

Sequence
SEQUENCE LISTING

<110> Meria1 Limited
Audonnet, Jean-Christophe
Minke, Jules

<120> RECOMBINANT EQUINE HERPESVIRUS-1 VACCINE CONTAINING MUTATED
GLYCOPROTEIN C AND USES THEREOF

<130> MER 11-174

<150> 61/613,151
<151> 2012-03-20

<160> 37

<170> PatentIn version 3.5

<210> 1
<211> 3663
<212> DNA
<213> artificial

<220>
<223> EHV-1 DNA polymerase (Pol) gene (AY464052) from EHV-1 V592 strain

<400> 1
tcagctttga tggggagctg cttctagagt acaaaaaact gtatgcagta ttcgacgact 60
ttcttcctcc ggtgtaaagg gcgtcagctt ttcaaagccg gcgcgctcaa gcagtgcctg 120
ggttttcgtg ggggtcttgt ggggggtttc cggaataaac cgctttaaaa gatctttctgt 180
tgttctcaca tcatttccga atagagcctt aaaggtcacg cttatggtac ccaacaggtg 240
ggagaaatag tagtctgtgt ttagcggtag gtcattctcg gaaacatagg tcgggtcttc 300
ggcgaggctg gaaaccagca gtttgcggtt aggttggggg cgtgcggtct tggttaccac 360
gggggttttg gcggtaccgc gcattgagtt tactacaccc gcttcgcggt ccgcggcctc 420
ggtctgcgca actatcacat acggaattct ctcttttacg ctgggcagtt cttcattcct 480
catggcgagc ttaaagtaga cggtagagtg cggcaggcgc ttggttggtat acgattcggg 540
tgagcggctc agctcagcag tcataacgaa ctgcgcgacg tccaagttgg gggcagtgat 600
acggttgtag gcctctacca gcactcgccc aaacttgtag aagccgctcg gtagcgggag 660
ccccacccat tctgcgggag gcacgtctgt cacctttgct gccgccgtgg ccacatcctc 720
gtcgtacaac aaaagatcta ccagatgtcg cgcgtagaag tttatgaaag agcagttatt 780
tttgcggaac aggtcgaccc cttcatgag catcttcccc ccgtttatga cacctatgta 840
cttcttcttg gtgatcagca gcagtcgctg aaaggtcttc tcacactcca gtttgatggg 900
cgctctaaag aggtccgctg aaatctgacg cgacatagca tccccagct ccgatacccc 960
ctcgtacgtc agggccacaa acttgataaa cacggagtcg gtgtctccgt agataaccct 1020
gacggagtaa ggcttggtgt ttcggaaacc tatagcccct ggaaaattgt cctccagcag 1080
ctcgcgcgtc gcccaacgag agtgaacgta atctcgggtc ttgaggagca tgctcgcgtcc 1140
tatcgtggta acggtagccg ctatcctcag acacggcaac aggccgtttg ccacccccgt 1200
gaatccgtaa accgagttgc atatcacctt aatcgagac tgctgcttat ctagtaaaac 1260

Sequence

tgccctcctcg	ggggtgctgg	tggggattcg	cgccctcacc	gccttttcgca	tggccagcca	1320
gtcgcgcagc	aagatgccaa	gcaggctttc	gcgaatatgg	gcgtggacaa	aaaataaactt	1380
ttggtcaccc	acctcgaacg	tcgagtagtt	gacggatggg	tgaagcccgg	ccagatccac	1440
ttcatcgagc	gccagggtgg	tgaaacagag	gttatggggc	tggataatgc	ttgggtataa	1500
gctagcgaag	tcaaacacaa	ccacgggggc	cacatgaaag	ccggatacgg	ggtctagaac	1560
ctttgctccc	tggtagccca	cggccctccc	gacgccgggc	ttcccgccctc	cgttttcaga	1620
agtagcgcca	gatcctgcgg	cgtccggggg	accgtccaca	ccgtcggggt	cgtctgtact	1680
gtcgaaggcg	tggctttggc	tatccatagc	caactccgaa	gtctctgacg	cggcgtctgc	1740
ctgactgtca	aaccggcgct	tgttgtctgg	caaaatgaaa	tttctctcgc	gggcgagttt	1800
cagcaagcac	gtgtacacgc	gaatttgctg	accgtcaaaa	attaccgcg	ttaggggtgat	1860
acgggcgagt	ttggccaccg	ccgatagttc	cagatggggg	aggtacttaa	aaaacagctt	1920
gcccaccagc	ctagagtcct	ggatacaata	ctctcctatt	acgcccctcc	ggtcaggccc	1980
tcccgcgtaa	taggagggta	tttctttata	gggaaggctc	atcttatgct	cgccgaggac	2040
gtctcccacg	accgcgtcga	gtttgtagct	gggtagcttt	agcttttccg	tcgccacaga	2100
atacatgtct	agagatatca	ggccattgat	tttcaccttg	ctcttcttct	gaaaatgggt	2160
cgtggcgatg	tcccacacct	taaacagccc	ccctttgttg	aacttgccgt	accgcgtccag	2220
cttgatgtta	tacaccgacg	ttaccttggt	aactatgtac	gcccagtcga	aattaacgat	2280
gtttagaccg	gtggcgaact	cgggagagta	ctgcttgaga	aaggtcagga	aggcaaccag	2340
cagctcgtag	tcgctgtcaa	actccaaaac	cgtcgggtctg	ggctcgccgc	gctggacgca	2400
tgcaaacgag	tattcctcag	agatatcgca	tgacccgagg	gaaaacagca	gggtgtgttc	2460
gtggttctga	gtagcaagcg	agtacagcag	acaggagatc	tggatgacca	ggtcctcttg	2520
gttagttgcc	actgggaacg	ccatttcggt	accggttcca	gctttacact	ctatatcaaa	2580
gcacatgagc	ttatagtcgg	gccaggcagc	ctcgtctggg	atcggtcca	ggttatcggg	2640
agtacagtta	atctccacgt	cgttgagggt	gacgtgtcgc	tcaacggggc	gaagttgaac	2700
acgctctccg	tgggtgccgg	gtcgcaggcg	gtaccaccca	aaactggtaa	aattttcatt	2760
gtccaacaac	agccgcgtgg	tcacgtccac	gtccccctcg	aattttgtaa	tctccgggtg	2820
aaagtgtcg	cagatgaacc	ctcccaggcg	gctgctggag	gcagatactc	tatagtagag	2880
agctggctta	gatccaaagt	agtacagcgt	cgtgtggcac	acgggtctcca	ctttgaagca	2940
gtccgcagac	acgtgctttc	cgccccacca	tcccccgccg	ctgccgccgc	tctgtttgcc	3000
gccgttgcca	tttcccaggg	ccgcgctcaa	agccgagctg	tgcgcgagct	ccaccattgc	3060
gcgcacgagt	tctgcctcgg	tggttatttc	acaagcgcta	tccacctccg	cctttgccat	3120
gtaaaaataa	tggcgcacac	catagacgtg	aaccgcgact	cgctttccac	actcgctcat	3180
tcccagcagt	gttaccacag	acccgcttgg	gcgggatagc	tcagcaaacc	tggatgggtc	3240
atcgtgtgag	gcgctctccg	aagtctctac	tatgtcgtac	acgtgaaatc	tctcaaattc	3300

Sequence

```

ggggttgaat ccacgcccc gaaaatcctg gccgttccaa acccgaatcc tgcgaggcca 3360
gcaacctccg gaggcaaagt tcagcacgtc gtactctgag ccacgacagt acactttggg 3420
tgggcgctcc aagggtgcca cgtgtacacc gcgtcgctgg tcggcggggg cttcttcatc 3480
gaggcatctt ggagctataa acttaaagct acccacctct gtgcagtacg agtggtgggg 3540
gggccttggg cgctctgtct ccgcggtctg cccgcttccc ggcccgaaaa atggcctctt 3600
gccaataaac ggattaaaaa acccgctcct gcgaacggag ttggcctggt cgcgcgccgc 3660
cat 3663

```

```

<210> 2
<211> 1220
<212> PRT
<213> artificial

```

```

<220>
<223> EHV-1 DNA polymerase (pol) protein (AAS45914.1) encoded by
AY464052 from EHV-1 V592 strain

```

```

<400> 2

```

```

Met Ala Ala Arg Glu Gln Ala Asn Ser Val Arg Arg Ser Gly Phe Phe
1 5 10 15

```

```

Asn Pro Phe Ile Gly Lys Arg Pro Phe Phe Arg Pro Gly Ser Gly Gln
20 25 30

```

```

Thr Ala Glu Thr Glu Arg Pro Arg Pro Pro Gln His Ser Tyr Cys Thr
35 40 45

```

```

Glu Val Gly Ser Phe Lys Phe Ile Ala Pro Arg Cys Leu Asp Glu Glu
50 55 60

```

```

Ala Pro Ala Asp Gln Arg Arg Gly Val His Val Gly Thr Leu Glu Arg
65 70 75 80

```

```

Pro Pro Lys Val Tyr Cys Asp Gly Ser Glu Tyr Asp Val Leu Asn Phe
85 90 95

```

```

Ala Ser Gly Gly Cys Trp Pro Arg Arg Ile Arg Val Trp Asn Gly Gln
100 105 110

```

```

Asp Phe Arg Gly Asp Gly Phe Asn Pro Arg Phe Glu Arg Phe His Val
115 120 125

```

```

Tyr Asp Ile Val Glu Thr Ser Glu Ser Ala Ser His Asp Asp Pro Ser
130 135 140

```

```

Arg Phe Ala Glu Leu Ser Arg Pro Ser Gly Ser Val Val Thr Leu Leu
145 150 155 160

```

```

Gly Met Ser Glu Cys Gly Lys Arg Val Ala Val His Val Tyr Gly Val

```

															Sequence															
165										170					175															
Arg	His	Tyr	Phe	Tyr	Met	Ala	Lys	Ala	Glu	Val	Asp	Ser	Ala	Cys	Gly															
			180					185					190																	
Ile	Thr	Thr	Glu	Ala	Glu	Leu	Val	Arg	Ala	Met	Val	Asp	Cys	Ala	His															
		195					200					205																		
Ser	Ser	Ala	Leu	Ser	Ala	Ala	Leu	Gly	Asn	Gly	Asn	Gly	Gly	Lys	Gln															
	210					215					220																			
Ser	Gly	Gly	Ser	Gly	Gly	Gly	Trp	Trp	Gly	Gly	Lys	His	Val	Ser	Ala															
225					230					235					240															
Asp	Cys	Phe	Lys	Val	Glu	Thr	Val	Cys	His	Thr	Thr	Leu	Tyr	Tyr	Phe															
				245					250																					
Gly	Ser	Lys	Pro	Ala	Leu	Tyr	Tyr	Arg	Val	Ser	Ala	Ser	Ser	Ser	Arg															
			260					265					270																	
Leu	Gly	Gly	Phe	Ile	Cys	Asp	Asn	Phe	His	Pro	Glu	Ile	Thr	Lys	Phe															
		275					280					285																		
Glu	Gly	Ser	Val	Asp	Val	Thr	Thr	Arg	Leu	Leu	Leu	Asp	Asn	Glu	Asn															
	290					295					300																			
Phe	Thr	Ser	Phe	Gly	Trp	Tyr	Arg	Leu	Arg	Pro	Gly	Thr	His	Gly	Glu															
305					310					315					320															
Arg	Val	Gln	Leu	Arg	Pro	Val	Glu	Arg	His	Val	Thr	Ser	Ser	Asp	Val															
				325					330					335																
Glu	Ile	Asn	Cys	Thr	Pro	Asp	Asn	Leu	Glu	Pro	Ile	Pro	Asp	Glu	Ala															
			340					345					350																	
Ala	Trp	Pro	Asp	Tyr	Lys	Leu	Met	Cys	Phe	Asp	Ile	Glu	Cys	Lys	Ala															
		355					360					365																		
Gly	Thr	Gly	Asn	Glu	Met	Ala	Phe	Pro	Val	Ala	Thr	Asn	Gln	Glu	Asp															
	370					375					380																			
Leu	Val	Ile	Gln	Ile	Ser	Cys	Leu	Leu	Tyr	Ser	Leu	Ala	Thr	Gln	Asn															
385					390					395					400															
His	Glu	His	Thr	Leu	Leu	Phe	Ser	Leu	Gly	Ser	Cys	Asp	Ile	Ser	Glu															
				405					410					415																
Glu	Tyr	Ser	Phe	Ala	Cys	Val	Gln	Arg	Gly	Glu	Pro	Arg	Pro	Thr	Val															
			420					425					430																	
Leu	Glu	Phe	Asp	Ser	Glu	Tyr	Glu	Leu	Leu	Val	Ala	Phe	Leu	Thr	Phe															

Sequence															
435					440					445					
Leu	Lys	Gln	Tyr	Ser	Pro	Glu	Phe	Ala	Thr	Gly	Tyr	Asn	Ile	Val	Asn
	450					455					460				
Phe	Asp	Trp	Ala	Tyr	Ile	Val	Asn	Lys	Val	Thr	Ser	Val	Tyr	Asn	Ile
465					470					475					480
Lys	Leu	Asp	Gly	Tyr	Gly	Lys	Phe	Asn	Lys	Gly	Gly	Leu	Phe	Lys	Val
				485					490					495	
Trp	Asp	Ile	Ala	Thr	Asn	His	Phe	Gln	Lys	Lys	Ser	Lys	Val	Lys	Ile
			500					505					510		
Asn	Gly	Leu	Ile	Ser	Leu	Asp	Met	Tyr	Ser	Val	Ala	Thr	Glu	Lys	Leu
		515					520					525			
Lys	Leu	Pro	Ser	Tyr	Lys	Leu	Asp	Ala	Val	Val	Gly	Asp	Val	Leu	Gly
	530					535					540				
Glu	His	Lys	Ile	Asp	Leu	Pro	Tyr	Lys	Glu	Ile	Pro	Ser	Tyr	Tyr	Ala
545					550					555					560
Gly	Gly	Pro	Asp	Arg	Arg	Gly	Val	Ile	Gly	Glu	Tyr	Cys	Ile	Gln	Asp
				565					570					575	
Ser	Arg	Leu	Val	Gly	Lys	Leu	Phe	Phe	Lys	Tyr	Leu	Pro	His	Leu	Glu
			580					585					590		
Leu	Ser	Ala	Val	Ala	Lys	Leu	Ala	Arg	Ile	Thr	Leu	Thr	Arg	Val	Ile
		595					600					605			
Phe	Asp	Gly	Gln	Gln	Ile	Arg	Val	Tyr	Thr	Cys	Leu	Leu	Lys	Leu	Ala
	610					615					620				
Arg	Glu	Arg	Asn	Phe	Ile	Leu	Pro	Asp	Asn	Arg	Arg	Arg	Phe	Asp	Ser
625					630					635					640
Gln	Ala	Asp	Ala	Ala	Ser	Glu	Thr	Ser	Glu	Leu	Ala	Met	Asp	Ser	Gln
				645					650					655	
Ser	His	Ala	Phe	Asp	Ser	Thr	Asp	Glu	Pro	Asp	Gly	Val	Asp	Gly	Thr
			660					665					670		
Pro	Asp	Ala	Ala	Gly	Ser	Gly	Ala	Thr	Ser	Glu	Asn	Gly	Gly	Gly	Lys
		675					680					685			
Pro	Gly	Val	Gly	Arg	Ala	Val	Gly	Tyr	Gln	Gly	Ala	Lys	Val	Leu	Asp
	690					695					700				
Pro	Val	Ser	Gly	Phe	His	Val	Asp	Pro	Val	Val	Val	Phe	Asp	Phe	Ala

Sequence																
705						710	715					720				
Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Gln	Ala	His	Asn	Leu	Cys	Phe	Thr	Thr	
				725					730					735		
Leu	Ala	Leu	Asp	Glu	Val	Asp	Leu	Ala	Gly	Leu	Gln	Pro	Ser	Val	Asn	
			740					745					750			
Tyr	Ser	Thr	Phe	Glu	Val	Gly	Asp	Gln	Lys	Leu	Phe	Phe	Val	His	Ala	
		755					760					765				
His	Ile	Arg	Glu	Ser	Leu	Leu	Gly	Ile	Leu	Leu	Arg	Asp	Trp	Leu	Ala	
	770					775					780					
Met	Arg	Lys	Ala	Val	Arg	Ala	Arg	Ile	Pro	Thr	Ser	Thr	Pro	Glu	Glu	
785					790					795					800	
Ala	Val	Leu	Leu	Asp	Lys	Gln	Gln	Ser	Ala	Ile	Lys	Val	Ile	Cys	Asn	
				805					810					815		
Ser	Val	Tyr	Gly	Phe	Thr	Gly	Val	Ala	Asn	Gly	Leu	Leu	Pro	Cys	Leu	
			820					825					830			
Arg	Ile	Ala	Ala	Thr	Val	Thr	Thr	Ile	Gly	Arg	Asp	Met	Leu	Leu	Lys	
		835					840					845				
Thr	Arg	Asp	Tyr	Val	His	Ser	Arg	Trp	Ala	Thr	Arg	Glu	Leu	Leu	Glu	
	850					855					860					
Asp	Asn	Phe	Pro	Gly	Ala	Ile	Gly	Phe	Arg	Asn	His	Lys	Pro	Tyr	Ser	
865					870					875					880	
Val	Arg	Val	Ile	Tyr	Gly	Asp	Thr	Asp	Ser	Val	Phe	Ile	Lys	Phe	Val	
				885					890					895		
Gly	Leu	Thr	Tyr	Glu	Gly	Val	Ser	Glu	Leu	Gly	Asp	Ala	Met	Ser	Arg	
			900					905					910			
Gln	Ile	Ser	Ala	Asp	Leu	Phe	Arg	Ala	Pro	Ile	Lys	Leu	Glu	Cys	Glu	
		915					920					925				
Lys	Thr	Phe	Gln	Arg	Leu	Leu	Leu	Ile	Thr	Lys	Lys	Lys	Tyr	Ile	Gly	
	930					935					940					
Val	Ile	Asn	Gly	Gly	Lys	Met	Leu	Met	Lys	Gly	Val	Asp	Leu	Val	Arg	
945					950					955					960	
Lys	Asn	Asn	Cys	Ser	Phe	Ile	Asn	Leu	Tyr	Ala	Arg	His	Leu	Val	Asp	
				965					970					975		
Leu	Leu	Leu	Tyr	Asp	Glu	Asp	Val	Ala	Thr	Ala	Ala	Ala	Lys	Val	Thr	

Sequence															
980					985					990					
Asp	Val	Pro	Pro	Ala	Glu	Trp	Val	Gly	Arg	Pro	Leu	Pro	Ser	Gly	Phe
		995					1000					1005			
Asp	Lys	Phe	Gly	Arg	Val	Leu	Val	Glu	Ala	Tyr	Asn	Arg	Ile	Thr	
	1010					1015					1020				
Ala	Pro	Asn	Leu	Asp	Val	Arg	Glu	Phe	Val	Met	Thr	Ala	Glu	Leu	
	1025					1030					1035				
Ser	Arg	Ser	Pro	Glu	Ser	Tyr	Thr	Asn	Lys	Arg	Leu	Pro	His	Leu	
	1040					1045					1050				
Thr	Val	Tyr	Phe	Lys	Leu	Ala	Met	Arg	Asn	Glu	Glu	Leu	Pro	Ser	
	1055					1060					1065				
Val	Lys	Glu	Arg	Ile	Pro	Tyr	Val	Ile	Val	Ala	Gln	Thr	Glu	Ala	
	1070					1075					1080				
Ala	Glu	Arg	Glu	Ala	Gly	Val	Val	Asn	Ser	Met	Arg	Gly	Thr	Ala	
	1085					1090					1095				
Gln	Asn	Pro	Val	Val	Thr	Lys	Thr	Ala	Arg	Pro	Gln	Pro	Lys	Arg	
	1100					1105					1110				
Lys	Leu	Leu	Val	Ser	Asp	Leu	Ala	Glu	Asp	Pro	Thr	Tyr	Val	Ser	
	1115					1120					1125				
Glu	Asn	Asp	Val	Pro	Leu	Asn	Thr	Asp	Tyr	Tyr	Phe	Ser	His	Leu	
	1130					1135					1140				
Leu	Gly	Thr	Ile	Ser	Val	Thr	Phe	Lys	Ala	Leu	Phe	Gly	Asn	Asp	
	1145					1150					1155				
Val	Arg	Thr	Thr	Glu	Asn	Leu	Leu	Lys	Arg	Phe	Ile	Pro	Glu	Thr	
	1160					1165					1170				
Pro	His	Lys	Thr	Pro	Thr	Lys	Thr	Gln	Ala	Leu	Leu	Glu	Arg	Ala	
	1175					1180					1185				
Gly	Phe	Glu	Lys	Leu	Thr	Pro	Phe	Thr	Pro	Glu	Glu	Glu	Ser	Arg	
	1190					1195					1200				
Arg	Ile	Leu	His	Thr	Val	Phe	Cys	Thr	Leu	Glu	Ala	Ala	Pro	His	
	1205					1210					1215				
Gln	Ser														
	1220														

<210> 3

Sequence

<211> 3663
<212> DNA
<213> artificial

<220>
<223> EHV-1 DNA polymerase (Pol) (AY665713) from EHV-1 Ab4 strain

```

<400> 3
tcagctttga tggggagctg cttctagagt acaaaaaact gtatgcagta ttcgacgact      60
ttcttcctcc ggtgtaaagg gcgtcagctt ttcaaagccg gcgcgctcaa gcagtgcctg      120
ggttttcgtg ggggtcttgt ggggggtttc cggaataaac cgctttaaaa gattttctgt      180
tgttctcaca tcatttccga atagagcctt aaaggtcacg cttatggtac ccaacagggtg      240
ggagaaatag tagtctgtgt ttagcggtag gtcattctcg gaaacatagg tcgggtcttc      300
ggcgaggctg gaaaccagca gtttgcgttt aggttggggg cgtgcggtct tggttaccac      360
ggggttttgg gcggtaccgc gcattgagtt tactacaccc gcttcgctgt ccgcggcctc      420
ggtctgcgca actatcacat acggaattct ctcttttacg ctgggcagtt cttcattcct      480
catggcgagc ttaaagtaga cggtgaggtg cggcaggcgc ttgttggtat acgattcggg      540
tgagcggctc agctcagcag tcataacgaa ctgcgcacg tccaagttgg gggcagtgat      600
acggttgtag gcctctacca gactcgcgcc aaacttgtag aagccgctcg gtagcgggag      660
ccccacccat tctgcgggag gcacgtctgt cacctctgct gccgccgtgg ccacatcctc      720
gtcgtacaac aaaagatcta ccagatgtcg cgcgtacaag tttatgaaag agcagttatt      780
tttgcgacc aggtcgaccc cttcatgag catcttcccc ccgtttatga cacctatgta      840
cttcttcttg gtgatcagca gcagtcgctg aaaggcttct tcacactcca gtttgatggg      900
cgctctaaag aggtccgctg aaatctgacg cgacatagca tccccagct ccgatacccc      960
ctcgtacgtc agggccacaa acttgataaa cacggagtcg gtgtctccgt agataaccct     1020
gacggagtaa ggcttggtgt ttcggaaacc tatagccctt ggaaaattgt cctccagcag     1080
ctcgcgctc gcccaacgag agtgaacgta atctcgggtc ttgaggagca tgtcgcgtcc     1140
tatcgtggta acggtagccg ctatcctcag acacggcaac aggccgtttg ccacccccgt     1200
gaatccgtaa accgagttgc atatcacctt aatcgagac tgctgcttat ctagtaaaac     1260
tgctcctcg ggggtgctgg tggggattcg gccctcacc gcctttcgca tggccagcca     1320
gtcgcgcgag aagatgcaa gcaggctttc gcgaatatgg gcgtggacaa aaaataactt     1380
ttggtcaccc acctgaacg tcgagtagtc gacggatggt tgaagcccgg ccagatccac     1440
ttcatcgagc gccagggtgg tgaaacagag gttatgggcc tggataatgc ttgggtataa     1500
gctagcgaag tcaaacacaa ccacgggggt cacatgaaag ccggatacgg ggtctagaac     1560
ctttgctccc tggtagccca cggccctccc gacgccgggc ttcccgcctc cgttttcaga     1620
agtagcgcca gatcctgcgg cgtccggggg accgtccaca ccgtcgggtt cgtctgtact     1680
gtcgaaggcg tggctttggc tatccatagc caactccgaa gtctctgacg cggcgtctgc     1740
ctgactgtca aaccggcgtc tgttgtctgg caaaatgaaa tttctctcgc gggcgagttt     1800

```

Sequence						
cagcaagcac	gtgtacacgc	gaatttgctg	accgtcaaaa	attaccgcgc	ttagggatgat	1860
acgggcgagt	ttggccaccg	ccgatagttc	cagatggggg	aggacttaaa	aaaacagctt	1920
gcccaccagc	ctagagtcct	ggatacaata	ctctcctatt	acgcccctcc	ggtcaggccc	1980
tcccgcgtaa	taggagggta	tttctttata	gggaaggtct	atcttatgct	cgccgaggac	2040
gtctcccacg	accgcgtcga	gtttgtagct	gggtagcttt	agcttttccg	tcgccacaga	2100
atacatgtct	agagatatca	ggccattgat	tttcaccttg	ctcttcttct	gaaaatgggt	2160
cgtggcgatg	tcccacacct	taaacagccc	ccctttgttg	aacttgccgt	accggtccag	2220
cttgatgtta	tacaccgacg	ttaccttggt	aactatgtac	gcccagtcga	aattaacgat	2280
gtttagaccg	gtggcgaact	cgggagagta	ctgcttgaga	aaggtcagga	aggcaaccag	2340
cagctcgtag	tcgctgtcaa	actccaaaac	cgctcggctg	ggctcgccgc	gctggacgca	2400
tgcaaacgag	tattcctcag	agatatcgca	tgacccgagg	gaaaacagca	gggtgtgttc	2460
gtggttctga	gtagcaagcg	agtacagcag	acaggagatc	tggatgacca	ggctcctctg	2520
gttagttgcc	actgggaacg	ccatttcgtt	accggttcca	gctttacact	ctatatcaaa	2580
gcacatgagc	ttatagtcgg	gccaggcagc	ctcgtctggt	atcggtcca	ggttatcggg	2640
agtacagtta	atctccacgt	cgcttgaggt	gacgtgtcgc	tcaacggggc	gaagttgaac	2700
acgctctccg	tgggtgccgg	gtcgcaggcg	gtaccaccgc	aaactggtaa	aattttcatt	2760
gtccaacaac	agccgcgtgg	tcacgtccac	gctcccctcg	aattttgtaa	tctccgggtg	2820
aaagtgtgctg	cagatgaacc	ctcccaggcg	gctgctggag	gcagatactc	tatagtagag	2880
agctggctta	gatccaaagt	agtacagcgt	cgtgtggcac	acggtctcca	ctttgaagca	2940
gtccgcagac	acgtgctttc	cgccccacca	tccccgcgcg	ctgccgcccgc	tctgtttgcc	3000
gccgttgcca	tttcccaggg	ccgcgctcaa	agccgagctg	tgcgcgagct	ccaccattgc	3060
gcgcacgagt	tctgcctcgg	tggttattcc	acaagcgcta	tccacctccg	cctttgccat	3120
gtaaaaataa	tggcgcacac	catagacgtg	aaccgcgact	cgctttccac	actcgctcat	3180
tcccagcagt	gttaccacag	accgcttggt	gcgggatagc	tcagcaaacc	tggatgggtc	3240
atcgtgtgag	gcgctctccg	aagtctctac	tatgtcgtac	acgtgaaatc	tctcaaattc	3300
ggggttgaat	ccatcgcccc	gaaaatcctg	gccgttccaa	accggaatcc	tgcgaggcca	3360
gcaacctccg	gaggcaaagt	tcagcacgtc	gtactctgag	ccatcgagct	acactttggg	3420
tgggcgctcc	aagggtgcca	cgtgtacacc	gcgtcgtggg	tcggcggggg	cttcttcac	3480
gaggcatctt	ggagctataa	acttaaagct	accacctct	gtgcagtacg	agtgttgggg	3540
gggccttggg	cgctctgtct	ccgcggtctg	cccgttccc	ggcctgaaaa	atggcctctt	3600
gccaataaac	ggattaaaaa	accgcctcct	gcgaacggag	ttggcctggt	cgcgcgccgc	3660
cat						3663

<210> 4
 <211> 1220
 <212> PRT

Sequence

<213> artificial

<220>

<223> EHV-1 DNA polymerase (pol) protein (AAT67287.1) encoded by AY665713 from EHV-1 Ab4 strain

<400> 4

Met Ala Ala Arg Glu Gln Ala Asn Ser Val Arg Arg Ser Gly Phe Phe
1 5 10 15

Asn Pro Phe Ile Gly Lys Arg Pro Phe Phe Arg Pro Gly Ser Gly Gln
20 25 30

Thr Ala Glu Thr Glu Arg Pro Arg Pro Pro Gln His Ser Tyr Cys Thr
35 40 45

Glu Val Gly Ser Phe Lys Phe Ile Ala Pro Arg Cys Leu Asp Glu Glu
50 55 60

Ala Pro Ala Asp Gln Arg Arg Gly Val His Val Gly Thr Leu Glu Arg
65 70 75 80

Pro Pro Lys Val Tyr Cys Asp Gly Ser Glu Tyr Asp Val Leu Asn Phe
85 90 95

Ala Ser Gly Gly Cys Trp Pro Arg Arg Ile Arg Val Trp Asn Gly Gln
100 105 110

Asp Phe Arg Gly Asp Gly Phe Asn Pro Arg Phe Glu Arg Phe His Val
115 120 125

Tyr Asp Ile Val Glu Thr Ser Glu Ser Ala Ser His Asp Asp Pro Ser
130 135 140

Arg Phe Ala Glu Leu Ser Arg Pro Ser Gly Ser Val Val Thr Leu Leu
145 150 155 160

Gly Met Ser Glu Cys Gly Lys Arg Val Ala Val His Val Tyr Gly Val
165 170 175

Arg His Tyr Phe Tyr Met Ala Lys Ala Glu Val Asp Ser Ala Cys Gly
180 185 190

Ile Thr Thr Glu Ala Glu Leu Val Arg Ala Met Val Asp Cys Ala His
195 200 205

Ser Ser Ala Leu Ser Ala Ala Leu Gly Asn Gly Asn Gly Gly Lys Gln
210 215 220

Ser Gly Gly Ser Gly Gly Trp Trp Gly Gly Lys His Val Ser Ala
225 230 235 240

Sequence

Asp Cys Phe Lys Val₂₄₅ Glu Thr Val Cys His₂₅₀ Thr Thr Leu Tyr Tyr₂₅₅ Phe

Gly Ser Lys Pro₂₆₀ Ala Leu Tyr Tyr Arg₂₆₅ Val Ser Ala Ser Ser₂₇₀ Ser Arg

Leu Gly Gly₂₇₅ Phe Ile Cys Asp Asn₂₈₀ Phe His Pro Glu Ile₂₈₅ Thr Lys Phe

Glu Gly₂₉₀ Ser Val Asp Val Thr₂₉₅ Thr Arg Leu Leu Leu₃₀₀ Asp Asn Glu Asn

Phe Thr Ser Phe Gly Trp₃₁₀ Tyr Arg Leu Arg Pro₃₁₅ Gly Thr His Gly Glu₃₂₀

Arg Val Gln Leu Arg₃₂₅ Pro Val Glu Arg His₃₃₀ Val Thr Ser Ser Asp₃₃₅ Val

Glu Ile Asn Cys₃₄₀ Thr Pro Asp Asn Leu₃₄₅ Glu Pro Ile Pro Asp₃₅₀ Glu Ala

Ala Trp Pro₃₅₅ Asp Tyr Lys Leu Met₃₆₀ Cys Phe Asp Ile Glu₃₆₅ Cys Lys Ala

Gly Thr Gly Asn Glu Met Ala₃₇₅ Phe Pro Val Ala Thr₃₈₀ Asn Gln Glu Asp

Leu Val Ile Gln Ile Ser₃₉₀ Cys Leu Leu Tyr Ser₃₉₅ Leu Ala Thr Gln Asn₄₀₀

His Glu His Thr Leu₄₀₅ Leu Phe Ser Leu Gly₄₁₀ Ser Cys Asp Ile Ser₄₁₅ Glu

Glu Tyr Ser Phe₄₂₀ Ala Cys Val Gln Arg Gly Glu Pro Arg Pro₄₃₀ Thr Val

Leu Glu Phe₄₃₅ Asp Ser Glu Tyr Glu₄₄₀ Leu Leu Val Ala Phe₄₄₅ Leu Thr Phe

Leu Lys₄₅₀ Gln Tyr Ser Pro Glu₄₅₅ Phe Ala Thr Gly Tyr₄₆₀ Asn Ile Val Asn

Phe Asp Trp Ala Tyr Ile₄₇₀ Val Asn Lys Val Thr₄₇₅ Ser Val Tyr Asn Ile₄₈₀

Lys Leu Asp Gly Tyr₄₈₅ Gly Lys Phe Asn Lys₄₉₀ Gly Gly Leu Phe Lys₄₉₅ Val

Trp Asp Ile Ala₅₀₀ Thr Asn His Phe Gln₅₀₅ Lys Lys Ser Lys Val₅₁₀ Lys Ile

Sequence

Asn Gly Leu₅₁₅ Ile Ser Leu Asp Met₅₂₀ Tyr Ser Val Ala Thr₅₂₅ Glu Lys Leu

Lys Leu₅₃₀ Pro Ser Tyr Lys Leu₅₃₅ Asp Ala Val Val Gly₅₄₀ Asp Val Leu Gly

Glu₅₄₅ His Lys Ile Asp Leu₅₅₀ Pro Tyr Lys Glu Ile₅₅₅ Pro Ser Tyr Tyr Ala₅₆₀

Gly Gly Pro Asp Arg₅₆₅ Arg Gly Val Ile Gly₅₇₀ Glu Tyr Cys Ile Gln₅₇₅ Asp

Ser Arg Leu Val₅₈₀ Gly Lys Leu Phe Phe₅₈₅ Lys Tyr Leu Pro His₅₉₀ Leu Glu

Leu Ser Ala₅₉₅ Val Ala Lys Leu Ala₆₀₀ Arg Ile Thr Leu Thr₆₀₅ Arg Val Ile

Phe Asp₆₁₀ Gly Gln Gln Ile Arg₆₁₅ Val Tyr Thr Cys Leu₆₂₀ Leu Lys Leu Ala

Arg Glu Arg Asn Phe Ile₆₃₀ Leu Pro Asp Asn Arg₆₃₅ Arg Arg Phe Asp Ser₆₄₀

Gln Ala Asp Ala Ala₆₄₅ Ser Glu Thr Ser Glu₆₅₀ Leu Ala Met Asp Ser₆₅₅ Gln

Ser His Ala Phe₆₆₀ Asp Ser Thr Asp Glu₆₆₅ Pro Asp Gly Val Asp₆₇₀ Gly Thr

Pro Asp Ala₆₇₅ Ala Gly Ser Gly Ala₆₈₀ Thr Ser Glu Asn Gly₆₈₅ Gly Gly Lys

Pro Gly₆₉₀ Val Gly Arg Ala Val₆₉₅ Gly Tyr Gln Gly Ala₇₀₀ Lys Val Leu Asp

Pro Val Ser Gly Phe His₇₁₀ Val Asp Pro Val Val₇₁₅ Val Phe Asp Phe Ala₇₂₀

Ser Leu Tyr Pro Ser₇₂₅ Ile Ile Gln Ala His₇₃₀ Asn Leu Cys Phe Thr₇₃₅ Thr

Leu Ala Leu Asp₇₄₀ Glu Val Asp Leu Ala₇₄₅ Gly Leu Gln Pro Ser Val Asp

Tyr Ser Thr₇₅₅ Phe Glu Val Gly Asp₇₆₀ Gln Lys Leu Phe Phe₇₆₅ Val His Ala

His Ile₇₇₀ Arg Glu Ser Leu Leu₇₇₅ Gly Ile Leu Leu Arg₇₈₀ Asp Trp Leu Ala

Sequence

Met Arg Lys Ala Val Arg Ala Arg Ile Pro Thr Ser Thr Pro Glu Glu
785 790 795 800

Ala Val Leu Leu Asp Lys Gln Gln Ser Ala Ile Lys Val Ile Cys Asn
805 810 815

Ser Val Tyr Gly Phe Thr Gly Val Ala Asn Gly Leu Leu Pro Cys Leu
820 825 830

Arg Ile Ala Ala Thr Val Thr Thr Ile Gly Arg Asp Met Leu Leu Lys
835 840 845

Thr Arg Asp Tyr Val His Ser Arg Trp Ala Thr Arg Glu Leu Leu Glu
850 855 860

Asp Asn Phe Pro Gly Ala Ile Gly Phe Arg Asn His Lys Pro Tyr Ser
865 870 875 880

Val Arg Val Ile Tyr Gly Asp Thr Asp Ser Val Phe Ile Lys Phe Val
885 890 895

Gly Leu Thr Tyr Glu Gly Val Ser Glu Leu Gly Asp Ala Met Ser Arg
900 905 910

Gln Ile Ser Ala Asp Leu Phe Arg Ala Pro Ile Lys Leu Glu Cys Glu
915 920 925

Lys Thr Phe Gln Arg Leu Leu Leu Ile Thr Lys Lys Lys Tyr Ile Gly
930 935 940

Val Ile Asn Gly Gly Lys Met Leu Met Lys Gly Val Asp Leu Val Arg
945 950 955 960

Lys Asn Asn Cys Ser Phe Ile Asn Leu Tyr Ala Arg His Leu Val Asp
965 970 975

Leu Leu Leu Tyr Asp Glu Asp Val Ala Thr Ala Ala Ala Glu Val Thr
980 985 990

Asp Val Pro Pro Ala Glu Trp Val Gly Arg Pro Leu Pro Ser Gly Phe
995 1000 1005

Asp Lys Phe Gly Arg Val Leu Val Glu Ala Tyr Asn Arg Ile Thr
1010 1015 1020

Ala Pro Asn Leu Asp Val Arg Glu Phe Val Met Thr Ala Glu Leu
1025 1030 1035

Ser Arg Ser Pro Glu Ser Tyr Thr Asn Lys Arg Leu Pro His Leu
1040 1045 1050

Sequence

Thr Val Tyr Phe Lys Leu Ala Met Arg Asn Glu Glu Leu Pro Ser
 1055 1060 1065
 Val Lys Glu Arg Ile Pro Tyr Val Ile Val Ala Gln Thr Glu Ala
 1070 1075 1080
 Ala Glu Arg Glu Ala Gly Val Val Asn Ser Met Arg Gly Thr Ala
 1085 1090 1095
 Gln Asn Pro Val Val Thr Lys Thr Ala Arg Pro Gln Pro Lys Arg
 1100 1105 1110
 Lys Leu Leu Val Ser Asp Leu Ala Glu Asp Pro Thr Tyr Val Ser
 1115 1120 1125
 Glu Asn Asp Val Pro Leu Asn Thr Asp Tyr Tyr Phe Ser His Leu
 1130 1135 1140
 Leu Gly Thr Ile Ser Val Thr Phe Lys Ala Leu Phe Gly Asn Asp
 1145 1150 1155
 Val Arg Thr Thr Glu Asn Leu Leu Lys Arg Phe Ile Pro Glu Thr
 1160 1165 1170
 Pro His Lys Thr Pro Thr Lys Thr Gln Ala Leu Leu Glu Arg Ala
 1175 1180 1185
 Gly Phe Glu Lys Leu Thr Pro Phe Thr Pro Glu Glu Glu Ser Arg
 1190 1195 1200
 Arg Ile Leu His Thr Val Phe Cys Thr Leu Glu Ala Ala Pro His
 1205 1210 1215
 Gln Ser
 1220

<210> 5
 <211> 3663
 <212> DNA
 <213> artificial sequence

<220>
 <223> EHV-1 DNA polymerase (Pol) (NC_001491) from EHV-1

<400> 5
 tcagctttga tggggagctg cttctagagt acaaaaaact gtatgcagta ttcgacgact 60
 ttcttcctcc ggtgtaaagg gcgtcagctt ttcaaagccg gcgcgctcaa gcagtgcctg 120
 ggttttcctg ggggtcttgt ggggggtttc cggaataaac cgcttttaaaa gattttctgt 180
 tgttttcaca tcatttccga atagagcctt aaagggtcacg cttatggtac ccaacaggtg 240
 ggagaaatag tagtctgtgt ttagcggtag gtcattctcg gaaacatagg tcgggtcttc 300
 ggcgaggtcg gaaaccagca gtttgcgttt aggttggggg cgtgcggtct tggttaccac 360

Sequence

ggggtttttg	gcggtaccgc	gcattgagtt	tactacaccc	gcttcgcgtt	ccgcggcctc	420
ggtctgcgca	actatcacat	acggaattct	ctctttttacg	ctgggcagtt	cttcatttcct	480
catggcgagc	ttaaagtaga	cggtgaggtg	cggcaggcgc	ttgttggtat	acgattcggg	540
tgagcggctc	agctcagcag	tcataacgaa	ctcgcgcacg	tccaagttgg	gggcagtgat	600
acggttgtac	gcctctacca	gcactcgcgc	aaacttgtca	aagccgctcg	gtagcgggcg	660
ccccacccat	tctgcgggag	gcacgtctgt	cacctctgct	gccgccgtgg	ccacatcctc	720
gtcgtacaac	aaaagatcta	ccagatgtcg	cgcgtagaac	tttatgaaag	agcagttatt	780
tttgcggaac	aggtcgaccc	ccttcatgag	catcttcccc	ccgtttatga	cacctatgta	840
cttcttcttg	gtgatcagca	gcagtcgctg	aaaggctctc	tcacactcca	gtttgatggg	900
cgctctaaa	aggtccgctg	aaatctgacg	cgacatagca	tccccagct	ccgatacccc	960
ctcgtacgtc	agggccacaa	acttgataaa	cacggagtcg	gtgtctccgt	agataaccct	1020
gacggagtaa	ggcttgtggg	ttcggaacc	tatagcccct	ggaaaattgt	cctccagcag	1080
ctcgcgcgtc	gccaacgag	agtgaacgta	atctcgggtc	ttgaggagca	tgctgcgtcc	1140
tatcgtggta	acggtagccg	ctatcctcag	acacggcaac	aggccgtttg	ccacccccgt	1200
gaatccgtaa	accgagttgc	atatcacctt	aatcgcagac	tgctgcttat	ctagtaaaac	1260
tgcttctctg	ggggtgctgg	tggggattcg	cgccctcacc	gcctttcgca	tggccagcca	1320
gtcgcgcagc	aagatgcaa	gcaggctttc	gcgaatatgg	gcgtggacaa	aaaataactt	1380
ttggtcacc	acctcgaacg	tcgagtagtc	gacggatggg	tgaagcccgg	ccagatccac	1440
ttcatcgagc	gccagggtgg	tgaacacagag	gttatgggccc	tggataatgc	ttgggtataa	1500
gctagcgaag	tcaaacacaa	ccacgggggc	cacatgaaag	ccggatacgg	ggtctagaac	1560
ctttgctccc	tggtagccca	cggccctccc	gacgccgggc	ttcccgcctc	cgttttcaga	1620
agtagcgcca	gatcctgcgg	cgtccggggg	accgtccaca	ccgtcggggt	cgtctgtact	1680
gtcgaaggcg	tggctttggc	tatccatagc	caactccgaa	gtctctgacg	cggcgtctgc	1740
ctgactgtca	aaccggcgct	tgttgtctgg	caaaatgaaa	tttctctcgc	gggcgagttt	1800
cagcaagcac	gtgtacacgc	gaatttgctg	accgtcaaaa	attaccgcgc	ttagggtgat	1860
acgggcgagt	ttggccaccg	ccgatagttc	cagatggggg	aggtacttaa	aaaacagctt	1920
gcccaccagc	ctagagtcct	ggatacaata	ctctcctatt	acgcccctcc	ggtcaggccc	1980
tcccgcgtaa	taggagggtg	tttctttata	gggaagggtc	atcttatgct	cgccgaggac	2040
gtctcccacg	accgcgtcga	gtttgtagct	gggtagcttt	agcttttccg	tcgccacaga	2100
atacatgtct	agagatatca	ggccattgat	tttcaccttg	ctcttcttct	gaaaatgggt	2160
cgtggcgatg	tcccacacct	taaacagccc	ccctttgttg	aacttgccgt	accgtccag	2220
cttgatgtta	tacaccgacg	ttaccttggt	aactatgtac	gcccagtcga	aattaacgat	2280
gtttagaccg	gtggcgaact	cgggagagta	ctgcttgaga	aaggtcagga	aggcaaccag	2340
cagctcgtac	tcgctgtcaa	actccaaaac	cgctcggctg	ggctcgcgcg	gctggacgca	2400

Sequence

```

tgcaaacgag tattcctcag agatatcgca tgacccgagg gaaaacagca ggggtgtgttc 2460
gtgggttctga gtagcaagcg agtacagcag acaggagatc tggatgacca ggtcctcttg 2520
gttagttgcc actgggaacg ccatttcgtt acccgttcca gctttacact ctatatcaaa 2580
gcacatgagc ttatagtcgg gccaggcagc ctcgtctggg atcgggtcca ggttatcggg 2640
agtacagtta atctccacgt cgcttgaggt gacgtgtcgc tcaacggggc gaagttgaac 2700
acgctctccg tgggtgccgg gtcgcaggcg gtaccacccg aaactggtaa aattttcatt 2760
gtccaacaac agccgcgtgg tcacgtccac gtcacctcg aattttgtaa tctccgggtg 2820
aaagttgtcg cagatgaacc ctcccaggcg gctgctggag gcagatactc tatagtagag 2880
agctggctta gatccaaagt agtacagcgt cgtgtggcac acggtctcca ctttgaagca 2940
gtccgcagac acgtgctttc cgccccacca tccccgccg ctgccgccgc tctgtttgcc 3000
gccgttgcca tttcccaggg ccgcgctcaa agccgagctg tgcgcgcagt ccaccattgc 3060
gcgcacgagt tctgcctcgg tggttattcc acaagcgcta tccacctccg cttttgcat 3120
gtaaaaataa tggcgcacac catagacgtg aaccgcgact cgctttccac actcgctcat 3180
tcccagcagt gttaccacag acccgcttgg gcgggatagc tcagcaaacc tggatgggtc 3240
atcgtgtgag gcgctctccg aagtctctac tatgtcgtac acgtgaaatc tctcaaattc 3300
ggggttgaat ccatcgcccc gaaaatcctg gccgttccaa acccgaatcc tgcgaggcca 3360
gcaacctccg gaggcaaagt tcagcacgtc gtactctgag ccatcgcagt acactttggg 3420
tgggcgctcc aaggtgcca cgtgtacacc gcgtcgttg tggcggggg cttcttcac 3480
gaggcatctt ggagctataa acttaaagct acccacctct gtgcagtacg agtgttgggg 3540
gggccttggg cgctctgtct ccgcggtctg cccgcttccc ggcctgaaaa atggcctctt 3600
gccaataaac ggattaaaaa acccgctcct gcgaacggag ttggcctgtt cgcgcgccgc 3660
cat 3663

```

<210> 6
 <211> 1220
 <212> PRT
 <213> artificial sequence

<220>
 <223> EHV-1 DNA polymerase (YP_053075.1) encoded by NC_001491
 <400> 6

Met Ala Ala Arg Glu Gln Ala Asn Ser Val Arg Arg Ser Gly Phe Phe
 1 5 10 15

Asn Pro Phe Ile Gly Lys Arg Pro Phe Phe Arg Pro Gly Ser Gly Gln
 20 25 30

Thr Ala Glu Thr Glu Arg Pro Arg Pro Pro Gln His Ser Tyr Cys Thr
 35 40 45

Sequence

Glu Val Gly Ser Phe Lys Phe Ile Ala Pro Arg Cys Leu Asp Glu Glu
50 55 60

Ala Pro Ala Asp Gln Arg Arg Gly Val His Val Gly Thr Leu Glu Arg
65 70 75 80

Pro Pro Lys Val Tyr Cys Asp Gly Ser Glu Tyr Asp Val Leu Asn Phe
85 90 95

Ala Ser Gly Gly Cys Trp Pro Arg Arg Ile Arg Val Trp Asn Gly Gln
100 105 110

Asp Phe Arg Gly Asp Gly Phe Asn Pro Arg Phe Glu Arg Phe His Val
115 120 125

Tyr Asp Ile Val Glu Thr Ser Glu Ser Ala Ser His Asp Asp Pro Ser
130 135 140

Arg Phe Ala Glu Leu Ser Arg Pro Ser Gly Ser Val Val Thr Leu Leu
145 150 155 160

Gly Met Ser Glu Cys Gly Lys Arg Val Ala Val His Val Tyr Gly Val
165 170 175

Arg His Tyr Phe Tyr Met Ala Lys Ala Glu Val Asp Ser Ala Cys Gly
180 185 190

Ile Thr Thr Glu Ala Glu Leu Val Arg Ala Met Val Asp Cys Ala His
195 200 205

Ser Ser Ala Leu Ser Ala Ala Leu Gly Asn Gly Asn Gly Gly Lys Gln
210 215 220

Ser Gly Gly Ser Gly Gly Gly Trp Trp Gly Gly Lys His Val Ser Ala
225 230 235 240

Asp Cys Phe Lys Val Glu Thr Val Cys His Thr Thr Leu Tyr Tyr Phe
245 250 255

Gly Ser Lys Pro Ala Leu Tyr Tyr Arg Val Ser Ala Ser Ser Ser Arg
260 265 270

Leu Gly Gly Phe Ile Cys Asp Asn Phe His Pro Glu Ile Thr Lys Phe
275 280 285

Glu Gly Ser Val Asp Val Thr Thr Arg Leu Leu Leu Asp Asn Glu Asn
290 295 300

Phe Thr Ser Phe Gly Trp Tyr Arg Leu Arg Pro Gly Thr His Gly Glu
305 310 315 320

															Sequence				
Arg	Val	Gln	Leu	Arg	Pro	Val	Glu	Arg	His	Val	Thr	Ser	Ser	Asp	Val	325	330	335	
Glu	Ile	Asn	Cys	Thr	Pro	Asp	Asn	Leu	Glu	Pro	Ile	Pro	Asp	Glu	Ala	340	345	350	
Ala	Trp	Pro	Asp	Tyr	Lys	Leu	Met	Cys	Phe	Asp	Ile	Glu	Cys	Lys	Ala	355	360	365	
Gly	Thr	Gly	Asn	Glu	Met	Ala	Phe	Pro	Val	Ala	Thr	Asn	Gln	Glu	Asp	370	375	380	
Leu	Val	Ile	Gln	Ile	Ser	Cys	Leu	Leu	Tyr	Ser	Leu	Ala	Thr	Gln	Asn	385	390	395	400
His	Glu	His	Thr	Leu	Leu	Phe	Ser	Leu	Gly	Ser	Cys	Asp	Ile	Ser	Glu	405	410	415	
Glu	Tyr	Ser	Phe	Ala	Cys	Val	Gln	Arg	Gly	Glu	Pro	Arg	Pro	Thr	Val	420	425	430	
Leu	Glu	Phe	Asp	Ser	Glu	Tyr	Glu	Leu	Leu	Val	Ala	Phe	Leu	Thr	Phe	435	440	445	
Leu	Lys	Gln	Tyr	Ser	Pro	Glu	Phe	Ala	Thr	Gly	Tyr	Asn	Ile	Val	Asn	450	455	460	
Phe	Asp	Trp	Ala	Tyr	Ile	Val	Asn	Lys	Val	Thr	Ser	Val	Tyr	Asn	Ile	465	470	475	480
Lys	Leu	Asp	Gly	Tyr	Gly	Lys	Phe	Asn	Lys	Gly	Gly	Leu	Phe	Lys	Val	485	490	495	
Trp	Asp	Ile	Ala	Thr	Asn	His	Phe	Gln	Lys	Lys	Ser	Lys	Val	Lys	Ile	500	505	510	
Asn	Gly	Leu	Ile	Ser	Leu	Asp	Met	Tyr	Ser	Val	Ala	Thr	Glu	Lys	Leu	515	520	525	
Lys	Leu	Pro	Ser	Tyr	Lys	Leu	Asp	Ala	Val	Val	Gly	Asp	Val	Leu	Gly	530	535	540	
Glu	His	Lys	Ile	Asp	Leu	Pro	Tyr	Lys	Glu	Ile	Pro	Ser	Tyr	Tyr	Ala	545	550	555	560
Gly	Gly	Pro	Asp	Arg	Arg	Gly	Val	Ile	Gly	Glu	Tyr	Cys	Ile	Gln	Asp	565	570	575	
Ser	Arg	Leu	Val	Gly	Lys	Leu	Phe	Phe	Lys	Tyr	Leu	Pro	His	Leu	Glu	580	585	590	

Sequence

Leu Ser Ala Val Ala Lys Leu Ala Arg Ile Thr Leu Thr Arg Val Ile
595 600 605

Phe Asp Gly Gln Gln Ile Arg Val Tyr Thr Cys Leu Leu Lys Leu Ala
610 615 620

Arg Glu Arg Asn Phe Ile Leu Pro Asp Asn Arg Arg Arg Phe Asp Ser
625 630 635 640

Gln Ala Asp Ala Ala Ser Glu Thr Ser Glu Leu Ala Met Asp Ser Gln
645 650 655

Ser His Ala Phe Asp Ser Thr Asp Glu Pro Asp Gly Val Asp Gly Thr
660 665 670

Pro Asp Ala Ala Gly Ser Gly Ala Thr Ser Glu Asn Gly Gly Gly Lys
675 680 685

Pro Gly Val Gly Arg Ala Val Gly Tyr Gln Gly Ala Lys Val Leu Asp
690 695 700

Pro Val Ser Gly Phe His Val Asp Pro Val Val Val Phe Asp Phe Ala
705 710 715 720

Ser Leu Tyr Pro Ser Ile Ile Gln Ala His Asn Leu Cys Phe Thr Thr
725 730 735

Leu Ala Leu Asp Glu Val Asp Leu Ala Gly Leu Gln Pro Ser Val Asp
740 745 750

Tyr Ser Thr Phe Glu Val Gly Asp Gln Lys Leu Phe Phe Val His Ala
755 760 765

His Ile Arg Glu Ser Leu Leu Gly Ile Leu Leu Arg Asp Trp Leu Ala
770 775 780

Met Arg Lys Ala Val Arg Ala Arg Ile Pro Thr Ser Thr Pro Glu Glu
785 790 795 800

Ala Val Leu Leu Asp Lys Gln Gln Ser Ala Ile Lys Val Ile Cys Asn
805 810 815

Ser Val Tyr Gly Phe Thr Gly Val Ala Asn Gly Leu Leu Pro Cys Leu
820 825 830

Arg Ile Ala Ala Thr Val Thr Thr Ile Gly Arg Asp Met Leu Leu Lys
835 840 845

Thr Arg Asp Tyr Val His Ser Arg Trp Ala Thr Arg Glu Leu Leu Glu
850 855 860

Sequence

Asp Asn Phe Pro Gly Ala Ile Gly Phe Arg Asn His Lys Pro Tyr Ser
 865 870 875 880
 Val Arg Val Ile Tyr Gly Asp Thr Asp Ser Val Phe Ile Lys Phe Val
 885 890 895
 Gly Leu Thr Tyr Glu Gly Val Ser Glu Leu Gly Asp Ala Met Ser Arg
 900 905 910
 Gln Ile Ser Ala Asp Leu Phe Arg Ala Pro Ile Lys Leu Glu Cys Glu
 915 920 925
 Lys Thr Phe Gln Arg Leu Leu Leu Ile Thr Lys Lys Lys Tyr Ile Gly
 930 935 940
 Val Ile Asn Gly Gly Lys Met Leu Met Lys Gly Val Asp Leu Val Arg
 945 950 955 960
 Lys Asn Asn Cys Ser Phe Ile Asn Leu Tyr Ala Arg His Leu Val Asp
 965 970 975
 Leu Leu Leu Tyr Asp Glu Asp Val Ala Thr Ala Ala Ala Glu Val Thr
 980 985 990
 Asp Val Pro Pro Ala Glu Trp Val Gly Arg Pro Leu Pro Ser Gly Phe
 995 1000 1005
 Asp Lys Phe Gly Arg Val Leu Val Glu Ala Tyr Asn Arg Ile Thr
 1010 1015 1020
 Ala Pro Asn Leu Asp Val Arg Glu Phe Val Met Thr Ala Glu Leu
 1025 1030 1035
 Ser Arg Ser Pro Glu Ser Tyr Thr Asn Lys Arg Leu Pro His Leu
 1040 1045 1050
 Thr Val Tyr Phe Lys Leu Ala Met Arg Asn Glu Glu Leu Pro Ser
 1055 1060 1065
 Val Lys Glu Arg Ile Pro Tyr Val Ile Val Ala Gln Thr Glu Ala
 1070 1075 1080
 Ala Glu Arg Glu Ala Gly Val Val Asn Ser Met Arg Gly Thr Ala
 1085 1090 1095
 Gln Asn Pro Val Val Thr Lys Thr Ala Arg Pro Gln Pro Lys Arg
 1100 1105 1110
 Lys Leu Leu Val Ser Asp Leu Ala Glu Asp Pro Thr Tyr Val Ser
 1115 1120 1125

Sequence

Glu Asn Asp Val Pro Leu Asn Thr Asp Tyr Tyr Phe Ser His Leu
1130 1135 1140

Leu Gly Thr Ile Ser Val Thr Phe Lys Ala Leu Phe Gly Asn Asp
1145 1150 1155

Val Arg Thr Thr Glu Asn Leu Leu Lys Arg Phe Ile Pro Glu Thr
1160 1165 1170

Pro His Lys Thr Pro Thr Lys Thr Gln Ala Leu Leu Glu Arg Ala
1175 1180 1185

Gly Phe Glu Lys Leu Thr Pro Phe Thr Pro Glu Glu Glu Ser Arg
1190 1195 1200

Arg Ile Leu His Thr Val Phe Cys Thr Leu Glu Ala Ala Pro His
1205 1210 1215

Gln Ser
1220

<210> 7
<211> 1407
<212> DNA
<213> artificial sequence

<220>
<223> EHV-1 glycoprotein (gC) gene (AY464052) from EHV-1 V592 strain

<400> 7
atgtggttgc ctaatctcgt gagatttgtg gcggtcgcgt atctaactctg tgccggggcg 60
atattaactt atgcctctgg agctagtgtc agctccagcc agagtacgcc cgctacacca 120
actcacacaa ctccgaatct aactaccgca cacggcgcg gctctgacaa cacaactaac 180
gcaaacggta cagaatctac aactcccat gaaaccacaa tcacctgcac caagagtctc 240
atatctgtgc cctactacaa atctgtcgat atgaactgta caacgtcggg aggcgtaaat 300
tatagcgagt accgcctcga gatttacttg aaccagcgca cccattttc gggtagcccc 360
cccggcgacg aagaaaacta catcaaccat aacgccacca aggatcagac tctgctgtta 420
tttcaacgg cagagaggaa aaaatctcga aggggtggcc agctgggagt tatcccagac 480
aggctaccaa agcgccagct gtttaacctt cccctccaca cggaagggtg taaaaagttt 540
ccactgacca tcaaatctgt agattggcgg acggccggca tttagctgtg gtccttgtat 600
gccaaaaatg gcacgctcgt taacagtacc agcgttaccg tctcaaccta caacgcaccg 660
ttgctggacc tttccgttca cccgagcctg aagggggaaa actacagggc cacgtgcgtc 720
gtcgcaagct actttccaca cagctccgtc aagctgcggg ggtacaaaaa tgcccgcgag 780
gtggacttta caaagtacgt tacgaacgcc tcaagcgtgt gggtagacgg gctaatacag 840
cgaatctcta cggtgtctat cccggttgat ccggaggagg aatacacacc cagtcttcgc 900
tgtagcatag actggtacag ggacgaagta tcatttgctc gcatagccaa agctggaaca 960

Sequence

```

ccctctgtgt ttgttgcccc aaccgtgtcc gtttcggtag aagacggaga cgccgtctgt      1020
acgggctaaat gcgtaccgag caccgggggtg ttcgtatcgt ggtcagtga cgaccaccta      1080
ccagggggttc cgtcgcaaga catgacaacc ggagtctgcc ctagccactc gggattgggt      1140
aacatgcaaa gccgccggcc cctctcagaa gagaatgggg agagggagta tagctgcata      1200
atagaggggt accccgacgg cctgcctatg ttttcggaca cagtgggtata tgacgcctcc      1260
ccgattgttg aggacaggcc ggttttgacg agcatcatcg cagttacttg cggggccgcg      1320
gcactggcgc tggtcgttct catcacagcc gtttgttttt actgctcaa gccctcacag      1380
gcgccgtaca agaagtctga cttttag                                           1407

```

<210> 8

<211> 468

<212> PRT

<213> artificial sequence

<220>

<223> EHV-1 glycoprotein (gC) protein (AAS45900.1) encoded by AY464052
from EHV-1 V592 strain

<400> 8

Met Trp Leu Pro Asn Leu Val Arg Phe Val Ala Val Ala Tyr Leu Ile
1 5 10 15

Cys Ala Gly Ala Ile Leu Thr Tyr Ala Ser Gly Ala Ser Ala Ser Ser
20 25 30

Ser Gln Ser Thr Pro Ala Thr Pro Thr His Thr Thr Pro Asn Leu Thr
35 40 45

Thr Ala His Gly Ala Gly Ser Asp Asn Thr Thr Asn Ala Asn Gly Thr
50 55 60

Glu Ser Thr His Ser His Glu Thr Thr Ile Thr Cys Thr Lys Ser Leu
65 70 75 80

Ile Ser Val Pro Tyr Tyr Lys Ser Val Asp Met Asn Cys Thr Thr Ser
85 90 95

Val Gly Val Asn Tyr Ser Glu Tyr Arg Leu Glu Ile Tyr Leu Asn Gln
100 105 110

Arg Thr Pro Phe Ser Gly Thr Pro Pro Gly Asp Glu Glu Asn Tyr Ile
115 120 125

Asn His Asn Ala Thr Lys Asp Gln Thr Leu Leu Leu Phe Ser Thr Ala
130 135 140

Glu Arg Lys Lys Ser Arg Arg Gly Gly Gln Leu Gly Val Ile Pro Asp
145 150 155 160

Sequence

Arg Leu Pro Lys Arg Gln Leu Phe Asn Leu Pro Leu His Thr Glu Gly
165 170 175

Gly Thr Lys Phe Pro Leu Thr Ile Lys Ser Val Asp Trp Arg Thr Ala
180 185 190

Gly Ile Tyr Val Trp Ser Leu Tyr Ala Lys Asn Gly Thr Leu Val Asn
195 200 205

Ser Thr Ser Val Thr Val Ser Thr Tyr Asn Ala Pro Leu Leu Asp Leu
210 215 220

Ser Val His Pro Ser Leu Lys Gly Glu Asn Tyr Arg Ala Thr Cys Val
225 230 235 240

Val Ala Ser Tyr Phe Pro His Ser Ser Val Lys Leu Arg Trp Tyr Lys
245 250 255

Asn Ala Arg Glu Val Asp Phe Thr Lys Tyr Val Thr Asn Ala Ser Ser
260 265 270

Val Trp Val Asp Gly Leu Ile Thr Arg Ile Ser Thr Val Ser Ile Pro
275 280 285

Val Asp Pro Glu Glu Glu Tyr Thr Pro Ser Leu Arg Cys Ser Ile Asp
290 295 300

Trp Tyr Arg Asp Glu Val Ser Phe Ala Arg Ile Ala Lys Ala Gly Thr
305 310 315 320

Pro Ser Val Phe Val Ala Pro Thr Val Ser Val Ser Val Glu Asp Gly
325 330 335

Asp Ala Val Cys Thr Ala Lys Cys Val Pro Ser Thr Gly Val Phe Val
340 345 350

Ser Trp Ser Val Asn Asp His Leu Pro Gly Val Pro Ser Gln Asp Met
355 360 365

Thr Thr Gly Val Cys Pro Ser His Ser Gly Leu Val Asn Met Gln Ser
370 375 380

Arg Arg Pro Leu Ser Glu Glu Asn Gly Glu Arg Glu Tyr Ser Cys Ile
385 390 395 400

Ile Glu Gly Tyr Pro Asp Gly Leu Pro Met Phe Ser Asp Thr Val Val
405 410 415

Tyr Asp Ala Ser Pro Ile Val Glu Asp Arg Pro Val Leu Thr Ser Ile
420 425 430

Sequence

Ile Ala Val Thr Cys Gly Ala Ala Ala Leu Ala Leu Val Val Leu Ile
435 440 445

Thr Ala Val Cys Phe Tyr Cys Ser Lys Pro Ser Gln Ala Pro Tyr Lys
450 455 460

Lys Ser Asp Phe
465

<210> 9
<211> 1407
<212> DNA
<213> artificial sequence

<220>
<223> EHV-1 glycoprotein (gC) gene (AY665713) from EHV-1 Ab4 strain

<400> 9
atgtggttgc ctaatctcgt gagatttgtg gcggtcgcgt atctaactctg tgccggggcg 60
atattaactt atgcctctgg agctagtgtg agctccagcc agagtacgcc cgctacacca 120
actcacacaa ctccgaatct aactaccgca cacggcgcg gctctgacaa cacaactaac 180
gcaaacggta cagaatctac acactcccat gaaaccacaa tcacctgcac caagagtctc 240
atatctgtgc cctactacaa atctgtcgat atgaactgta caacgtcggg aggcgtaaat 300
tatagcgagt accgcctcga gatttacttg aaccagcgca cccatttttc gggtagcccc 360
cccggcgacg aagaaaacta catcaaccat aacgccacca aggatcagac tctgctgtta 420
ttctcaacgg cagagaggaa aaaatctcga aggggtggcc agctgggagt tatcccagac 480
aggctaccaa agcgccagct gtttaacctt cccctccaca cggaagggtg taaaaagttt 540
ccactgacca tcaaactctgt agattggcgg acggccggca ttacgtgtg gtccttgtat 600
gccaaaaatg gcacgctcgt taacagtacc agcgttaccg tctcaaccta caacgcaccg 660
ttgctggacc tttccgttca cccgagcctg aagggggaaa actacagggc cacgtgcgtc 720
gtcgcaagct actttccaca cagctccgtc aagctgcggg ggtacaaaaa tgcccgcgag 780
gtggacttta caaagtacgt tacgaacgcc tcaagcgtgt gggtagacgg gctaatacag 840
cgaatctcta cgggtgtctat cccggttgat ccggaggagg aatacacacc cagtcttcgc 900
tgtagcatag actggtacag ggacgaagta tcatttgctc gcatagccaa agctggaaca 960
ccctctgtgt ttgttgcccc aaccgtgtcc gtttcggtag aagacggaga cgccgtctgt 1020
acggctaaat gcgtaccgag caccgggggtg ttcgtatcgt ggtcagtga cgaccaccta 1080
ccaggggttc cgtcgcaaga catgacaacc ggagtctgcc ctagccactc gggattgggt 1140
aacatgcaaa gccgccggcc cctctcagaa gagaatgggg agaggagta tagctgcata 1200
atagaggggt accccgacgg cctgcctatg ttttcggaca cagtgggtata tgacgcctcc 1260
ccgattgttg aggacaggcc ggttttgacg agcatcatcg cagttacttg cggggccgcg 1320
gcactggcgc tggtcgttct catcacagcc gtctgttttt actgctccaa gccctcacag 1380

Sequence

1407

gcgccgtaca agaagtctga ctttttag

<210> 10
 <211> 468
 <212> PRT
 <213> artificial sequence

<220>
 <223> EHV-1 glycoprotein (gC) protein (AAT67273.1) encoded by AY665713)
 from EHV-1 Ab4 strain

<400> 10

Met Trp Leu Pro Asn Leu Val Arg Phe Val Ala Val Ala Tyr Leu Ile
 1 5 10 15

Cys Ala Gly Ala Ile Leu Thr Tyr Ala Ser Gly Ala Ser Ala Ser Ser
 20 25 30

Ser Gln Ser Thr Pro Ala Thr Pro Thr His Thr Thr Pro Asn Leu Thr
 35 40 45

Thr Ala His Gly Ala Gly Ser Asp Asn Thr Thr Asn Ala Asn Gly Thr
 50 55 60

Glu Ser Thr His Ser His Glu Thr Thr Ile Thr Cys Thr Lys Ser Leu
 65 70 75 80

Ile Ser Val Pro Tyr Tyr Lys Ser Val Asp Met Asn Cys Thr Thr Ser
 85 90 95

Val Gly Val Asn Tyr Ser Glu Tyr Arg Leu Glu Ile Tyr Leu Asn Gln
 100 105 110

Arg Thr Pro Phe Ser Gly Thr Pro Pro Gly Asp Glu Glu Asn Tyr Ile
 115 120 125

Asn His Asn Ala Thr Lys Asp Gln Thr Leu Leu Leu Phe Ser Thr Ala
 130 135 140

Glu Arg Lys Lys Ser Arg Arg Gly Gly Gln Leu Gly Val Ile Pro Asp
 145 150 155 160

Arg Leu Pro Lys Arg Gln Leu Phe Asn Leu Pro Leu His Thr Glu Gly
 165 170 175

Gly Thr Lys Phe Pro Leu Thr Ile Lys Ser Val Asp Trp Arg Thr Ala
 180 185 190

Gly Ile Tyr Val Trp Ser Leu Tyr Ala Lys Asn Gly Thr Leu Val Asn
 195 200 205

Ser Thr Ser Val Thr Val Ser Thr Tyr Asn Ala Pro Leu Leu Asp Leu
 210 215 220

Sequence

Ser Val His Pro Ser Leu Lys Gly Glu Asn Tyr Arg Ala Thr Cys Val
225 230 235 240

Val Ala Ser Tyr Phe Pro His Ser Ser Val Lys Leu Arg Trp Tyr Lys
245 250 255

Asn Ala Arg Glu Val Asp Phe Thr Lys Tyr Val Thr Asn Ala Ser Ser
260 265 270

Val Trp Val Asp Gly Leu Ile Thr Arg Ile Ser Thr Val Ser Ile Pro
275 280 285

Val Asp Pro Glu Glu Glu Tyr Thr Pro Ser Leu Arg Cys Ser Ile Asp
290 295 300

Trp Tyr Arg Asp Glu Val Ser Phe Ala Arg Ile Ala Lys Ala Gly Thr
305 310 315 320

Pro Ser Val Phe Val Ala Pro Thr Val Ser Val Ser Val Glu Asp Gly
325 330 335

Asp Ala Val Cys Thr Ala Lys Cys Val Pro Ser Thr Gly Val Phe Val
340 345 350

Ser Trp Ser Val Asn Asp His Leu Pro Gly Val Pro Ser Gln Asp Met
355 360 365

Thr Thr Gly Val Cys Pro Ser His Ser Gly Leu Val Asn Met Gln Ser
370 375 380

Arg Arg Pro Leu Ser Glu Glu Asn Gly Glu Arg Glu Tyr Ser Cys Ile
385 390 395 400

Ile Glu Gly Tyr Pro Asp Gly Leu Pro Met Phe Ser Asp Thr Val Val
405 410 415

Tyr Asp Ala Ser Pro Ile Val Glu Asp Arg Pro Val Leu Thr Ser Ile
420 425 430

Ile Ala Val Thr Cys Gly Ala Ala Ala Leu Ala Leu Val Val Leu Ile
435 440 445

Thr Ala Val Cys Phe Tyr Cys Ser Lys Pro Ser Gln Ala Pro Tyr Lys
450 455 460

Lys Ser Asp Phe
465

<210> 11
<211> 1407

Sequence

<212> DNA
<213> artificial sequence

<220>
<223> EHV-1 glycoprotein (gC) gene (NC_001491) from EHV-1

```
<400> 11
atgtggttgc ctaatctcgt gagatttgtg gcggtcgcgt atctaactctg tgccggggcg      60
atattaactt atgcctctgg agctagtgtg agctccagcc agagtacgcc cgctacacca      120
actcacacaa ctccgaatct aactaccgca cacggcgcgg gctctgacaa cacaactaac      180
gcaaacggta cagaatctac aactcccat gaaaccacaa tcacctgcac caagagtctc      240
atatctgtgc cctactacaa atctgtcgat atgaactgta caacgtcggg aggcgtaaata      300
tatagcgagt accgcctcga gatttacttg aaccagcgca cccatttttc gggtagcccc      360
cccggcgacg aagaaaacta catcaaccat aacgccacca aggatcagac tctgctgtta      420
tttcaacggg cagagaggaa aaaatctcga aggggtggcc agctgggagt tatcccagac      480
aggctaccaa agcgccagct gtttaacctt cccctccaca cggaagggtg taaaaagttt      540
ccactgacca tcaaactctg agattggcgg acggccggca ttacgtgtg gtccttgtat      600
gccaaaaatg gcacgctcgt taacagtacc agcgttaccg tctcaaccta caacgcaccg      660
ttgctggacc tttccgttca cccgagcctg aagggggaaa actacagggc cacgtgcgtc      720
gtcgcaagct actttccaca cagctccgtc aagctgcggg ggtacaaaaa tgcccgcgag      780
gtggacttta caaagtacgt tacgaacgcc tcaagcgtgt gggtagacgg gctaatacag      840
cgaatctcta cgggtgtctat cccggttgat ccggaggagg aatacacacc cagtcttcgc      900
tgtagcatag actggtacag ggacgaagta tcatttgctc gcatagccaa agctggaaca      960
ccctctgtgt ttgttgcccc aaccgtgtcc gtttcggtag aagacggaga cgccgtctgt     1020
acggctaaat gcgtaccgag caccgggggtg ttcgtatcgt ggtcagtga cgcaccaccta     1080
ccaggggttc cgtcgcaaga catgacaacc ggagtctgcc ctagccactc gggatttggtt     1140
aacatgcaaa gccgccggcc cctctcagaa gagaatgggg agagggagta tagctgcata     1200
atagaggggt accccgacgg cctgcctatg ttttcggaca cagtgggtata tgacgcctcc     1260
ccgattgttg aggacaggcc ggttttgacg agcatcatcg cagttacttg cggggccgcg      1320
gcaactggcg tggtcgttct catcacagcc gtctgttttt actgctccaa gccctcacag      1380
gcgccgtaca agaagtctga cttttag                                     1407
```

<210> 12
<211> 468
<212> PRT
<213> artificial sequence

<220>
<223> EHV-1 glycoprotein (gC) protein (YP_053061.1) encoded by NC_001491

<400> 12

Met Trp Leu Pro Asn Leu Val Arg Phe Val Ala Val Ala Tyr Leu Ile

1	5	Sequence	10	15											
Cys	Ala	Gly	Ala 20	Ile	Leu	Thr	Tyr	Ala 25	Ser	Gly	Ala	Ser	Ala 30	Ser	Ser
Ser	Gln	Ser 35	Thr	Pro	Ala	Thr	Pro 40	Thr	His	Thr	Thr	Pro 45	Asn	Leu	Thr
Thr	Ala 50	His	Gly	Ala	Gly	Ser 55	Asp	Asn	Thr	Thr	Asn 60	Ala	Asn	Gly	Thr
Glu 65	Ser	Thr	His	Ser	His 70	Glu	Thr	Thr	Ile	Thr 75	Cys	Thr	Lys	Ser	Leu 80
Ile	Ser	Val	Pro	Tyr 85	Tyr	Lys	Ser	Val	Asp 90	Met	Asn	Cys	Thr	Thr 95	Ser
Val	Gly	Val	Asn 100	Tyr	Ser	Glu	Tyr	Arg 105	Leu	Glu	Ile	Tyr	Leu 110	Asn	Gln
Arg	Thr	Pro 115	Phe	Ser	Gly	Thr	Pro 120	Pro	Gly	Asp	Glu	Glu 125	Asn	Tyr	Ile
Asn	His 130	Asn	Ala	Thr	Lys	Asp 135	Gln	Thr	Leu	Leu	Leu 140	Phe	Ser	Thr	Ala
Glu 145	Arg	Lys	Lys	Ser	Arg 150	Arg	Gly	Gly	Gln	Leu 155	Gly	Val	Ile	Pro	Asp 160
Arg	Leu	Pro	Lys	Arg 165	Gln	Leu	Phe	Asn	Leu 170	Pro	Leu	His	Thr	Glu 175	Gly
Gly	Thr	Lys	Phe 180	Pro	Leu	Thr	Ile	Lys 185	Ser	Val	Asp	Trp	Arg 190	Thr	Ala
Gly	Ile	Tyr 195	Val	Trp	Ser	Leu	Tyr 200	Ala	Lys	Asn	Gly	Thr 205	Leu	Val	Asn
Ser	Thr 210	Ser	Val	Thr	Val	Ser 215	Thr	Tyr	Asn	Ala	Pro 220	Leu	Leu	Asp	Leu
Ser 225	Val	His	Pro	Ser	Leu 230	Lys	Gly	Glu	Asn	Tyr 235	Arg	Ala	Thr	Cys	Val 240
Val	Ala	Ser	Tyr	Phe 245	Pro	His	Ser	Ser	Val 250	Lys	Leu	Arg	Trp	Tyr 255	Lys
Asn	Ala	Arg	Glu 260	Val	Asp	Phe	Thr	Lys 265	Tyr	Val	Thr	Asn	Ala 270	Ser	Ser
Val	Trp	Val	Asp	Gly	Leu	Ile	Thr	Arg	Ile	Ser	Thr	Val	Ser	Ile	Pro

Sequence

275 280 285

Val Asp Pro Glu Glu Glu Tyr Thr Pro Ser Leu Arg Cys Ser Ile Asp
 290 295 300

Trp Tyr Arg Asp Glu Val Ser Phe Ala Arg Ile Ala Lys Ala Gly Thr
 305 310 315 320

Pro Ser Val Phe Val Ala Pro Thr Val Ser Val Ser Val Glu Asp Gly
 325 330 335

Asp Ala Val Cys Thr Ala Lys Cys Val Pro Ser Thr Gly Val Phe Val
 340 345 350

Ser Trp Ser Val Asn Asp His Leu Pro Gly Val Pro Ser Gln Asp Met
 355 360 365

Thr Thr Gly Val Cys Pro Ser His Ser Gly Leu Val Asn Met Gln Ser
 370 375 380

Arg Arg Pro Leu Ser Glu Glu Asn Gly Glu Arg Glu Tyr Ser Cys Ile
 385 390 395 400

Ile Glu Gly Tyr Pro Asp Gly Leu Pro Met Phe Ser Asp Thr Val Val
 405 410 415

Tyr Asp Ala Ser Pro Ile Val Glu Asp Arg Pro Val Leu Thr Ser Ile
 420 425 430

Ile Ala Val Thr Cys Gly Ala Ala Ala Leu Ala Leu Val Val Leu Ile
 435 440 445

Thr Ala Val Cys Phe Tyr Cys Ser Lys Pro Ser Gln Ala Pro Tyr Lys
 450 455 460

Lys Ser Asp Phe
 465

<210> 13
 <211> 195
 <212> PRT
 <213> artificial sequence

<220>
 <223> EHV-1 RaCL DNA polymerase partial sequence

<400> 13

Phe Asp Ser Gln Ala Asp Ala Ala Ser Glu Thr Ser Glu Leu Ala Met
 1 5 10 15

Asp Ser Gln Ser His Ala Phe Asp Ser Thr Asp Glu Pro Asp Gly Val
 20 25 30

Sequence

Asp Gly Thr Pro Asp Ala Ala Gly Ser Gly Ala Thr Ser Glu Asn Gly
35 40 45

Gly Gly Lys Pro Gly Val Gly Arg Ala Val Gly Tyr Gln Gly Ala Lys
50 55 60

Val Leu Asp Pro Val Ser Gly Phe His Val Asp Pro Val Val Val Phe
65 70 75 80

Asp Phe Ala Ser Leu Tyr Pro Ser Ile Ile Gln Ala His Asn Leu Cys
85 90 95

Phe Thr Thr Leu Ala Leu Asp Glu Val Asp Leu Ala Gly Leu Gln Pro
100 105 110

Ser Val Asp Tyr Ser Thr Phe Glu Val Gly Asp Gln Lys Leu Phe Phe
115 120 125

Val His Ala His Ile Arg Glu Ser Leu Leu Gly Ile Leu Leu Arg Asp
130 135 140

Trp Leu Ala Met Arg Lys Ala Val Arg Ala Arg Ile Pro Thr Ser Thr
145 150 155 160

Pro Glu Glu Ala Val Leu Leu Asp Lys Gln Gln Ser Ala Ile Lys Val
165 170 175

Ile Cys Asn Ser Val Tyr Gly Phe Thr Gly Val Ala Asn Gly Leu Leu
180 185 190

Pro Cys Leu
195

<210> 14
<211> 195
<212> PRT
<213> artificial sequence

<220>
<223> EHV-1 RaCL DNA polymerase partial sequence comprising N at 752 of full length EHV-1 DNA polymerase

<400> 14

Phe Asp Ser Gln Ala Asp Ala Ala Ser Glu Thr Ser Glu Leu Ala Met
1 5 10 15

Asp Ser Gln Ser His Ala Phe Asp Ser Thr Asp Glu Pro Asp Gly Val
20 25 30

Asp Gly Thr Pro Asp Ala Ala Gly Ser Gly Ala Thr Ser Glu Asn Gly
35 40 45

Sequence

Gly Gly Lys Pro Gly Val Gly Arg Ala Val Gly Tyr Gln Gly Ala Lys
50 55 60

Val Leu Asp Pro Val Ser Gly Phe His Val Asp Pro Val Val Val Phe
65 70 75 80

Asp Phe Ala Ser Leu Tyr Pro Ser Ile Ile Gln Ala His Asn Leu Cys
85 90 95

Phe Thr Thr Leu Ala Leu Asp Glu Val Asp Leu Ala Gly Leu Gln Pro
100 105 110

Ser Val Asn Tyr Ser Thr Phe Glu Val Gly Asp Gln Lys Leu Phe Phe
115 120 125

Val His Ala His Ile Arg Glu Ser Leu Leu Gly Ile Leu Leu Arg Asp
130 135 140

Trp Leu Ala Met Arg Lys Ala Val Arg Ala Arg Ile Pro Thr Ser Thr
145 150 155 160

Pro Glu Glu Ala Val Leu Leu Asp Lys Gln Gln Ser Ala Ile Lys Val
165 170 175

Ile Cys Asn Ser Val Tyr Gly Phe Thr Gly Val Ala Asn Gly Leu Leu
180 185 190

Pro Cys Leu
195

<210> 15
<211> 194
<212> PRT
<213> artificial sequence

<220>
<223> EHV-1 RaCL DNA polymerase partial sequence with amino acid deletion at 752 of full length EHV-1 DNA polymerase

<400> 15

Phe Asp Ser Gln Ala Asp Ala Ala Ser Glu Thr Ser Glu Leu Ala Met
1 5 10 15

Asp Ser Gln Ser His Ala Phe Asp Ser Thr Asp Glu Pro Asp Gly Val
20 25 30

Asp Gly Thr Pro Asp Ala Ala Gly Ser Gly Ala Thr Ser Glu Asn Gly
35 40 45

Gly Gly Lys Pro Gly Val Gly Arg Ala Val Gly Tyr Gln Gly Ala Lys
50 55 60

Val Leu Asp Pro Val Ser Gly Phe His Val Asp Pro Val Val Val Phe
Page 31

															Sequence															
65					70					75					80															
Asp	Phe	Ala	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Gln	Ala	His	Asn	Leu	Cys															
				85					90					95																
Phe	Thr	Thr	Leu	Ala	Leu	Asp	Glu	Val	Asp	Leu	Ala	Gly	Leu	Gln	Pro															
			100					105					110																	
Ser	Val	Tyr	Ser	Thr	Phe	Glu	Val	Gly	Asp	Gln	Lys	Leu	Phe	Phe	Val															
		115					120					125																		
His	Ala	His	Ile	Arg	Glu	Ser	Leu	Leu	Gly	Ile	Leu	Leu	Arg	Asp	Trp															
	130					135					140																			
Leu	Ala	Met	Arg	Lys	Ala	Val	Arg	Ala	Arg	Ile	Pro	Thr	Ser	Thr	Pro															
145					150					155					160															
Glu	Glu	Ala	Val	Leu	Leu	Asp	Lys	Gln	Gln	Ser	Ala	Ile	Lys	Val	Ile															
			165						170					175																
Cys	Asn	Ser	Val	Tyr	Gly	Phe	Thr	Gly	Val	Ala	Asn	Gly	Leu	Leu	Pro															
			180					185					190																	

Cys Leu

<210> 16
 <211> 34
 <212> DNA
 <213> artificial sequence

<220>
 <223> PN1 primer

<400> 16
 cccaagcttg agatggcggc ggcgcaacag gccca

34

<210> 17
 <211> 61
 <212> DNA
 <213> artificial sequence

<220>
 <223> PN2 primer

<400> 17
 cgcgatcct taagcgtagt ctgggacgtc gtatgggtag ctttgatggg gagctgcttc

60

t

61

<210> 18
 <211> 22
 <212> DNA
 <213> artificial sequence

<220>
 <223> P1 primer

Sequence

<400> 18
gcctgcgtgg aggagtattg gg 22

<210> 19
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> P2 primer

<400> 19
taattgatta ctattaataa ctattacacc ggaggaagaa agtcg 45

<210> 20
<211> 46
<212> DNA
<213> artificial sequence

<220>
<223> P3 primer

<400> 20
caaactcatc aatgtatctt aaggtctgtg taaatttaaa gtgcga 46

<210> 21
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> P4 primer

<400> 21
caaaggtgcc agcgtcacat cg 22

<210> 22
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> P5 primer

<400> 22
acgactttct tcctccggtg taatagttat taatagtaat caatt 45

<210> 23
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> P6 primer

<400> 23
cccttgctca ccatggtggc ggatctgacg gttcactaaa cc 42

<210> 24
<211> 42
<212> DNA

	Sequence	
<213> artificial sequence		
<220>		
<223> P7 primer		
<400> 24		
ggttttagtga accgtcagat ccgccaccat ggtgagcaag gg		42
<210> 25		
<211> 45		
<212> DNA		
<213> artificial sequence		
<220>		
<223> P8 primer		
<400> 25		
cgcacttttaa atttacacag accttaagat acattgatga gtttg		45
<210> 26		
<211> 64		
<212> DNA		
<213> artificial sequence		
<220>		
<223> P9 primer		
<400> 26		
tccccgcgga taacttcgta tagcatacat tatacgaagt tattagttat taatagtaat		60
caat		64
<210> 27		
<211> 64		
<212> DNA		
<213> artificial sequence		
<220>		
<223> P10 primer		
<400> 27		
ctagctagca taacttcgta taatgtatgc tatacgaagt tatcttaaga tacattgatg		60
agtt		64
<210> 28		
<211> 25		
<212> DNA		
<213> artificial sequence		
<220>		
<223> gC-1 primer		
<400> 28		
gactctgtcg acggccaccg ccgac		25
<210> 29		
<211> 25		
<212> DNA		
<213> artificial sequence		
<220>		
<223> gC-2 primer		

Sequence

<400> 29		
cctggatcca gactctattc ccatg		25
<210> 30		
<211> 20		
<212> DNA		
<213> artificial sequence		
<220>		
<223> delta gC-1 primer		
<400> 30		
ttggcctatg cggacgactt		20
<210> 31		
<211> 20		
<212> DNA		
<213> artificial sequence		
<220>		
<223> delta gC-2 primer		
<400> 31		
ccctttggtg catggtatgt		20
<210> 32		
<211> 21		
<212> DNA		
<213> artificial sequence		
<220>		
<223> Poly1 primer		
<400> 32		
tctggaacta tcggcgggtgg c		21
<210> 33		
<211> 21		
<212> DNA		
<213> artificial sequence		
<220>		
<223> Poly2 primer		
<400> 33		
cgggtcttga ggagcatgtc g		21
<210> 34		
<211> 1407		
<212> DNA		
<213> artificial sequence		
<220>		
<223> EHV-1 glycoprotein (gC) gene from EHV-1 RacL11 strain		
<400> 34		
atgtggttgc ctaatctcgt gagatttgtg gcggtcgcgt atctaacttg tgccggggcg		60
atattaactt atgcctctgg agctagtgtg agctccagcc agagtacgcc cgctacacca		120
actcacacaa ctccgaatct aactaccgca cacggcgcggt gctctgacaa cacaactaac		180

Sequence					
gcaaacggta	cagaatctac	acactcccat	gaaaccacaa	tcacctgcac caagagtctc	240
atatctgtgc	cctactacaa	atctgtcgat	atgaactgta	caacgtcggg aggcgtaa	300
tatagcgagt	accgcctcga	gatttacttg	aaccagcgca	ccccattttc gggtagcccc	360
cccggcgacg	aagaaaacta	catcaaccat	aacgccacca	aggatcagac tctgctgtta	420
ttctcaacgg	caaagaggaa	aaaatctcga	aggggtggcc	agctgggagt tatcccagac	480
aggctaccaa	agcgcaagct	gtttaacctt	cccctccaca	cggaagggtg taaaaagttt	540
ccactgacca	tcaaattctgt	agattggcgg	acggccggca	tttacgtgtg gtccttgtat	600
gccaaaaatg	gcacgctcgt	taacagtacc	agcgttaccg	tctcaaccta caacgcaccg	660
ttgctggacc	tttccgttca	cccagagcctg	aagggggaaa	actacagggc cacgtgcgtc	720
gtcgcaagct	actttccaca	cagctccgtc	aagctgcggg	ggtacaaaaa tgcccgcgag	780
gtggacttta	caaagtacgt	tacgaacgcc	tcaagcgtgt	gggcagacgg gctaatacag	840
cgaatctcta	cggtgtctat	cccggttggg	ccggaggagg	aatacacacc cagtcttcgc	900
tgtagcatag	actggtacag	ggacgaagta	tcatttgctc	gcatagccaa agctggaaca	960
ccctctgtgt	ttgttgcccc	aaccgtgtcc	gtttcggtag	aagacggaga cgccgtctgt	1020
acggctaaat	gcgtaccgag	caccgggggtg	ttcgtatcgt	ggtcagtga cgcaccaccta	1080
ccaggggttc	cgtcgcaaga	catgacaacc	ggagtctgcc	ctagccactc gggattgggt	1140
aacatgcaaa	gccgccggcc	cctctcagaa	gagaatgggg	agagggagta tagctgcata	1200
atagaggggt	accccagcgg	cctgcctatg	ttttcggaca	cagtgggtata tgacgcctcc	1260
ccgattgttg	aggacaggcc	ggttttgacg	agcatcatcg	cagttacttg cggggccgcg	1320
gcactggcgc	tggtcgttct	catcacagcc	gtctgttttt	actgctccaa gccctcacag	1380
gcgccgtaca	agaagtctga	cttttag			1407

<210> 35
 <211> 468
 <212> PRT
 <213> artificial sequence

<220>
 <223> EHV-1 glycoprotein (gC) protein from EHV-1 RacL11 strain

<400> 35

Met	Trp	Leu	Pro	Asn	Leu	Val	Arg	Phe	Val	Ala	Val	Ala	Tyr	Leu	Ile
1				5					10					15	

Cys	Ala	Gly	Ala	Ile	Leu	Thr	Tyr	Ala	Ser	Gly	Ala	Ser	Ala	Ser	Ser
		20						25					30		

Ser	Gln	Ser	Thr	Pro	Ala	Thr	Pro	Thr	His	Thr	Thr	Pro	Asn	Leu	Thr
		35					40					45			

Thr	Ala	His	Gly	Ala	Gly	Ser	Asp	Asn	Thr	Thr	Asn	Ala	Asn	Gly	Thr
		50				55					60				

Sequence

Glu Ser Thr His Ser His Glu Thr Thr Ile Thr Cys Thr Lys Ser Leu
 65 70 75 80
 Ile Ser Val Pro Tyr Tyr Lys Ser Val Asp Met Asn Cys Thr Thr Ser
 85 90 95
 Val Gly Val Asn Tyr Ser Glu Tyr Arg Leu Glu Ile Tyr Leu Asn Gln
 100 105 110
 Arg Thr Pro Phe Ser Gly Thr Pro Pro Gly Asp Glu Glu Asn Tyr Ile
 115 120 125
 Asn His Asn Ala Thr Lys Asp Gln Thr Leu Leu Leu Phe Ser Thr Ala
 130 135 140
 Lys Arg Lys Lys Ser Arg Arg Gly Gly Gln Leu Gly Val Ile Pro Asp
 145 150 155 160
 Arg Leu Pro Lys Arg Lys Leu Phe Asn Leu Pro Leu His Thr Glu Gly
 165 170 175
 Gly Thr Lys Phe Pro Leu Thr Ile Lys Ser Val Asp Trp Arg Thr Ala
 180 185 190
 Gly Ile Tyr Val Trp Ser Leu Tyr Ala Lys Asn Gly Thr Leu Val Asn
 195 200 205
 Ser Thr Ser Val Thr Val Ser Thr Tyr Asn Ala Pro Leu Leu Asp Leu
 210 215 220
 Ser Val His Pro Ser Leu Lys Gly Glu Asn Tyr Arg Ala Thr Cys Val
 225 230 235 240
 Val Ala Ser Tyr Phe Pro His Ser Ser Val Lys Leu Arg Trp Tyr Lys
 245 250 255
 Asn Ala Arg Glu Val Asp Phe Thr Lys Tyr Val Thr Asn Ala Ser Ser
 260 265 270
 Val Trp Ala Asp Gly Leu Ile Thr Arg Ile Ser Thr Val Ser Ile Pro
 275 280 285
 Val Gly Pro Glu Glu Glu Tyr Thr Pro Ser Leu Arg Cys Ser Ile Asp
 290 295 300
 Trp Tyr Arg Asp Glu Val Ser Phe Ala Arg Ile Ala Lys Ala Gly Thr
 305 310 315 320
 Pro Ser Val Phe Val Ala Pro Thr Val Ser Val Ser Val Glu Asp Gly
 325 330 335

Sequence

Asp Ala Val Cys Thr Ala Lys Cys Val Pro Ser Thr Gly Val Phe Val
340 345 350

Ser Trp Ser Val Asn Asp His Leu Pro Gly Val Pro Ser Gln Asp Met
355 360 365

Thr Thr Gly Val Cys Pro Ser His Ser Gly Leu Val Asn Met Gln Ser
370 375 380

Arg Arg Pro Leu Ser Glu Glu Asn Gly Glu Arg Glu Tyr Ser Cys Ile
385 390 395 400

Ile Glu Gly Tyr Pro Asp Gly Leu Pro Met Phe Ser Asp Thr Val Val
405 410 415

Tyr Asp Ala Ser Pro Ile Val Glu Asp Arg Pro Val Leu Thr Ser Ile
420 425 430

Ile Ala Val Thr Cys Gly Ala Ala Ala Leu Ala Leu Val Val Leu Ile
435 440 445

Thr Ala Val Cys Phe Tyr Cys Ser Lys Pro Ser Gln Ala Pro Tyr Lys
450 455 460

Lys Ser Asp Phe
465

<210> 36
<211> 3663
<212> DNA
<213> artificial sequence

<220>
<223> EHV-1 DNA polymerase (Pol) from EHV-1 NY03 strain

<400> 36
atggcggcgc gcgaacaggc caactccgtt cgcaggagcg ggttttttaa tccgtttatt 60
ggcaagaggc cttttttcag gccgggaagc gggcagaccg cggagacaga gcgccaagg 120
ccccccaac actcgtactg cacagagggtg ggtagcttta agtttatagc tccaagatgc 180
ctcgatgaag aagccccgc cgaccagcga cgcggtgtac acgtgggcac cttggagcgc 240
ccacccaaag tgtactgcga tggctcagag tacgacgtgc tgaactttgc ctccggagggt 300
tgctggcctc gcaggattcg ggtttggaac ggccaggatt ttcggggcga tggattcaac 360
cccagatttg agagatttca cgtgtacgac atagtagaga cttcggagag cgcctcacac 420
gatgaccat ccaggtttgc tgagctatcc cgccaagcg ggtctgtggt aacactgctg 480
ggaatgagcg agtgtggaaa gcgagtcgcg gttcacgtct atggtgtgcg ccattatatt 540
tacatggcaa aggcggagggt ggatagcgct tgtggaataa ccaccgaggc agaactcgtg 600
cgcgcaatgg tggactgcgc gcacagctcg gctttgagcg cggccctggg aaatggcaac 660

Sequence						
ggcggcaaac	agagcggcgg	cagcggcggg	ggatgggtggg	gcggaagca	cgtgtctgcg	720
gactgcttca	aagtggagac	cgtgtgccac	acgacgtgt	actactttgg	atctaagcca	780
gctctctact	atagagtatc	tgccctccagc	agccgcctgg	gaggggttcat	ctgcgacaac	840
tttcacccgg	agattacaaa	attcgagggg	agcgtggacg	tgaccacgcg	gctgtttgttg	900
gacaatgaaa	attttaccag	tttcgggtgg	taccgcctgc	gacccggcac	ccacggagag	960
cgtgttcaac	ttcgccccgt	tgagcgacac	gtcacctcaa	gcgacgtgga	gattaactgt	1020
actcccgata	acctggagcc	gataccagac	gaggctgcct	ggcccgacta	taagctcatg	1080
tgctttgata	tagagtgtaa	agctggaacg	ggtaacgaaa	tggcgttccc	agtggcaact	1140
aaccaagagg	acctgggtcat	ccagatctcc	tgtctgtgtg	actcgcttgc	tactcagaac	1200
cacgaacaca	ccctgctgtt	ttccctcggg	tcatgcgata	tctctgagga	atactcgttt	1260
gcatgcgtcc	agcgcggcga	gcccagaccg	acggtttttg	agtttgacag	cgagtacgag	1320
ctgctgggtg	ccttcctgac	ctttctcaag	cagtactctc	ccgagttcgc	caccggctac	1380
aacatcgta	attttgactg	ggcgtaata	gttaacaagg	taacgtcggg	gtataacatc	1440
aagctggacg	ggtacggcaa	gttcaacaaa	ggggggctgt	ttaagggtgtg	ggacatcgcc	1500
acgaaccatt	ttcagaagaa	gagcaagggtg	aaaatcaatg	gcctgatatc	tctagacatg	1560
tattctgtgg	cgacggaaaa	gctaaagcta	cccagctaca	aactcgacgc	ggtcgtggga	1620
gacgtcctcg	gcgagcataa	gatagacctt	ccctataaag	aaataccctc	ctattacgcg	1680
ggagggcctg	accggagggg	cgtaatagga	gagtattgta	tccaggactc	taggctgggtg	1740
ggcaagctgt	tttttaagta	cctcccccat	ctggaactat	cggcgggtggc	caaactcgcc	1800
cgtatcacc	taacgcgggt	aatttttgac	ggtcagcaaa	ttcgcgtgta	cacgtgcttg	1860
ctgaaactcg	cccgcgagag	aaatttcatt	ttgccagaca	acagacgccg	gtttgacagt	1920
caggcagacg	ccgcgtcaga	gacttcggag	ttggctatgg	atagccaaag	ccacgccttc	1980
gacagtacag	acgaaccgga	cgggtgtggac	ggtaccccg	acgccgcagg	atctggcgct	2040
acttctgaaa	acggaggcgg	gaagcccggc	gtcgggaggg	ccgtgggcta	ccaggagaca	2100
aaggttctag	accccgatc	cggctttcat	gtggaccccg	tggttgtgtt	tgacttcgct	2160
agcttatacc	caagcattat	ccaggcccat	aacctctgtt	tcaccaccct	ggcgctcgat	2220
gaagtggatc	tggccgggct	tcaaccatcc	gtcaactact	cgacgttcga	ggtgggtgac	2280
caaaagtatt	ttttgtcca	cgcccatatt	cgcgaaagcc	tgcttggcat	cttgctgcgc	2340
gactggctgg	ccatgcgaaa	ggcgggtgag	gcgcgaatcc	ccaccagcac	ccccgaggag	2400
gcagttttac	tagataagca	gcagtctgcg	attaagggtga	tatgcaactc	ggtttacgga	2460
ttcacggggg	tggcaaacgg	cctgttgccg	tgtctgagga	tagcggctac	cgttaccacg	2520
ataggacgcg	acatgtctct	caagaccgga	gattacgttc	actctcgttg	ggcgacgcgc	2580
gagctgctgg	aggacaatth	tccaggggct	ataggtttcc	gaaaccacaa	gccttactcc	2640
gtcagggtta	tctacggaga	caccgactcc	gtgtttatca	agtttgtggg	cctgacgtac	2700

Sequence		
gagggggtat cggagctggg ggatgctatg tcgctgcaga tttcagcgga cctctttaga	2760	
gcgcccatca aactggagtg tgagaagacc tttcagcgac tgctgctgat caccaagaag	2820	
aagtacatag gtgtcataaa cggggggaag atgctcatga aggggggtcga cctgggtccgc	2880	
aaaaataact gctctttcat aaacttgtac gcgcgacatc tggtagatct tttgttgtac	2940	
gacgaggatg tggccacggc ggcagcagag gtgacagacg tgcctcccgc agaatgggtg	3000	
gggcgcccgc taccgagcgg ctttgacaag tttgggagag tgctggtaga ggcgtacaac	3060	
cgtatcactg cccccaactt ggacgtgctc gagttcggtt tgactgctga gctgagccgc	3120	
tcacccgaat tgtataccta caagcgcctg ccgcacctca ccgtctactt taagctcgcc	3180	
atgaggaatg aagaactgcc cagcgtaaaa gagagaattc cgtatgtgat agttgcgcag	3240	
accgaggccg cggaacgcga agcgggtgta gtaaaactca tgcgcggtac cgcccaaac	3300	
cccgtggtaa ccaagaccgc acgcccccaa cctaaacgca aactgctggg ttccgacctc	3360	
gccgaagacc cgacctatgt ttccgagaat gacgtaccgc taaacacaga ctactatttc	3420	
tcccacctgt tgggtaccat aagcgtgacc tttaaggctc tattcggaat tgatgtgaga	3480	
acaacagaaa atcttttaaa gcgggtttatt ccggaaccc cccacaagac cccacgaaa	3540	
accaggcac tgcttgagcg cgccggcttt gaaaagctga cgccctttac accggaggaa	3600	
gaaagtcgtc gaatactgca tacagttttt tgtactctag aagcagctcc ccatcaaagc	3660	
tga	3663	

<210> 37
 <211> 1220
 <212> PRT
 <213> artificial sequence

<220>
 <223> EHV-1 DNA polymerase (pol) protein from EHV-1 NY03 strain
 <400> 37

Met Ala Ala Arg Glu Gln Ala Asn Ser Val Arg Arg Ser Gly Phe Phe
 1 5 10 15

Asn Pro Phe Ile Gly Lys Arg Pro Phe Phe Arg Pro Gly Ser Gly Gln
 20 25 30

Thr Ala Glu Thr Glu Arg Pro Arg Pro Pro Gln His Ser Tyr Cys Thr
 35 40 45

Glu Val Gly Ser Phe Lys Phe Ile Ala Pro Arg Cys Leu Asp Glu Glu
 50 55 60

Ala Pro Ala Asp Gln Arg Arg Gly Val His Val Gly Thr Leu Glu Arg
 65 70 75 80

Pro Pro Lys Val Tyr Cys Asp Gly Ser Glu Tyr Asp Val Leu Asn Phe
 85 90 95

Sequence

Ala Ser Gly Gly Cys Trp Pro Arg Arg Ile Arg Val Trp Asn Gly Gln
100 105 110

Asp Phe Arg Gly Asp Gly Phe Asn Pro Arg Phe Glu Arg Phe His Val
115 120 125

Tyr Asp Ile Val Glu Thr Ser Glu Ser Ala Ser His Asp Asp Pro Ser
130 135 140

Arg Phe Ala Glu Leu Ser Arg Pro Ser Gly Ser Val Val Thr Leu Leu
145 150 155 160

Gly Met Ser Glu Cys Gly Lys Arg Val Ala Val His Val Tyr Gly Val
165 170 175

Arg His Tyr Phe Tyr Met Ala Lys Ala Glu Val Asp Ser Ala Cys Gly
180 185 190

Ile Thr Thr Glu Ala Glu Leu Val Arg Ala Met Val Asp Cys Ala His
195 200 205

Ser Ser Ala Leu Ser Ala Ala Leu Gly Asn Gly Asn Gly Gly Lys Gln
210 215 220

Ser Gly Gly Ser Gly Gly Gly Trp Trp Gly Gly Lys His Val Ser Ala
225 230 235 240

Asp Cys Phe Lys Val Glu Thr Val Cys His Thr Thr Leu Tyr Tyr Phe
245 250 255

Gly Ser Lys Pro Ala Leu Tyr Tyr Arg Val Ser Ala Ser Ser Ser Arg
260 265 270

Leu Gly Gly Phe Ile Cys Asp Asn Phe His Pro Glu Ile Thr Lys Phe
275 280 285

Glu Gly Ser Val Asp Val Thr Thr Arg Leu Leu Leu Asp Asn Glu Asn
290 295 300

Phe Thr Ser Phe Gly Trp Tyr Arg Leu Arg Pro Gly Thr His Gly Glu
305 310 315 320

Arg Val Gln Leu Arg Pro Val Glu Arg His Val Thr Ser Ser Asp Val
325 330 335

Glu Ile Asn Cys Thr Pro Asp Asn Leu Glu Pro Ile Pro Asp Glu Ala
340 345 350

Ala Trp Pro Asp Tyr Lys Leu Met Cys Phe Asp Ile Glu Cys Lys Ala
355 360 365

Sequence

Gly Thr Gly Asn Glu Met Ala Phe Pro Val Ala Thr Asn Gln Glu Asp
 370 375 380
 Leu Val Ile Gln Ile Ser Cys Leu Leu Tyr Ser Leu Ala Thr Gln Asn
 385 390 395 400
 His Glu His Thr Leu Leu Phe Ser Leu Gly Ser Cys Asp Ile Ser Glu
 405 410 415
 Glu Tyr Ser Phe Ala Cys Val Gln Arg Gly Glu Pro Arg Pro Thr Val
 420 425 430
 Leu Glu Phe Asp Ser Glu Tyr Glu Leu Leu Val Ala Phe Leu Thr Phe
 435 440 445
 Leu Lys Gln Tyr Ser Pro Glu Phe Ala Thr Gly Tyr Asn Ile Val Asn
 450 455 460
 Phe Asp Trp Ala Tyr Ile Val Asn Lys Val Thr Ser Val Tyr Asn Ile
 465 470 475 480
 Lys Leu Asp Gly Tyr Gly Lys Phe Asn Lys Gly Gly Leu Phe Lys Val
 485 490 495
 Trp Asp Ile Ala Thr Asn His Phe Gln Lys Lys Ser Lys Val Lys Ile
 500 505 510
 Asn Gly Leu Ile Ser Leu Asp Met Tyr Ser Val Ala Thr Glu Lys Leu
 515 520 525
 Lys Leu Pro Ser Tyr Lys Leu Asp Ala Val Val Gly Asp Val Leu Gly
 530 535 540
 Glu His Lys Ile Asp Leu Pro Tyr Lys Glu Ile Pro Ser Tyr Tyr Ala
 545 550 555 560
 Gly Gly Pro Asp Arg Arg Gly Val Ile Gly Glu Tyr Cys Ile Gln Asp
 565 570 575
 Ser Arg Leu Val Gly Lys Leu Phe Phe Lys Tyr Leu Pro His Leu Glu
 580 585 590
 Leu Ser Ala Val Ala Lys Leu Ala Arg Ile Thr Leu Thr Arg Val Ile
 595 600 605
 Phe Asp Gly Gln Gln Ile Arg Val Tyr Thr Cys Leu Leu Lys Leu Ala
 610 615 620
 Arg Glu Arg Asn Phe Ile Leu Pro Asp Asn Arg Arg Arg Phe Asp Ser
 625 630 635 640

Sequence

Gln Ala Asp Ala Ala Ser Glu Thr Ser Glu Leu Ala Met Asp Ser Gln
645 650 655

Ser His Ala Phe Asp Ser Thr Asp Glu Pro Asp Gly Val Asp Gly Thr
660 665 670

Pro Asp Ala Ala Gly Ser Gly Ala Thr Ser Glu Asn Gly Gly Gly Lys
675 680 685

Pro Gly Val Gly Arg Ala Val Gly Tyr Gln Gly Ala Lys Val Leu Asp
690 695 700

Pro Val Ser Gly Phe His Val Asp Pro Val Val Val Phe Asp Phe Ala
705 710 715 720

Ser Leu Tyr Pro Ser Ile Ile Gln Ala His Asn Leu Cys Phe Thr Thr
725 730 735

Leu Ala Leu Asp Glu Val Asp Leu Ala Gly Leu Gln Pro Ser Val Asn
740 745 750

Tyr Ser Thr Phe Glu Val Gly Asp Gln Lys Leu Phe Phe Val His Ala
755 760 765

His Ile Arg Glu Ser Leu Leu Gly Ile Leu Leu Arg Asp Trp Leu Ala
770 775 780

Met Arg Lys Ala Val Arg Ala Arg Ile Pro Thr Ser Thr Pro Glu Glu
785 790 795 800

Ala Val Leu Leu Asp Lys Gln Gln Ser Ala Ile Lys Val Ile Cys Asn
805 810 815

Ser Val Tyr Gly Phe Thr Gly Val Ala Asn Gly Leu Leu Pro Cys Leu
820 825 830

Arg Ile Ala Ala Thr Val Thr Thr Ile Gly Arg Asp Met Leu Leu Lys
835 840 845

Thr Arg Asp Tyr Val His Ser Arg Trp Ala Thr Arg Glu Leu Leu Glu
850 855 860

Asp Asn Phe Pro Gly Ala Ile Gly Phe Arg Asn His Lys Pro Tyr Ser
865 870 875 880

Val Arg Val Ile Tyr Gly Asp Thr Asp Ser Val Phe Ile Lys Phe Val
885 890 895

Gly Leu Thr Tyr Glu Gly Val Ser Glu Leu Gly Asp Ala Met Ser Arg
900 905 910

Sequence

Gln Ile Ser Ala Asp Leu Phe Arg Ala Pro Ile Lys Leu Glu Cys Glu
 915 920 925
 Lys Thr Phe Gln Arg Leu Leu Leu Ile Thr Lys Lys Lys Tyr Ile Gly
 930 935 940
 Val Ile Asn Gly Gly Lys Met Leu Met Lys Gly Val Asp Leu Val Arg
 945 950 955 960
 Lys Asn Asn Cys Ser Phe Ile Asn Leu Tyr Ala Arg His Leu Val Asp
 965 970 975
 Leu Leu Leu Tyr Asp Glu Asp Val Ala Thr Ala Ala Ala Glu Val Thr
 980 985 990
 Asp Val Pro Pro Ala Glu Trp Val Gly Arg Pro Leu Pro Ser Gly Phe
 995 1000 1005
 Asp Lys Phe Gly Arg Val Leu Val Glu Ala Tyr Asn Arg Ile Thr
 1010 1015 1020
 Ala Pro Asn Leu Asp Val Arg Glu Phe Val Met Thr Ala Glu Leu
 1025 1030 1035
 Ser Arg Ser Pro Glu Leu Tyr Thr Asn Lys Arg Leu Pro His Leu
 1040 1045 1050
 Thr Val Tyr Phe Lys Leu Ala Met Arg Asn Glu Glu Leu Pro Ser
 1055 1060 1065
 Val Lys Glu Arg Ile Pro Tyr Val Ile Val Ala Gln Thr Glu Ala
 1070 1075 1080
 Ala Glu Arg Glu Ala Gly Val Val Asn Ser Met Arg Gly Thr Ala
 1085 1090 1095
 Gln Asn Pro Val Val Thr Lys Thr Ala Arg Pro Gln Pro Lys Arg
 1100 1105 1110
 Lys Leu Leu Val Ser Asp Leu Ala Glu Asp Pro Thr Tyr Val Ser
 1115 1120 1125
 Glu Asn Asp Val Pro Leu Asn Thr Asp Tyr Tyr Phe Ser His Leu
 1130 1135 1140
 Leu Gly Thr Ile Ser Val Thr Phe Lys Ala Leu Phe Gly Asn Asp
 1145 1150 1155
 Val Arg Thr Thr Glu Asn Leu Leu Lys Arg Phe Ile Pro Glu Thr
 1160 1165 1170

Sequence

Pro	His	Lys	Thr	Pro	Thr	Lys	Thr	Gln	Ala	Leu	Leu	Glu	Arg	Ala
	1175					1180					1185			
Gly	Phe	Glu	Lys	Leu	Thr	Pro	Phe	Thr	Pro	Glu	Glu	Glu	Ser	Arg
	1190					1195					1200			
Arg	Ile	Leu	His	Thr	Val	Phe	Cys	Thr	Leu	Glu	Ala	Ala	Pro	His
	1205					1210					1215			
Gln	Ser													
	1220													