCGTGTGGGTAGACGGGCTAATCAGCGAATCTCTA	
NC_001491 (gC)	(801)	TACGAACGCCTCAAGCGTGTGGGTAGACGGGCTAATCAGCGAATCTCTA	

Figure 15 (Continued)

		851	900
AY464052 (gC)	(851)	CGGTGTCTATCCCGGTTGATCCGGAGGAGGAATACACACCCAGTCTTCGC	
AY665713 (gC)	(851)	CGGTGTCTATCCCGGTTGATCCGGAGGAGGAATACACACCCAGTCTTCGC	
gC of RacL11	(851)	CGGTGTCTATCCCGGTTGATCCGGAGGAGGAATACACACCCAGTCTTCGC	
NC_001491 (gC)	(851)	CGGTGTCTATCCCGGTTGATCCGGAGGAGGAATACACACCCAGTCTTCGC	
		901	950
AY464052 (gC)	(901)	TGTAGCATAGACTGGTACAGGGACGAAGTATCATTTGCTCGCATAGCCAA	
AY665713 (gC)	(901)	TGTAGCATAGACTGGTACAGGGACGAAGTATCATTTGCTCGCATAGCCAA	
gC of RacL11	(901)	TGTAGCATAGACTGGTACAGGGACGAAGTATCATTTGCTCGCATAGCCAA	
NC_001491 (gC)	(901)	TGTAGCATAGACTGGTACAGGGACGAAGTATCATTTGCTCGCATAGCCAA	
		951	1000
AY464052 (gC)	(951)	AGCTGGAACACCCTCTGTGTTTGTGCCCCAACCGTGTCGGTTTCGGTAG	
AY665713 (gC)	(951)	AGCTGGAACACCCTCTGTGTTTGTGCCCCAACCGTGTCGGTTTCGGTAG	
gC of RacL11	(951)	AGCTGGAACACCCTCTGTGTTTGTGCCCCAACCGTGTCGGTTTCGGTAG	
NC_001491 (gC)	(951)	AGCTGGAACACCCTCTGTGTTTGTGCCCCAACCGTGTCGGTTTCGGTAG	
		1001	1050
AY464052 (gC)	(1001)	AAGACGGAGACGCCGTCTGTACGGCTAAATGCGTACCGAGCACCAGGGGTG	
AY665713 (gC)	(1001)	AAGACGGAGACGCCGTCTGTACGGCTAAATGCGTACCGAGCACCAGGGGTG	
gC of RacL11	(1001)	AAGACGGAGACGCCGTCTGTACGGCTAAATGCGTACCGAGCACCAGGGGTG	
NC_001491 (gC)	(1001)	AAGACGGAGACGCCGTCTGTACGGCTAAATGCGTACCGAGCACCAGGGGTG	
		1051	1100
AY464052 (gC)	(1051)	TTCGTATCGTGGTCAGTGAACGACCACCTACCAGGGGTTCCGTGCGAAGA	
AY665713 (gC)	(1051)	TTCGTATCGTGGTCAGTGAACGACCACCTACCAGGGGTTCCGTGCGAAGA	
gC of RacL11	(1051)	TTCGTATCGTGGTCAGTGAACGACCACCTACCAGGGGTTCCGTGCGAAGA	
NC_001491 (gC)	(1051)	TTCGTATCGTGGTCAGTGAACGACCACCTACCAGGGGTTCCGTGCGAAGA	
		1101	1150
AY464052 (gC)	(1101)	CATGACAACCGGAGTCTGCCCTAGCCACTCGGGATTGGTTAACATGCAAA	
AY665713 (gC)	(1101)	CATGACAACCGGAGTCTGCCCTAGCCACTCGGGATTGGTTAACATGCAAA	
gC of RacL11	(1101)	CATGACAACCGGAGTCTGCCCTAGCCACTCGGGATTGGTTAACATGCAAA	
NC_001491 (gC)	(1101)	CATGACAACCGGAGTCTGCCCTAGCCACTCGGGATTGGTTAACATGCAAA	
		1151	1200
AY464052 (gC)	(1151)	GCCGCCGGCCCCCTCTCAGAAGAGAATGGGGAGAGGGAGTATAGCTGCATA	
AY665713 (gC)	(1151)	GCCGCCGGCCCCCTCTCAGAAGAGAATGGGGAGAGGGAGTATAGCTGCATA	
gC of RacL11	(1151)	GCCGCCGGCCCCCTCTCAGAAGAGAATGGGGAGAGGGAGTATAGCTGCATA	
NC_001491 (gC)	(1151)	GCCGCCGGCCCCCTCTCAGAAGAGAATGGGGAGAGGGAGTATAGCTGCATA	
		1201	1250
AY464052 (gC)	(1201)	ATAGAGGGGTACCCCGACGGCCTGCCTATGTTTTCGGACACAGTGGTATA	
AY665713 (gC)	(1201)	ATAGAGGGGTACCCCGACGGCCTGCCTATGTTTTCGGACACAGTGGTATA	
gC of RacL11	(1201)	ATAGAGGGGTACCCCGACGGCCTGCCTATGTTTTCGGACACAGTGGTATA	
NC_001491 (gC)	(1201)	ATAGAGGGGTACCCCGACGGCCTGCCTATGTTTTCGGACACAGTGGTATA	
		1251	1300
AY464052 (gC)	(1251)	TGACGCCTCCCCGATTGTTGAGGACAGGCCGGTTTTGACGAGCATCATCG	
AY665713 (gC)	(1251)	TGACGCCTCCCCGATTGTTGAGGACAGGCCGGTTTTGACGAGCATCATCG	
gC of RacL11	(1251)	TGACGCCTCCCCGATTGTTGAGGACAGGCCGGTTTTGACGAGCATCATCG	
NC_001491 (gC)	(1251)	TGACGCCTCCCCGATTGTTGAGGACAGGCCGGTTTTGACGAGCATCATCG	

Figure 15 (Continued)

	1301	1350
AY464052 (gC) (1301)	CAGTTACTTGCGGGGCGCGGCACTGGCGCTGGTCGTTCTCATCACAGCC	
AY665713 (gC) (1301)	CAGTTACTTGCGGGGCGCGGCACTGGCGCTGGTCGTTCTCATCACAGCC	
gC of RacL11 (1301)	CAGTTACTTGCGGGGCGCGGCACTGGCGCTGGTCGTTCTCATCACAGCC	
NC_001491 (gC) (1301)	CAGTTACTTGCGGGGCGCGGCACTGGCGCTGGTCGTTCTCATCACAGCC	
	1351	1400
AY464052 (gC) (1351)	GTTTGTTTTTACTGCTCCAAGCCCTCACAGGCGCCGTACAAGAAGTCTGA	
AY665713 (gC) (1351)	GTCTGTTTTTACTGCTCCAAGCCCTCACAGGCGCCGTACAAGAAGTCTGA	
gC of RacL11 (1351)	GTCTGTTTTTACTGCTCCAAGCCCTCACAGGCGCCGTACAAGAAGTCTGA	
NC_001491 (gC) (1351)	GTCTGTTTTTACTGCTCCAAGCCCTCACAGGCGCCGTACAAGAAGTCTGA	
	1401	
AY464052 (gC) (1401)	CTTTTAG	
AY665713 (gC) (1401)	CTTTTAG	
gC of RacL11 (1401)	CTTTTAG	
NC_001491 (gC) (1401)	CTTTTAG	

Sequence identity percentage:

AY464052 (gC) (SEQ ID NO :7) : AY665713 (gC) (SEQ ID NO:9): 99.9%
 AY464052 (gC) (SEQ ID NO :7) : NC_001491 (gC) (SEQ ID NO:11): 99.9%
 AY665713 (gC) (SEQ ID NO:9) : NC_001491 (gC) (SEQ ID NO:11): 100%
 gC of RacL11 (SEQ ID NO:34) : AY464052 (gC) (SEQ ID NO :7): 99.6%
 gC of RacL11 (SEQ ID NO:34) : AY665713 (gC) (SEQ ID NO:9): 99.7%
 gC of RacL11 (SEQ ID NO:34) : NC_001491 (gC) (SEQ ID NO:11): 99.7%

Figure 15 (continued)

FIG. 15B EHV-1 glycoprotein C protein sequence alignment

		1	50
AAS45900.1 (gC)	(1)	MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTTTPNLTTA	
AAT67273.1 (gC)	(1)	MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTTTPNLTTA	
gC protein of RacL11	(1)	MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTTTPNLTTA	
YP_053061.1 (gC)	(1)	MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTTTPNLTTA	
		51	100
AAS45900.1 (gC)	(51)	HGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDNMCTTSVGVN	
AAT67273.1 (gC)	(51)	HGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDNMCTTSVGVN	
gC protein of RacL11	(51)	HGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDNMCTTSVGVN	
YP_053061.1 (gC)	(51)	HGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDNMCTTSVGVN	
		101	150
AAS45900.1 (gC)	(101)	YSEYRLIYILNQRTFFSGTFPGDEENYINHNATKDQTLILFSTAERKKSR	
AAT67273.1 (gC)	(101)	YSEYRLIYILNQRTFFSGTFPGDEENYINHNATKDQTLILFSTAERKKSR	
gC protein of RacL11	(101)	YSEYRLIYILNQRTFFSGTFPGDEENYINHNATKDQTLILFSTAERKKSR	
YP_053061.1 (gC)	(101)	YSEYRLIYILNQRTFFSGTFPGDEENYINHNATKDQTLILFSTAERKKSR	
		151	200
AAS45900.1 (gC)	(151)	RGGQLGVIPDRLPKRQLFNLPLHTEGGTKFFLTIKSVDWRTAGIYVWSLY	
AAT67273.1 (gC)	(151)	RGGQLGVIPDRLPKRQLFNLPLHTEGGTKFFLTIKSVDWRTAGIYVWSLY	
gC protein of RacL11	(151)	RGGQLGVIPDRLPKRQLFNLPLHTEGGTKFFLTIKSVDWRTAGIYVWSLY	
YP_053061.1 (gC)	(151)	RGGQLGVIPDRLPKRQLFNLPLHTEGGTKFFLTIKSVDWRTAGIYVWSLY	
		201	250
AAS45900.1 (gC)	(201)	AKNGTLVNSTSVTVSTYNAPLLDLSVHPSLKGNYRATCVVASYFFHSSV	
AAT67273.1 (gC)	(201)	AKNGTLVNSTSVTVSTYNAPLLDLSVHPSLKGNYRATCVVASYFFHSSV	
gC protein of RacL11	(201)	AKNGTLVNSTSVTVSTYNAPLLDLSVHPSLKGNYRATCVVASYFFHSSV	
YP_053061.1 (gC)	(201)	AKNGTLVNSTSVTVSTYNAPLLDLSVHPSLKGNYRATCVVASYFFHSSV	
		251	300
AAS45900.1 (gC)	(251)	KLRWYKNAREVDFTKYVTNASSVWVDGLITRISTVSIPIVDPPEEYTPSLR	
AAT67273.1 (gC)	(251)	KLRWYKNAREVDFTKYVTNASSVWVDGLITRISTVSIPIVDPPEEYTPSLR	
gC protein of RacL11	(251)	KLRWYKNAREVDFTKYVTNASSVWVDGLITRISTVSIPIVDPPEEYTPSLR	
YP_053061.1 (gC)	(251)	KLRWYKNAREVDFTKYVTNASSVWVDGLITRISTVSIPIVDPPEEYTPSLR	
		301	350
AAS45900.1 (gC)	(301)	CSIDWYRDEVSFARIAKAGTFSVFVAFTVSVSVEDGDAVCTAKCVPSTGV	
AAT67273.1 (gC)	(301)	CSIDWYRDEVSFARIAKAGTFSVFVAFTVSVSVEDGDAVCTAKCVPSTGV	
gC protein of RacL11	(301)	CSIDWYRDEVSFARIAKAGTFSVFVAFTVSVSVEDGDAVCTAKCVPSTGV	
YP_053061.1 (gC)	(301)	CSIDWYRDEVSFARIAKAGTFSVFVAFTVSVSVEDGDAVCTAKCVPSTGV	
		351	400
AAS45900.1 (gC)	(351)	FVSWSVNDHLEFGVPSQDMTTGVCPSHSGLVNMQSRPFLSENGEREYSICI	
AAT67273.1 (gC)	(351)	FVSWSVNDHLEFGVPSQDMTTGVCPSHSGLVNMQSRPFLSENGEREYSICI	
gC protein of RacL11	(351)	FVSWSVNDHLEFGVPSQDMTTGVCPSHSGLVNMQSRPFLSENGEREYSICI	
YP_053061.1 (gC)	(351)	FVSWSVNDHLEFGVPSQDMTTGVCPSHSGLVNMQSRPFLSENGEREYSICI	
		401	450
AAS45900.1 (gC)	(401)	IEGYFDGLPMFSDTVVYDASPIVEDRPFVLTSSIIAVTCGAAALALVVLITA	
AAT67273.1 (gC)	(401)	IEGYFDGLPMFSDTVVYDASPIVEDRPFVLTSSIIAVTCGAAALALVVLITA	
gC protein of RacL11	(401)	IEGYFDGLPMFSDTVVYDASPIVEDRPFVLTSSIIAVTCGAAALALVVLITA	
YP_053061.1 (gC)	(401)	IEGYFDGLPMFSDTVVYDASPIVEDRPFVLTSSIIAVTCGAAALALVVLITA	
		451	469
AAS45900.1 (gC)	(451)	VCFYCSKPSQAPYKKSDF-	
AAT67273.1 (gC)	(451)	VCFYCSKPSQAPYKKSDF-	
gC protein of RacL11	(451)	VCFYCSKPSQAPYKKSDF-	
YP_053061.1 (gC)	(451)	VCFYCSKPSQAPYKKSDF-	

Figure 15 (continued)

Sequence identity percentage:

AAS45900.1 (SEQ ID NO:8) : AAT67273.1 (SEQ ID NO:10): 100%
AAS45900.1 (SEQ ID NO:8) : YP_053061.1 (SEQ ID NO:12): 100%
AAT67273.1 (SEQ ID NO:10): YP_053061.1 (SEQ ID NO:12): 100%
gC protein of RacL11 (SEQ ID NO:35) : AAS45900.1 (SEQ ID NO:8): 98.9%
gC protein of RacL11 (SEQ ID NO:35) : AAT67273.1 (SEQ ID NO:10): 98.9%
gC protein of RacL11 (SEQ ID NO:35) : YP_053061.1 (SEQ ID NO:12): 98.9%

Figure 16

EHV-1 DNA polymerase (Pol) gene (AY464052) from EHV-1 V592 strain (SEQ ID NO:1)

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1  tcagctttga  tggggagctg  cttctagagt  acaaaaaact  gtatgcagta  ttgcagcact
61  ttcttctctc  ggtgtaaaag  gcgtcagctt  ttcaaaagcg  gcgcgctcaa  gcagtgcctg
121  ggttttctgt  ggggtcttgt  ggggggtttc  cggaataaac  cgctttaaaa  gattttctgt
181  tgttctcaca  tcatttccga  atagagcctt  aaaggtcacg  cttatggtac  ccaacagggtg
241  ggagaaaatg  tagtctgtgt  ttagcggtag  gtcattctcg  gaaacatagg  tcgggtcttc
301  ggcgaggctg  gaaaccagca  gtttgcgttt  aggttggggg  cgtgcgggtc  tggttaccac
361  ggggttttgg  gcggtacgcg  gcattgagtt  tactacaccc  gcttcgcgtt  ccgcggcctc
421  ggtctgcgca  actatcacat  acggaattct  ctcttttaag  ctgggcagtt  cttcattctc
481  catggcgagc  ttaaagtaga  cggtgagggt  oggcaggcgc  ttgttgggtt  acgattcggg
541  tgagcggctc  agctcagcag  tcataacgaa  ctgcgcacg  tccaagttgg  gggcagtgat
601  acggtttgac  gcctctacca  gcaactgcgc  aaacttgtca  aagccgctcg  gtacggggcg
661  cccaccccat  tctgcgggag  gcacgtctgt  cacctttgct  gccgcgctgg  ccacatcctc
721  ctgcgtaca  aaaagatcta  ccagatgtcg  cgcgtacaag  tttatgaaa  agcgtattt
781  tttgcggacc  aggtcgaccc  ccttcatgag  catcttcccc  ccgtttatga  caccatgta
841  cttcttcttg  gtgatcagca  gcagtgcgtg  aaaggtcttc  tcacactcca  gtttgatggg
901  cgctctaaag  aggtccgctg  aaatctgacg  cgacatagca  tccccagct  ccgatacccc
961  ctgcgtacgt  aggcacacaa  aottgataaa  caccgagtcg  gtgtctccgt  agataacct
1021  gacggagtaa  ggcttgggtt  ttgcgaaacc  tatagccctt  ggaaaattgt  cctccagcag
1081  ctgcgcgctc  gcccaacgag  agtgaacgta  atctcgggtc  ttgaggagca  tgtcgcgtcc
1141  tatcgtggta  acggtagcgg  ctatcctcag  acacggcaac  aggcggtttg  ccccccctgt
1201  gaatccgtaa  accgagttgc  atatcacctt  aatgcagac  tgcgtcttat  ctagtaaaac
1261  tgcctcctcg  ggggtgctgg  tggggattcg  cgcctcacc  gcctttcgca  tggccagcca
1321  gtgcgcgacg  aagatgccaa  gcaggctttc  gcgaatatgg  gcgtggacaa  aaaataactt
1381  ttgggtcacc  acctogaaag  tcgagtagtt  gacggatggt  tgaagcccg  ccagatccac
1441  ttcatcgagc  gccagggtgg  tgaaacagag  gttatgggac  tggataatgc  ttgggtataa
1501  gtgcgcgaa  tcaaacacaa  ccacggggtc  cacatgaaag  ccgataacgg  ggtctagaa
1561  ctttgcctcc  tggtagccca  oggcctctcc  gacgcggggc  ttccgcctc  cgttttcaga
1621  agtagcggca  gatcctgcgg  cgtccggggt  accgtccaca  ccgtcgggtt  cgtctgtact
1681  gtogaaggcg  tggctttggc  tatccatagc  caactccgaa  gtctctgacg  ogggtctgc
1741  ctgactgtca  aaccggcgct  tgttgcctgg  caaaatgaaa  tttctctcgc  ggcgcaggtt
1801  cagcaagcac  gtgtacacgc  gaatttgctg  accgtcaaaa  attacccgog  ttagggtgat
1861  acgggcgag  ttggccaccg  ccgatagttc  cagatggggg  aggtacttaa  aaaacagctt
1921  gccaccagc  cttagagctc  ggatacaata  ctctcctatt  acgcccctcc  ggtcaggccc
1981  tccgcgtgaa  ctgagggtga  tttctttata  gggaagggtc  atcttatgct  ccgcgaggac
2041  gtctccacg  accgcgtcga  gttttagctg  gggtagcttt  agcttttccg  tcgccacaga
2101  atacatgtct  agagatatca  ggccattgat  tttcaacctg  ctcttctctc  gaaaatggtt
2161  cgtggcgatg  tcccacacct  taaacagccc  ccctttgttg  aacttgcctg  acccgtccag
2221  ctgactgtta  tacaccgacg  ttacctgtgt  aactatgtac  gccagtcgaa  aattaaogct
2281  gttgtagcgg  gtggcgaaat  cgggagagta  ctgcttgaga  aaggtcagga  aggcaaccag
2341  cagctcgtac  tcgctgtcaa  actccaaaac  cgtcggctcg  ggctcgcgcg  gctggaogca
2401  tgcaaacgag  tattcctcag  agatatcgca  tgacccgagg  gaaaacagca  ggggtgtgtc
2461  gtgggtctga  gtagcaagcg  agtacagcag  acaggagatc  tggatgaoca  ggtcctcttg
2521  gttagttgcc  actgggaacg  ccatttctgt  acccgttcca  gctttacact  ctatatcaaa
2581  gcacatgagc  ttatagtcgg  gccaggcagc  ctgctctggt  atcggctcca  ggttatcggg
2641  agtacagtta  atctccacgt  cgcttgaggt  gacgtgtcgc  tcaacggggc  gaagttgaac
2701  acgctctccg  tgggtgcggg  gtgcgaggcg  gtaccaacca  aaactggtaa  aattttcatt
2761  gtccaacaac  agcgcgctgg  tcacgtccac  gctcccctcg  aattttgtaa  tctccgggtg
2821  aaagttgtcg  cagatgaacc  ctcccaggcg  gctgtcggag  gcagataact  tatagtagag
2881  agctggctta  gatccaaagt  agtacagcgt  cgtgtggcac  acggtctcca  ctttgaagca
2941  gtccgcagac  acgtgctttc  ogccccacca  tccccgcgcg  ctgcgcgcgc  tctgtttgcc
3001  gccgttgcca  tttcccaggg  ccgcgctcaa  agccgagctg  tgcgcgcagt  ccaccattgc
3061  gcgcaogagt  tctgcctcgg  tggttattcc  acaagcgcta  tccacctcog  cctttgccat
3121  gtaaaaaata  tggcgcacac  catagacgtg  aaccgcgact  cgctttccac  actcgtctat
3181  tcccagcagt  gttaccacag  accgccttgg  gcgggatagc  tcagcaaac  tggatgggtc
3241  atcgtgtgag  gcgctctccg  aagtctctac  tatgtcgtac  acgtgaaatc  tctcaaatct
3301  ggggttgaat  ccacgcgcgc  gaaaatcctg  gcggttccaa  acccgaatcc  tgcgaggcca
3361  gcaacctccg  gaggcaaaat  tcagcacgtc  gtactctgag  ccacgcgagt  acactttggg
3421  tgggcgctcc  aaggtgcoca  cgtgtacacc  gcgtgcgtgg  tcggcggggg  cttcttcac
3481  gaggcattct  ggagctataa  acttaaagct  acccactctc  gtgcagtaac  agtgttgggg
3541  gggccttggg  cgctctgtct  ccgcggtctg  ccgccttccc  ggctgaaaa  atggcctctt
3601  gccataaac  ggattaaaaa  accgcgtcct  gcgaacggag  ttggcctgtt  ccgcgcgcgc
3661  cat

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Figure 16 (Continued)

EHV-1 DNA polymerase (pol) protein (AAS45914.1) encoded by AY464052 from EHV-1 V592 strain (1220aa) (SEQ ID NO:2)

MAAREQANSVRRSGFFNPFIGKRPFFRPGSGQTAETERPRPPQH
 SYCTEVGSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNLFASGGCW
 PRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELSRPSGSSVVTLL
 GMSECGKRVAHVHYGVRHYFYMAKAEVDSACGITTEAELVRAMVDCAHSSALSAAALGN
 GNGGKQSGGSGGGWGGKHSVADCFKVETVCHTTLYYFGSKPALYYRVSASSSRLGGF
 ICDNFHPEITKFEQSVDTTRLLLDNENFTSFGWYRLRPGTHGERVQLRPVERHVTSS
 DVEINCTPDNLEPIPDEAAWPDYKLMCFDIECKAGTGNEMAFPVATNQEDLVIQISCL
 LYSLATQNHEHTLLFSLGSCDISEEYSFACVQRGEPRPTVLEFDSEYELLVAFITFLK
 QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNKGGLFKVWDIATNHFQKKS
 KVKINGLISLDMYSVATEKLLPSYKLDVAVGDLGEHKIDLPYKEIPSYAGGPDRR
 GVIGEYCIQDSRLVGKLFKYLPHLELSAVAKLARITLTRVIFDGQQIRVYTCLLKLA
 RERNFILPDNRRRFDSDADAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATS
 ENGGGKPGVGRAVGYQGAKVLDPVSGFHVDPVVVDFASLYPSIIQAHNLCFTTLALD
 EVDLAGLQPSVNYSTFEVGDQKLFFVHAHIRESLGILLRDWLAMRKAVRARIPTSTP
 EEAVLLDKQSSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTRDYVHSR
 WATRELLEDNFPGAIGFRNHKPYSVRVIYGDTSVFIKFVGLTYEGVSELGDAMSRQI
 SADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGKMLMKGVDLVRKNNCSFINLYAR
 HLVDLLLYDEDVATAAAKVTDVPPAEWVGRPLPSGFDKFGRLVEAYNRITAPNLDVR
 EFVMTAELSRSPESYTNKRLPHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREA
 GVVNSMRGTAQNPFVTKTARQPQRKLLVSDLAEDPTYVSENDVPLNTDYFSSHLLGT
 ISVTFKALFGNDVRTTENLLKRFIPETPHKTPKTQALLERAGFEKLTPTFPEEESRR
 ILHTVFCTLEAAPHQS

EHV-1 DNA polymerase (Pol) (AY665713) from EHV-1 Ab4 strain (SEQ ID NO:3)

1	tcagctttga	tggggagctg	cttctagagt	acaaaaaact	gtatgcagta	ttcgacgact
61	ttcttctctcc	ggtgtaaagg	gcgtcagctt	ttcaaagccg	gcgcgctcaa	gcagtgcctg
121	ggttttctgtg	ggggtcttgt	gggggggttc	cggaataaac	cgctttaaaa	gattttctgt
181	tgttctcaca	tcatttccga	atagagcctt	aaaggtcacg	cttatggtac	ccaacaggtg
241	ggagaaatag	tagtctgtgt	ttagcggtag	gtcattctcg	gaaacatagg	tcgggtcttc
301	ggcgaggtcg	gaaaccagca	gtttgcgttt	aggttggggg	cgtgcggtct	tggttaccac
361	ggggtttttg	gcggtaccgc	gcattgagtt	tactacaccc	gcttcgcggt	ccgcggcctc
421	ggtctgcgca	actatcacat	acggaattct	ctcttttaag	ctgggcaggt	cttcattcct
481	catggcgagc	ttaaagtaga	cggtagagtg	cggcaggcgc	ttgttggtat	acgattcggg
541	tgagcggctc	agctcagcag	tcataacgaa	ctcgcgcacg	tccaagttgg	gggcagtgat
601	acggttgtag	gcctctacca	gcactcgccc	aaacttgtea	aagccgctcg	gtagcgggag
661	ccccacccat	tctgcgggag	gcacgtctgt	cacctctgct	gccgcggtgg	ccacatcctc
721	gtcgtacaac	aaaagatcta	ccagatgtcg	cgcgtacaag	tttatgaaag	agcagttatt
781	tttgcgagacc	aggtcgaccc	ccttcagtag	catcttcccc	ccgtttatga	cacctatgta
841	cttcttcttg	gtgatcagca	gcagtcgctg	aaaggtcttc	tcacactcca	gtttgatggg
901	cgctctaaag	aggtccgctg	aaatctgacg	cgacatagca	tccccagct	ccgatacccc
961	ctcgtacgtc	aggcccacaa	acttgataaa	cacggagtcg	gtgtctccgt	agataaccct
1021	gacggagtaa	ggcttgtggt	ttcggaacc	tatagcccct	ggaaaattgt	cctccagcag
1081	ctcgcgcgctc	gcccacagag	agtgaacgta	atctcgggtc	ttgaggagca	tgctcgcgtcc
1141	tatcgtggta	acggtagccg	ctatcctcag	acacggcaac	aggccgtttg	ccacccccgt
1201	gaatccgtaa	accgagttgc	atatcacctt	aatcgagac	tgctgcttat	ctagtaaaac
1261	tgccctcctcg	ggggtgctgg	tggggattcg	gcacctcacc	gcctttcgca	tggccagcca
1321	gtcgcgcagc	aagatgccaa	gcaggctttc	gcgaatatgg	gcgtggacaa	aaaataactt
1381	ttggtcacc	acctcgaaag	tcgagtagtc	gacggatggg	tgaagcccg	ccagatccac
1441	ttcatcgagc	gccaggggtg	tgaaacagag	gttatgggoc	tggtataatgc	ttgggtataa
1501	gctagcgaag	tcaaacacaa	ccacgggggtc	cacatgaaag	ccggatacgg	ggtctagaac
1561	ctttgctccc	tggtagccca	cggccctccc	gacgcggggc	ttcccgccctc	cgttttcaga

Figure 16 (Continued)

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1621 agtagcgcca gatcctgagg cgteccgggt accgtccaca ccgtcggggt cgtctgtact
1681 gtcgaaggcg tggctttggc tatccatagc caactccgaa gtctctgacg cggcgtctgc
1741 ctgactgtca aaccggcgtc tgttgctcgg caaaatgaaa tttctctcgc gggcgagttt
1801 cagcaagcac gtgtacacgc gaatttgctg accgtcaaaa attaccgcgc ttaggggtgat
1861 acgggcgagt ttggccaccg ccgatagtcc cagatggggg aggtacttaa aaaacagctt
1921 gcccaccagc ctagagtcct ggatacaata ctctcctatt acgcccctcc ggtcaggccc
1981 tcccgcgtaa taggagggtg tttctttata ggggaagggt atcttatgct cgcgaggac
2041 gtctcccacg accgcgtcga gtttgtagct gggtagcttt agcttttccg tcgccacaga
2101 atacatgtct agagatatca ggccattgat tttcaccttg ctcttcttct gaaaatgggt
2161 cgtggcgatg tcccacacct taaacagccc ccctttggtg aacttgccgt acccgtccag
2221 cttgatgtta tacaccgacg ttaccttggt aactatgtac gccagtcaa aattaacgat
2281 gttgtagccg gtggcgaaact cgggagagta ctgcttgaga aaggtcagga aggcaaccag
2341 cagctcgtac tcgctgtcaa actccaaaac cgtegggtct ggctcgccgc gctggacgca
2401 tgcaaacgag tattcctcag agatatacga tgacccgagg gaaaacagca ggggtgtgtc
2461 gttggtctga gtagcaagcg agtacagcag acaggagatc tggatgacca ggtcctcttg
2521 gttagttgcc actgggaacg ccatttcggt accggtcca gctttacact ctatatcaaa
2581 gcacatgagc ttatagtcgg gccaggcagc ctgctctggt atcggtcca ggttatcggg
2641 agtacagtta atctccacgt cgcttgagggt gacgtgtcgc tcaacggggc gaagttgaac
2701 acgctctccg tgggtgccgg gtgcgaggcg gtaccaccgc aaactggtaa aattttcatt
2761 gtccaacaac agccgcgtgg tcacgtccac gctcccctcg aattttgtaa tctccgggtg
2821 aaagttgtcg cagatgaacc ctcccaggcg gctgctggag gcagatactc tatagtagag
2881 agctggctta gatccaaagt agtacagcgt cgtgtggcac acggctctca ctttgaagca
2941 gtccgcagac acgtgctttc cgccccacca tccccgcgc ctgcccgcgc tctgtttgcc
3001 gccgttgcca tttcccaggg ccgcgctcaa agccgagctg tgccgcgagt ccaccattgc
3061 gcgcacgagt tctgcctcgg tggttattcc acaagcgcta tccacctccg cctttgccat
3121 gtaaaaaataa tggcgcacac catagacgtg aaccgcgact cgctttccac actcgctcat
3181 tcccagcagt gttaccacag acccgcttgg gcgggatagc tcagcaaacc tggatgggtc
3241 atcgtgtgag gcgctctccg aagtctctac tatgtcgtac acgtgaaatc tctcaaactc
3301 ggggttgaat ccacgcccc gaaaatcctg gccgttccaa acccgaatcc tgcgaggcca
3361 gcaacctccg gaggcaaagt tcagcacgtc gtactctgag ccacgcagat acactttggg
3421 tgggcgctcc aaggtgccc cgtgtacacc gcgtcgctgg tcggcggggg cttcttcac
3481 gaggcatctt ggagctataa acttaaagct acccactct gtgcagtacg agtgttggg
3541 gggccttggg cgctctgtct ccgcggtctg ccgcctccc ggctgaaaa atggcctctt
3601 gccataaaac ggattaaaa accgcctcct gcgaacggag ttggcctggt cgcgcgcgcg
3661 cat

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EHV-1 DNA polymerase (pol) protein (AAT67287.1) encoded by AY665713 from EHV-1 Ab4 strain (1220aa) (SEQ ID NO:4)

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MAAREQANSVRRSGFFNPFIGKRPFRRPGSGQTAETERPRPPQH
SYCTEVGSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNLFASGGCW
PRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELSRPSGSSVVTLL
GMSECGKRVAVHVYGVRYFYMAKAEVDSACGITTEAELVRAMVDCAHSSALSALGN
GNGGKQSGSGGGWGGKHVSADCFKVETVCHTTLYYFGSKPALYYRVSASSRLGGF
ICDNFHPEITKFEGSVDVTTTRLLLDNENFTSFGWYRLRPGTHGERVQLRPVERHVTSS
DVEINCTPDNLEPIPDAAWPDYKLMCFDIECKAGTGNEMAFPVATNQEDLVIQISCL
LYSLATQNHEHTLLFSLGSCDISEEYSFACVQRGEPRPTVLEFDSEYELLVAFITFLK
QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNKGGLFKVWDIATNHFQKKS
KVINGLISLDMYSVATEKLLPSYKLDVAVGDLGEHKIDLPYKEIPSYAGGPDRR
GVIGEYCIQDSRLVGKLFKYLPHLELSAVAKLARITLTRVIFDGQQIRVYTCLLKLA
RERNFILPDNRRRFDSDADAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATS
ENGGGKPGVGRAVGYQGAQVLDPVSGFHVDPVVVDFASLYPSIIQAHNLCFTTLALD
EVDLAGLQPSVDYSTFEVGDQKLFFVHAHIRESLGILLRDWLAMRKAVRARIPTSTP

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Figure 16 (Continued)

EEAVLLDKQQSAIKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTRDYVHSR
 WATRELLEDNFGAIGFRNHKPYSVRVIYGDTSVFIKRVGLTYEGVSELGDAMSRQI
 SADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGKMLMKGVDLVRKNNCSFINLYAR
 HLVDLLLYDEDVATAAAEVDVPPAEWVGRPLPSGFDKFGRLVEAYNRITAPNLDVR
 EFVMTAELSRSPESYTNKRLPHLTVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREA
 GVVNSMRGTAQNPVVTKTARPQPKRKLVSDDLAEPTYVSENDVPLNTDYYFSHLLGT
 ISVTFKALFGNDVRTTENLLKRFIPETPHKTPTKTQALLERAGFEKLTPTTPEEESRR
 ILHTVFCTLEAAPHQ5

EHV-1 DNA polymerase (Pol) (NC_001491) from EHV-1 (SEQ ID NO:5)

1 tcagctttga tggggagctg cttctagagt acaaaaaact gtatgcagta ttcgacgact
 61 ttcttcctcc ggtgtaaagg gcgtcagctt ttcaaagccg gcgcgctcaa gcagtgcctg
 121 ggttttcgtg ggggtcctgt ggggggtttc cggaataaac cgctttaaaa gattttctgt
 181 tgttctcaca tcatttcgga atagagcctt aaagggtcacg cttatggtac ccaacagggtg
 241 ggagaaatag tagtctgtgt ttagcggtag gtcatctctg gaaacatagg tcgggtcttc
 301 ggcgaggtcg gaaaccagca gtttgcggtt aggttggggg cgtgcgggtc ttggtaccac
 361 ggggttttgg gcggtaccgc gcattgagtt tactacaccc gcttcgcgtt ccgcggcctc
 421 ggtctgcgca actatcacat acggaattct ctcttttaac ctgggcagtt cttcattcct
 481 catggcgagc ttaaagtaga cgggtgaggtg cggcagggcg ttggttggtat acgattcggg
 541 tgagcggctc agctcagcag tcataacgaa ctgcgcgacg tccaagttgg gggcagtgat
 601 acggttgtag gcctctacca gcactcgccc aaacttgta aagcgcgtcg gtacgggcg
 661 cccaccccat tctgcgggag gcacgtctgt cacctctgct gccgcggtg ccacatcctc
 721 gtcgtacaac aaaagatcta ccagatgtcg cgcgtacaag tttatgaaag agcagttatt
 781 tttgcggacc aggtcgaccc ccttcagtag catcttcccc ccgtttatga cacctatgta
 841 cttcttcttg gtgatcagca gcagtcgctg aaagggtctt tcacactcca gtttgatggg
 901 cgctctaaag aggtccgctg aaatctgacg cgacatagca tccccagct ccgatacccc
 961 ctctgtagtc agggccacaa acttgataaa cacggagtcg gtgtctccgt agataaccct
 1021 gacggagtaa ggcttgtggt ttcggaacc tatagcccct ggaaaattgt cctccagcag
 1081 ctgcgcgctc gcccaacgag agtgaacgta atctcggtc ttgaggagca tgcgcgtcc
 1141 tatcgtggtg acggtagccg ctatcctcag acacggcaac aggcggtttg ccacccccgt
 1201 gaatccgtaa accgagttgc atatcacctt aatcgagac tgctgcttat ctagtataaac
 1261 tgctcctcgc ggggtgctgg tggggattcg cgccctcacc gcctttcgca tggccagcca
 1321 gtcgcgcagc aagatgccaa gcaggtcttc gcgaatatgg gcgtggacaa aaaataactt
 1381 ttggtcacc acctcgaaag tcgagtagtc gacggatggg tgaagcccg ccagatccac
 1441 ttcatcgagc gccaggggtg tgaacagag gttatggggc tggataatgc ttgggtataa
 1501 gtagcgaag tcaaacacaa ccacggggtc cacatgaaag ccgatacgg ggtctagaac
 1561 ctttgctccc tggtagccca cggccctccc gacgcggggc ttccgcctc cgttttcaga
 1621 agtagcgcca gatcctgcgg cgtccggggt accgtccaca ccgtcgggt cgtctgtact
 1681 gtcgaaggcg tggctttggc tatccatagc caactccgaa gtctctgacg ccgctgtctg
 1741 ctgactgtca aaccggcgctc tgttgtctgg caaaatgaaa tttctctcgc gggcgagttt
 1801 cagcaagcac gtgtacacgc gaatttgctg accgtcaaaa attaccgcg ttaggggtgat
 1861 acgggcgagt ttggccaccg ccgatagttc cagatggggg aggtacttaa aaaacagctt
 1921 gccaccagc ctgagtcct ggatacaata ctctcctatt acgcccctcc ggtcaggccc
 1981 tcccgctaa taggagggta tttctttata ggggaaggtc atcttatgct cgccgaggac
 2041 gtctcccacg accgcgtcga gttttagct gggtagcttt agcttttccg tcgccacaga
 2101 atacatgtct agagatatca ggccattgat tttcaccttg ctcttcttct gaaaatgggt
 2161 cgtggcgatg tcccacacct taaacagccc ccctttgttg aacttgccgt acccgctccg
 2221 cttgatgtta tacaccgacg ttacctgtt aactatgtac gccagtcaa aattaacgat
 2281 gttgtagccg gtggcgaaact cgggagagta ctgcttgaga aagggtcagga aggcaaccag
 2341 cagctcgtac tcgctgtcaa actccaaaac cgtcgggtc ggctcgccgc gctggacgca
 2401 tgcaaacgag tattcctcag agatatcgca tgaccgagg gaaaacagca ggggtgtgtc
 2461 gtggttctga gtagcaagc agtacagcag acaggagatc tggatgacca ggtcctcttg
 2521 gtagttgccc actggaagc ccatttcgtt acccgttcca gctttacact ctatatcaaa

Figure 16 (Continued)

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2581 gcacatgagc ttatagtcgg gccaggcage ctcgctctggt atcggtccca gggtatcggg
2641 agtacagtta atctccacgt cgcttgaggt gacgtgtcgc tcaacggggc gaagttgaac
2701 acgctctccg tgggtgccgg gtcgcaggcg gtaccaccgc aaactggtaa aattttcatt
2761 gtccaacaac agccgcgtgg tcacgtccac gctcccctcg aattttgtaa tctccgggtg
2821 aaagttgtcg cagatgaacc ctcccaggcg gctgctggag gcagatactc tatagtagag
2881 agctggctta gatccaaagt agtacagcgt cgtgtggcac acggtctcca ctttgaagca
2941 gtccgcagac acgtgctttc cgccccacca tccccgcgcg ctgcccgcgc tctgtttgcc
3001 gccgttgcca tttcccaggg ccgcgctcaa agccgagctg tgcgcgcagt ccaccattgc
3061 gcgcacgagt tctgcctcgg tggttattcc acaagcgcta tccacctccg cctttgccat
3121 gtaaaaaataa tggcgcacac catagacgtg aaccgcgact cgctttccac actcgctcat
3181 tcccagcagt gttaccacag acccgcttgg gcgggatagc tcagcaaacc tggatgggtc
3241 atcgtgtgag gcgctctccg aagtctctac tatgtcgtac acgtgaaatc tctcaaatct
3301 ggggttgaat ccatacgcccc gaaaatcctg gccgttccaa acccgaatcc tgcgaggcca
3361 gcaacctccg gaggcaaagt tcagcacgtc gtactctgag ccatacgagt acactttggg
3421 tgggcgctcc aaggtgcccc cgtgtacacc gcgtcgctgg tcggcggggg cttcttcac
3481 gagcatctt ggagctataa acttaagct acccacctc gtgcagtac agtgttggg
3541 gggccttggg cgctctgtct ccgcggtctg cccgcttccc ggctgaaaa atggcctctt
3601 gccataaac ggattaaaaa acccgctcct gcgaacggag ttggcctgtt cgcgcgccgc
3661 cat

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EHV-1 DNA polymerase (YP_053075.1) encoded by NC_001491 (1220aa) (SEQ ID NO:6)

```

MAAREQANSVRRSGFFNPFIGKRPFRRPGSGQTAETERPRPPQH
SYCTEVGSFKFIAPRCLDEEAPADQRRGVHVGTLERPPKVYCDGSEYDVLNLFASGGCW
PRRIRVWNGQDFRGDGFNPRFERFHVYDIVETSESASHDDPSRFAELSRPSGSVVTLL
GMSECGKRVAVHVYGVRRHYFYMAKAEVDSACGITTEAELVRAMVDCAHSSALSAAALGN
GNGGKQSGSGSGGWGKHSVADCFKVVETVCHTTLTYFGSKPALYYRVSASSSRLGGF
ICDNFHP EITKFEGSVDVTRLLLDNENFTSFGWYRLRPGTHGERVQLRPVERHVTSS
DVEINCTPDNLEPIPDAAWPDYKLMCFDIECKAGTGNEMAFPVATNQEDLVIQISCL
LYSLATQNHEHTLLFSLGSCDISEEYSFACVQRGEPRPTVLEFDSEYELLVAFITFLK
QYSPEFATGYNIVNFDWAYIVNKVTSVYNIKLDGYGKFNKGGLFKVWDIATNHFQKKS
KVKINGLI SLDMYSVATEKLLPSYKLDVAVGVDLGEHKIDLPYKEIPSYAGGPDRR
GVIGEYCIQDSRLVGKLFKKYLPHELSAVAKLARITLTRVIFDGQQIRVYTCLLKLA
RERNFILPDNRRRFDSDAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATS
ENGGGKPGVGRAVGYYQAKVLDPVSGFHVDPVVVDFASLYPSIIQAHNLCFTTLALD
EVDLAGLQPSVDYSTFEVGDQKLFFVHAHIRESLGILLRDWLAMRKAVRARIPTSTP
EEAVLLDKQQAIAKVICNSVYGFTGVANGLLPCLRIAATVTTIGRDMLLKTRDYVHSR
WATRELLEDNFPGAIGFRNHKPYSVRVIYGDTSVFIKFVGLTYEGVSELGDAMSROI
SADLFRAPIKLECEKTFQRLLLITKKKYIGVINGGKMLMKGVDLVRKNNCSFINLYAR
HLVDLLLYDEDVATAAAEVDTPPAEWVGRPLPSGFDKFGFRLVEAYNRITAPNLDVR
EFVMTAELSRSPESYTNKRLPHLTIVYFKLAMRNEELPSVKERIPYVIVAQTEAAEREA
GVVNSMRGTAQNPNVTKTARPPKRLKLLVSDLAEDPTYVSENDVPLNTDYYFSHLLGT
ISVTFKALFGNDVRTTENLLKRFIPETPHKTPTKTQALLERAGFEKLTPTPEEESRR
ILHTVFCTLEAPHQS

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EHV-1 glycoprotein (gC) gene (AY464052) from EHV-1 V592 strain (SEQ ID NO:7)

```

Atgtggttgccctaatctcgtgagatttggtggcggtgcgctatctaactctgtgcggggcgatattaactta
tgcctctggagctagtgtcgtagctccagccagagtagcccgctacaccaactcacacaactccgaatctaa
ctaccgcacacggcgcgggctctgacaacacaactaacgcaaacggtacagaatctacacactcccatgaa
accacaatcacctgcaccaagagtctcatatctgtgcctactacaaatctgtcgatatgaactgtacaac
gtcggtaggcgtaaatatagcgagtagccgctcgagatttacttgaaccagcgacccccattttcgggta

```

Figure 16 (Continued)

cgccccccggcgacgaagaaaactacatcaaccataacgccaccaaggatcagactctgctgttattctca
acggcgagagaggaaaaaatctcgaaggggtggccagctgggagttatcccagacaggctaccaaagcgcca
gctgtttaaccttccccctccacacggaaggtggtacaaagtttccactgaccatcaaactctgtagattggc
ggacggccggcattttacgtgtggtccttgtatgccccaaatggcacgctcggttaacagtaccagcggtacc
gtctcaacctacaacgcaccgttgctggacctttccggttcacccgagcctgaagggggaaaactacagggc
cacgtgctgctcgcaagctactttccacacagctccgtcaagctgcggtggtacaaaaatgcccgcgagg
tggaactttacaaagtacgttacgaacgcctcaagcgtgtgggtagacgggctaatacgcgaatctctacg
gtgtctatccccggttgatccggaggaggaatacacacccagctcttcgctgtagcatagactgggtacagggga
cgaagtatcattttgctcgcatagccaaagctggaacaccctctgtgtttgttgccccaaacggtgtccgttt
cggtagaagacggagacgccgtctgtacggctaaatgcgtaccgagcaccgggggtgttcgtatcgtgggtca
gtgaacgaccacctaccaggggttcgctcgcaagacatgacaaccggagctctgccctagccactcgggatt
ggttaacatgcaaagccgcccggccccctctcagaagagaatggggagagggaggtatagctgcataatagagg
ggtaccccgacggcctgcctatgttttcggacacagtgggtatgatgcgcctccccgattgttgaggacagg
ccggttttgacgagcatcatcgagttacttgcggggccgcggcactggcgctgggtcgttctcatcacagc
cgtttgttttactgctccaagccctcacaggcgccgtacaagaagtctgacttttag

EHV-1 glycoprotein (gC) protein (AAS45900.1) encoded by AY464052 from EHV-1 V592 strain (468aa) (SEQ ID NO:8)

MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTT
PNLTTAHGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDNMCTTSVGVNYS
EYRLEIYLNQRTPFSGTPPGDEENYINHNATKDQTLLEFSTAERKKSRRGGQLGVIPD
RLPKRQLFNLPLHTEGGTKFPLTIKSVDWRTAGIYVWSLYAKNGTLVNSTSVTVSTYN
APLLDLSVHPSLKGENYRATCVVASYPHSSVKLRWYKNAREVDFTKYVTNASSVWVD
GLITRISTVSI PVDPEEEYTPSLRCSIDWYRDEVSFARIAKAGTPSVFVAPT VSVSVE
DGDVACTAKCVPSTGVFVSWSVNDHLPGVPSQDMTTGVCPSHGLVNMQSRRLSEEN
GEREYSCIIEGYPDGLPMFSDTVVYDASPIVEDRPVLTSIIAVTCGAAALALVVLITA
VCFYCSKPSQAPYKKSDF

EHV-1 glycoprotein (gC) gene (AY665713) from EHV-1 Ab4 strain (SEQ ID NO:9)

Atgtggttgcctaatactctgctgagatttgtggcggtcgcgatatctaactctgtgccggggc
gatattaacttatgcctctggagctagtgttagctccagccagagtagcggcgctacac
caactcacacaactccgaatctaactaccgcacacggcgcgggctctgacaacacaact
aacgcaaacggtacagaatctacacactcccatgaaaccacaatcacctgcaccaagag
tctcatatctgtgccctactacaaatctgtcgatatgaactgtacaacgtcggtaggcg
taaattatagcgagtaccgcctcgagatttacttgaaccagcgcacccccattttcgggt
acgccccccggcgacgaagaaaactacatcaaccataacgccaccaaggatcagactct
gctgttattctcaacggcgagagaggaaaaaatctcgaaggggtggccagctgggagttat
tcccagacaggctaccaaagcgccagctgtttaaccttccccctccacacggaaggtggt
acaaagtttccactgaccatcaaactctgtagattggcgacggcgccggtattttacgtgtg
gtccttgtatgccccaaatggcacgctcggttaacagtaccagcggtaccgtctcaacct
acaacgcaccgttgctggacctttccggttcacccgagcctgaaggggggaaaactacagg
gccacgtgctgctcgcaagctactttccacacagctccgtcaagctgcggtggtacaa
aatgcccgcgaggtggactttacaaagtacgttacgaacgcctcaagcgtgtgggttag
acgggctaatacgcgaatctctacgggtgtctatcccgggttgatccggaggaggaatac
acacccagctcttcgctgtagcatagactgggtacagggacgaagtatcattttgctcgcat

Figure 16 (Continued)

agccaaagctggaacaccctctgtgtttgttgccccaaccgtgtccggtttcggtagaag
 acggagacgccgtctgtacggctaaatgcgtaccgagcaccggggtgttcgtatcgtgg
 tcagtgaacgaccacctaccaggggttcgctcgcaagacatgacaaccggagtctgccc
 tagccactcgggattgggttaacatgcaaagccgcccggccccctctcagaagagaatgggg
 agagggagtatagctgcataatagaggggtaccccgacggcctgcctatgttttcggac
 acagtgggtatatgacgcctccccgattgttgaggacaggccgggttttgacgagcatcat
 cgcagttacttgcgggggccgcggcactggcgctggctgttctcatcacagccgtctgtt
 ttactgctccaagccctcacaggcgccgtacaagaagtctgacttttag

EHV-1 glycoprotein (gC) protein (AAT67273.1) encoded by AY665713) from EHV-1 Ab4 strain (468aa) (SEQ ID NO:10)

MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTT
 PNLTTAHGAGSDNTTNANGTESTHSHETTITCTKSLISVPYYKSVDMNCTTSVGVNYS
 EYRLEIYLNQRTPFSGTPPGDEENYINHNATKDQTLLEFSTAERKKSRRGGQLGVIPD
 RLPKRQLFNLPLHTEGGTKFPLTIKSVDWRTAGIYVWSLYAKNGTLVNSTSVTVSTYN
 APLLDLSVHPSLKGENYRATCVVASYFPHSSVKLRWYKNAREVDFTKYVTNASSVWVD
 GLITRISTVSI PVDPEEEYTPSLRCSIDWYRDEVSFARIAKAGTPSVFVAPT VSVSVE
 DGDAVCTAKCVPSTGVFVSWSVNDHLPGVPSQDMTTGVCPSHSGLVNMQSRRLPSEEN
 GEREYSCIIEGYPDGLPMFSDTVVYDASPIVEDRPVLTSIIAVTCGAAALALVVLITA
 VCFYCSKPSQAPYKKSDF

EHV-1 glycoprotein (gC) gene (NC_001491) from EHV-1 (SEQ ID NO:11)

atgtggttgccctaattctcgtgagatttgtggcgggtcgcgatctctaattctgtgccggggcgatattaactta
 tgcctctggagctagtgtcgtacgtccagccagagtagcggccgtacaccaactcacacaactccgaatctaa
 ctaccgcacacggcgcggggtctgacaacacaactaacgcaaaccgtacagaatctacacactcccatgaa
 accacaatcacctgcaccaagagtctcatatctgtgccctactacaaatctgtcgatatagaactgtacaac
 gtcggtaggcgtaaattatagcgagtagccgcctcgagatttacttgaaccagcgcacccccattttcgggta
 cgcccccggcgacgaagaaaactacatcaaccataacgccaccaaggatcagactctgctgttattctca
 acggcagagagggaaaaaatctcgaaggggtggccagctgggagttatccagacaggctaccaaaagcgcca
 gctgtttaaccttccccctccacacggaagggtggtacaaagtttccactgacctcaaatctgtagattggc
 ggacggccggcattttacgtgtggtccttgtatgccccaaatggcacgctcggttaacagtaccagcgttacc
 gtctcaacctacaacgcacgggttgctggacctttccggttaccgcagcctgaagggggaaaactacagggc
 cacgtgcgtcgtcgcaagctactttccacacagctccgtcaagctgcgggtggtacaaaaatgcccgcgagg
 tggactttacaaagtacgttacgaacgcctcaagcgtgtgggtagacgggctaatacgcgaatctctacg
 gtgtctatcccggttgatccggaggaggaatacacacccagctcttcgctgtagcatagactggtacagggga
 cgaagtatcatttgctcgcatagccaaagctggaacaccctctgtgtttgttgccccaaccgtgtccggtt
 cggtagaagacggagacgccgtctgtacggctaaatgcgtaccgagcaccggggtgttcgtatcgtggtca
 gtgaacgaccacctaccaggggttcgctcgcaagacatgacaaccggagctgtgcctagccactcgggatt
 ggttaacatgcaaagccgcccggccccctctcagaagagaatggggagagggagtagctgcataatagagg
 ggtaccccgacggcctgcctatgttttcggacacagtgggtatatgacgcctccccgattgttgaggacagg
 ccgggttttgacgagcatcatcgagttacttgcgggggccgcggcactggcgctggctgttctcatcacagc
 cgtctgtttttactgctccaagccctcacaggcgccgtacaagaagtctgacttttag

Figure 16 (Continued)

EHV-1 glycoprotein (gC) protein (YP_053061.1) encoded by NC_001491 (468aa) (SEQ ID NO:12)

MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTT
 PNLTTAHGAGSDNTTNANGTESTSHETTITCTKSLISVPYYKSVDNMCTTSVGVNYS
 EYRLEIYLNQRTPFSGTPPGDEENYINHNATKDQTLLEFSTAERKKSRRGGQLGVIPD
 RLPKRQLFNLPLHTEGGTKFPLTIKSVDWRTAGIYVWSLYAKNGTLVNSTSVTVSTYN
 APLLDLSVHPSLKGENYRATCVVASYPHSSVKLRWYKNAREVDFTKYVTNASSVWVD
 GLITRISTVSI PVDPEEEYTPSLRCSIDWYRDEVSFARIAKAGTPSVFVAPT VSVSVE
 DGDAVCTAKCVPSTGVFVSWSVNDHLPGVPSQDMTTGVCPSHGLVNMQSRRLSEEN
 GEREYSCIIEGYPDGLPMFSDTVVYDASPIVEDRPVLTSIIAVTCGAAALALVVLITA
 VCFYCSKPSQAPYKKSDF

EHV-1 RacL DNA polymerase partial sequence (SEQ ID NO:13)

FDSQADAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATSENGGGKPGVGRAVGYQGAKVLDPVSG
 FHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPSVNYSTFEVGDQKLFFVHAHIRESLLGILL
 RDWLAMRKAVRARIPTSTPEEAVLLDKQQSAIKVICNSVYGFTGVANGLLPCL

EHV-1 RacL DNA polymerase partial sequence comprising N at 752 of full length EHV-1 DNA polymerase (SEQ ID NO:14)

FDSQADAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATSENGGGKPGVGRAVGYQGAKVLDPVSG
 FHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPSVNYSTFEVGDQKLFFVHAHIRESLLGILL
 RDWLAMRKAVRARIPTSTPEEAVLLDKQQSAIKVICNSVYGFTGVANGLLPCL

EHV-1 RacL DNA polymerase partial sequence with amino acid deletion at 752 of full length EHV-1 DNA polymerase (SEQ ID NO:15)

FDSQADAASETSELAMDSQSHAFDSTDEPDGVDGTPDAAGSGATSENGGGKPGVGRAVGYQGAKVLDPVSG
 FHVDPVVVDFDASLYPSIIQAHNLCFTTLALDEVDLAGLQPSVYSTFEVGDQKLFFVHAHIRESLLGILLR
 DWLAMRKAVRARIPTSTPEEAVLLDKQQSAIKVICNSVYGFTGVANGLLPCL

EHV-1 glycoprotein (gC) gene from EHV-1 RacL11 strain (SEQ ID NO:34)

Atgtggttgccctaattctcgtgagatttgtggcggctcgctatctaatctgtgccggggcgatattaactta
 tgcctctggagctagtgttagctccagccagagtacgcccgtacaccaactcacacaactccgaatctaa
 ctaccgcacacggcgcgggctctgacaacacaactaacgcaaacggtacagaatctacacactcccatgaa
 accacaatcacctgcaccaagagtctcatatctgtgccctactacaaatctgtcgatatgaactgtacaac
 gtcggttaggcgtaaattatagcgagtaccgcctcgagatttacttgaaccagcgcacccccattttcgggta
 cgccccccggcgacgaagaaaactacatcaaccataacgccaccaaggatcagactctgctgttattctca
 acggcaaagaggaaaaaatctcgaaggggtggccagctgggagttatcccagacagggtaccaaagcgcaa
 gctgtttaaccttcccctccacacggaaggtggtacaaagtctccactgaccatcaaactctgtagattggc
 ggacggccggcatttacgtgtggtccttgtatgccaaaaatggcacgctcggttaacagtaccagcggtacc
 gtctcaacctacaacgcacgggtgctggacctttccgttcacccgagcctgaagggggaaaactacagggc
 cacgtgcgtcgtcgcaagctactttccacacagctccgtcaagctgcggtggtacaaaaatgcccgcgagg
 tggactttacaaagtacgttacgaacgcctcaagcgtgtgggcagacgggctaatacgcgaatctctacg
 gtgtctatcccgggttggtccggaggaggaatacacaccagctcttcgctgtagcatagactgggtacaggga
 cgaagtatcatttgcctgcgatagccaaagctggaacacctctgtgtttgttgccccaaacggtgtccgttt
 cggtagaagacgggagacggcgtctgtacggctaaatgcgtaccgagcaccgggggtgttcgtatcgtggtca
 gtgaacgaccacctaccaggggttccgtcgcaagacatgacaaccggagctctgccctagccactcgggatt

Figure 16 (Continued)

ggttaacatgcaaagccgcccggccctctcagaagagaatggggagagggagtagctgcataatagagg
 ggtacccccgacggcctgcctatgttttcggacacagtgggtatatgacgcctccccgattggtgaggacagg
 ccggttttgacgagcatcatcgagttacttgccggggccgcccactggcgctggctgcttctcatcacagc
 cgtctgtttttactgctccaagccctcacaggcgccgtacaagaagtctgacttttag

EHV-1 glycoprotein (gC) protein from EHV-1 RacL11 strain (SEQ ID NO:35)

MWLPNLVRFVAVAYLICAGAILTYASGASASSSQSTPATPTHTTTPNLTTAHGAGSDNTTNANGTESTHSHE
 TTITCTKSLISVPYKSVDMNCTTSVGVNYSYRLEIYLNQRTFFSGTPPGDEENYINHNATKDQTLLEFS
 TAKRKSRRGGQLGVI PDRLPKRKLFNLPLHTEGGTKFPLTIKSVDWRTAGIYVWSLYAKNGTLVNSTSVT
 VSTYNAPLLDLSVHPSLKGENYRATCVVASYFPHSSVKLRWYKNAREVDFTKYVTNASSVWADGLITRIST
 VSI PVGPEEEYTPSLRCSIDWYRDEVSFARIAKAGTPSVFVAPT VSVSVEDGDAVCTAKCVPSTGVFVWS
 VNDHLPVPSQDMTTGVCPSHSLVNMQSRRPLSEENGEREYSCIIEGYPDGLPMFSDTVVYDASPIVEDR
 PVLTSIIAVTCGAAALALVVLITAVCFYCSKPSQAPYKKSDF*

EHV-1 DNA polymerase (Pol) from EHV-1 NY03 strain (SEQ ID NO:36)

atggcggcgcgcaacaggccaactccgttcgcaggagcgggtttttaatccgtttattggcaagaggccattttcaggccgg
 gaagcgggcagaccgaggagacagagcggcccaaggcccccaacactcgtactgcacagaggtgggtagctttaagttat
 agctccaagatgcctcgatgaagaagcccccgccaccagcgacgcggtgtacacgtgggcaccttgagcggccacccaa
 agtgtagctcgatggctcagagtagcagctgctgaactttgcctccggaggtgctggcctcgaggattcgggttggaacggc
 caggattttcggggcgatggattcaacccagatttgagagatttcacgtgtacgacatagtagagacttcggagagcgcctcac
 acgatgacctatccaggtttgctgagctatcccggcaagcgggtctgtggaactgctgggaatgagcagtggtggaagc
 gagtcgggttcacgtctatggtgtgcgcattttttacatggcaaggcggaggtggatagcgtttggaataaccaccga
 ggcagaactcgtgcgcgaatggtggactgcgcgcacagctcggcttgagcgcggccctgggaatggcaacggcggcaa
 acagagcggcgagcggcgggggatggtggggcggaagcacgtgtctgcggactgcttcaaagtggagaccgtgtgcc
 acacgacgctgtactactttggtatcaagccagctctctactatagatctgcctccagcagccgctgggaggggtcatctgc
 gacaactttaccggagattacaaaattcgaggggagcgtggacgtgaccacgcggctgtgttggaatgaaattttacca
 gtttcgggtggtaccgcctgcgacccggcaccacggagagcgtgtcaactcgccttgagcgcacacgtcacctcaagc
 gacgtggagattaactgtactcccataacctggagccgataccagacgaggtgctgcccactataagctcatgtgctttg
 atatagagtgtaaagctggaacgggtaacgaaatggcgttccagtggaactaaccaagaggacgtggtcatccagatctct
 gtctgtgtactcgttgcctcagaaccacgaacacacctgctgtttccctcgggtcatgcgatatctctgaggaatactcgtt
 tgcattgcgtccagcgcggcgagcccagaccgaggttttgagtttgacagcagtagcagctgctggtgcttctgacctt
 ctcaagcagtagctctccgagttcgccaccggctacaacatcgtaattttgactgggcgtacatagttacaaggtaacgtcgg
 gtataacatcaagctggacgggtacggcaagttcaacaaggggggctgtttaaggtgtgggacatcgccacgaaccattttca
 gaagaagagcaaggtgaaatcaatggcctgatatcttagacatgtattctgtggcgacggaaaagctaaagctaccagcta
 caaactcgacgcggctgtgggagacgtcctcggcgagcataagatagacctccctataaagaaataccctctattacgcggg
 agggcctgaccggagggcgtaataaggagagtattgtatccaggactctaggctggtgggcaagctgtttttaagtaacctccc
 catctggaactatcggcggtggccaaactcggcgatcacctaaccgcgggtaattttgacggtcagcaaatcgcggtgtaca
 cgtgctgtgtaaaactcggcgagagaaattcattttgcagacaacagacgccggttgacagtcaggcagacgccgcgt
 cagagacttcggagttggctatggatagccaaagccacgccttcgacagtacagacgaaccgacggtgtggacggtacccc
 ggacgccgcaggatctggcgctacttctgaaaacggagggcggaagcccggcgctcgggagggccgtgggctaccaggggag
 caaaggttctagacccgatatccggcttcatgtggaccccggtgtgtgttgacttcgtagcttataccaagcattatccaggc
 ccataacctctgttaccacctggcgctcgatgaagtggatctggccgggcttcaacctccgtcaactactcgacgttcgagg

Figure 16 (Continued)

tgggtgacaaaaagtatttttgtccacgcccatttcgcgaaagcctgcttggcatcttctgctgcgcgactggctggccatgcgaa
 aggcggtgagggcgcgaaatccccaccagcacccccaggaggcagttttactagataagcagcagctctgcgattaaggtgata
 tgcaactcggtttacggattcacgggggtggcacaacggcctgttgccgtgtctgaggatagcggctaccgttaccacgatagga
 cgcgacatgctcctcaagaccgagattacgttcactctcgttggcgacgcgcgagctgctggaggacaattttccaggggct
 ataggtttccgaaaccacaagccttactccgtcagggttatctacggagacaccgactccgtgtttatcaagtttggggcctgacg
 tacgaggggggtatcgagctgggggatgctatgtcgcgtcagatttcagcggacctcttagagcgcccatcaaaactggagtgt
 gagaagacctttcagcgactgctgctgacccaagaagaagtacataggtgtcataaacggggggaagtgtcatgaaggg
 ggtcgacctggtccgcaaaaataactgctctttcataaactgtacgcgcgacatctggtagatcttttgtgtacgacgaggtgtg
 gccacggcggcagcagaggtgacagacgtgcctcccgagaatgggtggggcgcccgctaccgagcgggctttgacaagttt
 gggcgagtgtgtagaggcgtacaaccgtatcactgccccaaactggacgtgcgcgagttcgttatgactgctgagctgagc
 cgctcacccgaattgtataccaacaagcgctgccgcacctaccgtctactttaagctcgccatgaggaatgaagaactgccc
 gcgtaaaagagagaattccgtatgtgatagttgcgcagaccgaggccgcggaacgcgaagcgggtgtagtaaaactaatgcg
 cggtagccgccccaaacccgtgtaaccaagaccgcacgccccaaactaaacgcaaaactgctggttccgacctgcgcgaa
 gacctgacctatgtttccgagaatgacgtaccgtaaacacagactactatttctccacctgttgggtaccataagcgtgaccttt
 aaggctctattcgaaatgatgtgagaacaacagaaaatcttttaaagcgggttattccggaaacccccacaaagacccccacga
 aaacccaggcactgcttgagcgcgcgggcttggaaaagctgacgccctttacaccggaggaagaaagtcgtcgaataactgcat
 acagtttttgtactctagaagcagctcccatcaaagctga

EHV-1 DNA polymerase (pol) protein from EHV-1 NY03 strain (SEQ ID NO:37)

maareqansvrrsgffnfigkrpffirpgsgqtaeterprppqhsyctevgsfkfiaprcldceapadqrrgvhvtlerppk
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