(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
10 September 2021 (10.09.2021)

WIPO | PCT

(10) International Publication Number
WO 2021/176234 A1

(51) International Patent Classification:
A61K 39/12 (2006.01) *A61K 39/00* (2006.01)
A61P 31/20 (2006.01)

(21) International Application Number:
PCT/GB2021/050560

(22) International Filing Date:
05 March 2021 (05.03.2021)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

2003292.6	06 March 2020 (06.03.2020)	GB
2003289.2	06 March 2020 (06.03.2020)	GB
2005880.6	22 April 2020 (22.04.2020)	GB
2005878.0	22 April 2020 (22.04.2020)	GB
2013541.4	28 August 2020 (28.08.2020)	GB

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*

WO 2021/176234 A1

(54) Title: VACCINE AGAINST AFRICAN SWINE FEVER VIRUS INFECTION

(57) Abstract: The present invention relates to attenuated African Swine Fever viruses. The attenuated viruses protect pigs against subsequent challenge with virulent virus. The present invention also relates to the use of such attenuated viruses to treat and/or prevent African Swine Fever.

VACCINE AGAINST AFRICAN SWINE FEVER VIRUS INFECTION

FIELD OF THE INVENTION

The present invention relates to attenuated African Swine Fever viruses. The attenuated viruses protect pigs against subsequent challenge with virulent virus. The present invention also relates to the use of such attenuated viruses to treat and/or prevent African Swine Fever.

BACKGROUND TO THE INVENTION

African Swine Fever (ASF)

African swine fever is a devastating haemorrhagic disease of domestic pigs caused by a double-stranded DNA virus, African swine fever virus (ASFV). ASFV is the only member of the *Asfarviridae* family and replicates predominantly in the cytoplasm of cells. Virulent strains of ASFV can kill domestic pigs within about 5-14 days of infection with a mortality rate approaching 100%.

ASFV can infect and replicate in warthogs (Phacochoerus sp.), bushpigs (Potamocherus sp.) and soft ticks of the Ornithodoros species (which are thought to be a vector), but in these species few if any clinical signs are observed and long term persistent infections can be established. ASFV was first described after European settlers brought pigs into areas endemic with ASFV and, as such, is an example of an “emerging infection”. The disease is currently endemic in many sub-Saharan countries and in Europe in Sardinia. Following its introduction to Georgia in the Trans Caucasus region in 2007, ASFV has spread extensively through neighbouring countries including the Russian Federation. In 2012 the first outbreak was reported in Ukraine and in 2013 the first outbreaks in Belarus. In 2014 further outbreaks were reported in pigs in Ukraine and detection in wild boar in Lithuania and Poland.

There is currently no treatment for ASF. Prevention in countries outside Africa has been attempted on a national basis by restrictions on incoming pigs and pork products, compulsory boiling of waste animal products under licence before feeding to pigs and the application of a slaughter policy when the disease is diagnosed. Prevention in Africa is based on measures to keep warthogs and materials contaminated by warthogs away from the herd.

There is thus a need for improved measures to control ASFV infection and prevent spread of the disease.

African Swine Fever Virus (ASFV)

The complete genome sequences of ASFV isolate Benin 97/1 (a highly pathogenic virus from West Africa, Group1), isolate OURT88/3 (non-pathogenic, attenuated virus from Portugal, Group 1) and isolate BA71V (Vero cell tissue culture adapted non-pathogenic virus, Group 1) have been compared (Chapman et al. 2008 J. Gen. Virol. 89: 397-408).

In the OURT88/3 genome, the multigene family (MGF) 360 18R (DP148R) gene, EP153R gene and EP402R gene are each interrupted by frameshift mutations. Additionally, the following MGF genes are absent from the OURT88/3 genome: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L, MGF 300 3L, MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and MGF 505 1R, 2R and 6R. The MGF 505 3R gene is also truncated.

The sequences of the high-virulence Lisboa60 strain and the low-virulence NH/P68 strain have also been compared (Portugal et al. 2015 J. Gen. Virol. 96: 408-419).

In the NH/P68 genome, the MGF 360 18R (DP148R) gene, EP153R gene and EP402R gene are each interrupted by a premature stop codon. Additionally, the following MGF genes are absent from the NH/P68 genome: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L, MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and MGF 505 1R, 2R and 6R. The MGF 360 9L and MGF 505 3R genes are also truncated.

Deletion of the DP148R gene from the virulent Benin 97/1 isolate reduced virulence and induced protection against challenge with the parental virus (Reis et al. 2017 J. Virol. 91, 24: e01428-17).

SUMMARY OF THE INVENTION

Generally, the invention relates to an attenuated African Swine Fever virus in which expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted, whilst expression and/or activity of particular MGF genes is not disrupted.

The invention provides an attenuated African Swine Fever (ASF) virus in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted; and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

In a further aspect the invention provides an attenuated African Swine Fever (ASF) virus in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 11L and 12L,
MGF 360 6L, 10L, 11L, 12L, 13L, and 14L, and
MGF 505 1R and 2R.

In a further aspect the invention provides an attenuated African Swine Fever (ASF) virus in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 5L, 6L, 8L and 12L,
MGF 360 6L, 10L, 11L, 12L, 13L, 14L and 21R, and
MGF 505 1R and 2R.

The invention also provides a vaccine comprising an attenuated ASF virus of the invention.

The invention further provides a vaccine of the invention for use in treating and/or preventing ASF in a subject.

The invention further provides a method for treating and/or preventing ASF in a subject which comprises the step of administering to the subject an effective amount of a vaccine according to the invention.

The invention yet further provides a method of attenuating an ASF virus which comprises the step of disrupting the expression and/or activity of the following genes: DP148R, EP153R and EP402R.

DESCRIPTION OF THE FIGURES

Figure 1 shows confocal microscopy images of non-permeabilised cells expressing wild-type (**A**) or mutant (**B**) CD2v stained with sera from pigs immunised with attenuated ASFV containing a wild-type CD2v gene to detect surface expression.

Figure 2 shows exemplary images from a HAD assay. Vero cells were infected with modified vaccinia virus Ankara expressing T7RNA polymerase and transfected with plasmids (pcDNA3) expressing wild-type or mutant CD2v full-length proteins with a C-terminal HA epitope tag. Pig red blood cells were added and cells observed for attachment of red blood cells to the surface. HAD of red blood cells is observed around three cells

transfected with a plasmid expressing wild-type Benin CD2v (**A**). Partial HAD is observed around one cell expressing CD2v with the Y102 residue mutated to D (**B**). No HAD is observed for cells expressing CD2v with residue E99 mutated to R (**C**).

Figure 3 depicts an alignment of the amino acid sequence of CD2v ligand-binding domain from different ASFV isolates of varying genotypes. E99 and equivalent residues in other isolates are highlighted in yellow.

Figure 4 shows exemplary images from a HAD assay. Vero cells were infected with modified vaccinia virus Ankara expressing T7RNA polymerase and transfected with plasmids (pcDNA3) expressing wild-type or mutant CD2v full-length proteins from Benin or Georgia strains with a C-terminal HA epitope tag. Pig red blood cells were added and cells observed for attachment of red blood cells to the surface. HAD of red blood cells is observed around four cells transfected with a plasmid expressing wild-type Benin CD2v (**A**) and around four cells transfected with a plasmid expressing wild-type Georgia CD2v (**B**). No HAD is observed for cells expressing Georgia CD2v with residue Q96 mutated to R (**C**) or for untransfected Vero cells (**D**).

Figure 5 shows WSL cells expressing CD2vE99R infected with BeninΔCD2v virus (**A**) or OURT88/3 virus (**B**), which has frame-shift interruptions in the EP153R and EP402R/CD2v genes. HAD is observed upon infected with BeninΔCD2v but not with OURT88/3.

Figure 6 shows porcine marrow cells infected with ASFV Benin 97/1 wild-type (**B** left panel) or ASFV Benin 97/1 ΔDP148RΔEP153R-CD2vE99R (**A**, **B** right panel).

Figure 7 shows levels of luciferase expression from an NF-κB dependent promoter in HEK293T cells transfected with an empty pcDNA3 vector (negative control) or a plasmid expressing DP148R. Cells were stimulated with IL-1β (**A**) or TNF-α (**B**) to induce NF-κB activation. Alternatively, NF-κB activation was induced by overexpression of the the two main kinases of the NF-κB pathway, IKKα (**C**) or IKKβ (**D**).

Figure 8 shows immunofluorescence images of HeLa cells transfected with HA-tagged DP148R and stained for HA tag (red) and NF-κB p65 sub-unit (green). Nuclei are shown in blue. Cells were unstimulated (top row) or stimulated with TNFα (middle row) or IL-1β (bottom row) to induce NF-κB activation and p65 translocation to the nucleus. Arrows point to cells expressing DP148R. In stimulated cells expressing DP148R, p65 doe snot translocate to the nucleus.

Figure 9 depicts the experimental protocol used to immunise, boost and challenge pigs with BeninΔDP148RΔEP153RΔCD2v (Group A) and BeninΔDP148RΔEP153R-CD2vE99R (Group B) viruses.

Figure 10 shows rectal temperatures of pigs in Group A (**A**) and B (**B**) and the control Group E (**C**) during immunisation and challenge.

Figure 11 shows clinical scores of pigs in Group A (**A**) and B (**B**) and the control Group E (**C**) during immunisation and challenge.

Figure 12 shows viremia of pigs in Group A (**A**) and B (**B**) during immunisation and challenge.

Figure 13 shows the antibody response of pigs in Group A (**A**) and B (**B**) during immunisation and challenge measured using a commercially available competitive ELISA based on the VP72 (B646L) major capsid protein.

Figure 14 shows the cell-mediated immune response in Group A (**A**) and B (**B**) during immunisation and challenge. Peripheral blood mononuclear cells were collected pre-immunization, boost and challenge from pigs in Groups A and B and stimulated with ASFV Benin virus. Numbers of IFN gamma producing cells were measured by Elispot assay.

Figure 15 shows the number of ASFV specific lesions found in pigs from Groups E, A and B at post-mortem.

Figure 16 directly compares virus genome in blood after immunisation with BeninΔDP148R (**A**), BeninΔDP148RΔCD2v (**B**), BeninΔDP148RΔEP153RΔCD2v (**C**) and BeninΔDP148RΔEP153R-CD2vE99R (**D**).

DETAILED DESCRIPTION

African Swine Fever Virus (ASFV)

African swine fever virus (ASFV) is the causative agent of African swine fever (ASF). The genome structure of ASFV is known in the art, as detailed in Chapman et al. 2008 J. Gen. Virol. 89: 397-408. ASFV is a large, icosahedral, double-stranded DNA virus with a linear genome containing at least 150 genes. The number of genes differs slightly between different isolates of the virus. ASFV has similarities to the other large DNA viruses, e.g., poxvirus, iridovirus and mimivirus. In common with other viral haemorrhagic fevers, the main target cells for replication are those of monocyte, macrophage lineage.

Based on sequence variation in the C-terminal region of the B646L gene encoding the major capsid protein p72, 22 ASFV genotypes (I-XXII) have been identified. All ASFV p72 genotypes have been circulating in eastern and southern Africa. Genotype I has been circulating in Europe, South America, the Caribbean and western Africa. Genotype VIII is confined to four East African countries.

Examples of strains from some of the genotypes are given below:

Genotype I : OURT88/3; Brazil/79; Lisbon/60; BA715; Pret; Benin 97/1; IC/1/96; IC/576; CAM/82; Madrid/62; Malta/78; ZAR85; Katange63; Togo; Dakar59; Ourt88/1; BEN/1/97; Dom_Rep; VAL/76; IC/2/96; Awoshie/99; NIG/1/99; NIG/1/98; ANG/70; BEL/85; SPEC120; Lisbon/57; ASFV-Warm; GHA/1/00; GAM/1/00; Ghana; HOL/86; NAM/1/80; NUR/90/1; CAM/4/85; ASFV-Teng; Tegani; ASFV-E75.

Genotype II: Georgia 2007/1; POL/2015/Podlaskie (Polish strain); Belgium/Etalle/wb/2018; ASFV/Kyiv/2016/131; China/2018/AnhuiXCGQ

Genotype III: BOT 1/99

Genotype IV: ASFV-War; RSA/1/99/W

Genotype VI: MOZ 94/1

Genotype VII: VICT/90/1; ASFV-Mku; RSA/1/98

Genotype VIII: NDA/1/90; KAL88/1; ZAM/2/84; JON89/13; KAV89/1; DEZda; AFSV-Mal; Malawi LIL 20/1

Genotype IX: UGA/1/95

Genotype X: BUR/1/84; BUR/2/84; BUR/90/1; UGA/3/95; TAN/Kwh12; HindeII; ASFV-Ken; Virulent Uganda 65.

ASFV isolates

The attenuated ASF virus of the present invention may be derivable from a wild-type ASF virus isolate, but includes mutations in its genome such that the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted.

The term “wild-type” indicates that the virus existed (at some point) in the field, and was isolated from a natural host, such as a domestic pig, tick or warthog. ASFV isolates described to date are summarised in Table 1 below, together with their Genbank Accession numbers.

Table 1

Isolate	Country	Host	Year	Virulence	GenBank accession no.
BA71qqV	Spain	Pig	1971	Tissue culture adapted	U18466
Benin 97/1	Spain	Pig	1997	High	AM712239
Georgia 2007/1	Georgia	Pig	2007	High	FR682468
Kenya	Kenya	Pig	1950	High	AY261360
Malawi Lil20/1	Malawi	Tick	1983	High	AY261361
Mkuzi	Zululand	Tick	1978	Unknown	AY261362
OURT88/3	Portugal	Tick	1988	Low	AM712240
Pretorisuskop/96/4	South Africa	Tick	1996	High	AY261363
Tangani 62	Malawi	Pig	1962	High	AY261364
Warmbaths	South Africa	Tick	1987	Unknown	AY261365
Warthog	Namibia	Warthog	1980	Unknown	AY261366
Pol16_20186_07	Poland	Pig	2018	High	MG939583
Pig/HLJ/2018	China	Pig	2018	Virulent	MK333180
DB/LN/2018	China	Dried blood pig feed	2018	Unknown	MK333181
Belgium 2018/1	Belgium	Wild boar	2018	Virulent	LR536725
China /2018/AnhuiXCGQ	China	Pig	2018	Virulent	MK128995
Ken05/TK1, Ken06 Bus	Kenya		2005/06	Unknown	NC_044945 KM111295
R35, R25, R7, R8, N10	Uganda		2018	Unknown	MH025920, MH025918, MH025917, MH025916, MH025919
Pol_17_03029_C201	Poland	Pig	2017	Unknown	MG939587
26544/OG10	Sardinia/Italy	Pig	2017	Unknown	KM102979
47/Ss?2008	Sardinia/Italy	Pig	2008	Unknown	KX354450
Belgium/Etalle/wb/2018	Belgium	Wild boar	2018	Virulent	MK543947
ASFV/Kyiv/2016/131	Ukraine	Pig	2016	Unknown	MN194591
ASFV-SY18	China	Pig	2018	Unknown	MH766894
ASFV_HU_2018	Hungary	Wild boar	2019	Unknown	MN715134
ASFV-wbBS01	China	Wild boar	2019	Unknown	MK645909
ASFV Georgia 2007/1 (new version)	Georgia	Pig	2007	Virulent	LR743116
ASFV/pig/China/CAS19-01/2019	China	Pig	2019	Unknown	MN172368
ASFV/LT14/1490	Latvia	Wild boar	2019	Unknown	MK628478
Odintsovo_02/14	Russia	Pig	2014		NC_044948
ASFV CzechRepublic 2017/1	Czech Republic	Wild boar	2017	Unknown	LR722600
ASFV Moldova 2017/1	Moldova	Pig	2019	Unknown	LR722599
RSA_2_2008	South Africa	Pig	2008	Unknown	MN336500
LIV_5_40	Zambia	Tick		Unknown	MN318203
ASFV/POL/2015/Podlaskie	Poland	Wild boar	2015	Virulent	MH681419

The genome of the attenuated ASFV of the invention may correspond to any ASFV genotype. The genome of the attenuated ASFV of the invention may essentially correspond to any ASFV genotype.

The term "corresponds to" means that the remainder of the genome of the attenuated ASFV of the invention is the same as a wild-type strain (i.e. a virus that existed at some point in the field). "The remainder of the genome" refers to all genes other than the disrupted genes DP148R, EP153R and EP402R. In other words, the genes of the attenuated ASFV of the invention may be the same as the genes of the wild-type strain, except for the genes DP148R, EP153R and EP402R. In an embodiment the genes of the attenuated ASFV of the invention are the same as the genes of the wild-type strain, except for DP148R, EP153R and EP402R.

The disrupted genes DP148R, EP153R and EP402R may also correspond to the wild-type strain. In an embodiment the genes DP148R, EP153R and EP402R correspond to the wild-type strain. In such an embodiment (i.e. where DP148R, EP153R and EP402R correspond to the wild-type strain) expression and/or activity of DP148R, EP153R and EP402R may be disrupted by one or more mutation in an intergenic region such as a promoter. In other words, the DP148R, EP153R and EP402R genes are the same as in the wild-type genome but their expression or activity is altered by mutation of a non-genic sequence. Thus all of the genes of the attenuated ASFV of the invention may be the same as the genes of the wild-type strain. In an embodiment all genes of the attenuated ASFV of the invention are the same as the genes of the wild-type strain.

The term "essentially corresponds to" means the same as "corresponds to" with the additional exception that the remainder of the genome may comprise one or more mutations. The one or more mutations may be in other genes (i.e. not in the genes DP148R, EP153R and EP402R).

The genome of the attenuated ASFV may correspond or essentially correspond to genotype I. The genome of the attenuated ASFV may correspond or essentially correspond to genotype II. The genome of the attenuated ASFV may correspond or essentially correspond to genotype III. The genome of the attenuated ASFV may correspond or essentially correspond to genotype IV. The genome of the attenuated ASFV may correspond or essentially correspond to genotype V. The genome of the attenuated ASFV may correspond or essentially correspond to genotype VI. The genome of the attenuated ASFV may correspond or essentially correspond to genotype VII. The genome of the attenuated ASFV

may correspond or essentially correspond to genotype VIII. The genome of the attenuated ASFV may correspond or essentially correspond to genotype IX. The genome of the attenuated ASFV may correspond or essentially correspond to genotype X.

The genome of the attenuated ASFV may correspond or essentially correspond to genotype I. The genome of the attenuated ASFV may correspond or essentially correspond to genotype II.

Preferably, the genome of the attenuated ASFV may correspond or essentially correspond to genotype I.

The genome of the attenuated ASFV of the invention may correspond or essentially correspond to that of a virulent ASFV strain. Known virulent ASF virus strains include: Georgia 2007/1, Benin 97/1, Kenyan, Malawi Lil20/1, Pretorisuskop/96/4 and Tengani 62. The genome of the attenuated ASFV may correspond or essentially correspond to that of the Benin 97/1 strain. The genome of the attenuated ASFV may correspond or essentially correspond to that of the Georgia 2007/1 strain.

The genome of the attenuated ASFV may correspond or essentially correspond to that of the Benin 97/1 strain.

The genome of the attenuated ASFV of the invention may correspond or essentially correspond to that of an ASFV strain whose virulence is currently unknown, for example: Mkuzi, Warmbaths and Warthog.

In an embodiment the genome of the attenuated ASFV of the invention does not correspond to that of OURT88/3. In an embodiment the genome of the attenuated ASFV of the invention does not correspond to that of NH/P68. In an embodiment the attenuated ASFV of the invention is not OURT88/3. In an embodiment the attenuated ASFV of the invention is not NH/P68. In an embodiment the attenuated ASFV of the invention is neither OURT88/3 nor NH/P68.

The complete genome for the African swine fever virus Benin 97/1 pathogenic isolate is given in Genbank Locus: AM712239.1. The complete BA71 isolate genome encodes 151 open reading frames (ORFs), the Benin 97/1 isolate encodes 157 ORFs and the OURT88/3 isolate encodes 151 ORFs.

Multigene families (MGFs)

ASFV contains five multi-gene families which are present in the left and right variable regions of the genome. The MGFs are named after the average number of codons present

in each gene: MGF100, 110, 300, 360 and 505/530. The N-terminal regions of members of MGFs 300, 360 and 505/530 share significant similarity with each other. It has been shown the MGF 360 and 505 families encode genes essential for host range function that involves promotion of infected-cell survival and suppression of type I interferon response.

The attenuated ASFV according to the present invention comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

In a further aspect the invention provides an attenuated African Swine Fever (ASF) virus in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 11L and 12L,
MGF 360 6L, 10L, 11L, 12L, 13L, and 14L, and
MGF 505 1R and 2R.

Suitably, in one embodiment the invention provides an ASFV in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 5L, 6L, 8L, and 12L, and
MGF 360 6L, 10L, 11L, 12L, 13L, 14L and 21R, and
MGF 505 1R and 2R.

Suitably, in one embodiment the invention provides an ASFV in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 6L, 8L, and 12L, and
MGF 360 6L, 10L, 11L, 12L, 13L, 14L and 21R, and
MGF 505 1R and 2R.

Suitably, in one embodiment the invention provides an ASFV in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 12L, and
MGF 360 6L, 10L, 11L, 12L, 13L, 14L, and
MGF 505 1R and 2R.

Suitably, in one embodiment the invention provides an ASFV in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:
multigene family (MGF) 360 6L, 10L, 11L, 12L, 13L, and 14L, and
MGF 505 1R and 2R.

The location of some of these genes in the genomes of a variety of ASFV strains is provided below in Table 2. The sequence identity of each gene to the corresponding Benin 97/1 gene is also provided.

Table 2a – MGF 360-10L

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	20677	19607	100
Georgia 2007/1	26438	25368	93
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	30628	29563	82
Malawi-Lil/20	24802	23763	91
Mkuzi 1979	28139	27069	99
Pretorisuskop/96/4	27186	26116	96
Tengani 62	21600	20530	92
Warmbaths	26361	25322	94
Warthog	23130	22091	95
E75	19981	18911	100

Table 2b – MGF 360-11L

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	21764	20703	100
Georgia 2007/1	27526	26465	97
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	31716	30655	84
Malawi-Lil/20	25892	24831	86
Mkuzi 1979	29225	28164	99
Pretorisuskop/96/4	28275	27214	97
Tengani 62	22688	21627	97
Warmbaths	27449	26388	97
Warthog	24218	23157	97
E75	21068	20007	100

Table 2c – MGF 360-12L

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	24668	23616	100
Georgia 2007/1	30434	29382	96
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	34566	33549	90
Malawi-Lil/20	28731	27682	92
Mkuzi 1979	32125	31073	97
Pretorisuskop/96/4	31150	30098	95
Tengani 62	25592	24540	96
Warmbaths	30346	29294	96
Warthog	27088	26036	96
E75	23971	22920	99

Table 2d – MGF 360-13L

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	25901	24840	100
Georgia 2007/1	31656	30595	97
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	35812	34757	90
Malawi-Lil/20	29980	28925	91
Mkuzi 1979	33347	32286	99
Pretorisuskop/96/4	32368	31307	95
Tengani 62	26814	25753	95
Warmbaths	31559	30498	95
Warthog	28338	27277	95
E75	25204	24143	99

Table 2e – MGF 360-14L

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	27146	26073	100
Georgia 2007/1	32913	31840	99
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	37194	36121	92
Malawi-Lil/20	31266	30193	92
Mkuzi 1979	34620	33547	99
Pretorisuskop/96/4	33598	32525	97
Tengani 62	28056	26983	97
Warmbaths	32820	31747	96

Warthog	29568	28495	97
E75	26449	25376	100

Table 2f – MGF 505-1R

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	21971	23566	100
Georgia 2007/1	27734	29329	95
BA71V	Deleted		
OURT88/3	Deleted		
Kenya 1950	31904	33496	91
Malawi-Lil/20	26041	27627	93
Mkuzi 1979	29425	31020	96
Pretorisuskop/96/4	28449	30044	94
Tengani 62	22891	24486	95
Warmbaths	27651	29246	95
Warthog	24387	25982	95
E75	21275	22870	100

Table 2g – MGF 505-2R

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	27352	28932	100
Georgia 2007/1	33119	34699	99
BA71V	17725	19304	99
OURT88/3	29532	29981	76
Kenya 1950	37419	38985	90
Malawi-Lil/20	31541	33121	93
Mkuzi 1979	34826	36406	99
Pretorisuskop/96/4	33795	35374	97
Tengani 62	28261	29830	98
Warmbaths	33029	34597	96
Warthog	29773	31352	97
E75	26655	28236	99

5

Table 2h – MGF 505-3R

Strain	Start Nucleotide Number	Stop Nucleotide number	% Nucleotide Identity
Benin 97/1	29019	29861	100
Georgia 2007/1	34786	35625	96
BA71V	20398	21915	100
OURT88/3	20850	22367	100
Kenya 1950	40295	41815	89
Malawi-Lil/20	34322	35842	89
Mkuzi 1979	37500	39017	99

Pretorisuskop/96/4	36480	37985	89
Tengani 62	30926	32443	90
Warmbaths	35712	37232	93
Warthog	32449	33954	90
E75	29330	30847	100

The gene (i.e. nucleotide) sequences of these genes from different strains are given below.

MGF 110 5L gene sequences

SEQ ID No. 266 – China/2018/AnhuiXCGQ (genotype II) 9145-8528 MGF 110 5L/6L fusion

ATGTTGGTGATCTTCTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGAGCCTCCAGAGGAAGAACTCGAATACTGGTGTGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGACGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAGGGTATCTACCATACCATGAATTGCAACCAGGTCTTAGGGCTACCTAATCAACCAGCTGGACAACT
TCATCCAACGGATAATCCTCCACAAGAAGAACTTGAATACTGGTGCACTTATACAGAAAACTGCAAGTTTTGCTGGAATTGTC
AAAATGGCCTTTGTGAGGGCAAATTGGAGAATACAACAATTCTTGAAAATGAGTATGTGCAATCATGTATAGTTTCCCGCTGG
CTAAATAAATGTATGTATGATCTAGGACAGGGGATTCACCATGTAATGGCCTGTTCTGAACCAAAGCCCTGGAATCCTTACAA
AATCTTAAAGAGAGAGTGGAAAGAAAATAATAGTTAA

SEQ ID No. 267 – Georgia 2007/1 (genotype II) 9140-8523 MGF 110 5L/6L fusion

ATGTTGGTGATCTTCTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGAGCCTCCAGAGGAAGAACTCGAATACTGGTGTGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGACGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAGGGTATCTACCATACCATGAATTGCAACCAGGTCTTAGGGCTACCTAATCAACCAGCTGGACAACT
TCATCCAACGGATAATCCTCCACAAGAAGAACTTGAATACTGGTGCACTTATACAGAAAACTGCAAGTTTTGCTGGAATTGTC
AAAATGGCCTTTGTGAGGGCAAATTGGAGAATACAACAATTCTTGAAAATGAGTATGTGCAATCATGTATAGTTTCCCGCTGG
CTAAATAAATGTATGTATGATCTAGGACAGGGGATTCACCATGTAATGGCCTGTTCTGAACCAAAGCCCTGGAATCCTTACAA
AATCTTAAAGAGAGAGTGGAAAGAAAATAATAGTTAA

SEQ ID No. 268 – Ken05/Tk1 9698-9327 MGF 110 5L

ATGTTGGTGATCTTCTTGGGACTCCTTGGCCTGCTGGCCAACCAGGTCTTAGGGCTACCTAATCAACCAGCTGGACAACTTCA
TCCAACGGATAATCCTCCAAAAGAAGAACTTGGATACTGGTGCACTTACACGGAAAGCTGTAAATTTTGCTGGAACTGTCAAA
ATGGCCTTTGTGAGGGCAAATTGGAGAATACAACAATTCTTGAAAATGAGTATGTGCAATCATGTATAGTTTCCCGCTGGCTA
AATAAATGTATGTATGATCTAGGACAGGGGATTGACCATGTAATGGCCTGTTCTGAACCAAAGCCCTGGAATCCTTACAAAAT
CTTAAAGAGAGAGTGGAAAAAAAATGTCAGCCAAAATTAA

SEQ ID No. 269 – Ken06.Bus 6224-5853 MGF 110 5L

ATGTTGGTGATCTTCTTGGGACTCCTTGGCCTGCTGGCCAACCAGGTCTTAGGGCTACCTAATCAACCAGCTGGACAACTTCA
TCCAACGGATAATCCTCCAAAAGAAGAACTTGGATACTGGTGCACTTACACGGAAAGCTGTAAATTTTGCTGGAACTGTCAAA
ATGGCCTTTGTGAGGGCAAATTGGAGAATACAACAATTCTTGAAAATGAGTATGTGCAATCATGTATAGTTTCCCGCTGGCTA
AATAAATGTATGTATGATCTAGGACAGGGGATTCACCATGTAATGCCCTGTTCTGAACCAAAGCCCTGGAATCCTTACAAAAT
CTTAAAGAAAGAGTGGAAAGAAAATGTCAGCCAAAATTAA

SEQ ID No. 270 – Malawi Lil-20/1/1983 7878-7516 MGF 110 5L

ATGTTGGTTATCTTCTTGGGAATTCTTGGCCTTCTGGCCAACCAGGTCTCAAGCCAGCTCGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAGATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGT
ATGTATGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAACCAAAGTACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAACAGCCAAAATTAA

SEQ ID No. 271 – Mkuzi 1979 (genotype XII) 10334-9972 MGF 110 5L

ATGTTAGTAATCTTCTTGGGAATTCTTGGCCTTCTGGCCAACCAGGTCTCAAGCCAGCTCGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAGATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGC
ATGTATGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAACCAAAGTACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAACAGTCAAAATTAA

SEQ ID No. 272 – Pretorisuskop/96/4 (genotype XX/I) 9424-9059 MGF 110 5L

ATGTTAGTAATCTTCTTGGGAATTCTTGGCCTTCTGGCCAACCAGGTCTCAAGCCAGCTCGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAAATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGT
ATGTATGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAGCCAAAATACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAACAGCCAAAATAAATAA

SEQ ID No. 273 – Tengani62 (genotype V/I) 8803-8447 MGF 110 5L

ATGTTAGTCATCTTCTTGGGAATTCTTGGCCTTCTGGTCAACCAGGTCTCAAGCCAGCCAGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAAATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGT
ATGTATGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAACCAAAATACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAATAGTTAA

SEQ ID No. 274 – Warmbaths (genotype III/I) 8649-8284 MGF 110 5L

ATGTTAGTAATCTTTTTGGGAATTCTTGGCCTTCTGGCCAACCAGGTCTCAAGCCAGCTCGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAAATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGT
ATGTACGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAACCAAAATACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAACAGCCAAAATAAATAA

SEQ ID No. 275 – Warthog (genotype IV) 7349-6984 MGF 110 5L

ATGTTAGTAATCTTCTTGGGAATTCTTGGCCTTCTGGCCAACCAGGTCTCAAGCCAGCTCGTTGGACAACTTCATCCAACGGA
AAATCCTTCAGAGAATGAACTTGAATACTGGTGCACTTACATGGAATGTTGCCAGTTTTGCTGGGACTGTCAAAATGGCCTTT
GTGTGAATAAGTTGGGAAATACAACAATTCTTGAAAATGAGTATGTGCATCCATGTATAGTTTCCCGCTGGCTAAATAAATGT
ATGTACGATCTGGGTCAAGGCATTGATCATGTAATGGTCTGTTCTCAACCAAAATACTGGAATCCTTATAAAATCTTAAAGAA
AGAGTGGAAAGAAAATAACAGCCAAAATAAATAA

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 110 5L. Suitably the functional version of MGF 110 5L comprises the sequence of SEQ ID No. 266, 267, 268, 269, 270, 271, 272, 273, 274 or 275. Suitably the functional version of MGF 110 5L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 266, 267, 268, 269, 270, 271, 272, 273, 274 or 275. Suitably the functional version of MGF 110 5L consists of the sequence of SEQ ID No. 266, 267, 268, 269, 270, 271, 272, 273, 274 or 275.

MGF 110 6L gene sequences

SEQ ID No. 35 – Ken05/Tk1 MGF 110 6L

ATGTTGGTAATCTTTTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTCTCAAGTCAACCAGATGGACAACTTCGTCCAACAGA
GGATCCTCCAGAAGAAGAACTTAAATATTGGTGCACCTACATGGAAAGTTGCCAGTTTTGTTGGGACTGCCAAGATGGCAATT
GTATAAACAAAGTAGATGGGTCAGTCATTTATAAAAATGAGTTTGTGCGACCATGTTCAGTTTCCCGCTGGATGAATAAATGT
ATGTATGATTTAAATAAGGGTATCTATCATACAATGAATTGTTCTCAGCCACAGTCTTGGAATCCCTACAAATACTTCAGGAA
GGAGTGGAAAAAAGATGAACTCTAG

SEQ ID No. 36 – Ken06.Bus MGF 110 6L

ATGTTGGTGATCTTTTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTCTCAAGTCAGCCAGTTGGACAACTTCGTCCAACAGA
GGACCCTCCAGAGAATGAACTCGAATATTGGTGCACCTACATGGAAAGTTGCCAGTTTTGCTGGGACTGTCAAGATGGCAATT
GTATAAACAAAGTAGATGGGTCAGTCATTTATAAAAATGAGTATGTGCAACCATGTTCAGTTTCCCGCTGGCTAAATAAATGT
ATGTATGATTTAGATAAGGGTATCTATCATACAATGAACTGTTCTCAGCCACGGTCTTGGAATCCCTACAAATGTTTCAGGAA
GGAGTGGAAAAAAGATGAACTCTAG

SEQ ID No. 37 – Kenya 1950 MGF 110 6L

ATGTTGGTGATCTTTTTGGGAATTCTTGGCCTTATGGCCAGCCAGGTCTTAGGGCTACCATCTAATCAACCAACTGGACAACT
TCGTCCAACAGAGGATCCTCCAGAGGAAGAACTCGAATACTGGTGTGCCTACATGGAAAGTTGCCAGTTTTGCTGGGACTGCC
AAGATGGCAATTGCATAAACAAAATAGATGGGTCAGTCATTTATAAAAATGAGTTTGTGCGACCATGTTCAGTTTCCCGCTGG
ATGGATAAATGTATGTATGATTTAAATAAGGGTATCTATCATACAATGAATTGTTCTCAGCCACAGTCTTGGAATCCCTACAA
ATACTTCAGGAAGGAGTGGAAAAAAGATGAACTCTAG

SEQ ID No. 38 – Malawi Lil-20/1 (1983) MGF 110 6L

ATGTTGGTGACCTTTTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTCTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGCGCCTACATGGAAAGTTGCCAGTTTTGCTGGGACTGCCAAGATGGCAATT
GTATAAACAAAATAGATGGGTCAGTCATTTATAAAAATGAGTATGTGCGACCATGTTCAGTTTCCCGTTCGATGGATAAATGT
ATGTATGATTTAAATAAGGGTATCTACCATAGCATGAGCTGTTCTGACCCAAAGGCCTGGAATCCCTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

SEQ ID No. 39 – Mkuzi 1979 MGF 110 6L

ATGTTGGTGATCTTTTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAACTCGTTGGACAACTTCGACCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGCGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGATGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAAGCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAAGGTATCTACCATACCATGAATTGTTCTCAGCCATGGTCTTGGAATCCTTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

SEQ ID No. 40 – Pretorisuskop/96/4 MGF 110 6L

ATGTTGGTGATCTTCTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGCGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGATGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAAGGTATCTACCATACCATGAATTGTTCTCAGCCATGGTCTTGGAATCCTTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

SEQ ID No. 41 – Tengani62 MGF 110 6L

ATGTTGGTGATCTTCTTGGGAATTTTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGTGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGATGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAGGGTATCTACCATACCATGAATTGTTCTCAGCCATGGTCTTGGAATCCTTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

SEQ ID No. 42 – Warmbaths MGF 110 6L

ATGTTGGTGATCTTCTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGTCCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGCGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGATGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT
ATGTATGATTTAGATAAAGGTATCTACCATACCATGAATTGTTCTCAGCCATGGTCTTGGAATCCTTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

SEQ ID No. 43 – Warthog MGF 110 6L

ATGTTGGTGATCTTCTTGGGAATTCTTGGCCTTCTGGCCAGCCAGGTTTCAAGTCAGCTCGTTGGACAACTTCGACCAACAGA
GGATCCTCCAGAGGAAGAACTCGAATACTGGTGCGCCTACATGGAAAGTTGCCAATTTTGCTGGGACTGCCAAGATGGCACTT
GTATAAACAAAATAGATGGGTCAGTAATTTACAAGAATGAGTATGTGAAATCATGTCTGGTTTCCCGTTGGCTGGATAAATGT

ATGTATGATTTAGATAAAGGTATCTACCATACCATGAATTGTTCTCAGCCATGGTCTTGGAATCCTTACAAATACTTCAGGAA
GGAATGGAAAAAAGATGAACTCTAG

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 110 6L. Suitably the functional version of MGF 110 6L comprises the sequence of SEQ ID No. 35, 36, 37, 38, 39, 40, 41, 42 or 43. Suitably the functional version of MGF 110 6L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 35, 36, 37, 38, 39, 40, 41, 42 or 43. Suitably the functional version of MGF 110 6L consists of the sequence of SEQ ID No. 35, 36, 37, 38, 39, 40, 41, 42 or 43.

MGF 110 7L gene sequences

SEQ ID No. 247 – China/2018/AnhuiXCGQ MGF 110 7L

ATGCTGGTGATTATCCTGGGAATTATTGGCCTGCTGGCCAGTAGCAACCTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGAACCCCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACCAGCAGGGTTTGGGGAAACAACTCCACAAGTATTATTGAGAATGACTATGTAAAATATTGT
GAGGTTTCCCGCTGGGGTGACCTATGTAGATATGATGTGGAGGAGCACATTTACCATAGCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATCCCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 248 – Georgia 2007/1 MGF 110 7L

ATGCTGGTGATTATCCTGGGAATTATTGGCCTGCTGGCCAGTAGCAACCTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGAACCCCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACCAGCAGGGTTTGGGGAAACAACTCCACAAGTATTATTGAGAATGACTATGTAAAATATTGT
GAGGTTTCCCGCTGGGGTGACCTATGTAGATATGATGTGGAGGAGCACATTTACCATAGCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATCCCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 249 – Ken05/Tk1 MGF 110 7L

ATGCTGGTGATTATCCTGGGAGTTATTGGCCTGCTGGCCAGTAGCAACTTGGTTTCATCCTCCACTTCTACTCGGATAGGTGG
ACATCTTCCTCTAACATTTGATCCTCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGGTCTGTACTAGCAGGATCTGGGGGAACAACTCCACAAGTATTGTTGAGAACAGCTATGTAAAATATTGT
GAAGTTTCCCGCTGGGGTGACCAGTGTAGATATGATGTGGAGGAGCGCATTTACCATACCATGAACTGTTCTGACCCAAAACC
CTGGAATCCTTATAAAATTACAAGGGTGGAGTGGAAAAAGAATGAACATTTCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 250 – Kenya 1950 MGF 110 7L

ATGCTGGTGATTATCCTGGGAGTTATTGGCCTGCTGGCCAGTAGCAACTTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGATCCTCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGGTCTGTACTAGCAGGATCTGGGGGAACAACTCCACAAGTATTGTTGAGAACAGCTATATAAAATATTGT
GAAGTTTCCCGCTGGGGTGACCAGTGTAGATATGATGTGGAGGAGCACATTTACTATACCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATTTCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 251 – Malawi Lil-20/1 (1983) MGF 110 7L

ATGCTGGTGATTATCCTGGGAGTTATTGGCCTGCTGGCCAGTAGCAACTTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGATCCTCCAGAGAATGAACTTGGATACTGGTACACTTATGTGGAAAGTTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGGTCTGTACTAGCAGGGTTTGGGGAAACAACTCCACAAGTATTGTTGAGAATGACTATGTAAAATATTGT
GAGGTTTCTCGCTGGGGTGACCAATGTAGATATGATGTGGAGGAGCACATTTACTATACCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAAGGAAGGAGTGGAAAAAGGATGA

SEQ ID No. 252 – Mkuzi 1979 MGF 110 7L

ATGCTGGTGATTATCCTGGGAGTTATTGGCCTGCTGGCCAGTAGCAACTTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACAGAGGATCCTCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACTAGCAGGGTTTGGGGAAACAACTCCACAAGTATTGTTGAGAACGACTATGTAAAATATTGT

GAGGTTTCTCGCTGGGGTGACCAATGTAGATATGATGTAGAGGAGCACATTTACTATACCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGGATGAACATTCCAGAAAGAATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 253 – Pretorisuskop/96/4 MGF 110 7L

ATGCTGGTGATTATCCTGGGAATTATTGGCCTGCTGGCCAGTAGCAACCTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGATCCCCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACCAGCAGGGTTTGGGGAAACAACTCCACAAGTATTGTTGAGAATGACTATGTAAAATATTGT
GAGGTTTCCCGCTGGGGAAACCTATGTAGATATGATGTGGAGGAGCACATTTACTATAGCATGAACTGTTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAATATCTCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 254 – Tengani 62 MGF 110 7L

ATGAACTGTTCTGACCCAAAGCCCTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATCCCAGAAAGGA
TTTGAAAAAAGATGAATTCTAG

SEQ ID No. 255 – Warmbaths MGF 110 7L

ATGCTGGTGATTATCCTGGGAATTATTGGCCTGCTGGCCAGTAGCAACCTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGATCCCCCAGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACCAGCAGGGTTTGGGGAAACAACTCCACAAGTATTGTTGAGAATGACTATGTAAAATATTGT
GAGGTTTCCCGCTGGGGTAACCTATGTAGATATGATGTGGAGGAGCACATTTACCATAGCATGAACTGCTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATCCCAGAAAGGATTTGAAAAAAGATGAATTCTAG

SEQ ID No. 256 – Warthog MGF 110 7L

ATGCTGGTGATTATCCTGGGAATTATTGGCCTGCTGGCCAGTAGCAACCTGGTTTCATCCTCCACTTCTACTCGGGTAGGTGG
ACATCTTCCTCTAACATTTGATCCCCCCGAGAATGAACTTGGATACTGGTGCACTTATGTGGAAAGCTGTCGGTTCTGCTGGG
ATTGTGAAGATGGGATTTGTACCAGCAGGGTTTGGGGAAACAACTCCACAAGTATTGTTGAGAATGACTATGTAAAATATTGT
GAGGTTTCCCGCTGGGGTAACCTATGTAGATATGATGTGGAGGAGCACATTTACCATAGCATGAACTGCTCTGACCCAAAGCC
CTGGAATCCTTATAAAATTGCAAGGAAGGAGTGGAAAAAGAATGAACATCCCAGAAAGGATTTGAAAAAAGATGAATTCTAG

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 110 7L. Suitably the functional version of MGF 110 7L comprises the sequence of SEQ ID No. 247, 248, 249, 250, 251, 252, 253, 254, 255 or 256. Suitably the functional version of MGF 110 7L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 247, 248, 249, 250, 251, 252, 253, 254, 255 or 256. Suitably the functional version of MGF 110 7L consists of the sequence of SEQ ID No. 247, 248, 249, 250, 251, 252, 253, 254, 255 or 256.

MGF 110 8L gene sequences

SEQ ID No. 44 – Ken05/Tk1 MGF 110 8L

ATGAAGGTGCTGATTCTAGTACTACTGGGGGTCGTTATCCTTCAGGCTGCTCCTATACGTAAATTAGAAGACCTACTGCCAAC
CCGTAATCCTCCCCAAAATGAGCTAGTTTACTGGTGCACCTACGCAAACCAATGTGACTTTTGCTGGGAATGTGTACACGGAA
TCTGCCGAAACAGAATTCAAGCAGATTGGCCTGTGATTCACCAAAATGACTGGATTATAAATTGCACCGTTTCCCGCTGGAAT
GGTATATGTAGGTATTATGAAGGACCCAGAGTCCATATAGATCATGAAATGGACTGTGCAAATCCAACATCCCATACTTATCC
ACACATTGAATACATGAAGATCTATGAAAGAGATGACCTATGA

SEQ ID No. 45 – Kenya 1950 MGF 110 8L

ATGAAGGTGCTGATTCTAGTACTACTGGGGGTCGTTATCCTTCAGGCTGCTCCTATACGTAAATTAGAAGACCTACTGCCAAC
CCGTAATCCTCCCCAAAATGAGTTAGTTTATTGGTGCACCTACGCAAACCAATGTGATTTTTGCTGGGAATGTATACACGGAA
TCTGCCGAAACAGAATTCAAGCAGATTGGCCTGTGATTCACCAAAATGACTGGATTATAAATTGCACCGTTTCCCGCTGGAAT

GGTATATGTAGGTATTATGAAGGACCCAGAGGCCATATAGATCATGAAATGGACTGTGCAAATCCAACATACCATACTTATCC
ACACATTGAATACATGAAGATTTATGTAAGAGATGACCTATGA

SEQ ID No. 46 – Malawi Lil-20/1 (1983) MGF 110 8L

ATGAAGGTGCTGATTCTAGTACTGCTGGCGGTGGTTATCCTTCAAGCCGCTCCTATACGTAAATTAGAAGATCTACTACCAAC
CCGTTATCCTCCTGACCATGAGCTAGTTTATTGGTGCACCTACGCAAACCAATGTGACTTTTGCTGGGAATGCGTACACGGTA
TCTGCCGAAATAGGATTCAAGCAGATTGGCCGGTTATTCACCAAAATGACTGGATTATAAATTGCACGGTTTCCCGCTGGAAT
GGTATATGTAGTTATTATGAAGGACCCAGAAACCATACAGATCATCAAATGGACTGTGCAAATCCAACATCCCATACCTATCC
ACATAGAGAATACATGAAAATTTATGAAAGAGATGACTTATAA

SEQ ID No. 47 – Mkuzi 1979 MGF 110 8L

ATGAAGGTGCTGATTCTAGTACTACTGGGGGGGGGGGGTATTATTCTTCAGGCCGCTCCTATACGTAAATTAGAAGATCTACT
ACCAACCCGTTATCCTCCTGAACATGAGCTGGTTTATTGGTGCACCTACGCAAACCAATGTGACTTTTGCTGGGAATGCGTCC
ACGGTATTTGCCGAAACAGGATTCAAGCAGATTGGCCGGTTATTCATCAAAATGACTGGATTATAAATTGCACGGTTTCCCGC
TGGAATGGCCAATGTCATTATTATGAAGGTTCTCAACAATATCTACATCATGAAATGGACTGTACAAATCCAACATCCCATAC
CTATCCACATACAGAATACATGAAGATCTATGAAAGAGATGACTTATGA

SEQ ID No. 48 – Pretorisuskop/96/4 MGF 110 8L

ATGAAGGTGCTAATTCTAGTACTACTGGGGGTGGTTATCCTTCAGGCCGCTCCTATACGTAAATTAGAAGATCTACTACCAAC
CCGTTATCCTCCTGAACATGAGCTAGTTTATTGGTGCACTTACGCAAACCAATGTGACTTTTGCTGGGAATGCGTCCACGGTA
TCTGCCGAAACAGGATTCAAGCAGATTGGCCAGTTATTCATCAAAATGACTGGATTATAAATTGCACGGTTTCCCGCTGGAAT
GGTATATGTAGTTATTATGAAGGACCCAGAAACCATACAGATCATCAAATGGACTGTGCAAATCCAACATCCCATACTTATCC
ACATAGAGAATACATGAAGATCTATGAAAGAGATGACTTATGA

SEQ ID No. 49 – Warmbaths MGF 110 8L

ATGAAGGTGCTAATTCTAGTACTACTGGGGGTGGTTATTCTTCAGGCCGCTCCTATACGTAAATTAGAAGATCTACTACCAAC
CCGTTATCCTCCTGAACATGAGCTAGTTTATTGGTGCACTTACGCAAACCAATGTGACTTTTGCTGGGAATGCGTCCACGGTA
TCTGCCGAAACAGGATTCAAGCAGATTGGCCAGTTATTCACCAAAATGACTGGATTATAAATTGCACAGTTTCTCGCTGGAAT
GGTATATGTAGTTATTATGAAGGACCCAGAAACCATACAGATCATCAAATGGACTGTGCAAATCCAACATCCCATACTTATCC
ACATAGAGAATACATGAAGATCTATGAAAGAGATGACTTATGA

SEQ ID No. 50 – Warthog MGF 110 8L

ATGAAGGTGCTAATTCTAGTACTACTGGGGGTGGTTATTCTTCAGGCCGCTCCTATACGTAAAGTAGAAAATCTACTGCCAAC
CCGTAATCCTCCCCAAAATGAATTAGTTTATTGGTGCACCTATGCAAACCAATGTGACTTTTGCTGGGAATGCATTCACGGCA
TCTGCCGAAACAGGATTCAAGCAGATTGGCCAGTTATTCATCAAAATGACTGGATTATAAATTGCACGGTTTCCCGCTGGAAT
GGCCAATGTCATTATTATGAAGGTTCTCAACAATATCTGCATCATGAAATGGACTGTATAAATCCAACATCCCATACCTATCC
ACATACAGAATACATGAAGATCTATGAAAGAGATGACTTATGA

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 110 8L. Suitably the functional version of MGF 110 8L comprises the sequence of SEQ ID No. 44, 45, 46, 47, 48, 49 or 50. Suitably the functional version of MGF 110 8L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 44, 45, 46, 47, 48, 49 or 50. Suitably the functional version of MGF 110 8L consists of the sequence of SEQ ID No. 44, 45, 46, 47, 48, 49 or 50.

MGF 110 12L gene sequences

SEQ ID No. 276 – Benin 97/1 (genotype I) 7643-7332 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCAACAACCCAGTGGTGTTT
TTATGAAATATCACTTAAAATACTTAATCATCATAGCATGGAAAAATGGAGGGATAAGAATTGGTCAATCATTATAAGGTATT

ATTGTTTTTACCTTGTATTTAGCTTTGCATTTGCTGGTTGCGTTGCATTTGCGATCTGCAAAAATCTACGACTGTGTACAACC
ATGAAATTACTTATGCTTTTGAATATTTTGGTTTTGTTATCTCAGCCAATTTTGAATAATTGA

SEQ ID No. 277 – China/2018/AnhuiXCGQ (genotype II) 14155-13796 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTTATTCTTACCTATCAATCACCAACAACCCCGTGGTGTTT
TTATGAAATATCACTTAAAATACCTAATCATCATAGCATGAAATGTTGTTCGTATCCTAGACTTTATGAACATGAAATGTTCA
TGGAAAAATGGAGGGATAAGAATTGGCCAATCATTATAAGGTATTATTGTTTTTACCTTGTATTTAGCTTTGTATTTGCTGGT
TGCGTTGCATTTGCGATCTGCAAAAATCTACGACTGAGTACAACCATGAAATTACTTATGCTTTTGAGTATTTTGGTTTTGTT
GTTATCTCAGCCAATCTTGAATAATTGA

SEQ ID No. 278 – Georgia 2007/1 (genotype II) 14151-13792 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTTATTCTTACCTATCAATCACCAACAACCCCGTGGTGTTT
TTATGAAATATCACTTAAAATACCTAATCATCATAGCATGAAATGTTGTTCGTATCCTAGACTTTATGAACATGAAATGTTCA
TGGAAAAATGGAGGGATAAGAATTGGCCAATCATTATAAGGTATTATTGTTTTTACCTTGTATTTAGCTTTGTATTTGCTGGT
TGCGTTGCATTTGCGATCTGCAAAAATCTACGACTGAGTACAACCATGAAATTACTTATGCTTTTGAGTATTTTGGTTTTGTT
GTTATCTCAGCCAATCTTGAATAATTGA

SEQ ID No. 279 – Ken05/Tk1 (genotype IX) 15456-14950 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTTTTCAATCATCCTCATTCTTACATATCAATCACCGACAACTCAGCATCCTCC
TAAGGAAGAGCTTGCGTACTGGTGCACTTATGCAAAATCTTGTGACTTCTGCTGGGATTGCCAAAATGACACTTGTATAAATA
AGGTAATAAATGAGTCTATTTCGATAACTTCGATTGTAAACTGTAGAGTTACTCGCGATTCCCAATCCTGTTTTTATGAAATA
TCAGTTAAAATACCTAATCATCATAGCATGGAATGTTCATATCCTAGACTTTATGAACATGAAATGTTTATGGAAAAATGGAG
GGATGAGTATTGGCCAATCATTATAAAACAGTGTTGTTTTTACCTTGTATTTAGCATTGCATTTGCTGGATGCGTTGCATTTG
CGATCTGCAAAAATCTACGACTGCGTACAACTATAAAACTACTTATTCTTTTGAGTATTTTGGTTTGGTTGTCTCAACCAGTC
TTGAATTGA

SEQ ID No. 280 – Ken06.Bus (genotype X) 11961-11446 MGF 110 12L

ATGAAGGTTTTTCTGGCACTTTTACTAGGTTATTTAACTATCCTCATTCTTACATATCAAACACCAACAACCCAGCATCCTCC
TAAGGAGGAGCTTCCATATTGGTGTACGTATGTAAAGAATTGCGACCTCTGTTGGGATTGTCAAGATAGCATCTATTGGAACA
AGGTAATAAGTGAGTCTATTTCGATAAATTCGATTATAAACTGTAGAGTTACTTGCGATTCCCAATCTCAGTCCTGCTTTTAT
GAAATATTACTTAAAATACCTAATCATCATAGCATGGAATGTTCTTATCCTGGATCGTATGAAAATGAAATGTTCATGGAAAA
ATGGAGGGATGAGAATTGGTCAATCATTATAAAACATTATTGTTTTTACCTTGTATTTAGCTTTGCATTTGCTGGTTGCGTTG
CATTTGCGATCTGCAAAAATCTACGACTGAGTACAACTATGAAATTACTTATGCTTTTGAGTATTTTGGTTTGCTTATCTCAG
CCAATCTTGAATAATTGA

SEQ ID No. 281 – Kenya 1950 (genotype X) 16240-15731 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTTTTCAATCATCCTCATTCTTACATATCAATCACCGACAACCCAGCATCCTCC
TAAGGAAGAGCTTGCGTACTGGTGCACTTATGCAAAATCTTGTGACTTCTGCTGGGATTGCCAAAATGACACTTGTATAAATA
AGGTAATAAATGAGTCTATTTCGATAACTTCGATTGTAAACTGTAGAGTTACTCGCGATTCCCAGTCCTGTTTTTATGATATA
TCAGTTAAAATACCTAATCATCATAGCATGGAATGTTCATATCCTAGACTTTATGAACATGAAATGTTTATGGAAAAATGGAG
GGATGAGTATTGGCCAATCATTATAAAACAGTGTTGTTTTTACCTTGTATTTAGCTTTGCATTTGCTGGTTGCGTTGCATTTG
CGATCTGCAAAAACCTACGACTGCGTACAACTATAAAACTACTTATTCTTTTGAGTATTTTGGTTTGGTTATCTCAGCCAATC
TTGAATAATTGA

SEQ ID No. 282 – L60 (genotype I) 7993-7682 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCAACAACCCAGTGGTGTTT
TTATGAAATATCACTTAAAATACTTAATCATCATAGCATGGAAAAATGGAGGGATAAGAATTGGTCAATCATTATAAGGTATT
ATTGTTTTTACCTTGTATTTAGCTTTGCATTTGCTGGTTGCGTTGCATTTGCGATCTGCAAAAATCTACGACTGTGTACAACC
ATGAAATTACTTATGCTTTTGAATATTTTGGTTTTGTTATCTCAGCCAATTTTGAATAATTGA

SEQ ID No. 283 – Malawi Lil-20/1/1983 (genotype VIII) 12584-12069 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCAACAACCCAGCATCCTCC
TAAGGAAGAGCTTGAGTATTGGTGCACTTATGCAAAAACTTGTGACTTCTGCTGGGATTGCCAAAATGACACTTGTATAAATA
AGGTAATAAATGAATCTATTTCGATGAATTCGATTGTAAACTGTAGAGTTACTCGCGATTCCCAATCCCAGTCCTGTTTTTAT

GAAATATCACTTAAAATACCTAATTATCATAGCATGGAATGTTCATATCCTAGACTTTATAAACATTTCATGTCCATGGAAAA
ATGGAGGGATGAGAATTGGCCAATCCTTATAAGACATTATTGTTTTTACCTTGTATTTAGCTTTGCATTTGCTGGTTGCGTTG
CATTTGCGATCTGCAAAAATCTACGACTGCGTACAACCATGAAATTACTTATGCTTTTGAGTATTTTGGTTTTGTTATCTCAG
CCAATCTTGAATAATTGA

SEQ ID No. 284 – Mkuzi 1979 (genotype XII) 15894-15571 MGF 110 12L

ATGAACGCAACCATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCGACAAC
CCAGTGGTGTTTTTATGAAATATCACTTAAAATACTTAATCATCATAGCATGGAAAAATGGAGGGATAAGAATTGGTCAATCA
TTATAAGGTATTATTGTTTTTACCTTGTGTTTAGCTTTGCATTTGCCGGTTGCGTTGCATTTGCGATCTGCAAAAATCTACGA
CTGTGTACAACCATGAAATTACTTATGCTTTTGGGTATTTTGGTTTTGTTATCTCAGCCAATCTTGAATAATTGA

SEQ ID No. 285 – Warmbaths (genotype III/I) 14212-13859 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCAGCAACCCAGTGGTGTTT
TTATGAAATATCACTTAAAATACCTAATCATCATAGCATGGAATGTTCATATCCTAGACTTTATAAACATTTCATATTCATGG
AAAAATGGAGGGATAAGAATTGGTCAATCATTATAAGGTATTATTGTTTTTACCTTGTATTTAGTTTTGCATTTGCTGGTTGC
ATTGCATTTGCGATCTGCAAAAATCTACGACTGTGTACAACTATGAAATTACTTATGCTTTTGAGTATTTTGGTTTTGTTATC
TCAGCCAATCTTGAATAATTGA

SEQ ID No. 286 – Warthog (genotype IV) 12897-12544 MGF 110 12L

ATGAAGGTTTTTCTAGGACTTTTACTAGGTTATTCAACCATCCTCATTCTTACATATCAATCACCAGCAACCCAGTGGTGTTT
TTATGAAATATCACTTAAAATACCTAATCATCATAGCATGGAATGCTCATATCCTAGACTTTATAAACATTTCATGTTCATGA
AAAAATGGAGGGATAAGAATTGGTCAATCATTATAAGGTATTATTGTTTTTACCTTGTATTTAGTTTTGCATTTGCTGGTTGC
ATTGCATTTGCGATCTGCAAAAATCTACGACTGTGTACAACTATGAAATTACTTATGCTTTTGAGTATTTTGGTTTTGTTATC
TCAGCCAATCTTGAATAATTGA

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 110 12L. Suitably the functional version of MGF 110 8L comprises the sequence of SEQ ID No. 276, 277, 278, 279, 280, 281, 282, 283, 284, 285 or 286. Suitably the functional version of MGF 110 12L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 276, 277, 278, 279, 280, 281, 282, 283, 284, 285 or 286. Suitably the functional version of MGF 110 12L consists of the sequence of SEQ ID No. 276, 277, 278, 279, 280, 281, 282, 283, 284, 285 or 286.

MGF 360 6L gene sequences

SEQ ID No. 51 – Georgia 2007/1 MGF 360 6L (NC_044959.1:17222-18349)

TTACCGCAAATTGTCTCTCAGCGAAGAAAATGAATGAAACGTTTCTGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATCATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCCGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCCAATTTATTTTGAGGGTACATACAAGCAAGCGACATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATAATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACGATTGTAAATAAAGTCTATCAACACGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATCGAAATATTGTCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAATACACAGAACTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACATCAGAACATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGTCCGTTTTCCCACCATAATCCAAGCTGCTGTAAAATAAAAATATCATCCTCATGATAATTTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 52 – China/2018/AnhuiXCGQ MGF 360 6L (MK128995.1:17221-18348)

TTACCGCAAATTGTCTCTCAGCGAAGAAAATGAATGAAACGTTTCTGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATCATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCCGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCCAATTTATTTTGAGGGTACATACAAGCAAGCGACATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATAATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACGATTGTAAATAAAGTCTATCAACACGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATCGAAATATTGTCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAATACACAGAACTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACATCAGAACATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGTCCGTTTTCCCACCATAATCCAAGCTGCTGTAAAATAAAAATATCATCCTCATGATAATTTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 53 – Warmbaths MGF 360 6L (AY261365.1:17236-18363

TTACCGCAAATTGTCTCTCAGTAAAGAAAATGAATGAAACGTTTCTGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
CAGGTTCTAATATTTTTTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATTATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCACCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAGCGGCATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATAATC
TAGGTAAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACAATTGTAAATAAAGTCTATCAACACGTAAAAA
TCATGGCTATCAAACCTGTCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAATACACAGAGCTTTCATCCTTTCTG
TCTTGGCGCATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGCGCCACTAGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGACCGTTTTCCCACCATAGTCCAAGCTGCTGTAAAATAAAAATATCATCTTCATGATATTTTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 54 – L60 MGF 360 6L (NC_044941.1:11041-12168)

TTACCGCAAATTGTCTCTCAGCAAAGAAAATGAATGAAACGTTTCCGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATTATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAGCGACATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATAATC
TAGATGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACAATTGTAAATAAAGTCTATCAATACGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACATATTATACAATCCTACATCTAAAAATTCTGGATTGGCTCCTAGTTCAATACACAGGTCTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAACAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTTACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGGCCATTATGCCACCACAATCCAAGCTGCTGTAAAATAAAAATATCATCCTCATGATATTCTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 55 – Benin 97/1 MGF 360 6L (NC_044956.1:10692-11819)

TTACCGCAAATTGTCTCTCAGCAAAGAAAATGAATGAAACGTTTCCGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATTATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAGCGACATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATAATC
TAGATGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACAATTGTAAATAAAGTCTATCAATACGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACATATTATACAATCCTACATCTAAAAATTCTGGATTGGCTCCTAGTTCAATACACAGGTCTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAACAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTTACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGGCCATTATGCCACCACAATCCAAGCTGCTGTAAAATAAAAATATCATCCTCATGATATTCTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 56 – Pretorisuskop/96/4 MGF 360 6L (AY261363.1:17123-18250)

TTACCGCAAATTGTCTCTCAGCAAAGAAAATGAATGAAACGTTTCCGTATATTCGTAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCCTAAAAAGAAGTTTCATTATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCCATTTACTTCATGATTAATGTAACGTATCAATGTCTCTAAGGCAGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAGCGGCATCATGTCATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATCATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CATATGTATTTTTTATCATTTTTTCTTTTTCATCTAAATTTAAGATAAAACAATTGTAAATAAAGTCTATCAACACGTAAAAA
TCATGACTATCAAACCTGTCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAG
ATCAACAAACAAATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGGATACATAGAACTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGGCCATTATGCCACCATAGTCCAAGCTGCTGTAAAATAAAAATATCATCTTCATGATAATTTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 57 – Mkuzi 1979 MGF 360 6L (AY261362.1:18925-20052)

TTACTGCAAATTGTCTCTCAGCAAAGAAAATGAATGAAACGTTTCTGTATATTCATAGGTTGAAATTATTTTACGCACTTCAT
TAGGTTCTATTATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGAAGTTTCATTATAACATTCTTT
TCTTGTCTAAGAAGAGTTTCTTGTATTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTCCTTCATGATTAATGAAACCTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAGCGACATCATGTCATTTGGATCT
AAACGTATATTTTCTTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATCATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTGTATGGCGAACTTAAACCAAAATTTTAATA
CAAGTGTATTTTTTGTCATTTCTTCTTTTTCATCTAAGTATAGGATAAAACGATTGTACATAAAGTCTATCAACACGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATCGAAACATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAAGTAG
ATCAACAAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAATACACAGAACTTTCGTCCTTTCCG
TCTTGGCACATATGATGCCATAATTAATGTTGGCACCCCATAAAATAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCCTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGGCCATTATGCCACCATAGTCCAAGCTGCTGTAAAATAAAAATATCATCTTCATGATATTCTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 58 – Ken05/Tk1 MGF 360 6L (NC_044945.1:19166-20293)

TTATCGTAAATTGTCTCTTAGCGAAGAAAATGAATGAACCGTTTCCGTATATTGATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGTAGTTTCATTATAACATTCTTT
TCTTCTCTAAGAAGAGTTTCTTGTATTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACGTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCCCCTAAGGCAAAACAATAGTATATACCTAACTTATTTTGAGGGTACATACAAGCAAGCGACATCATGTTATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCGTTTTTAAACGCCAATGATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATCGCGAACTTATACCAAAATTTTAATA
CAAGTGTATTTCTTGTCATTTCTTCTTTTTCATCTAAATTTAAGATAAAACGATTGTAAATAAAGTCTATCAACGTGTAAAAA
TCATGGTCATCAAAACTATCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACTTTTTGTTGTTTAAGTAG
ATCAACAAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAAGACACAGAACTTTTGTCCTTTCCG
TCTTGGCACACATAATGCCATAATTAACGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGGTTTTTCTTCACA
GCCGTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACATCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATGGGGCCATCATGCCACCACAACCCTAGCTGCTGTAAAATAAAAATATCATCCTCATGATAATTTGAAAAGG
CCTTGGTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 59 – Malawi Lil-20/1 (1983) MGF 360 6L (AY261361.1:15478-16605)

TTACCGCAAATTGTCTCTCAGCGAAGAAAATGAATGAAACGTTTCCGTATATTCATAGGTTGAAATTATTTTACGCACTTCAC
CAGGTTCTAATATTTTTTTATGAAGTATTGAATGGGAGGTTAAAAGTCCTTTCTTAAAAAAGAGTTTCATTATAACATTCTTT
TCTTCTCTAAGAAGAGTTTCTTGTATTTTTTTTTATATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATCTACTTCATGATTAATGAAACGTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCACCTAAGGCAAAACAATAGTATATACCTAATTTATTTTGAGGGTACATACAAGCAAGCGACATCATGTGATTTGGATCT
AAACGTATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTACCTAAGTATACAGCCATTTTTAAACGCCAATCATC
TAGGTGAGGAAATTTCTTACTAAGAAAACGAATAGGTTTTATAAGATTAAACTCTATGGCGATCTTAAACCAAAATTTTAATA
CAAGTGTATTTCTTGTCATTTCTTCTTTTTCATCTAAGTATAGGATATAACGATTGTAAATAAAGTTTATCAATGCGTAAAAA
TCATGGCTATCAAAACTGTCGAGAATGGGAATGTTTTCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAAATAG
ATCAACAAACATAGTATACAACCCTACCTCTAAAAATGTTGGATCAGCTCCTAGTTGAATACACAGAACTTTCGTCCTTTCCA
TCTTGGCACATATGATGCCATAATTGATGTTGGCACCCCATAAAACAAATAACTTGATTAGATCAGTCTGATTTTTCTTTACA

GCCTTCACCAAGGCTCTGTCAAGCTCATAGCTGTCAACGTCAGAGCATGACATAGAGCCACTGGTTACCATTTTACATTGTTT
ACAAAAACCTATAGGTCCGTTTTCCCACCATAATTCTAGCTGCTGTAAAATAAAAACATCATCTTCATGATAATTTGAAAAAG
CCTTGTTTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

SEQ ID No. 60 – Kenya 1950 MGF 360 6L (AY261360.1:19341-20462)

TTACCGCACATTGTCTCTCAGCGAAGAAAATGAATGAAACGTTTCCGTATATTGATAGGTTGAAATTATTTTACGCACTTCAC
TAGGTTCTAATATTTTCTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTCTTAAAAAGTAGTTTCATTATATCATACTTT
TCTTCTCTAAGAAGAATTTCTTGTATTTTTTTTTGTATAAGGATTGGCACCCAAACTTATACAAAAATGTACATTACTCCAAAT
ACCATAATTTGAAAAGAAAGGTCTATTTAGTTCATGATTAATGAAACGTATCAACGCCTCTAAGGCAGTATTGATATTTGCCC
CTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGATACATACAAGCAAGCGACATCATGTGATTTGGATCTAAACGT
ATATTTTCCTGAAAATATGCATGATGGATTTCATCAACATTCCCTAAGTATACAGCCGTTTTTAAACGCCAATCATCTAGGTG
AGGAAATTTCTTACCAAGAAAACGAATAGGTTTTACAAGATTAAACTCTATGGCAAACTTATACCAAAATTTTAATACAAGTG
TATTTTTTGTTATTTTTTCTTTTTCATCTAAATTTAAGATAAAACCATTGTAAATAAAGTCTATCAACACGTAAAAATCATGG
CTATCAAAACTGTCGAGAATCGAAATATTATCATAATAAATATCTATAGCTAATAAGACCTTTTGTTGTTTAATTAGATCAAC
AAACATATTATACAACCCTACATCTAAAAATTTTGGATCAGCTCCTAGTTGAATACATAGAACTTTCGTCCTTTCCGTCTTGG
CACACACGATGCCAAAATTAATTTCGGCGCCCCATAAAACAAATAACTTGATTAGATCAGTTTGGTTTTCCTTCACAGCTTTT
ACTAAGGCTCTGTCAAGCTCATAGCTGTCGACATCAGAACATGACATAGAGCCACCGGTTACCATTTTACATTGTTTACAAAA
ACCTATGGGTCCGTTTTCCCACCACAGTCCAAGCTGCTGTAAAATGAAACTATCATCTTCATGATAATTTGAAAAAGCCTTGT
TTTCTATCAAGACTTTTTTTGTAAGAACCTGTAAAGAGTTCAT

SEQ ID No. 61 – Ken06.Bus MGF 360 6L (NC_044946.1:15081-16208)

TTACCGCAAATTATCTCTCAGTGAAGAAAATGAATGAAACGTTTCCGTATGTTCATAGGTTGAAATTATTTTACGCACCTCAC
TAGGTTCTAATATTTTTTTTATGAAGTATTGAATGGGGGCTTAAAAGTCCTTTTTTTAAAAAGTAGTTTCATTATAACATTCTTT
TCTTCTCTAAGAAGAGTTTCTTGTATTTTTTTTTGTATCAGGGTTGGCACCCAAACTTATACAAAAATGTATATTACTCCAAAT
ACCATAATTTGAAAAGAAAGTTATTTCCCTATTTACTTCATGATTAATGAAACGTATCAACGTCTCTAAGGCAGTATTGATAT
TTGCGCCTAAGGCAAAACAATAGTATATACCTAATTTATTCTGAGGGTACATACAAGCAAACGACATCATGTGATTTGGATCT
AAACGTATATTTTCTTGAAAATATGCATGATGGATTTCATCAACATTCCCTAAGTATACAGCCGTTTTTAAACGCCAATCATC
TAGGTGAGGAAATTTCTTACTAAGATAACGGATAGGTTTTACAAGATTAAACTCTATGGCGAACTTAAACCAAAATTTTAATA
CAAATGTGTTTCTTGTCATTTTTTCTTTTTCATCTAAATTTAGGATAAAACGATTGTAAATAAAGTTTATCAACGCGTGAAAA
TCATGGCTATTAAAGCTGTCGAGAATCAAAATATTATCATAATAAATATCTATGGCTAATAAGACCTTTTGTTGTTTAATTAG
ATTAACAAACATATTATACAGCTTTTTATCTAAAAATTCTGGATCGGCTCCTAGTTGAATACACAGGTCTTTCGTCCTTTCCA
TCTTAGCACACATAATGCCATAATTAATGTTGGCACCCCATAAAACAAATAATATGATTAGATCAGTTTGGTTTTCCTTCACA
GCTTTTACTAAGGCCCTGTCAAGCTCATAGCTGTCAACATCAGAGCATGACATTGAGCCAATGGTTACTATTTTACATTGTTT
ACAAAAACCTATGGGGCCGTTTTCCCACCACAATCCTAGCTGCTGTAAAATAAAACTATCATCTTCATGATAATTTGAAAAGG
CCTTGTTTTCTATTAAGACTTTTTTTGTAAGAACCTGTAAAGAATTCAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 6L. Suitably the functional version of MGF 360 6L comprises the sequence of SEQ ID No. 51, 52, 53, 54, 55, 56, 57, 58, 59, 60 or 61. Suitably the functional version of MGF 360 6L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 51, 52, 53, 54, 55, 56, 57, 58, 59, 60 or 61. Suitably the functional version of MGF 360 6L consists of the sequence of SEQ ID No. 51, 52, 53, 54, 55, 56, 57, 58, 59, 60 or 61.

MGF 360 10L gene sequences

SEQ ID No. 62 – Georgia 2007/1 MGF 360 10L (LR743116.1:26373-27410)

CTAGGCCAACATACTTTTTAATTTATAGTTTTTTAATAGATGATATATTTTGTTAGGATCTGCTTCTTTTAACGTTAATAGCG
AGGAGTCTGCACTATAAATGTCTAATGATAAATGATGAGATATCAAATAGTAATTCCGTTGCTCTGCTAGGGCCTTTGCCTCT
TCAAAGGCGTCGGCTCCCAGATCTATACAAAAGAACAAGTTATCCATATTATAAAATCGTACGCAGGCAAGCATAGCTGAATT
AATATTAGCTCCTAAGAGAAAACAATAATATATGGTTAAAAAATTGTTATCTTTTGTGCAGGCCATCCGCATCATTTCATCCA
CGTCCATGCGGATCTTTTCCTTTTCATACAAATTATGTAGGTCAAACAGCTTATTAAAACAAAGAGCACAGATTAACCACCAC
GTATTTAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAGATTATCCTGCAATGCCACTATAAAACAGTATAT
CGTTAACATATCACCATCCGACATATTACTTAATATGTCGGTGTCTTCTACTAACCTTTTCAACTTCCAATATATGGATGACC
TTATTTCCCTTATAATGACATAGGCTGGAAAGGGATTATCATTAAAAAGTTTAAGACATAAGATAATATTACTGCTAGTAGTG
CCAGGGTGTATTAATTTAAAGAACATGTGCATAATCTTCTTTTTATCCACGCGGTACTTGGCTCCTAATTCCCAGCAAAATTC

TCGAACAGGCGGCGTATTGGCGCAAATTAACCCATAGTTGATGTCTGCGCCCCATTCTGTAAACAGTTTTATTAACTGATAGT
TGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCGTCTGCAAAGCTTGGCAGCTTTATCAGCATATGTTTG
CAATCAAGGGAAATTGGGGCCTTATACCACCATAGTCCGCAGCGTTCTAAGATAACATGGTACTCAATAGATACTTGCTGTCT
GGCTAGTACCTTTTTGGCGAAGGATTGTAAGGAAGGAAACAT

SEQ ID No. 63 – China/2018/AnhuiXCGQ MGF 360 10L (MK128995.1:25402-26439)

CTAGGCCAACATACTTTTTAATTTATAGTTTTTTAATAGATGATATATTTTGCTAGGATCTGCTTCTTTTAACGTTAATAGCG
AGGAGTCTGCACTATAAATGTCTAATGATAAATGATGAGATATCAAATAGTAATTCCGTTGCTCTGCTAGGGCCTTTGCCTCT
TCAAAGGCGTCGGCTCCCAGATCTATACAAAAGAACAAGTTATCCATATTATAAAATCGTACGCAGGCAAGCATAGCTGAATT
AATATTAGCTCCTAAGAGAAAACAATAATATATGGTTAAAAAATTGTTATCTTTTGTGCAGGCCATCCGCATCATTTCATCCA
CGTCCATGCGGATCTTTTCCTTTTCATACAAATTATGTAGGTCAAACAGCTTATTAAAACAAAGAGCACAGATTAACCACCAC
GTATTTAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAGATTATCCTGCAATGCCACTATAAAACAGTATAT
CGTTAACATATCACCATCCGACATATTACTTAATATGTCGGTGTCTTCTACTAACCTTTTCAACTTCCAATATATGGATGACC
TTATTTCCCTTATAATGACATAGGCTGGAAAGGGATTATCATTAAAAAGTTTAAGACATAAGATAATATTACTGCTAGTAGTG
CCAGGGTGTATTAATTTAAAGAACATGTGCATAATCTTCTTTTTATCCACGCGGTACTTGGCTCCTAATTCCCAGCAAAATTC
TCGAACAGGCGGCGTATTGGCGCAAATTAACCCATAGTTGATGTCTGCGCCCCATTCTGTAAACAGTTTTATTAACTGATAGT
TGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCGTCTGCAAAGCTTGGCAGCTTTATCAGCATATGTTTG
CAATCAAGGGAAATTGGGGCCTTATACCACCATAGTCCGCAGCGTTCTAAGATAACATGGTACTCAATAGATACTTGCTGTCT
GGCTAGTACCTTTTTGGCGAAGGATTGTAAGGAAGGAAACAT

SEQ ID No. 64 – Ken06.Bus MGF 360 10L (NC_044946.1:23437-24507)

TTACGACGTTGTATCATTGATGTGATAATCCAAATAGGCCAACATACTTTTTGATTTATAGTTGTTTAATAGATGGTATATTT
TTTTAGGGTTCGCTTCTTTTAGCGTGAATAGAGAGGGATCTGGATGATAGATATCTAATGACAAACGTTGTGATATTAAATAA
TAGTCCCGCTGCTCTGCTAGGGCTTTTGCCTCTTCGAAGGCATTGGCTCCCAAGTCTATACAAAAGAACAGATTATCTATATT
AAAGAACTGTATGGCAGCAAGCATGGCCATATTGATATCGGCCCCTAAAATAAAACAATAATACATCGTTAAAAAGTTATTAT
CTTTCGTGCAAGCTATGCGCATCATTTCATTAATGTCTATGCGAATCTTTTCCTGCTCATAGAGATAATGGAGGTCAGACAGT
TTATTAAAATACAGAGCACAGATTAACCACCACGTATTCATGTGCTTAAAATGTTCGTAAAAATACGAGACGGCCTCCCTAAG
ATCATTCTGCAAGGCCACCATAAAACAATATATAGTTAGCATATCGCCGTCCGAAACATCACGTAGTAGGTCTTCATCTTCTA
CTAACCTCCTCAGCCTCCAATAAAGAGACGACTTTATTTCCCTTATAATCACATAGGTAGGAAAAGGATTCTCATTAAAAAGC
TTATGACATAAGATAATATATTGACTTGTTTTGTTCTCTATAAATTTAAAGAACATGTGTATCACCTTTTTTTTATCCATGCG
ATAGTTCGCTCCTAATTCCCAACAAAACTCTCGGGTAGGCTGTGTATTGGCACAAATGTATCCATAGTTGATGTTTGCACCCC
ACTCCGTGAATAGTTTTATTAATTGATAGTTGTTTTCCTTTGCAGCTATCATCAATGCCGTATTGAGATCCAGGCCATCCGCA
AAGTATGGCAACCTTATTAACATGTGTTTGCAATCAAGTGAAATTGGAGCCGTATACCACCATAACCCGCAGTATTTCAAAAT
ATGATAGTAGTCTTCAGGCAGCACATGCTGACTGGCTAATATCTTTTTGGCGAAAGACTGTAAAGAAGGAAACAT

SEQ ID No. 65 – Ken05/Tk1 MGF 360 10L (NC_044945.1:27310-28380)

TTACGACGTTGTATCATTATTGTGATAATCCAAATAGGCCGACATACTTTTTGATTTATAATTGTTTAATAGATGGTATATTT
TTTTAGGGTTCGCTTCTTTTAGCGTGAATAGAGAGGGATCTGGATGATAGATATCTAATGACAAACGATGTGATATTAAATAA
TAGTCCCGCTGCTCTGCTAGGGCTTTTGCCTCTTCGAAGGCATTGGCCCCCAAGTCTATACAAAAGAACAGATTATCTATATT
AAAAAACTGTATGGCAGCAAGCATCGCCATATTGATATCGGCCCCTAAAATAAAACAATAATACATCGTTAAAAAGTTGTTAT
CTTTCGTGCAAGCTATGCGCATCATTTCATTAATGTCTATGCGAATTTTTTCCTGCTCATAGAGATAATGGAGGTCAAACAGT
TTATTAAAACACAGAGCACAGATTAACCACCACGTATTCAGGTGCTTAAAATGTTGGTAAAAATACGAGACGGCCTCCCTAAG
ACCATTCTGCAAGGCCACCATAAAACAATATAAAGTTAGCATATCGCCGTCCGAAACATCGCGTAGTAGGTCTTCGTCTTCTA
CTAACCTCCTCAGCCTCCAATAAAGAGACGACTTTATTTCCCTTATAATCACATAGGTAGGAAAAGGATTCTCATTAAAAAGC
TTATGACATAAGATAATATATTGACTCGTTTTGTTCTCTATAAATTTAAAAAACATATGCATCACCTTTTTTTTATCTAAGCG
ATAGTTCGCTCCTAATTCCCAACAAAACTCTCGAGTAGGCTGTGTATTGGCACAAATGTATCCATAGTTGATGTTTGCACCCC
ACTCCGTGAACAGTTTTATTAATTGATAGTTGTTTTCCTTTGCAGCTATCATCAATGCCGTATTGAGGTCCAGGCCATCCGCA
AAGTATGGCAACCTTATTAACATGTGTTTACAATCAAGTGAAATTGGAGCCTTATACCACCATAACCCGCAGCGCTTCAAAAT
ATGATAGTAGTCTTCAGGCAGCACATGCTGGCTGGCTAATATCTTTTTGGCGAAAGATTGCAGGGAAGGAAACAT

SEQ ID No. 66 – Kenya 1950 MGF 360 10L (AY261360.1:29558-30628)

TTACGACGTTGTATCATTAATGTGATAATCCAAATAGGCCGACATACTTTTTGATTTATAGTTGTTTAATAGATGGTATATTT
TTTTAGGGTTCGCTTCTTTTAGCGTGAATAGAGAGGGATCTGGATGATAGATATCTAATGACAAACGATGTGATATTAAATAA
TAGTCCCGCTGCTCTGCTAGGGCTTTTGCCTCTTCGAAGGCATTGGCCCCCAAGTCTATACAAAAGAACAGATTATCCATATT
AAAGAACTGTATGGCAGCAAGCATGGCCATATTGATATCGGCCCCTAAAATAAAACAATAATACATCGTTAAAAAGTTGTTAT
CTTTCGTGCAAGCTATGCGCATCATTTCATTAATGTCTATGCGAATTTTTTCCTGCTCATAGAGATAATGGAGGTCAAACAGT
TTATTAAAACACAGAGCACAGATTAACCACCACGTATTCAGGTGCTTAAAATGTTGGTAAAAATACGAGACGGCCTCCCTAAG
ATCATTCTGCAAGGCCACCATAAAACAATATAAAGTTAGCATATCGTCGTCCGAAACATCGCGTAGTAGGTCTTCGTCTTCTA
CTAATCTCCTCAGCCTCCAATAAAGAGACGACTTTATTTCCCTTATAATCACATAGGTAGGAAAAGGATTCTCATTAAAAAGC
TTATGACATAAGATAATATACTGACTCGTTTTGTTCTCTATAAATTTAAAAAACATATGCATCACCTTTTTTTTATCTAAGCG
ATAGTTTGCTCCTAATTCCCAACAAAACTCTCGAGTAGGCTGTGTATTGGCACAAATGTATCCATAGTTGATGTTTGCACCCC

ACTCCGTGAACAGTTTTATTAATTGATAGTTGTTTTCCTTTGCAGCTATCATCAATGCCGTATTGAGGTCCAGGCCATCCGCA
AAGTATGGCAACCTTATTAACATGTGTTTACAATCAAGTGAAATTGGAGCCTTATACCACCATAACCCGCAGCGCTTCAAAAT
ATGATAGTAGTCTTCAGGCAGCACATGCTGGCTGGCTAATATCTTTTTGGCGAAAGATTGCAGGGAAGGAAACAT

SEQ ID No. 67 – L60 MGF 360 10L (NC_044941.1:19956-21026)

TTATAACGATGTATCATTGATGTCATAATTCAAATAGGCCAACATACTTTTTGATTTATAGTTTTTTTAATAGACGATATATTT
TGTTAGGATCTGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATGTCTAATGATAAACGATGAGATATCAAATAG
TAATTCTGTTGCTCTGCCAAGGCTTTTGCCTCTTCAAAGGCATCGGCCCCCAGATCTATACAAAAGAACAGGTTATCCATATT
ATAGAATCGTATGGAGGCAATCATGGCCAAATTAATATTAGCTCCTAAGATAAAACAATAATATATAGTTAAAAAATTGTTAT
CTTTTGTGCAGGCTATCCGCATCATTTCATCCATGTCCATACGGATTTTTTCTTTTTCGTACAAATTATGTAGGTCAAACAGC
TTATTATAGCAAAGAGCACATGTTAACCACCACGTATTCAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAG
ATTATCCTGCAATGCCACGATAAAACAGTATATAGTTAACATATCACCATCCGAAATATTACTTAATACGTTGGTATCTTCTG
CTAAATTTTTTAGCTTCCAATGTATACACGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGATTGTCATTAAAAAAT
TTAAGACATAAGATAATATTATTACTAGTAGTGTTAGGATGTATTAATTTAAAGAATATGTGCATAATCTTCTTTTTATCCAC
TTGGTACTTGGCTCCTAATTCCCAGCAAAATTCTCGAATAGGTGGCGTATTCGCGCAAATTAACCCATAGTTGATGTCTGCGC
CCCAATCCGTAAACATTTTTATTAATTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCT
GCAAAGTTTGGCAGCTTTATCAGCATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGCCCGCAGCGTTCTAA
GATAACATGGTAATCAATAGATACATGCTGACTGGCTAATACCTTTTTGGCGAAGGATTGCAAGGAAGGAACCAT

SEQ ID No. 68 – Benin 97/1 MGF 360 10L (NC_044956.1:19607-20677)

TTATAACGATGTATCATTGATGTCATAATTCAAATAGGCCAACATACTTTTTGATTTATAGTTTTTTAATAGACGATATATTT
TGTTAGGATCTGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATGTCTAATGATAAACGATGAGATATCAAATAG
TAATTCTGTTGCTCTGCCAAGGCTTTTGCCTCTTCAAAGGCATCGGCCCCCAGATCTATACAAAAGAACAGGTTATCCATATT
ATAGAATCGTATGGAGGCAATCATGGCCAAATTAATATTAGCTCCTAAGATAAAACAATAATATATAGTTAAAAAATTGTTAT
CTTTTGTGCAGGCTATCCGCATCATTTCATCCATGTCCATACGGATTTTTTCTTTTTCGTACAAATTATGTAGGTCAAACAGC
TTATTATAGCAAAGAGCACATGTTAACCACCACGTATTCAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAG
ATTATCCTGCAATGCCACGATAAAACAGTATATAGTTAACATATCACCATCCGAAATATTACTTAATACGTTGGTATCTTCTG
CTAAATTTTTTAGCTTCCAATGTATACACGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGATTGTCATTAAAAAAT
TTAAGACATAAGATAATATTATTACTAGTAGTGTTAGGATGTATTAATTTAAAGAATATGTGCATAATCTTCTTTTTATCCAC
TTGGTACTTGGCTCCTAATTCCCAGCAAAATTCTCGAATAGGTGGCGTATTCGCGCAAATTAACCCATAGTTGATGTCTGCGC
CCCAATCCGTAAACATTTTTATTAATTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCT
GCAAAGTTTGGCAGCTTTATCAGCATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGCCCGCAGCGTTCTAA
GATAACATGGTAATCAATAGATACATGCTGACTGGCTAATACCTTTTTGGCGAAGGATTGCAAGGAAGGAACCAT

SEQ ID No. 69 – Mkuzi 1979 MGF 360 10L (AY261362.1:27069-28139)

TTATAACGATGTATCATTGATGTCATAATTCAAATAGGCCAACATACTTTTTGATTTATAGTTTTTTAATAGACGATATATTT
TGTTAGGATCTGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATGTCTAATGATAAACGATGAGATATCAAATAG
TAATTCTGTTGCTCTGCCAAGGCCTTTGCCTCTTCAAAGGCATCGGCCCCCAGATCTATACAAAAGAACAGGTTATCCATATT
ATAGAATCGTATGGAGGCAATCATGGCCAAATTAATATTAGCTCCTAAGATAAAACAATAATATATAGTTAAAAAATTGTTAT
CTTTTGTGCAGGCTATCCGCATCATTTCATCCATGTCCATACGGATTTTTTCTTTTTCGTACAAATTATGTAGGTCAAACAGC
TTATTATAGCAAAGAGCACATGTTAACCACCACGTATTCAAATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAG
ATTATCCTGCAATGCCACGATAAAACAGTATATAGTTAACATATCACCATCCGAAATATTACTTAATACGTTGGTATCTTCTG
CTAAATTTTTTAGCTTCCAATGTATACACGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGATTGTCATTAAAAAAT
TTAAGACATAAGATAATATTACTACTAGTAGTGCTAGGATGTATTAATTTAAAGAATATGTGCATAATCTTCTTTTTATCCAC
TTGGTGCTTGGCTCCTAATTCCCAGCAAAATTCTCGAATAGGTGGCGTATTCGCGCAAATTAACCCATAGTTGATGTCTGCGC
CCCAATCCGTAAACATTTTTATTAATTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCT
GCAAAGTTTGGCAGCTTTATCAGCATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGCCCGCAGCGTTCTAA
GATAACATGGTGATCAATAGATACATGCTGACTGGCTAATACCTTTTTGGCGAAGGATTGCAAGGAAGGAAACAT

SEQ ID No. 70 – Pretorisuskop/96/4 MGF 360 10L (AY261363.1:26116-27186)

TTATAACGTTGTATTATTGACGTCATAATTCAAATAGGCCAATATACTTTTTGATTTATAGTTTTTTAATAGATGATATATTT
TGTTAGGATCCGCTTCTTTTAACGTTAATAACGAGGAATCTGGACTATAAATGTCTAATGATAAACAATGAGATATCAAAAAG
TAATTCCGTTGCTCTGCCAGGGCTTTTGCCTCCTCAAAGGCATCGGCCCCCAGGTCTATACAAAAGAATAAGTTATCTATGTT
ATAGAATTGTATGGAGGCAATCATAGCTAAATTAATATTAGCTCCTAAGATAAAACAATAATATATGGTTAAAAAATTGTTAT
CTTTTGTGCAGGCTATCCGCATCATTTCATCCATGTCCATGCGGATCTTTTCCTTTTCATACAAATGATGTAGGTCAAACACC
TTATTATAGCAAAGAACACATGTTAACCACCACGTATTCAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAG
ATTATCCTGCAATGCCACGATAAAACAGTATATAGTTAACATATCTCCATCCGAAATATTACTTAATACGTTGGTATCTTCTG
CTAACTTTTTTAGCTTCCAATGTATACACGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGATTGTCATTAAAAAGT
TTAAGACATAAGATAATATTACTACTAGTAGTGCTAGGATGTATTAATTTAAAGAATATGTGCATAATCTTCTTTTTATCCAC
TTGGTACTTGGCTCCTAATTCCCAGCAAAATTCTCGAACAGGTGGCGTATTCGCGCAAATTAACCCATAGTTGATGTCTGCGC
CCCAATCCGTAAACATTTTTATTAATTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCT

GCAAAGTTTGGCAGCTTTATCAGCATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGCCCGCAGCGTTCTAA
GATAATATGGTGATCAATGGATACATGCTGTCTGGCTAGTACCTTTTTGGCGAAGGATTGTAAGGAAGGAAACAT

SEQ ID No. 71 – Tengani 62 MGF 360 10L (AY261364.1:20530-21600)

TTATAACAATGTATCATTGATATCATCATTCAAATAGGCCAACATATTTTTTGATTTATAGTTTTTTAATAGATGATTTATTT
TGTTAGGATCTGTTTCTTTTAACGTTAATAGCAAGGAGTCTGGCTTATAAATGTCTAATGATAAACGATGAGATATTAAATAG
TAATTCCGTTGCTCTGCCAGGGCTTTTGCCTCTTCAAAGGCGTCGGCTCCCAGATCTATACAAAAGAACAAGTTATCCATATT
ATAAAATCGTACGCAGGCAAGCATAGCTGAATTAATATTAGCTCCTAAGAGAAAACAATAATATATAGTTAAAAAATTGTTAT
CTTTTGTGCAGGCCATCCGCATCATTTCATCCACGTCCATGCGGATCTTTTCCTTTTCATACAAATTATGTAGGTCAAACAGC
TTATTAAAACAAAGAGCACAGATTAACCACCACGTATTTAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAG
ATTATCCTGCAATGCCACTATAAAACAGTATATCATTAACATATCACCATCCGACATATTACTTAATATGTCGGTGTCTTCTA
CTAACCTTTTCAGCTTCCAATATATGGATATCCTTATTTCCCTTATAATGACATAGGCTGGAAAGGGATTATCATTAAAAAGT
TTAAGACATAAGATAATATTACTGCTAGTAGTGCCAGGATGTATTAATTTAAAGAACATGTGTATAATCTTCTTTTTATCCAC
GCGGTGCTTGGCTCCTAATTCCCAGCAAAATTCTCGAACAGACGGCGTATTGGCGCAAATTAACCCATAGTTGATGTCTGCGC
CCCATTCCGTAAACAGTTTTATTAACTGATAGTTATTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCGTCT
GCAAAGCTTGGCAGCTTTATCAGCATATGTTTGCAGTCAAGTGAAATTGGAGCCTTATACCACCATAGTCCGCAACGTTCTAA
GATAACATGGTACTCAATAGATACTTGCTGTCTGGCTAGTACCTTTTTGGCGAAGGATTGTAAGGAAGGAAACAT

SEQ ID No. 72 – Warthog MGF 360 10L (AY261366.1:22069-23130)

TCATATTGTATCATCATGGTTAAAATATGCCGTCATATTTTTTGATTTATAGTTTTTTAATAGATGATATATTTTGTTAGGGT
CCGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATGTCTAATGATAAACGATGAGATATCAAAAAGTAATTCCGT
TGCTCTGCCAGGGCTTTTGCCTCTTCAAAGGCATCGGCCCCCAAGTCTATACAAAAGAACAGGTTATCCATATTATAAAATCG
TATGGAGGCAATCATGGCCAAATTAATATTAGCTCCTAAGATAAAACAATAATATATAGTTAAAAAATTGTTATCTTTTGTGC
AGGCTATCCGCATCATTTCATCCATGTCCATGCGGATTTTTTCCTTTTCGTACAAATTATGTAGGTCAAACAGCTTATTAAAA
CAAAGAGCACAGATTAGCCACCACGTATTCAGATATTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAGATTATCCTG
CAATGCCACCATAAAACAGTATATCGTTAACATATCACCATCCGAAATATTACTTAATACGTCGGTGTCTTCTACTAACTTTT
TCAGCTTCCAATATATGGATGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGGTTATCATTAAAAAGTTTAAGACAT
AAGATAATATTACTGCTAGTAGTGCCAGGATGTATTAATTTAAAGAACATGTGCATAATCTTCTTTTTATCCACGCGGTACTT
GGCTCCTAGTTCCCAGCACAATTCTCGAACAGGCGGCGTATTGGCGCAAATTAACCCATAGTTGATGTCTGCGCCCCATTCCG
TAAACAGTTTTATTAACTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCTGCAAAGCTT
GGCAGCTTTATCAGCATATGTTTGCAATCAAGGGAAATTGGAGCCTTATACCACCATAGTCCGCAGCGTTCTAAGATAACATG
GTAATCAATAGATACATGCTGTCTGGCTAGTACCTTTTTGGCGAAGGATTGTAA
GGAAGGAAACAT

SEQ ID No. 73 – Warmbaths MGF 360 10L (AY261365.1:25300-26361)

TCATATTGTATCATCATGGTTAAAATATGCCGTCATATTTTTTGATTTATAGTTTTTTAATAGATGATATATTTTGTTAGGGT
CCGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATGTCTAATGATAAACGATGAGATATCAAAAAGTAATTCCGT
TGCTCTGCCAGAGCCTTTGCCTCTTCAAAGGCGTCGGCCCCCAGGTCTATACAAAAGAACAGGTTATCCATATTATAGAATCG
TATGGAGGCAATCATGGCCAAATTAATATTAGCTCCTAAGATAAAACAATAATATATAGTTAAAAAATTGTTATCTTTTGTGC
AGGCTATCCGCATCATTTCATCCATGTCCATGCGGATTTTTTCCTTTTCGTACAAATTATGTAGGTCAAACAGCTTATTAAAA
CAAAGAGCACAGATTAGCCACCACATATTCAGATACTTAAAATGTTGGTAAACATAAGAAATGGCCTCCCTAAGATTATCCTG
CAATGCCACCATAAAACAGTATATCGTTAACATATCACCATCTGAAATATCACTTAATACGTCGGTGTCTTCTACTAACTTTC
TCAGCTTCCAATATATGGATGACTTTATTTCCCTTATAATGACATAGGCTGAAAAGGGGTTATCATTAAAAAGTTTAAGACAT
AAGATAATATTACTGCTAGTAGTGCCAGGATGTATTAATTTAAAGAACATGTGCATAATCTTCTTTTTATCCACGCGGTACTT
GGCTCCTAGTTCCCAGCACAATTCTCGAACAGGCGGTGTATTGGCGCAAATTAACCCATAGTTGATGTCTGCGCCCCATTCCG
TAAACAGTTTTATTAACTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCTGCAAAGCTT
GGCAGCTTTATCAGCATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGTCCGCAGCGTTCTAAGATAACATG
GTAATCAATAGATACATGCTGTCTGGCTAGTACCTTTTTGGCGAAGGATTGTAA
GGAAGGAAACAT

SEQ ID No. 74 – Malawi Lil-20/1 (1983) MGF 360 10L (AY261361.1:23735-24802)

TTACACTGTGTCATGCCCATCATAGTCAAAATATACCATCATATTTTTTGATTTATAGTTTTTTAATAGATGATATATTTTTT
TAGGATCTGCTTCTTTTAACGTTAATAGCGAGGAGTCTGGACTATAAATATCTATTGATAAACGATGATACATCAAAAAGTAA
TTCCGCTGGTCTGCCAGGGCTTTTGCCTCTTCAAAGGCATCGGCTCCCAGGTCTATACAAAAGAACAAGTTATCCATATTATA
GAATTGTACGCAGGCAAGCATAGCCTGATTAATATTAGCTCCTAAGAGAAAACAGTAATATATGGTTAAAAAGTTGTTATCTT
TAGTGCAGGCTATGCACATCATTTCATCCATGTCCATGCGGATCTTTTCCTTTTCATACAAATCATGTAGGTCAAACAGCTTA
TTAAAACAAAGAGCACAGATTAACCACCACGTATTCAGATGCTTAAAATGTTGGTAAAAATAAGAAATGGCCTCCCTAAGATT
ATCCTGCAATGCCAGGATAAAACAGTATATAGTCAACATATCATCATCCGACATATTACTTAATATGTCAGTGTCTTCTACTA
ACCTTCTCAGCTTCCAATATATAGACGACTTTATTTCCCTTATAATGACATAGGTTGGAAAAGGATTATTATTAAAAAGTTTA
AGACATAAGATAATATTACTACTAGTAGTGCCATGATGTATTAATTTAAAAAACATATGCATAACCTTATTTTTATCCACTTG
GTACTTGGCTCCTAATTCCCAGCAAAATTCTCGAACAGGCGGCGTATTAGCGCAAATTAATCCATAGTTGATGTCCGCGCCCC

ATTCCGTAAACAGTTTTATTAACTGATAGTTGTTTTCCTTTGTAGCCAACATTAGTGCCGTATTAAGGTCCAAGCCATCTGCA
AAGCTTGGCAGCTTTATTAACATATGTTTGCAATCAAGTGAAATTGGAGCCTTATACCACCATAGTCCGCAATGTTTTAAGAT
ATAATGATAATCAATGGATACATGATGTCTAGCTAATACCTTTTTGGCGAAGGATTGTAAAGAAGGAAACAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 10L. Suitably the functional version of MGF 360 10L comprises the sequence of SEQ ID No. 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73 or 74. Suitably the functional version of MGF 360 10L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73 or 74. Suitably the functional version of MGF 360 10L consists of the sequence of SEQ ID No. 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73 or 74.

MGF 360 11L gene sequences

SEQ ID No. 75 – Georgia 2007/1 MGF 360 11L (NC_044959.1:26465-27526)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCAATTTATTTTTTCAGGGTCCG
TAACGATCGACAACAGAGAAATAACCGGATTGTAATGCTTTAATGATAAGGCATGGGCTATCAGATAATTTTCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCATCGGCACCCAGGTCTATACAAAAGAACAGGTTTCCAAGATTATAGTTTTGTATGGA
AACAAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCCGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATTTCATCAATATCCATGCGGACCCTTTCTATTTCGTACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGACGCGGGTATTTCTGGTAAAAGTAGCGGATAGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGCTACTGGTTTTATCGCGCGTTGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAACAGGTTGAC
CTTATAAATAATTTATTGCGTCGAATATGAAGCATAATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGACATGATA
TTGATCTACCGGTATACACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 76 – China/2018/AnhuiXCGQ MGF 360 11L (MK128995.1:26467-27528)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCAATTTATTTTTTCAGGGTCCG
TAACGATCGACAACAGAGAAATAACCGGATTGTAATGCTTTAATGATAAGGCATGGGCTATCAGATAATTTTCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCATCGGCACCCAGGTCTATACAAAAGAACAGGTTTCCAAGATTATAGTTTTGTATGGA
AACAAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCCGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATTTCATCAATATCCATGCGGACCCTTTCTATTTCGTACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGACGCGGGTATTTCTGGTAAAAGTAGCGGATAGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGCTACTGGTTTTATCGCGCGTTGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAACAGGTTGAC
CTTATAAATAATTTATTGCGTCGAATATGAAGCATAATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGACATGATA
TTGATCTACCGGTATACACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 77 – L60 MGF 360 11L (NC_044941.1:21052-22113)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGTAATTTATTTTTTCAGGGTCCA
TAACGTTCGACAACAGAGAAATGACTGGATTGTAATGCTTTAATGATAAGGCATGGGCTATCAGATAATTTTCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCGTTGGCGCCCAGGTCTATACAAAAGAACAGGTTTCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCCGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATTTCATCGATATCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCGATGTAGGCGCGGGTATTTCTGGTAAAAGTAGCGAATAGCATCTTTGAGGTCATAGTCCACCGC
TATAGCATACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCTAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGCTACTGGTTTTATCGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC

CTTATAAATAGTTTATTACGTCGAATATGAAGCATAATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGACACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 78 – Benin 97/1 MGF 360 11L (NC_044956.1:20703-21764)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGTAATTTATTTTTTCAGGGTCCA
TAACGTTCGACAACAGAGAAATGACTGGATTGTAATGCTTTAATGATAAGGCATGGGCTATCAGATAATTTTCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCGTTGGCGCCCAGGTCTATACAAAAGAACAGGTTTCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCCGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATTTCATCGATATCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCGATGTAGGCGCGGGTATTTCTGGTAAAAGTAGCGAATAGCATCTTTGAGGTCATAGTCCACCGC
TATAGCATACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCTAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGCTACTGGTTTTATCGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC
CTTATAAATAGTTTATTACGTCGAATATGAAGCATAATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGACACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 79 – Mkuzi 1979 MGF 360 11L (AY261362.1:28164-29225)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGTAATTTATTTTTTCAGGGTCCA
TAACGATCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATGGGCTATCAGATAATTTCCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCGTTGGCGCCCAGGTCTATACAAAAGAACAGGTTTCCAAGATTATAGTTTTGTATGGA
AACCAGCATAGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGACCGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATTTCATCAATATCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGGCGCGGGTATTTCTGGTAAAAGTAGCGAATAGCATCTTTGAGGTCATAGTCCACCGC
TATAGCATACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCTAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCTCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGCTACTGGTTTTATCGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC
CTTATAAATAGTTTATTACGTCGAATATGAAGCATAATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGACACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 80 – Warmbaths MGF 360 11L (AY261365.1:26388-27449)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCGATTTATTTTTTCAGGGTCCG
TAACCACCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATTGGCTATCAGATAATTTCCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCGTTGGCACCCAGGTCTATACAAAAGAACAGGTTCCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAGATGGCTGAATAGCTATAATCTTGGACGCAGGCTA
TGTGCATCATTTCATCAATGTCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGCCGCGGGTATTTCTGGTAAAAGTAGCGGATAGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGTTACTGGTTTTATCGCGCGTTGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC
CTTATAAATATTCTATTACGTCGAATATGAAGCATTATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGACACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 81 – Pretorisuskop/96/4 MGF 360 11L (AY261363.1:27214-28275)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCGATTTATTTTTTCAGGGTCCG
TAACCACCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATTGGCTATCAGATAATTTCCCTTTTGTTCT
GCCAAAGCTTTGCCCTCTTCAAAGGCGTTGGCACCCAGGTCTATACAAAAGAACAGGTTCCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCTGAATAGCTATAATCTTGGACGCAGGCTA
TGTGCATCATTTCATCAATGTCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGCCGCGGGTATTTCTGGTAAAAGTAGCGGATAGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGTTACTGGTTTTATCGCGCGTTGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC

CTTATAAATATTCTATTACGTCGAATATGAAGCATTATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCTACCGACACGCACTGCCCAGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 82 – Tengani 62 MGF 360 11L (AY261364.1:21627-22688)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCAATTTATTTTTTTAGGGTCTG
TAACGACCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATCGGCTATCAGATAATTTCCCTTTTGTTCT
GCCAAAGCTTTGCCTTCCTCAAAGGCGTTGGCTCCCAGGTCTATACAAAAGAACAGGTTCCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCCGAATAGCTATAATCTTGGACGCAGGCTA
TGTGCATCATTTCATCAATGTCCATGCGGACCCTTTCTATTTCGTACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATGAGCCGCCACCTATGTAGACGCGGGTATTTCTGGTAAAAGTAGCGGATCGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTGCTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCCCCCCTCAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGTTACTGGTTTTATCGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCACC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC
CTTATAAATAGTTTATTACGTCGAATCTGAAGCATAATGGGTCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGACACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 83 – Warthog MGF 360 11L (AY261366.1:23157-24218)

TTATCTTTGTTCATAATCAAGAAAAATCCCCATATTTATTGAGTGATAATTTTTTAACATGCGATTTATTTTTTCAGGGTCCG
TAACCACCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATTGGCTATCAGATAATTTCCCTTTTGTTCT
GCCAAAGCTTTGCCCTCCTCAAAGGCGTTGGCCCCCAGGTCTATACAAAAGAACAGGTTCCCAAGATTATAGTTTTGTATGGA
AACCAGCATGGCTTGATTGATGTTGGCTCCCATGATAAAACAGTAGTAAATGGCTGAATAGCTATAATCTTGGACGCAGGCTA
TGTGCATCATTTCATCAATGTCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGA
GCGCACATGAGCCGCCACCTATGTAGCCGCGGGTATTTCTGGTAAAAGTAGCGGATAGCATCTTTGAGGTCATAGTCCACCGC
TATCGCGTACCAGTATTTGGTTAAAACAGTACTAAAGCTATCATCATGGTCCAGCATGAAGGTTATCTCCATGAGCCCTCTTA
ACTCCCACATGATTTCTCCCCTTAGATCCAGATTATCTATAATCCTTAAATTGGGGTTATTGGAAAACACCTCGTGGCAAAAG
ATAATATTGTTACTGGTTTTATCGCGCGTTGTATCAAAGAAAATTTTTAAAATATACTCTCTTTCTAAATATTCTTTGGCTCC
CAGCTCTTTGCACAGATCACGGGTATTTTCCGTGAGAGCACAAATCATTCCATAGTTAATATCTGCACCCCATTCAGTAAACA
GCTTTATCAAGTCATGATTATTCTCCTTCACGGCTTTCATCAGTCCTATGTTTAACTCGATACCTTGACTAAAGCAGGTTGAC
CTTATAAATATTCTATTACGTCGAATATGAAGCATTATGGGGCCATTATGCCACCACAGGCCACAACACTTCAGGATATGATA
ATGATCCACCGATACGCACTGCCCGGCCAGTACTTTCTTCGTGAGGGATTGCAGGGAAGGCAACAT

SEQ ID No. 84 – Malawi Lil-20/1 (1983) MGF 360 11L (AY261361.1:24831-25892)

TTATCTTCGTTCATAATCAAGAAAAACCCTCATATTTATTGAGTGATAATTTTTTAACATGCAATTTATTTTTTCAGGGTCCA
TAATGACCGACAACAGAGAAATGACCGGATTGTAATGCTTTAATGATAAGGCATCGGCTATCAGATAATTTTCCTTTTGTTCT
GCCAAAGCTTTCCCCTCCTCAAAGGCGTTGGCCCCCAGATCTATACAAAAGAACATGTTCCCAAGATTATAGTTTTGTATAGA
AACAAGCATGGCTTGATTGATGTTGGCCCCCATGATAAAACAGTAATAAATAGCCGCATAGCTATAATCTTGGACGCAGGCTA
TGTGCATCATTTCATCAATATCCATGCGGACCCTTTCTATTACATACAGCTCGTGAAGGTCGAACACGTTGTTGTAAAAAAGG
GCGCACATAAGCCGCCAGTGGTGTAGATGGGTATACCTCTGATAAAAATAATGGATAGCCTTTTTGAGGCCATAGTCTACCGC
TATGGCGTACCAGTATTTGGTTAACATATTGCTAAAGGAGTTGTCATGGTCCAACATGTAGGTTATCTCCATGAGTCCCCTTA
GCTCCCACATGATTTCCTCCCTCAGATCCAAATTATCCACATTTTTCAGGTTGGGGTTATTGGAAAACATTTCGTGGCATAAG
ATAATATTACTGTCGGTTTTGTTGCGCGTCGTATCAAAGAAAATTTTTAAAATATAATCTCTATCTAAACGATCTTTGGCTCC
TAGTTCTCTGCATAGATTACGGGTGTGCTCCGTATGGGCACAAATCAGTCCATAATTAATATCGGCACCCCACTCGGCAAACA
GCCTTATCAAGTCATGGTTGTTTTCCTTCGCGGCTTTCATCAGTACGGTGTTCAATTCAATACCCTCGCTAAAACAGGTTGAC
CTTATAAACATTTTGTGACGATAAACGTAAAATGTAATAGGGCCATCATACCACCACAACCCGCAGCACTTTAAGACATGATA
TTGATCTACCGGTACACACTGTTTGGCCAGCACTTTCTTAGTTAAAGATTGTAAGGAAGGCAACAT

SEQ ID No. 85 – Kenya 1950 MGF 360 11L (AY261360.1:30655-31716)

TTATCTGCGTTCATAATCGAGAAAAACCACCATATTCTTTGAGTGATAATTTTTTAACATAGAATTTATCTTTTCTGGGTCGG
TCACGGCCGACAACAGGGAAATCACCGGGTTATAATGTTTTAATGATAAGGCATCGGCTATCAAATAATTTTCCTTTTGTATT
GCTAGGGTTTTGCCTTCTTCAAAGGCGTTGGCACCCAGGTCTATACAAAAGAACATGTTCCCGAGATTATAGTTTTGTATGGA
AACAAACATGGCTTGATTGATGTTGGCCCCCATGATAAAACAGTAGTAGATAGCTGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATCTCATCGATATCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACATTGTTATAAAAAAGG
GCGCACATAAGCCGCCACCGATGTAGATGGGTATACTTCTGATAAAAATAGTGGATGGCCTTTTTGAGGCCGTAGTCTACCGC
TATGGCGTACCAGTATTTGGTTAACATATTGCTGAAGGAGTTGTCATGGTCCAACATGTAGGTTATCTCCATGAGTCCCCTTA
GCTCCCACATGATTTCCTCCCTCAGATCCAAATCATCCACATGTTTCAGATTGGGGTTATTGGAAAACATTTCGTGGCATAAG
ATAATATTACTGTCGGTTTTGTTGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTATCTAAACGGTCTTTGGCTCC
AAGTTCTCTGCATAGATTGCGGGTGTGCTCCGAATGAGCACAAACCAGTCCATAATTAATATCGGCACCCCACTCAACAAACA
GCCTTATCAAGTCATGATTGTTTTCCTTCGCGGCTTTCATCAGTACGGTGTTCAATTCAATACCCTCGCTAAAACAGGTTGAC

TTTATAAACATTTTGTTACGATACGTATAAAATGTAATAGGGCCATCATACCACCACAACCCGCAGCATTTCAGGATATGATA
TTGATCTACCGGTATACACTGTTTGGCCAGCACTTTCTTGGATAGGGATTGCAAGGAAGGCAACAT

SEQ ID No. 86 – Ken05/Tk1 MGF 360 11L (NC_044945.1:28407-29468)

TTATCTGCGTTCATAATCGAGAAAAACCACCATATTCTTTGAGTGATAATTTTTTAACATAGAATTTATCTTTTCTGGGTCGG
TCACGGCCGACAACAGGGAAATCACCGGGTTATAATGTTTTAATGATAAGGCATCGGCTATCAAATAATTTTCCTTTTGTATT
GCTAGGGCTTTGCCTTCTTCAAAGGCGTTGGCACCCAGGTCTATACAAAAGAACATGTTCCCGAGATTATAGTTTTGTATGGA
AACAAACATGGCTTGATTGATGTTGGCCCCCATGATAAAACAGTAGTAAATAGCTGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATCTCATCGATATCCATGCGGACCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACATTGTTATAAAAAAGG
GCGCACATAAGCCGCCACCGATGTAGATGGGTATACTTCTGATAAAAATAGTGGATGGCCTTTTTGAGGCCGTAGTCTACCGC
TATGGCGTACCAGTATTTGGTTAACATATTGCTGAAGGAGTTGTCATGGTCCAACATGTAGGTTATTTCCATGAGTCCCCTTA
GCTCCCACATGATTTCCTCCCTCAGATCCAAATCATCCACATGTTTCAGATTGGCGTTATTGGAAAACATTTCGTGGCATAAG
ATAATATTACTGTCGGTTTTGTTGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTCTATCTAAACGGTCTTTGGCTCC
AAGTTCTCTACATAGATTGCGGGTGTGCTCCGAATGAGCACAAACCAGTCCATAATTAATATCGGCACCCCACTCAACAAACA
GCCTTATCAAGTCATGATTGTTTTCCTTCGCGGCTTTCATCAGTACGGTGTTCAATTCAATACCCTCGCTAAAACAGGTTGAC
TTTATAAACATTTTGTTACGATACGTATAAAATGTAATAGGGCCATCATACCACCACAACCCGCAGCATTTCAGGATATGATA
TTGATCTACCGGTATACACTGTTTGGCCAGCACTTTCTTGGATAGGGATTGCAAGGAAGGCAACAT

SEQ ID No. 87 – Ken06.Bus MGF 360 11L (NC_044946.1:24534-25595)

TTATCTGCGTTCATAATCGAGAAAAACCACCATATTCTTTGAGTGATAATTTTTTAACATAGAATTTATCTTTTCCGGGTCGG
TCACGGCCGACAACAGGGAAATCACCGGGTTATAATGTTTTAATGATAAGGCATCGGCTATCAAATAATTTTCCTTTTGTATT
GCTAGGGCTTTGCCTTCTTCAAAGGCGTTGGCACCCAGGTCTATACAAAAGAACATGTTCCCGAGATTATAGTTTTGTATGGA
AACAAACATGGCTTGATTGATGTTGGCACCCATGATAAAACAGTAGTAAATAGTTGAATAGCTATAATCTTGGATGCAGGCTA
TGTGCATCATCTCATCGATATCCATGCGGATCCTTTCTATTTCATACAGCTCGTGAAGGTCGAACACATTGTTATAAAAAAGG
GCGCACATGAGCCGCCACCGATGTAGATGGGTATACTTCTGATAAAAATAGTGGATGGCCTTTTTGAGGCCGTAGTCTACCGC
TATGGCGTACCAGTATTTGGTTAACATGTTGCTGAAGGAGTTGTCATGGTCCAACATGTAGGTTATCTCCATGAGTCCCCTTA
GCTCCCACATGATTTCCTCCCTCAGGTCCAAATCATCCACATGTTTCAGATTGGGGTTATTGGAAAACATTTCGTGGCATAAG
ATAATATTACTGTCGGTTTTGTTGCGCGTCGTATCAAAGAAAATTTTTAAAATATACTCTTTATCTAAACGGTCTTTGGCCCC
TAGTTCTCTGCATAGATCGCGGGTGTGCTCCGAATGAGCACAAACCAGTCCATAATTAATATCGGCACCCCACTCAGTAAATA
ATTTTATTAGGTCATGATTGTTTTCCTTCGCGGCTTTCATCAGTACGGTGTTCAATTCAATACCCTCGCTAAAACAGGTTGAC
TTTATAAACATTTTGTTACGATACGTATAAAATGTAATAGGGCCATCATACCACCACAACCCGCAACTTTTCAGGATATGATA
TTGATCTACCGGTATACACTGTTTGGCCAGCACTTTTTTGGATAGGGATTGCAAGGAAGGCAACAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 11L. Suitably the functional version of MGF 360 11L comprises the sequence of SEQ ID No. 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86 or 87. Suitably the functional version of MGF 360 11L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86 or 87. Suitably the functional version of MGF 360 11L consists of the sequence of SEQ ID No. 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86 or 87.

MGF 360 12L gene sequences

SEQ ID No. 88 – Georgia 2007/1 MGF 360 12L (LR743116.1:30355-31407)

TCATCTTAAATCATAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCTATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGCT
AAGCATGGCTTGATTGATGTTGGCGCCCAGGACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTACTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTTTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATACCAGCCCGTAGTTGATGTCCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAGTTGTTTTCCCTTACAGCCTTCACTAACGCCGTATTTAGGTTTAAGCCCTCTTTAATACCTGCTGATTTT

ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATCATGCCACCATAGGTCATAACACTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 89 – China/2018/AnhuiXCGQ MGF 360 12L (MK128995.1:29384-30436)

TCATCTTAAATCATAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCTATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGCT
AAGCATGGCTTGATTGATGTTGGCGCCCAGGACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTACTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTTTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATACCAGCCCGTAGTTGATGTCCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAGTTGTTTTCCCTTACAGCCTTCACTAACGCCGTATTTAGGTTTAAGCCCTCTTTAATACCTGCTGATTTT
ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATCATGCCACCATAGGTCATAACACTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 90 – Tengani 62 MGF 360 12L (AY261364.1:24540-25592)

TCATCTTAAATCATAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCA
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCTATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGCT
AAGCATGGCCTGATTGATGTTGGCGCCCAGGACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTCTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATACCAGCCCGTAGTTGATGTCCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAGTTGTTTTCCCTTACAGCCTTTACTAACGCCGTATTTAGGTTTAAGCCCTCTTTAATACCTGCTGATTTT
ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATCATGCCACCATAGGTCATAACACTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 91 – Warthog MGF 360 12L (AY261366.1:26036-27088)

TCATCTTAAATCGTAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTAACGCATGATCTATAATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTTATACCCTTCCCCTAAA
GCTATAGTGCCCTCTTCGAAAGCATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGGCGCCCAGGACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGCACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTCTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCGGGTGTGCTCCGTGTTGACAGATACCAGCCCATAGTTGATGTTCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAATTGTTTTCCCTTACAGCCTTCACTAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGCTGATTTT
ATGAGCTTTAGGTTATGATCAAACGTGATCGGACCATCATGCCACCATAGGTCATAACACTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 92 – Warmbaths MGF 360 12L (AY261365.1:29294-30346)

TCATCTTAAATCGTAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTACCGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTTATACCCTTCCCCTAAA
GCTATAGTACCCTCTTCGAAAGCATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTACATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGGCGCCCAGAACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATAGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCATGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTCTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCGGGTGTGCTCCGTGTTGACAGATACCAGCCCATAGTTGATGTCCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAGTTGTTTTCCCTTACAGCCTTCACTAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGCTGATTTT

ATGAGCTTTAGGTTATGATCAAACGTGATCGGACCATCATGCCACCATAGGTCATAACACTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 93 – Pretorisuskop/96/4 MGF 360 12L (AY261363.1:30098-31150)

TCATCTTAAATCGTAGGTAAGGAAGATCATCATATTTTTTGAAACGTAATTTTTTAACGCATGATCTATAATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGACTATAAATCTTTAGGGATAAAATGTTCTTTATAAGCTTATACCCTTCCCCTAAA
GCTATAGTGCCCTCTTCGAAAGCATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGCCCCCCAGGACATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATGAATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTAAGTAGTAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTCTTCATTCAAGGTCTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATACCAGCCCATAGTTGATGTTCGCCCCCCACTCTGCAAACAGTT
TTATAAGGTTGTAGTTGTTTTCCCTTACAGCCTTCACTAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGCTGATTTT
ATGAGCTTTAGGTTATGATCAAACGTGATCGGACCATCATGCCACCATAGGTCGTAACACTTTAAAAGATAATGTTGGTTTGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 94 – Mkuzi 1979 MGF 360 12L (AY261362.1:31073-32125)

TCATCTTAAATCATAGGAAAGGAAGATCATCATATTTTTTGAAAAGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGATGGTGGTCGGACTATAAATCTTTAGAGATAAAATGTTTTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGGCGCCCAACATATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTAATGCAGGCGATCC
GCATCATCTCTTCTATGTCCATATAGATCTTGTCCTTTTCATACGCCTCATGGAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCTTCTTTCAGGTTATAGCGTATGGCTAT
AGCGTACCAGTATTTGAGTAGCAATGTACTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAAAAAATTTCTATCCTCATTTTTATATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATAAAAATTTGTAAAATTTCTTTTTCATTCAAGGTCTCCTTGGCACCTAG
CTCTCGACAGAGGTCCCAGGTGTGCTCCGAGCTGACAGATACCAGCCCATAGTTGATGTCCGCCCCCCACTCTGCAAACAATT
TTATAAGGTTGTAGTTGTTTTCCTTTACAGCCTTCACCAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGCTGATTTT
ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATCATGCCACCATAGGTCATAATATTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCGGCCAACACCTTTTTGGTCAAAGATTGCAGGGAAGGCAACAT

SEQ ID No. 95 – L60 MGF 360 12L (NC_044941.1:23965-25017)

TCATCTTAAATCATAGGAAAGGAAGATCATCATATTTTTTGAAAAGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGATGGTGGTCGGACTATAAATCTTTAGAGATAAAATGTTTTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGGCGCCCAACATATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCAATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGGAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGCTATAGCGTACGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCAAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCAATTTCAGATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATGAAAATTTGTAAAATTTCCTCTTCATTCAAGATCTCCTTGGCACCTAA
CTCTTGACAGAGGTCCCGGGTATGCTCCGTGTTGACAGATACCAGCCCATAGTTGATGTCCGCCCCCCACTCTGTAAATAGTT
TTATAAGGCTGTAGTTGTTTTCCCTTACAGCCTTTACTAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGATGATTTT
ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATTATACCACCATAGATCATAATATTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAAAGATTGCAGGGAAGGCAACAT

SEQ ID No. 96 – Benin 97/1 MGF 360 12L (NC_044956.1:23616-24668)

TCATCTTAAATCATAGGAAAGGAAGATCATCATATTTTTTGAAAAGTAATTTTTTAACGCATGATCTATGATTTCAGGGTCCG
TGCTTTTAGGCAACGGGATGGTGGTCGGACTATAAATCTTTAGAGATAAAATGTTTTTTATAAGCTCATACCCTTCCCCTAAA
GCTGTAGTACCCTCTTCGAAAACATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGT
AAGCATGGCCTGATTGATGTTGGCGCCCAACATATAGCAGTAGTACATGGTTGAAAGGTTGTGGTCTTTGATGCAGGCAATCC
GCATCATCTCTTCTATGTCCATATGGATCTTGTCCTTTTCATACGCCTCATGGAGGTCAAACACATTATTAAAACAAAGAGCA
CATGTTAACCGCCACGTATTCATGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAGGCTATAGCGTACGGCTAT
AGCGTACCAGTATTTGAGTAGTAATGTACTGAGCAAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTAACTCCCTTAACT
CCCAGAAAATTTCTATCCTCAATTTCAGATTATTTACTTTTTGTAATATCGGATTGTTGGAAAACACCTCATGGCATAAAATA
ATGTTACTACTAGTTTTATGAAACTTTAGATCTATGAAAATTTGTAAAATTTCCTCTTCATTCAAGATCTCCTTGGCACCTAA
CTCTTGACAGAGGTCCCGGGTATGCTCCGTGTTGACAGATACCAGCCCATAGTTGATGTCCGCCCCCCACTCTGTAAATAGTT
TTATAAGGCTGTAGTTGTTTTCCCTTACAGCCTTTACTAACGCCGTATTTAGGTCTAAGCCCTCTTTAATGCCTGATGATTTT

ATGAGCCTTAGGTTATGATCAAACGTGATCGGAGCATTATACCACCATAGATCATAATATTTTAAAAGATAATGTTGGTTCGT
GGGCACGCATTGTCCAGCCAACACCTTTTTGGTCAAAGATTGCAGGGAAGGCAACAT

SEQ ID No. 97 – Malawi Lil-20/1 (1983) MGF 360 12L (AY261361.1:27682-28731)

TCATCTTAAATCGTAGGAAAGGAAGGTCATCATATTTTTTGATTTATAATTTTTTAACACATGATCTATTATTTCAGGGTCCG
TGTTTTTAGGTAACGGGGCAGTGGACGGACTATAGATCTTTAGGGATAAAATGTTCCTTATAAGCTCATACCCTTCCCCTACA
GGCATATTCTCTTCGAAAACATCAGCCCCCAGATCCATACAAAAGAACATGTTTTCTATATTATAGTACTGTATTGAGGCAAG
CATGGCCTGATTAATGTTGGCGCCCAGGACATAGCAGTAGTATATCGTTGAAAGGTTGTGGTCTTTGATGCAGGCTACTCGCA
TCATCTCTTCTAAGTCCATATAGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACATTATTAAAACAAAGAGCACAT
GTTAACCGCCACGTATTCAGGTGTGTATATTTTTGATAAAAATACTGTATGGCCTCTTTCAGGTTATAGCGTACGGCTATAGC
GTACCAGTATTTGAGTAATAATGTATTGAGTGAAAACTCATTATTTAACAGATCGGTTTTTTTTATTAACTCCCTTAACTCCC
AGAAAATTTCTATCCTCATTTTCAGATTATTTACTTTTTGTAATAACGGATTGTTGGAAAACACCTCATGGCATAAAATAATG
TTACTACTAGTTTTATAAAACTTTAGATCGATGAAAATTCGTAAAATTTCCTCTTCATTTAAGGTCTCCTTGGCGCCTAGCTC
TCTGCAGAGGTCCCGGGTGTGCTCCGTGTTGACAGATACCAGCCCGTAGTTGATGTCCGCCCCCCACTCTGTAAAAAGCTTTA
TAAGGTTGTAGTTGTTTTCCCTTACAGCCTTTACTAACGCCGTATTTAGGTCTAAGCCATCTTTAATGCCTGCTGATTTTATC
AGCCCTAGGTTATGATCAAACGTGATCGGAGAATCATACCACCATAGGTCGTAACACTTTAAAAGATAATATTGGTCCGTCGG
CAGGCATTGTCCAGCCAGTACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 98 – Kenya 1950 MGF 360 12L (AY261360.1:33549-34604)

TCATCTTAGATCATAAGTAAGGAAGACCATCATATTTTTTGAAAAGTAATTTTTTAACTCATGATCTATAATTTCAGGGTCCG
TGCTTTTAGGCAACGGGGTGGTGGCCGGGCTATAAATCTTTAGGGATAAAATATTCCTTATAGGCTCATACCCTTCCTGTCCC
ACTAGAGCCATACCCTCTTCAAAAGCATCGGCCCCCAGATCCATACAAAAGAATATGTTTTCTATATTATAGTACTGTATTGA
GGTAAGCATGGCCTGATTGATGTTGGCGCCCAGCATATAGCAGTAGTATATCGTTGAAAGGCTGTGGTCTTTGATGCAGGCTA
TCCGCATCATCTCTTCTAAATCCATACAGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACGTTATTAAAACAAAGA
GCACATGTTAATCGCCACGTATTCAGGTGCGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAAGTTGTAGCGTACGGC
TATAGCGTACCAGTATTTGAGTAATAGTGTATTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTATCTCCCTTA
ACTCCCAAAAAATTTCTATCCTCATTTTCAGGTTATTTACCTTTTTTAAAAGTAGATTATCGGAAAACACCTCATGACATAAG
ATAATGTTACTACTGGTTTTATGAAACTTTAAATCTATGAAAATTTGTAAAATATCCCCTTCATTTAAGGTCTTCTTGGCGCC
TAGCTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATATCAGCCCGTAGTTGATGTTCGCTCCCCACTCCGTAAATA
GTTTTATAAGACTGTAGTTGTTTTCCTTTACAGCCTTCACTAATGCCATGTTTAGGTCTAAGCCTTCTTGAAGGCCTGCTGAT
TTTATCAGCCTTAGGTTATGATCAAACGTGATCGGAGCATTATTCCACCATAGATCGTAACACTTTAAAAGATAATGTTGGTC
CTCGGGCAGACATTGTCCAGCCAGCACCTTTTTGGTCAGAGATTGCAGGGAAGGCAACAT

SEQ ID No. 99 – Ken06.Bus MGF 360 12L (NC_044946.1:27428-28483)

TCATCTTAGATCATAAGTAAGGAAGACCATCATATTTTTTGAAAAGTAATTTTTTAACGCATGATCTATAATTTCAGGGTCCG
TGCTTTTAGGCAATGGGGTAGTGGCCGGGCTATAAATCTTTAGGGATAAAATATTCCTTATAGGCTCATACCCTTCCTGTCCC
ACTAGAGCCATACCCTCTTCAAAAGCATCGGCCCCCAGATCCATACAAAAGAATATGTTTTCTATATTATAGTACTGTATTGA
GGTAAGCATGGCCTGATTGATGTTGGCGCCCAGCATATAGCAGTAGTATATTGTTGAAAGGTTGTGGTCTTTGATGCAGGCTA
TCCGCATCATCTCTTCTAAATCCATACAGATCTTGTCCTTTTCATACGCCTCATGAAGGTCAAACACGTTATTAAAACAAAGA
GCACATGTTAACCGCCACGTATTCAGGTGTGTATATTTTTGGTAAAAATACTGTATGGCCTCTTTCAAGTTGTAGCGTACGGC
TATAGCGTACCAGTATTTGAGTAATAGTGTATTGAGCGAAAACTCATTATTTAGCAGATCGGTTTTTTCTATTATCTCCCTTA
ACTCCCAAAAAATTTCTATCCTCATTTTCAGGTTATTTACCCTTTTTAAAAGTAAATTATCGGAAAACACCTCATGACATAAG
ATAATGTTACTACTGGTTTTATAAAATTTTAAATCTATGAAAATTTGTAAAATATCCCCTTCATTTAAGGTCTTCTTGGCGCC
TAGCTCTCGACAGAGGTCCCAGGTGTGCTCCGTGTTGACAGATATCAGCCCGTAGTTAATGTTCGCCCCCCACTCCGTAAATA
GTTTTATAAGACTGTAGTTGTTTTCCTTTACAGCCTTCACTAATGCCATGTTTAGGTCTAAGCCTTCTTGAATGCCTGCTAAT
TTTATCAGCCTTAGGTTATGATCAAACGTGATCGGAGCATTATTCCACCATAGATCGTAACACTTTAAAAGATAATGTTGGTC
CTCGGGCAGACATTGTCTAGCCAGCACCTTTTTGGTCAAAGATTGCAGGGAAGGCAACAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 12L. Suitably the functional version of MGF 360 12L comprises the sequence of SEQ ID No. 88, 89, 90, 91, 92, 93, 94 95, 96, 97, 98 or 99. Suitably the functional version of MGF 360 12L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 88, 89, 90, 91, 92, 93, 94 95, 96, 97, 98 or 99. Suitably the functional version of MGF 360 12L consists of the sequence of SEQ ID No. 88, 89, 90, 91, 92, 93, 94 95, 96, 97, 98 or 99.

MGF 360 13L gene sequences

SEQ ID No. 100 – Georgia 2007/1 MGF 360 13L (LR743116.1:31568-32629)

CTATAGTATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGTAAATATCCAAAGCCAAACTATGGCTCAGAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGCGCGTAACAGTAATATATTGTTAATGGATTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGATGTTTTCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCATCTAGAAAACAAATGGCGTCCTTACAATCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAACCATTTAACTCGTCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAACAAATTTGTTTTCTAAAATAGGATTATTCATAAAAATTTCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCCTGGTAAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACCATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACGAAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTCGGCCACGATCCATACAAAGCTTGAGAGGAGCATCATGCCACCATAGGCCACAATATTTCAAAATGCAGTGTTCATC
TATTGACAAACACTGGCTGGCTATCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 101 – China/2018/AnhuiXCGQ MGF 360 13L (MK128995.1:30597-31658)

CTATAGTATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGTAAATATCCAAAGCCAAACTATGGCTCAGAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGCGCGTAACAGTAATATATTGTTAATGGATTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGATGTTTTCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCATCTAGAAAACAAATGGCGTCCTTACAATCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAACCATTTAACTCGTCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAACAAATTTGTTTTCTAAAATAGGATTATTCATAAAAATTTCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCCTGGTAAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACCATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACGAAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTCGGCCACGATCCATACAAAGCTTGAGAGGAGCATCATGCCACCATAGGCCACAATATTTCAAAATGCAGTGTTCATC
TATTGACAAACACTGGCTGGCTATCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 102 – Tengani 62 MGF 360 13L (AY261364.1:25753-26814)

CTATAGTATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGTAAATATCCAAAGCCAAACTATGGCTCAGAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGCGCGTAACAGTAATATATTGTTAATGGGTTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGATGTTTTCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCATCTAGAAAGCAAATGGCGTCCTTACACTCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAACCGTTTAACTCATCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAGTAAATTTATCTTCTATATTAGGATTATTCATAAATATATCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCTTGGTGAAAATACGGAAAATATCGTCGTCTTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACTATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCTATATGGAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTTGGCCACGATCCATACAAAGCTTGAGGGGGACATCATGCCACCATAGGCCACAGTGTTTCAGAATGCAGTGTTCATC
TATCGACAAAGACTGGTTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGTAATGACAT

SEQ ID No. 103 – Warthog MGF 360 13L (AY261366.1:27277-28338)

CTATAGTATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCCTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGTAAATATCCAAAGTCAAACTATGGCTTAGAAAATGATAACCTTTT
TGTTCCGCTATAGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCGTAACAATAATATATTGTTAATGGATTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTTTCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCATCTAGAAAGCAAATGGCGTCCTTACACTCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAATCGTTTAACTCATCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TACAAATTAAGCCCCTTAATTGTATAGTAAATTTGTTTTCTATATTAGGATTATTCATAAATATCTCATGGCACAAAATAATA
CGGCCGCTGGTTTTATTGTGCATTATCTTGGTGAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCACCTAGCTG
TCTACACAACTCTCGGATGTGCTCCGTATTGATAGAAAGCAAACTATAGTTGATATGTGCGCCCCATTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCTATATGGAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT

TGTATTTGGCCACGATCCATACAAAGCTTGAGGGGGACATCATGCCACCATAGGCCACAGTGTTTCAGAATGCAGTGTTCATC
TGTCGACAAACACTGGCTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 104 – Warmbaths MGF 360 13L (AY261365.1:30498-31559)

CTATAGTATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAACCCTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGTAAATATCCAAAGCCAAACTATGGCTTAGAAAATGATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCGTAACAGTAATATATTGTTAATGGATTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTATCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCATTAAGACCCGTATATTTCTCATCTAGAAAGCAAATGGCGTCCTTACACTCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAATCGTTTAACTCATCCGTTTCTTTTATTTCTATGAGCCTCCATAGTCTTT
TACAAATTAAGCCCCTTAATTGTATAGTAAATTTGTTTTCTATATTAGGATTATTCATAAATATCTCATGGCACAAAATAATA
CGGCCGCTGGTTTTATTGTGCATTATCTTGGTGAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTTTTTGGCACCTAGCTG
TCTACACAACTCTCGGATGTGTTCCGTATTGATAGAAAGCAAACTATAGTTGATATGTGCGCCCCATTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCTACATGGAGATCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTTGGCCACGATCCATACAAAGCTTGAGGGGGACATCATGCCACCATAGGCCACAGTGTTTCAGAATGCAGTGTTCATC
TGTCGACAAACACTGGCTGGCTACCGTTTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 105 – Pretorisuskop/96/4 MGF 360 13L (AY261363.1:31307-32368)

CTATAGTATATTATGAGAATATTCCCAAATTATGGATAAGTTTTTTGATTTATAATCCTTTAAAAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAGTGGCAAGGAAGCATCTGAGCTGAAAATATCCAAAGCCAAACTATGGCTTAGAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TATTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCGTAACAGTAATATATTGTTAATGGATTGTTATCCTTGGTAG
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTTTCCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTAAAA
TACAGGAGACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCTTCTAGAAAGCAAATGGCGTCCTTACACTCGTATTG
TACTGCTTTGGCGTACCAATACTTCACTAGTAAATCGTTTAACTCATCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TACAAATTAAGCCCCTTAATTGTATAGTAAATTTGTTTTCTATATTAGGATTATTCATAAATATATCATGGCACAAAATAATA
CGGCCGCTGGTTTTATTGTGCATTATCTTGGTGAAAATACGGAAAACATCGTCGTCTTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTCCGTATTAATAGAAAGCAAACTATAGTTGATATGTGCGCCCCATTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCTATATGGAGGTCTATATCCTCTCCTAAAAATCCTGATTTTATT
TGTATTTGGCCACGATCCATACAAAGCTTGAGGGGGACATCATGCCACCATAGGCCACAGTGTTTCAGAATGCAGTGTTCATC
TATCGACAAACACTGGCTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 106 – Mkuzi 1979 MGF 360 13L (AY261362.1:32286-33347)

CTATAATATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAATGGCAAGGAAGCATCTGAACTGTAAATATCCAAAGTCAAGCTATGGCTTAAAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCCCCCAAATCTATACAGAAAAATATATTACCGATGTTATAATATTG
TACTGAAGTGAGCATAGCTTGGTTGATGTTGCTCCCCAGGGCGTAACAGTAATATATTGTTAATAGATTGTTATCCTTGGCAC
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTTTTCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCATTCGTTAAGATCCGTATATTTCTCATCTAGAAAGCAAATGGCGTTCTTACAAACGTATTG
TACTGCTTTGGCATACCAATACTTCACTAGTAAATCATTTAACTTGTCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAACAAATTTGTTTTCTAAAATAGGATTATTCATAAAAATTTCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCCTGGTGAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACTATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACGAAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTCGGCCACGATCCATACAAAGCTTGAGAGGAGCATCATGCCACCATAGGCCACAGTATTTCAAAATGCAGTGTTCATC
TATTGACAAACACTGGCTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 107 – L60 MGF 360 13L (NC_044941.1:25189-26250)

CTATAATATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTTTTCGG
GGTCCTTTAAGTTTAATGGCAAGGAAGCATCTGAACTGTAAATATCCAAAGTCAAGCTATGGCTTAAAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGACGTTATAATATTG
TACTGAAGTGAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCGTAACAGTAATATATTGTTAATAGATTGTTATCCTTGGCAC
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTTTTCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCACTCGTTAAGATCCGTATATTTCTCATCTAGAAAGCAAATGGCGTTCTTACAAACGTATTG
TACTGCTTTGGCATACCAATACTTCACTAGTAAATCATTTAACTCGTCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAACAAATTTGTTTTCTAACATAGGATTATTCATAAAAATTTCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCCTGGTGAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACTATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACGAAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT

TGTATTCGGCCACGATCCATACAAAGCTTGAGAGGAGCATCATGCCACCATAGGCCACAGTATTTCAAAATGCAGTGTTCATC
TATTGACAAACACTGGCTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 108 – Benin 97/1 MGF 360 13L (NC_044956.1:24840-25901)

CTATAATATATTATGAGAATATTCCCAAATGATGGATAAGTTTTTTGATTTATAATCTTTTAATAAACTGCTTATTTTTTCGG
GGTCCTTTAAGTTTAATGGCAAGGAAGCATCTGAACTGTAAATATCCAAAGTCAAGCTATGGCTTAAAAAATTATAACCTTTT
TGTTCCGCTATGGCACGACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAAAATATATTACCGACGTTATAATATTG
TACTGAAGTGAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCGTAACAGTAATATATTGTTAATAGATTGTTATCCTTGGCAC
AAGCCAGACATATCATGTCATGGACGTCTATTTGGACTTTTTTCTTGTGGTACATCTCATGAAGCTCATATATTTTGTTATAA
TACAGGAGACATTTTAATCGCCACTCGTTAAGATCCGTATATTTCTCATCTAGAAAGCAAATGGCGTTCTTACAAACGTATTG
TACTGCTTTGGCATACCAATACTTCACTAGTAAATCATTTAACTCGTCCGTTTCTTTTATTTCTATGAGCCCCCATAGTCTTT
TATAAATTAAGCCCCTTAATTGTATAACAAATTTGTTTTCTAACATAGGATTATTCATAAAAATTTCATGGCACAAAATAATA
CTGCCGCTGGTTTTATTGTGCATTATCCTGGTGAAAATACGGAAAATATCGTTGTCCTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAACTCTCGGATGTGCTTCGTATTGATAGAAAGCAAACTATAGTTGATATTTGCGCCCCACTCTGTAAAGAGCTTTA
TCAGACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACGAAGGTCTATATCTTCTCCTAAAAATCCTGATTTTATT
TGTATTCGGCCACGATCCATACAAAGCTTGAGAGGAGCATCATGCCACCATAGGCCACAATATTTCAAAATGCAGTGTTCATC
TATTGACAAACACTGGCTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCAACGACAT

SEQ ID No. 109 – Malawi Lil-20/1 (1983) MGF 360 13L (AY261361.1:28920-29980)

TTAGAGTATATTATGAGAGTAATCCAAAATGATGGATAAATTTTTTGATTTATAATTTTTTAACAAACTGCTTATTTCTTCGG
GGTCCTTTAAGTTTAATGGCAAGGAAGCATCCGAGCTATAAATATTCAAAACCAAACTATGGCTTAGAAAATTATAACCTTTT
TGTCTCGCTATGGCACTACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAATATATATTACCGATGTTATAATATTG
CACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCATAACAGTAATATATTGTTAATGGATTGTTATCCCTGATAC
AAGCCAGGGATAACATTTCATTAACGTCTATTTGGATTTTTTCCTTGTGGTATATATCATGAAGCTCATATATTTTGTTATAA
TATAGGTAACATTTTAATCGCCATTCATTAAGATCCGTATATTTCTCATCCAGAAAGCAAATGGCATCTTTATAATCGTATTG
TACTGCTTTGGCGTACCAATATTTCACTAGTAATTCACTTAACTCGTCCGTTTCTTTTATTTCTATAAGCCCGCATAGTCTTT
TATAAATTAAGCGCCTTAATTGTGCAGCAAATTTGTTTTCTAAATTAGGATTATTTATAAATATCTCATGGCACAAAATAACA
CTGCCGCTGGTTTTATTATGCATTATCTTGTTGAAAATACAGAAAATATCGTAGTCCTCCAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAAATCTCGGACGTGCTTCGTATTGATAGAAAGCAGACTATAGTTGATATTTGCGCCCAACTCTGTAAAAAGCTTTA
TTAGATTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACAAAGGTCTATATCTTCTCCTAAAAATCCCGATTTTATT
TGTATTCGGCCACGATCCATATAAAGCTTGAGAGGGGCATCATGCCACCATAAGTCACAGTATTTCAAAATGTGTTCATCTAT
CGACAAACATGATGTACTGGCTACCGTCTTTTTGACGAGGGTTTGTAGAGAGAGCGGCGCCGACAT

SEQ ID No. 110 – Kenya 1950 MGF 360 13L (AY261360.1:34752-35812)

TTAGAGTATTTTATGAGAGTAATCCAGAATGATGGATAAATTTTTTGATTTATAATTTTTTAATAAACTGCTTATTTCTTCGG
GAACCTTTAAGTTTAATGGCAAGGAAGCATCTGAGCTATAAATATTCAAAATTAAACTATGGCATAAAAAATTATAACCATTT
TGTCTCGCTATGGCACTACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAATATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGGTTGATGTTGCCCCCCAGGGCATAACAATAATATATTGTTAATAGATTGTTATCCCTGATAC
AAGCCAGAGATAACATTTCATTGACGTCTATTTGGATTTTTTTCTTGTGGTATATATCATGAAGCTCATATATTTTGTTATAA
CATAGGTAACATTTTAATCGCCATTCATCAAGATCCGTATATTTTTCATCCAGAAAGCAAATGGCATCTTTATGATCGTATTG
TACTGCATTGGCGTACCAATATTTCACTAGTAATTCGCTTAACTCGTCCGTTTCTTTTATTTCTATAAGCCCGCATAATCTTT
TATAAATTAAGCGCCTTAATTGTGCAGCAAAGTTGTTTTCTAATTTAGGATTATTTATAAATATCTCATGGCACAAAATAATA
CTGCCGCTAGTTTTATTATGCATTATTTTATTGAAAATACAGAAAATATCGTAGTCGTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAAATCTCGGGCGTGCTTCGTATTGATAGAAAGCAGACTATAGTTGATATATGCGCCCCACTCTGTAAATAACTTTA
TCAGACTATAGTTATTTTCCTTAACAGCTATTATTAATGCCACACAAAGGTCTATATCTTCTCCTAGGAATCCCGATTTTATG
TATATTCGTCCACGATCTATGTAAAGCTTGAGGGGAGCATCATGCCACCATAAGCCACAGTATTTCAAAATGTGTTCATCTAT
CGACAAACATGATGTACTGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCGACGACAT

SEQ ID No. 111 – Ken06.Bus MGF 360 13L (NC_044946.1:28644-29704)

TTAGAGTATTTTATGAGAGTAATCCAGAATGATGGATAAATTTTTTGATTTATAATTTTTTAATAAACTGCTTATTTCTTCGG
GATCCTTTAAGTTTAATGGCAAGGAAGCATCTGAGCTATAAATATTCAAAACCAAACTATGGCTTAAAAAATTATAACCATTT
TGTCTCGCTATGGCACTACCCTCTTCAAAGGCATTACCACCCAAATCTATACAGAAATATATATTACCGATGTTATAATATTG
TACTGAAGTAAGCATAGCTTGATTGATGTTGCCCCCCAGGGCATAACAATAATATATTGTTAATAGATTGTTATCCCTGATAC
AAGCCAGAGATAACATTTCATTGACGTCTATTTGGATTTTTTCCTTGTGGTATATATCATGAAGCTCATATATTTTGTTATAA
CATAGGTAACATTTTAATCACCATTCATCAAGATCCGTATATTTTTCATCCAGAAAGCAAATGGCATCTTTATGGTCGTATTG
TACTGCATTGGCGTACCAATATTTCACTAGCAATTCGCTTAACTCGTCCGTTTCTTTTATTTCTATAAGCCCGCATAGTCTTT
TATAAATTAAGCGCCTTAATTGTGCAGCAAAGTTGTTTTCTAAATTAGGATTATTTATAAATATCTCATGGCACAAAATAATA
CTGCCGCTAGTTTTATTATGCATTATCTTGTTGAAAATACAGAAAATATCGTAGTCGTCTAGAGTTTCTTTGGCGCCTAGCTG
TCTACACAAATCTCGGGCGTGCTTCGTATTGATAGAAAGCAGACTATAGTTGATATATGCGCCCCACTCTGTAAATAACTTTA
TCATACTATAGTTGTTTTCCTTAACAGCTATTATTAATGCCACACAAAGGTCTATATCTTCTCCTAGGAATCCCGATTTTATG

TATATTCGCCCACGATCTATGTAAAGCTTGAGGGGAGCATCATGCCACCATAAGCCACAGTATTTCAAAATGTGTTCATCTAT
CGACAAACATGATGTACCGGCTACCGTCTTTTTGACGAGGGTCTGCAGAGAGAGCGGCGACGACAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 13L. Suitably the functional version of MGF 360 13L comprises the sequence of SEQ ID No. 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110 or 111. Suitably the functional version of MGF 360 13L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110 or 111. Suitably the functional version of MGF 360 13L consists of the sequence of SEQ ID No. 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110 or 111.

MGF 360 14L gene sequences

SEQ ID No. 112 – Georgia 2007/1 MGF 360 14L (LR743116.1:32814-33887)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCAGATTTTTTGAAGTATATGTCTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATACCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGAGTTGTGCCCTATCAAAATCGGCAGCCCCCAAATCAATACAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCCAACCTATGACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTGATGCAAATCTCTTTTTCACGACACAACTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAGAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGTGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGCAGAACTCCTGCACAGGATTTTAGCCTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTTAA
GCCTCCCAGTTCCGCACACAGCCGCTTTAGATACACGGCAGGAACACGTATAAGCCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGTTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCGAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAACTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 113 – China/2018/AnhuiXCGQ MGF 360 14L (MK128995.1:31843-32916)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCAGATTTTTTGAAGTATATGTCTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATACCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGAGTTGTGCCCTATCAAAATCGGCAGCCCCCAAATCAATACAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCCAACCTATGACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTGATGCAAATCTCTTTTTCACGACACAACTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAGAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGTGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGCAGAACTCCTGCACAGGATTTTAGCCTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTTAA
GCCTCCCAGTTCCGCACACAGCCGCTTTAGATACACGGCAGGAACACGTATAAGCCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGTTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCGAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAACTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 114 – Tengani 62 MGF 360 14L (AY261364.1:26983-28056)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCAGCTCGTTTCAGATTTTTTGAAGTATATGACTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATGCCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGCGTTGTGCCCTATCAAAATCAGTAGCCCCCAAATCGATGCAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCTAACCTATAACAGTAATAAATGGCCG
CATAATTTTTTTTCTGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTGATGCAAATCTCTTTTTCACGACACAACTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAGAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGTGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGCAGAACTCCTGCACAGGATTTTAGCCTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGATTCGGATACAGGCGTTAA
GCCACCCAGTTCCGTGCACAGCCGCTTTAGATGCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA

CACTGTACATGTTTATACGAAAAAATTTGCTTACAATTATTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACCTTTTTGGCCAATGTTTGTAAAGACAACAT

SEQ ID No. 115 – Warthog MGF 360 14L (AY261366.1:28495-29568)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCAGATTTTTTGAAGTATATGACTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATGCCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAAAAAATGTTG
CTCAAGTTATACATATAAGTTTTGTGCGCAATGCGTTGTGCCCTATCAAAATCAGTAGCCCCCAAATCGATGCAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCTAACCTATAACAGTAATAAATGGCCG
CATAATTTTTTTTCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTGATACAAATCTCTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAAAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGTGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGCTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTTAA
GCCTCCCAGTTCCGTGCACAGCCGCTTTAGATGCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAATTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACATATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACCTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 116 – Warmbaths MGF 360 14L (AY261365.1:31747-32820)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCATATTTTTTGAAGTATATGCCTTTAGCC
TATCATATATTTCCTGGGGTTCGGTTACATCTAATGCCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAAAGAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGCGTTGTGCCCTATCAAAATCAGTAGCCCCCAAATCGATGCAGAAAAACAG
GTTTAAAGAATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCTCCCAACCTATAACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTAATGCAAATCTCTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAGAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGCGCAAACCAAAACTTTGTTAATAGGTGGTGCGCCGTATCCCCCATCAACGGAA
TTTTTGAACAGCTGTACATAACTGTGTCTAAAGTGGTTCTAGTTATGGTTTCCAAGAGTGGGTTATAACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGGTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGTGTTAA
GCCTCCCAGTTCTGTGCACAGCCGCTTTAGATGCACGGTAGGAACACATATAAGTCCATATTCAGGATTTGCACCCCAATCCA
CAAATAAACGTATAAGCTCAAGATTATCCCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAGAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAATTTGCTTACAATTGTTACACAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACATATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACCTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 117 – Pretorisuskop/96/4 MGF 360 14L (AY261363.1:32525-33598)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCAGATTTTTTGAAGTATATGACTTTAGCC
TATCATATATTTCCTGGGGTTCGGTTACATCTAATGCCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGTGTTGTGCCCTATCAAAATCAGTAGCCCCCAAATCGATGCAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCTAACCTATAACAGTAATAAATGGCCG
CATAATTTTTTTTCTGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTGATGCAAATCTCTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGGTGATTTTTATGCCTTTTATAGAAATAGTGAAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGCTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGTTACAGGCGTTAA
GCCTCCCAGTTCCGTGCACAGCCGCTTTAGATGCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAATTTGCTTACAATTGTTACACAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACCTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 118 – Mkuzi 1979 MGF 360 14L (AY261362.1:33547-34620)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCCCGTTTCATATTTTTTGAAGTATATGTCTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATACCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGAGTTGTGCCCTATCAAAATCGGCAGCCCCCAAATCAATACAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCCAACCTATGACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTAATGCAAATCTCTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGCTGATTTTTATGCCTTTTATAAAAATAGTGGAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGGTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTTAA
GCCTCCCAGTTCCGCACACAGCCGCTTTAGATACACGGCAGGAACACGTATAAGCCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGTTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA

CACTGTAAATGTTTATACGAAAAAACTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 119 – L60 MGF 360 14L (NC_044941.1:26422-27495)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCATATTTTTTGAAGTATATGTCTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATACCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGAGTTGTGCCCTATCAAAATCGGCGGCCCCCAAATCAATACAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCCAACCTATGACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTAATGCAAATCTCTTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGCTGATTTTTATGCCTTTTATAAAAATAGTGGAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGGTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTCAA
GCCTCCCAGTTCCGCACACAGCCGCTTTAGATACACGGCAGGAACACGTATAAGCCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGTTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAACTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 120 – Benin 97/1 MGF 360 14L (NC_044956.1:26073-27146)

TTAGTCTATAACTATAATTTCTGGATGGGCTGTAAGATACTCTTCGGCTCGTTTCATATTTTTTGAAGTATATGTCTTTAGCA
TATCATATATTTCCTGGGGTTCGGTTACATCTAATACCAAGGTCACATCACGGCTGAAAAGCTGCTTTACTAAGAAAATGTTG
CTCAAGTTATACATATAAGCTTTGTGCGCAATGAGTTGTGCCCTATCAAAATCGGCGGCCCCCAAATCAATACAGAAAAACAT
GTTTAAAGTATTATTGTTATAGATAGAAAGATTCATGCCATAATCGAGACTAGCCCCCAACCTATGACAGTAATAAATGGCCG
CGTAATTTTTTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTAATGCAAATCTCTTTTTTCACGACACAGCTCGTGT
ATGTCAAAAATGTTATTAAAATAAAGGCTACAAGCTACCCGCCAATAGAGCTGATTTTTATGCCTTTTATAAAAATAGTGGAT
AGCCTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TGTTTGAACAGGTGTACGTAACTGTGTCTAAAGTGGTTCTAGTTACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTTAGGTTGGCCACTTCTTTTAAAATTTCCAGAAGACGGGGTTCGGATACAGGCGTCAA
GCCTCCCAGTTCCGCACACAGCCGCTTTAGATACACGGCAGGAACACGTATAAGCCCATATTCAGGATTTGCGCCCCAATCCA
CAAATAAACGTATAAGTTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATACGAAAAAACTTGCTTACAATTGTTACATAGGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAACGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 121 – Malawi Lil-20/1 (1983) MGF 360 14L (AY261361.1:30193-31266)

TTAGTCTATAACTACAATTTCTGGATGGGCTGTAAAATACTCTTCGGCTTGTTTTAGATTTTTTGACGTATATGTATTTAGCA
TATCATATATTGCCTGGGGCTCAGTTAGATCTAATATCAAGCTCACATCACGGCTGAAAAGCTGTTTTACTAAAAAAAGGTTG
CTCAAGTTATACATATAAACTCTACGCGCAATGAGTCGCGCCCTATCAAAGTTAGTAGCCCCCAAATCAATGCAGAAAAATAG
GTTTAAAGTATTATTGTTATAGATAGATAGATTCATGCCATAATCAAGACTAGCCCCTAACATATGACAGTAATAAATGGCTG
CATAATTTTCTTCCCGCAAGCAAGCAAATTTCATCATCAGATTAGGGCTAATGCAAATCTCTTTTTTTACAACACAGCTCATGC
AAGTCAAAAATGTTGTTAAAATAAAGGCTACAAGTCAGTCGCCAATAGAGCTGATTTTTATGCTTTTCGTAGAAATAGTGAAT
AGCTTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTTGATAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TTTTTGAACGGGTGTACATAACTGTGTCTAAGGTGGTTCTAGTCACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTCAGATCGGCCACTTCTTTTAAAATCTCCAGAAGACGAGATTCGGATACAGGTGTTAA
GCCTCCTAGTTCCATGCACAGCCGCTTTAGATGCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAACAATCGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCTTCAAGACAAAGATCATCCTCAGAAAAA
CACTGTAAATGTTTATATGAAAAAATTTGCTTACATGTATTACATAAGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAGCGTATAATCATAATCACTTGAAAGATAATTGCATGCCACAACTTTTTTGGCCAGCGTTTGTAAAGACAACAT

SEQ ID No. 122 – Kenya 1950 MGF 360 14L (AY261360.1:36121-37194)

TTAGTCTATAACTACAATTTCTGGATGGGCTGTAAAATACTCTTCGGCTCGTTTTAGATTTTTTGACGTATATGTCTTTAGCA
TATCATATATTGCCTGGGGTTCGGTTATATTTAATACCAAGCTCGCATCACGGCTGAAAAGCTGTTTTACTAAAAAAATGTTG
CTCAAGTTATACATATAAACTCTATGCGCAATGAGTCGCGCTCTATCAAAGTTAGTAGCCCCCAAATCAATACAGAAAAATAG
GTTTAAAGTATTATTGTTATAGATAGATAGATTCATGCCATAATCGGGACTAGCCCCCAACATATGACAGTAATAAATGGCTG
CATAATTTTCTTCCCGCAGGCAAGCAAATTTCATCATTAGATTAGGGCTAATGCAAATCTCTTTTTTTAGAACACAGCTCATGC
AAGTCAAAAATATTATTAAAATAAAGGCTACAAGCCAGCCGCCAATAGAGCTGATTTTTATGCTTTTCATAGAAATAGTGAAT
CGCTTTTGTAAAATTATGTCGTAATGCCAGGGCAAACCAAAACTTCGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TTTTTGAACGGGTGTACATAACGGTGTTTAAAGTGGTTCTAGTCACGGTTTCCAAGAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTCAGATCGGCCACTTCTTTTAAAATTTCCAGAAGACGAGATTCGGAGACAGGTGTTAA
GCCTCCTAGTTCTGTGCACAGCCGTTTTAGATCCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAACAATCGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCGTCAAGACAAAGATCATCCTCAGAAAAA

CACTGCAAATGTTGATACGAAAAAATTTGCTTACATGTATTACATAAGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAGCGTATAATCATAGTCACTTGAAAGATAATTGCATGCCACAACCTTTTTGGCCAACGTTTGTAAAGACAACAT

SEQ ID No. 123 – Ken06.Bus MGF 360 14L (NC_044946.1:29917-30990)

TTAGTCTATAACGACAATTTCTGGATGGGCTGTAAAATACTCTTCGGCTCGTTTTAGATTTTTTGACGTATATGTCTTTAGCA
TATCATATATTGCCTGGGGTTCGGTTATATTTAATACCAAGCTCGCATCACGGCTGAAAAGCTGTTTTACTAAAAAAATGTTG
CTCAAGTTATACATATAAACTCTATGCGCAATGAGTCGCGCTCTATCAAAGTTAGTAGCCCCCAAATCAATGCAGAAAAATAG
GTTTAAAGTATTATTGTTATAGATAGATAGATTCATGCCATAATCGGGACTAGCCCCCAACATATGACAGTAATAAATGGCTG
CATAATTTTCTTCCCGCAGGCAAGCAAATTTCATCATTAGATTAGGGCTAATGCAAATCTCTTTTTTAGAACACAGCTCATGC
AAGTCAAAAATGTTATTAAAATAAAGGCTACAAGTTAGCCGCCAATACAGCTGATTTTTATGTTTTTCGTAGAAATAGTGAAT
CGCTTTTGTAAAATTATGCCGTAATGCCAGGGCAAACCAAAACTTCGTTAATAGGAGGTGCGCCGTATCCCCCGTCAACGGAA
TTTTTGAACGGGTATACATAACTGTGTTTAAAGTGGTTCTAGTCACGGTTTCCATAAGTGGATTATGACAAAACATGTCATAA
CCCAGTAGAACTCCTGCACAGGATTTCAGATCGGCCACTTCTTTTAAAATTTCCAGAAGACGAGATTCGGAGACAGGTGTTAA
GCCTCCTAGTTCCGTGCACAGCCGTTTTAGATGCACGGCAGGAACACGTATAAGTCCATATTCAGGATTTGCGCCCCAATCCA
CAAACAATCGTATAAGCTCAAGATTATCGCTCTTCACGGCCTTTACTAGCGCCGCGTCAAGACAAAGATCATCCACAGAAAAA
CACTGCAAATGTTGATACGAAAAAATTTGCTTACATGTATTACATAAGTGAATAGGACCTAAATCCCACCACAAACCAAAACG
CTGCAGCGTATAATCATAGTCACTTGAAAGATAATTGCACGCCACAACTTTTTTGGCCAACGTTTGTAAAGACAACAT

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 14L. Suitably the functional version of MGF 360 14L comprises the sequence of SEQ ID No. 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, or 123. Suitably the functional version of MGF 360 14L comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, or 123. Suitably the functional version of MGF 360 14L consists of the sequence of SEQ ID No. 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, or 123.

MGF 360 21R gene sequences

SEQ ID No. 124 – Georgia 2007/1 MGF 360 14L

ATGTCTACTCCACTTTCTCTACAGACTCTTGTTAAAAAAGTGCTGGCCACACAGCACATATCTAAAGAACACTACTTTATTTT
GAAATATTGTGGTTTATGGTGGCATGAAGCGCCGATTACGATTTGCATTGATGAGGATAGCCAAATATTGATAAAATCGGCAA
GCTTCAAAGAAGGCTTATCTTTAGATATCGCATTAATGAAAGTCGTGCAAGAAAATAACCATGATTTAATAGAGTTGTTTACC
AAGTGGGGTGCAGATATCAACTCTAGCTTAGTTACTGTTAATACGGAGTATACCCGGAACCTTTGTCAGAAATTAGGCGCAAA
GGAAGCTTTGAATGAAAGGGATATTTTACAAATATTTTATAAAACACGTCATCTTAAAACTAGCAGTAATATTATTTTATATA
ATGAATTGTTTTCTAATAATCTCCTTTTCCAAAATATAGAGAGATTGAGTTTAATAGTTTATAGGGGCTTGAAAAACTTATCA
ATCAACTTTATATTGGATGATATTTCATTTAGCGAAATGTTAACTAGATACTGGTATAGTATGGCGATATTATATAACCTTAC
TGAAGCCATCCAATATTTTTATCAACGATATAGGCATTTTAAAGATTGGCGGCTTATATGTGGGCTTTCTTTTAACAATTTGT
CTGACCTTCATGAAGTATATAACTTAGAGAAGACGGATATAGACATTGATGAAATGATGAAGTTGACCTGTAGTACGTATGAT
GGTAATTATTCGACTATTTATTATTGTTTTATGTTGGGGGCTGACATCAATCGGGCAATGTTAACCTCGGTAATAAACTTTCA
TATTGGTAACTTGTTCCTTTGTATAGATTTAGGAGCTGATGCTTTCGAAGACAGCATGGAACTAGCAAAACAAAAGAATAATA
ATATATTAGTAGAAATATTATCATTTAAAAATTATTATAGTTCAAATACCTCTCTTTTATCAATAAAAACGACAGATCCGGAA
AAAATTAATGCCTTATTAGATGAAGAAAAGTATGAGTCAAAAAATATGTTAATGTATGAAGAATTATCTCATTGA

SEQ ID No. 125 – China/2018/AnhuiXCGQ MGF 360 14L

ATGTCTACTCCACTTTCTCTACAGACTCTTGTTAAAAAAGTGCTGGCCACACAGCACATATCTAAAGAACACTACTTTATTTT
GAAATATTGTGGTTTATGGTGGCATGAAGCGCCGATTACGATTTGCATTGATGAGGATAGCCAAATATTGATAAAATCGGCAA
GCTTCAAAGAAGGCTTATCTTTAGATATCGCATTAATGAAAGTCGTGCAAGAAAATAACCATGATTTAATAGAGTTGTTTACC
AAGTGGGGTGCAGATATCAACTCTAGCTTAGTTACTGTTAATACGGAGTATACCCGGAACCTTTGTCAGAAATTAGGCGCAAA
GGAAGCTTTGAATGAAAGGGATATTTTACAAATATTTTATAAAACACGTCATCTTAAAACTAGCAGTAATATTATTTTATATA
ATGAATTGTTTTCTAATAATCTCCTTTTCCAAAATATAGAGAGATTGAGTTTAATAGTTTATAGGGGCTTGAAAAACTTATCA
ATCAACTTTATATTGGATGATATTTCATTTAGCGAAATGTTAACTAGATACTGGTATAGTATGGCGATATTATATAACCTTAC
TGAAGCCATCCAATATTTTTATCAACGATATAGGCATTTTAAAGATTGGCGGCTTATATGTGGGCTTTCTTTTAACAATTTGT
CTGACCTTCATGAAGTATATAACTTAGAGAAGACGGATATAGACATTGATGAAATGATGAAGTTGACCTGTAGTACGTATGAT
GGTAATTATTCGACTATTTATTATTGTTTTATGTTGGGGGCTGACATCAATCGGGCAATGTTAACCTCGGTAATAAACTTTCA
TATTGGTAACTTGTTCCTTTGTATAGATTTAGGAGCTGATGCTTTCGAAGACAGCATGGAACTAGCAAAACAAAAGAATAATA

ATATATTAGTAGAAATATTATCATTTAAAAATTATTATAGTTCAAATACCTCTCTTTTATCAATAAAAACGACAGATCCGGAA
AAAATTAATGCCTTATTAGATGAAGAAAAGTATGAGTCAAAAAATATGTTAATGTATGAAGAATTATCTCATTGA

SEQ ID No. 126 – Tengani 62 MGF 360 14L

ATGTCTACTCCACTTTCTCTACAGACTCTTGTTAAAAAAGTGCTGGCCACACAGCACGTATCTAAAGATCACTACTTTATTTT
AAAATATTGTGGTTTGTGGTGGCATAAGGCCCCGATTACGATTTGCATTGATGAGGATAGCCAAATATTGATAAAATCGGCAA
GCTTTAAAGAAGGCTTACCTTTAGATATGGCATTAATGAAAGCTGTACAGGAAAACAACTATGAAATGATCATGTTGTTTACT
GAGTGGGGTGCAGACATTAACTCTAGCTTAGTCACTGTTAATACGGAGCGTACCCGGAACCTTTGTCGAGAATTAGGCGCGAA
GGAAATTTTGAATGAAAAAGAAATTTTAGAAATATTTTATAAAACATGTCATATTAAAACTAGCAGTAATTTTATTCTATGCC
ATGAATTGTTATCCAATAATCCCCTTTTCCAAAATATAGAGAGTTTGAGTTTAATAGTTTATAGGGGCTTGAAAAACTTATCA
ATTAACTTTATATTGGATGATATTTCATTTAGCGAAATGTTAACTAGATACTGGTATAGCTGGGCGATATTATATAACCTTAC
TGAAGCTATTCAATATTTCTATCAAACATACAAGCATTTTAAAGATTGGCGGCTAATATGTGGACTTGCTTATAATAACGTGT
TTGATCTTCATGAAATTTATAACATAGAAAAGACTGATTTAGATATTGATGAAATGATGCAGTTGGCTTGTATGTATGATAGT
AATTATTCAACTATTTATTATTGTTTTATGTTGGGGGCTAATATCAATCAGGCAATGTTAACCTCGGTAATAAACCATTATAT
TAATAACTTGTTCCTTTGTATAGATTTGGGAGCTGACGCCGTCAAAGACAGCATGGAACTAGCAAAACAAAAGAATTATAATA
TATTAGTAAAAATATTAACATTTAAAAATTATAGTCCAGACTCTTCTCTTTTATCATTAAAAACGACAGATCCGGAAAAAATT
AATGCCTTACTAGATGAAGAAAAGTATGAGTCGAAAAATATGTTAATGTATGAAGAATCATCTCGTTGA

SEQ ID No. 127 – Pretorisuskop/96/4 MGF 360 14L

ATGCCTTCTCCACATTCTCTACAGACTCTTGCTAAAAAAATACTGGCTACACAGCAGATATCTACAGATCACTACTTTATTTT
AAAATATTGTGGTTTATGGTGGCATGGAGCTCCAATTATGCTTTCTACTAATGAGGATAATCAATTGATGATAAAATCGGCAA
GCTTCAAAGAAGGCTTATCTTTAGATTTGGCATTAATGAAAGTCGTGCAAGAAAACAATCATGATTTAATAAAGCTGTTTACC
GAGTGGGGTGCAGACATCAACTCTAGCTTCGTCACTGTTAATATGGAGTGTACCCGAAACCTCTGTCGGGAATTAGGCGCGAA
GGAAGCTTTGAATGAAAGGGATATTTTACAAATATTTTATAAAACACGTGATATTAAAACTAGCAGTCATGTTATTTTATGCC
ATGAATTATTATCCAATAACCCCCTTTTCCAGAATATAGAGAGAATGCGTTCAATAATTTATAGGAGTCTGGAAAAACTATCA
ATCAACTTTATATTGGATGATATTTCATTTAGTGAAATGTTAACTAGACACTGGTATGGGTTGGCGATATTATATAACCTAAC
TGAAGCTATCCAATATTTCTATGAAAAATACAAGCATTTTAAAAATTGGCGGCTAATATGTGGACTTTCTTTTAACAATCTGT
CTGATCTTTATGAAATATATAATTTAGAGAAGGTTGATATGAACATTGATGAAATGATGTATCTGGCCTGTAGTATATATGAT
GGTAATTATTCAACTATTTATTATTGTTTTGTATTGGGAGCTGATATCAATCAGGCAATGTTAACCTCAGTAATAAACCATTG
TATTGGTAACTTGTTCCTTTGTATAGATTTAGGGGCTGATGCTTTCGAAGACAGCATGGAACTAGCAAAGCAAAAAAATGATA
ATATTTTTATTAGTATATTATCATTTAAAAATTACAGTCCAGACTCTTCTCTTTTGTCATTAAAAATGACAGATCCGGAAAAA
ATTAATGCCTTACTAGATGAAGAAAAGTATGAGTCAAAAAATATGTTAATGTTTGA

SEQ ID No. 128 – Mkuzi 1979 MGF 360 14L

ATGCCTACTCCACTTTCTCTACAGACTCTTGCTAAAAAAGTACTGGCCACACAGTATATATCCATAGATTATTACTTTATTTT
GAAATATTGTGGTTTATGGTGGCATGGAGCCCCTATTATGATTTCCATTGATAAGAATAAAAGCCAAATACTGATAAAATCGG
CAAGCTTCAAAGAAGGCTTATCTTTAGATATCGCATTAATGAAAGCTGTGCAGGAAAACAATCATGATTTAATAAAGCTGTTT
ACCGAGTGGGGTGCAGACATCAACTCTAGCTTAGTCACTGTTAATACGGAGTGTACCCGAAACCTCTGTCGGGAATTAGGCGC
GAAGGAAGCTTTGAATGAAAGGGATATTTTACAAATATTTTATAAAACACGTGATATTAAAACTAGCAGTAATGTTATACTAT
GCCATGAATTGTTATCCAATAACCCCCTTTTCCAAAATATAGAGAGAATGCGTTCAATAATTTATAGGAGTCTGGAAAAACTA
TCAATTAACTTTATATTGGATGATATTTCATTTAGCGAAATGTTAACTAGACACTGGTATAGGTTGGCGATATTATATAACCT
AACTGAAGCTATCCAATATTTCTATGAAAAATACAAGCATTTTAAAGATTGGCGGCTAATATGTGGGCTTTCTTTTAACAATC
TGTCTGACCTTCATGAAATATATAACTTAGAGAAGGTTGATATGGACATTGATATAATGATGTATCTGGCCTGTAGTACGTAT
GATGGTAATTATTCAACTATTTATTATTGTTTTGTATTGGGGGCTGATATCAATCAGGCAATGTTAACCTCGGTAATAAACCA
TCGTATTGGTAACTTGTTCCTTTGTATAGATTTAGGGGCTGATGCCTTCGAAGACAGTATGAAACTAGCAAAACAAAAGAATC
ATAATATATTAGTACATATATTATCGTTTAAAAACTATAGTCCAGACTTCTCCCTTTTATCAATAAAAACGACAGATCCAGAG
AAAATTAATGCCTTACTAGATGAAGAAAAGTATGAGTCAAAAAATATGTTAATGTATGATGAATTTGACGCCTGTACTAATAA
TGTTTAA

SEQ ID No. 129 – Warmbaths MGF 360 14L

ATGCCTACTCCACTTTCTCTACAGACTCTTGCTAAAAAAGTACTGGCCACACAGTATATATCCATAGATTATTACTTTATTTT
GAAATATTGTGGTTTATGGTGGCATGGAGCCCCTATTATGATTTCCATTGATAAGAATAAAAGCCAAATACTGATAAAATCGG
CAAGCTTCAAAGAAGGCTTATCTTTAGATATCGCATTAATGAAAGCTGTGCAGGAAAACAATCATGATTTAATAAAGCTGTTT
ACCGAGTGGGGTGCAGACATCAACTCTAGCTTAGTCACTGTTAATACGGAGTGTACCCGAAACCTCTGTCGGGAATTAGGCGC
GAAGGAAGCTTTGAATGAAAGGGATATTTTACAAATATTTTATAAAACACGTGATATTAAAACTAGCAGTAATGTTATACTAT
GCCATGAATTGTTATCCAATAACCCCCTTTTCCAAAATATAGAGAGAATGCGTTCAATAATTTATAGGAGTCTGGAAAAACTA
TCAATTAACTTTATATTGGATGATATTTCATTTAGCGAAATGTTAACTAGACACTGGTATAGGTTGGCGATATTATATAACCT
AACTGAAGCTATCCAATATTTCTATGAAAAATACAAGCATTTTAAAGATTGGCGGCTAATATGTGGGCTTTCTTTTAACAATC
TGTCTGACCTTCATGAAATATATAACTTAGAGAAGGTTGATATGGACATTGATATAATGATGTATCTGGCCTGTAGTACGTAT
GATGGTAATTATTCAACTATTTATTATTGTTTTGTATTGGGGGCTGATATCAATCAGGCAATGTTAACCTCGGTAATAAACCA
TCGTATTGGTAACTTGTTCCTTTGTATAGATTTAGGGGCTGATGCCTTCGAAGACAGTATGAAACTAGCAAAACAAAAGAATC

ATAATATATTAGTACATATATTATCGTTTAAAAACTATAGTCCAGACTTCTCCCTTTTATCAATAAAAACGACAGATCCAGAG
AAAATTAATGCCTTACTAGATGAAGAAAAGTATGAGTCAAAAAATATGTTAATGTATGATGAATTTGACGCCTGTACTAATAA
TGTTTAA

SEQ ID No. 130 – Ken05/Tk1 MGF 360 14L

ATGCCTACACCGTCTTCTTTACAAGTCCTTGTCAAAAGGGTGTTGGACTACCAGCATCATGTATCTGAAGATGATTATTGTAT
TTTACAGCATTGTGGGTTGTGGTGGCATGGAAGTCCAATTATGTTTTTTACTAATGAAAATCATCAAAGGATGATAAAATCAG
CAAGCTTTAAAGATGGTTTAGAAATAAATCTCGCATTAATGAAGGCCGTACAGGAAAACAATTGTATCTTAATAGAGCTGTTT
ACCGAATGGGGTGCAGACATTAATTATGGATTGATTACTGTCAATACGGAATATACCCGAAACCTATGTCGAAATCTAGGTGC
CAAGGAGGCGTTAAATACACGGAAAATTTTAGATGTATTTTTAAATTTAAAGGATTTTAAAAGTAGTAATCATATTATTCTAT
GCCATGAATTGTTATCTAATAATCCTCTTTTACTAAGTGAAAATAATGATTATTTGAGAAAAATAATTAATTGTAATCTAAGG
AGAATATCAATTAACTTTATATTGGATGAAATTTCATTTAATGAAAAGCTAACCAGATTCTGGTATAAACAGGCAGTACTAAA
TAATCTTACTGAAGCTATCCAATATTTCTATCAAAAATATAAGCAGTTTAAAGACTGGCGACTAATATGTGGACTTGCTTTAA
ATAATGTATTTGATCTTCATGAAATATATAACAAAGAGAAGGCTGATATAGATATTAATCAAATGATAGAGATAACCTGTACA
TATATGTGTAGTTATCCCACCATTTACTATTGTTTTGTAATGGGGGCTGACATTAATCGGGCAATGATTACCTCAGTTACAAA
ATCTTATACTGGTAACTTGTTCTTTTGTATAGATTTAGGAGCTACTGCCTTCGAAGAGTGCTTAGAAATAGCAAAACAACAGA
ATGATAATGAATTGGTAAAGGTATTATCATTGAAAAACTATTACAGTCCAGATAGCTCCCTTTTATCATTAAAAATAACAGAT
CCGGAAAAAATTAATATCTTATTAGATGATGAAACATATGAGTCAAAAAATGAGTTAATATATGAAGAATTAATATAA

SEQ ID No. 131 – Kenya 1950 MGF 360 14L

ATGTCCACACCATCTTCTTTACAAGTCCTTGTCAAAAGGGTGCTGGACTTCCAGCATGTGTCTGAAGATGATTACTGTATTTT
AAAATGTTGTGGGTTATGGTGGCATGGAGGCCCAATCATGCTTTCTACGAATGAGGATAATCAAATGATGATAAAATCAGCAA
GTTTTAAAGATGGTTTAGAGATAAATCTCGCATTAATGATGGCCGTACAAGAAAACAATTGTAGCCTAATAGAGCTGTTTACC
GAATGGGGTGCAGACATTAATTCTGGATTGGTTACTGTCAACACGGAATACACCCGAAACCTATGTCGAAATCTAGGTGCTAA
GGAGACATTAAATAAACGGGAAATTTTAGATGTATTTTTAAAATTAAAGAATTTTAAAAGTAGTAATAATATTATTCTATCCC
ATGAATTATTATCTAATAATCCTCTTTTCCTAAGTGAAGATAATGATTATTTTAGAAGAATAATTAATTGTAATCTAAGGAGA
ATATCAATTAACTTTATATTGGATGAAATTTCATTTAATGAAAAGCTAACCAGATTCTGGTATAGTCAGGCGGTACTATATAA
TCTTACTGAAGCTATCCAATATTTCTATCAAAAATATGAACATCTCAATGAGTGGCGTTTAATTTGTGCGCTTTCTTTTAATA
ATGTGTTTGATCTTCATGAAATATATAACAAAGAAAAGGTTGGTATGGATATTAATCAAATGATAGAGATAACCTGTGCATAT
ATGTGTAGTTATTCCACCATTTACTATTGTTTTGTAATGGGAGCTGACATTAATCGGGCAATGATTATCTCGGTTACAAAATC
TTATACTTATAACTTGTTCTTTTGTATAGATTTAGGAGCTACTGCCTTCGAAGAGTGTTTAGAAATAGCAAAACAACAGAATA
ATAATGAATTAGTAAAAATATTATCATTGAAAAACTATTATAGTCCAGATAGCTCCCTTATATCATTAAAAATAACAGATCCG
GAGAAAATTAATATCTTATTAGATGAGGAAAATTATGAGTCAAAAAATGAGTTAATATATGAAGAATCTAATATAAATAATAG
CGATGATATATTTTGA

SEQ ID No. 132 – Ken06.Bus MGF 360 14L

ATGCCATCTACTTTACAAGCACTTGCTAAAAAAGTACTGGCCACACCGCATATATCTAAAAAATATTGTCAGTCTAAGGAGTA
CTGTCATATATTAAAATGTTGTGGTTTATGGTGGCATGATGCTCCAATTACAATTTATCCTTGTATAAATAAAATATTGATAA
AAACAGCAAGCTTTAAACATGGTTTAGAGTTGAATGTCGCATTCATGAAAGCTGTACAGGAAAATAATTATGATCTAATAAGG
CTGTTTATTGAGTGGGGTGCGGATATCAACTTTGGGTTGGCCACTGTTAATACAGACCGTACCCGGGACCTGTGCCGGGAACT
AGGTGCGAAGGAAGCTTTAAGTGAAAAAGAAATTTTAGAAATATTTGATAAAATACAGTATATTAAAAGTAGCAGTAATATTA
TTGTATCCCATGAATTATTATCTAATAACCCCCTTTTCTTAAATAATGATCAATTGAAATTAAGAATGTTCGATGAACTACAT
AAACTATCAATCAACTTTGTATTACATGAGATATCATTTAATGAAATGCTAACTAGGTATTGGTATAGTATGGCGATACTATA
TAACCTCACCGCAGCCATTCAATATTTTTATCAATCCTACAAGCATTTTAAAGATTGGCGGTTAATATGTGGGCTTGCTTATA
ACAACGTGTTTGATCTTCATGAAATATATAACAAAGAGAAGGTTGATATGGATATTAATCAAATGATGCAGTTGGCCTGTATG
TATGATGGTAATTATACAACCATTTATTATTGTTTTATGTTGGGAGCTGACATTAATCGGGCAATGATTACCTCGGTTACAAA
ATCTTGTGATGGTAACTTATTCCTTTGTATAGATTTGGGGGCTGATGTATTTGAAGAGAGTATGAAAATGGCAATAGAAGATC
ATAATGACGTATTAGAAAGTATCTTATCATTTAAAAATTATTATAGTTCAGACGTTTCTCTGTTATCATTAAAGACGACAGAT
CCAGAAAAAATTAATGCCTTGTTAGAAGAAGAAAGTTACAAATCAAAAAATAGGTTGATATATAAAAGTTATTGA

SEQ ID No. 133 – Malawi Lil-20/1 (1983) MGF 360 14L

ATGATGCCATCTACTTTACAAACACTTGCTAAAAAAACATTGGCCACACAGCATATATCTAAAAAATATTGGCCGTCTGAGGA
GTATTGTTATATATTAAAATGTTGTGGTTTATGGTGGCATGATTCTCCAATCACGATTTTTACTTGTATAAAACAAATATTAA
TAAAAACAGCAAACTTTAAACATGGTTTAGACTTAAACCTTGCATTAATGAAAGCTGTACAAGAAAATAACTATGAATTGATC
ATGTTGTTTACTGAGTGGGGTGCGGATATCAACTTGGGGTTGATCACTGTTAATACAGAGTGCACCCGAGATTTGTGCCAAAA
GTTAGGTGCAAAGGAAGCTTTGAGTGCAAAGGAAATTTTAGAAATATTTTATAAAATACAGTATATTAAGAGTAGCAATAATA
TTATTATATCTCATGAATTAATATCTAATCATCCCCTTTTCCTAAATAATGATCAATTGAAATTAAGAATTGTTGGTGAACTA
AATGCTATATCAATCAACTTTATATTGGATGAGATATCATTCAATGAAATGCTAACTAGGTATTGGTATAGTATGGCGATACT
ATATAAACTCCCTGCAGCCATTCAATATTTTTATCAATCATACAAGTATTTTAAAGATTGGCGGTTAATATGTAGCCTTGCTT
ATAACAACGTGTTTGACCTTCATGAAATTTATAATAAAGAGAAGACTGATATAAACATTGATGAAATGATGCGGTTGGCCTGT
AGGTATGATGGTAATTATACAACTATTTATTATTGTTTTATGTTGGGGGCTGACATTAATCAGGCAATGATTACCTCGGTCAT

GAATCTTTGGGACGGTAACTTATTTCTTTGTATAGATTTGGGGGCTGATGTATTTGAAGAGTGTATGAAAATAGCAATAGAAG
ATCATAATGGTGTATTAGAAAGTATCTTATCATTTAAAAATTATTATAGTCCAGACGTTTCTCTGTTATCATTAAAAACGACA
GATCCGGAAAAAATTAATGACTTGCTAGATGAAGATATCTATAAATCAAAAAATAGGTTGATATATAAAAGTTGTTGA

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 360 21R. Suitably the functional version of MGF 360 21R comprises the sequence of SEQ ID No. 124, 125, 126, 127, 128, 129, 130, 131, 132 or 133. Suitably the functional version of MGF 360 21R comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 124, 125, 126, 127, 128, 129, 130, 131, 132 or 133. Suitably the functional version of MGF 360 21R consists of the sequence of SEQ ID No. 124, 125, 126, 127, 128, 129, 130, 131, 132 or 133.

MGF 505 1R gene sequences

SEQ ID No. 134 – Georgia 2007/1 MGF 505 1R (LR743116.1:28707-30302)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTAACCGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATACAGCAACATACCCTCATTC
CCGTAAATGAAGCCCTGAGAACAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTCATATTTCACAAATGCCATATCATGCGGCAATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTACTTTAAACATAGATTAGAGGATGATTTGCCCTTCACTCATTTACTT
ATTGAAAAGGCATGTAAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATATCTACAATATGATAGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACATCTATATTGTTTGGGGTATAGATTTATATATAACAGAATCGTACCCGATA
AGTATCATCATTTAGATATTCGCATGCTTTCAAGCCTACAACTCCTACATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATAAAGATAATATAAATATTATTCTAACACAAGCTGCAACCTATAACCATAGAAAAAT
TTTAATCTATTTCATTCCTCAATCAACCCACGCACAGATAGAACAATGTTTACTAGTGGCGATAAAAGCAAAATCTTCCAGGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAACCTCATCAAAAAAATAAGCCATTATGTTGCCACTTACAAT
TCAACAAATATAATAGGCATTCTGAGTATGCGGCGGAAAAAGAAGATATATTTAGATATCATATTGACAAAATTTGTAAAAAA
AGCTATTTTTAATAAGTTTGTCGTTCGATGTATGGATACATTTTCTATAAACCCGGAAAGAATCCTTAAAATAGCCGCGCGAA
TAAATAGGATGATGTTAGTGAAAAAAATATCTGAACATGTTTGGAAAAATCATGCGGTTAGACTTAAATACCTTAAACATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGATCGCTGTTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACCAATATCAACATC
GTGAACAAGTATATCGGCAACCTGTTTGTTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATTTATTC
TAAACAATACATGCCTTAG

SEQ ID No. 135 – China/2018/AnhuiXCGQ MGF 505 1R (MK128995.1:27736-29331)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTAACCGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATACAGCAACATACCCTCATTC
CCGTAAATGAAGCCCTGAGAACAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTCATATTTCACAAATGCCATATCATGCGGCAATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTACTTTAAACATAGATTAGAGGATGATTTGCCCTTCACTCATTTACTT
ATTGAAAAGGCATGTAAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATATCTACAATATGATAGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACATCTATATTGTTTGGGGTATAGATTTATATATAACAGAATCGTACCCGATA
AGTATCATCATTTAGATATTCGCATGCTTTCAAGCCTACAACTCCTACATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATAAAGATAATATAAATATTATTCTAACACAAGCTGCAACCTATAACCATAGAAAAAT
TTTAATCTATTTCATTCCTCAATCAACCCACGCACAGATAGAACAATGTTTACTAGTGGCGATAAAAGCAAAATCTTCCAGGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAACCTCATCAAAAAAATAAGCCATTATGTTGCCACTTACAAT
TCAACAAATATAATAGGCATTCTGAGTATGCGGCGGAAAAAGAAGATATATTTAGATATCATATTGACAAAATTTGTAAAAAA
AGCTATTTTTAATAAGTTTGTCGTTCGATGTATGGATACATTTTCTATAAACCCGGAAAGAATCCTTAAAATAGCCGCGCGAA
TAAATAGGATGATGTTAGTGAAAAAAATATCTGAACATGTTTGGAAAAATCATGCGGTTAGACTTAAATACCTTAAACATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGATCGCTGTTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACCAATATCAACATC
GTGAACAAGTATATCGGCAACCTGTTTGTTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATTTATTC
TAAACAATACATGCCTTAG

SEQ ID No. 136 – Tengani 62 MGF 505 1R (AY261364.1:22891-24486)

ATGTTCTCTCTTCAGAACCTATGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATACAGCAACATAACCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGAGTCTTTTATTAGCATGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAGTATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTAATATTTCACAAATGCCATATCATGCGGCAATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTCTTTTAAACATAGATTAAGGGATGATTTGCCCTTCACTCATTTACTT
ATTGAAAAGGCATGTAAAGATCATAATTATGAAGTAATTAAATGGATATATGAAAACCTACATATCTACAATATGATAGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACGTCTATATTGTTTGGGGTATAGATTTATATATAACAGGATCGTACCCGATA
AGTATCATCATTTAGATATTCGCATGCTTTCAAGCCTACAACTCCTGCATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATAAAGATAATATAAATATTATTCTAACACAAGCTGCAACCTATAACCATAGAAAAAT
TTTAATCTATTTCATTCCTCAATCAACCCACGCACAGATAGAACAATGTTTACTAGTGGCGATAAAAACAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAATCTCATCAAAAAAATAAGCCATTATGTTGCCACTTACAAT
TCAACAAATATAATAGGCATTCTGAGTATGCGGCGGAAAAAGAAGATATATTTAGATATCATATTGACAAAATTTGTAAAAAA
AGCTATTTTTAATAAATTTGTCGTTCGATGTATGGATACATTTTCTATAAACCCGGAAAGAATCCTTAAAATAGCCGCGCGAA
TAAATAGGACGATGTTAGTGAAAAAAATATCTGAACATGTTTGGAAAAATCATGCGGTTAGACTTAAATACCTTAAACATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGATCGCTGTTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACCAATATCAACATC
GTGAACAAGTATATCGGCAACCTGTTTGTTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATCTATTC
TAAACATTACATGCCTTAG

SEQ ID No. 137 – Warmbaths MGF 505 1R (AY261365.1:27651-29246)

ATGTTCTCTCTCCAGAACCTATGTCGAAAAACTTTACCTGACTGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATACAGCAACGTACCCTCATTC
CCGTAAATGAAGCCCTGAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGGGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGAGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTCATATTTCACAAATGCCATATAATCCGACGATGCTTTTTTAATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTACTTTAAACATAGATTAGAGGATGATTTGCCCCTCACTCATTTACTT
ATTGAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATACCTACGATATAATGGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACGTCTATATTGTTTGGGGTATACATTTATATATAACAGGATCGTACCCTATG
AGTATCATCATTTAGATATTCTCATTCTTTCAAGCCTACAACTCCTGCATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAACAATGATAATTTAGATATTATTCTAACACAAGCTGCAACATATAACCATAGAAAAAT
TTTAACCTATTTCATTCCTCAATTAACCTACGCACAAATAGAACAATGTTTGTTCATGGCGATAAAAAGAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAACCCTTTCCATCGAACTCATCAAAAAAATAAGCCAATATGTTGTCACTTACAAT
TCAACAAATATAATAGGCATTCTGAGTATGAAGCGGAAAAAGAAGATATATTTAGATATCATGTTGACAAAATATGTAAAATA
CGCTATTTTTAATAAATATGTCGTTCGATGTATGGATAGATTTTCCATAAACCCGGAAAGAATCATCAAAATGGCCGCGCGAA
TAAATAGGATGATGTTAGTGAAAAAAATATCTGAACATGTTTGGAAAAATCATGCGGCTAGACTTAAACACCTTAAGCATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGATCGCTGCTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTATCCTAG
ATACTATACAATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACCAATATCAACATC
GTGAACAAGTATATTGGCGACCTGTTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATCTATTC
TAAACATTACATGCTTTAG

SEQ ID No. 138 – Mkuzi 1979 MGF 505 1R (AY261362.1:29425-31020)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTGATTGTAAACTTCCTGAATTTTTTGACGATTATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGGGCAGGAAACAACTGTGTGCTTATACAGCAACATACCCTTATTC
CCATAAATGAAGCCCTGAGAACAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCATGGGAGGGGAATCTT
TACTATGCTATTATAGGGGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTAATATTTCACAAATGCCATATCATGCGGCGATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTATTTTAAATATAGGTTAGAGGATGATTTACCCCTCACTCATTTACTT
ATTGAAAAGGCATGTGAAAATCATAATTATGAAGTTATTAGATGGATATATGAAAACCTACATATCTACAATATGATAGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACGTCTATATTGTTTGGGGTATACATTTATATATAACAGGATCGTACCCAATA
AGTATCATCATATAGATATTCTCATTCTTTCAAGCCTACAACTCCTGCATAAGGTGGCAGCCAAAGGATACTTAGACTTTATC
CTAGAAACCTTAAAGTATGATCATAACAATGATAATTTAGATATTATTCTAACACAAGCTGCAACATATAACCATAGAAAAAT
TTTAACCTATTTTATTCCTCAATCAACCTACGCACAAATAGAACAATGTTTGATGGTGGCGATAAAAACAAAATCTTCCAAGA
AAACCTTGAATTTACTATTGTCCCACCTAAACCTTTCCATCAAACTCATCAAAAAAATAAGCCAATATGTTGTCACTTACAAT
TCAACAAATATAATAGGCATTCTGAGTATGAAGCGAAAAAAGAAGATATATTTAGATATCTTGTTGACAAAATTTGTAAAAAA
TGCTATTTTTAATAAATTTGTCGTTCGATATATGGATACGTTTTCTATAAACCCGGAAAAAATCGTCAAAATGGCCGCGCGAA
TAAATAAGATGATGTTAGTGAAAAAAATATCTGAACATATTTGGAAAAATCATGCGGCTAGACTTGAACACCTTAAACATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGAGTACTGCTATTACCATATGCAAGGGGA

AGAAATTTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTCGACGTTTTTTATAATTGTTGTATCCTAG
ATACGATACGATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACTAATATCAACATC
GTGAACAAGTATATTGACAACCTGTTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATTTATTC
TAAACATTATATGCCTTAG

SEQ ID No. 139 – Warthog MGF 505 1R (AY261366.1:24387-25982)

ATGTTTTCTCTCCAGAACTTGTGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATACAGCAACATACCCTCATTC
CCGTAAACGAAGCCCTGAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGAAACCTT
TACTATGCTATTATAGGAGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACGATCCAGTCATATTTCACAAATGCCATATCATGCGGCGATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTATTTTAAATATAGGTTAGAGAATGATTTGCCCCTCGCTCATTTACTT
ATTAAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATATCTACAATATAATGGATAC
CTTTGGATGTGCTATTGCCCATAAGGATCTACGTCTATATCGTTTGGGGTATACATTTATATATAACAGGATCGTACCCTATA
AGTATCATTATTTAGATGTTCTCATTCTTTCAGGCCTACATCTCCTGTATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAACAATGATAATTTAGATATTATTCTAACACAAGCTGCAACATATAACCATAGAAAAAT
TTTAACCTATTACATTCCTCAATTAACCTATGCACAAATAGAACAATGTTTGTTCATGGCGATTAAAAAAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAAGCTTTCCATCAAACTCATCAAAAAAATAAGCCAATATGTTGCCACTTACAAT
TCAACAAATATAATAGGCATTCTGAATATGCGGCGGAAAAAGAAGATATATTTAGATATCATATTGACAAAATTTGTAAAAAA
AGCTATTTTTAATAAATTTGTCGTTCGATGTATGGATACATTTTCCATAAACCCGGAAAGAATCATCAAAATGGCCGCGCGAA
TAAATAAGATGTTGTTAGTGAAAAAAATATCTGAACATGCTTGGAAAAATCATGCGGCTAGACTTAAACACCTTAAGCATGCG
GTATACACGATGAAACATAAAGATGGGAAAAATAGACTCATGAACTTGATCTATGATCACTACTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTCTCCTAG
ATACTATACGATTTAAAAACCTTCTTTTAGATTGTTCACACATCATAGGTAAAAACGCTCATGATGCTACTAATATCACTATC
GTGAACAAGTATATTGGCAACCTGTTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATCTATTC
TAAACATTACATGCCTTAG

SEQ ID No. 140 – L60 MGF 505 1R (NC_044941.1:22320-23915)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGATTATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGGGCAGGAAACAACTGTGTGCTTATACAACAACATACCCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGGGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGTAACCGCTACAACTTAATTCGTAAATATGATGATCAAATCAAGGACCATCATGA
CATTCTGCCATTCATTGATGATCCAATCATATTTCACAAATGCCATATCATGCGGCGATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGTGTTCTTCTTTATTTTAAATATACATTAGAGGATGATTTGCCCCTCGTTCATTTACTT
ATTGAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATGTCTGCCATATAATAGATAC
CTTTGACTGTGCTATTGCCCATAAAGATCTACGTTTATATTGTTTGGGGTATACATTTATATACAACAGGATTGTACCCTATA
AGTATCATCATTTAGATATTCTCATACTTTCAAGCCTACAACTCCTACATAAGGTGGCGGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATATAGATAATTTAGATGTTATTCTAACACAAGCTGCAACATATAACCATAGAAAAAT
TTTAACCTATTTTATTCCTCAATCAACCTACGCACAAATAGAACAATGTTTGTTCGTGGCGATAAAAACAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAAACTCATCCAAAAAATCAGCCAATATGTTGCCACTTTCAAT

SEQ ID No. 141 – Benin 97/1 MGF 505 1R (NC_044956.1:21971-23566)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGATTATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGGGCAGGAAACAACTGTGTGCTTATACAACAACATACCCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGGGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGTAACCGCTACAACTTAATTCGTAAATATGATGATCAAATCAAGGACCATCATGA
CATTCTGCCATTCATTGATGATCCAATCATATTTCACAAATGCCATATCATGCGGCGATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGTGTTCTTCTTTATTTTAAATATACATTAGAGGATGATTTGCCCCTCGTTCATTTACTT
ATTGAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGATATATGAAAACCTACATGTCTGCCATATAATAGATAC
CTTTGACTGTGCTATTGCCCATAAAGATCTACGTTTATATTGTTTGGGGTATACATTTATATACAACAGGATTGTACCCTATA
AGTATCATCATTTAGATATTCTCATACTTTCAAGCCTACAACTCCTACATAAGGTGGCGGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATATAGATAATTTAGATGTTATTCTAACACAAGCTGCAACATATAACCATAGAAAAAT
TTTAACCTATTTTATTCCTCAATCAACCTACGCACAAATAGAACAATGTTTGTTCGTGGCGATAAAAACAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAAACTCATCCAAAAAATCAGCCAATATGTTGCCACTTTCAAT

TCAACAAATATAATAGGCATTCTGAGTATGAAGCGGAAAAAGAAGATATATTTGGATATCATATTGACAAAATTTGTAAAAAA
TGCTATTTTTAATAAATTTGTCGTTCGATGTATGGAGAGATTTTCTATAAACCCGGAAAGAATCGTCAAAATGGCTGCGCGTA
TAAATAAGATGATGTTAGTGAAAAAAATATCTGAACATGTTTGGAAAAATCATGCGGCTAGACTTAAACACCTTAAACATGCG
GTACACACGATGAAGCATAAAGATGGGAAAAATAGACTCATGAACTTTATCTATGAACACTGCTATTACCATATGCAAGGGGA
AGAAATTTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTCGACGTTTTTTATAATTGTTGTATCCTAG
ATACGATACGATTCAAAAGCCTTCTTTTAGATTGTTCACATATCATAGGTAAAAACGCTCATGATGCTACTAATATCAACATC
GTGAACAAGTATATTGGCAACCTGTTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATCTATTC
TAAACATTATATGCCTTAG

SEQ ID No. 142 – Pretorisuskop/96/4 MGF 505 1R (AY261363.1:28449-30044)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTGTACAACAACATACCCTCATTC
CCGTAAACGAAGCCCTGAGAATAGCAGCGTCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGAAACCTT
TACTATGCTATTATAGGAGCTCTAGAGGGCAACCGCCACGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTCATTGACAATCCAGTCATATTTCACAAATGCCATATAATGCGGCGATGCTTTTTTGATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGCGTTCTTCTTTATTTTAAATATAGGTTAGAGAATGATTTGCCCCTCGCTCATTTACTT
GTTGAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGTTATATGAAAACCTACATATCTACAATATAATGGAGAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACGTCTATATCGTTTGGGGTATACATTTATATATAACAGGATCGTACCCTATA
AGTATCATTATTTAGATGTTCTCATTCTTTCAGGCCTACATCTCCTGTATAAGGTGGCAGCCAAAGGATACTTAGATTTTATC
CTAGAAACCTTAAAGTATGATCATAACAATGATAATTTAGATATTATTCTAACACAAGCTGTAACATATAACCATAGAAAAAT
TTTAACCTATTACATTCCTCAATTAACCTATGCACAAATAGAACAATGTTTGTTCATGGCGATTAAAAAAAAATCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAAGCTTTCCATCAAACTCATCAAAAAAATAAGCCAATATGTTGCCACTTACAAT
TCAACAAATATAATAGGCATTCTGAATATGAAGCGGAAAAAGAAGATATATTTAGATATCATATTGACAAAATTTGTAAAATA
CGCTATTTTTAATAAATATGTCGTTCGTTGTATGGATACATTTTCCATAAACCCGGAAAGAATCATCAAAATGGCCGCGCGAA
TAAATAAGATGTTGTTAGTGAAAAAAATATCTCAACATGCTTGGAAAAATCATGCGGCTAGACTTAAACACCTTAAGCATGCG
GTATACACGATGAAACATAAAGATGGGAAAAATAGACTCATGAACTTGATCTATGATCACTACTATTACCATATGCAAGGGGA
AGAAATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCACCAAAGTTGTTTGACGTTTTTTATGATTGTTGTCTCCTAG
ATACTATACGATTTAAAAGCCTTCTTTTAGATTGTTCACACATCATAGGTAAAAACGCTCATGATGCTACTAATATCACTATC
GTGAACAAGTATATTGGCAACCTGTTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCCATCTATTC
TAAACATTACATGCCTTAG

SEQ ID No. 143 – Kenya 1950 MGF 505 1R (AY261360.1:31904-33496)

ATGTTTTCTCTCCAGAACTTATGTCGAAAAACCTTACCTGACCGTAAACTTCCTGAATTTTTTGACGATTATGTATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACGATTCAACGAGCAGGAAACAACTGTGTACTTATCCAACAACATAACCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCTTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGTAATCGCCACAACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTTATTGACGATCCAGTCATATTTCACAAATGTCATATGATGCGGCGATGCTTTTTTAATTGTATTTTGTATC
AAGCTGTAAAATATAGTAAGTTTAGCGTTCTTCTATATTTTAAATATATATTAAAGGAGAATTTGCCCCTCGTTCATTCACTT
ATTGAAAAGGCGTGTGAAGATCATAATTATGAAGTTATTAAATGGATCTATGAAAACCTACATATCTATGAAATAATGGATAC
CTTTAAATGTGCTATTGCCCATAAAGATCTACATTTATATAGTTTAGGATATACATTTATATATAATAGGATCGTACCCTATA
AGTATCATCATTTAGATATTCGCATACTTTCAAGGCTACAACTTCTACATAAGGTGACAGCCAAAGGATACTTGGACTTTATC
CTAGAAACCTTAAAGTATGATCATAATAAAGATAATATAAATATTATTCTGACACAAGCTGCAACCTATAACCATAGAAACAT
TTTAACCTATTTCATTCCTCAATCAACCTACGCGCAGATAGAACAATGCTTATTCGTGGCAATAAAAACAAACGCTTCCAAGA
AAACCTTGAATTTACTATTATCTCACCTAAACCTTTCTATCAAACTCGTCAAAAAATTAAGCCAATATGTTGTTGCTTACAAG
TCAACAAATATCATAAGCATTCTGAGTATGCAGCAAAAAAAGAAGATATATTTAGATATCATTTTGACAAAGGTTGTAAAAAA
CGCTATTTTTATTAAATTTGTCATTGGATGTATGGTTACATTTTCCATAAACCCAGAAAGAATTGTCAAAATGGCCGCGCGAA
TAAAAAAGATGAAGTTAGTGAAAAATATATCTGAACATGTTTGGAAAAATCATGCGGCTAAACTTAAACACCTTAAGCATGCG
GTACACACGATGAAGCATCAAGAAGGAAAAAATAGATTAATGAACTTTATCTATGATCACTGTTATTACCACATGCAAGGAGA
AGAGATCTTTAGTCTTGCAAGATTTTATGCAATCCATCATGCGCCAAAATTGTTCGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTTAAAAGCCTGCTTTTAGATTGTTCATATATCATAGCTAAAAACGCTCATGATGCTAGTATTAACATCGTG
AATAAGTATATTGGCAATCTATTTGCTATGGGGGTTCTTAGCAAAAAAGAAATCTTACAAGACTATCCATCCATCTATTCTAA
GGATTACATGCTTTAG

SEQ ID No. 144 – Ken06.Bus MGF 505 1R (NC_044946.1:25784-27376)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACCTTACCTGACTGTAAACTTCCTGAGTTTTTTGACGATTATGTATTACAACT
GCTGGGCTTATACTGGGAAAATCATGGTACGATTCAACGAGCAGGAAACAACTGTGTACTTATCCAACAACATAACCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAGGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGGAACCACCACAACTTAATTCGTAAATACGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTTATTGACGATCCAGTCATATTTCACAAATGTCATACAATGCGGCGATGCTTTTTTAATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTCAGCGTTCTTCTATACTTTAAATATATATTAAAGGAGAATTTGCCCCTCGTCCACTCACTT
ATTGAAAAGGCGTATAAATATCATAATTATGAGGTTATTAAATGGATCTATGAAAACCTACATATCTATGATATCATAAATAC
TTTTAAATGTGCTATTGCCCATAAAGATCTACGTTTATATTGTTTAGGGTATACATTTGTATATAATAGAATCGTACCCTATA

AGTATTATCATTTAGATATTCGCATCCTTTTAAGGCTACAACTTCTACATAAGGTGACAGCCAAAGGATACTTGGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATACAAACAATATAGATATTATCCTAACACAGGCTGCAACCTATAACCATAGAAACAT
TTTAACCTATTTCATTCCTCAATCAACCTACGCACAAATAGAACAATGTTTATTCGTGGCGATAAAAACAAATGCTTCCAAGA
AAACCTTGAATTTACTATTATCTCACCTAAATCTTTCTATCAAACTCGTCAAAAAATTAAGCCAATATGTTGTCGCTTACAAG
TCAACAAATATCATAAGCATTCTGAGTAGGCAGCAAAAAAAGAAGATATATTTAGATATCATTTTGACAAAGGTTGTAAAAAA
TGCTGTTTTTAATAAATTTGTCATTGGATGTATGGTTACATTTTCCATAAACCCAGAAAGAATTGTCAAAATGGCCGCGCGAA
TAAAAAAGATGAAGTTAGTAAAAAATATATCTGAACATGTTTGGAAAAATCATGCGGTTAAACTTAAATATCTTAAGCATGCG
GTACACACGATGAAGCATCAAGAAGGAAAAAATAGATTAATGAACTTTATCTATGATCACTGTTATTACCACATGCAAGAAGA
AGAGATCTTTAGCCTCGCAAGATTTTATGCAATCCATCATGCGCCAAAATTGTTCGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTTAAAAGCCTGCTTTTAGATTGTTCACATATCATAGTTAAAAACGCTCATGATGCTAGTATTAACATCGTG
AACAAGTATATTGGCAATCTATTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAAGACTATCCATCTATCTATTCTAA
GGATTACATGCTTTAG

SEQ ID No. 145 – Ken05/Tk1 MGF 505 1R (NC_044945.1:29657-31249)

ATGTTCTCTCTCCAAAACTTATGTCGAAAAACCTTACCTGACTGTAAACTTCCTGAATTTTTTGACGATTATGTATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACGATTCAACGAGCAGGAAACAACTGTGTACTTATCCAACAACATAACCTCATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGGAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGTAACCGCCACAACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTCTGCCATTTATTGACGATCCAGTTATATTTCACAAATGTCATATAATGCGGCGATGCTTTTTTAATTGTATGTTGTATC
AAGCTGTAAAATATAGTAAGTTTAGCGTTCTTCTATATTTTAAATATATATTAAAGGAAAATTTGCCCCTCGTCCACTCACTC
ATTGAAAAAGCGTATAAATATCATAATTATGAGGTTATTAAATGGATCTATGAAAATCTACATATCTATGATATCATAAATAC
TTTTAAATATGCTATTGCCCATAAAGATCTACGTTTATATTGTTTAGGGTATACATTTGTATATAATAGGATCGTACCCTATA
AGTATTATCATTTAGATATTCGCATCCTTTTAAGGCTACAACTTCTACATAAGGTGACAGCCAAAGGATACTTGGATTTTATC
CTAGAAACCTTAAAGTATGATCATAATACAAACAATATAGATATTATCCTAACACAGGCTGCAACCTATAACCATAGAAACAT
TTTAACCTATTTCATTCCTCAATCAACCTACGCACAAATAGAACAATGCTTATTCGTGGCAATAAAAACAAACGCTTCCAAAA
AAACCTTGAATTTACTATTATCTCACCTAAACCTTTCTATCAAACTCGTCAAAAAATTAAGCCAATATGTTGTCGCTTACAAG
TCAACAAATATCATAAGCATTCTGAGTATGCAGCAAAAAAAGAAGATATATTTAGATATCATTTTGACAAAGGTTGTAAAAAA
CGCTGTTTTTATTAAATTTGTCATTGGATGTATGGTTACATTTTCCATAAACCCAGAAAGAATTGTCAAAATGGCCGCGCGAA
TAAAAAAGATGAAGTTAGTAAAAAATATATCTGAACATGTTTGGAAAAATCATGCGGCTAAACTTAAACATCTTAAGCATGCG
GTACACACGATGAAGCATCAAGAAGGAAAAAATAGACTCATGAACTTTATCTATGATCACTGCTATTACCACATGCAAGGAGA
AGAGATCTTTAGTCTTGCAAGATTTTATGCAATCCATCATGCGCCAAAATTGTTCGACGTTTTTTATGATTGTTGTATCCTAG
ATACGATACGATTTAAAAGCCTGCTTTTAGATTGTTCACATATTATAGCTAAAAACGCTCATGATGCTAGTATTAACATCGTG
AATAAGTATATTGGCAATCTATTTGCTATGGGAGTTCTTAGCAAAAAAGAAATCTTACAAGACTATCCATCCATCTATTCTAA
ATATGACATACTTTAG

SEQ ID No. 146 – Malawi Lil-20/1 (1983) MGF 505 1R (AY261361.1:26041-27633)

ATGTTCTCTCTCCAGAACTTATGTCGAAAAACATTACCTGACTGTAAACTTCCTGAATTTTTTGACGAATATATATTACAACT
GCTGGGATTATACTGGGAAAACCATGGAACTATTCAACGAGCAGGAAACAACTGTGTGCTTATCCAGCAACATAACCTTATTC
CCGTAAATGAAGCCCTAAGAATAGCAGCATCTGAAGAAAATTATGAGATCGTGAGCCTTTTATTAGCGTGGGAGGGAAACCTT
TACTATGCTATTATAGGGGCTCTAGAGGGCAACCGCCCCGACTTAATTCGTAAATATGATGACCAAATCAAGGACCATCATGA
AATTTTGCCATTCATCGACGATCCAATCATATTTCACAAATGTCACATAATGCGGCGATGCTTTTTTAATTGTATTTTATATC
AAGCTGTAAAATATAGTAAGTTTCGTGTTCTTCTTTATTTTAAACATAGGTTAGGGGATGATTTGCCCCTCACTCATTTACTT
ATTGAAAAGGCATGTGAAGATCATAATTATGAAGTTATTAAATGGATCTATGAAAACCTACATAGCTACAATATAATGGATAC
CTTTGAATGTGCTATTGCCCATAAGGATCTACGTCTATATTGTTTGGGGTATACATTTATATATAATAGGATCGTACCCTATA
AGTATCATCATTTAGATATTTGCATACTTTCAAGCCTACAACTCCTGCATAAGGTGGCAGCCAAAGGATACTTGGATTTTATC
CTAGAAACCTTAAAGTATGATCATAACATAAATAATATAGATATTATTCTAACACAAGCTGCAACCTATAACCATAGAAAAAT
TTTAACCTATTTCATTCCTCAATTAACCTACGCACAGATAGAACAATGTTTACTAGTGGCGATAAAAACAAAAGCTTCCAAGA
AAACCTTGAACTTACTACTGTCTCACCTAAACCTTTCCATCAAACTCATCAAAAAAATAAGCCAATATGTTGTCACTTACAAT
TCAACAAATATCATAAGCATTCTGAGTATGCGGCGGAAAAAGAAGATATATTTAGATATCATTTTGACAGAGTTTGTAAAAAA
CGCTATTTTTAATAAATTTGTCGTTCGATGTATGGATACATTTTCCATAAACCCGGAAAGAATTGTCAAAATGGCCGCACGAA
TAAATAGGATGATGTTAGTGAAAAATATATCTGAACGTGTTTGGAAAAATCATGCGGTTAAACTTAAACACCTTAAGCATGCG
GTACATACGATGAAGCATCAAGAAGGAAAAAATAGACTCATGAACTTTATCTATGATCACTGCTATTACCACATGCAAGGGGA
AGAGATCTTTGGCCTCGCAAGATTTTATGCAATCCATCATGCACCCAAGTTGTTTGACGTTTTTTATGATTGCTGCATGCTAG
ATGCTACACGATTTAAAAGCCTGCTTTTAGATTGTCCACATATCATAGGTAAAAACGCTTATGATGCTGGTATCAACCTCGTG
AACAAATATATTGGCAACCTATTTGCTATGGGGGTTCTTAGCAAAAAAGAAATCTTACAGGACTATCCATCTATCTATTCTAA
ACATGATATGTTTTAG

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 505 1R. Suitably the functional version of MGF 505 1R comprises the sequence of SEQ ID No. 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145 or 146. Suitably the functional version of MGF 505 1R comprises a sequence having at least 70%, at least 80%,

at least 90% or at least 95% identity with SEQ ID No. 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145 or 146. Suitably the functional version of MGF 505 1R consists of the sequence of SEQ ID No. 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145 or 146.

MGF 505 2R gene sequences

SEQ ID No. 147 – Georgia 2007/1 MGF 505 2R (NC_044959.1:33119-34699)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCATAGGAGACGACCACATACTCATACGACGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCTTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATTTTATCTT
ACCATTGATTCAAGACGCGAATACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATGAGAGCGTATCTTCACGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAAACCATACATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCAAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGCAAC
ATAGATACCGTCCTGACCCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAACTTTTGTTGCTGGCCGTGCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTACCGCGCTATGTGATAGAGTACGAGTCCACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTGAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGTCTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGGGAAAAAGTCATGTTTTATTTAGCCAAGCTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TATTAGACTGTTTAGAAATTATTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTGTTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAAAACAATACAATG
TTAA

SEQ ID No. 148 – China/2018/AnhuiXCGQ MGF 505 2R

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCATAGGAGACGACCACATACTCATACGACGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCTTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATTTTATCTT
ACCATTGATTCAAGACGCGAATACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATGAGAGCGTATCTTCACGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAAACCATACATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCAAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGCAAC
ATAGATACCGTCCTGACCCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAACTTTTGTTGCTGGCCGTGCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTACCGCGCTATGTGATAGAGTACGAGTCCACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTGAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGTCTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGGGAAAAAGTCATGTTTTATTTAGCCAAGCTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TATTAGACTGTTTAGAAATTATTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTGTTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAAAACAATACAATG
TTAA

SEQ ID No. 149 – Mkuzi 1979 MGF 505 2R (AY261362.1:34826-36406)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCATAGGAGACGACCACATACTCATACGACGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCTTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATTTTATCTT
ACCATTGATTCAAGACGCGAATACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATGAGAGCGTATCTTCACGAAACCCTATTT

GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAGACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGCAAC
ATAGATACCGTCCTGACCCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAACTTTTGTTGCTGGCTGTTCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTATGAGTCCACCTTGGTGATAAAGATTTTGTTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACAAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGTTTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGGGAAAAAGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
TGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TATTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTATTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAAAACAATACAATG
TTAA

SEQ ID No. 150 – L60 MGF 505 2R (NC_044941.1:27701-29281)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCATAGGAGACGACCACATACTCATACGACGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCCTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATTTTATCTT
ACCATTGATTCAAGACGCGAATACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATGAGAGCGTATCTTCACGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAGACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGCAAC
ATAGATACCGTCCTGACCCAAGCCGTAAAGTACAACCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAGCTTTTGTTGCTGGCTGTTCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTATGAGTCCACCTTGGTGATAAAGATTTTGTTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGTCTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGGGAAAAAGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
TGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TATTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTATTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAAAACAATACAATG
TTAA

SEQ ID No. 151 – Benin 97/1 MGF 505 2R (NC_044956.1:27352-28932)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCATAGGAGACGACCACATACTCATACGACGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCCTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATTTTATCTT
ACCATTGATTCAAGACGCGAATACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATGAGAGCGTATCTTCACGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAGACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGCAAC
ATAGATACCGTCCTGACCCAAGCCGTAAAGTACAACCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAGCTTTTGTTGCTGGCTGTTCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTATGAGTCCACCTTGGTGATAAAGATTTTGTTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGTCTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGGGAAAAAGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
TGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TATTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTATTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAAAACAATACAATG
TTAA

SEQ ID No. 152 – Tengani 62 MGF 505 2R (AY261364.1:28261-29830)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCGTAGGAGACGACCACATACTCATACGGCGGGATCTCATCCTTTCCACCA

ACGAGGCCTTAAGAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCGTCATAGGAGCCTTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATCTTATCTT
ACCATTGATTCAAGACGCGAAAACGTTTGAAAAATGCCATGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTGTTCTCCAAAAATACCAAGAAGAGCTGTCCATGAGAGCATATCTTTGCGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAAACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACTATGTACTCCTTAGGATATATTTTCCTTTTTGATAGAGGGAACACCGAAGCTA
CGTTGCTAACGCAATATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
ATAGATATTGTCCTGACCCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAGCTTTTGTTGCTGGCCGTGCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCCACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTT
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTATGGGAGG
ATGATCTAGAACGACTTACTCGTCTTAAAGATATGGTATACACCGTAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATACACGGCATATACAAAAACTTATTATACGGCGAAAAAGAAAAGGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TGTTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTATAGTATTCTGGAAATCTTAGAAAAACATATGATTTCCCTATTT
ACTATGAAAGTTATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAGTAA

SEQ ID No. 153 – Pretorisuskop/96/4 MGF 505 2R (AY261363.1:33795-35374)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCGTAGGAGACGACCACATCCTCATACGGCGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAAGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCATCATAGGAGCCTTGCAGGGTGATCAATATGACCTGATCCATAAGTATGAAAACCAAATCGGCGACTTTCATCTTATCTT
ACCATTGATTCAAGATGCGAAAACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAGAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAACATACCAAGAAGAGCTGTCTATGAGAGCATATCTTCGCGAAACCCTATTT
GAACTAGCGTGCCTGTGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAAACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTGACGATGTATTCCTTAGGATATATTCTTCTTTTTGATAGAGAGAACACCGAAGCTA
CGTTGTTAACACAACATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCTACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
ATAGATATCGTCCTGACTCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAACA
TATTGAAAAGCTTTTGTTGCTGGCCGTGCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCCCATCTAAACTACT
CCGTGAAACGTATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCCACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTT
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACGGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGACTTACTCGTCTTAAAAATATGGTATACACCATAAAGTACGAACATGGGAAAAAAATGTTAATTAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGACGAAAGAGAAAAGGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAACCGCGGTTTAAGCAACTAA
TGTTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTATAGTATCCTGGAAATCTTAGAAAAACATATTATTTCCCTATTT
ACTATGAAAGTTATGACTGAAGAGGAAAAAAACCTATGTTTAGAAATATTATATAAGTAA

SEQ ID No. 154 – Warmbaths MGF 505 2R (AY261365.1:33029-34597)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTATTACAACGATTAGG
ACTGTATTGGAGATGTCACGGCTCCCTTCAACGCGTAGGAGACGACCACATACTCATACGGCGGGATCTCATCCTTTCCACCA
ACGAGGCCTTAAGAATGGCGGGAGAAGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAC
GCCATCATAGGAGCCTTGCAGGGTGATCAATATGACCTAATCCATAAGTATGAAAACCAAATCGGCGACTTTCATCTTATCTT
ACCATTGATTCAAGATGCGAAAACGTTTGAAAAATGCCACGCTTTAGAACGTTTTTGTGGTGTTTCATGTCTGCTAAAACATG
CTACAAAATACAACATGCTCCCTATTCTCCAAACATACCAAGAAGAGCTGTCTATGAGAGTATATCTTCGCGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATGTCCTTAAATGGATAGAGCAAACCATGCATGTTTACGACCTAAAGGTTATGTT
TAATATTGCCATCTCCAAGAGAGATCTGACTATGTATTCCTTAGGATATATTCTTCTTTTTGATAGAGAGAACACCGAAGCTA
CGTTGCTAACGCAACATCTCGAGAAAACAGCGGCCAAGGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
ATAGATATCGTCCTGTCCCAAGCCGTAAAGTACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAAAA
TATTGAAAAACTTTTGTTGCTGGCTGTTCAGGAAAAGGCTTCTAAAAAAACATTGAACTTACTGTTGTCCCATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCCACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTAAACCTGATAGATGCCATGTTGGAAAAGATGGTAAGATATTTTTCTGCGACGAAAGTGAGGACGATCATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCTATACAGAAAATGAGAACAGATATCGTAATCCATACTTCTTATGTTTGGGAGG
ATGATCTAGAACGACTTACTCGTCTTAAAAATATGGTATACGCCATAAAGTATGAACATGGGAAAAAAATGTTAATGAAAGTC
ATGCACGGCATATACAAAAACTTATTATACGGCGAAAGAGAAAAGGTCATGTTTCATTTAGCCAAGCTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAGGACTGTTACAAACTGGATGTGGCACGGTTTAAGCAACTAACGTTAAACTGTT
TAGAAATTATTACTAAAAAATCTTGCTATAGTATCCTGGAAATCCTAGAAAAACATATTATTTCCCTATTTACTATGAAAGTT
ATGACTGAAGAAGAAAAAAACCTATGTTTAGAAATATTATATAAAGTAATTCATTATAATACAATACAATGTTAA

SEQ ID No. 155 – Malawi Lil-20/1 (1983) MGF 505 2R (AY261361.1:31541-33121)

ATGTTTTCCCTTCAAGATCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACAGTTAGG
ACTGTACTGGAAACGTCACGGCTCTCTTCAACGCATAGGAGACGACCACATACTCATACGGCGGGACCTCATCCTTTCCACCA
ACGAGGCCTTAAAAATGGCGGGAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGGAGGGAAACCTTCATTAT
GCCATCATAGGGGCCTTACAGGGTGATCAATATGATCTGATCCATAAGTATGAAAACCAAATCGAAGACTATCATCATATCTT
GCCATTGATTCAAGATGCGAAAACGTTTGAAAAATGCCACGCCTTAGAACGTTTTTGTGATGTTCCATGTCTGCTAGAACATG
CTACAAAACACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTCTATAAGAGTGTATCTTCGCGAAACCCTATTC
GAACTAGCATGCCTATGGCAGAGGTATGATGTTCTTAAATGGATAGAGCAAACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTAAGCATGTACTCCTTAGGATATGTTCTCCTTTTTGATAGAGGAAACATCGAAGCTA
CGTTCCTAACGCAACATCTCGAGAAGACAGCGGCCAAAGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
TTAAATATCGTCCTGTCCCAAGCCGTAAAATACAATCATAGAAAACTTTTGGATTATTTTCTGCGTCAACTACCTCGTAAAAA
TATTGAAAAACTTTTGTTGCTGGCCGTGCAGGAAAAGGCTTCTAAAAAAACATTGAACCTACTGTTGTCACACTTAAACTACT
CCGTGAAACACATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCTACCTTGGTGATAAAACTTTTATTGAAAAAAAGA
GTAAACCTGATAGACGCCGTGTTGGAAAAGAATGTAAGATATTTTTCTGCGATTAAAGTGAGGACTATTATGGATGAGCTTTC
GATTAGTCCGGAAAGAGTCATTAAGATGGCCATACAGAAAATGAGAACGGATATTGTGATTCAGACTTCTTATATTTGGGAGG
ATGATCTAGAAAGACTTATTCGTCTTAAAAATATGGTATACACCATAAAGTATGAACATGGGAAAAAAATGTTAATTAAAGTT
ATTCACGGCATATACAAAAACTTATTATACGGCGAAAAAGAAAAAGTCATGTTTCATTTAGCCAAACTCTATGTTGCTCAAAA
CGCGGCCACCCAATTCAGGGACATTTGTAAGGACTGTTGCAAACTGGATGTGGCGCGGTTTAAACCGCGGTTTAAACAACTAA
TTTTAGACTGTTTAGAAATGGTTACTAAAAAATCTTGCTTTAGTATTATAGAAATCTTAGAAAACTATATTATTTCCCTATTT
GTGATGAAAGTCATCACTGAAGAAGAAAAAAACCTATGTTTAGAACTATTATATAAAGTAATTAGTTACAAAACGATATAATG
TTAA

SEQ ID No. 156 – Ken05/Tk1 MGF 505 2R (NC_044945.1:35094-36674)

ATGTTTTCCCTTCAAGACCATTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACGGTTAGG
ACTGTACTGGGGACGTCACGGCTCTCTTCAACGAATCGGGGACGATCACATACTCATACGGCGGGACCTCATCCTTTCCACCA
ACGAGGCCTTAAAAATGGCGGGAGAAGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGGAGGGAAATCTTCATTAT
GCTATCATAGGGGCTTTACAGGGTGATCAATATGACCTAATCCATAAGTATGAAAACCAAATCGAAGACTATCATCATATCTT
ACCATTGATTCAAGATGCGGAAACGTTTGAAAAATGCCACGCCTTAGAACGTTTTTGTGATGTTCCATGTCTGCTAGAACATG
CTACAAAACACAACATGCTCCCTATTCTCCAAAAATATCAAGAAGAGTTGTCTATAAGAGTGTATCTACGCGAAACCCTATTC
GAACTAGCATGCCTATGGCAGAGGTATGATATTCTTAAATGGATAGAGCAAACCATGCATGTTTACGATCTAAAAATTATATT
TAATATTGCCATCTCCAAGAGGGATCTAAGCATGTACTCCTTAGGATATGTTCTCCTTTTTGATAGAGGGAACACCGAAGCTA
CCTTGTTAACGCAACACCTCGAGAAGACAGCGGCCAAGGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
TTAAATATCGTCCTGTTCCAAGCCGTAAAATACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACCCCGTAAAAA
TATTGAAAAACTTTTGTTGCTGGCTGTGCAGGAAAAAGCTTCTAAGAAAACATTGAACTTACTGTTGTCACATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCTACCTTGGTGATAAAGATTTTATTAAAAAAAAGA
GTAAACCTAATAGACGCCGTGTTGGAAAAGACTGTAAGATATTTTTCTGAGACGAAAGTAAAGACTATTATGGATGAGCTTTC
GATTAATCCGGAAAAAGTCATTAAGATGGCCATACAGAAAATGAGAACGGATATTGTGATCCAAACTTCTTATATTTGGGAGG
ATGATCTAGAAAGACTTATTCGTCTTAAAAATATGGTATACACCATAAAGTATGAACATGGGAAAAAAATGTTAATGAAAGTT
ATTCACGGCATATACAAAAACTTATTACACGATGAAAAAGAAAAAGTCATGTTTCATTTAGCCAAGTTCTATATTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAAGACTGTTGCAAACTGGATGTGGCGCGGTTTAAACCGCGGTTTAAACAACTAA
TTTTAGACTGTTTAGAAATTGTTACTAAAAAATCTTGCTTTAGTATTATAGAAATTTTAGAAAACCATATTATTTCCCTATTT
ATGATGAAAGTTATCACTGAAGATGAAAAAAACCTAGGTTTAGAATTATTATATAAAGTAATTAGTTACAAAATGATATCATA
TTAA

SEQ ID No. 157 – Kenya 1950 MGF 505 2R (AY261360.1:37419-38999)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCACGTACTACAACAATTGGG
GCTGTACTGGGAAAAACACGGCTCTCTTCAACGAATAGGGAACGATCACATACTCATACGGCGGGATCTCATCCTTTCTATCA
ACGAGGCCTTAAAAATAGCGGCAGAGGAAGGAAACAATGAAGTAGTAAAGCTTTTGTTACTATGGAAGGGAAATCTTCATTAT
GCCATCATAGGAGCTTTGGAGGGTGACCAATATGACCTGATCTATACGTATGAAAACCAAATTGAAGACTATCATCATATCTT
GCCATTGATTCAAGATGCGAAAACGTTTGAAAAATGCCACGCCTTGGAACGTTTTTGTGATGTTCCATGCCTGCTAGAGCATG
CTATAAAACACAACATGCTCCCTATTCTCCAAAAATATCAAGAAGAACTGTTTATAAGAGTGTATCTCCGCGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATATTCTTAAATGGATAGAGCAAACCATGCATGTTTACGATCTAAAAATTATATT
TAATATTGCCATCTCCAAGAGGGATCTAAGCATGTACTCCTTAGGATATGTTCTCCTTTTTGATAGAGGGAACACCGAAGCTA
CCTTGTTAACGCAACACCTCGAGAAGACAGCGGCCAAGGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATACGGCGGTAAC
ATAAACATCGTCCTATCCCAAGCCGTAAAATACAATCATAGGAAACTTTTAGATTATTTTCTGCGTCAACTACCTCGTAAAAA
TATTGAAAAACTTTTGTTGTTAGCCGTACAGGAAAAGGCTTCTAAGAAAACATTGAACTTACTGTTGTCTTATTTAAACTACT
CCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGTACGAGTCCACACTGGTGATAAGGATTTTATTAAAAAAAAGA
ATAAACCTAATAGACGCCGTGTTGGAAAAGACTGTAAGATATTTTTCTGAGACGAAAGTAAAGACTATTATGGATGAGCTTTC
GATTAATCCGGAAAAAGTTATTAAGATGGCCATACAGAAAATGAGAACGGATATTGTGATCCAAACTTCTTATATTTGGGAGG
ATGATCTAGAAAGACTTATTCGTCTTAAAAATATGGTATACACCATAAAGTATGAACATGGGAAAAAAATGTTAATGAAAGTT
ATTCACGGCATATACAAAAACTTATTACACGATGAAAAAGAAAAAGTCATGTTTCATTTAGCCAAGTTCTATATTGCTCAAAA
CGCGGCCACCCAATTCAGAGACATTTGTAAAGACTGTTGCAAACTGGATGTGGCGCGGTTTAAACCGCGGTTTAAACAACTAA
TTTTAGACTGTTTAGATATTATTACTAAAAAAACGTGCCTCAATATTATGGAAATCTTAGAAAATCATATTATTTCGCTATTT
GCTATGAAAATGATGACTGAAGATGAAAAAAACCTAGGTTTAGAATTATTATATAAAGTAATTAGTTACAAAATGATATCATA
TTAA

SEQ ID No. 158 – Ken06.Bus MGF 505 2R (NC_044946.1:31225-32799)

ATGTTTTCCCTTCAAGACCTTTGCCGAAAGCATCTTTTTATTCTTCCCGATGTTTTTGGCGAGCATGTACTACAACAATTGGG
GCTGTACTGGGAAAAACACGGCTCTCTTCAACGAATAGGGAACGATCACATACTCATACGGCGGGATCTCATCCTTTCTATCA
ACGAGGCCTTAAAAATAGCGGCAGAGGAAGGAAACAATGAAGTAGTAAAGCTCTTGTTACTGTGGAAGGGAAATCTTCATTAT
GCCATCATAGGAGCCTTGCAGGGTGACCAATATGACCTCATCCATACGTACGAAAACCAAATCGAAGACTATCATCATATCTT
GCCATTGATTCAAGATGCGAAAACGTTTGAAAAATGCCACGCCTTGGAACGTTTTTGTGATGTTCCATGCCTACTAGAACATG
CTACAAAACACAACATGCTCCCTATTCTCCAAAAATACCAAGAAGAGCTGTTTATAAGAGTGTATCTCCGCGAAACCCTATTT
GAACTAGCATGCCTATGGCAGAGGTATGATATCCTTAAATGGATAGAGCAAACCATGCATGTTTACGACCTAAAGATTATGTT
TAATATTGCCATCTCCAAGAGGGATCTAAGCATGTACTCTTTAGAATATATTCTCTTTTTTAATAGAGGGAACACCGATGTTG
CGTTAGCAACGTTGCTAACGCAACATCTCGAGAAGACAGCGGCCAAGGGGCTCCTCCACTTTGTGCTAGAAACGTTAAAATAC
GGCGGTAACATAAACATCGTCCTCTCCCAAGCCGTAAAATACAATCATAGAAAACTTTTAGATTATTTTCTGCGTCAACTACC
TCGTAAAAATATTGAAAAACTTTTGTTGCTGGCCGTACAGGAAAGGGCTTCTAAGAAAACATTGAACTTACTGTTGTCTTATT
TAAACTACTCCGTGAAACGCATCAAAAAACTGCTGCGCTATGTGATAGAGCATGAGTCCACACTGGTGATAAGGATTTTATTA
AAAAAAAGAATAAACCTAATAGACGCCGTGTTGGAAAAGACTGTAAGATATTTTTCTATGACTAAAGTGAGGACGATCATGGA
TGAGCTTTCGATTAATCCGGAAAAAGTCATTAAAATGGCCGTGCAGAAAATGAGAACGGATATCGTGATCCATACTTCTTATG
TTTGGGAGGATGATCTAGAAAGACTTATTCGTCTTAAAAATATGCTATACACTATAAAGTATGAGCATGGAAAAAAAATGCTA
ATTAAAGTCATTCACGGCATATACAAAAACTTATACGGCGAAAAAGAAAAAGTCATGTTTAATTTGGCCAAGTTCTATGCTGC
TCAAAACGCGGCCACCCAATTCAAAGACACTTGTAAAGACTGTTGCAAACTGGATGTGGCGCGGTTTAAACAACTAATTTTAG
ACTGTTTAGACATTATTACTAAAAAAACGTGCCTCAGTATCATGGAAATCTTAGAAAATCATATTATTTCGCTATTTGCTATG
AAAATGATGACGGAGGATGAAAAAAACTTAGGTTTAGAAATATTATATAAAGTAATTAGTTACAAAATGATATCATATTAA

In an embodiment the attenuated ASFV of the invention comprises a functional version of MGF 505 2R. Suitably the functional version of MGF 505 2R comprises the sequence of SEQ ID No. 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157 or 158. Suitably the functional version of MGF 505 2R comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157 or 158. Suitably the functional version of MGF 505 2R consists of the sequence of SEQ ID No. 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157 or 158.

MGF 505 6R gene sequences

SEQ ID No. 257 – Benin 97/1 MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACACTTTCTTCCTTCCAAATGATTTTAGCAAGCATACTCTACAACGGCTGGG
GTTGTATTGGAAAGAGCATGGATCCGTCCATCGAATAGAAAAGGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGAGAGGAGGGGGACACAGATGTGGTACAGCTCTTGTTACTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCTTTGAAGACTGAGAATTATAATCTAGTATGTGAGTACCATAGCCAAATTCAGGACTGGCATATTCTCCT
ACCCTTGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGGATGTGACCTTATATGCCTTCTCCAACATG
CTGTAAAATGTGATATGCTTTCTATTCTTGTTAAATATAAGGAGGATTTACTAAATGTAAGGATTAGGCATCGTACCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGATTTGAGATTATTGAATGGATAGGTCAAAATCTGTCAATTCCTGAACCTGAGGC
CATTTTTAGCATTGCTATTGTTACAAAAGATGTAGAACTGTTTTCCTTAGGATATAAAATTATTTTTGATTACATGCAAAGAC
AAGGAATTTTTCAATTAACCAATGTAGTTCGCATGCTTCTGCTAAATCGTCATATTGGTATGGCAATAGAAAAAGGACTTTTA
CCTTTTATTCTGGAAACTTTAAAATATGGTGGTAGTGTAAAAAGAGCTTTATCTTATGCAGTAATAGATAATAAAAGAAAAAT
TATAGACTATCTTGTACGCCATGAAAATATACCCCGAGGAACTATTGAAAGACTTTTGCATCTAGCTGTGAAAAAACAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAGAT
CACAAATCCACTCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGGTTTTTGATAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAATCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGCTTGGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAATATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCTTATGCTTTAGAGTATGA
CATGTATTAA

SEQ ID No. 258 – L60 MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACACTTTCTTCCTTCCAAATGATTTTAGCAAGCATACTCTACAACGGCTGGG
GTTGTATTGGAAAGAGCATGGATCCGTCCATCGAATAGAAAAGGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGAGAGGAGGGGGACACAGATGTGGTACAGCTCTTGTTACTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCTTTGAAGACTGAGAATTATAATCTAGTATGTGAGTACCATAGCCAAATTCAGGACTGGCATATTCTCCT
ACCCTTGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGGATGTGACCTTATATGCCTTCTCCAACATG
CTGTAAAATGTGATATGCTTTCTATTCTTGTTAAATATAAGGAGGATTTACTAAATGTAAGGATTAGGCATCGTACCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGATTTGAGATTATTGAATGGATAGGTCAAAATCTGTCAATTCCTGAACCTGAGGC
CATTTTTAGCATTGCTATTGTTACAAAAGATGTAGAACTGTTTTCCTTAGGATATAAAATTATTTTTGATTACATGCAAAGAC
AAGGAATTTTTCAATTAACCAATGTAGTTCGCATGCTTCTGCTAAATCGTCATATTGGTATGGCAATAGAAAAAGGACTTTTA
CCTTTTATTCTGGAAACTTTAAAATATGGTGGTAGTGTAAAAAGAGCTTTATCTTATGCAGTAATAGATAATAAAAGAAAAAT
TATAGACTATCTTGTACGCCATGAAAATATACCCCGAGGAACTATTGAAAGACTTTTGCATCTAGCTGTGAAAAAACAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAGAT
CACAAATCCACTCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGGTTTTTGATAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAATCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGCTTGGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGTATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCTTATGCTTTAGAGTATGA
CATGTATTAA

SEQ ID No. 259 – China/2018/AnhuiXCGQ MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACATTTTCTTCCTTCCAAATGATTTTAGCAAGCATACCCTACAATGGCTGGG
ATTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGAGAGGAGGGGGACACAGATGTAGTACAGCTCTTGTTATTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAAAAATATAACCTAATATGTGAGTATCATAGCCAAATTCAGGACTGGCATATTCTCCT
ACCCATGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGGATGTGACTTTATTTGCCTTCTCCAACATG
CTGTAAAATACAACATGCTTTCTATTCTTGTCAAATATAAGGAGGATCTACTAAATGCAAGGATTAGGCATCGTATCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGAATTGAAATTATTGATTGGATAGGCCAAAATCTGCCAATTCCTGAACCTGATGC
CATTTTTAGCATTGCTGTTGCTACAAGAGATTTAGAACTGTTTTCCTTAGGGTACAAGATTATTTTTGATTACATGCAAAGAC
AGGGAATCATTCAATTAACCAATGGAGTTCGCATGGTTGTGCTAAATCGTCACATTAGCATGGCAATAGATAATGGTCTTTTA
CCTTTTGTTCTGGAAACTTTAAAACATGGTGGGAATATACATAGAGCCTTATCTTATGCAGTAACACACAATAGAAGAAAAAT
TCTGGATTATCTTATTCGCCAGAAAAATATAGCCCCTAATACAATTGAAAGACTTTTATATCTGGCCGTGAAAAATCAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAAAT
GAGAAATCCACTCTTGTGTTAAAAATTTTATTAGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGATTTTTGGTAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAATCACCCATTTTAAAGACCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGTTTAGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGTATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCCTATGATGCTTTAGAGTA
G

SEQ ID No. 260 – Georgia 2007/1 MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACATTTTCTTCCTTCCAAATGATTTTAGCAAGCATACCCTACAATGGCTGGG
ATTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGAGAGGAGGGGGACACAGATGTAGTACAGCTCTTGTTATTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAAAAATATAACCTAATATGTGAGTATCATAGCCAAATTCAGGACTGGCATATTCTCCT
ACCCATGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGGATGTGACTTTATTTGCCTTCTCCAACATG
CTGTAAAATACAACATGCTTTCTATTCTTGTCAAATATAAGGAGGATCTACTAAATGCAAGGATTAGGCATCGTATCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGAATTGAAATTATTGATTGGATAGGCCAAAATCTGCCAATTCCTGAACCTGATGC
CATTTTTAGCATTGCTGTTGCTACAAGAGATTTAGAACTGTTTTCCTTAGGGTACAAGATTATTTTTGATTACATGCAAAGAC
AGGGAATCATTCAATTAACCAATGGAGTTCGCATGGTTGTGCTAAATCGTCACATTAGCATGGCAATAGATAATGGTCTTTTA
CCTTTTGTTCTGGAAACTTTAAAACATGGTGGGAATATACATAGAGCCTTATCTTATGCAGTAACACACAATAGAAGAAAAAT
TCTGGATTATCTTATTCGCCAGAAAAATATAGCCCCTAATACAATTGAAAGACTTTTATATCTGGCCGTGAAAAATCAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAAAT
GAGAAATCCACTCTTGTGTTAAAAATTTTATTAGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGATTTTTGGTAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAATCACCCATTTTAAAGACCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGTTTAGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGTATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCCTATGATGCTTTAGAGTA
G

SEQ ID No. 261 – Mkuzi 1979 MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACACTTTCTTCCTTCCAAATGATTTTAGCAATCATACCCTACAACGGCTGGG
GTTATATTGGAAAGAGCATGGATCCGTCCATCGAATAGAAAAGGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACATCTTGCAGGAGAGGAGGGGAACACAGATGTAGTACAGCTCTTGTTATTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAGAAATATAACCTAATATGTGAGTACCATAGCCAAATTCAGAACTGGCATGTTCTCCT
CCCCTTGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGGATGTGACTTTATTTGCCTTCTCCAACATG
CTGTAAAATGTGACATGCTTTCTATTCTTGTTAAATATAAGGAGGATCTACTAAATGCAAGGATTAGGCATCGTATCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGATTTGAGATTATTGAATGGATAGGTCAAAATCTGCCAATTCCTGAACCTGAGGC
CATTTTTAGCATTGCTATTGTTACAAAAGATATAGAACTGTTTTCCTTAGCGTACAAGCTTATTTTTGATTACATGCAAAGAC
AAGGAACTTTTCAATTAACCAATATGGTCCGCATGCTTCTGCTAAATCGGTACATTGGTATGGCAATAGAAAAAGGACTTTTA
CCCTTTATTCTGGAAACTTTAAAATATGGTGGTAGTGTAAATAGAGCTTTATCTTATGCAGTAATAGATAATAAAAGAAAAAT
TATAGACTATCTTGTACGCCATGAAAATATACCCCGTGGAACTATTGAAAGACTTTTGCATCTAGCTGTGAAAAAACAATCTT
CCAGAAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAGAT
CACAACTCTACTCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCGGGTAAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGGTTTTTGATAGACATCATTCACAGCATTTACCAAAGTTATTCACTAAAACATGA
AGATATTTTTAAACTGGCAACATTTTATGTCAAACACAATGCAATCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGCTTGGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGCATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCCTATAATGCTTTAGAGTA
G

SEQ ID No. 262 – Pretorisuskop/96/4 MGF 505 6R

ATGTTCTCCCTTCAGGACCTCTGTCGGAAGAACATTTTCTTCCTTCCAAACGATTTTAGCAAGCATACCCTACAATGGCTGGG
GTTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACTGCTTGCAGGAGAGGAGGGGGACACAGATGTAGTACAGCTCTTGTTGCTATGGGAAGGAAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAGAAATATAGCCTAGTATGTGAGTACCATAGCCAAATTCAGGACTGGCATGTTCTCCT
CCCCTTGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGAATGTGACTTTATATGCCTTCTACAACATG
CTGTAAAATGTGACATGCTTTCTATTCTTGTTAAATATAAAGAGGATCTACTAAATGTAAGGATTAGGCATCGTATCCAATCC
CTGTTTGTTTTGGCATGCGAAAATCGGAGATTTGAGATTATTGAATGGATAGGTCAAAATCTGCCAATTCCTGAACCTGAGGC
CATTTTTAGCATTGCTATTGTTACAAAAGATATAGAACTGTTTTCCTTAGGATACAAGCTTATTTTTGATTACATGCAAAGAC
AAGGAACTTTTCAATTAACCAATATGGTTCGCATGCTTCTGCTAAATCGTTACATTGGTATGGCAATAGAAAAAGGCCTTTTA
CCCTTTATCGTGGAAACTTTAAAATATGGTGGTAGTGTAAATAGAGCTTTATCTTATGCAGTCATAGATAATAAAAGAAAAAT
TATAGACTATCTTGTACGTCATGAAAATATACCCCGTGGAACTATTGAAAGACTTTTGCATCTAGCTGTGAAAAAACAATCTT
CCAGAAAAACTTTGAACTTGTTGCTATCTTACATAAACTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAGAT
CACAACTCTACCCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATTTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCGGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAC
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGGTTTTTGATAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAATATTTTATGTCAAATACAATGCAATCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGCTTGGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGCATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACTAAGGAAGAAATCATATAA

SEQ ID No. 263 – Tengani 62 MGF 505 6R

ATGTTCTCCCTTCAGGACCTCTGTCGGAAGAACACTTTCTTCCTTCCAAATGATTTTAGCAAGCATACCCTACAACGGCTGGG
GTTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGAGAGGAGGGGGACACAGATGTAGTACAGCTCTTATTATTATGGGAAGGAAATCTTCATTAT
GCCATCATAGGAGCCTTGAAGACTGAGAAATATAACCTAATATATGAGTACCATAGCCAAATTCAGGACTGGCATGTTCTCTT
ACCCATGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGCATGTGACTTTATATGCCTTCTCCAACATG
CTATAAAATATAACATGCTTTCTATCCTTGTCAAATATAAGGAAGACTTACTAAATGTAAGGATTAGGTATCGTATCCAATCC
CTGTTTGTTTTGGCATGTGAAAACCGGAGAATTGAGATTATTGAATGGATAGGTCAAAATCTGCCAATTCCTGAACCTGATGC
CATTTTTAGCATTGCTGTTGCTACAAGAGATTTAGAACTGTTTTCCTTAGGGTACAAGATTATTTTTGATTACATGCAAAGAC
AGGGAATCTTTCAATTAACCAATGGAGTTCGCATGGTTGTGCTAAATCGTCACATTAGCATGGCAATAGATAATGGTCTTTTA
CCCTTTGTTCTGGAAACTTTAAAACATGGTGGGAATATACATAGAGCCTTATCTTATGCAGTAACACACAATAAAAGAAAAAT
TCTGGATTATCTTATTCGCCAGAAAAATATAGCCCCTAATACAATTGAAAGACTTTTATATCTGGCCGTGAAAAATCAATCAT
CCAGAAAAACTTTGAACTTGTTACTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAAAT
GAGAAATCCACTCTTGTGTTAAAAATTTTATTAGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTGATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGGCGATTTTTGGTAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAACCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA

ACAGAGGAACAGAAAGTAAAAAACTCTTTTTAGAGTGTTTAGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGCATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAGCCTATGGATGCTTTAGAGTAGCCATGTA
TTAA

SEQ ID No. 264 – Warmbaths MGF 505 6R

ATGTTCTCCCTACAGGACCTCTGTCGGAAGAACATTTTCTTCCTTCCAAACGATTTTAGCAAGCATACCCTACAATGGCTGGG
GTTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAGACAGCATAATGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACTGCTTGCAGGAGAGGAGGGGGACATAGATGTAGTACAGCTCTTGTTATTATGGGAGGGTAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAGAAATATAACCTAATATGTGAGTACCATAGCCAAATTCAGGACTGGCATATTCTCCT
ACCCATGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGCATGTGACTTTATATGCCTTCTCCAACATG
CTGTAAAATATAACATGCTTTCTATCCTTGTCAAATATAAGGAAGACTTACTAAATGTAAGGATTAGGTATCGTATCCAATCC
CTGTTTGTTTTGGCATGCGAAAACCGGAGAATTGAGATTATTCATTGGATAGGCCAAAATCTGCCAATTCCTGAACCTGATGC
CATTTTTAGCATTGCTGTTGCTACAAGAGATTTAGAACTGTTTTCCTTAGGGTACAAGATTATTTTTGATTACATGCAAAGAC
AGGGAATCTTTCAATTATCCAATGGAGTTCGCATGGTTGTGCTAAATCGTCACATTAGCATGGCAATAGATAATGGACTTTTA
CCCTTTGTTCTGGAAACTTTAAAACATGGTGGGAATATACATAGAGCCTTATCTTATGCAGTAACACACAATAGAAGAAAAAT
TCTGGATTATCTTATTCGCCAGAAAAATATAGCCCCTAATACAATTGAAAGACTTTTATATCTGGCCGTGAAAAATCAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTGGTAGAGCATGTAGTAAAT
GAGAAATCCACTCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGACGATTTTTGATAGAGATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAACACAATGCAACCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGTTTAGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGTATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAACTATTACCAAGGAAGAAATCATGCAAGCCTATGATGCTTTAGAGTA
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SEQ ID No. 265 – Warthog MGF 505 6R

ATGTTCTCCCTTCAGGACCTCTGTCGGAAGAACATTTTCTTCCTTCCAAATGATTTTAGCAAGCATACCCTACAATGGCTGGG
GTTATATTGGAAAGAGCATGGATCCGTCCATCGAGCAGAAAAAAACAGCATAGTGATACAGAATGAATTGGTTCTTTCTATCA
ATGATGCTTTACAGCTTGCAGGGGAAGAGGGGGACACAGATGTAGTACAGCTCTTGTTATTATGGGAGGGAAATCTGCATTAT
GCCATCATAGGAGCCTTGAAGACTGAGAAATATAATCTAATATGTGAGTACCATAGCCAAATTCAGGACTGGCATGTTCTCCT
CCCCTTGATTCAAGATCCAGAAACATTCGAAAAATGTCATGATTTAAGCCTTGCATGTGACTTTATATGCCTTCTACAACATG
CTGTAAAATATAACATGCTTTCTATCCTTGTCAAATATAAGGAAGACTTACTAAATGTAAGGATTAGGTATCGTATCCAATCC
CTGTTTGTTTTGGCATGTGAAAACCGGAGAATTGAGATTATTGATTGGATAGGCCAAAATCTGCCAATTCCTGAACCTGATGC
CATTTTTAGCATTGCTGTTGCTACAAGAGATTTAGAACTGTTTTCCTTAGGGTACAAGATTATTTTTGATTACATGCAAAGAC
AGGGAATCTTTCAATTATCCAATGGAGTTCGCATGGTTGTGCTAAATCGTCACATTAGCATGGCAATAGATAATGGACTTTTA
CCCTTTGTTCTGGAAACTTTAAAACATGGTGGGAATATACATAGAGCCTTATCTTATGCAGTAACACACAATAGAAGAAAAAT
TCTGGATTATCTTATTCGCCAGAAAAATATAGCCCCTAATACAATTGAAAGACTTTTATATCTGGCCGTGAAAAATCAATCTT
CCAGGAAAACTTTGAACTTGTTGCTATCTTACATAAATTACAAGGTGAAAAATGTTAAAAAGCTAGTAGAGCATGTAGTAAAT
GAGAAATCCACTCTTGTGTTAAAAATTTTATTGGAAAAAAAGGAAAATCTAGTGGATGCTGTTTTAACAAGACTTGTAAAACA
TTCTACATATTTCCAGGTGAGAGAATTTATCCAGGAGTTTTCCATCAGCCCAGAAAAATTCATTAAAATAGCTGTGCGGGAAA
AGAAAAATGTGTTAATCGAGGCTATTTCTGAAGATATTTGGGAAAATCCCACAGAAAGAATTACTTATCTCAAACAGATAGTG
CACACCATAAAATATGAAAGTGGAAGACGATTTTTGATAGACATCATTCACAGCATTTACCAAAGTTACTCACTAAAACACGA
AGATATTCTTAAACTGGCAACATTTTATGTCAAATACAATGCAATCACCCATTTTAAAGATCTCTGCAAATATCTTTGGCTGA
ACAGAGGAACAGAAAGTAAGAAACTGTTTTTAGAGTGTTTAGAAATTGCTGATGAGAAGGAGTTTCCTGATATTAAAAGCATT
GTGAGTGAATATATTAACTACTTGTTTACTGCAGGAGCTATTACCAAGGAAGAAATCATGCAAGCCTATGATGCTTTAGAGTA
G

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Benin 97/1 strain:

SEQ ID No. 55 (MGF 360 6L), SEQ ID No. 68 (MGF 360 10L), SEQ ID No. 78 (MGF 360 11L), SEQ ID No. 96 (MGF 360 12L), SEQ ID No. 108 (MGF 360 13L) and SEQ ID No. 120 (MGF 360 14L), and

SEQ ID No. 141 (MGF 505 1R) and SEQ ID No. 151 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the China/2018/AnhuiXCGQ strain:

SEQ ID No. 52 (MGF 360 6L), SEQ ID No. 63 (MGF 360 10L), SEQ ID No. 76 (MGF 360 11L), SEQ ID No. 89 (MGF 360 12L), SEQ ID No. 101 (MGF 360 13L), SEQ ID No. 113 (MGF 360 14L) and SEQ ID No. 125 (MGF 360 21R), and
SEQ ID No. 135 (MGF 505 1R) and SEQ ID No. 148 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Georgia 2007/1 strain:
SEQ ID No. 51 (MGF 360 6L), SEQ ID No. 62 (MGF 360 10L), SEQ ID No. 75 (MGF 360 11L), SEQ ID No. 88 (MGF 360 12L), SEQ ID No. 100 (MGF 360 13L), SEQ ID No. 112 (MGF 360 14L) and SEQ ID No. 124 (MGF 360 21R), and
SEQ ID No. 134 (MGF 505 1R) and SEQ ID No. 147 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Ken05/Tk1 strain:
SEQ ID No. 35 (MGF 110 6L), SEQ ID No. 44 (MGF 110 8L), and
SEQ ID No. 58 (MGF 360 6L), SEQ ID No. 65 (MGF 360 10L), SEQ ID No. 86 (MGF 360 11L) and SEQ ID No. 130 (MGF 360 21R), and
SEQ ID No. 145 (MGF 505 1R) and SEQ ID No. 156 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Ken06.Bus strain:
SEQ ID No. 36 (MGF 110 6L), and
SEQ ID No. 61 (MGF 360 6L), SEQ ID No. 64 (MGF 360 10L), SEQ ID No. 87 (MGF 360 11L), SEQ ID No. 99 (MGF 360 12L), SEQ ID No. 111 (MGF 360 13L), SEQ ID No. 123 (MGF 360 14L) and SEQ ID No. 132 (MGF 360 21R), and
SEQ ID No. 144 (MGF 505 1R) and SEQ ID No. 158 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Kenya 1950 strain:
SEQ ID No. 37 (MGF 110 6L), SEQ ID No. 45 (MGF 110 8L), and
SEQ ID No. 60 (MGF 360 6L), SEQ ID No. 66 (MGF 360 10L), SEQ ID No. 85 (MGF 360 11L), SEQ ID No. 98 (MGF 360 12L), SEQ ID No. 110 (MGF 360 13L), SEQ ID No. 122 (MGF 360 14L) and SEQ ID No. 131 (MGF 360 21R), and
SEQ ID No. 143 (MGF 505 1R) and SEQ ID No. 157 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the L60 strain:

SEQ ID No. 54 (MGF 360 6L), SEQ ID No. 67 (MGF 360 10L), SEQ ID No. 77 (MGF 360 11L), SEQ ID No. 95 (MGF 360 12L), SEQ ID No. 107 (MGF 360 13L) and SEQ ID No. 119 (MGF 360 14L), and
SEQ ID No. 140 (MGF 505 1R) and SEQ ID No. 150 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Malawi Lil-20/1 (1983) strain:
SEQ ID No. 38 (MGF 110 6L), SEQ ID No. 46 (MGF 110 8L), and
SEQ ID No. 59 (MGF 360 6L), SEQ ID No. 74 (MGF 360 10L), SEQ ID No. 84 (MGF 360 11L), SEQ ID No. 97 (MGF 360 12L), SEQ ID No. 109 (MGF 360 13L), SEQ ID No. 121 (MGF 360 14L) and SEQ ID No. 133 (MGF 360 21R), and
SEQ ID No. 146 (MGF 505 1R) and SEQ ID No. 155 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Mkuzi 1979 strain:
SEQ ID No. 39 (MGF 110 6L), SEQ ID No. 47 (MGF 110 8L), and
SEQ ID No. 57 (MGF 360 6L), SEQ ID No. 69 (MGF 360 10L), SEQ ID No. 79 (MGF 360 11L), SEQ ID No. 94 (MGF 360 12L), SEQ ID No. 106 (MGF 360 13L), SEQ ID No. 118 (MGF 360 14L) and SEQ ID No. 128 (MGF 360 21R), and
SEQ ID No. 138 (MGF 505 1R) and SEQ ID No. 149 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Pretorisuskop/96/4 strain:
SEQ ID No. 40 (MGF 110 6L), SEQ ID No. 48 (MGF 110 8L), and
SEQ ID No. 56 (MGF 360 6L), SEQ ID No. 70 (MGF 360 10L), SEQ ID No. 81 (MGF 360 11L), SEQ ID No. 93 (MGF 360 12L), SEQ ID No. 105 (MGF 360 13L), SEQ ID No. 117 (MGF 360 14L) and SEQ ID No. 127 (MGF 360 21R), and
SEQ ID No. 142 (MGF 505 1R) and SEQ ID No. 153 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Tengani 62 strain:
SEQ ID No. 41 (MGF 110 6L), and
SEQ ID No. 71 (MGF 360 10L), SEQ ID No. 82 (MGF 360 11L), SEQ ID No. 90 (MGF 360 12L), SEQ ID No. 102 (MGF 360 13L), SEQ ID No. 114 (MGF 360 14L) and SEQ ID No. 126 (MGF 360 21R), and
SEQ ID No. 136 (MGF 505 1R) and SEQ ID No. 152 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Warmbaths strain:

SEQ ID No. 42 (MGF 110 6L), SEQ ID No. 49 (MGF 110 8L), and
SEQ ID No. 53 (MGF 360 6L), SEQ ID No. 73 (MGF 360 10L), SEQ ID No. 80 (MGF 360 11L), SEQ ID No. 92 (MGF 360 12L), SEQ ID No. 104 (MGF 360 13L), SEQ ID No. 116 (MGF 360 14L) and SEQ ID No. 129 (MGF 360 21R), and
SEQ ID No. 137 (MGF 505 1R) and SEQ ID No. 154 (MGF 505 2R).

In an embodiment the invention provides an ASFV which comprises one or more, such as all, of the following sequences from the Warthog strain:
SEQ ID No. 43 (MGF 110 6L), SEQ ID No. 50 (MGF 110 8L), and
SEQ ID No. 72 (MGF 360 10L), SEQ ID No. 83 (MGF 360 11L), SEQ ID No. 91 (MGF 360 12L), SEQ ID No. 103 (MGF 360 13L), SEQ ID No. 115 (MGF 360 14L), and
SEQ ID No. 139 (MGF 505 1R).

The translation products (i.e. protein sequences) of these genes are given below:

Benin 97/1 MGF gene protein sequences

SEQ ID No. 1 – translation of Benin 97/1 MGF 110-11L (A9JKR9)

MKYSWKNGGGDYWPIIIRHCCFYLVFSIAFVGYIVFAYYKNLHLNTAMKLLALLCILIWLSQPGLNRPLSIFYMKQNLPRTYT
PPIRELEYWCTYGKHCDFCWECRNGICKNKVWDDMSSVQEHSYPMEHCMIHRQCKYIRDGPIFQVECTMQTSDATHLINA

SEQ ID No. 2 – translation of Benin 97/1 MGF 110-12L (A9JKS1)

MKVFLGLLLGYSTILILTYQSPTTQWCFYEISLKILNHHSMEKWRDKNWSIIIRYYCFYLVFSFAFAGCVAFAICKNLRLCTT
MKLLMLLNILVLLSQPILNN

SEQ ID No. 3 – translation of Benin 97/1 MGF 360-6L (A9JKS8)

MNSLQVLTKKVLIENKAFSEYHEDDIFILQQLGLWWHNGPIGFCKQCKMVTSGSMSCSDVDSYELDRALVRAVKKNQTDLIKL
FVLWGANINYGIICAKTERTKDLCIELGANPEFLDVGLYNMFVDLIKQQKVLLAIDIYYDNISILDSFDSHDFYVLIDFIYNC
FILNLDEKEKMIKNTYVLKFWFKIAIEFNLIKPIRFLSKKFPHLDYWRLKTAVYLGNVDEIHHAYFQENIRLDPNDMMSLACM
YPQNKLGIYYCFALGANINTALETLIGFINHEVNREITFFSNYGIWSNVHFCISLGANPYTKKIQETLLRQEKNVIMKLLFKK
GLLSPHSILHKKILEPSEVRKIISTYEYTETFHSFSLLRDNLR

SEQ ID No. 4 – translation of Benin 97/1 MGF 360-10L

MVPSLQSFAKKVLASQHVSIDYHVILERCGLWWYKAPISLDCKHMLIKLPNFADGLDLNTALMLATKENNYQLIKMFTDWGAD
INYGLICANTPPIREFCWELGAKYQVDKKKIMHIFFKLIHPNTTSNNIILCLKFFNDNPFSAYVIIREIKSCIHWKLKNLAED
TNVLSNISDGDMLTIYCFIVALQDNLREAISYVYQHFKYLNTWWLTCALCYNKLFDLHNLYEKEKIRMDMDEMMRIACTKDNN
FLTIYYCFILGANINLAMIASIRFYNMDNLFFCIDLGADAFEEAKALAEQQNYYLISHRLSLDIYSPDSSLLTLKEADPNKIY
RLLKNYKSKSMLAYLNYDINDTSL

SEQ ID No. 5 – translation of Benin 97/1 MGF 360-11L (A9JKU4)

MLPSLQSLTKKVLAGQCVSVDHYHILKCCGLWWHNGPIMLHIRRNKLFIRSTCFSQGIELNIGLMKAVKENNHDLIKLFTEWG
ADINYGMICALTENTRDLCKELGAKEYLEREYILKIFFDTTRDKTSSNIIFCHEVFSNNPNLRIIDNLDLRGEIMWELRGLME
ITFMLDHDDSFSTVLTKYWYAIAVDYDLKDAIRYFYQKYPRLHRWRLMCALFYNNVFDLHELYEIERVRMDIDEMMHIACIQD
YSYSAIYYCFIMGANINQAMLVSIQNYNLGNLFFCIDLGANAFEEGKALAEQKENYLIAHALSLKHYNPVISLLSNVMDPEKI
NYMLKNYHSINMGIFLDYEQR

SEQ ID No. 6 – translation of Benin 97/1 MGF 360-12L (A9JKU9)

MLPSLQSLTKKVLAGQCVPTNQHYLLKYYDLWWYNAPITFDHNLRLIKSSGIKEGLDLNTALVKAVRENNYSLIKLFTEWGAD
INYGLVSVNTEHTRDLCQELGAKEILNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNLKLRIEIFWELRELIEKT
DLLNNEFLLSTLLLKYWYAIAVRYSLKEAIQYFYQKYTHMNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYMLGANINQAMLTSIQYYNIENMFFCMDLGADVFEEGTTALGEGYELIKNILSLKIYSPTTIPLPKSTDPEIIDHA
LKNYFSKNMMIFLSYDLR

SEQ ID No. 7 – translation of Benin 97/1 MGF 360-13L (A9JKU7)

MSLPLSLQTLVKKTVASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYSLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPMLENKFVIQLRGLIYKRLWGL
IEIKETDELNDLLVKYWYAKAVQYVCKNAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKKKVQIDVHDMICLACAKDNN
LLTIYYCYALGGNINQAMLTSVQYYNVGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLTLDIYSSDASLPLNLKDPEKISS
LLKDYKSKNLSIIWEYSHNIL

SEQ ID No. 8 – translation of Benin 97/1 MGF 360-14L (A9JKV1)

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVANLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYKRHKNQLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNMKRAEEYLTAHPEIIVID

SEQ ID No. 9 – translation of Benin 97/1 MGF 505-1R (A9JKU5)

MFSLQNLCRKTLPDCKLPEFFDDYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRIAASEENYEIVGLLLAWEGNL
YYAIIGALEGNRYNLIRKYDDQIKDHHDILPFIDDPIIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYTLEDDLPLVHLL
IEKACEDHNYEVIKWIYENLHVCHIIDTFDCAIAHKDLRLYCLGYTFIYNRIVPYKYHHLDILILSSLQLLHKVAAKGYLDFI
LETLKYDHNIDNLDVILTQAATYNHRKILTYFIPQSTYAQIEQCLFVAIKTKSSKKTLNLLLSHLNLSIKLIQKISQYVATFN
STNIIGILSMKRKKKIYLDIILTKFVKNAIFNKFVVRCMERFSINPERIVKMAARINKMMLVKKISEHVWKNHAARLKHLKHA
VHTMKHKDGKNRLMNFIYEHCYYHMQGEEIFSLARFYAIHHAPKLFDVFYNCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFAMGVLSKKEILQDYPSIYSKHYMP

SEQ ID No. 10 – translation of Benin 97/1 MGF 505-2R (A9JKV3)

MFSLQDLCRKHLFILPDVFGEHVLQRLGLYWRCHGSLQRIGDDHILIRRDLILSTNEALRMAGEEGNNEVVKLLLLWKGNLHY
AVIGALQGDQYDLIHKYENQIGDFHFILPLIQDANTFEKCHALERFCGVSCLLKHATKYNMLPILQKYQEELSMRAYLHETLF
ELACLWQRYDVLKWIEQTMHVYDLKIMFNIAISKRDLTMYSLGYIFLFDRGNTEATLLTQHLEKTAAKGLLHFVLETLKYGGN
IDTVLTQAVKYNHRKLLDYFLRQLPRKHIEKLLLLAVQEKASKKTLNLLLSHLNYSVKRIKKLLRYVIEYESTLVIKILLKKR
VNLIDAMLEKMVRYFSATKVRTIMDELSISPERVIKMAIQKMRTDIVIHTSYVWEDDLERLTRLKNMVYTIKYEHGKKMLIKV
MHGIYKNLLYGEREKVMFHLAKLYVAQNAATQFRDICKDCYKLDVARFKPRFKQLILDCLEIVTKKSCYSILEILEKHIISLF
TMKVMTEEEKNLCLEILYKVIHYKTIQC

MGF 110 5L protein sequences

SEQ ID No. 306 – Ken05/Tk1 MGF 110 5L protein

MLVIFLGLLGLLANQVLGLPNQPAGQLHPTDNPPKEELGYWCTYTESCKFCWNCQNGLCEGKLENTTILENEYVQSCIVSRWL
NKCMYDLGQGIDHVMACSEPKPWNPYKILKREWKKNVSQN

SEQ ID No. 307 – Ken06.Bus MGF 110 5L protein

MLVIFLGLLGLLANQVLGLPNQPAGQLHPTDNPPKEELGYWCTYTESCKFCWNCQNGLCEGKLENTTILENEYVQSCIVSRWL
NKCMYDLGQGIHHVMPCSEPKPWNPYKILKKEWKENVSQN

SEQ ID No. 308 – Malawi Lil-20/1/1983 MGF 110 5L protein

MLVIFLGILGLLANQVSSQLVGQLHPTENPSENELEYWCTYMECCQFCWDCQDGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNSQN

SEQ ID No. 309 – Mkuzi 1979 MGF 110 5L protein

MLVIFLGILGLLANQVSSQLVGQLHPTENPSENELEYWCTYMECCQFCWDCQDGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNSQN

SEQ ID No. 310 – Pretorisuskop/96/4 MGF 110 5L protein

MLVIFLGILGLLANQVSSQLVGQLHPTENPSENELEYWCTYMECCQFCWDCQNGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNSQNK

SEQ ID No. 311 – Tengani62 MGF 110 5L protein

MLVIFLGILGLLVNQVSSQPVGQLHPTENPSENELEYWCTYMECCQFCWDCQNGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNS

SEQ ID No. 312 – Warmbaths MGF 110 5L protein

MLVIFLGILGLLANQVSSQLVGQLHPTENPSENELEYWCTYMECCQFCWDCQNGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNSQNK

SEQ ID No. 313 – Warthog MGF 110 5L protein

MLVIFLGILGLLANQVSSQLVGQLHPTENPSENELEYWCTYMECCQFCWDCQNGLCVNKLGNTTILENEYVHPCIVSRWLNKC
MYDLGQGIDHVMVCSQPKYWNPYKILKKEWKENNSQNK

SEQ ID No. 314 – China/2018/AnhuiXCGQ MGF 110 5L/6L fusion protein

MLVIFLGILGLLASQVSSQLVGQLRPTEEPPEEELEYWCAYMESCQFCWDCQDGTCINKIDGSVIYKNEYVKSCLVSRWLDKC
MYDLDKGIYHTMNCNQVLGLPNQPAGQLHPTDNPPQEELEYWCTYTENCKFCWNCQNGLCEGKLENTTILENEYVQSCIVSRW
LNKCMYDLGQGIHHVMACSEPKPWNPYKILKREWKENNS

SEQ ID No. 315 – Georgia 2007/1 MGF110 5L/6L fusion protein

MLVIFLGILGLLASQVSSQLVGQLRPTEEPPEEELEYWCAYMESCQFCWDCQDGTCINKIDGSVIYKNEYVKSCLVSRWLDKC
MYDLDKGIYHTMNCNQVLGLPNQPAGQLHPTDNPPQEELEYWCTYTENCKFCWNCQNGLCEGKLENTTILENEYVQSCIVSRW
LNKCMYDLGQGIHHVMACSEPKPWNPYKILKREWKENNS

MGF 110 12L protein sequences

SEQ ID No. 316 – Benin 97/1 MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPTTQWCFYEISLKILNHHSMEKWRDKNWSIIIRYYCFYLVFSFAFAGCVAFAICKNLRLCTT
MKLLMLLNILVLLSQPILNN

SEQ ID No. 317 – China/2018/AnhuiXCGQ MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPTTPWCFYEISLKIPNHHSMKCCSYPRLYEHEMFMEKWRDKNWPIIIRYYCFYLVFSFVFAG
CVAFAICKNLRLSTTMKLLMLLSILVLLLSQPILNN

SEQ ID No. 318 – Georgia 2007/1 MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPTTPWCFYEISLKIPNHHSMKCCSYPRLYEHEMFMEKWRDKNWPIIIRYYCFYLVFSFVFAG
CVAFAICKNLRLSTTMKLLMLLSILVLLLSQPILNN

SEQ ID No. 319 – Ken05/Tk1 MGF 110 12L protein

MKVFLGLLLGFSIILILTYQSPTTQHPPKEELAYWCTYAKSCDFCWDCQNDTCINKVINESISITSIVNCRVTRDSQSCFYEI
SVKIPNHHSMECSYPRLYEHEMFMEKWRDEYWPIIIKQCCFYLVFSIAFAGCVAFAICKNLRLRTTIKLLILLSILVWLSQPV
LN

SEQ ID No. 320 – Ken06.Bus MGF 110 12L protein

MKVFLALLLGYLTILILTYQTPTTQHPPKEELPYWCTYVKNCDLCWDCQDSIYWNKVISESISINSIINCRVTCDSQSQSCFY
EILLKIPNHHSMECSYPGSYENEMFMEKWRDENWSIIIKHYCFYLVFSFAFAGCVAFAICKNLRLSTTMKLLMLLSILVCLSQ
PILNN

SEQ ID No. 321 – Kenya 1950 MGF 110 12L protein

MKVFLGLLLGFSIILILTYQSPTTQHPPKEELAYWCTYAKSCDFCWDCQNDTCINKVINESISITSIVNCRVTRDSQSCFYDI
SVKIPNHHSMECSYPRLYEHEMFMEKWRDEYWPIIIKQCCFYLVFSFAFAGCVAFAICKNLRLRTTIKLLILLSILVWLSQPI
LNN

SEQ ID No. 322 – L60 MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPTTQWCFYEISLKILNHHSMEKWRDKNWSIIIRYYCFYLVFSFAFAGCVAFAICKNLRLCTT
MKLLMLLNILVLLSQPILNN

SEQ ID No. 323 – Malawi Lil-20/1/1983 MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPTTQHPPKEELEYWCTYAKTCDFCWDCQNDTCINKVINESISMNSIVNCRVTRDSQSQSCFY
EISLKIPNYHSMECSYPRLYKHFMSMEKWRDENWPILIRHYCFYLVFSFAFAGCVAFAICKNLRLRTTMKLLMLLSILVLLSQ
PILNN

SEQ ID No. 324 – Mkuzi 1979 MGF 110 12L protein

MNATMKVFLGLLLGYSTILILTYQSPTTQWCFYEISLKILNHHSMEKWRDKNWSIIIRYYCFYLVFSFAFAGCVAFAICKNLR
LCTTMKLLMLLGILVLLSQPILNN

SEQ ID No. 325 – Warmbaths MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPATQWCFYEISLKIPNHHSMECSYPRLYKHFIFMEKWRDKNWSIIIRYYCFYLVFSFAFAGC
IAFAICKNLRLCTTMKLLMLLSILVLLSQPILNN

SEQ ID No. 326 – Warthog MGF 110 12L protein

MKVFLGLLLGYSTILILTYQSPATQWCFYEISLKIPNHHSMECSYPRLYKHFMFMKKWRDKNWSIIIRYYCFYLVFSFAFAGC
IAFAICKNLRLCTTMKLLMLLSILVLLSQPILNN

MGF 360 12L protein sequences

SEQ ID No. 159 – Georgia 2007/1 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDAPITFDHNLRLIKSAGIKEGLNLNTALVKAVRENNYNLIKLFAEWGAD
INYGLVSVNTEHTWDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIVKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYVLGANINQAMLSSIQYYNIENMFFCIDLGADVFEEGTTALGEGYELIKNILSLKIYSPATTPLPKSTDPEIIDHA
LKNYVSKNMMIFLTYDLR*

SEQ ID No. 160 – China/2018/AnhuiXCGQ MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDAPITFDHNLRLIKSAGIKEGLNLNTALVKAVRENNYNLIKLFAEWGAD
INYGLVSVNTEHTWDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIVKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYVLGANINQAMLSSIQYYNIENMFFCIDLGADVFEEGTTALGEGYELIKNILSLKIYSPATTPLPKSTDPEIIDHA
LKNYVSKNMMIFLTYDLR*

SEQ ID No. 161 – Tengani 62 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDAPITFDHNLRLIKSAGIKEGLNLNTALVKAVRENNYNLIKLFAEWGAD
INYGLVSVNTEHTWDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIEKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN

LSTMYYCYVLGANINQAMLSSIQYYNIENMFFCIDLGADVFEEGTTALGEGYELIKNILSLKIYSPATTPLPKSMDPEIIDHA
LKNYVSKNMMIFLTYDLR*

SEQ ID No. 162 – Warthog MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDGPITFDHNLKLIKSAGIKEGLDLNTALVKAVRENNYNLIKLFAEWGAN
INYGLVSVNTEHTRDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIEKT
DLLNNEFSLSALLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYVLGANINQAMLTSIQYYNIENMFFCMDLGADAFEEGTIALGEGYKLIKNILSLKIYSPATTPLPKSTDPEIIDHA
LKNYVSKNMMIFLTYDLR*

SEQ ID No. 163 – Warmbaths MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDGPITFDHNLKLIKSAGIKEGLDLNTALVKAVRENNYNLIKLFAEWGAD
INYGLVSVNTEHTRDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIEKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIYMDIEEMMRIACIKDHN
LSTMYYCYVLGANINQAMLTSIQYYNVENMFFCMDLGADAFEEGTIALGEGYKLIKNILSLKIYSPATTPLPKSTDPEIIDHA
VKNYVSKNMMIFLTYDLR*

SEQ ID No. 164 – Pretorisuskop/96/4 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKCYDLWWHDGPITFDHNLKLIKSAGIKEGLDLNTALVKAVRENNYNLIKLFAEWGAN
INYGLVSVNTEHTWDLCRELGAKETLNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIEKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYVLGGNINQAMLTSIQYYNIENMFFCMDLGADAFEEGTIALGEGYKLIKNILSLKIYSPATTPLPKSTDPEIIDHA
LKNYVSKNMMIFLTYDLR*

SEQ ID No. 165 – Mkuzi 1979 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKYYDLWWHDAPITFDHNLRLIKSAGIKEGLDLNTALVKAVKENNYNLIKLFAEWGAD
INYGLVSVSSEHTWDLCRELGAKETLNEKEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNIKMRIEIFWELRELIEKT
DLLNNEFSLSTLLLKYWYAIAIRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIYMDIEEMMRIACIKDHN
LSTMYYCYMLGANINQAMLTSIQYYNIENMFFCMDLGADVFEEGTTALGEGYELIKNILSLKIYSPTTIPLPKSTDPEIIDHA
LKNYFSKNMMIFLSYDLR*

SEQ ID No. 166 – L60 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKYYDLWWYNAPITFDHNLRLIKSSGIKEGLDLNTALVKAVRENNYSLIKLFTEWGAD
INYGLVSVNTEHTRDLCQELGAKEILNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNLKLRIEIFWELRELIEKT
DLLNNEFLLSTLLLKYWYAIAVRYSLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYMLGANINQAMLTSIQYYNIENMFFCMDLGADVFEEGTTALGEGYELIKNILSLKIYSPTTIPLPKSTDPEIIDHA
LKNYFSKNMMIFLSYDLR*

SEQ ID No. 6 – Benin 97/1 MGF 360 12L protein

MLPSLQSLTKKVLAGQCVPTNQHYLLKYYDLWWYNAPITFDHNLRLIKSSGIKEGLDLNTALVKAVRENNYSLIKLFTEWGAD
INYGLVSVNTEHTRDLCQELGAKEILNEEEILQIFIDLKFHKTSSNIILCHEVFSNNPILQKVNNLKLRIEIFWELRELIEKT
DLLNNEFLLSTLLLKYWYAIAVRYSLKEAIQYFYQKYTHMNTWRLTCALCFNNVFDLHEAYEKDKIHMDIEEMMRIACIKDHN
LSTMYYCYMLGANINQAMLTSIQYYNIENMFFCMDLGADVFEEGTTALGEGYELIKNILSLKIYSPTTIPLPKSTDPEIIDHA
LKNYFSKNMMIFLSYDLR*

SEQ ID No. 167 – Malawi Lil-20/1 MGF 360 12L protein

MLPSLQSLTKKVLAGQCLPTDQYYLLKCYDLWWYDSPITFDHNLGLIKSAGIKDGLDLNTALVKAVRENNYNLIKLFTEWGAD
INYGLVSVNTEHTRDLCRELGAKETLNEEEILRIFIDLKFYKTSSNIILCHEVFSNNPLLQKVNNLKMRIEIFWELRELIKKT
DLLNNEFSLNTLLLKYWYAIAVRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKIYMDLEEMMRVACIKDHN
LSTIYYCYVLGANINQAMLASIQYYNIENMFFCMDLGADVFEENMPVGEGYELIRNILSLKIYSPSTAPLPKNTDPEIIDHVL
KNYKSKNMMTFLSYDLR*

SEQ ID No. 168 – Kenya 1950 MGF 360 12L protein

MLPSLQSLTKKVLAGQCLPEDQHYLLKCYDLWWNNAPITFDHNLRLIKSAGLQEGLDLNMALVKAVKENNYSLIKLFTEWGAN
INYGLISVNTEHTWDLCRELGAKKTLNEGDILQIFIDLKFHKTSSNIILCHEVFSDNLLLKKVNNLKMRIEIFWELREIIEKT
DLLNNEFSLNTLLLKYWYAIAVRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKICMDLEEMMRIACIKDHS
LSTIYYCYMLGANINQAMLTSIQYYNIENIFFCMDLGADAFEEGMALVGQEGYEPIRNILSLKIYSPATTPLPKSTDPEIIDH
ELKNYFSKNMMVFLTYDLR*

SEQ ID No. 169 – Ken06.Bus MGF 360 12L protein

MLPSLQSLTKKVLARQCLPEDQHYLLKCYDLWWNNAPITFDHNLRLIKLAGIQEGLDLNMALVKAVKENNYSLIKLFTEWGAN
INYGLISVNTEHTWDLCRELGAKKTLNEGDILQIFIDLKFYKTSSNIILCHEVFSDNLLLKRVNNLKMRIEIFWELREIIEKT
DLLNNEFSLNTLLLKYWYAIAVRYNLKEAIQYFYQKYTHLNTWRLTCALCFNNVFDLHEAYEKDKICMDLEEMMRIACIKDHN
LSTIYYCYMLGANINQAMLTSIQYYNIENIFFCMDLGADAFEEGMALVGQEGYEPIRNILSLKIYSPATTPLPKSTDPEIIDH
ALKNYFSKNMMVFLTYDLR*

MGF 360 13L protein sequences

SEQ ID No. 170 – Georgia 2007/1 MGF 360 13L protein

MSLPLSLQTLVKKTIASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYGLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPILENKFVIQLRGLIYKRLWGL
IEIKETDELNGLLVKYWYAKAVQYDCKDAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKENIQIDVHDMICLASTKDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLALDIYSSDASLPLNLKDPEEISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 171 – China/2018/AnhuiXCGQ MGF 360 13L protein

MSLPLSLQTLVKKTIASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYGLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPILENKFVIQLRGLIYKRLWGL
IEIKETDELNGLLVKYWYAKAVQYDCKDAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKENIQIDVHDMICLASTKDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLALDIYSSDASLPLNLKDPEEISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 172 – Tengani 62 MGF 360 13L protein

MSLPLSLQTLVKKTVANQSLSIDEHCILKHCGLWWHDVPLKLCMDRGQIQIKSGFLGEDIDLHIALIIAVKENNYSLIKLFTE
WGANINYSLLSINTKHIRELCRQLGAKETLEDDDIFRIFTKIMHNKTSGSIILCHDIFMNNPNIEDKFTIQLRGLIYKRLWGL
IEIKETDELNGLLVKYWYAKAVQYECKDAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKENIQIDVHDMICLASTKDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLALDIYSSDASLPLNLKDPEEISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 173 – Warthog MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSTDEHCILKHCGLWWHDVPLKLCMDRGQIQIKSGFLGEDIDLHIALIIAVKENNYSLIKLFTE
WGAHINYSLLSINTEHIRELCRQLGAKETLEDNDIFRIFTKIMHNKTSGRIILCHEIFMNNPNIENKFTIQLRGLICKRLWGL
IEIKETDELNDLLVKYWYAKAVQYECKDAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKEKVQIDVHDMICLASTKDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYHFLSHSLTLDIYSSDASLPLNLKDPEEISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 174 – Warmbaths MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSTDEHCILKHCGLWWHDVPLKLCMDRGQIQIKSGFLGEDIDLHVALIIAVKENNYSLIKLFTE
WGAHINYSLLSINTEHIRELCRQLGAKKTLEDNDIFRIFTKIMHNKTSGRIILCHEIFMNNPNIENKFTIQLRGLICKRLWRL
IEIKETDELNDLLVKYWYAKAVQYECKDAICFLDEKYTGLNEWRLKCLLYYNKIYELHEMYHKDKVQIDVHDMICLASTKDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYHFLSHSLALDIYSSDASLPLNLKDPEEISS
LLKGYKSKNLSIIWEYSHNIL*

SEQ ID No. 175 – Pretorisuskop/96/4 MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSIDEHCILKHCGLWWHDVPLKLCMDRGQIQIKSGFLGEDIDLHIALIIAVKENNYSLIKLFTE
WGAHINYSLLSINTEHIRELCRQLGAKETLEDDDVFRIFTKIMHNKTSGRIILCHDIFMNNPNIENKFTIQLRGLICKRLWGL
IEIKETDELNDLLVKYWYAKAVQYECKDAICFLEEKYTDLNEWRLKCLLYFNKIYELHEMYHKEKVQIDVHDMICLASTKDNN

PLTIYYCYALGGNINQAMLTSIQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLALDIFSSDASLPLNLKDPEEISS
FLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 176 – Mkuzi 1979 MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYSLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPILENKFVIQLRGLIYKRLWGL
IEIKETDKLNDLLVKYWYAKAVQYVCKNAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKKKVQIDVHDMICLACAKDNN
LLTIYYCYALGSNINQAMLTSVQYYNIGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLTLDIYSSDASLPLNLKDPEEISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 177 – L60 MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYSLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPMLENKFVIQLRGLIYKRLWGL
IEIKETDELNDLLVKYWYAKAVQYVCKNAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKKKVQIDVHDMICLACAKDNN
LLTIYYCYALGGNINQAMLTSVQYYNVGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLTLDIYSSDASLPLNLKDPEKISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 7 – Benin 97/1 MGF 360 13L protein

MSLPLSLQTLVKKTVASQCLSIDEHCILKYCGLWWHDAPLKLCMDRGRIQIKSGFLGEDIDLRVALIIAVKENNYSLIKLFTE
WGANINYSLLSINTKHIRELCRQLGAKETLEDNDIFRIFTRIMHNKTSGSIILCHEIFMNNPMLENKFVIQLRGLIYKRLWGL
IEIKETDELNDLLVKYWYAKAVQYVCKNAICFLDEKYTDLNEWRLKCLLYYNKIYELHEMYHKKKVQIDVHDMICLACAKDNN
LLTIYYCYALGGNINQAMLTSVQYYNVGNIFFCIDLGGNAFEEGRAIAEQKGYNFLSHSLTLDIYSSDASLPLNLKDPEKISS
LLKDYKSKNLSIIWEYSHNIL*

SEQ ID No. 178 – Malawi Lil-20/1 (1983) MGF 360 13L protein

MSAPLSLQTLVKKTVASTSCLSIDEHILKYCDLWWHDAPLKLYMDRGRIQIKSGFLGEDIDLCVALIIAVKENNYNLIKLFTE
LGANINYSLLSINTKHVRDLCRQLGAKETLEDYDIFCIFNKIMHNKTSGSVILCHEIFINNPNLENKFAAQLRRLIYKRLCGL
IEIKETDELSELLVKYWYAKAVQYDYKDAICFLDEKYTDLNEWRLKCYLYYNKIYELHDIYHKEKIQIDVNEMLSLACIRDNN
PLTIYYCYALGGNINQAMLTSVQYYNIGNIYFCIDLGGNAFEEGSAIARQKGYNFLSHSLVLNIYSSDASLPLNLKDPEEISS
LLKNYKSKNLSIILDYSHNIL*

SEQ ID No. 179 – Kenya 1950 MGF 360 13L protein

MSSPLSLQTLVKKTVASTSCLSIDEHILKYCGLWWHDAPLKLYIDRGRIYIKSGFLGEDIDLCVALIIAVKENNYSLIKLFTE
WGAYINYSLLSINTKHARDLCRQLGAKETLDDYDIFCIFNKIMHNKTSGSIILCHEIFINNPKLENNFAAQLRRLIYKRLCGL
IEIKETDELSELLVKYWYANAVQYDHKDAICFLDEKYTDLDEWRLKCYLCYNKIYELHDIYHKKKIQIDVNEMLSLACIRDNN
LLTIYYCYALGGNINQAMLTSVQYYNIGNIYFCIDLGGNAFEEGSAIARQNGYNFLCHSLILNIYSSDASLPLNLKVPEEISS
LLKNYKSKNLSIILDYSHKIL*

SEQ ID No. 180 – Ken06.Bus MGF 360 13L protein

MSSPLSLQTLVKKTVAGTSCLSIDEHILKYCGLWWHDAPLKLYIDRGRIYIKSGFLGEDIDLCVALIIAVKENNYSMIKLFTE
WGAYINYSLLSINTKHARDLCRQLGAKETLDDYDIFCIFNKIMHNKTSGSIILCHEIFINNPNLENNFAAQLRRLIYKRLCGL
IEIKETDELSELLVKYWYANAVQYDHKDAICFLDEKYTDLDEW*LKCYLCYNKIYELHDIYHKEKIQIDVNEMLSLACIRDNN
LLTIYYCYALGGNINQAMLTSVQYYNIGNIYFCIDLGGNAFEEGSAIARQNGYNFLSHSLVLNIYSSDASLPLNLKDPEEISS
LLKNYKSKNLSIILDYSHKIL*

MGF 360 14L protein sequences

SEQ ID No. 181 – Georgia 2007/1 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVARLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHHLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNLKRAEEYLTAHPEIIVID*

SEQ ID No. 182 – China/2018/AnhuiXCGQ MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVARLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHHLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNLKRAEEYLTAHPEIIVID*

SEQ ID No. 183 – Tengani 62 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQIFSYKHVQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVHLKRLCTELGGLTPVSESRLLEILKEVARLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHHLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLQKKNYAA
IYYCYRLGASLDYGMNLSIYNNNTLNMFFCIDLGATDFDRAQRIAHKAYMYNLSNIFLVKQLFSRDVTLALDVTEPQEIYDML
KSYTSKNLKRAEEYLTAHPEIIVID*

SEQ ID No. 184 – Warthog MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYMLQRFGLWWDLGPIHLCNNCKQIFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVHLKRLCTELGGLTPVSEPRLLEILKEVAKLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHHLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLRKKNYAA
IYYCYRLGASLDYGMNLSIYNNNTLNMFFCIDLGATDFDRAQRIAHKTYMYNLSNIFLVKQLFSRDVTLALDVTEPQEIYDML
KSYTSKNLKRAEEYLTAHPEIIVID*

SEQ ID No. 185 – Warmbaths MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYMLQRFGLWWDLGPIHLCNNCKQIFSYKHLQCFSEDDLCLEAALVKAVKRDNLELIRLFVD
WGANPEYGLICVPTVHLKRLCTELGGLTPVSEPRLLEILKEVANLKSCAGVLLGYDMFCYNPLLETITRTTLDTVMYSCSKIP
LMGDTAHHLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCYRLGASLDYGMNLSIYNNNSLNLFFCIDLGATDFDRAQRIAHKAYMYNLSNILLVKQLFSRDVTLALDVTEPQEIYDRL
KAYTSKNMKRAEEYLTAHPEIIVID*

SEQ ID No. 186 – Pretorisuskop/96/4 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQIFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVHLKRLCTELGGLTPVTEPRLLEILKEVAKLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYKRHKNHLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLQKKNYAA
IYYCYRLGASLDYGMNLSIYNNNTLNMFFCIDLGATDFDRAQHIAHKAYMYNLSNIFLVKQLFSRDVTLALDVTEPQEIYDRL
KSYTSKNLKRAEEYLTAHPEIIVID*

SEQ ID No. 187 – Mkuzi 1979 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVANLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYKRHKNQLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNMKRAEEYLTAHPEIIVID*

SEQ ID No. 188 – L60 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVANLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYKRHKNQLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA
IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNMKRAEEYLTAHPEIIVID*

SEQ ID No. 8 – Benin 97/1 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNNCKQVFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVYLKRLCAELGGLTPVSEPRLLEILKEVANLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVTYTCSNIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYKRHKNQLYWRVACSLYFNNIFDIHELCREKEICISPNLMMKFACLREKNYAA

IYYCHRLGASLDYGMNLSIYNNNTLNMFFCIDLGAADFDRAQLIAHKAYMYNLSNIFLVKQLFSRDVTLVLDVTEPQEIYDML
KTYTSKNMKRAEEYLTAHPEIIVID*

SEQ ID No. 189 – Malawi Lil-20/1 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNTCKQIFSYKHLQCFSEDDLCLEAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVHLKRLCMELGGLTPVSESRLLEILKEVADLKSCAGVLLGYDMFCHNPLLETVTRTTLDTVMYTRSKIP
LTGDTAHLLLSKFWFALALRHNFTKAIHYFYEKHKNQLYWRLTCSLYFNNIFDLHELCCKKEICISPNLMMKFACLREENYAA
IYYCHMLGASLDYGMNLSIYNNNTLNLFFCIDLGATNFDRARLIARRVYMYNLSNLFLVKQLFSRDVSLILDLTEPQAIYDML
NTYTSKNLKQAEEYFTAHPEIVVID*

SEQ ID No. 190 – Kenya 1950 MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNTCKQIFSYQHLQCFSEDDLCLDAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVDLKRLCTELGGLTPVSESRLLEILKEVADLKSCAGVLLGYDMFCHNPLLETVTRTTLNTVMYTRSKIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYEKHKNQLYWRLACSLYFNNIFDLHELCSKKEICISPNLMMKFACLREENYAA
IYYCHMLGASPDYGMNLSIYNNNTLNLFFCIDLGATNFDRARLIAHRVYMYNLSNIFLVKQLFSRDASLVLNITEPQAIYDML
KTYTSKNLKRAEEYFTAHPEIVVID*

SEQ ID No. 191 – Ken06.Bus MGF 360 14L protein

MLSLQTLAKKVVACNYLSSDYDYTLQRFGLWWDLGPIHLCNTCKQIFSYQHLQCFSVDDLCLDAALVKAVKSDNLELIRLFVD
WGANPEYGLIRVPAVHLKRLCTELGGLTPVSESRLLEILKEVADLKSCAGVLLGYDMFCHNPLMETVTRTTLNTVMYTRSKIP
LTGDTAHLLLTKFWFALALRHNFTKAIHYFYEKHKNQLYWRLTCSLYFNNIFDLHELCSKKEICISPNLMMKFACLREENYAA
IYYCHMLGASPDYGMNLSIYNNNTLNLFFCIDLGATNFDRARLIAHRVYMYNLSNIFLVKQLFSRDASLVLNITEPQAIYDML
KTYTSKNLKRAEEYFTAHPEIVVID*

MGF 505 1R protein sequences

SEQ ID No. 192 – Georgia 2007/1 MGF 505 1R protein

MFSLQNLCRKTLPNRKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRTAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRQCFFDCILYQAVKYSKFRVLLYFKHRLEDDLPFTHLL
IEKACKDHNYEVIKWIYENLHIYNMIDTFECAIAHKDLHLYCLGYRFIYNRIVPDKYHHLDIRMLSSLQLLHKVAAKGYLDFI
LETLKYDHNKDNINIILTQAATYNHRKILIYFIPQSTHAQIEQCLLVAIKAKSSRKTLNLLLSHLNLSINLIKKISHYVATYN
STNIIGILSMRRKKKIYLDIILTKFVKKAIFNKFVVRCMDTFSINPERILKIAARINRMMLVKKISEHVWKNHAVRLKYLKHA
VHTMKHKDGKNRLMNFIYDRCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFVMGVLSKKEILQDYPSIYSKQYMP*

SEQ ID No. 193 – China/2018/AnhuiXCGQ MGF 505 1R protein

MFSLQNLCRKTLPNRKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRTAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRQCFFDCILYQAVKYSKFRVLLYFKHRLEDDLPFTHLL
IEKACKDHNYEVIKWIYENLHIYNMIDTFECAIAHKDLHLYCLGYRFIYNRIVPDKYHHLDIRMLSSLQLLHKVAAKGYLDFI
LETLKYDHNKDNINIILTQAATYNHRKILIYFIPQSTHAQIEQCLLVAIKAKSSRKTLNLLLSHLNLSINLIKKISHYVATYN
STNIIGILSMRRKKKIYLDIILTKFVKKAIFNKFVVRCMDTFSINPERILKIAARINRMMLVKKISEHVWKNHAVRLKYLKHA
VHTMKHKDGKNRLMNFIYDRCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFVMGVLSKKEILQDYPSIYSKQYMP*

SEQ ID No. 194 – Tengani 62 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQHNLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRQCFFDCILYQAVKYSKFRVLLSFKHRLRDDLPFTHLL
IEKACKDHNYEVIKWIYENLHIYNMIDTFECAIAHKDLRLYCLGYRFIYNRIVPDKYHHLDIRMLSSLQLLHKVAAKGYLDFI
LETLKYDHNKDNINIILTQAATYNHRKILIYFIPQSTHAQIEQCLLVAIKTKSSKKTLNLLLSHLNLSINLIKKISHYVATYN
STNIIGILSMRRKKKIYLDIILTKFVKKAIFNKFVVRCMDTFSINPERILKIAARINRTMLVKKISEHVWKNHAVRLKYLKHA
VHTMKHKDGKNRLMNFIYDRCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFVMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 195 – Warmbaths MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQRTLIPVNEALRIAASEENYEIVGLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIIRRCFFNCILYQAVKYSKFRVLLYFKHRLEDDLPLTHLL
IEKACEDHNYEVIKWIYENLHTYDIMDTFECAIAHKDLRLYCLGYTFIYNRIVPYEYHHLDILILSSLQLLHKVAAKGYLDFI
LETLKYDHNNDNLDIILTQAATYNHRKILTYFIPQLTYAQIEQCLFMAIKRKSSKKTLNLLLSHLTLSIELIKKISQYVVTYN
STNIIGILSMKRKKKIYLDIMLTKYVKYAIFNKYVVRCMDRFSINPERIIKMAARINRMMLVKKISEHVWKNHAARLKHLKHA
VHTMKHKDGKNRLMNFIYDRCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIQFKSLLLDCSHIIGKNAHDATNINI
VNKYIGDLFAMGVLSKKEILQDYPSIYSKHYML*

SEQ ID No. 196 – Mkuzi1979 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDDYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPINEALRTAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYRLEDDLPLTHLL
IEKACENHNYEVIRWIYENLHIYNMIDTFECAIAHKDLRLYCLGYTFIYNRIVPNKYHHIDILILSSLQLLHKVAAKGYLDFI
LETLKYDHNNDNLDIILTQAATYNHRKILTYFIPQSTYAQIEQCLMVAIKTKSSKKTLNLLLSHLNLSIKLIKKISQYVVTYN
STNIIGILSMKRKKKIYLDILLTKFVKNAIFNKFVVRYMDTFSINPEKIVKMAARINKMMLVKKISEHIWKNHAARLEHLKHA
VHTMKHKDGKNRLMNFIYEYCYYHMQGEEIFSLARFYAIHHAPKLFDVFYNCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIDNLFAMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 197 – Warthog MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYRLENDLPLAHLL
IKKACEDHNYEVIKWIYENLHIYNIMDTFGCAIAHKDLRLYRLGYTFIYNRIVPYKYHYLDVLILSGLHLLYKVAAKGYLDFI
LETLKYDHNNDNLDIILTQAATYNHRKILTYYIPQLTYAQIEQCLFMAIKKKSSKKTLNLLLSHLKLSIKLIKKISQYVATYN
STNIIGILNMRRKKKIYLDIILTKFVKKAIFNKFVVRCMDTFSINPERIIKMAARINKMLLVKKISEHAWKNHAARLKHLKHA
VYTMKHKDGKNRLMNLIYDHYYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCLLDTIRFKNLLLDCSHIIGKNAHDATNITI
VNKYIGNLFAMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 198 – L60 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDDYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRIAASEENYEIVGLLLAWEGNL
YYAIIGALEGNRYNLIRKYDDQIKDHHDILPFIDDPIIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYTLEDDLPLVHLL
IEKACEDHNYEVIKWIYENLHVCHIIDTFDCAIAHKDLRLYCLGYTFIYNRIVPYKYHHLDILILSSLQLLHKVAAKGYLDFI
LETLKYDHNIDNLDVILTQAATYNHRKILTYFIPQSTYAQIEQCLFVAIKTKSSKKTLNLLLSHLNLSIKLIQKISQYVATFN
STNIIGILSMKRKKKIYLDIILTKFVKNAIFNKFVVRCMERFSINPERIVKMAARINKMMLVKKISEHVWKNHAARLKHLKHA
VHTMKHKDGKNRLMNFIYEHCYYHMQGEEIFSLARFYAIHHAPKLFDVFYNCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFAMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 9 – Benin 97/1 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDDYILQLLGLYWENHGTIQRAGNNCVLIQQHTLIPVNEALRIAASEENYEIVGLLLAWEGNL
YYAIIGALEGNRYNLIRKYDDQIKDHHDILPFIDDPIIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYTLEDDLPLVHLL
IEKACEDHNYEVIKWIYENLHVCHIIDTFDCAIAHKDLRLYCLGYTFIYNRIVPYKYHHLDILILSSLQLLHKVAAKGYLDFI
LETLKYDHNIDNLDVILTQAATYNHRKILTYFIPQSTYAQIEQCLFVAIKTKSSKKTLNLLLSHLNLSIKLIQKISQYVATFN
STNIIGILSMKRKKKIYLDIILTKFVKNAIFNKFVVRCMERFSINPERIVKMAARINKMMLVKKISEHVWKNHAARLKHLKHA
VHTMKHKDGKNRLMNFIYEHCYYHMQGEEIFSLARFYAIHHAPKLFDVFYNCCILDTIRFKSLLLDCSHIIGKNAHDATNINI
VNKYIGNLFAMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 199 – Pretorisuskop/96/4 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLVQQHTLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHDLIRKYDDQIKDHHEILPFIDNPVIFHKCHIMRRCFFDCILYQAVKYSKFRVLLYFKYRLENDLPLAHLL
VEKACEDHNYEVIKWLYENLHIYNIMETFECAIAHKDLRLYRLGYTFIYNRIVPYKYHYLDVLILSGLHLLYKVAAKGYLDFI
LETLKYDHNNDNLDIILTQAVTYNHRKILTYYIPQLTYAQIEQCLFMAIKKKSSKKTLNLLLSHLKLSIKLIKKISQYVATYN
STNIIGILNMKRKKKIYLDIILTKFVKYAIFNKYVVRCMDTFSINPERIIKMAARINKMLLVKKISQHAWKNHAARLKHLKHA
VYTMKHKDGKNRLMNLIYDHYYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCLLDTIRFKSLLLDCSHIIGKNAHDATNITI
VNKYIGNLFAMGVLSKKEILQDYPSIYSKHYMP*

SEQ ID No. 200 – Kenya 1950 MGF 505 1R protein

MFSLQNLCRKTLPDRKLPEFFDDYVLQLLGLYWENHGTIQRAGNNCVLIQQHNLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHNLIRKYDDQIKDHHEILPFIDDPVIFHKCHMMRRCFFNCILYQAVKYSKFSVLLYFKYILKENLPLVHSL
IEKACEDHNYEVIKWIYENLHIYEIMDTFKCAIAHKDLHLYSLGYTFIYNRIVPYKYHHLDIRILSRLQLLHKVTAKGYLDFI

LETLKYDHNKDNINIILTQAATYNHRNILTYFIPQSTYAQIEQCLFVAIKTNASKKTLNLLLSHLNLSIKLVKKLSQYVVAYK
STNIISILSMQQKKKIYLDIILTKVVKNAIFIKFVIGCMVTFSINPERIVKMAARIKKMKLVKNISEHVWKNHAAKLKHLKHA
VHTMKHQEGKNRLMNFIYDHCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSYIIAKNAHDASINIV
NKYIGNLFAMGVLSKKEILQDYPSIYSKDYML*

SEQ ID No. 201 – Ken06.Bus MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDDYVLQLLGLYWENHGTIQRAGNNCVLIQQHNLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNHHNLIRKYDDQIKDHHEILPFIDDPVIFHKCHTMRRCFFNCILYQAVKYSKFSVLLYFKYILKENLPLVHSL
IEKAYKYHNYEVIKWIYENLHIYDIINTFKCAIAHKDLRLYCLGYTFVYNRIVPYKYYHLDIRILLRLQLLHKVTAKGYLDFI
LETLKYDHNTNNIDIILTQAATYNHRNILTYFIPQSTYAQIEQCLFVAIKTNASKKTLNLLLSHLNLSIKLVKKLSQYVVAYK
STNIISILSRQQKKKIYLDIILTKVVKNAVFNKFVIGCMVTFSINPERIVKMAARIKKMKLVKNISEHVWKNHAVKLKYLKHA
VHTMKHQEGKNRLMNFIYDHCYYHMQEEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSHIIVKNAHDASINIV
NKYIGNLFAMGVLSKKEILQDYPSIYSKDYML*

SEQ ID No. 202 – Ken05/Tk1 MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDDYVLQLLGLYWENHGTIQRAGNNCVLIQQHNLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRHNLIRKYDDQIKDHHEILPFIDDPVIFHKCHIMRRCFFNCMLYQAVKYSKFSVLLYFKYILKENLPLVHSL
IEKAYKYHNYEVIKWIYENLHIYDIINTFKYAIAHKDLRLYCLGYTFVYNRIVPYKYYHLDIRILLRLQLLHKVTAKGYLDFI
LETLKYDHNTNNIDIILTQAATYNHRNILTYFIPQSTYAQIEQCLFVAIKTNASKKTLNLLLSHLNLSIKLVKKLSQYVVAYK
STNIISILSMQQKKKIYLDIILTKVVKNAVFIKFVIGCMVTFSINPERIVKMAARIKKMKLVKNISEHVWKNHAAKLKHLKHA
VHTMKHQEGKNRLMNFIYDHCYYHMQGEEIFSLARFYAIHHAPKLFDVFYDCCILDTIRFKSLLLDCSHIIAKNAHDASINIV
NKYIGNLFAMGVLSKKEILQDYPSIYSKYDIL*

SEQ ID No. 203 – Malawi Lil-20/1 (1983) MGF 505 1R protein

MFSLQNLCRKTLPDCKLPEFFDEYILQLLGLYWENHGTIQRAGNNCVLIQQHNLIPVNEALRIAASEENYEIVSLLLAWEGNL
YYAIIGALEGNRPDLIRKYDDQIKDHHEILPFIDDPIIFHKCHIMRRCFFNCILYQAVKYSKFRVLLYFKHRLGDDLPLTHLL
IEKACEDHNYEVIKWIYENLHSYNIMDTFECAIAHKDLRLYCLGYTFIYNRIVPYKYHHLDICILSSLQLLHKVAAKGYLDFI
LETLKYDHNINNIDIILTQAATYNHRKILTYFIPQLTYAQIEQCLLVAIKTKASKKTLNLLLSHLNLSIKLIKKISQYVVTYN
STNIISILSMRRKKKIYLDIILTEFVKNAIFNKFVVRCMDTFSINPERIVKMAARINRMMLVKNISERVWKNHAVKLKHLKHA
VHTMKHQEGKNRLMNFIYDHCYYHMQGEEIFGLARFYAIHHAPKLFDVFYDCCMLDATRFKSLLLDCPHIIGKNAYDAGINLV
NKYIGNLFAMGVLSKKEILQDYPSIYSKHDMF*

DP148R

The DP148R gene is located close to the right end of the ASFV genome, at position 177915 to 178679 on the Benin 97/1 genome. The DP148R gene may also be referred to as MGF 360 18R. DP148R is expressed at early times post-infection. The amino acid sequence of the DP148R protein has no significant similarity to other proteins; the secondary structure is predicted to be predominantly helical, but no signal peptide or transmembrane domains are evident.

DP148R inhibits type I interferon. DP148R also inhibits activation of the NF-kB transcription factor (see Figure 7). DP148R inhibits nuclear translocation of the p65 subunit of NF-kB (see Figure 8). NF-κB controls expression of interferon and pro-inflammatory cytokines as part of the host's innate immune system response to viral infection. The inhibition of NF-κB by DP148R would results in decreased amounts of type I interferon (IFN) and pro-inflammatory cytokines and chemokines produced by cells infected with ASFV and allow ASFV to circumvent the host innate immune response, favouring virus replication and disrupting the development of adaptive responses.

The gene (i.e. nucleotide) sequences and positions in the genome of DP148R genes from different ASFV strains are presented below.

SEQ ID No. 287 – Georgia 2008/1 DP148R (MH910495.1:183350-184063)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGCGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCAGTTGCCTT
CTTTCGAGCCAATACTAAGGAGCTAGAGGACTTCTTATGCTCAGATGGGCAGTCTGAGGAGGTACTGTCTGGCCCCCTTCTTA
ACCGTCTACTAGAACCCTCAGGCCCTCTTGATATTTTAACCGGATATCACCTATTTCGTCAGAATCCCAAGGCAGGTCAGTTG
CGCGGCCTTGAGGTCAAGATGCTTGAACGGTTATACGATGCTAATATTTACAATATACTGTCTCGGCTGCGGCCTGAAAAAGT
TCGCAACAAGGCTATTGAGCTATACTGGGTTTTCCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGAT
ATGAGGAACCGGACTTTGCTGAACTGGCCTTTATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAA
TATATGCCTCTGACCCGCGCAGTTCTTACGGATGCCATCCGGATAAGTCTTGAGAGCAACAACCAGGTAGGGATTTGCTATGC
TTACTTGATGGGAGGCAGCCTCAAGGGACTAGTCTCCGCCCCACTGCGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCA
AAAAGAAGGACGTTCTTTCACCCCACGACTTCTTACTGCTGCTCCAGTAG

SEQ ID No. 288 – China/2018/AnhuiXCGQ DP148R (MK128995.1:183372-184085)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGCGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCAGTTGCCTT
CTTTCGAGCCAATACTAAGGAGCTAGAGGACTTCTTATGCTCAGATGGGCAGTCTGAGGAGGTACTGTCTGGCCCCCTTCTTA
ACCGTCTACTAGAACCCTCAGGCCCTCTTGATATTTTAACCGGATATCACCTATTTCGTCAGAATCCCAAGGCAGGTCAGTTG
CGCGGCCTTGAGGTCAAGATGCTTGAACGGTTATACGATGCTAATATTTACAATATACTGTCTCGGCTGCGGCCTGAAAAAGT
TCGCAACAAGGCTATTGAGCTATACTGGGTTTTCCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGAT
ATGAGGAACCGGACTTTGCTGAACTGGCCTTTATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAA
TATATGCCTCTGACCCGCGCAGTTCTTACGGATGCCATCCGGATAAGTCTTGAGAGCAACAACCAGGTAGGGATTTGCTATGC
TTACTTGATGGGAGGCAGCCTCAAGGGACTAGTCTCCGCCCCACTGCGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCA
AAAAGAAGGACGTTCTTTCACCCCACGACTTCTTACTGCTGCTCCAGTAG

SEQ ID No. 289 – OURT 88/3 DP148R (NC_044957.1:168827-169045)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAGGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
CGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTTCTTTCGAGCCAATACTAAGGAGCTAGAGGACT
TCTTACGCTCAGATGGGCAATCTGAGGAGATACTGTCTGGCCCCCCTCCTTAA

SEQ ID No. 290 – L60 DP148R (NC_044941.1:177973-178737)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAGGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
CGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTTCTTTCGAGCCAATACTAAGGAGCTAGAGGACT
TCTTACGCTCAGATGGGCAATCTGAGGAGATACTGTCTGGCCCCCTCCTTAACCGTCTACTAGAACCCTCATGCCCTCTTGAT
ATTTTAACCGGATATCACCTATTTCGTCAGAATCCCAAGGCAGGTCAGTTGCGCGGCCTTGAGGTCAAGATGCTTGAACGGTT
ATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTGAAAAAGTCCGCAACAAGGCTATTGAGCTATACTGGGTTT
TCCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGATATGAGGAACCGGACTTTGCTGAACTGGCCTTT
ATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAATATATGCCTCTGACCCGCGCAGTTCTTACGGA
TGCCATCCAGATAAGTCTTGAGAGCAACAACCAGGTAGGGATTTGCTATGCTTACTTGATGGGAGGCAGCCTCAAGGGACTAG
TCTCCGCCCCACTGCGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCAAAAAGAAGGACGTTCTTTCACCCCACGACTTC
TTACTGCTGCTCCAGTAG

SEQ ID No. 291 – Benin 97/1 DP148R (NC_044956.1:177915-178679)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAGGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
CGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTTCTTTCGAGCCAATACTAAGGAGCTAGAGGACT
TCTTACGCTCAGATGGGCAATCTGAGGAGATACTGTCTGGCCCCCTCCTTAACCGTCTACTAGAACCCTCATGCCCTCTTGAT
ATTTTAACCGGATATCACCTATTTCGTCAGAATCCCAAGGCAGGTCAGTTGCGCGGCCTTGAGGTCAAGATGCTTGAACGGTT
ATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTAAAAAAGTCCGCAACAAGGCTATTGAGCTATACTGGGTTT
TCCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGATATGAGGAACCGGACTTTGCTGAACTGGCCTTT
ATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAATATATGCCTCTGACCCGCGCAGTTCTTACGGA
TGCCATCCAGATAAGTCTTGAGAGCAACAACCAGGTAGGGATTTGCTATGCTTACTTGATGGGAGGCAGCCTCAAGGGACTAG
TCTCCGCCCCACTGCGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCAAAAAGAAGGACGTTCTTTCACCCCACGACTTC
TTACTGCTGCTCCAGTAG

SEQ ID No. 292 – Warthog DP148R (AY261366.1:180836-181548)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGTGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTT
CTTTCGAGCCAATACTAAGGAGCTAGAGGACTTTTTATGCTCAGATGGGCAGTCTGAGGAGATACTGTCCGGCCCCCTCCTTA
ACCGTCTACTAGAACCCTCAGGCCCTCTTGATATTTTAACCGGATATCACTTATTTCGTCAGAATCCCAAGGCAGGTCAGGTG
CGCGGCCTTGAGGTCAAGATGCTTGAACGGTTATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTGAAAAAGT
TCGCAACAAGGCTGTTGAGCTATACTGGGTTTTTCGGGCTATCAATATGTGTCATGCTCCTTTAGTTTTAGATATTGTACGAT
ATGAGGAACCGGACTTTGCTGAACTGGCCTTTATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAA
TATATGCCTCTGACCCGCGCAGTTCTTACGGATGCCATCCAGATAAGTCTTGAGAGCAACAGCCAGGTAGGGATTTGCTATGC
CTACTTGATGGGAGGCAGCCTCAAGGGCCTAGTCCGTGCCCCACTACGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCA
AAAAGAAGGACGTTCTTCCACCCCATGACTTCTTACTGCTGCTCCAGTAA

SEQ ID No. 293 – Pretorisuskop/96/4 DP148R (AY261363.1:185149-185861)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGTGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTT
CTTTCGAGCCAATACTAAGGAGGTAGAAGACTTCTTATGCTCAGATGGGCAGTCTGAGGAGGTACTGTCCGGCCCCCTCCTTA
ACCGTCTACTAGAACCCTCAGGCCCTCTTGATATTTTAACCGGATATCACTTATTTCGTCAGAATCCCAAGGCGGGTCAGGTG
CGCGGCCTTGAGGTCAAGATGCTTGAACGGTTATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTGAAAAAGT
TCGCAACAAGGCTGTTGAGCTATACTGGGTTTTTCGGGCTATCAATATGTGTCATGCTCCTTTAGTTTTAGATATTGTACGAT
ATGAGGAACCGGACTTTGCTGAACTGGCCTTTATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAA
TATATGCCTCTGAGCCGCGCAGTTCTTACGGATGCCATCCAGATAAGTCTTGAGAGCAACAGCCAGGTAGGGATTTGCTATGC
CTACTTGATGGGAGGCAGCCTCAAGGGCCTAGTCCGTGCCCCACTACGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCA
AAAAGAAGGACGTTCTTCCACCCCACGACTTCTTACTGCTGCTCCAGTAA

SEQ ID No. 294 – Tengani 62 DP148R (AY261364.1:179845-180557)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGTGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTT
CTTTCGAGCCAATACTAAAGAGCTAGAGGACTTCTTATGTCCAGATGGGCAGTCTGAGGAGGTGCTGTCTGGCTCCCTCCTTA
ACCGTCTACTAGAACCCTCAGGCCCTCTTGATATTTTAACTGGATATCACCTATTTCGTCAGAATCCCAAGGCAGGTCAGTTG
CGCGGCCTTGAGGTCAAGATGCTTGAACGGTTATACGATGCTAATATTTACAACATATTGTCCCGGCTGCGACCTGAAAAAGT
TCGCAACAAGGCTGTTGAGCTATACTGGGTTTTTCGGGCTATCAATATGTGTCATGCTCCTTTAGTTTTAGATATTGTACGAA
ATGAGGAACTGGACTTTGCTGAACTGGCCTTTATTTGTGCTGCTTACTTTGGTGAGCCTCAGGTAATGTATTTGCTCTACAAA
TATATGCCTCTGACCCGCGCAGTTCTTACGGATGCCATCCAGATAAGTCTTGAGAGCAACAGCCAGGTGGGGATTTGCTATGC
CTACTTGATGGGAGGCAGCCTCAAGGGACTAGTCCGTGCCCCGCTACGTAAACGTCTGCGCGCCAAACTACGCTCGCAGCGCA
AAAAGAAGGATGTTCTTCCACCCCACGACTTCTTACTGCTGCTCCAGTAA

SEQ ID No. 295 – Ken06.Bus DP148R (NC_044946.1:181097-181870)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAAGATGTTAGAAATAGTATTGGCAACGCTGCTGGG
TGATCTGCAGCAACTTAAGGATCTTACACCTAAGCAGCGGGCCGTAGCTTTCTTCCGAGCCAACACCAAAGAGCTAGAGGACT
TTCTCTACCCCGATGGGCAGACTGAGGAGTTACTCCCTGGATTTCTTCTTAACCATTTACTAGAACCCTCAGGCCCTATTGAA
ATTTTAACCGGATATCACCTCTTTCGTCAGAATCCAAAGGCAGGTCGCTTGCGAGGCCTTGAGGTGAAAATGCTTGAACGGTT
ATATGATGCTAATATTTACAATATGCTGGCTCGGCTACGGCCTGAGTTGGTTCGTGACAAGGCTGTTGAGCTATATTGGCTTT
TTCGAGCTATTTTAATATGTCATGGTCCCTTGGTTTTGGAGATTGTACGACATGAGACGTTGGACTTTGCAGAAACCGCCTTT
ATCTGTGCTGCTTACTTTAGTGAACCTCAGGTAATGTACGCTCTTTATAACTTTATACCACCCACTCATGCAGTCCTTGCTGA
TGCCATCCAGATGTGTCTTGAGAGCAACAGCGAGGCAGGGATTTGCTATGTCTACCTAATGGGAGGTAACCTCAAGGGCAAGG
TGCCCGGCTCGCTGCGCAAACGTCTGCGTGCCAGTCCACTTCGGCAAGAACGCAAAAAGAAAAACGTCCTTCCGCCCCACGAA
TTCCTACTCCTGCTCCACGGGATTTAA

SEQ ID No. 296 – Kenya 1950 DP148R (AY261360.1:189099-189872)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAAGATGTTAGAAATAGTATTGGCCACGCTGCTAGG
TGATCTGCAGAAACTTAAGGATCTTACACCTCCGCAGCGGGCTGTGGCTTTCTTTCGAGCCAACACCAAAGAGCTAGAGGACT
TTCTCTACCCCGATGGGCAGTCTGAGGAGTTACTCCCTGGACTTCTCCTTAACCGTTTACTAGAACCTTCAGGTTCTATTGAC
ATTTTAACCGGTTACCACCTATTTCGTGAGAATCCAAAGGCAGGTCGCTTGCGAGGCCTTGAGGTGAAAATGCTTGAACGGTT
ATATGATGCTAATATTTACAATATGCTGGCTCGGCTACGGCCTGAGTTGGTTCGTGACAAGGCTATTGAGCTATATTGGCTCT
TTCGGGCTATTTTAATGTGTCATAGTCCCTTAGTTTTGGAGATTGTACGACATGAGACAATGGATTTTGCAGAAACCGCCTTT
ATCTGTGCCGCTTACTTTAGTGAACCTCAGGTAATGTACGCTCTTTATAAATTTATACCTATCTCTCGTGCAGTCCTTGCTGA
TGCCATTCAGATGTGTCTTGAGAGCAACAGCGAGGCGGGGATTTGCTATGCTTACCTAATGGGGGGTAGCCTCAAGGGCAAGG
TGCCTGGCTCGCTGCGCAAACGTCTGCGTGCCAGTCCACTTCGGCAAGAGCGCAAAAAGAAAAACGTCCTCCCGCCCCATGAA
TTCCTACTCATGCTCCATGGGATTTAA

SEQ ID No. 297 – Warmbaths DP148R (AY261365.1:184288-185048)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAGGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
TGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTTCTTTCGAGCCAATACTAAGGAGCTAGAGGACT

TCTTATGCTCAGATGGGCAGTCTGAGGAGATACTGTCCGGCCCCCTCCTTAACCGTCTACTAGAACCCTCAGGCCCTCTTGAT
ATTTTAACCGGATATCACTTATTTCGTCAGAATCCCAAGGCAGGTCAGTTGCGCGGTCTTGAGGTCAAGATGCTTGAACGGTT
ATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTGAAAAAGTTCGCAACAAGGCTATTGAGCTATACTGGGTTT
TCCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGATATGAGGAACCGGACTTTGCTGAACTGGCCTTT
ATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAATATATGCCTCTGACCCGCGCAGTTCTTACGGA
TGCCATCCGGATAAGTCTTGAGAGTAACAACCAGGTAGGGATTTGCTATGCTTACTTGATGGGAGGCAGCCTCAAGGGACTAG
TCTCCGCCCCACTGCGTAAACGTCTGCGCGCCAAACTACGCTCACAGCGCAAAAAGAAAGACGTTCTTTCACCCCACGACTTC
TTACTGCTGCTCCAGTAA

SEQ ID No. 298 – Mkuzi 1979 DP148R (AY261362.1:185751-186511)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAGGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
CGACCTGCAGCGGCTCCGGGTTCTTACCCCTCAGCAGCGGGCGGTTGCCTTCTTTCGAGCCAATACTAAGGAGCTAGAGGACT
TCTTATGCTCAGATGGGCAGTCTGAGGAGATACTATCTGGCCCCCTTCTTAACCGTCTACTAGAACCCTCAGGCCCTCTTGAT
ATTTTAACTGGATATCACCTATTTCGTCAGAACCCCAAGGCAGGTCAGTTACGCGGCCTTGAGGTCAAGATGCTTGAACGGTT
ATACGATGCTAATATTTACAATATATTGTCTCGGCTGCGACCTGAAAAAGTTCGCAACAAGGCTATTGAGCTTTACTGGGTTT
TTCGAGCTATCCATATTTGTCATGCTCCTTTAGTTTTAGATATTGTACGATATGAGGAACCGGACTTTGCTGAACTGGCCTTT
ATTTGTGCTGCTTACTTTGGTGAACCTCAGGTAATGTATTTGCTCTACAAATATATGCCTCTGACCCGCGCAGTTCTTACGGA
TGCCATCCGGATAAGTCTTGAGAGTAACAACCAGGTAGGGATTTGCTATGCTTACTTGATGGGAGGCAGCCTCAAGGGACTAG
TCTCCGCCCCACTGCGTAAACGTCTGTGCGCCAAACTACGCTCGCAGCGCAAAAAGAAGGACGTTCTTTCACCCCACGACTTC
TTACTGCTGCTCCAGTAA

SEQ ID No. 299 – Ken05/Tk1 DP148R (NC_044945.1:186074-186847)

ATGCAAAATAAAATCCCAAATTTTAACCTTTTCTTTTTTTTTCTATACAAGATGTTAGAAATAGTATTGGCAACGCTGCTAGG
TGATCTGCAGAAACTTAAAGATCTTACACCTATGCAGCGGGCTGTGGCTTTCTTTCGAGCCAACACTAAAGAGCTAGAGGACT
TCCTCTGCCCCGATGGGCAGTCTGAGGAGTTACTCCCTGGACTTCTCCTTAACCGTTTATTAGAACCTTCAGGTCCTATTGAC
ATTTTAACCGGTTACCACCTATTTCGTGAGAATCCGAAGGCAGGTCGGCTGCGTGGCCTTGAGGTCAAGCTGCTTGAACGGTT
ATATGATGCTAACATCTACAATATATTGGCCCAGCTACGGCCTGAGTTGGTTCGCAATAAGGCTGTTGAGTTATATTGGCTCT
TTCGGGCTATTTTGATGTGTCATGGTCCCTTAGTTTTGGAGATTGTACGACATGAGACAATGGATTTTGCAGAATTAGCCTTT
ATCTGTGCTGCTTACTTTAGTGAACCTCAGGTAATGTACGCTATTTATAAATTTATACCTATCTCTTGCGCAGTCCTTGCTGA
TGCCATTCAGATGTGTCTTGAGAGTAACAGCGAGGCGGGGATTTGCTATGCTTACCTAATGGGGGGTAGCCTCAAGGGCAAGG
TGCCTGGCGCGCTGCGCAAACGTCTGCGTGCCAGTCCACTTCGGCAAGAGCGCAAAAAGAAAAACGTTCTTCCACCCCATGAA
TTCCTACTCATGCTTCATGGGATTTAA

SEQ ID No. 300 – Malawi Lil-20/1 (1983) DP148R (AY261361.1:183573-184346)

ATGTTAGAAATAGTATTGGCAACGCTGCTAGGTGATCTGCAGAAGCTTAGGGATCTTACACCTATGCAGCGGGCTGTGGCTTT
CTTTCGAGTCAACACTAAAGAGCTAGAGGACTTCCTCTACCCCGATGGGCAGTCTGAGGAGTTGCTCCCTGGACTTCTCCTTA
ACCGTTTACTAGAACCTTCAGGCCCTATTGACATTTTAACCGGTTACCACCTATTTCGTGAGAACCCAAAGGCAGGTCGGCTG
CGTGGCCTTGAGGTTAAGCTGCTTGAACGGTTATATGATGCTAACATCTACAATATGTTGGCCCAAATACGACCTGAGTTGGT
TCGTATCAAGGCTATTGAGTTATATTGGCTCTTTCGGGCTATTTTAATGTGTCATAGTCCCTTAGTTTTGGAGATTGTACGAC
ATGAGACAATGGATTTTGCAGAATTAGCCTTTATCTGTGCTGCTTACTTTAGTGAACCTCAGGTAATGTACGCTCTTTATAAA
TTTATACCTATTTCTCGCGCAGTCCTTGCTGATGCCATCGAGATGTCTCTTGAGAGCAACAGCGAGACGGGGATTTGCTATGC
CTACCTAATGGGGGGTAGCCTCAAGGGCAAGGTGCCCGGCCCGCTGCGCAAACGTCTGCGTGCCAGTCCACTTCGGCAAGAGC
GCAAAAAGAAAAACGTCCTTCCGCCCCATGAATTTCTACTCATGCTCCATGGGATTTAA

In an embodiment the invention provides an attenuated ASF virus in which the expression and/or activity of the DP148R gene is disrupted. Suitably, the DP148R gene comprises the sequence of SEQ ID No. 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 or 300. Suitably, the DP148R gene comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 or 300. Suitably, the DP148R gene consists of the sequence of SEQ ID No. 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 or 300.

The amino acid sequence of the Benin 97/1 DP148R protein is depicted below as SEQ ID No. 11:

SEQ ID No. 11 – Benin 97/1 DP148R protein

MQNKIPNFNLFFFFLYRMLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLRSDGQSEEILSGPLLNRLLEPSCPLD
ILTGYHLFRQNPKAGQLRGLEVKMLERLYDANIYNILSRLRPKKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAF
ICAAYFGEPQVMYLLYKYMPLTRAVLTDAIQISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLRAKLRSQRKKKDVLSPHDF
LLLLQ

Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 11. Suitably, the DP148R gene encodes a protein comprising a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 11. Suitably, the DP148R gene encodes a protein consisting of the sequence of SEQ ID No. 11.

Orthologous DP148R sequences from other genomes share between 74 and 99% amino acid identity. The orthologous DP148R genes from other ASFV isolates are depicted below as SEQ ID Nos 12 to 19, and their location in the ASFV genome is indicated:

SEQ ID No. 12 – Warthog DP148R protein: 181103 to 181549

MLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCSDGQSEEILSGPLLNRLLEPSGPLDILTGYHLFRQNPKAGQV
RGLEVKMLERLYDANIYNILSRLRPEKVRNKAVELYWVFRAINMCHAPLVLDIVRYEEPDFAELAFICAAYFGEPQVMYLLYK
YMPLTRAVLTDAIQISLESNSQVGICYAYLMGGSLKGLVRAPLRKRLRAKLRSQRKKKDVLPPHDFLLLLQ

SEQ ID No. 13 – Kenya 1950 DP148R protein: 189417 to 189872

MQNKIPNFNLFFFFLYKMLEIVLATLLGDLQKLKDLTPPQRAVAFFRANTKELEDFLYPDGQSEELLPGLLLNRLLEPSGSID
ILTGYHLFRENPKAGRLRGLEVKMLERLYDANIYNMLARLRPELVRDKAIELYWLFRAILMCHSPLVLEIVRHETMDFAETAF
ICAAYFSEPQVMYALYKFIPISRAVLADAIQMCLESNSEAGICYAYLMGGSLKGKVPGSLRKRLRASPLRQERKKKNVLPPHE
FLLMLHGI

SEQ ID No. 14 – Malawi LIL20/1 DP148R protein: 183687 to 184346

MLEIVLATLLGDLQKLRDLTPMQRAVAFFRVNTKELEDFLYPDGQSEELLPGLLLNRLLEPSGPIDILTGYHLFRENPKAGRL
RGLEVKLLERLYDANIYNMLAQIRPELVRIKAIELYWLFRAILMCHSPLVLEIVRHETMDFAELAFICAAYFSEPQVMYALYK
FIPISRAVLADAIEMSLESNSETGICYAYLMGGSLKGKVPGPLRKRLRASPLRQERKKKNVLPPHEFLLMLHGI

SEQ ID No. 15 – Mkuzi DP148R protein: 185751 to 186515

MQNKIPNFNLFFFFLYRMLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCSDGQSEEILSGPLLNRLLEPSGPLD
ILTGYHLFRQNPKAGQLRGLEVKMLERLYDANIYNILSRLRPEKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAF
ICAAYFGEPQVMYLLYKYMPLTRAVLTDAIRISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLCAKLRSQRKKKDVLSPHDF
LLLLQ

SEQ ID No. 16 – Pretorisuskop DP148R protein: 185416 to 185862

MLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKEVEDFLCSDGQSEEVLSGPLLNRLLEPSGPLDILTGYHLFRQNPKAGQV
RGLEVKMLERLYDANIYNILSRLRPEKVRNKAVELYWVFRAINMCHAPLVLDIVRYEEPDFAELAFICAAYFGEPQVMYLLYK
YMPLSRAVLTDAIQISLESNSQVGICYAYLMGGSLKGLVRAPLRKRLRAKLRSQRKKKDVLPPHDFLLLLQ

SEQ ID No. 17 – Tengani62 DP148R protein: 180112 to 180558

MLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCPDGQSEEVLSGSLLNRLLEPSGPLDILTGYHLFRQNPKAGQL
RGLEVKMLERLYDANIYNILSRLRPEKVRNKAVELYWVFRAINMCHAPLVLDIVRNEELDFAELAFICAAYFGEPQVMYLLYK
YMPLTRAVLTDAIQISLESNSQVGICYAYLMGGSLKGLVRAPLRKRLRAKLRSQRKKKDVLPPHDFLLLLQ

SEQ ID No. 18 – Warmbaths DP148R protein: 184606 to 185052

MQNKIPNFNLFFFFLYRMLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCSDGQSEEILSGPLLNRLLEPSGPLD
ILTGYHLFRQNPKAGQLRGLEVKMLERLYDANIYNILSRLRPEKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAF
ICAAYFGEPQVMYLLYKYMPLTRAVLTDAIRISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLRAKLRSQRKKKDVLSPHDF
LLLLQSEQ ID No. 19 – OURT88/3 DP148R protein: 169146 to 169592

MQNKIPNFNLFFFFLYRMLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLRSDGQSEEILSGPPPSEQ ID No. 301 – China/2018/Anhui DP148R protein

MLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCSDGQSEEVLSGPLLNRLLEPSGPLDILTGYHLFRQNPKAGQL
RGLEVKMLERLYDANIYNILSRLRPEKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAFICAAYFGEPQVMYLLYK
YMPLTRAVLTDAIRISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLRAKLRSQRKKKDVLSPHDFLLLLQ

SEQ ID No. 302 – Georgia2007/1 DP148R protein

MLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLCSDGQSEEVLSGPLLNRLLEPSGPLDILTGYHLFRQNPKAGQL
RGLEVKMLERLYDANIYNILSRLRPEKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAFICAAYFGEPQVMYLLYK
YMPLTRAVLTDAIRISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLRAKLRSQRKKKDVLSPHDFLLLLQ

SEQ ID No. 303 – Ken05/Tk1 DP148R protein

MQNKIPNFNLFFFFLYKMLEIVLATLLGDLQKLKDLTPMQRAVAFFRANTKELEDFLCPDGQSEELLPGLLLNRLLEPSGPID
ILTGYHLFRENPKAGRLRGLEVKLLERLYDANIYNILAQLRPELVRNKAVELYWLFRAILMCHGPLVLEIVRHETMDFAELAF
ICAAYFSEPQVMYAIYKFIPISCAVLADAIQMCLESNSEAGICYAYLMGGSLKGKVPGALRKRLRASPLRQERKKKNVLPPHE
FLLMLHGI

SEQ ID No. 304 – Ken06 DP148R protein

MQNKIPNFNLFFFFLYKMLEIVLATLLGDLQQLKDLTPKQRAVAFFRANTKELEDFLYPDGQTEELLPGFLLNHLLEPSGPIE
ILTGYHLFRQNPKAGRLRGLEVKMLERLYDANIYNMLARLRPELVRDKAVELYWLFRAILICHGPLVLEIVRHETLDFAETAF
ICAAYFSEPQVMYALYNFIPPTHAVLADAIQMCLESNSEAGICYVYLMGGNLKGKVPGSLRKRLRASPLRQERKKKNVLPPHE
FLLLLHGI

SEQ ID No. 305 – L60 DP148R protein

MQNKIPNFNLFFFFLYRMLEIVLATLLGDLQRLRVLTPQQRAVAFFRANTKELEDFLRSDGQSEEILSGPLLNRLLEPSCPLD
ILTGYHLFRQNPKAGQLRGLEVKMLERLYDANIYNILSRLRPEKVRNKAIELYWVFRAIHICHAPLVLDIVRYEEPDFAELAF
ICAAYFGEPQVMYLLYKYMPLTRAVLTDAIQISLESNNQVGICYAYLMGGSLKGLVSAPLRKRLRAKLRSQRKKKDVLSPHDF
LLLLQ

Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 12.Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 13. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 14. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 15. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 16. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 17. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 18. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 19. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 301. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 302. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 303. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No.

304. Suitably, the DP148R gene encodes a protein comprising the sequence of SEQ ID No. 305.

EP153R

The EP153R gene is expressed both early and late in infection. EP153R may also be referred to as 8CR. The EP153R protein is a C-type lectin. C-type animal lectins are found in serum, the extracellular matrix and cell membranes and are thought to act as receptors for carbohydrate ligands. The EP153R protein comprises a C-type lectin domain, a cell attachment sequence (RGD) and a transmembrane domain, and has similarity with CD44 molecules involved in T cell activation.

The gene (i.e. nucleotide) sequences and positions in the genome of EP153R genes from different ASFV strains are presented below.

SEQ ID No. 204 – Benin 97/1 EP153R (NC_044956.1:67030-67491)

ATGTATTTTAAGAAAAAATACATCGGTCTTATTGATAAGAACTGTGAAAAAAAAAATATTAGATGATTCTAGTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTCTGGGATAATTATATAA
AATGTTACCGAAATAATGATAAAATGTTTTACTGTCCTAATGATTGGGTTGGATATAATAATATTTGTTACTATTTTAGTAAT
GGTAGTTTTTCTAAAAATTATACAGCTGCTAGTAATTTTTGTAGACAATTAAATGGTACACTTGCTAATAATGATACTAATTT
ATTAAATCTAACTAAAATATATAATAATCAATCTATGTATTGGGTTAACAATACGGTAATATTACGTGGTGATAATAAATATA
GTCAAAAAGTTAACTATACAGATTTATTATTTATTTGTGGTAAATAA

SEQ ID No. 205 – Georgia 2007/1 EP153R (NC_044959.1:73369-74451)

ATGTTTTCTAACAAAAAGTACATCGGTCTTATCAATAAGAAGGAGGGTTTGAAAAAAAAAAATAGATGATTATAGTATATTAAT
AATTGGAATATTAATTGGAACTAACATCTTAAGCCTTATTATAAATATAATAGGAGAGATTAATAAACCAATATGTTACCAAA
ATGATGATAAGATATTTTATTGCCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTGGCAATGAAGAAAAAAAT
TATAATAATGCAAGTAATTATTGTAAGCAATTAAATAGTACGCTTACTAATAATAATACTATTTTAGTAAATCTTACTAAAAC
ATTAAATCTTACTAAAACATATAATCACGAATCTAATTATTGGGTTAATTATTCTTTAATTAAAAATGAGTCAGTACTATTAC
GTGATAGTGGATATTACAAAAAACAAAAACATGTAAGTTTATTATATATTTGTAGTAAATAA

SEQ ID No. 206 – Ken05/Tk1 EP153R (NC_044945.1:73544-74038)

ATGTATTCTAAGAAAAAGTACATCGGTCTTATTGACAAGAACTGTGAAAAAAAAAATATTAGATGATGCTACTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATTATAACTCTTATCTATAATTTCATATTTTGGGAGAATTATATAA
AATGTATCCAAAATGATGATAAGATGTTTTACTGTCCTAAAGATTGGGTTGGGTATAATAATGCGTGTTATTATTTTAGTAAT
AACAATAAAAATTATACAGATGCAAATAATTATTGTAAAAATTCACATAATAGTACACTTGCTAATAATGATACTAAATTATT
AAATCTTACTAAATTATTAAATCTTTCTAAATTATATTACAATGATTCTACATATTGGGTTAAATATTCTTTACCTAAAAATA
AAGCAGTAACATTACGTAACAGTACCTACAAATATGATAGAGTTAAATCTACAGAAACATTTTTTATTTGTAGTAACTAA

SEQ ID No. 207 – Ken06.Bus EP153R (NC_044946.1:69244-69741)

ATGTATTCTAAGAAAAAGTACATCGGTCTTATTGACAAAAGCTGTGAAAAAAAAAATATTAGATGATCCTACTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATTATAACTCTTATCTATAATTTCATATTTTGGGAGAATTATATAA
AATGTATCCGAAATGATGATAAGATGTTTTACTGCCCTAAAGATTGGGTTGGATATAATAATGTGTGTTATTATTTTAGTAAC
GATAATGGAAAAAATTATATGAATGCAAGTAATTTTTGTAATAAAAAAAATAGCACGCTTGCTAATAATACGACTAATTTAGT
AAATCTTACTAAAATATTAAATTTTACCAAACAATATAATCATGAATCACTTTATTGGGTTAATTATTCTTTAAGTAATAATA
TGTCATTAGCATTACAGAATAGTAATTTTCCTTCTTCAGGAAGACGTAAATATATGGACTTATTATATATATGTAGTATATAA

SEQ ID No. 208 – L60 EP153R (NC_044941.1:67379-67840)

ATGTATTTTAAGAAAAAATACATCGGTCTTATTGATAAGAACTGTGAAAAAAAAATATTAGATGATTCTAGTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTCTGGGATAATTATATAA
AATGTTACCGAAATAATGATAAAATGTTTTACTGTCCTAATGATTGGGTTGGATATAATAATATTTGTTACTATTTTAGTAAT
GGTAGTTTTTTCTAAAAATTATACAGCTGCTAGTAATTTTTGTAGACAATTAAATGGTACACTTGCTAATAATGATACTAATTT
ATTAAATCTAACTAAAATATATAATAATCAATCTATGTATTGGGTTAACAATACGGTAATATTACGTGGTGATAATAAATATA
GTCAAAAAGTTAACTATACAGATTTATTATTTATTTGTGGTAAATAA

SEQ ID No. 209 – China/2018/AnhuiXCGQ EP153R (MK128995.1:72837-73313)

ATGTTTTCTAACAAAAAGTACATCGGTCTTATCAATAAGAAGGAGGGTTTGAAAAAAAAAATAGATGATTATAGTATATTAAT
AATTGGAATATTAATTGGAACTAACATCTTAAGCCTTATTATAAATATAATAGGAGAGATTAATAAACCAATATGTTACCAAA
ATGATGATAAGATATTTTATTGCCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTGGCAATGAAGAAAAAAAT
TATAATAATGCAAGTAATTATTGTAAGCAATTAAATAGTACGCTTACTAATAATAATACTATTTTAGTAAATCTTACTAAAAC
ATTAAATCTTACTAAAACATATAATCACGAATCTAATTATTGGGTTAATTATTCTTTAATTAAAAATGAGTCAGTACTATTAC
GTGATAGTGGATATTACAAAAAACAAAAACATGTAAGTTTATTATATATTTGTAGTAAATAA

SEQ ID No. 210 – Malawi Lil-20/1 (1983) EP153R (AY261361.1:70776-71261)

ATGTTTTCTAACAAAAAGTACATCGGTCTTATTGACAAGTACTGTGAAAAAAAAATATTAGATGATTCTAGTACAATAAAAAT
TTGTTACATATTAATTGGAATACTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTTTGGGAGAATTATATAA
CATGTAACCAAAAAGATAAGACGTTTTACTGTCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTGGCAATGAT
GAAAAAAATTATAATAATGCAAGTAATTATTGTAAGCAATTAAATAGTACGCTTACTAATAATAATACTAATTTAGTAAATCT
TACTAAAACATTAAATCTTACTAAAACATATAATCACGAATCTAATTATTGGGTTAATTATTCTTTAATTAAAAATGAGTCAG
TACTATTACGCAATAGTGGATATTATAAAAAACAAAAACATGTAAGTTTATTATATATTTGTAGTAAATAA

SEQ ID No. 211 – Warthog EP153R (AY261366.1:69453-69944)

ATGTTTTCTAATAAAAAGTACATTGGTCTTATCAATAAGAAGGAGGGATTGAAAAAAAAAATAGATGATTATAGTATATTAAT
AATTGGAATATTAATTGGAACTAACATCTTAAGCCTTATTATAAATATAATAGGAGAGATTAATAAACCAATATGTTACCAAA
ATAATGATAAGATATTTTATTGCCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTAGTAATGATAATGGCAAT
AATTATACAACTGCGGATAATAAATGTAAACAATTAAATAATAGTACACTGGCTAATAATCTTACTGATTTATTAAATCTTAC
GAGTTTCTTAAATCTTACTAAATTATATCATCATCATTCTCATTATTGGGTTAATTATTCTTTAAATAATAATTATTCAGTAC
CATTAATTGATAGTAAATATAATTTAAATAGGAAAAAAAGTCACTATACAGATTTACTATTTATTTGCAGCAAATAA

SEQ ID No. 212 – Mkuzi 1979 EP153R (AY261362.1:74549-75013)

ATGTATTTTAAGAAAAAATACATCGGTCTTATTGATAAGAACTGTGAAAAAAAAAATATTAGATGATTCTAGTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTCTGGGATAATTATATAA
AATGTTACCGAAATAATGATAAAATGTTTTACTGTCCTAATGATTGGGTTGGATATAATAATGTTTGTTACTATTTTAGTAAT
GGTAGTTTTTTTTAAAAATTATACAGATGCTAATAATTATTGTAAAAAAATAAATAGTACTCTTGCTAATAATGATACTAATTT
ATTAAGTTTAACTAAAATATACAATAATCAATCTATGTATTGGGTTAACAATACAGTAGCATTACGTGGTGATAGTGTATATG
CACAAAGAAAAGTTAATAATTCAGATCTATTATTTATTTGTAGTAAATAA

SEQ ID No. 213 – Warmbaths EP153R (AY261365.1:72727-73191)

ATGTATTTTAAGAAAAAGTACATCGGTCTTATTGATAAGAACTGTGAAAAAAAAAATATTAGATGATTGTACTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTTTGGGATCATTATATGA
CATGTAACAAAAAAGATAAGATGTTTTACTGTCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTAGTAATGAT
AGTTTTACTAAGAATTATACATATGCAAGTAATTCTTGTAAAAAAATAAATAGTACACTTGCTAATAATGATACTAATTTACT
AAATCTTATTAAAGTATATAATAATGTATCTGAGTATTGGGTTAATAATACAGTAACATTACGTGGTGATCATAAATACATAA
ATAAGCAAAATAATTGTAATACAGAATTTTTATTTATTTGTAGTAGATAG

SEQ ID No. 214 – Tengani 62 EP153R (AY261364.1:68134-68604)

ATGTTTTCTAACAAAAAGTATCCGAGTCTTATCGAAAAAAAAATGGATGACTTGATGACTTTAAAGTTTTGTTACATCATTAT
TGCAATCTTGATCATGACTAATATTTTTAGCCTTGTTGTGAATATATGGGGGGGGGGGTGATCGACAATCTTATGAGAATGTAT
TTTATTGTCCTAAAGATTGGGTTGGATATAATAATGCATGTTATTATTTTAGTAATGATATGAAAAATTATACAGAAGCAAGT
AATTATTGTAAAAATTTATATAATAGTACAATTGTTAATAATAATACTAATATAGTAAATCTTACTAAAACATTAAATCTTAC
TAAAATATATAATCATGAAAGTAATTATTGGGTTAATTATTCTTTAATTAATAATGAGTCATTAACATTACGGGACAGTAATT
TTCCTTCTTCAGGAAAACGTACATATATAGATTTATTATATATATGTAGTATATAA

SEQ ID No. 215 – Pretorisuskop/96/4 EP153R (AY261363.1:73562-74029)

ATGTATTTTAAGAAAAAGTACATCGGTCTTATTGATAAGAACTGTGAAAAAAAAATATTAGATGATTGTACTACAATAAAAAT
TTGTTACATATTAATTGGAATATTGATTGGAACTAATATGATAACTCTTATTTATAATTTCATATTTTGGGATCATTATATGA
CATGTAACAAAAAAGATAAGATGTTTTACTGTCCTAAAGATTGGGTTGGATATAATAATGTTTGTTATTATTTTAATAATGAT
AGTAAGAATTATACAACTGCTACTAATTCTTGTAAACAATTAAATAGTACACTTGCTAATAATGATACTAATTTATTAAATCT
TACTAAAGTATATCACCATGATAAATTATATTGGGTTAACTATTCTTTAAATGACAATTTTTCATTATCATTACGTAATAGTA
CATATGAAAAAAGATCTAAATATTTGCCATTATTATTTATTTGCAGTAAATAA

SEQ ID No. 216 – Kenya 1950 EP153R (AY261360.1:76255-76731)

ATGTTTTTGAACAAAAAGTATCCGAGTCTTATCGAAAAAAAAATGGATGATTTGATGACTTTAAAGTTTTGTTACTTAATAAT
CACATTTTTAATCATAACCAATATTTTTAGCCTTGCTATAAATATATGGGGGGGGGGGTGATATGATAGATCGACAAAGTTGTG
AAAATATATTTTACTGTCCTAAAGATTGGGTTGGCTATAATAATGCGTGTTATTATTTTAGTAATAACAATAAAAATTATACA
GATGCAAATAATTATTGTAAAAATTCACATAATAGTACACTTGCTAATAATGATACTAAATTATTAAATCTTACTAAATTATT
AAATCTTTCTAAATTATATTACAATGATTCTACATATTGGGTTAAATATTCTTTACCTAAAAATAAAGCAGTAACATTACGTA
ACAGTACCTACAAATATGATAGAGTTAAATATACAGAAACATTTTTTATTTGTAGTAACTAA

In an embodiment the invention provides an attenuated ASF virus in which the expression and/or activity of the EP153R gene is disrupted. Suitably, the EP153R gene comprises the sequence of SEQ ID No. 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215 or 216. Suitably, the EP153R gene comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215 or 216. Suitably, the EP153R gene consists of the sequence of SEQ ID No. 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215 or 216.

The accession numbers of EP153R proteins from different strains of ASFV are listed below in Table 3.

Table 3

Strain	**EP153R protein accession number**
BA71V	Q65150
Benin 97/1	A9L06
E75	D4I5P5
Georgia 2007/1	E0WMJ5
Kenya	P0CA63
Malawi	P0CA64
Portugal/OURT88/1988	A9JLS3
PretorisuskopPr4/1996	O89335
Warthog	P0CA65

The amino acid sequences of the EP153R proteins from different ASFV strains are depicted below.

SEQ ID No. 20 – Benin 97/1 EP153R protein

MYFKKKYIGLIDKNCEKKILDDSSTIKICYILIGILIGTNMITLIYNFIFWDNYIKCYRNNDKMFYCPNDWVGYNNICYYFSN
GSFSKNYTAASNFCRQLNGTLANNDTNLLNLTKIYNNQSMYWVNNTVILRGDNKYSQKVNYTDLLFICGK

SEQ ID No. 217 – Georgia 2007/1 EP153R protein

MFSNKKYIGLINKKEGLKKKIDDYSILIIGILIGTNILSLIINIIGEINKPICYQNDDKIFYCPKDWVGYNNVCYYFGNEEKN
YNNASNYCKQLNSTLTNNNTILVNLTKTLNLTKTYNHESNYWVNYSLIKNESVLLRDSGYYKKQKHVSLLYICSK*

SEQ ID No. 218 – Ken05/Tk1 EP153R protein

MYSKKKYIGLIDKNCEKKILDDATTIKICYILIGILIGTNIITLIYNFIFWENYIKCIQNDDKMFYCPKDWVGYNNACYYFSN
NNKNYTDANNYCKNSHNSTLANNDTKLLNLTKLLNLSKLYYNDSTYWVKYSLPKNKAVTLRNSTYKYDRVKSTETFFICSN*

SEQ ID No. 219 – Ken06.Bus EP153R protein

MYSKKKYIGLIDKSCEKKILDDPTTIKICYILIGILIGTNIITLIYNFIFWENYIKCIRNDDKMFYCPKDWVGYNNVCYYFSN
DNGKNYMNASNFCNKKNSTLANNTTNLVNLTKILNFTKQYNHESLYWVNYSLSNNMSLALQNSNFPSSGRRKYMDLLYICSI*

SEQ ID No. 220 – L60 EP153R protein

MYFKKKYIGLIDKNCEKKILDDSSTIKICYILIGILIGTNMITLIYNFIFWDNYIKCYRNNDKMFYCPNDWVGYNNICYYFSN
GSFSKNYTAASNFCRQLNGTLANNDTNLLNLTKIYNNQSMYWVNNTVILRGDNKYSQKVNYTDLLFICGK*

SEQ ID No. 221 – China/2018/AnhuiXCGQ EP153R protein

MFSNKKYIGLINKKEGLKKKIDDYSILIIGILIGTNILSLIINIIGEINKPICYQNDDKIFYCPKDWVGYNNVCYYFGNEEKN
YNNASNYCKQLNSTLTNNNTILVNLTKTLNLTKTYNHESNYWVNYSLIKNESVLLRDSGYYKKQKHVSLLYICSK*

SEQ ID No. 222 – Malawi Lil-20/1 (1983) EP153R protein

MFSNKKYIGLIDKYCEKKILDDSSTIKICYILIGILIGTNMITLIYNFIFWENYITCNQKDKTFYCPKDWVGYNNVCYYFGND
EKNYNNASNYCKQLNSTLTNNNTNLVNLTKTLNLTKTYNHESNYWVNYSLIKNESVLLRNSGYYKKQKHVSLLYICSK*

SEQ ID No. 223 – Warthog EP153R protein

MFSNKKYIGLINKKEGLKKKIDDYSILIIGILIGTNILSLIINIIGEINKPICYQNNDKIFYCPKDWVGYNNVCYYFSNDNGN
NYTTADNKCKQLNNSTLANNLTDLLNLTSFLNLTKLYHHHSHYWVNYSLNNNYSVPLIDSKYNLNRKKSHYTDLLFICSK*

SEQ ID No. 224 – Mkuzi 1979 EP153R protein

MYFKKKYIGLIDKNCEKKILDDSSTIKICYILIGILIGTNMITLIYNFIFWDNYIKCYRNNDKMFYCPNDWVGYNNVCYYFSN
GSFFKNYTDANNYCKKINSTLANNDTNLLSLTKIYNNQSMYWVNNTVALRGDSVYAQRKVNNSDLLFICSK*

SEQ ID No. 225 – Warmbaths EP153R protein

MYFKKKYIGLIDKNCEKKILDDCTTIKICYILIGILIGTNMITLIYNFIFWDHYMTCNKKDKMFYCPKDWVGYNNVCYYFSND
SFTKNYTYASNSCKKINSTLANNDTNLLNLIKVYNNVSEYWVNNTVTLRGDHKYINKQNNCNTEFLFICSR*

SEQ ID No. 226 – Tengani 62 EP153R protein

MFSNKKYPSLIEKKMDDLMTLKFCYIIIAILIMTNIFSLVVNIWGGGDRQSYENVFYCPKDWVGYNNACYYFSNDMKNYTEAS
NYCKNLYNSTIVNNNTNIVNLTKTLNLTKIYNHESNYWVNYSLINNESLTLRDSNFPSSGKRTYIDLLYICSI*

SEQ ID No. 227 – Pretorisuskop/96/4 EP153R protein

MYFKKKYIGLIDKNCEKKILDDCTTIKICYILIGILIGTNMITLIYNFIFWDHYMTCNKKDKMFYCPKDWVGYNNVCYYFNND
SKNYTTATNSCKQLNSTLANNDTNLLNLTKVYHHDKLYWVNYSLNDNFSLSLRNSTYEKRSKYLPLLFICSK*

SEQ ID No. 228 – Kenya 1950 EP153R protein

MFLNKKYPSLIEKKMDDLMTLKFCYLIITFLIITNIFSLAINIWGGGDMIDRQSCENIFYCPKDWVGYNNACYYFSNNNKNYT
DANNYCKNSHNSTLANNDTKLLNLTKLLNLSKLYYNDSTYWVKYSLPKNKAVTLRNSTYKYDRVKYTETFFICSN*

Suitably, the EP153R gene encodes a protein comprising the sequence of SEQ ID No. 20, 217, 218, 219, 220, 221, 222, 223, 224, 225 226, 227 or 228. Suitably, the EP153R gene encodes a protein comprising a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 20, 217, 218, 219, 220, 221, 222, 223, 224, 225 226, 227 or 228. Suitably, the EP153R gene encodes a protein consisting of the sequence of SEQ ID No. 20, 217, 218, 219, 220, 221, 222, 223, 224, 225 226, 227 or 228.

EP153R is immunogenic (i.e. evokes an immune response) (Burmakina et al. 2019 J. Gen. Virol. 100: 259-265). EP153R inhibits capsase-3 activation during ASFV infection and thereby has an inhibitory effect on apoptosis. EP153R is required for haemadsorption. EP153R also inhibits MHC-I expression in infected cells.

EP402R

The EP402R gene encodes a protein which is incorporated in the external layer of the virus and is partly similar to the mammalian T-lymphocyte surface adhesion receptor CD2. In particular, the N-terminal extracellular region of the EP402R protein consists of two immunoglobulin-like (Ig-like) domains similar to the extracellular ligand-binding region of CD2. The N-terminal extracellular domain of the EP402R protein may be referred to as the "ligand-binding domain". The cytoplasmic domain of EP402R protein is dissimilar to CD2. The EP402R protein may be referred to as CD2v due to this similarity.

EP402R is immunogenic (i.e. evokes an immune response) (Netherton et al. 2019 Front. Immunol. 10, 1318). EP402R is required for haemadsorption and may have a role in virus entry or spread. EP402R can bind the host protein AP-1. The functions of EP402R may be mediated by its extracellular, N-terminal, Ig-like domain binding to ligands in the same manner that mammalian CD2 binds extracellular adhesion molecules.

The gene (i.e. nucleotide) sequences and positions in the genome of EP402R genes from different ASFV strains are presented below.

SEQ ID No. 229 – Georgia 2007/1 EP402R (NC_044959.1:73369-74451)

ATGATAATACTTATTTTTTTAATATTTTCTAACATAGTTTTAAGTATTGATTATTGGGTTAGTTTTAATAAAACAATAATTTT
AGATAGTAATATTACTAATGATAATAATGATATAAATGGAGTATCATGGAATTTTTTTAATAATTCTTTTAATACACTAGCTA
CATGTGGAAAAGCAGGTAACTTTTGTGAATGTTCTAATTATAGTACATCAATATATAATATAACAAATAATTGTAGCTTAACT
ATTTTTCCTCATAATGATGTATTTGATACAACATATCAAGTAGTATGGAATCAAATAATTAATTATACAATAAAATTATTAAC
ACCTGCTACTCCCCCAAATATCACATATAATTGTACTAATTTTTTAATAACATGTAAAAAAAATAATGGAACAAACACTAATA
TATATTTAAATATAAATGATACTTTTGTTAAATATACTAATGAAAGTATACTTGAATATAACTGGAATAATAGTAACATTAAC
AATTTTACAGCTACATGTATAATTAATAATACAATTAGTACATCTAATGAAACAACACTTATAAATTGTACTTATTTAACATT
GTCATCTAACTATTTTTATACTTTTTTTAAATTATATTATATTCCATTAAGCATCATAATTGGGATAACAATAAGTATTCTTC
TTATATCCATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCACCACCTGAATCTAAT
GAAGAAGAACAATGTCAGCATGATGACACCACTTCCATACATGAACCATCTCCCAGAGAACCATTACTTCCTAAGCCTTACAG
TCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCTTACCTAAACCGTGTC
CTCCACCCAAACCATGTCCGCCACCCAAACCATGTCCTCCACCTAAACCATGTCCTTCAGCTGAATCCTATTCTCCACCCAAA

CCACTACCTAGTATCCCGCTACTACCCAATATCCCGCCATTATCTACCCAAAATATTTCGCTTATTCACGTAGATAGAATTAT
TTAA

SEQ ID No. 230 – China/2018/AnhuiXCGQ EP402R (MK128995.1:73383-74465)

ATGATAATACTTATTTTTTTAATATTTTCTAACATAGTTTTAAGTATTGATTATTGGGTTAGTTTTAATAAAACAATAATTTT
AGATAGTAATATTACTAATGATAATAATGATATAAATGGAGTATCATGGAATTTTTTTAATAATTCTTTTAATACACTAGCTA
CATGTGGAAAAGCAGGTAACTTTTGTGAATGTTCTAATTATAGTACATCAATATATAATATAACAAATAATTGTAGCTTAACT
ATTTTTCCTCATAATGATGTATTTGATACAACATATCAAGTAGTATGGAATCAAATAATTAATTATACAATAAAATTATTAAC
ACCTGCTACTCCCCCAAATATCACATATAATTGTACTAATTTTTTAATAACATGTAAAAAAAATAATGGAACAAACACTAATA
TATATTTAAATATAAATGATACTTTTGTTAAATATACTAATGAAAGTATACTTGAATATAACTGGAATAATAGTAACATTAAC
AATTTTACAGCTACATGTATAATTAATAATACAATTAGTACATCTAATGAAACAACACTTATAAATTGTACTTATTTAACATT
GTCATCTAACTATTTTTATACTTTTTTTAAATTATATTATATTCCATTAAGCATCATAATTGGGATAACAATAAGTATTCTTC
TTATATCCATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCACCACCTGAATCTAAT
GAAGAAGAACAATGTCAGCATGATGACACCACTTCCATACATGAACCATCTCCCAGAGAACCATTACTTCCTAAGCCTTACAG
TCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCTTACCTAAACCGTGTC
CTCCACCCAAACCATGTCCGCCACCCAAACCATGTCCTCCACCTAAACCATGTCCTTCAGCTGAATCCTATTCTCCACCCAAA
CCACTACCTAGTATCCCGCTACTACCCAATATCCCGCCATTATCTACCCAAAATATTTCGCTTATTCACGTAGATAGAATTAT
TTAA

SEQ ID No. 231 – Warthog EP402R (AY261365.1:73281-74450)

ATGATAATAATCCTTATTTTTTTAATATATTTAAAACTGGTCTTAAATAATAATATTATTATATGGCATCCTACTTTAAATGA
AACAATTTTTTTAAATGTTACAACTATAGGGAATATTAGTGGTCTATTTTGGAATACATATTATAATAATAATCGTAGTGAAC
TTACTAAGTGCGGAATATATAATAATTATTGTTCATGTGATAGTCTTAATACATCATTGTATAATATAAATAATTGTAGTTTA
GTTATTTTTCCAAATAATACAAAAATATTTAATACAATATATGAATTAATATATTCAGGTAATCAAACTAATTATACAATAAA
ATTGCTAGAATCTACTACTCCTCCAAATATTACATATAATTGTACTACATCTGTAATAACATGTAAAAAAAATAATGGGACAA
ATACTAATATATTTTTAACTATAAATAATACGATTGTTAATTCTACTAATGAAGATGTTATTTACTACTATTGGAATAGAAGT
GAATTTAATAACTTTACAGCTACATGTATGATTAATAATACAATTAATTCATCAAATATATCAGAAATTATAGACTGTACTAA
TACATTATTATTAAACAGTTATTTAGACTTTTTTCAAGTAGCCGGTTATATGTTTTATATGATAATTTTTATTGTAACTGGAA
TAACAGTAAGTATTTTTATTTCAATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCTA
CCACCTGAATCTAATGAAGAAGAATGTCAGCATGATGATGACACCACTTCCATACATGAACCATCCCCCAGAGAACCATTACT
TCCTAAACCTTACAGTCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCC
TACCTAAACCATGCCCACCACCTAAACCGTGTCCGCCACCCAAACCATGTCCTCCACCCAAACCATGCCCGCCACCCAAACCA
TGCCCGCCACCTAAACCATGTCCTCCACCTGAATCATGTTCTTCACCTGAATCATGTTCTTCACCTGAATCATATTCTCCACC
CAAACCACTACCTAGTATCCCGCTGCTACCCAATATCCCGCCATTATCTACACAAAATATTTCGCTTATTCATGTAGATAGAA
TTATTTAA

SEQ ID No. 232 – Pretorisuskop/96/4 EP402R (AY261363.1:74089-75309)

ATGATAATGTTCATAACACTTATTTTTTTAAGTTATATTAATATAGTTTTAAGTAATAATTATTGGGCTAGACTTAACGAAAC
AATAACTTTAAATAGTAACATTACTAATGATACTAATAATGAATTAGGTATATTTTGGAATTCTTATAATAATACTTATTATA
ATAATACATTTAATAATATTGCTATATGTGGAAAAAAAGGTATTTTTTGTGAATGTAATATTAATTATAATACATCTATATCT
AATACATCTATATCTAATACATCAATATATAATGTAACAAATAATTGTAGTTTAACGATTTTTCTTTATGATGATAATATATT
TAAAACATATCAATTAGTATATCAGAATTACAAAATTAATTATACAATAAACTTATTATTACCTGTTACTTCTCCAAATATTA
CATATAATTGTACTAACTCTTTAATAACATGTGAAAAAAATGATGGGACAAACACTAATATGTTTTTATCTATAAATAATATA
ACCATTAATCATACTAATCAAGATATTCTTACTTACTATTGGAATAATAGTGAGTTTAATAATTTTACAGCTACATGTATGAT
TAATAATACACTTAATTCAGCAAATACCACAAAAGTTATCAATTGCACTAATCCATTATTAAATTCTTACCAAAATTATTTTC
TTGAAAATATTCATACATTATTTTATATCATAATTTTTATTGTGAGTGGATTAATAGCAAGTATTTTTATTTCAATTATAACT
TTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCACCACCTGAATCTAATGAAGAAGAACAATGTCA
GCATGATGACACCACTTCCATACATGAACCATCTCCCAGAGAACCATTACTTCCTAAACCTTACAGTCGTTATCAATATAATA
CACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCCTACCTAACCCATGTCCTCCACCTAAACCGTGT
CCTCCACCCAAACCATGCCCGCCACCTAAACCATGTCCCCCACCCAAACCATGCCCGCCACCTAAACCGTGTCCTCCACCCAA
ACCATGTCCACCACCTAAACCATGTTCTTCACCTGAATCATATTCTCCACCCAAACCACTACCTAGTATCCCGCTACTACCCA
ATATCCCACCATTATCTACACAAAATATTTCACTTATTCATGTAGATAGAATTATTTAA

SEQ ID No. 233 – L60 EP402R (NC_044941.1:67916-69037)

ATGATAATAATAGTTATTTTTTTAATGTGTTTAAAAATAGTTTTAAACAATATTATAATATGGAGTACTTTAAATCAAACTGT
ATTTTTAAATAATATTTTTACAATTAATGATACATATGGTGGTCTATTTTGGAATACATATTATGATAATAATCGTAGTAATT
TTACTTATTGTGGAATAGCAGGAAATTATTGTTCATGTTGTGGTCATAACATATCATTGTATAATACAACAAATAATTGTAGT
TTAATTATTTTTCCTAACAATACAGAAATATTTAATAGAACATATGAATTAGTATATTTGGACAAAAAAATTAATTATACAGT
AAAACTATTAAAATCTGTTGATTCCCCAACTATTACATATAATTGTACTAATTCTTTAATAACATGTAAAAATAATAATGGGA
CAAATGTTAATATATATTTAATTATTAATAATACAATTAGTTCATTGAATGAAACAGAAAATATAAATTGTACTAATCCAATA
TTAAAATATCAAAATTATTTATCCACATTATTTTATATCATAATTTTTATTGTGAGTGGATTAATAATAGGTATTTTTATTTC

AATCATATCTGTATTATCTATACGAAGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCACCACCCTCTGAATCTAATG
AAGAAGATATTTCTCACGATGACACCACTTCCATACATGAACCATCTCCCAGAGAACCATTACTTCCTAAGCCTTACAGTCGT
TATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCCTACCTAAACCATGCCCGCC
ACCTAAACCATGTCCTCCACCCAAGCCATGCCCGCCACCCAAACCATGTCCTCCACCTAAACCGTGTTCTCCACCCAAACCGT
GTCGTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCCATCC
AAACCATGTCCTTCACCTGAATCCTATTCTCCACCCAAACCACTACCTAGTATCCCGTTACTACCCAATATCCCGCCATTATC
TACACAAAATATTTCGCTTATTCATGTAGATAGAATTATTTAA

SEQ ID No. 234 – Benin 97/1 EP402R (NC_044956.1:67567-68775)

ATGATAATAATAGTTATTTTTTTAATGTGTTTAAAAATAGTTTTAAACAATATTATAATATGGAGTACTTTAAATCAAACTGT
ATTTTTAAATAATATTTTTACAATTAATGATACATATGGTGGTCTATTTTGGAATACATATTATGATAATAATCGTAGTAATT
TTACTTATTGTGGAATAGCAGGAAATTATTGTTCATGTTGTGGTCATAACATATCATTGTATAATACAACAAATAATTGTAGT
TTAATTATTTTTCCTAACAATACAGAAATATTTAATAGAACATATGAATTAGTATATTTGGACAAAAAAATTAATTATACAGT
AAAACTATTAAAATCTGTTGATTCCCCAACTATTACATATAATTGTACTAATTCTTTAATAACATGTAAAAATAATAATGGGA
CAAATGTTAATATATATTTAATTATTAACAATACAATTGTTAATGATACTAATGGAGATATCCTTAATTATTATTGGAATGGT
AATAATAATTTTACAGCTACATGTATGATTAATAATACAATTAGTTCATTGAATGAAACAGAAAATATAAATTGTACTAATCC
AATATTAAAATATCAAAATTATTTATCCACATTATTTTATATCATAATTTTTATTGTGAGTGGATTAATAATAGGTATTTTTA
TTTCAATCATATCTGTATTATCTATACGAAGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCACCACCCTCTGAATCT
AATGAAGAAGATATTTCTCACGATGACACCACTTCCATACATGAACCATCTCCCAGAGAACCATTACTTCCTAAGCCTTACAG
TCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCCTACCTAAACCATGCC
CGCCACCTAAACCATGTCCTCCACCCAAGCCATGCCCGCCACCCAAACCATGTCCTCCACCTAAACCGTGTTCTCCACCCAAA
CCGTGTCGTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCCACCTAAACCATGTCCTCC
ATCCAAACCATGTCCTTCACCTGAATCCTATTCTCCACCCAAACCACTACCTAGTATCCCGTTACTACCCAATATCCCGCCAT
TATCTACACAAAATATTTCGCTTATTCATGTAGATAGAATTATTTAA

SEQ ID No. 235 – Tengani 62 EP402R (AY261364.1:68693-69841)

ATGATAATAAAGGTTATTTTTTTAGTTTTCTTTAAAATGGTTTTAAGTAATATTATAATATGGAGTACTTTAAATAACACAAT
ATATTTAAATATTAATTATTCAGATAGTAATTTATATACTGGTCTATTTTGGAATAAATATTATAATAATACTCGTAATAATT
TTACTACTTGTGTAACATCAAATAGTAGCTATTGTACATGTAAAGGCCATAACACATCATTGTATAATATAACAAATAATTGT
AGTTTAATCATTTTTCCAAATAATACAAAAATATTTAATACAACATATGAATTAGTATATTTAAATAATAAAATTAATTATAC
AATACAAATGGTACAACCTGTTGATCCTCCAATTATTATATATAATGATACTAATAATTCTTTAATAACATGTGAAAAAAATA
ATGGAACGAATACTGAAATCTATTTATATTTAAATGATACATTTATTAATAATACTAATGAAAATAGTATTAAATACTATTGG
AATTGTAGCGAATTAAACCATAATATTACAACTACATGTATTATTAATAATACACTTAATTCGGCAAATACCACAAAAGTTAT
AAATTGCACTAATCTATTGTTAAAATCTGACCAAAATTATTTTCTTAAAAATATTCATACATTATTTTATATCATAATTTTTA
TTGTGGGTGGAACATTAATAAGCATTATTATATCAATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAA
ATAGAAAGTCCACCACCCTCTGAATCTAATGAAGAAGAACATTGTCAGCATGATGATACCACTTCCATACATGAACCATCTCC
CAGAGAACCATTACTTCCTAAGCCTTACAGTCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCAC
TCAACCCATTTCCCCTACCTAAACCATGTCCTCCACCTAAACCGTGTCCTCCACCCAAACCATGTCCTCCACCTAAACCGTGT
CCTCCACCTAAACCGTGTCCCCCACCTAAACCATGTCCTTCACCTGAATCCCATTCTCCACCCAAACCACTACCTAGTATCCC
GCTGCTACCCAATATTCCCCCATTATCTACACAAAATATTTCGCTTATTCATGTAGATAGAATTATTTAA

SEQ ID No. 236 – Malawi Lil-20/1 (1983) EP402R (AY261361.1:72275-72458)

ATGATAATAATACTTATTTTTTTTAATAATTCCTAACATAGTTTTAAGTATTGATTATTGGGTTAGTTTTAATAAAACAATAAT
TTTAGATAGTAATATTACTAATGATAATAATGATATAAATGGAGTATCATGGAATTTCCTTAATAATTCTCTTAATACACTAG
CTACATGTGGAAAAGCAGGTAACTTTTGTGAATGCTCTAATTATAGTACATCACTATATAATATAGCACATAATTGTAGCTTA
ACTATTTTCCCTCATAATGATGTATTTGGTACACCATATCAAGTAGTATGGAATCAAATAATTAATTATACAATAAAATTATT
AACACCTGTTACTCCCCCAAATATTACATATAATTGTACTAATTTTTTAATAACATGTAAAAAAAATAATGGAACAAATACTA
TTATATATTTCAATATAAATGATACTAATGTTAAATATACTAATGAAAGTATACTTGAATATAACTGGAATAATAGTAACTTT
AACAATTTTACAGCTACATGTATAATTAATAATACAATTAATTCATCAAATGATACACAAACTATAGACTGCATCAATACATT
ATTAAGCAGTTATTTAGACTTTTTTCAAGTAGCCAGTTATATGTTTTATATGATAATTTTTATTGCAACTGGAATAATAGCAA
GTATTTTTATATCAATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCATCGCCATCT
GAATCTAATGAAGAAGAACAATGTCAGCATGATGACACCACTTCCATACATGAACCGTCTCCCAGAGAACCATTACTTCCTAA
GCCTTACAGTCGATATCAGTATAATACACCTATTTACTATATGCGTCCCTTAACACAACCACTCAATCCATCTCCCCTACCCA
AACTGTGTCCTCCACCCAAACCGTGTCCTCCACCCAAACCGTGTCCTCCACCCAAACCGTGTCCTCCACCCAAACCGTGTCCT
TCATCTGAATCATGTTCTCCACCTGAATCATATTCTCTACCCAAACCACTACCTAATATCCCGCTACTACCCAATATCCCGCC
ATTATCTACACAAAATATCTCGCTTATTCACGTAGATAGAATTATTTAA

SEQ ID No. 237 – Ken06.Bus EP402R (NC_044946.1:69827-70984)

ATGATAATAAAGCTTATTTTTTTTAATATCATTTAAAATGATTTTAGGTATTGATTATTGGGTTAGTCTTAATAATACAATAAT
TTTAGATAGTAACATTACTATTAATAATATTACTAATACTACTAATAATCCTACATTAAATGGTATATTTTGGAATATTTATA

ATAATAGTTATAATAATACTTTTAATTTACTTACCACATGTGGGAATACATATAATATATGTTCTTGTTCTAATAATTATAAT
ACAATATTATTTAATTATAATACCACAAATAATTGTAGTTTAATTATTTCTCCTCATGATGAAAAAATTTTTGATACGATGTT
TCAGATAATATATTTAACTAATAAAATTAATTATACAATACGATGGTTACAACCTGTTGATCCCCCAAATATTTCATTTAATG
ATAGTAATTCTTTAATAAAATGTGAAAAAAATAATGGAACAAATACTGAAATCTATTTATATTTAAATGATACATTTATTAAT
AATACTAATGAAAATGATCTTAAATATTATTGGAATTGTAGTGAGTTAAACTATAATATTACAGCTACATGTATTATTAATAA
TACACTTAATTCGGCAAATACCACAAAAGTTATAAATTGCACTAATCTATTATTAAAATCTGACCAAAATTATTTTCTTAAAA
ACATTCATACATTATTTTATATCATAATTTTTATTGTAACTGGGATAATAATAAGTATTTTTATAGCAATCATAACTTTTTTA
TCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAAAGTCCATCGCCTGAATCTAATGAAGAGGAAGAACAACAACATCA
TCATGACACTACTTCCATACATGAACCGTCTCCCAGAGAACCATTACTTCCTAAGCCTTACAGTCGTTATCAGTATAATACAC
CTATTTATTACATGCGTCCCTCAACACAACAACTATTTAAATCATATTCTTTACCCAAACCATGTCCCCCACCTAAACCATGT
CCTCCACCTAAACCATGTCCCCCACCCAAACCATGTCCCTCACCAGAATCATATCCCTCACCTGAACCATATCCTCTACTACC
TAATATCCCACTACCACCCAATATCCCGCCATTATCTACACAAAATATTTCGCTTATTCACGTAGATAGAATTATTTAA

SEQ ID No. 238 – Ken05/Tk1 EP402R (NC_044945.1:74107-75249)

ATGATAATAAAACTTATTTTTTTAATTTGTTTTAAAATAGTTTTAAGTATTGATAATAAAACAAAATTTAATGAAACATTAAT
TTTAGATAATATTGATTATTGGGTAAAGTTTAATGATACAATAACTTTAGATAGTAATATTACTAGTGAAATAGAAGCTGTAT
CTTGGAATTTTTATAATAATACTTTTAATCTACTTGCTACATGTGGAAAAGCAAGTAACTTTTGTAGTTGTTCTAATTATAGT
ACATCATTTTTTAATATTACAAATAATTGTAGTTTAACTATTTTTTTAATAGACGAGACGTTATTTAATACAACATATCAAAT
AGTATATTCAACTAATATAATTAATTATAAAATAAACTTATTAATACCTGTTACTCCTCCAATTATTTCATATAATTGTACTA
ATTGTTCTATAAATTGTAAAAAAAGTAATGGTACAAATACTAATATTTTTTTATCTATAAATGATACAATTGTTACATATACT
AATGAAAGTATTCTTAATTATGATTATAACTGTAGTATTTTAAATAATAATTTTACAGTTACATGTATAATTAATAATACAAT
TAGTACATCAAATACTACAGAATTTATAAACTGCACTAATATATTATTAAGTAGTTATCTAGATTTTTTTCAAGTAACTAGTT
ATATATTTTATATGATAATTTTTATTGTAACTGGAATAACAGTAAGTATTCTTATATCCATCATAACTTTCTTATTTATACGA
AAAAGAAAACATGTTGAAGAAATAGAAAGTCCACCGCCTGAATCTAATGAAGAAGAACAACAATGTCATCATGACACCACTTC
TATACATGAACCGTCTCCCAGAGAACCATTACTTCCTAAGCCTTACAGTCGTTATCAATATAATACACCTATTTACTACATGC
GTCCCTCAACACAACAACTATTTAAATCATATTCTTTACCCAAACCATGTCCCCCACCTAAACCATGTCCTCCACCCAAACCA
TGTCCCCCACCCAAACCATGTCCTCCACCCAAACCATGTCCTCCATCCAAACCATATCCTTCACTACCTAGTATCCCGCTACC
ACCCGATATCCCGCCATTATCTACACAAAATATTTCGCTTATTCACGTAGATAGAATTATTTAA

SEQ ID No. 239 – Kenya 1950 EP402R (AY261360.1:76800-77978)

ATGATAATAAAACTTATTTTTTTAATTTGTTTTAAAATAGTTTTAAGTATTGATAATAAAACAAAATTTAATGAAACATTAAT
TTTAGATAATATTGATTATTGGGTAAAGTTTAATGATACAATAACTTTAGATAGTAATATTACTAGTGAAATAGAAGCTGTAT
CTTGGAATTTTTATAATAATACTTTTAATCTACTTGCTATATGTGGAAAAGCAAGTAACTTTTGTAGTTGTTCTAATTATAGT
ACATCATTTTTTAATATTACAAATAATTGTAGTTTAACTATTTTTTTAATAGACGAGACGTTATTTAATACAACATATCAAAT
AGTATATTCAACTAATATAATTAATTATAAAATAAACTTATTAATACCTGTTACTCCTCCAATTATTTCATATAATTGTGCTA
ATTGTTCTATAAATTGTAAAAAAAGTAATGGTACAAATACTAATATTTTTTTATCTATAAATGATACAATTGTTACATATACT
AATGAAAGTATTCTTAATTATGATTATAACTGTAGTATTTTAAATAATAATTTTACAGTTACATGTATAATTAATAATACAAT
TAGCACATCAAATACTACAGAATTTATAAACTGCACTAATATATTATTAAGTAGTTATCTAGATTTTTTTCAAGTAACTAGTT
ATATATTTTATATGATAATTTTTATTGTAACTGGAATAACAGTAAGTATTCTTATATCCATCATAACTTTCTTATTTATACGA
AAAAGAAAACATGTTGAAGAAATAGAAAGTCCACCGCCTGAATCTAATGAAGAAGAACAACAATGTCATCATGACACCACTTC
TATACATGAACCGTCTCCCAGAGAACCATTACTTCCTAAGCCTTACAGTCGTTATCAATATAATACACCTATTTACTACATGC
GTCCCTCAACACAACAACTATTTAAATCATATTCTTTACCCAAACCATGTCCCCCACCTAAACCATGTCCTCCACCTAAACCA
TGTCCCCCACCTAAACCATGTCCTCCATCCAAACCATGTCCTCCACCTGAACCATATTCTCCACCCAAACCATGTCCTCCACC
CAAACCATATCCTTCACTACCTAGTATCCCGCTACCACCCGATATCCCGCCATTATCTACACAAAATATTTCGCTTATTCACG
TAGATAGAATTATTTAA

SEQ ID No. 240 – Warthog EP402R (AY261366.1:70011-71156)

ATGATAATTAAACTTATTTTTTTAATTTGTTTCAAAATAGTTTTAAGTATTAATTATTGGGTTAGGTATAATGATACAGTAAC
TTTAAATAGTAATATCAATAGCGAGACAGAAGGTATATTTTGGAATTTTTATAATAATACTTTTAATACTATTGCCACATGTG
GAAAAAAAAATAATGTTTGTGAATGTTCTAATTATGATAAATCCTTATATAATATAACAAATAATTGTAGTTTAACAATTTTT
CCAAATAATACAAAAATATTTAATACAACATATCAATTAGTATATTCACGCAATAGAATTAATTACACAATAAATTTGTTATT
ACCTGTTACATCTCCAATTATTACATATAATTGTACTCAATCTTTAATAACATGTGAAAAAACTAATGGAACAAATATTCATT
TATTCTTAAATTTAAATGATACAATTAATGAATATACTAACAAAAGTTTTCTCAATTACTATTGGAATAGTAGTGAGTTAAAT
AATATTTTTCTTGCTACATGTATTATTAATAATACACTTAATTCAGCAAATACTACAAAAGTTATCAATTGCACTAACCCATT
ATTAAAATCTTACCAAAATTATTTTCTTGAAAATATTCATACATTATTTTATATGATAATTTTTATTGTATCTGGAATAACAA
TAAGTATTTTTATATCAATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAAATAGAGAGTCCACCACCT
GAATCTAATGAAGAAGAACAATGTCAGCATGATGACACCACTTCTATACATGAACCATCTCCCAGAGAACCATTACTTCCTAA
ACCTTACAGTCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCAACCCATTTCCCCTACCTA
AACCATGCCCGCCACCTAAACCGTGTCCTCCACCCAAACCATGCCCGCCACCCAAACCATGCCCGCCACCTAAACCATGTCCT
CCACCCAAACCATGCCCGCCACCTAAACCATGTCCTCCACCTGAATCATATTCTCCACCCAAACCACTACCTAGTATCCCGCT
GCTACCCAATATCCCGCCATTATCTACACAAAATATTTCGCTTATTCATGTAGATAGAATTATTTAA

SEQ ID No. 241 – Mkuzi 1979 EP402R (AY261362.1:75106-76287)

ATGATGATAATTATACTTATTTTTTTAATATGTTTAAAAATAGTTTTAAATAATAATATTATAATATGGCATACTTTAAATGA
AACAATTTTTTTAAATAATAGTATTACATTTACGGATAATCTTGGTGGTCTATTTTGGAATACATATTATAATAATAATCATA
GTATCCTTACTAGTTGCGGAATATATCAAAATTATTGTTCATGCACTAATAATTATAGCACATCATTATATAATATAACAAAT
AATTGTGGTTTAATAATTTTTCCAAATAATACAAAAAGATTTAACACAACGTATGAATTAGTATATTTAAATAATAGTACTAA
ATATACAATAAACTTATTAGTACCTGTTACTCCTCCAAATATTACATATAATTGTACTACATCTGTAATAACATGTAAAAAAA
ATGATGGCACAAATACTAATATGTTTTTAAAAATAAATGATACAATCGTTAAAAGTAGTAATGAAAGTGTTTTTGAATACTCT
TGGAATAGTACTGATTTAAATAACAATTTTACGGCTATATGTATAATTAATAATACAATTAATTCATCAAATGACACACAAAC
TATAGAATGTCCCAATATATTATTAAACAATTATTTAGACTTTTTTCAAGTAACTAGTTACATGTTTTATATGATAATTTTTA
TTGTAACTGGAATAATAGCAAGTATTTTTATTTCAATCATAACTTTTTTATCTTTACGAAAAAGAAAAAAACATGTTGAAGAA
ATAGAAAGTCCACCACCCTCTGAATCTAATGAAGAAGATATTTCTCACGATGACACCACTTCCATACATGAACCATCTCCCAG
AGAACCATTACTTCCTAAGCCTTACAGTCGTTATCAGTATAATACACCTATTTACTACATGCGTCCCTCAACACAACCACTCA
ACCCATTTCCCCTACCTAAACCATGCCCGCCACCTAAACCATGCCCGCCACCCAAACCATGTCCTCCACCTAAACCGTGTCCT
CCACCCAAACCGTGTCGTCCACCTAAACCATGTCCTCCACCTAAACCATGCCCACCACCTAAACCATGTCCTTCACCTGAAAC
ATATTCTCCACCCAAACCACTACCTAATATCCCGCTGCTACCCAATATCCCGCCATTATCTACACAAAATATTTCGCTTATTC
ACGTAGATAGGATTATTTAA

In an embodiment the invention provides an attenuated ASF virus in which the expression and/or activity of the EP402R gene is disrupted. Suitably, the EP402R gene comprises the sequence of SEQ ID No. 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240 or 241. Suitably, the EP402R gene comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240 or 241. Suitably, the EP402R gene consists of the sequence of SEQ ID No. 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240 or 241.

The amino acid sequence of the EP402R protein from the Benin 97/1 strain is depicted below as SEQ ID No. 21.

SEQ ID No. 21 – Benin 97/1 EP402R protein

MIIIVIFLMCLKIVLNNIIIWSTLNQTVFLNNIFTINDTYGGLFWNTYYDNNRSNFTYCGIAGNYCSCCGHNISLYNTTNNCS
LIIFPNNTEIFNRTYELVYLDKKINYTVKLLKSVDSPTITYNCTNSLITCKNNNGTNVNIYLIINNTIVNDTNGDILNYYWNG
NNNFTATCMINNTISSLNETENINCTNPILKYQNYLSTLFYIIIFIVSGLIIGIFISIISVLSIRRKRKKHVEEIESPPPSES
NEEDISHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCSPPK
PCRPPKPCPPPKPCPPPKPCPPPKPCPPSKPCPSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 21. Suitably, the EP402R gene encodes a protein comprising a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 21. Suitably, the EP402R gene encodes a protein consisting of the sequence of SEQ ID No. 21.

The ligand-binding domain of Benin 97/1 EP402R is formed by amino acids 1-198 of SEQ ID No. 21 which are presented below as SEQ ID No. 34.

SEQ ID No. 34 – Benin 97/1 EP402R protein ligand-binding domain

MIIIVIFLMCLKIVLNNIIIWSTLNQTVFLNNIFTINDTYGGLFWNTYYDNNRSNFTYCGIAGNYCSCCGHNISLYNTTNNCS
LIIFPNNTEIFNRTYELVYLDKKINYTVKLLKSVDSPTITYNCTNSLITCKNNNGTNVNIYLIINNTIVNDTNGDILNYYWNG
NNNFTATCMINNTISSLNETENINCTNPILKY

Suitably, the ligand-binding domain of the EP402R protein comprises the sequence of SEQ ID No. 34. Suitably, the ligand-binding domain of the EP402R protein comprises a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 34. Suitably, the ligand-binding domain of the EP402R protein consists of the sequence of SEQ ID No. 34.

The orthologous EP402R genes from other ASFV isolates are depicted below as SEQ ID Nos 22 to 30:

SEQ ID No. 22 – Mkuzi EP402R protein

MIIILIFLICLKIVLNNNIIIWHTLNETIFLNNSITFTDNLGGLFWNTYYNNNHSILTSCGIYQNYCSCTNNYSTSLYNITNN
CGLIIFPNNTKRFNTTYELVYLNNSTKYTINLLVPVTPPNITYNCTTSVITCKKNDGTNTNMFLKINDTIVKSSNESVFEYSW
NSTDLNNNFTAICIINNTINSSNDTQTIECPNILLNNYLDFFQVTSYMFYMIIFIVTGIIASIFISIITFLSLRKRKKHVEEI
ESPPPSESNEEDISHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPP
PKPCRPPKPCPP PKPCPPPKPCPSPETYSPPKPLPNIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 23 – Warmbaths EP402R protein

MIIILIFLIYLKLVLNNNIIIWHPTLNETIFLNVTTIGNISGLFWNTYYNNNRSELTKCGIYNNYCSCDSLNTSLYNINNCSL
VIFPNNTKIFNTIYELIYSGNQTNYTIKLLESTTPPNITYNCTTSVITCKKNNGTNTNIFLTINNTIVNSTNEDVIYYYWNRS
EFNNFTATCMINNTINSSNISEIIDCTNTLLLNSYLDFFQVAGYMFYMIIFIVTGITVSIFISIITFLSLRKRKKHVEEIESL
PPESNEEECQHDDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKP
CPPPKPCPPPESCSSPESCSSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 24 – Georgia 2007/1 EP402R protein

MIILIFLIFSNIVLSIDYWVSFNKTIILDSNITNDNNDINGVSWNFFNNSFNTLATCGKAGNFCECSNYSTSIYNITNNCSLT
IFPHNDVFDTTYQVVWNQIINYTIKLLTPATPPNITYNCTNFLITCKKNNGTNTNIYLNINDTFVKYTNESILEYNWNNSNIN
NFTATCIINNTISTSNETTLINCTYLTLSSNYFYTFFKLYYIPLSIIIGITISILLISIITFLSLRKRKKHVEEIESPPPESN
EEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPSAESYSPPK
PLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 25 – Malawi Lil-20/1 (1983) EP402R protein

MIIILIFLIIPNIVLSIDYWVSFNKTIILDSNITNDNNDINGVSWNFLNNSLNTLATCGKAGNFCECSNYSTSLYNIAHNCSL
TIFPHNDVFGTPYQVVWNQIINYTIKLLTPVTPPNITYNCTNFLITCKKNNGTNTIIYFNINDTNVKYTNESILEYNWNNSNF
NNFTATCIINNTINSSNDTQTIDCINTLLSSYLDFFQVASYMFYMIIFIATGIIASIFISIITFLSLRKRKKHVEEIESPSPS
ESNEEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPLTQPLNPSPLPKLCPPPKPCPPPKPCPPPKPCPPPKPCP
SSESCSPPESYSLPKPLPNIPLLPNIPPLSTQN ISLIHVDRII

SEQ ID No. 26 – Kenya 1950 EP402R protein

MIIKLIFLICFKIVLSIDNKTKFNETLILDNIDYWVKFNDTITLDSNITSEIEAVSWNFYNNTFNLLAICGKASNFCSCSNYS
TSFFNITNNCSLTIFLIDETLFNTTYQIVYSTNIINYKINLLIPVTPPIISYNCANCSINCKKSNGTNTNIFLSINDTIVTYT
NESILNYDYNCSILNNNFTVTCIINNTISTSNTTEFINCTNILLSSYLDFFQVTSYIFYMIIFIVTGITVSILISIITFLFIR
KRKHVEEIESPPPESNEEEQQCHHDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQQLFKSYSLPKPCPPPKPCPPPKP
CPPPKPCPPSKPCPPPEPYSPPKPCPPPKPYPSLPSIPLPPDIPPLSTQNISLIHVDRII

SEQ ID No. 27 – N10 EP402R protein

MIIKLIFLISFKMILGIDYWVSLNNTIILDSNITINNITNTTNNPTLNGIFWNIYNNSYNNTFNLLTTCGNTYNICSCSNNYN
TILFNYNTTNNCSLIISPHDEKIFDTMFQIIYLTNKINYTIRWLQPVDPPNISFNDSNSLIKCEKNNGTNTEIYLYLNDTFIN
NTNENDLKYYWNCSELNYNITATCIINNTLNSANTTKVINCTNLLLKSDQNYFLKNIHTLFYIIIFIVTGIIISIFIAIITFL
SLRKRKKHVEEIESPSPESNEEEEQQHHHDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQQLFKSYSLPKPCPPPKPC
PPPKPCPPPKPCPSPESYPSPEPYPLLPNIPLPPNIPPLSTQNISLIHVDRII

SEQ ID No. 28 – Tengani 62 EP402R protein

MIIKVIFLVFFKMVLSNIIIWSTLNNTIYLNINYSDSNLYTGLFWNKYYNNTRNNFTTCVTSNSSYCTCKGHNTSLYNITNNC
SLIIFPNNTKIFNTTYELVYLNNKINYTIQMVQPVDPPIIIYNDTNNSLITCEKNNGTNTEIYLYLNDTFINNTNENSIKYYW
NCSELNHNITTTCIINNTLNSANTTKVINCTNLLLKSDQNYFLKNIHTLFYIIIFIVGGTLISIIISIITFLSLRKRKKHVEE
IESPPPSESNEEEHCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPC
PPPKPCPPPKPCPSPESHSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 29 – Pr4 EP402R protein

MFITLIFLSYINIVLSNNYWARLNETITLNSNITNDTNNELGIFWNSYNNTYYNNTFNNIAICGKKGIFCECNINYNTSISNT
SISNTSIYNVTNNCSLTIFLYDDNIFKTYQLVYQNYKINYTINLLLPVTSPNITYNCTNSLITCEKNDGTNTNMFLSINNITI
NHTNQDILTYYWNNSEFNNFTATCMINNTLNSANTTKVINCTNPLLNSYQNYFLENIHTLFYIIIFIVSGLIASIFISIITFL
SLRKRKKHVEEIESPPPESNEEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPNPCPPPKPCPP
PKPCPPPKPCPPPKPCPPPKPCPPPKPCPPPKPCSSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 30 – Warthog EP402R protein

MIIKLIFLICFKIVLSINYWVRYNDTVTLNSNINSETEGIFWNFYNNTFNTIATCGKKNNVCECSNYDKSLYNITNNCSLTIF
PNNTKIFNTTYQLVYSRNRINYTINLLLLPVTSPIITYNCTQSLITCEKTNGTNIHLFLNLNDTINEYTNKSFLNYYWNSSELN
NIFLATCIINNTLNSANTTKVINCTNPLLKSYQNYFLENIHTLFYMIIFIVSGITISIFISIITFLSLRKRKKHVEEIESPPP
ESNEEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCP
PPKPCPP PKPCPPPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 242 – China/2018/AnhuiXCGQ EP402R protein

MIILIFLIFSNIVLSIDYWVSFNKTIILDSNITNDNNDINGVSWNFFNNSFNTLATCGKAGNFCECSNYSTSIYNITNNCSLT
IFPHNDVFDTTYQVVWNQIINYTIKLLTPATPPNITYNCTNFLITCKKNNGTNTNIYLNINDTFVKYTNESILEYNWNNSNIN
NFTATCIINNTISTSNETTLINCTYLTLSSNYFYTFFKLYYIPLSIIIGITISILLISIITFLSLRKRKKHVEEIESPPPESN
EEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPSAESYSPPK
PLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 243 – Pretorisuskop/96/4 EP402R protein

MIMFITLIFLSYINIVLSNNYWARLNETITLNSNITNDTNNELGIFWNSYNNTYYNNTFNNIAICGKKGIFCECNINYNTSIS
NTSISNTSIYNVTNNCSLTIFLYDDNIFKTYQLVYQNYKINYTINLLLPVTSPNITYNCTNSLITCEKNDGTNTNMFLSINNI
TINHTNQDILTYYWNNSEFNNFTATCMINNTLNSANTTKVINCTNPLLNSYQNYFLENIHTLFYIIIFIVSGLIASIFISIIT
FLSLRKRKKHVEEIESPPPESNEEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPNPCPPPKPC
PPPKPCPPPKPCPPPKPCPPPKPCPPPKPCPPPKPCSSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 244 – L60 EP402R protein

MIIIVIFLMCLKIVLNNIIIWSTLNQTVFLNNIFTINDTYGGLFWNTYYDNNRSNFTYCGIAGNYCSCCGHNISLYNTTNNCS
LIIFPNNTEIFNRTYELVYLDKKINYTVKLLKSVDSPTITYNCTNSLITCKNNNGTNVNIYLIINNTISSLNETENINCTNPI
LKYQNYLSTLFYIIIFIVSGLIIGIFISIISVLSIRRKRKKHVEEIESPPPSESNEEDISHDDTTSIHEPSPREPLLPKPYSR
YQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCPPPKPCSPPKPCRPPKPCPPPKPCPPPKPCPPS
KPCPSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

SEQ ID No. 245 – Ken06.Bus EP402R protein

MIIKLIFLISFKMILGIDYWVSLNNTIILDSNITINNITNTTNNPTLNGIFWNIYNNSYNNTFNLLTTCGNTYNICSCSNNYN
TILFNYNTTNNCSLIISPHDEKIFDTMFQIIYLTNKINYTIRWLQPVDPPNISFNDSNSLIKCEKNNGTNTEIYLYLNDTFIN
NTNENDLKYYWNCSELNYNITATCIINNTLNSANTTKVINCTNLLLKSDQNYFLKNIHTLFYIIIFIVTGIIISIFIAIITFL
SLRKRKKHVEEIESPSPESNEEEEQQHHHDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQQLFKSYSLPKPCPPPKPC
PPPKPCPPPKPCPSPESYPSPEPYPLLPNIPLPPNIPPLSTQNISLIHVDRII

SEQ ID No. 246 – Ken05/Tk1 EP402R protein

MIIKLIFLICFKIVLSIDNKTKFNETLILDNIDYWVKFNDTITLDSNITSEIEAVSWNFYNNTFNLLATCGKASNFCSCSNYS
TSFFNITNNCSLTIFLIDETLFNTTYQIVYSTNIINYKINLLIPVTPPIISYNCTNCSINCKKSNGTNTNIFLSINDTIVTYT
NESILNYDYNCSILNNNFTVTCIINNTISTSNTTEFINCTNILLSSYLDFFQVTSYIFYMIIFIVTGITVSILISIITFLFIR

KRKHVEEIESPPPESNEEEQQCHHDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQQLFKSYSLPKPCPPPKPCPPPKP
CPPPKPCPPPKPCPPSKPYPSLPSIPLPPDIPPLSTQNISLIHVDRII

The ligand-binding domain of the EP402R protein from other strains can be readily identified by alignment with the sequence of Benin 97/1 EP402R protein, such as shown in Figure 3.

In an embodiment the invention provides an attenuated ASF virus in which the expression and/or activity of the EP402R gene is disrupted. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 22. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 23. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 24. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 25. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 26. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 27. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 28. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 29. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 30. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 242. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 243. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 244. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 245. Suitably, the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 246.

Haemadsorption

Haemadsorption is the phenomenon whereby cells infected with ASFV adsorb erythrocytes (red blood cells) on their surface. The degree of haemadsorption induced by an ASFV may be measured using a haemadsorption assay such as described herein. For example, cells may be transfected with a protein or infected with an ASFV, then red blood cells added and the degree of haemadsorption detected by imaging. In this way, different proteins and viruses can be tested for their effect on haemadsorption.

EP402R and EP153R are involved in mediating haemadsorption of ASFV-infected cells.

In an embodiment the invention provides an attenuated ASF virus which has reduced haemadsorption.

In an embodiment of the attenuated ASF virus of the invention, the ability of the EP153R gene and/or the EP402R gene to mediate haemadsorption may be disrupted. In an embodiment, the ability of the EP153R gene to mediate haemadsorption may be disrupted.

In an embodiment, the ability of the EP402R gene to mediate haemadsorption may be disrupted.

Reducing haemadsorption or disrupting the ability to mediate haemadsorption means that cells infected with the attenuated ASFV of the invention or transfected with a mutant, non-functional EP153R or EP402R protein adsorb fewer red blood cells to their surface than cells infected with a wild-type ASFV or transfected with a wild-type EP153R or EP402R protein. The number of red blood cells adsorbed to the surface of the infected/transfected cells may be decreased by at least 50, 60, 70, 80 or 90%. In an embodiment, haemadsorption is abolished i.e. no red blood cells adsorb to the surface of cells infected with the attenuated ASFV of the invention or transfected with a mutant, non-functional EP153R or EP402R protein.

Gene expression

The attenuated African Swine Fever (ASF) virus of one embodiment of the present invention has disrupted expression and/or activity of the genes DP148R, EP153R and EP402R. These genes may be referred to herein as the “disrupted genes”.

In an embodiment the invention provides an attenuated ASFV in which expression of the genes DP148R, EP153R and EP402R is disrupted.

The term “expression” with respect to a gene refers to the ability of the ASF virus to produce the product of the gene, such as RNA and/or protein. Disruption of expression of a gene means that production of the gene product is decreased. Expression of the gene may be decreased by at least 50%, at least 60%, at least 70%, at least 80%, at least 90% and/or at least 95%. Expression of the gene may be decreased to the extent that production of the gene product, such as RNA and/or protein, is entirely abolished (i.e. the gene product is not produced at all). Disruption of gene expression decreases expression of the gene relative to the expression of the gene when it is not disrupted. For example, a mutated gene may have decreased expression in comparison to a wild-type version of the gene.

A gene the expression of which is disrupted may not be fully transcribed and translated. Transcription of the gene may be decreased by at least 50%, at least 60%, at least 70%, at least 80%, at least 90% and/or at least 95%. Transcription of the gene may be abolished (i.e. the gene may not be transcribed). Translation of the gene may be decreased by at least 50%, at least 60%, at least 70%, at least 80%, at least 90% and/or at least 95%. Translation of the gene may be abolished. The gene may be transcribed but not translated. The gene

may be transcribed and translated but the protein too rapidly degraded to carry out its function. The gene may be transcribed and translated but the protein may be non-functional.

Gene expression may be measured by techniques known in the art. For example, the amount of mRNA transcribed from a gene may be quantified, such as by using quantitative polymerase chain reaction (qPCR). Alternatively or additionally, the amount of protein may be quantified, such as by using Western blotting or mass spectrometry.

Gene activity

In an embodiment the invention provides an attenuated ASFV in which activity of the genes DP148R, EP153R and EP402R is disrupted.

The term "activity" with respect to a gene refers to the ability of the gene to carry out its functions. Different genes have different activities i.e. different functions they fulfil. A given gene may have multiple activities; disruption of gene activity means disruption of one or more of those activities. One or more activity of the gene may be disrupted whilst one or more other activities are not disrupted. Disruption of gene activity decreases the activity of the gene relative to the activity of the gene when it is not disrupted. For example, a mutated gene may have decreased activity in comparison to a wild-type version of the gene. Gene activity may be decreased to the extent that gene activity is entirely abolished.

The attenuated ASFV according to the present invention may comprise a non-functional version of the disrupted genes.

Disruption of expression of a gene may also disrupt activity of that gene as the decreased amount of gene product means the gene cannot as effectively carry out one or more of its activities.

Gene expression and/or activity are disrupted by mutating the ASFV genome i.e. by mutating the ASFV genome. A "mutation" means a change in the nucleotide sequence of the ASFV genome relative to a known ASFV genotype. Mutations include changing one or more nucleotides to different nucleotides (i.e. substitution), adding nucleotides, deleting nucleotides and/or a combination of these.

In an embodiment the attenuated ASF virus of the invention comprises mutations that disrupt the expression and/or activity of the genes DP148R, EP153R and EP402R.

Gene expression and/or activity may be disrupted by disrupting transcription of the gene into mRNA i.e. by decreasing gene transcription, such as completely abolishing gene transcription. Gene expression and/or activity may be disrupted by disrupting translation of

mRNA into protein. In an embodiment the attenuated ASF virus comprises mutations that decrease transcription and/or translation of the genes. In an embodiment the attenuated ASF virus comprises mutations that cause the genes to not be transcribed and/or translated (i.e. complete abolition of transcription and/or translation).

Gene expression and/or activity may be disrupted by mutating a non-coding sequence associated with the gene, such as a promoter. In an embodiment the attenuated ASF virus comprises mutations in promoters of one or more of the disrupted genes.

Gene expression and/or activity may be disrupted by mutating a coding sequence of one or more of the disrupted genes.

Activity of DP148R

In an embodiment of the attenuated ASFV of the invention, DP148R activity may be disrupted.

In an embodiment the activity of DP148R that may be disrupted is its ability to inhibit type I interferon. In other words, the ability of DP148R to inhibit type I interferon may be decreased. The ability of DP148R to inhibit type I interferon may be decreased by at least 50, 60, 70, 80 or 90%. The ability of DP148R to inhibit type I interferon may be completely abolished.

In an embodiment the activity of DP148R that may be disrupted is its ability to inhibit NF-κB activity. In an embodiment, the invention provides an attenuated ASF virus in which the ability of the DP148R gene to inhibit NFκB activity is disrupted. NFκB activity may be measured using a luciferase reporter assay as described herein.

Disruption of the ability to inhibit NFκB activity means that the ability to inhibit NFκB activity is decreased. In other words, the DP148R gene of the attenuated ASF virus of the invention inhibits NFκB activity less than would a wild-type version of the DP148R gene. The ability to inhibit NFκB activity may be decreased by at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In an embodiment the ability of the DP148R gene to inhibit NFκB activity may be abolished i.e. the DP148R gene does not inhibit NFκB activity. In that case, the activity of NFκB would be as high as if no DP148R gene were present. A decrease in inhibition means NFκB activity is higher than it would be with the wild-type version of the DP148R gene. NFκB activity may be twice as high as it would be with the wild type version of the DP148R gene, such as three times as high, four times as high, five times as high or six times as high.

NFκB is a transcription factor that activates transcription of various genes, controlling expression of interferon and pro-inflammatory cytokines as part of the host's innate immune system response to viral infection. Inhibition of NFκB activity means decreasing activation of expression of its target genes. The degree of activation of NFκB target gene expression may be measured using a luciferase reporter assay in which an NFκB-activatable promoter is linked to a luciferase reporter.

In an embodiment the activity of DP148R that may be disrupted is its ability to inhibit translocation of the p65 sub-unit of NFκB to the nucleus. In an embodiment, the invention provides an attenuated ASF virus in which the ability of the DP148R gene to inhibit translocation of the p65 sub-unit of NFκB to the nucleus is disrupted. Translocation of p65 to the nucleus can be measured by immunofluorescence of cells stimulated with NF-κB activators as described herein. The relative and absolute amounts of p65 that translocate to the nucleus may quantified by using differential cell lysis conditions known in the art to either break open the nucleus or leave it intact then quantify the amount of p65 using techniques known in the art such as Western blotting or mass spectrometry. For example, cells expressing a wild type or mutant DP148R protein may be stimulated to activate NF-κB then differentially lysed to produce whole cell lysate, a cytoplasmic fraction and a nuclear fraction. The amount of p65 in each fraction may then be quantified for the different conditions (wild type or mutant DP148R protein).

Disruption of the ability to inhibit translocation of p65 to the nucleus means that the ability to inhibit translocation of p65 to the nucleus is decreased. In other words, the version of the DP148R gene in the attenuated ASF virus of the invention inhibits translocation of p65 to the nucleus less than would a wild-type version of the DP148R gene. The ability to inhibit translocation of p65 to the nucleus may be decreased by at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In an embodiment the ability of the DP148R gene to inhibit translocation of p65 to the nucleus may be abolished i.e. the DP148R gene does not inhibit translocation of p65 to the nucleus. In that case, as much p65 would translate to the nucleus as if no DP148R gene were present. A decrease in inhibition means the proportion of p65 that translocates to the nucleus is higher than it would be with the wild-type version of the DP148R gene. The proportion of p65 that translocates to the nucleus may be twice as high as it would be with the wild type version of the DP148R gene, such as three times as high, four times as high, five times as high or six times as high.

Activity of EP153R

In an embodiment of the attenuated ASFV of the invention, EP153R activity may be disrupted.

In an embodiment the activity of EP153R that may be disrupted is its ability to mediate haemadsorption. In other words, the ability of EP153R to mediate haemadsorption may be decreased. The ability of EP153R to mediate haemadsorption may be decreased by at least 50, 60, 70, 80 or 90%. The ability of EP153R to mediate haemadsorption may be completely abolished.

In an embodiment the activity of EP153R that may be disrupted is its ability to inhibit caspase-3. In other words, the ability of EP153R to inhibit caspase-3 may be decreased. The ability of EP153R to inhibit caspase-3 may be decreased by at least 50, 60, 70, 80 or 90%. The ability of EP153R to inhibit caspase-3 may be completely abolished. Caspase-3 activity may be measured by assays known in the art, such as described by Hurtado et al. (Hurtado et al. 2004 Virology 326: 160-170). For example, the cleaved active caspase-3 fragment of 17 kDa and the inactive procaspase-3 protein of 34 kDa may be quantified using Western blot or mass spectrometry and compared to ascertain the degree of activation of caspase-3. Alternatively or additionally, the ability of caspase-3 in cell extract to cleave a fluorescent substrate may be measured using high performance liquid chromatography.

In an embodiment the activity of EP153R that may be disrupted is its ability to inhibit MHC-I expression. In other words, the ability of EP153R to inhibit MHC-I expression may be decreased. The ability of EP153R to inhibit MHC-I expression may be decreased by at least 50, 60, 70, 80 or 90%. The ability of EP153R to inhibit MHC-I expression may be completely abolished. MHC-I expression may be measured by assays known in the art, such as described by Hurtado et al. (Hurtado et al. 2011 Arch. Virol. 156(2): 219-234). For example, cell surface expression of MHC-I may be measured using antibody staining of non-permeabilised cells followed by flow cytometry.

Activity of EP402R

In an embodiment of the attenuated ASFV of the invention, EP402R activity is disrupted.

In an embodiment the activity of EP402R that is disrupted is its ability to mediate haemadsorption. In other words, the ability of EP402R to mediate haemadsorption may be decreased. The ability of EP402R to mediate haemadsorption may be decreased by at least 50, 60, 70, 80 or 90%. The ability of EP402R to mediate haemadsorption may be completely abolished.

The activity of EP402R that is disrupted may be the ability of the EP402R protein to bind ligands via its extracellular N-terminal Ig-like domain (i.e. its ligand-binding domain). Thus in an embodiment the invention provides an attenuated ASF virus wherein the EP402R gene

comprises one or more mutations that disrupt ligand binding by the EP402R protein. The ability of the EP402R protein to bind one or more ligands may be disrupted. The ability of EP402R to bind one or more ligands may be decreased by at least 50, 60, 70, 80 or 90%. The ability of the EP402R protein to bind one or more ligands may be completely abolished. The ability of the EP402R protein to bind one or more ligands may be completely abolished whilst retaining the ability to bind other ligands. In an embodiment, the invention provides an attenuated ASF virus wherein the EP402R gene comprises one or more mutations that disrupt ligand binding by the EP402R protein. Ligand binding may be measured using assays such as immunoprecipitation, surface plasmon resonance and/or isothermal calorimetry.

Functional version of a gene

The attenuated ASFV of the invention comprises a functional version of one or more of the following genes:

multigene family (MGF) 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

In some embodiments the attenuated ASFV of the invention may comprise a functional version of one or more of the following genes: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R. Suitably, the attenuated ASFV comprises functional versions of two or more, such as three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, thirteen or more, fourteen or more, fifteen or more, sixteen or more, seventeen or more, eighteen or more, nineteen or more, twenty or more, twenty one, or twenty two of the following genes: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R. In an embodiment the attenuated ASFV comprises functional versions of all of the following genes: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R.

The expression “functional version” of a gene refers to a gene the expression and activity of which have not been disrupted. A functional version of a gene may not be mutated in a manner that disrupts gene expression or gene activity. A functional version of a gene may not comprise any mutations. The coding sequence of a functional version of a gene may be complete and uninterrupted. A functional version of a gene may be fully transcribed and translated.

A functional version of a gene may correspond to the gene in a wild-type ASFV isolate. A functional version of a gene may correspond to the gene in a virulent ASFV strain. The sequence of a functional version of a gene may be identical to the sequence of the gene in a wild-type ASFV isolate or virulent ASFV strain. The sequence of a functional version of a gene may be identical to the sequence of the gene in the wild-type ASFV isolate from which the attenuated ASFV of the invention is derived. A functional version of a gene may be a natural variant of the gene in a wild-type ASFV isolate.

A functional version of a gene may comprise mutations. However, the mutations should not disrupt the expression or activity of the gene. In other words, the mutations should not affect the function of the gene. A functional version of a gene may comprise one or more synonymous mutations (i.e. mutations which do not alter the amino acid sequence of the protein the gene encodes). A functional version of a gene may comprise one or more silent mutations, which may be synonymous or non-synonymous. A functional version of a gene may comprise deletions that do not disrupt the expression or activity of the gene. A functional version of a gene may comprise one or more single nucleotide polymorphisms (SNPs) that do not disrupt the expression or activity of the gene.

Deletions

In the attenuated ASFV of the invention, expression and/or activity of genes may be disrupted by deletion. In other words, expression and/or activity of a gene may be disrupted by a mutation that is a deletion.

An attenuated ASFV of the invention may be made to lack a functional version of a gene by deletion. In other words, the mutation that causes the ASFV to lack a functional version of a gene may be a deletion.

"Deletion" means removal of part of the ASFV genome nucleotide sequence. The deletion may be continuous, or may comprise deletion of a plurality of sections of sequence. Deletion may disrupt gene expression and/or activity in any of the ways described herein. Deletion may cause the ASFV to lack a functional version of the gene in any of the ways described herein.

Deletion may disrupt transcription of the gene into mRNA. For example, deleting a promoter of a gene would disrupt transcription. Deletion may disrupt translation of mRNA into protein. For example, deleting a start codon would disrupt translation. Gene expression and/or activity may be disrupted by deleting non-coding sequence associated with the gene, such as a promoter.

Gene expression and/or activity may be disrupted by deleting coding sequence of the gene. The ASFV may be made to lack a functional version of the gene by deleting coding sequence of the gene. Deletion of coding sequence may be partial (i.e. part of the coding sequence is deleted). The deletion may, for example, remove at least 50, 60, 70, 80 or 90% of the coding sequence of the gene. The deletion may be complete, in which case 100% of the coding sequence of the gene is absent when compared to the corresponding genome of the wild-type isolate.

Deletion of coding sequence may be continuous, or may comprise deletion of a plurality of sections of coding sequence. The deletion should remove a sufficient amount of coding sequence such that deletion disrupts the expression and/or activity of the gene i.e. a functional gene product, such as a protein, is no longer produced from the gene. The expression “deletion of a gene” (such as “partially deleted”) refers to deletion of a sufficient amount of coding sequence such that expression and/or activity of the gene is disrupted. The amount of coding sequence required to be deleted to disrupt gene expression and/or activity may be very small. For example, deletion of just the start codon (ATG) may be sufficient to disrupt expression and/or activity of the gene to attenuate the virus.

Partial and full deletions of a gene can be made using known techniques in the art, such as conditional targeting via Cre-LoxP and Flp-FRT systems, or by inducing a double strand break (DSB) and repair using engineered nucleases such as meganucleases, zinc finger nucleases (ZFNs), transcription-activator like effector nucleases (TALENs) and Cas in CRISPR-Cas systems. The DSB repair can be exploited to introduce a desired mutation by providing a vector comprising the desired mutated nucleotide sequence within a sequence that is homologous to the sequences flanking either side of the DSB. This results in the desired mutation being inserted at the site of the DSB. Nucleases such as those above can be engineered to induce DSB at a specific site within the genome. For example, chimeric meganucleases can be readily generated by combining known protein units to recognise a target recognition sequence within a gene or genomic region of interest. ZFNs can also be designed to target specific sequences, for example combining zinc-finger units with known specificities to bind specific regions of DNA. TALENs are artificial restriction enzymes designed by fusing a nuclease domain to DNA-binding TALE (transcription activator-like effector) domains. TALE domains are tandem arrays of amino acid repeats that recognise a single nucleotide and can be designed to target a specific region of DNA. CRISPR-Cas systems consist of a Cas (CRISPR-associated protein) nuclease and a CRISPR (clustered regularly interspaced short palindromic repeat) RNA sequence that guides the Cas protein to recognise and cleave a specific strand of DNA complementary to the CRISPR sequence. Single-stranded guide RNA (sgRNA) can therefore be designed to bind to a specific region

of DNA and guide the Cas to introduce a DSB. Accordingly, provided the nucleotide (e.g. DNA or cDNA) sequence of a gene is known, a known nuclease system can be utilised to introduce a partial or full deletion to the gene.

In an embodiment of the attenuated ASF virus of the present invention the genes DP148R, EP153R and EP402R may be at least partially deleted.

The DP148R gene may be at least partially deleted. The EP153R gene may be at least partially deleted. The EP402R gene may be at least partially deleted. The DP148R and EP153R genes may each be at least partially deleted. The DP148R, EP153R and EP402R genes may each be at least partially deleted.

In an embodiment of the attenuated ASF virus of the present invention the genes DP148R, EP153R and EP402R may be completely deleted.

The DP148R gene may be completely deleted. The EP153R gene may be completely deleted. The EP402R gene may be completely deleted. The DP148R and EP153R genes may each be completely deleted. The DP148R, EP153R and EP402R genes may each be completely deleted.

Interruptions

The expression and/or activity of the genes may be disrupted by interruption of the gene. In other words, the mutation that disrupts expression and/or activity of a gene may be one that interrupts the gene.

In an embodiment of the attenuated ASFV of the present invention the genes DP148R, EP153R and EP402R may interrupted. The DP148R gene may be interrupted. The EP153R gene may be interrupted. The EP402R gene may be interrupted. The DP148R and EP153R genes may each be interrupted. The DP148R, EP153R and EP402R genes may each be interrupted.

"Interruption" means the mutation alters the coding sequence of the gene such that a functional gene product, such as a protein, is no longer produced. The term "interruption" may be used herein to refer to a mutation that interrupts a gene. The mutation(s) should interrupt the coding sequence in a manner such that expression and/or activity of the gene is disrupted i.e. a functional gene product, such as a protein, is no longer produced from the gene.

The interruption may entirely abolish gene product production. For example, where the gene product is a protein, the interruption may render the mRNA nonsensical, causing the mRNA

to be degraded and the protein to not be translated, thereby abolishing protein production. The interruption may alter the gene product that is produced. The interruption may cause the gene to not be transcribed and/or translated.

The interruption may be a point mutation (i.e. substitution, insertion or deletion of a single nucleotide). An interruption may be a deletion. A gene may comprise multiple mutations that lead to interruption of the gene.

The interruption may be a frame shift mutation. A frame shift causes the codons downstream of the frame shift to be read as different amino acids. The protein produced may be non-functional.

The interruption may be mutation of a start codon. A start codon is typically ATG. Mutation of a start codon (e.g. point mutation of one, two or three of the nucleotides) means that translation will not start at that codon. Translation may begin at a subsequent start codon further downstream. If the subsequent start codon is in frame a version of the protein is produced that is N-terminally truncated and so may be non-functional. If the subsequent start codon is not in frame an entirely different or nonsense protein is produced, which would be non-functional. If there is no subsequent start codon, translation is entirely abolished and no protein is produced.

The interruption may be mutation of a stop codon (TAG, TAA or TGA). Mutation of a stop codon (also referred to as a nonstop mutation) causes continued translation of mRNA into a sequence that should not be translated. The resulting protein may be non-functional due to its excessive length.

Amino acid changes

In an embodiment of the attenuated ASF virus of the invention, the EP402R gene comprises one or more mutations that change one or more amino acids in the ligand-binding domain of the EP402R protein. Suitably the EP402R gene comprises one or more mutations (such as two or more, three or more, four or more or five or more mutations) that change one or more amino acids (such as two or more, three or more, four or more or five or more amino acids) in the ligand-binding domain of the EP402R protein.

Changing of the one or more amino acids in the ligand-binding domain of the EP402R protein should disrupt expression and/or activity of the EP402R protein. In an embodiment, changing the one or more amino acids in the ligand-binding domain of the EP402R protein may disrupt haemadsorption mediated by the EP402R protein. In an embodiment, changing

the one or more amino acids in the ligand-binding domain of the EP402R protein may disrupt ligand binding by the EP402R protein.

In an embodiment, the one or more mutations in the ligand-binding domain may be a deletion or an interruption as described herein. For example, deletion of part of the coding sequence for the ligand-binding domain of the EP402R protein would result in the absence of the encoded amino acids from the ligand-binding domain, which may disrupt ligand binding.

In an embodiment, one or more of the mutations may be a point mutation. Suitably one or more of the mutations may be point mutations that change a single amino acid into a different amino acid. Such an amino change may be referred to as a substitution. Changing even a single amino acid may disrupt the activity of the EP402R protein, such as ligand binding activity. For example, changing an amino acid that can be charged to an amino acid that can have the opposite charge may disrupt folding of the EP402R ligand-domain such that a binding pocket is deformed, which prevents ligand binding. Alternatively or additionally, substitution with an amino acid that can have an opposite charge may prevent electrostatic binding of a ligand. Another possibility is that changing an amino acid with a small side-chain to an amino acid with a bulky side-chain, or vice versa, may disrupt folding of the EP402R ligand-binding domain so that a binding pocket does not form which prevents ligand binding.

Thus in an embodiment the one or more changed amino acids in the ligand-binding domain may comprise a negatively charged amino acid that is changed to a positively charged amino acid. In an embodiment the one or more changed amino acids in the ligand-binding domain may comprise a positively charged amino acid that is changed to a negatively charged amino acid. Positively charged amino acids (i.e. amino acids that can have a positive charge) include histidine (H), lysine (K) and arginine (R). Negatively charged amino acids (i.e. amino acids that can have a negative charge) include aspartic acid (D) and glutamic acid (E).

In an embodiment the one or more changed amino acids in the ligand-binding domain may comprise an amino acid with a small side-chain that is changed to an amino acid with a bulky side-chain. In an embodiment the one or more changed amino acids in the ligand-binding domain may comprise an amino acid with a bulky side-chain that is changed to an amino acid with a small side-chain. Amino acids with a bulky side-chain include tryptophan (W). Amino acids with a small side-chain include glycine (G) and alanine (A).

In an embodiment the one or more changed amino acids in the ligand-binding domain may comprise an amino acid with a hydrophilic side-chain that is changed to an amino acid with a hydrophobic side-chain. In an embodiment the one or more changed amino acids in the ligand-binding domain may comprise an amino acid with a hydrophobic side-chain that is changed to an amino acid with a hydrophilic side-chain. Amino acids with a hydrophobic side-chain include alanine (A), valine (V), isoleucine (I), leucine (L), methionine (M), phenylalanine (F), tyrosine (Y) and tryptophan (W). Amino acids with a hydrophilic side-chain include arginine (R), histidine (H), lysine (K), aspartic acid (D), glutamic acid (E), serine (S), threonine (T), asparagine (N) and glutamine (Q).

Changing amino acid E99 to R or amino acid Y102 to D disrupts the ability of EP402R protein from Benin 97/1 strain to mediate haemadsorption (see Figures 4, 5 and 6). Furthermore, changing the amino acid Q96 to R disrupts the ability of EP402R protein from Georgia 2007/1 strain to mediate haemadsorption (see Figure 4C). Accordingly, in an embodiment the one or more mutations change an amino acid at a position in the EP402R protein which corresponds to E99 and/or Y102 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In other words, the EP402R protein expressed by the attenuated ASF virus of the invention may be the EP402R protein from any ASF virus strain, and the amino acid that is changed corresponds to E99 and/or Y102 of the amino acid sequence of the EP402R protein from the Benin 97/1 strain, which is presented herein as SEQ ID NO. 11. The positions E99 and Y102 refer to amino acids glutamic acid and tyrosine at positions 99 and 102 respectively of the Benin 97/1 EP402R protein. In an embodiment the one or more mutations change the amino acid at position E99 and/or Y102 of the EP402R protein of the Benin 97/1 strain, or the corresponding position in the EP402R protein of any other ASFV strain. In an embodiment the one or more mutations change amino acids at positions in the EP402R protein which corresponds to E99 and Y102 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change an amino acid at a position in the EP402R protein corresponding to E99 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change an amino acid at a position in the EP402R protein which corresponds to Y102 of the Benin 97/1 EP402R protein (SEQ ID NO. 11).

Whether an amino acid corresponds to E99 and/or Y102 of the Benin 97/1 EP402R protein may be assessed by sequence alignment. For example, Figure 3 shows an alignment of EP402R proteins from Benin, Mkuzi, Warmbaths, Tengnani, Warthog, Georgia and Malawi strains. The amino acid in the EP402R protein from each strain that corresponds to E99 of Benin 97/1 EP402R protein is the amino acid shown below the Benin E99 residue (highlighted in yellow). The amino acid in the EP402R protein from each strain that

corresponds to Y102 of Benin 97/1 EP402R protein is the amino acid shown below the Benin Y102 residue (three amino acids to the right of the amino acids highlighted in yellow). The amino acids in the EP402R protein from the strains in Figure 3 that corresponds to E99 and Y102 in Benin 97/1 EP402R are given in Table 4 below.

Table 4

	Corresponding Amino acid	
Strain	**E99**	**Y102**
Mkuzi	E101	E104
Warmbaths	E98	Y101
Tengani	E100	Y103
Warthog	Q95	Y98
Georgia	Q96	W99
Malawi	Q97	W100

Amino acids corresponding to E99 and Y102 of Benin 97/1 EP402R exist in EP402R proteins from strains other than those shown in Figure 3 and listed in Table 4 above (such as other strains listed in Table 1 herein). The skilled person can readily determine using sequence alignment which amino acid in an EP402R protein from a given strain, such as a strain from Table 1, corresponds to E99 or Y102 of Benin 97/1 EP402R. The corresponding amino acid may be identical to E99 or Y102 of Benin 97/1 EP402R. For example, an amino acid corresponding to E99 of Benin 97/1 EP402R may also be an E (glutamic acid). The corresponding amino acid may be similar to E99 or Y102. Suitably the corresponding amino acid has the same charge as E99 or Y102. Suitably the corresponding amino acid to E99 is a Q (glutamine). Suitably the corresponding amino acid to Y102 is a W (tryptophan). The expression “corresponding to E99 and/or Y102 of Benin 97/1 EP402R protein” encompasses E99 and/or Y102D of Benin 97/1 EP402R protein.

In an embodiment the one or more mutations change an amino acid at position E99 and/or Y102 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change an amino acid at position E99 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change an amino acid at position Y102 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change an amino acid at position Q96 of Georgia 2007/1 EP402R protein (SEQ ID NO. 24).

In an embodiment the one or more mutations change an amino acid at a position in the EP402R protein corresponding to N16, I19, W21, Y76, E99, Y102 and/or N108 of Benin 97/1 EP402R protein (SEQ ID NO. 11). In an embodiment the one or more mutations change the amino acid at position N16, I19, W21, Y76, E99, Y102 and/or N108 of the EP402R protein of

the Benin 97/1 strain, or the corresponding position in the EP402R protein of any other ASFV strain. In an embodiment the one or more mutations change an amino acid at a position in the EP402R protein corresponding to S15, W19, Q96, N104, and/or K108D of Georgia 2007/1 EP402R protein (SEQ ID NO. 24). In an embodiment the one or more mutations change the amino acid at position S15, W19, Q96, N104, and/or K108D of the EP402R protein of the Georgia 2007/1 EP402R protein (SEQ ID NO. 24), or the corresponding position in the EP402R protein of any other ASFV strain. In an embodiment the one or more mutations change an amino acid at a position in the EP402R protein corresponding to W20, Q112, N121 and/or R125 of N10 Genotype IX EP402R protein (SEQ ID NO. 27). In an embodiment the one or more mutations change the amino acid at position S15, W19, Q96, N104, and/or K108D of the EP402R protein of the N10 Genotype IX EP402R protein (SEQ ID NO. 27), or the corresponding position in the EP402R protein of any other ASFV strain. These amino acids are in the ligand-binding domain of the EP402R protein and are surface exposed.

Suitably, the mutation is selected from N16R, I19R, W21D, Y 76D, E99R, Y102D and/or N108R at a position corresponding to the position in the Benin 97/1 EP402R protein (SEQ ID NO. 11). Suitably, the mutation is a combination of E99R and N108R at the positions corresponding to the positions in the Georgia 2007/1 EP402R protein (SEQ ID NO. 11).

Suitably, the mutation is selected from S15R, W19D, Q96R, N104R and/or K108D at a position corresponding to the position in the Georgia 2007/1 EP402R protein (SEQ ID NO. 24). Suitably, the mutation is a combination of Q96R and N104R at the positions corresponding to the positions in the Georgia 2007/1 EP402R protein (SEQ ID NO. 24).

Suitably, the mutation is selected from W20D, Q112R, N121R and/or R125D at a position corresponding to the position in the N10 Genotype IX EP402R protein (SEQ ID NO. 27). Suitably, the mutation is a combination of Q112R and N121R at the positions corresponding to the positions in the N10 Genotype IX EP402R protein (SEQ ID NO. 27).

Suitably, where the attenuated ASFV is genotype I, the one or more mutations change an amino acid at a position in the EP402R protein corresponding to Y76, E99, Y102, and/or N108 of Benin 97/1 EP402R protein (SEQ ID NO. 11). Suitably, where the attenuated ASFV is genotype I, the mutation is selected from Y76D, E99R, Y102D, and/or N108R at a position corresponding to the position in the Benin 97/1 EP402R protein (SEQ ID NO. 11).

Suitably, where the attenuated ASFV is genotype II, the one or more mutations change an amino acid at a position in the EP402R protein corresponding to S15, W19, Q96, N104, and/or K108D of Georgia 2007/1 EP402R protein (SEQ ID NO. 24). Suitably, where there

attenuated ASFV is genotype II, the mutation is selected from S15R, W19D, Q96R, N104R and/or K108D at a position corresponding to the position in the Georgia 2007/1 EP402R protein (SEQ ID NO. 24). Suitably, where the attenuated ASFV is genotype II, the mutation may be a combination of Q96R and N104R at the positions corresponding to the positions in the Georgia 2007/1 EP402R protein (SEQ ID NO. 24).

In an embodiment the amino acid at the position corresponding to E99 is changed to R and/or the amino acid at the position corresponding to Y102 is changed to D. In an embodiment the amino acid at the position corresponding to E99 is changed to R. In an embodiment the amino acid at the position corresponding to Y102 is changed to D. In an embodiment E99 of Benin 97/1 EP402R is changed to R and/or Y102 of Benin 97/1 EP402R is changed to D. In an embodiment E99 of Benin 97/1 EP402R is changed to R. In an embodiment Y102 of Benin 97/1 EP402R is changed to D. In an embodiment Q96 of Georgia 2007/1 EP402R is changed to R.

The amino acid sequence of the EP402R protein from Benin 97/1 strain comprising the E99R substitution is depicted below as SEQ ID No. 31.

SEQ ID No. 31 – Benin 97/1 EP402R E99R protein

MIIIVIFLMCLKIVLNNIIIWSTLNQTVFLNNIFTINDTYGGLFWNTYYDNNRSNFTYCGIAGNYCSCCGHNISLYNTTNNCS
LIIFPNNTEIFNRTYRLVYLDKKINYTVKLLKSVDSPTITYNCTNSLITCKNNNGTNVNIYLIINNTIVNDTNGDILNYYWNG
NNNFTATCMINNTISSLNETENINCTNPILKYQNYLSTLFYIIIFIVSGLIIGIFISIISVLSIRRKRKKHVEEIESPPPSES
NEEDISHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCSPPK
PCRPPKPCPPPKPCPPPKPCPPPKPCPPSKPCPSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

In an embodiment the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 31. Suitably, the EP402R gene encodes a protein comprising a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 31, wherein amino acid 99 is R. Suitably, the EP402R gene encodes a protein consisting of the sequence of SEQ ID No. 31.

The amino acid sequence of the EP402R protein from Benin 97/1 strain comprising the Y102D substitution is depicted below as SEQ ID No. 32.

SEQ ID No. 32 – Benin 97/1 EP402R Y102D protein

MIIIVIFLMCLKIVLNNIIIWSTLNQTVFLNNIFTINDTYGGLFWNTYYDNNRSNFTYCGIAGNYCSCCGHNISLYNTTNNCS
LIIFPNNTEIFNRTYELVDLDKKINYTVKLLKSVDSPTITYNCTNSLITCKNNNGTNVNIYLIINNTIVNDTNGDILNYYWNG
NNNFTATCMINNTISSLNETENINCTNPILKYQNYLSTLFYIIIFIVSGLIIGIFISIISVLSIRRKRKKHVEEIESPPPSES
NEEDISHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCSPPK
PCRPPKPCPPPKPCPPPKPCPPPKPCPPSKPCPSPESYSPPKPLPSIPLLPNIPPLSTQNISLIHVDRII

In an embodiment the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 32. Suitably, the EP402R gene encodes a protein comprising a sequence having at least

70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 32, wherein amino acid 102 is D. Suitably, the EP402R gene encodes a protein consisting of the sequence of SEQ ID No. 32.

The amino acid sequence of the EP402R protein from Georgia 2007/1 strain comprising the Q96R substitution is depicted below as SEQ ID No. 33.

SEQ ID No. 33 – Georgia 2007/1 EP402R Q96R protein

MIILIFLIFSNIVLSIDYWVSFNKTIILDSNITNDNNDINGVSWNFFNNSFNTLATCGKAGNFCECSNYSTSIYNITNNCSLT
IFPHNDVFDTTYRVVWNQIINYTIKLLTPATPPNITYNCTNFLITCKKNNGTNTNIYLNINDTFVKYTNESILEYNWNNSNIN
NFTATCIINNTISTSNETTLINCTYLTLSSNYFYTFFKLYYIPLSIIIGITISILLISIITFLSLRKRKKHVEEIESPPPESN
EEEQCQHDDTTSIHEPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPPPKPCPPPKPCPPPKPCPPPKPCPSAESYSPPK
PLPSIPLLPNIPPLSTQNISLIHVDRII

In an embodiment the EP402R gene encodes a protein comprising the sequence of SEQ ID No. 33. Suitably, the EP402R gene encodes a protein comprising a sequence having at least 70%, at least 80%, at least 90% or at least 95% identity with SEQ ID No. 33, wherein amino acid 96 is R. Suitably, the EP402R gene encodes a protein consisting of the sequence of SEQ ID No. 33.In an embodiment the EP402R gene encodes a protein comprising a sequence selected from SEQ ID No. 31, 32 or 33.

Mutation combinations

The mutations that disrupt gene expression and/or activity described herein may be combined in an attenuated ASFV of the invention. In other words, each of the DP148R, EP153R and EP402R genes in an attenuated ASFV of the invention may be disrupted by the same type of mutation as any of the other genes or by a different type of mutation as any of the other genes.

For example, in an attenuated ASFV of the invention, DP148R may be disrupted by mutation of a promoter sequence, EP153R may be disrupted by complete deletion and EP402R may be disrupted by an amino acid change in its ligand-binding domain. As an alternative example, DP148R may be disrupted by partial deletion, EP153R may be disrupted by interruption and EP402R may be disrupted by complete deletion.

In an embodiment the invention provides an attenuated ASFV in which

the DP148R gene and EP153R gene are each completely deleted, and

the EP402R gene comprises a mutation that changes an amino acid at a position in the EP402R protein which corresponds to E99 of Benin 97/1 EP402R protein (SEQ ID No. 11) to R;

and which comprises a functional version of one or more of the following genes:

MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

The attenuated ASFV may comprise a functional version of one or more of the MGF genes as described herein.

In an embodiment the invention provides an attenuated ASFV in which
the DP148R gene and EP153R gene are each completely deleted, and
the EP402R gene comprises a mutation that changes an amino acid at a position in the EP402R protein which corresponds to E99 of Benin 97/1 EP402R protein (SEQ ID No. 11) to R;
and which comprises a functional version of one or more of the following genes:
MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

The attenuated ASFV may comprise a functional version of one or more of the MGF genes as described herein.

In an embodiment the invention provides an attenuated ASFV in which
the DP148R gene and EP153R gene are each completely deleted, and
the EP402R gene comprises a mutation that changes an amino acid at a position in the EP402R protein equivalent to Y102 of Benin 97/1 EP402R protein (SEQ ID No. 11) to D;
and which comprises a functional version of one or more of the following genes:
MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

The attenuated ASFV may comprise a functional version of one or more of the MGF genes as described herein.

Vaccine/pharmaceutical composition

The present invention also provides a vaccine comprising an attenuated ASF virus of the invention.

The term “vaccine” as used herein refers to a preparation which, when administered to a subject, induces or stimulates a protective immune response. A vaccine can render an organism immune to a particular disease, in the present case ASF. The vaccine of the present invention thus induces an immune response in a subject which is protective against subsequent ASF virus challenge. A vaccine comprising an attenuated ASFV of the invention may be capable of inducing a cross-protective immune response against a plurality of ASF virus genotypes. In an embodiment a vaccine comprising an attenuated ASFV of the invention of a single genotype may be capable of inducing a cross-protective immune response against a plurality of ASF virus genotypes.

The vaccine may comprise a plurality of attenuated ASF viruses. The plurality of attenuated ASF viruses may correspond to a plurality of different isolates, for example, different isolates of high or unknown virulence. Such a vaccine may be capable of inducing a cross-protective immune response against a plurality of ASF virus genotypes.

The vaccine may be useful in preventing African Swine Fever. Accordingly the invention provides a vaccine of the invention for use in treating and/or preventing African Swine Fever in a subject.

The present invention also provides a pharmaceutical composition which comprises one or more attenuated ASF virus(es) of the invention. The pharmaceutical composition may be used for treating African Swine Fever.

The vaccine or pharmaceutical composition may comprise one or more attenuated ASF virus(es) of the invention and optionally one or more adjuvants, excipients, carriers and diluents. The choice of pharmaceutical excipient, carrier or diluent can be selected with regard to the intended route of administration and standard pharmaceutical practice. The pharmaceutical compositions may comprise as (or in addition to) the carrier, excipient or diluent, any suitable binder(s), lubricant(s), suspending agent(s), coating agent(s), solubilising agent(s) and other carrier agents. The pharmaceutical compositions typically should be sterile and stable under the conditions of manufacture and storage. Formulations for parenteral administration include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations. Sterile injectable formulations may be prepared using a non-toxic parenterally acceptable diluent or solvent. A pharmaceutical composition of the present invention may include pharmaceutically acceptable dispersing agents, wetting agents, suspending agents, isotonic agents, coatings, antibacterial and antifungal agents, carriers, excipients, salts, or stabilizers which are nontoxic to the subjects at the dosages and concentrations employed. Preferably, such a composition can further comprise a

pharmaceutically acceptable carrier or excipient for use in the treatment of disease that that is compatible with a given method and/or site of administration, for instance for parenteral (e.g. sub-cutaneous, intradermal, or intravenous injection) or intrathecal administration.

The vaccine or pharmaceutical composition may comprise one or more attenuated ASF virus(es) of the invention in an effective amount.

In an embodiment the invention provides an attenuated ASF virus of the invention which when administered to a subject induces an immune response which is protective against subsequent challenge with virulent ASF virus. In an embodiment the invention provides an attenuated ASF virus of the invention which when administered to a subject induces an immune response which is protective against subsequent challenge with virulent ASF virus of a different genotype to the attenuated ASF virus of the vaccine.

Methods of prevention/treatment

The present invention also provides a method of preventing and/or treating ASF in a subject by administration to the subject of an effective amount of an attenuated virus, vaccine, or pharmaceutical composition of the invention.

The term “preventing” is intended to refer to averting, delaying, impeding or hindering the contraction of ASF. The vaccine may, for example, prevent or reduce the likelihood of an infectious ASFV entering a cell.

The term “treating” is intended to refer to reducing or alleviating at least one symptom of an existing ASF infection.

The subject may be any animal which is susceptible to ASF infection. ASF susceptible animals include domestic pigs, warthogs, bush pigs and ticks.

The subject vaccinated according to the present invention may be a domestic pig.

Administration

The vaccine of the invention may be administered by any convenient route, such as by intramuscular injection. Other suitable routes of administration include intranasal, oral, subcutaneous, transdermal and vaginal (e.g. during artificial insemination). In one embodiment, oral administration comprises adding the vaccine to animal feed or drinking water. In another embodiment, the vaccine may be added to bait for a wild animal, for example bait suitable for wild boar, wild pigs, bushpigs or warthogs.

The dose for pig immunisation may be less than 10^4 HAD_{50} or $TCID_{50}$ per pig. For example the dose may be between 10^2-10^3 HAD_{50} or $TCID_{50}$. The dose may be about 10^2 HAD_{50} or $TCID_{50}$ per pig. The dose may be determined by a veterinary practitioner within the scope of sound veterinary judgment.

The vaccine may be administered following a prime-boost regime. For example, after the first inoculation, the subjects may receive a second boosting administration some time (such as about 7, 14, 21 or 28 days) later. Typically the boosting administration is at a higher dose than the priming administration. The boosting dose may be about 10^2, 10^3 or 10^4 HAD_{50} or $TCID_{50}$ of the recombinant attenuated virus per pig.

Method for preparing an attenuated virus

The present invention also provides a method of attenuating an ASF virus which comprises the step of disrupting the expression and/or activity of the genes DP148R, EP153R and EP402R.

Disruption of gene expression and/or activity may be achieved by mutating the ASFV genome in any of the ways described herein.

The DP148R, EP153R and/or EP402R genes may be partially or completely deleted.

The DP148R gene may be at least partially or completely deleted. The EP153R gene may be at least partially or completely deleted. The EP402R gene may be at least partially or completely deleted. The DP148R and EP153R genes may be at least partially or completely deleted. The DP148R, EP153R and EP402R genes may each be partially or completely deleted. The coding sequences of one or more (such as two or more, or all three) of the disrupted genes may be at least partially or completely deleted.

The DP148R, EP153R and/or EP402R genes may be interrupted.

The DP148R gene may be interrupted. The EP153R gene may be interrupted. The EP402R gene may be interrupted. The DP148R and EP153R genes may be interrupted. The DP148R, EP153R and EP402R genes may each be interrupted. The coding sequences of one or more (such as two or more, or all three) of the disrupted genes may be interrupted.

In an embodiment the method of attenuating an ASF virus comprises disrupting the ability of the EP402R gene to mediate haemadsorption.

In an embodiment the method of attenuating an ASF virus comprises comprising introducing one or more mutations in the EP402R gene that disrupt ligand binding by the EP402R protein.

In an embodiment the method of attenuating an ASF virus comprises introducing one or more mutations in the EP402R gene that change one or more amino acids in the ligand-binding domain of the EP402R protein. The mutation may be one or more of the mutation as described herein.

In an embodiment the method of attenuating an ASF virus comprises changing the amino acid at position R96, E99 and/or Y102 of the EP402R protein.

In an embodiment the method of attenuating an ASF virus comprises changing the amino acid at position R96 to Q, the amino acid at position E99 to R and/or the amino acid at position Y102 to D. Suitably the method comprises changing the amino acid at position R96 to Q. Suitably the method comprises changing the amino acid at position E99 to R. Suitably the method comprises changing the amino acid at position Y102 to D.

In an embodiment the method of attenuating an ASF virus comprises completely deleting the DP148R gene, completely deleting the EP153R gene and introducing a mutation in the EP402R gene that changes the amino acid at position R96 of the EP402R protein to Q. In an embodiment the method of attenuating an ASF virus comprises completely deleting the DP148R gene, completely deleting the EP153R gene and introducing a mutation in the EP402R gene that changes the amino acid at position E99 of the EP402R protein to R. In an embodiment the method of attenuating an ASF virus comprises completely deleting the DP148R gene, completely deleting the EP153R gene and introducing a mutation in the EP402R gene that changes the amino acid at position Y102 of the EP402R protein to D.

Methods for mutation of viral genes are known in the art. In particular, methods for deletion of viral genes are known in the art. For example, homologous recombination may be used, in which a transfer vector is created in which the relevant gene(s) are missing and used to transfect virus-infected cells. Recombinant viruses expressing the new portion of sequence may then be selected. Similar procedures may be used in order to interrupt gene expression, for example by deletion of the ATG start codon.

"Retaining the function" of a gene means that expression and activity of the gene is not affected during the attenuation process. The resultant attenuated virus should express a functional version of the gene. Suitably, the genes the function of which is to be retained are

unaltered by the method of attenuation. Suitably, the sequences of the genes the function of which is to be retained are unaltered by the method of attenuation.

In some embodiments, the method of attenuating an ASF virus may comprise retaining the function of one or more of the following genes: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R. Suitably, the function of two or more, such as three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, eleven or more, twelve or more, thirteen or more, fourteen or more, fifteen or more, sixteen or more, seventeen or more, eighteen or more, nineteen or more, twenty or more, twenty one, or twenty two of the following genes are retained: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R. In an embodiment the method of attenuating an ASF virus may comprise retaining the function of all of the following genes: MGF 110 3L, 6L, 7L, 8L, 10L, 11L and 12L; MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R; and MGF 505 1R, 2R and 6R.

This disclosure is not limited by the exemplary methods and materials disclosed herein, and any methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of this disclosure. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, any nucleic acid sequences are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively.

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural referents unless the context clearly dictates otherwise.

The terms "comprising", "comprises" and "comprised of' as used herein are synonymous with "including", "includes" or "containing", "contains", and are inclusive or open-ended and do not exclude additional, non-recited members, elements or method steps. The terms "comprising", "comprises" and "comprised of' also include the term "consisting of'.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that such publications constitute prior art to the claims appended hereto.

The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not intended in any way to limit the scope of the invention.

EXAMPLES

Example 1 – Identification of EP402R/CD2v mutants that reduce HAD

Mutations were made in African swine fever virus (ASFV) Benin isolate EP402R protein (CD2v) and tested for their effect on haemadsorption (HAD).

A model of the extracellular, N-terminal, IgG-like, ligand-binding domain of CD2v was generated and used to predict the functional amino acid residues involved in binding of CD2v to its ligand. These residues were individually mutated to generate a set of mutant CD2v proteins.

Vero cells were infected with modified vaccinia virus Ankara expressing T7RNA polymerase and transfected with plasmids (pcDNA3) expressing wild-type or mutant CD2v full-length proteins with a C-terminal HA epitope tag. Pig red blood cells were added and cells observed for attachment of red blood cells to the surface. Expression of the wild-type or mutant CD2v proteins was confirmed both by confocal microscopy using permeabilised cells and Western blotting using an antibody recognising the HA tag and a secondary antibody. Cell surface expression of the wild-type or mutant CD2v was also confirmed by staining non-permeabilised cells with sera from pigs immunised with attenuated ASFV containing a wild-type CD2v gene and a secondary antibody (**Figure 1**).

Mutation of residues E99 or Y102 abrogated HAD. **Figure 2** shows exemplary images from the HAD assay. **Figure 2A** shows cells transfected with a plasmid expressing wild-type Benin CD2v. HAD of red blood cells is observed around three cells. **Figure 2B** shows cells expressing CD2v with the Y102 residue mutated to D. Partial HAD is observed around one cell. **Figure 2C** shows cells expressing CD2v with residue E99 mutated to R. No HAD is observed.

CD2v residue E99 is strongly conserved in ASFV, as shown by an alignment of the amino acid sequence of CD2v ligand-binding domain from different ASFV isolates of varying genotypes (**Figure 3**). The equivalent residue in other isolates (highlighted in yellow in Figure 3) is either identical (E) or has the same charge (Q).

The equivalent residue to Benin CD2v E99 in Georgia CD2v, Q96, was mutated to R and the ability of the mutant protein to induce HAD was tested using the HAD assay described above. Mutation of Q96 in Georgia CD2v abrogated HAD. **Figure 4** shows exemplary images from the HAD assay of Vero cells with pig red blood cells. **Figure 4A** shows Vero cells transfected with a plasmid expressing wild-type Benin CD2v. HAD of red blood cells is observed around four cells. **Figure 4B** shows Vero cells expressing wild-type Georgia CD2v. HAD is observed around two cells. **Figure 4C** shows Vero cells expressing Georgia CD2v

with residue Q96 mutated to R. No HAD is observed. **Figure 4D** shows non-transfected Vero cells. No HAD is observed.

Using the same assay, the following mutations were determined to impact HAD in Benin: N16R, I 19R, W21D, Y 76D, E99R, Y102D. In addition, a combination of E99R + N108R was determined to impact HAD in Benin.

The following mutations were determined to impact HAD in Georgia: S15R, W19D, Q96R, N104R, and K108D. In addition, combinations of S15R + W19D and Q96R + N104R were determined to impact HAD in Georgia.

The following mutations were determined to impact HAD in N10 Genotype IX: W20D, R125D, Q112R + N121R.

Example 2 – Generation of ASFV lacking functional DP148R, EP153R and EP402R

The ability to induce HAD could be restored by infecting WSL cells expressing the CD2vE99R mutant with BeninΔCD2v virus (**Figure 4A**).

However, HAD could not be restored by infecting WSL cells expressing the CD2vE99R mutant with OURT88/3 virus (**Figure 4B**). OURT88/3 has frame-shift interruptions in the EP153R and EP402R/CD2v genes, which suggests a role for EP153R in rescuing HAD caused by the CD2vE99R mutant.

Based on these results, two gene deleted Benin viruses were constructed using as backbone the attenuated BeninΔDP148R virus. One virus had in addition to DP148R further deletions of EP153R and EP402R (BeninΔDP148RΔEP153RΔCD2v) and the second had EP153R deleted and the wild-type EP402R gene replaced with the gene expressing CD2vE99R mutant (BeninΔDP148RΔEP153R-CD2vE99R).

The Benin CD2vE99R mutant protein was expressed at the cell surface, as shown in **Figure 6A**. Porcine bone marrow cells were infected with BeninΔDP148RΔEP153R-CD2vE99R, fixed and permeabilised at 8 hours post-infection then stained with an antibody which recognises the HA-tag fused in frame with the CD2vE99R gene and secondary antibody. The CD2vE99R is shown in red on the cell surface. The mNeon green was inserted in place of the EP153R gene and is shown in green. Nuclear DNA and virus cytoplasmic factories are stained blue. The panel on the right shows a larger field to indicate numbers of infected cells.

Cells infected with these viruses did not induce HAD. **Figure 6B** shows porcine bone marrow cells infected with wild type Benin97/1 virus (left panel) or BeninΔDP148RΔEP153R-CD2vE99R (right panel). Red blood cells are observed forming rosettes around the

Benin97/1 infected cells (left panel) but not around the cells infected with virus expressing mutant CD2vE99R (right panel). The inset bottom right shows cells infected with BeninΔDP148RΔEP153R-CD2vE99R expressing mNeon protein to confirm the cells were infected.

Example 3 – DP148R inhibits activation of NF-κB by inhibiting nuclear translocation of the p65 sub-unit

HEK293T cells were transfected with an NF-κB dependent luciferase reporter plasmid and either a plasmid encoding the DP148R gene or an empty plasmid (pcDNA3) as a negative control. Twenty four hours post transfection the cells were treated with IL-1β (**Figure 7A**) or TNF-α (**Figure 7B**) for eight hours to induce NF-κB activation. Following cell lysis, luciferase activity was measured. **Figure 7A** and **Figure 7B** show that in the presence of DP148R, luciferase values were significantly lower than those obtained from cells transfected with pcDNA3. This indicates that DP148R is able to inhibit NF-KB mediated signalling.

In a pair of alternative experiments, NF-κB activation was instead induced by overexpression of the two main kinases of the NF-κB signalling pathway, namely IKKα (**Figure 7C**) and IKKβ (**Figure 7D**). **Figure 7C** and **Figure 7D** show that, again, in the presence of DP148R, luciferase values were significantly lower than those obtained from cells transfected with pcDNA3, indicating that DP148R is able to inhibit the NF-κB pathway at the level of the kinases activation.

To further elucidate the mechanism by which DP148R inhibits NF-kB activation, the effect of DP148R on nuclear translocation of the p65 sub-unit of NF-kB was investigated. HeLa cells were transfected with a plasmid expressing HA-tagged DP148R and were then stimulated with TNF-alpha or IL-1β to activate NF-kB. Unstimulated cells were used as a negative control. Cells were fixed and permeabilised then stained for HA-tagged DP148R using an anti-HA tag antibody and an appropriate secondary antibody. The p65 subunit of NF-kB was stained with a primary antibody and secondary antibody. **Figure 8** shows immunofluorescence images of the cells. HA-tagged DP148R is shown in red, p65 is shown in green and nuclei are shown in blue. In cells not expressing DP148R, in unstimulated cells p65 remains in the cytoplasm but translocates into the nucleus following stimulation with TNF-alpha or IL-1beta. In contrast, in cells expressing DP148R, p65 nuclear translocation is not observed upon stimulation and lower amounts of p65 are detected in the cytoplasm. The results show that DP148R is an efficient inhibitor of NF-kB which would inhibit activation of genes dependent on NF-kB. These include for example proinflammatory cytokines and chemokines.

Example 4 – Lack of functional DP148R, EP153R and EP402R attenuates ASFV and induces protection against challenge

Vaccination experimental protocol

Groups of large white/landrace pigs were immunised intramuscularly with 10^4 TCID50 BeninΔDP148RΔEP153RΔCD2v (Group A – eight pigs) and BeninΔDP148RΔEP153R-CD2vE99R (Group B – six pigs).

Pigs were boosted on day 21 (10^4 TCID50/ml) and day 28 (10^6 TCID50/ml) post-immunisation and then challenged with 10^3 TCID50/ml parental virulent Benin 97/1 strain on day 45 post-immunisation, in parallel with three non-immunised pigs (control Group E).

The experimental protocol is depicted in **Figure 9**.

Temperature

Rectal temperatures were recorded daily for all pigs in Group A and B and the control Group E (**Figure 10**). In Group A, no increase in temperature was observed before challenge. After challenge an increase in temperature at or above 41 °C was observed in one pig at day 3 post-challenge and in the remaining pigs at day 4 post-challenge. Two pigs (A3 and A4) reached the humane end-point at day 5 post-challenge and were culled. The remaining pigs had an increased temperature above 40.5 °C for two days in total, except for pig A7 in which a temperature of 40.6 °C persisted for a 3rd day. All then survived to the end of the experiment at day 20 post-challenge without further increase in temperature (**Figure 10A**).

Three pigs in Group B had an increase in temperature above 40.5 °C at day 5 post-immunisation. One pig had a temperature of 41.1 °C by day 3 post-challenge and this was maintained a further 2 days when the animal was culled at the humane endpoint. From the other pigs all survived, one had a single day temperature above 40.5 °C at day 4 post-challenge, three had 2 days increase temperature (days 4 and 5) and one had no increased temperature. All survivors had no further temperature increase until the end of the experiment (day 20 post-challenge) (**Figure 10B**).

Control pigs had temperatures above 40.5 °C from day 4 post-challenge and were culled at the humane endpoint on day 6 post-challenge (**Figure 10C**).

Clinical scores

Clinical scores, including increased temperature and other signs such as lethargy and loss of appetite were collected daily (**Figure 11**). In Group A no signs were observed before

challenge. After challenge clinical scores were observed in all pigs coincident with increased temperatures and reaching higher levels in the two pigs that were culled at the humane endpoint (**Figure 11A**).

In Group B mild signs were observed in pigs post-immunization coincident with temperature increases. After challenge mild signs were observed except for the pig which was culled at the humane endpoint and the pig which did not show an increase in temperature which had no clinical signs (**Figure 11B**).

Viremia

Levels of virus genome in blood were measured by qPCR (**Figure 12**). No virus genome was detected in blood from pigs in Group A before challenge. After challenge variable levels of genome were detected from day 3 or 4 post-challenge. Maximum levels were detected in the pigs which were culled (~10e6 genome copies per ml). In other pigs the maximum levels detected varied between ~10e2 per ml and 10e5.5 per ml. Levels of virus genome decreased until termination at day 20 post-challenge becoming undetectable in 2 pigs and reduced to 10e2.6 in others except 1 pig in which levels remained at 10e4.5 at termination (**Figure 12A**).

In group B low levels of virus genome were detected in blood from 3 pigs at day 6 post-immunization. After challenge virus genome was detected at low levels (below 10e4 genome copies per ml) from day 7 post-challenge (**Figure 12B**).

Antibody response

ASFV specific antibody responses were measured using a commercially available competitive ELISA based on the VP72 (B646L) major capsid protein (**Figure 13**). In Group A antibody responses were first detected at day 27 post-immunization after the first boost and just before the second boost. Levels were maintained for the rest of the experiment (**Figure 13A**).

In pigs in Group B antibody responses were detected by day 14 (1 week before the boost) and increased maintaining a plateau after day 21 to 28 (**Figure 13B**).

Cell-mediated immune response

Peripheral blood mononuclear cells were collected pre-immunization, boost and challenge from pigs in Groups A and B and stimulated with ASFV Benin virus. Numbers of IFN gamma producing cells were measured by Elispot assay (**Figure 14**). In Group A low levels of IFN gamma producing cells were induced after immunisation and before boost and these

increased uniformly in all pigs before challenge (**Figure 14A**). In Group B responses were more variable between pigs and pigs had had higher numbers of IFN gamma producing cells before boost. However at the time of challenge these numbers had decreased slightly in all except 1 pig. The pig which was culled at the humane end point (B4) had a lower number of IFN gamma producing cells although similar in number to a pig which survive challenge (B5) (**Figure 14B**).

Scoring of macroscopic lesions at post-mortem

Control non-immune pigs (Group E) showed lesions typical of acute ASFV including enlarged and haemmorhagic lymph nodes and spleen. Those pigs which survived challenge had few, if any, ASFV specific lesions (**Figure 15**). The pigs culled at humane end points showed higher scores but less than the control pigs (data not shown).

Viremia comparison

Figure 16 directly compares virus genome in blood after immunisation with different viruses. Immunisation with BeninΔDP148R induces moderate levels of virus genome transiently, which decrease slowly over 60 days. No increase in replication or detectable challenge virus is observed (**Figure 16A**). Deletion of the EP402R/CD2v gene (BeninΔDP148RΔCD2v virus) dramatically reduces the persistence of genome in blood (~15 days maximum) and reduces the level in some pigs. No virus genome was detected post-challenge (**Figure 16B**). The triple deletion BeninΔDP148RΔEP153RΔCD2v induces no detectable genome in blood post-immunisation and moderate to low levels after challenge decreasing to low or undetectable levels by the end of the experiment (**Figure 16C**). The BeninΔDP148RΔEP153R-CD2vE99R virus induces a transient low level of virus genome in blood after immunisation and low levels after challenge (**Figure 16D**).

All publications mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in virology, molecular biology or related fields are intended to be within the scope of the following claims.

CLAIMS

1. An attenuated African Swine Fever (ASF) virus in which the expression and/or activity of the genes DP148R, EP153R and EP402R is disrupted;
and which comprises a functional version of one or more of the following genes:
multigene family (MGF) 110 3L, 6L, 7L, 8L, 10L, 11L and 12L,
MGF 360 5L, 6L, 7L, 10L, 11L, 12L, 13L, 14L, 20R, 21R and 22R, and
MGF 505 1R, 2R and 6R.

2. An attenuated ASF virus according to claim 1 wherein the DP148R gene and/or the EP153R gene is at least partially deleted.

3. An attenuated ASF virus according to claim 2 wherein the DP148R gene and/or the EP153R gene is completely deleted.

4. An attenuated ASF virus according to claim 1 wherein the DP148R gene and/or the EP153R gene is interrupted.

5. An attenuated ASF virus according to any of claims 1 to 4 wherein the ability of the DP148R gene to inhibit NF-κB activity is disrupted.

6. An attenuated ASF virus according to any of claims 1 to 5 wherein the ability of the DP148R gene to inhibit translocation of the p65 sub-unit of NF-κB activity to the nucleus is disrupted.

5. An attenuated ASF virus according to any of claims 1 to 4 wherein the ability of the EP153R gene and/or the EP402R gene to mediate haemadsorption is disrupted.

6. An attenuated ASF virus according to any of claims 1 to 5 wherein the EP402R gene comprises one or more mutations that disrupt ligand binding by the EP402R protein.

7. An attenuated ASF virus according to claim 6 wherein the EP402R gene comprises one or more mutations that change one or more amino acids in the ligand-binding domain of the EP402R protein.

8. An attenuated ASF virus according to claim 7 wherein the one or more mutations change an amino acid at a position in the EP402R protein which corresponds to E99 and/or Y102 of Benin 97/1 EP402R protein (SEQ ID No. 11).

9. An attenuated ASF virus according to claim 8 wherein the amino acid at the position which corresponds to E99 is changed to R and/or the amino acid at the position equivalent to Y102 is changed to D.

10. An attenuated ASF virus according to any of claims 1 to 6 wherein the EP402R gene is at least partially deleted.

11. An attenuated ASF virus according to claim 10 wherein the EP402R gene is completely deleted.

12. An attenuated ASF virus according to any of claim 1 to 11 which comprises functional versions of all ASF virus genes other than DP148R, EP153R and EP402R.

13. A vaccine comprising an attenuated ASF virus according to any of claims 1 to 12.

14. A vaccine according to claim 13 for use in treating and/or preventing African Swine Fever in a subject.

15. A method for treating and/or preventing African Swine Fever in a subject which comprises the step of administering to the subject an effective amount of a vaccine according to claim 13.

16. A vaccine for use according to claim 14, or a method according to claim 15, wherein the subject is a domestic pig.

17. A vaccine for use according to claim 14 or 16, or a method according to claim 15 or 16, in which the vaccine is administered following a prime-boost regime.

18. A method of attenuating an ASF virus which comprises the step of disrupting the expression and/or activity of the following genes:

DP148R

EP153R and

EP402R.

19. A method according to claim 18 wherein the DP148R gene and/or the EP153R gene is at least partially deleted.

20. A method according to claim 19 wherein the DP148R gene and/or the EP153R gene is completely deleted.

21. A method according to claim 18 wherein the DP148R gene and/or the EP153R gene is interrupted.

22. A method according to any of claims 18 to 21 comprising disrupting the ability of the EP402R gene to mediate haemadsorption.

23. A method according to any of claims 18 to 22 comprising introducing one or more mutations in the EP402R gene that disrupt ligand binding by the EP402R protein.

24. A method according to claim 23 comprising introducing one or more mutations in the EP402R gene that change one or more amino acids in the ligand-binding domain of the EP402R protein.

25. A method according to claim 24 comprising changing the amino acid at position R96, E99 and/or Y102 of the EP402R protein.

26. A method according to claim 25 comprising changing the amino acid at position R96 to Q, the amino acid at position E99 to R and/or the amino acid at position Y102 to D.

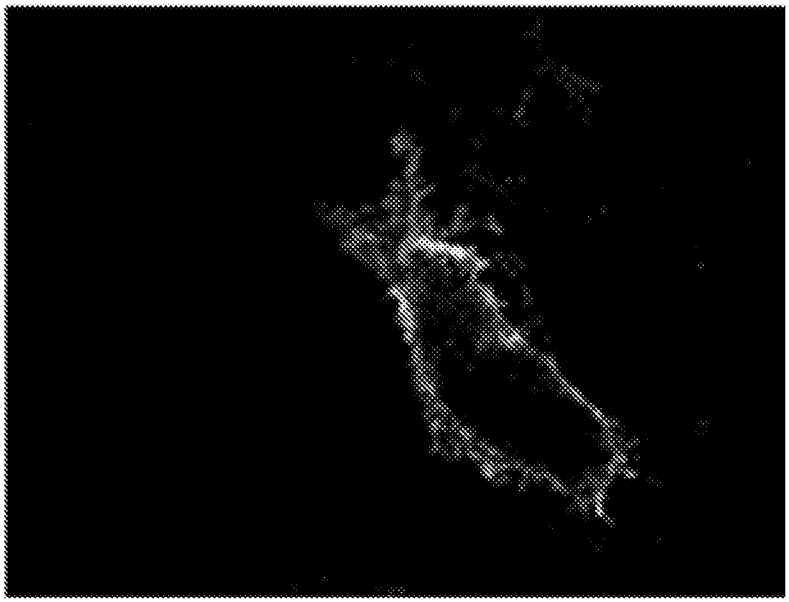
27. A method according to any of claims 18 to 23 wherein the EP402R gene is at least partially deleted.

28. A method according to claim 28 wherein the EP402R gene is completely deleted.

29. A method according to claim 28 wherein the EP402R gene is interrupted.

Figure 1

A



B

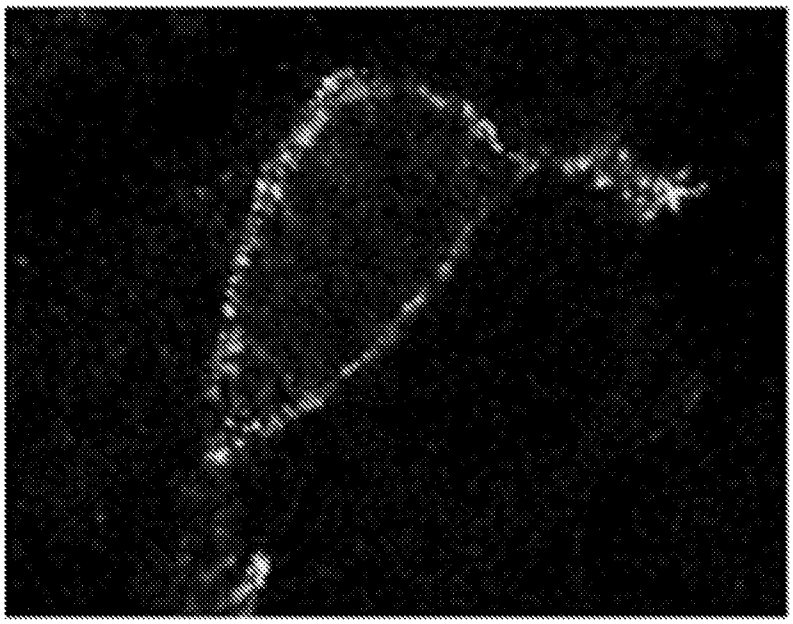
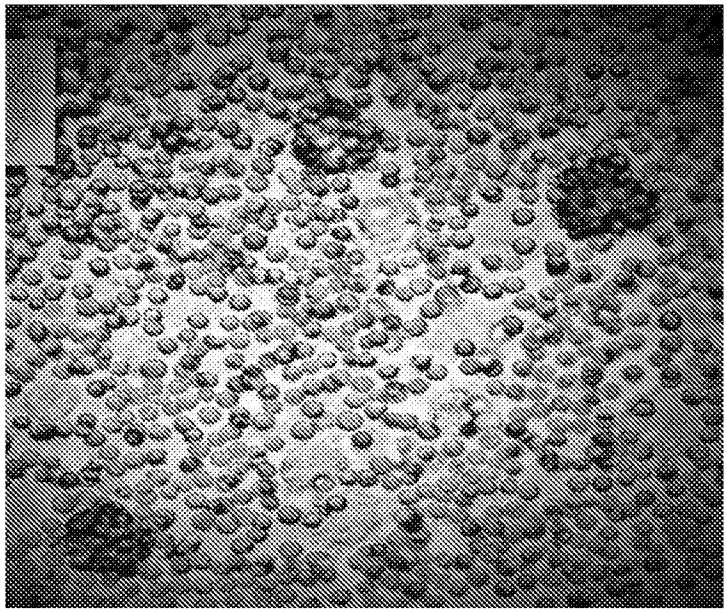


Figure 2

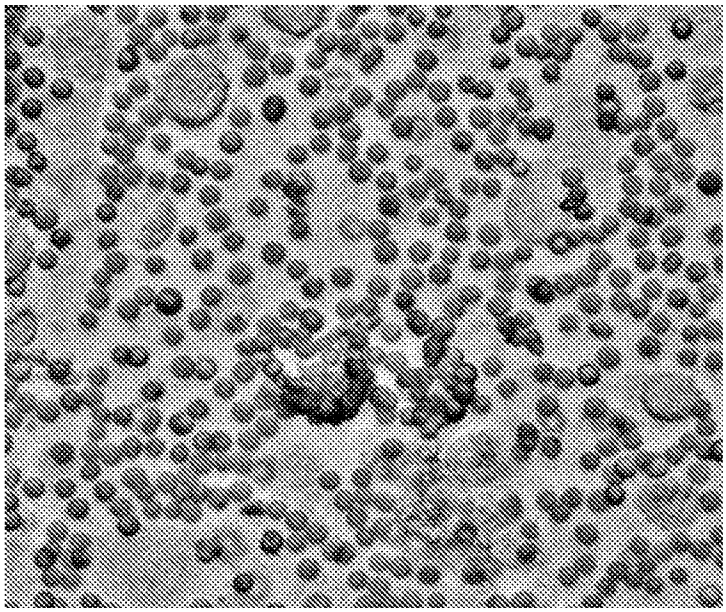
A

WT-CD2v



B

Mutant Y102D



C

Mutant E99R

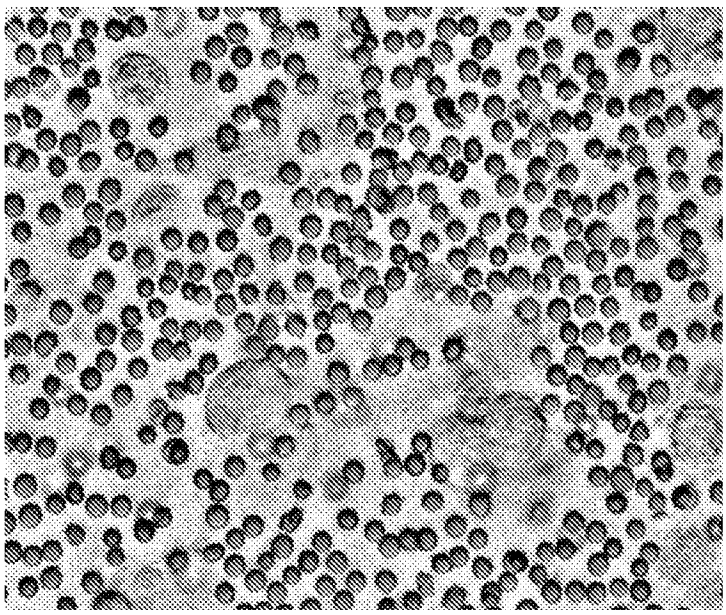


Figure 3

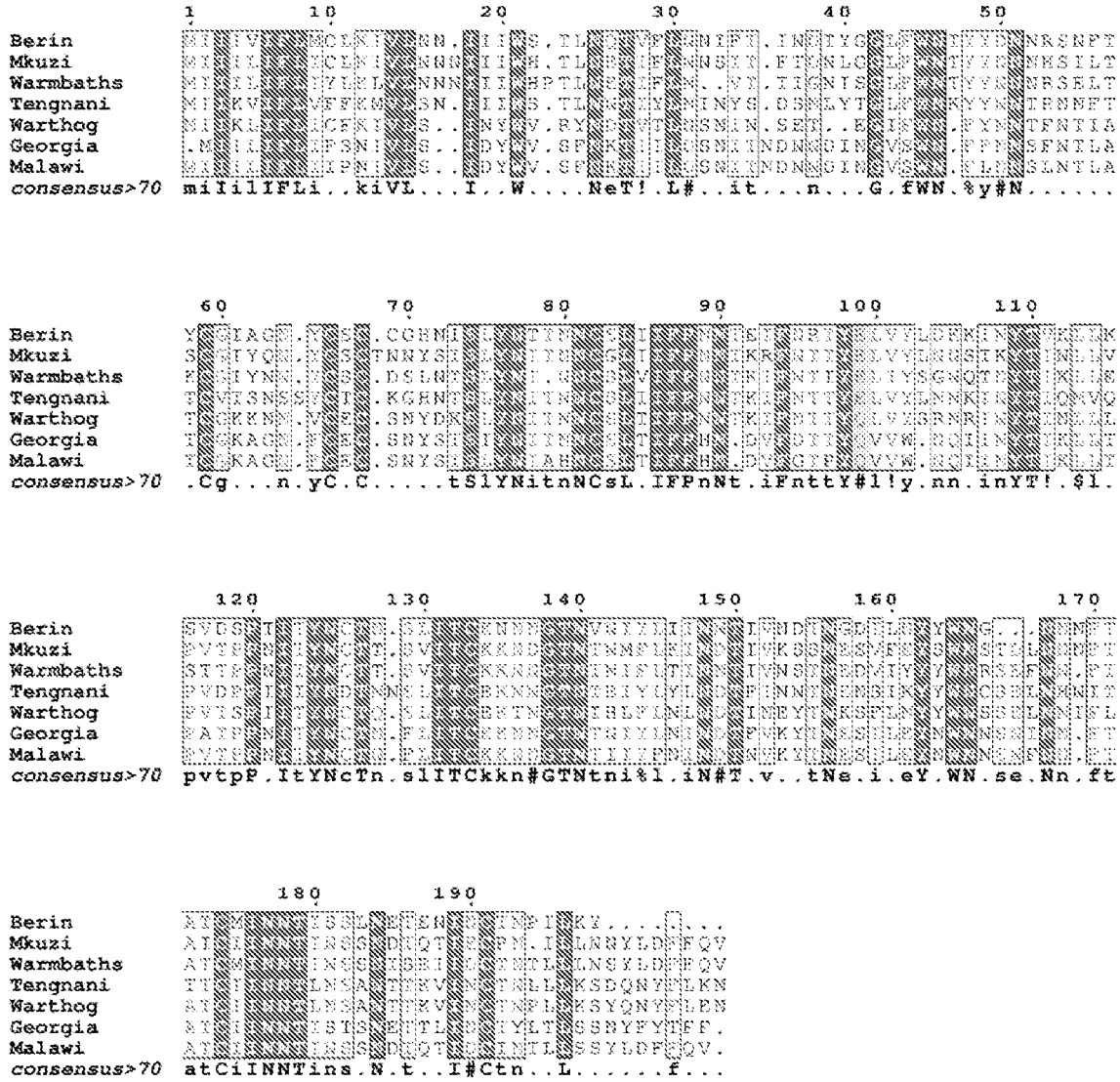

Berin
Mkuzi
Warmbaths
Tengnani
Warthog
Georgia
Malawi
consensus>70

Figure 4

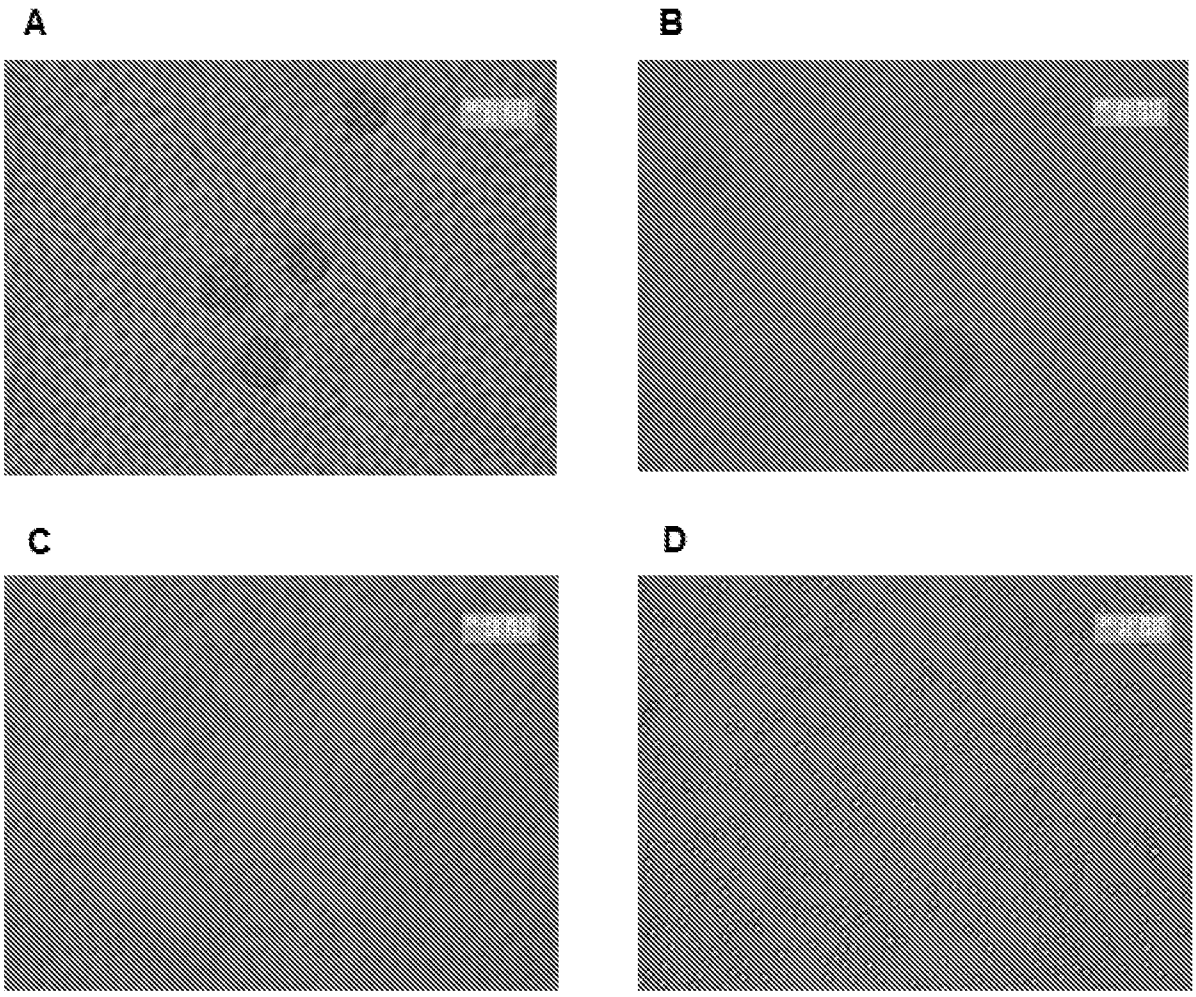


Figure 5

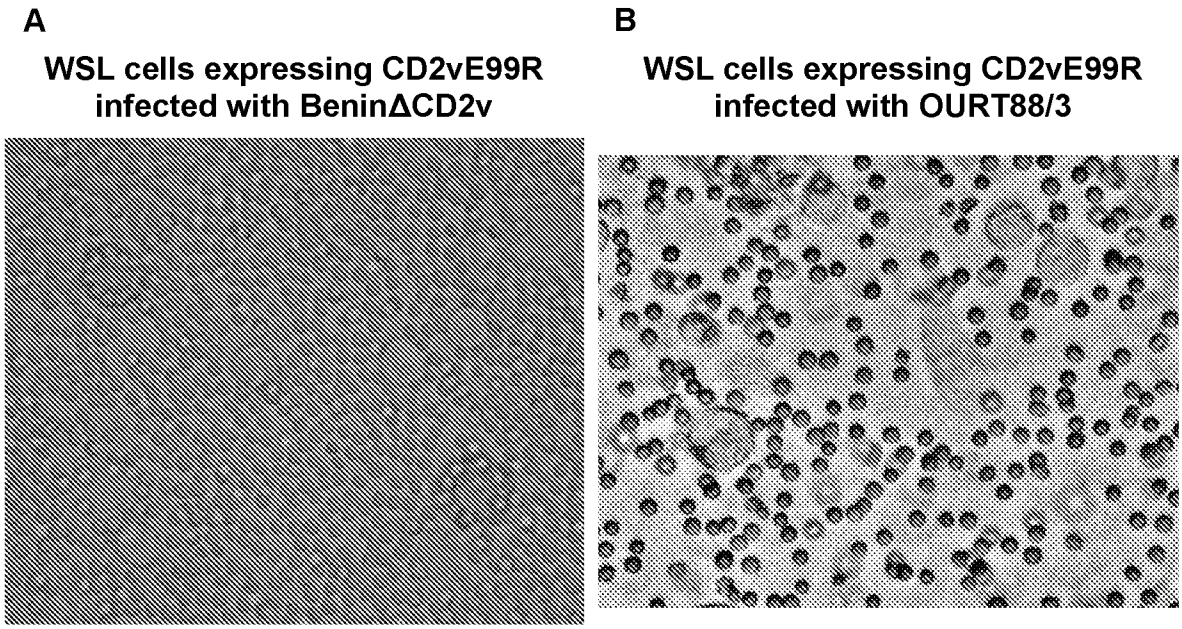

A
WSL cells expressing CD2vE99R infected with BeninΔCD2v
B
WSL cells expressing CD2vE99R infected with OURT88/3

Figure 6

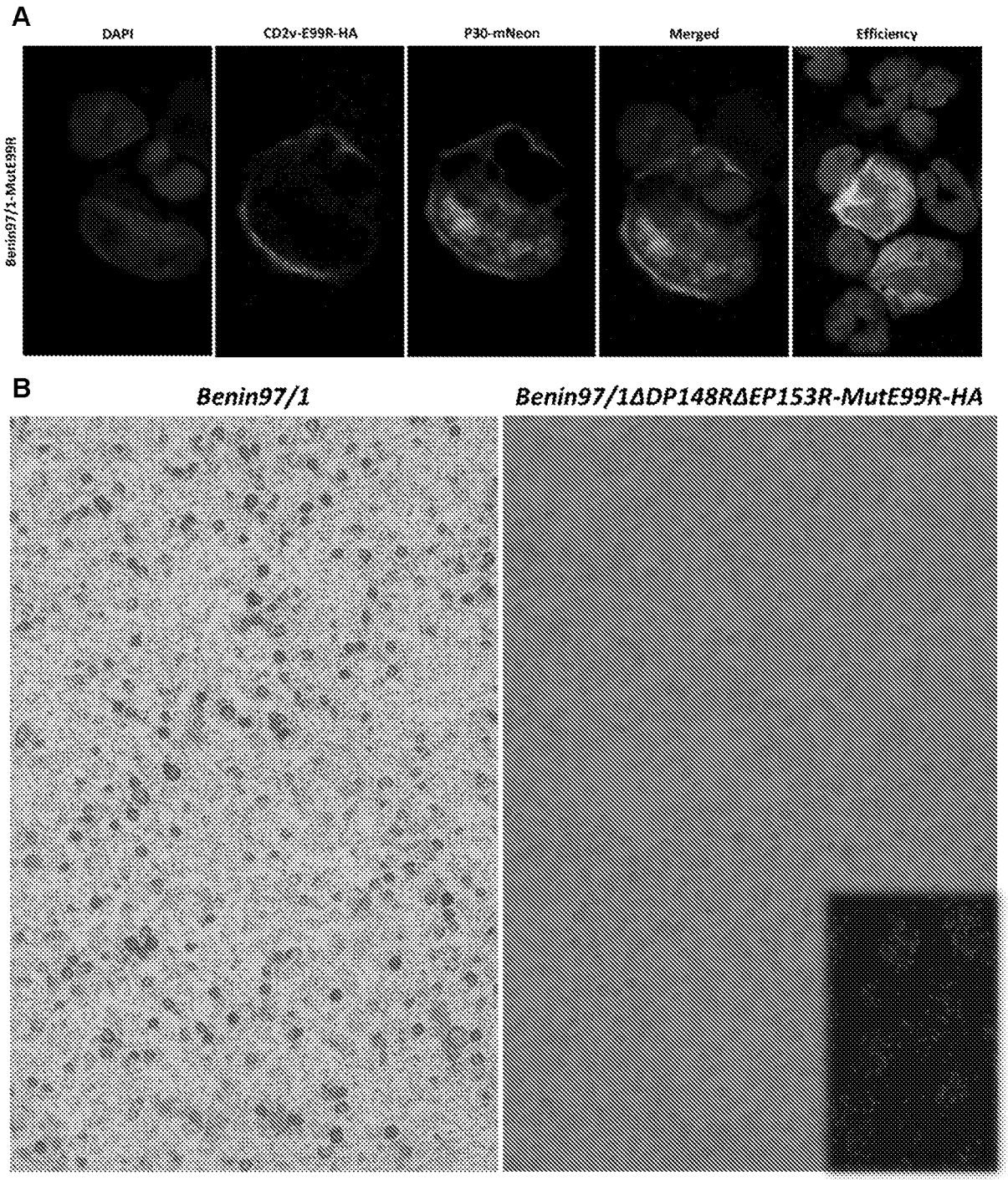

A
DAPI
CD2v-E99R-HA
P30-mNeon
Merged
Efficiency
Benin97/1-MutE99R
B
Benin97/1
Benin97/1ΔDP148RΔEP153R-MutE99R-HA

Figure 7

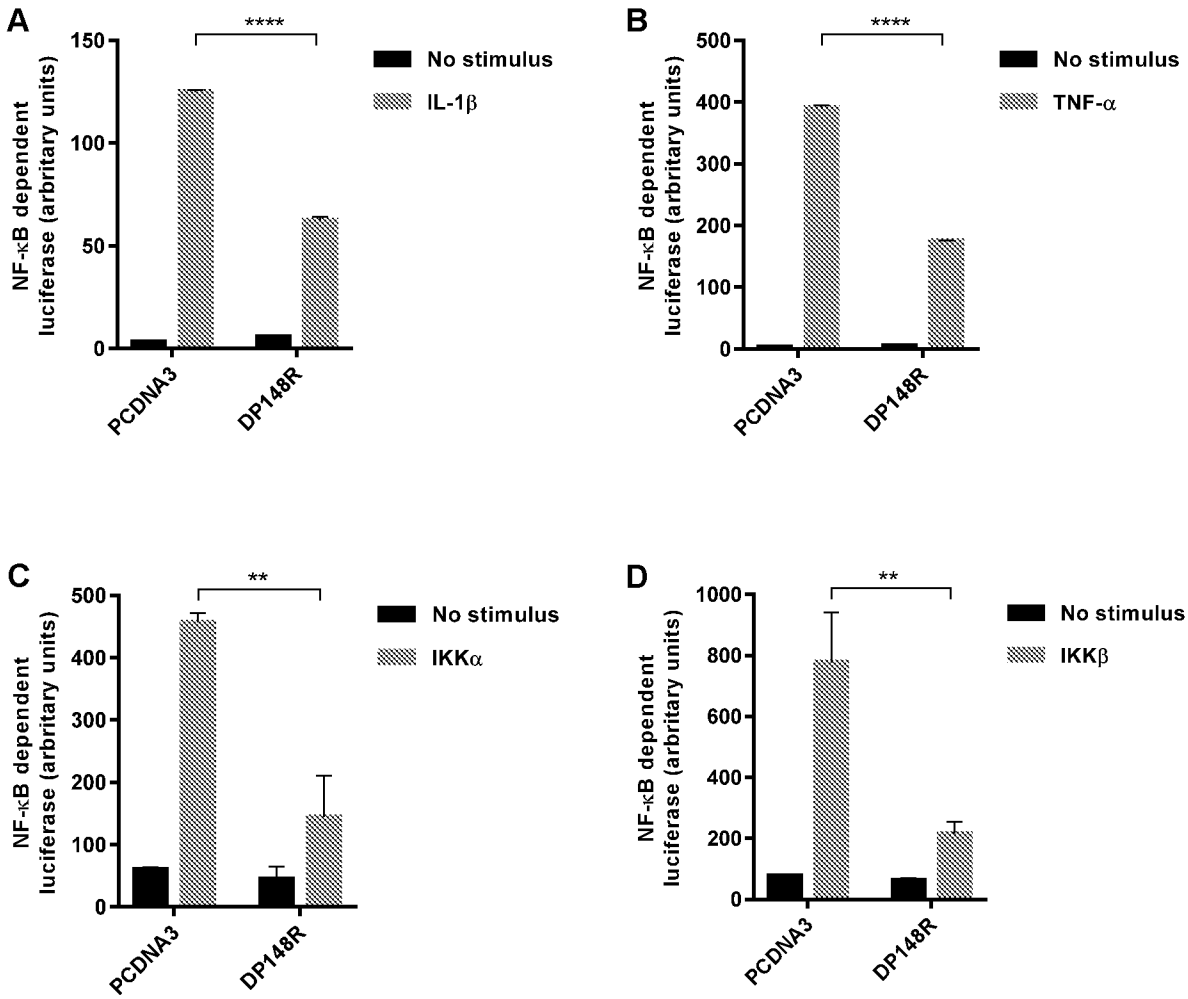

A
NF-κB dependent luciferase (arbritary units)
150
100
50
0
****
No stimulus
IL-1β
PCDNA3
DP148R
B
NF-κB dependent luciferase (arbritary units)
500
400
300
200
100
0
****
No stimulus
TNF-α
PCDNA3
DP148R
C
NF-κB dependent luciferase (arbritary units)
500
400
300
200
100
0
**
No stimulus
IKKα
PCDNA3
DP148R
D
NF-κB dependent luciferase (arbritary units)
1000
800
600
400
200
0
**
No stimulus
IKKβ
PCDNA3
DP148R

Figure 8

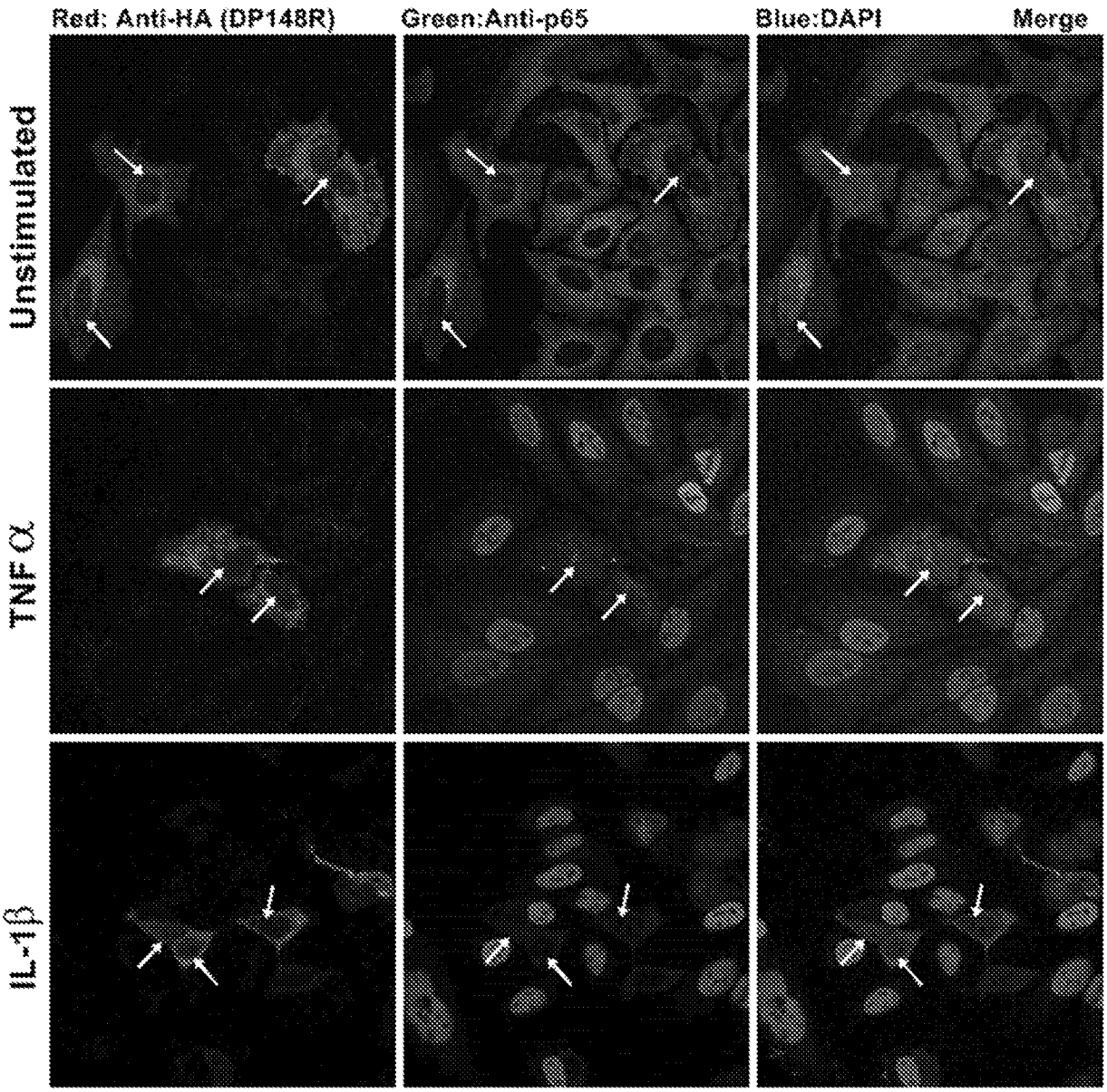
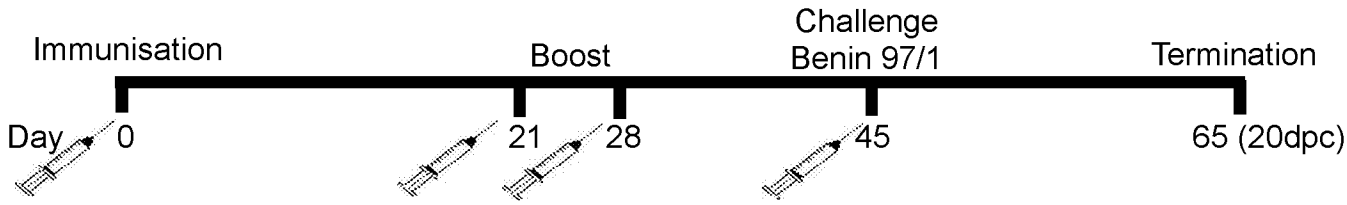

Red: Anti-HA (DP148R)
Green:Anti-p65
Blue:DAPI
Merge
Unstimulated
TNFα
IL-1β

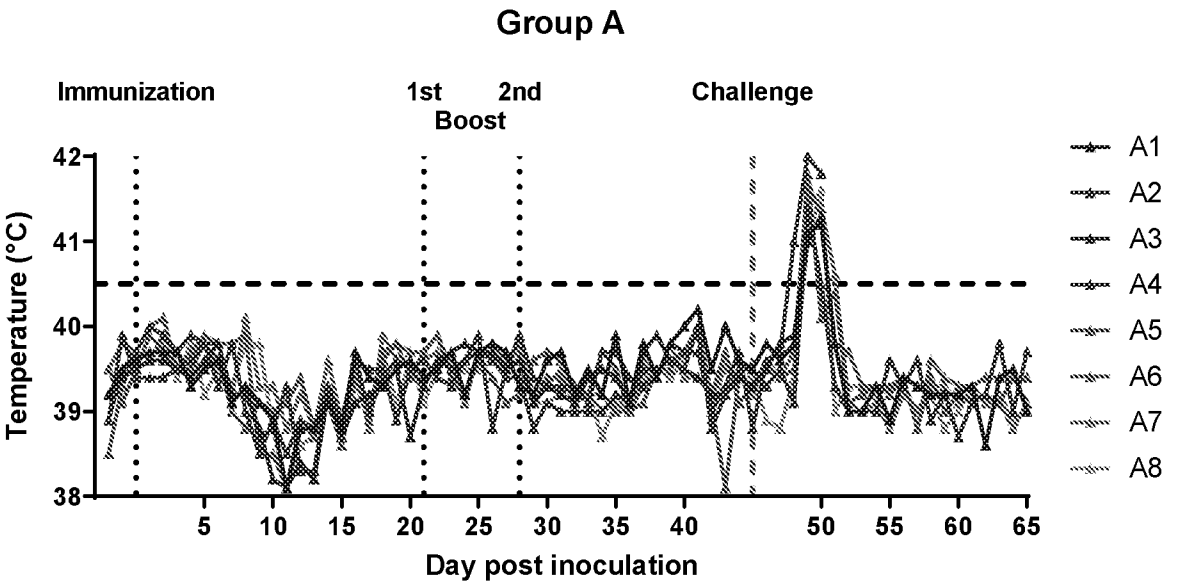
Figure 9



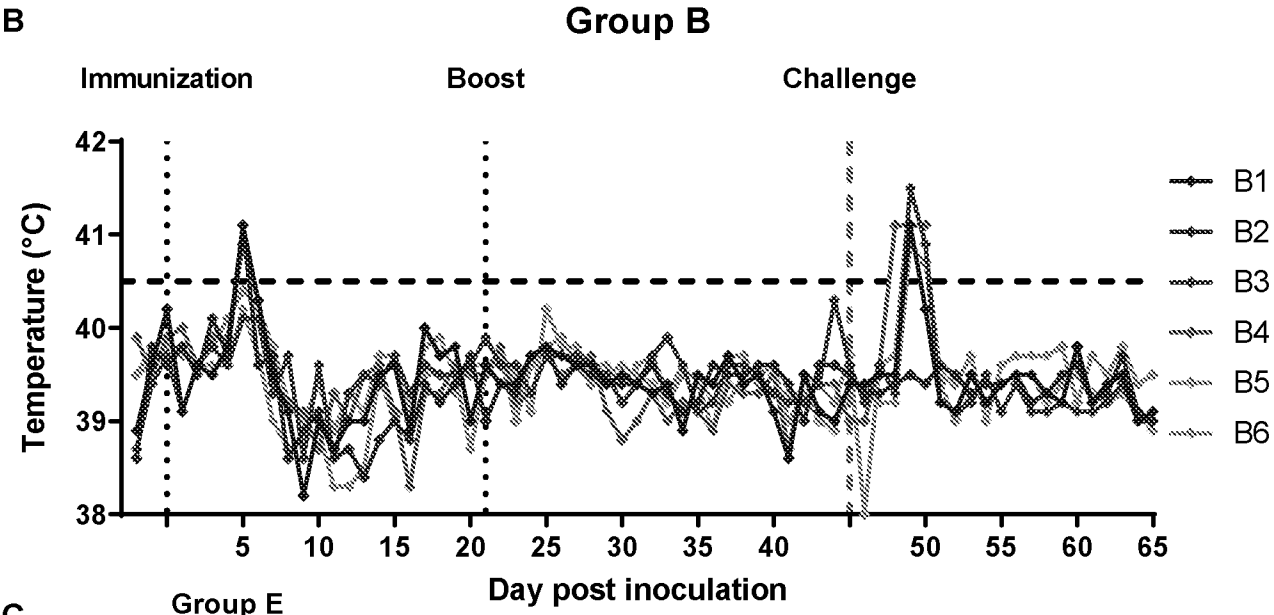
- Pigs: Large White/Landrace, 8 pigs in Group A, 6 pigs in group B
- Age: >8 weeks ; Weight: >20kg
- Route of immunization/challenge: Intramuscular
- Immunization and Boost with:
    A. Group A: 10^4 TCID50/ml **BeninΔDP148RΔEP153RΔCD2v** and additional boost with 10^6 TCID50/ml
    B. Group B: 10^4 TCID50/ml **BeninΔDP148RΔEP153R-CD2v_mutantE99R**
- Challenge: day 45 with 10^3 TCID50/ml virulent Benin 97/1 isolate

Figure 10

A



B



C

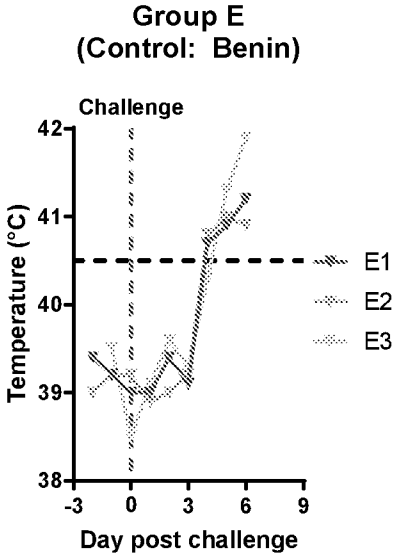


Figure 11

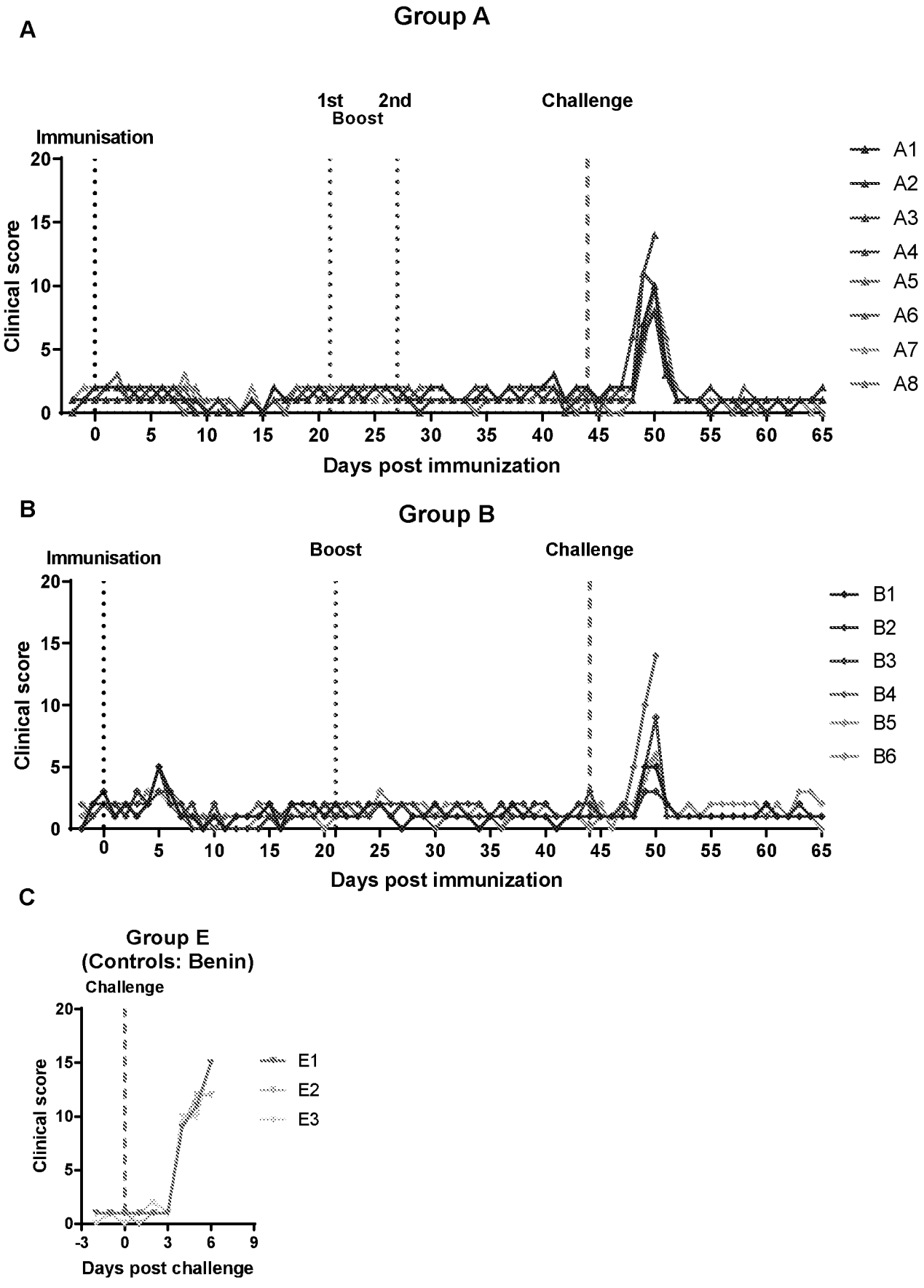
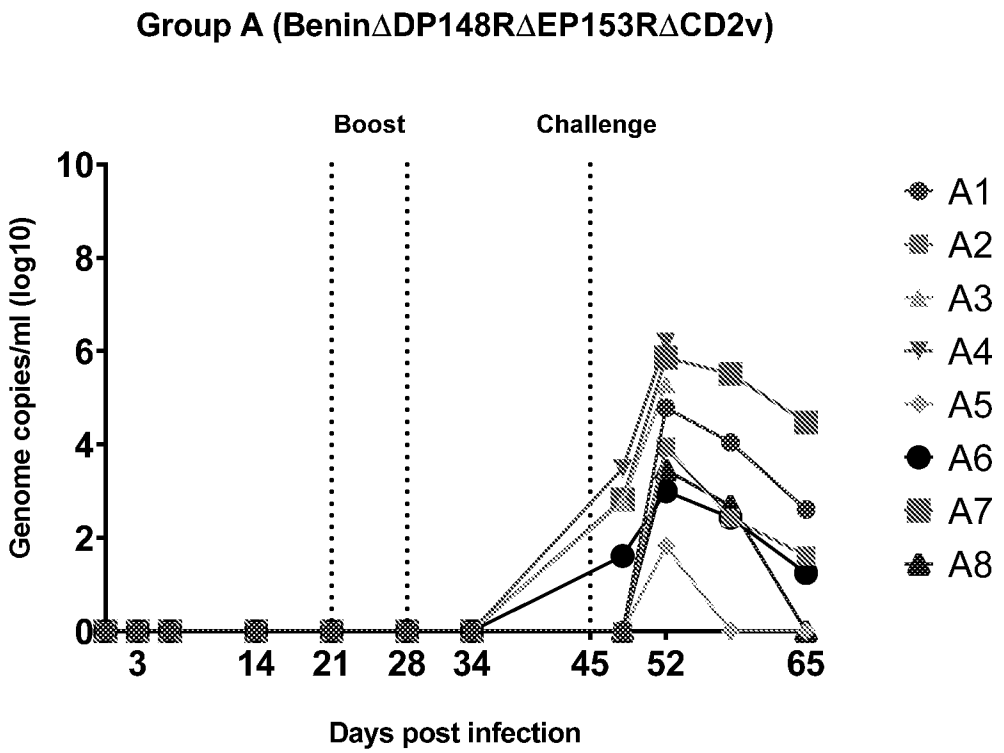

A
Group A
1st
2nd
Boost
Challenge
Immunisation
Clinical score
Days post immunization
A1
A2
A3
A4
A5
A6
A7
A8
B
Group B
Immunisation
Boost
Challenge
Clinical score
Days post immunization
B1
B2
B3
B4
B5
B6
C
Group E
(Controls: Benin)
Challenge
Clinical score
Days post challenge
E1
E2
E3

Figure 12

A


Group A (BeninΔDP148RΔEP153RΔCD2v)
Boost
Challenge
Genome copies/ml (log10)
10
8
6
4
2
0
3
14
21
28
34
45
52
65
Days post infection
A1
A2
A3
A4
A5
A6
A7
A8

B

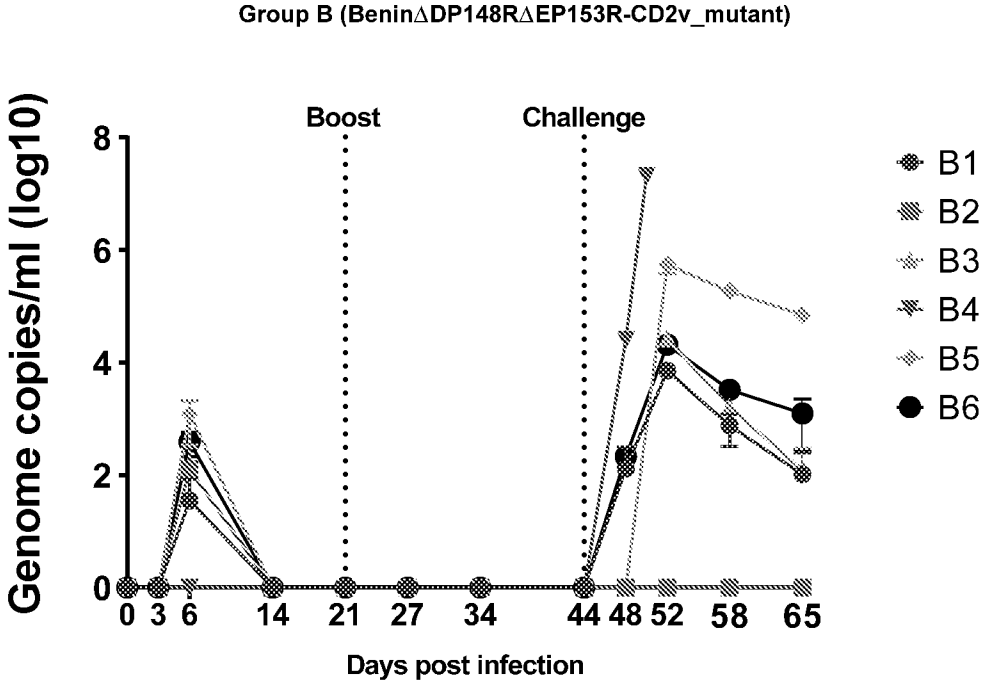
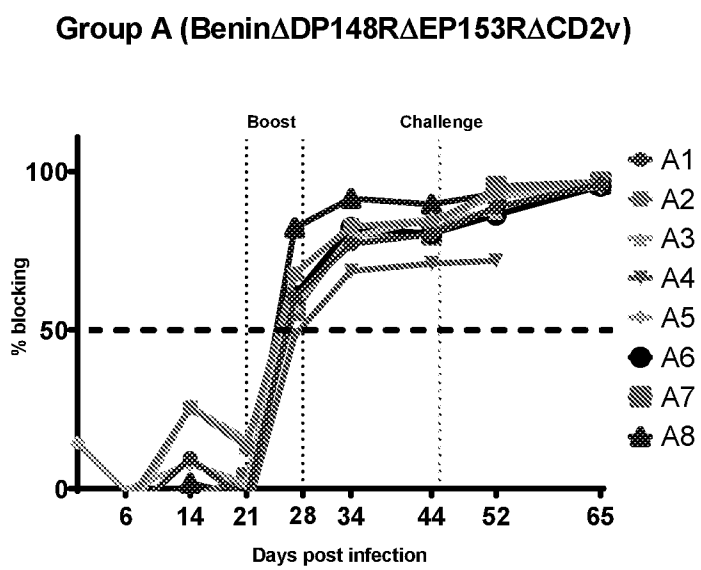
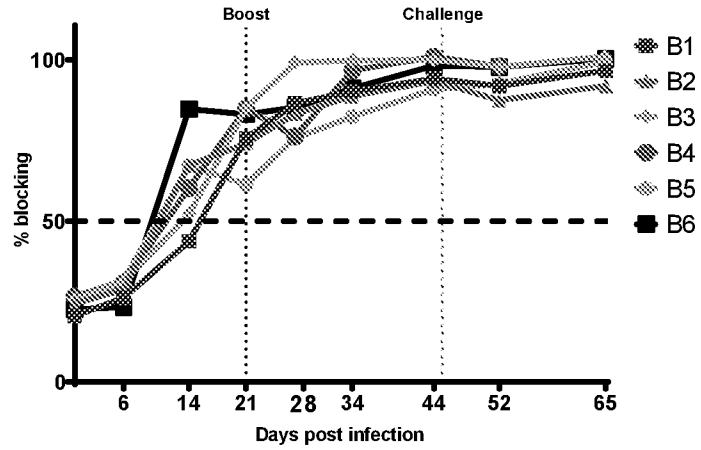

Group B (BeninΔDP148RΔEP153R-CD2v_mutant)
Boost
Challenge
Genome copies/ml (log10)
8
6
4
2
0
0 3 6
14
21
27
34
44 48 52
58
65
Days post infection
B1
B2
B3
B4
B5
B6

Figure 13

A



B



C

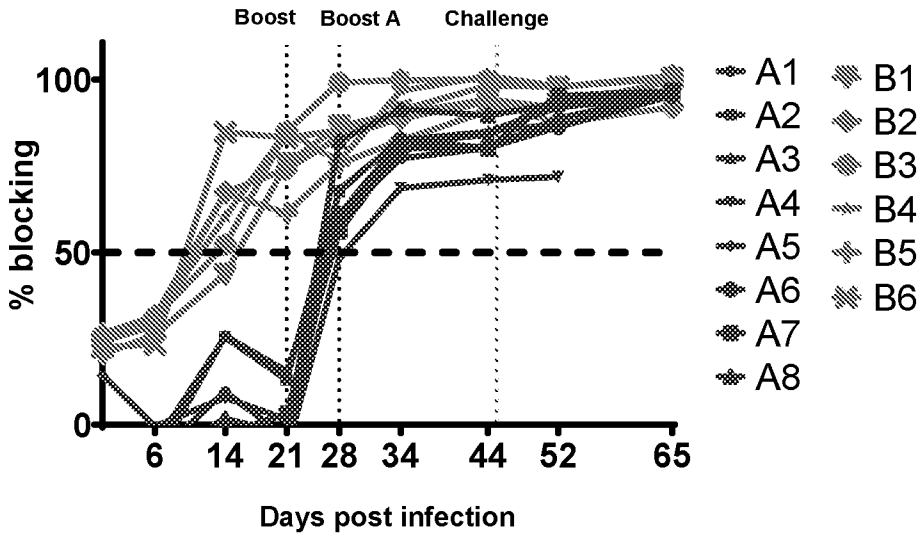
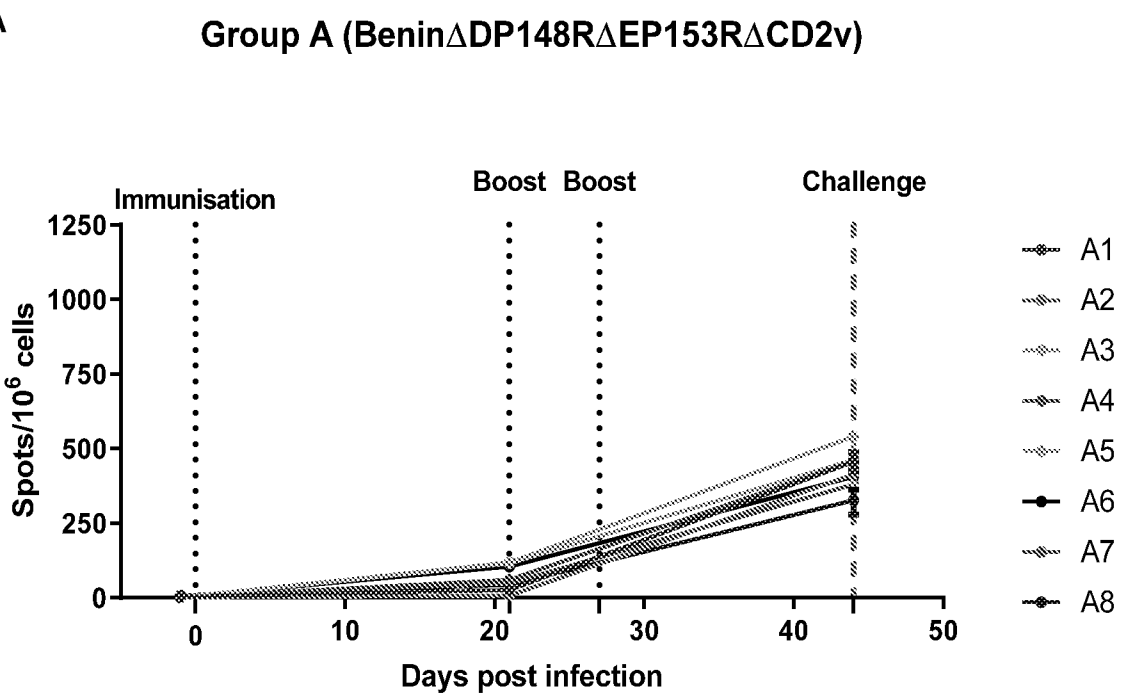


Figure 14

A


Group A (BeninΔDP148RΔEP153RΔCD2v)
Immunisation
Boost Boost
Challenge
Spots/10^6 cells
1250
1000
750
500
250
0
0
10
20
30
40
50
Days post infection
A1
A2
A3
A4
A5
A6
A7
A8

B

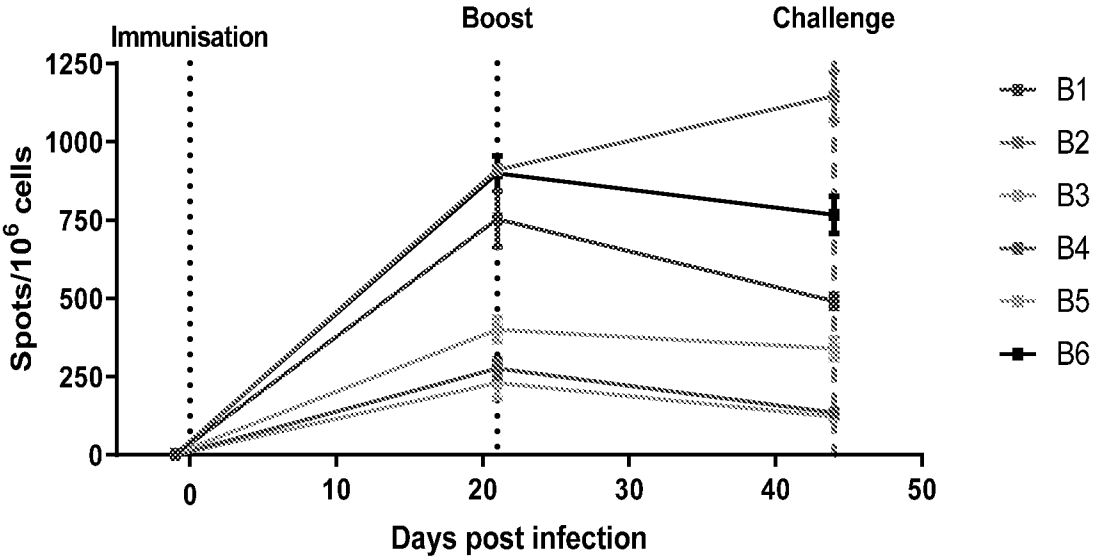

Group B (BeninΔDP148RΔEP153R-CD2v mutant)
Immunisation
Boost
Challenge
Spots/10^6 cells
1250
1000
750
500
250
0
0
10
20
30
40
50
Days post infection
B1
B2
B3
B4
B5
B6

Figure 15

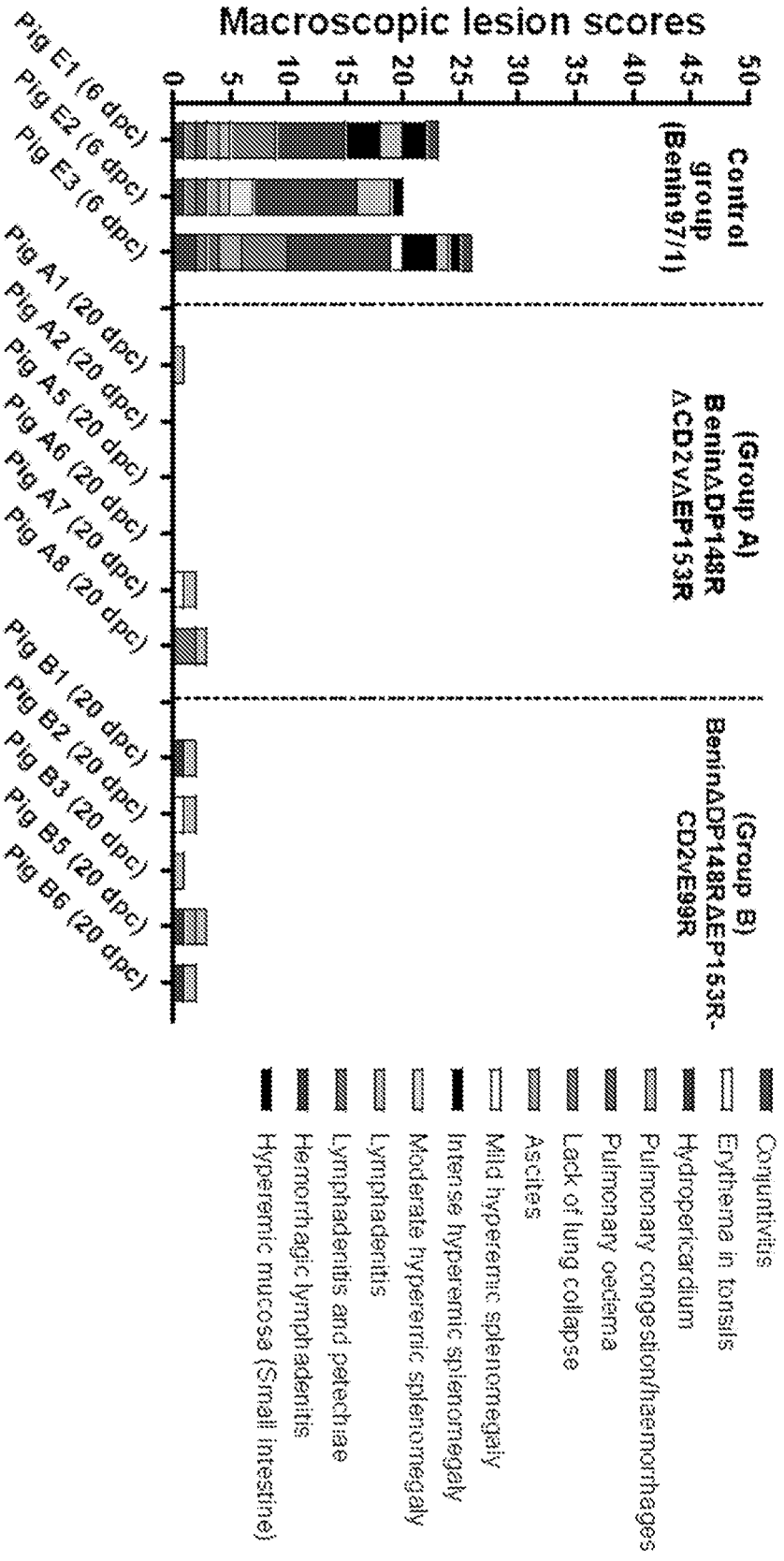
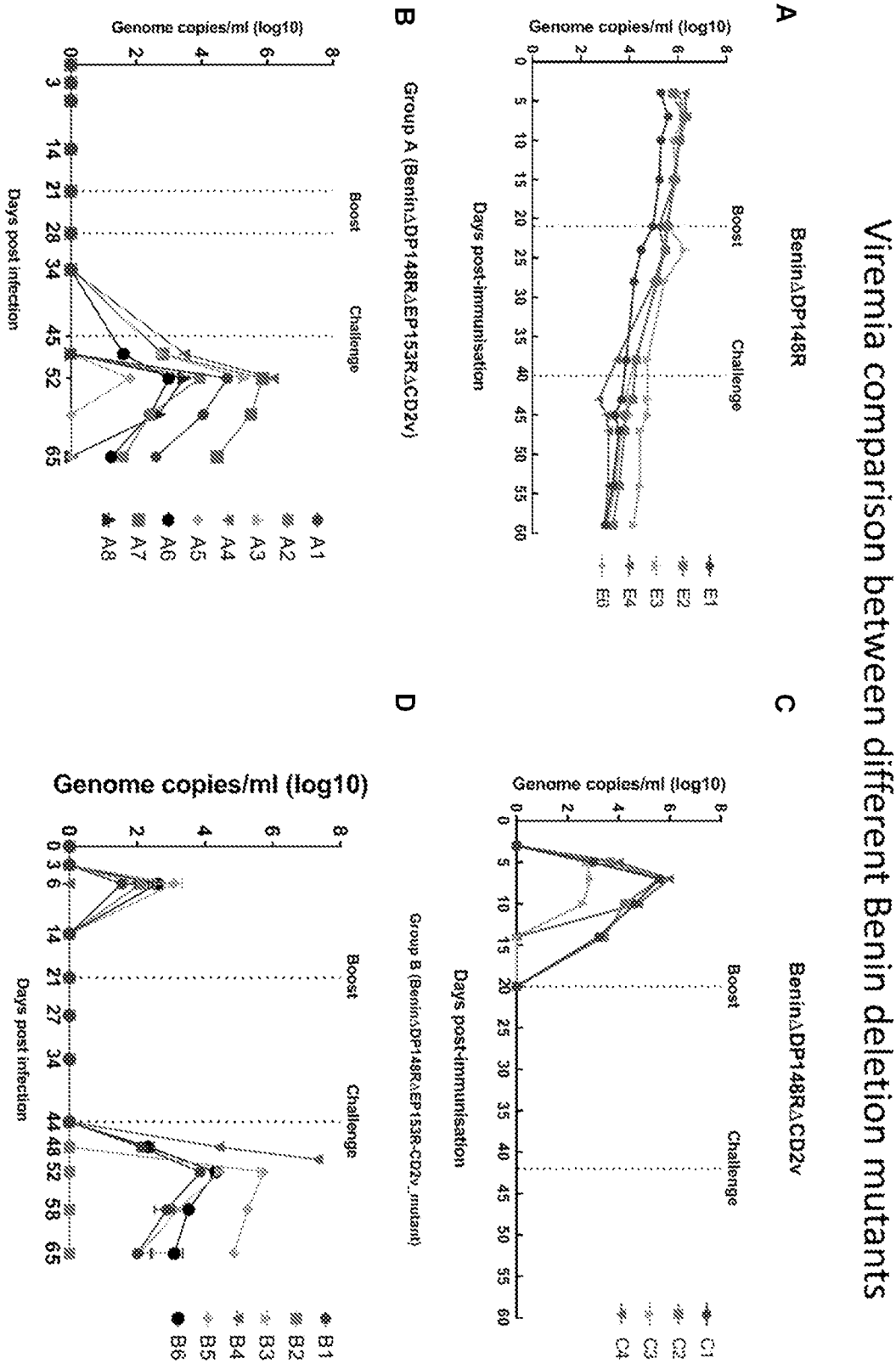

Macroscopic lesion scores
0
5
10
15
20
25
30
35
40
45
50
Control group (Benin97/1)
(Group A) BeninΔDP148R ΔCD2vΔEP153R
(Group B) BeninΔDP148RΔEP153R-CD2vE99R
Pig E1 (6 dpc)
Pig E2 (6 dpc)
Pig E3 (6 dpc)
Pig A1 (20 dpc)
Pig A2 (20 dpc)
Pig A5 (20 dpc)
Pig A6 (20 dpc)
Pig A7 (20 dpc)
Pig A8 (20 dpc)
Pig B1 (20 dpc)
Pig B2 (20 dpc)
Pig B3 (20 dpc)
Pig B5 (20 dpc)
Pig B6 (20 dpc)
Conjunctivitis
Erythema in tonsils
Hydropericardium
Pulmonary congestion/haemorrhages
Pulmonary oedema
Lack of lung collapse
Ascites
Mild hyperemic splenomegaly
Intense hyperemic splenomegaly
Moderate hyperemic splenomegaly
Lymphadenitis
Lymphadenitis and petechiae
Hemorrhagic lymphadenitis
Hyperemic mucosa (Small intestine)

Figure 16


Viremia comparison between different Benin deletion mutants
A
BeninΔDP148R
Genome copies/ml (log10)
Boost
Challenge
Days post-immunisation
E1
E2
E3
E4
E6
B
Group A (BeninΔDP148RΔEP153RΔCD2v)
Genome copies/ml (log10)
Boost
Challenge
Days post infection
A1
A2
A3
A4
A5
A6
A7
A8
C
BeninΔDP148RΔCD2v
Genome copies/ml (log10)
Boost
Challenge
Days post-immunisation
C1
C2
C3
C4
D
Group B (BeninΔDP148RΔEP153R-CD2v_mutant)
Genome copies/ml (log10)
Boost
Challenge
Days post infection
B1
B2
B3
B4
B5
B6

SEQUENCE LISTING

<110> The Pirbright Institute

<120> VACCINE

<130> P119271PCT

<150> GB 2003292.6
<151> 2020-03-06

<150> GB 2005878.0
<151> 2020-04-22

<160> 332

<170> PatentIn version 3.5

<210> 1
<211> 163
<212> PRT
<213> African swine fever virus

<400> 1

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Met Lys Tyr Ser Trp Lys Asn Gly Gly Gly Asp Tyr Trp Pro Ile Ile
1               5                  10                  15


Ile Arg His Cys Cys Phe Tyr Leu Val Phe Ser Ile Ala Phe Val Gly
            20                  25                  30


Tyr Ile Val Phe Ala Tyr Tyr Lys Asn Leu His Leu Asn Thr Ala Met
        35                  40                  45


Lys Leu Leu Ala Leu Leu Cys Ile Leu Ile Trp Leu Ser Gln Pro Gly
    50                  55                  60


Leu Asn Arg Pro Leu Ser Ile Phe Tyr Met Lys Gln Asn Leu Pro Arg
65                  70                  75                  80


Thr Tyr Thr Pro Pro Ile Arg Glu Leu Glu Tyr Trp Cys Thr Tyr Gly
                85                  90                  95


Lys His Cys Asp Phe Cys Trp Glu Cys Arg Asn Gly Ile Cys Lys Asn
            100                 105                 110


Lys Val Trp Asp Asp Met Ser Ser Val Gln Glu His Ser Tyr Pro Met
```

```
        115                 120                 125

Glu His Cys Met Ile His Arg Gln Cys Lys Tyr Ile Arg Asp Gly Pro
    130                 135                 140

Ile Phe Gln Val Glu Cys Thr Met Gln Thr Ser Asp Ala Thr His Leu
145                 150                 155                 160

Ile Asn Ala
```

<210> 2
<211> 103
<212> PRT
<213> African swine fever virus

<400> 2

```
Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln Trp Cys Phe Tyr Glu Ile Ser
            20                  25                  30

Leu Lys Ile Leu Asn His His Ser Met Glu Lys Trp Arg Asp Lys Asn
        35                  40                  45

Trp Ser Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe
    50                  55                  60

Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu
65                  70                  75                  80

Cys Thr Thr Met Lys Leu Leu Met Leu Leu Asn Ile Leu Val Leu Leu
                85                  90                  95

Ser Gln Pro Ile Leu Asn Asn
            100
```

<210> 3
<211> 375
<212> PRT
<213> African swine fever virus

<400> 3

```
Met Asn Ser Leu Gln Val Leu Thr Lys Lys Val Leu Ile Glu Asn Lys
1               5                  10                  15

Ala Phe Ser Glu Tyr His Glu Asp Asp Ile Phe Ile Leu Gln Gln Leu
            20                  25                  30

Gly Leu Trp Trp His Asn Gly Pro Ile Gly Phe Cys Lys Gln Cys Lys
        35                  40                  45

Met Val Thr Ser Gly Ser Met Ser Cys Ser Asp Val Asp Ser Tyr Glu
    50                  55                  60

Leu Asp Arg Ala Leu Val Arg Ala Val Lys Lys Asn Gln Thr Asp Leu
65                  70                  75                  80

Ile Lys Leu Phe Val Leu Trp Gly Ala Asn Ile Asn Tyr Gly Ile Ile
                85                  90                  95

Cys Ala Lys Thr Glu Arg Thr Lys Asp Leu Cys Ile Glu Leu Gly Ala
            100                 105                 110

Asn Pro Glu Phe Leu Asp Val Gly Leu Tyr Asn Met Phe Val Asp Leu
        115                 120                 125

Ile Lys Gln Gln Lys Val Leu Leu Ala Ile Asp Ile Tyr Tyr Asp Asn
    130                 135                 140

Ile Ser Ile Leu Asp Ser Phe Asp Ser His Asp Phe Tyr Val Leu Ile
145                 150                 155                 160

Asp Phe Ile Tyr Asn Cys Phe Ile Leu Asn Leu Asp Glu Lys Glu Lys
                165                 170                 175

Met Ile Lys Asn Thr Tyr Val Leu Lys Phe Trp Phe Lys Ile Ala Ile
            180                 185                 190

Glu Phe Asn Leu Ile Lys Pro Ile Arg Phe Leu Ser Lys Lys Phe Pro
        195                 200                 205
```

```
His Leu Asp Tyr Trp Arg Leu Lys Thr Ala Val Tyr Leu Gly Asn Val
    210                 215                 220

Asp Glu Ile His His Ala Tyr Phe Gln Glu Asn Ile Arg Leu Asp Pro
225                 230                 235                 240

Asn Asp Met Met Ser Leu Ala Cys Met Tyr Pro Gln Asn Lys Leu Gly
                245                 250                 255

Ile Tyr Tyr Cys Phe Ala Leu Gly Ala Asn Ile Asn Thr Ala Leu Glu
            260                 265                 270

Thr Leu Ile Gly Phe Ile Asn His Glu Val Asn Arg Glu Ile Thr Phe
        275                 280                 285

Phe Ser Asn Tyr Gly Ile Trp Ser Asn Val His Phe Cys Ile Ser Leu
    290                 295                 300

Gly Ala Asn Pro Tyr Thr Lys Lys Ile Gln Glu Thr Leu Leu Arg Gln
305                 310                 315                 320

Glu Lys Asn Val Ile Met Lys Leu Leu Phe Lys Lys Gly Leu Leu Ser
                325                 330                 335

Pro His Ser Ile Leu His Lys Lys Ile Leu Glu Pro Ser Glu Val Arg
            340                 345                 350

Lys Ile Ile Ser Thr Tyr Glu Tyr Thr Glu Thr Phe His Ser Phe Ser
        355                 360                 365

Leu Leu Arg Asp Asn Leu Arg
    370                 375
```

<210> 4
<211> 356
<212> PRT
<213> African swine fever virus

<400> 4

```
Met Val Pro Ser Leu Gln Ser Phe Ala Lys Lys Val Leu Ala Ser Gln
1               5                   10                  15
```

```
His Val Ser Ile Asp Tyr His Val Ile Leu Glu Arg Cys Gly Leu Trp
            20                  25                  30

Trp Tyr Lys Ala Pro Ile Ser Leu Asp Cys Lys His Met Leu Ile Lys
        35                  40                  45

Leu Pro Asn Phe Ala Asp Gly Leu Asp Leu Asn Thr Ala Leu Met Leu
    50                  55                  60

Ala Thr Lys Glu Asn Asn Tyr Gln Leu Ile Lys Met Phe Thr Asp Trp
65                  70                  75                  80

Gly Ala Asp Ile Asn Tyr Gly Leu Ile Cys Ala Asn Thr Pro Pro Ile
                85                  90                  95

Arg Glu Phe Cys Trp Glu Leu Gly Ala Lys Tyr Gln Val Asp Lys Lys
            100                 105                 110

Lys Ile Met His Ile Phe Phe Lys Leu Ile His Pro Asn Thr Thr Ser
        115                 120                 125

Asn Asn Ile Ile Leu Cys Leu Lys Phe Phe Asn Asp Asn Pro Phe Ser
    130                 135                 140

Ala Tyr Val Ile Ile Arg Glu Ile Lys Ser Cys Ile His Trp Lys Leu
145                 150                 155                 160

Lys Asn Leu Ala Glu Asp Thr Asn Val Leu Ser Asn Ile Ser Asp Gly
                165                 170                 175

Asp Met Leu Thr Ile Tyr Cys Phe Ile Val Ala Leu Gln Asp Asn Leu
            180                 185                 190

Arg Glu Ala Ile Ser Tyr Val Tyr Gln His Phe Lys Tyr Leu Asn Thr
        195                 200                 205

Trp Trp Leu Thr Cys Ala Leu Cys Tyr Asn Lys Leu Phe Asp Leu His
    210                 215                 220
```

```
Asn Leu Tyr Glu Lys Glu Lys Ile Arg Met Asp Met Asp Glu Met Met
225                 230                 235                 240


Arg Ile Ala Cys Thr Lys Asp Asn Asn Phe Leu Thr Ile Tyr Tyr Cys
                245                 250                 255


Phe Ile Leu Gly Ala Asn Ile Asn Leu Ala Met Ile Ala Ser Ile Arg
            260                 265                 270


Phe Tyr Asn Met Asp Asn Leu Phe Phe Cys Ile Asp Leu Gly Ala Asp
        275                 280                 285


Ala Phe Glu Glu Ala Lys Ala Leu Ala Glu Gln Gln Asn Tyr Tyr Leu
    290                 295                 300


Ile Ser His Arg Leu Ser Leu Asp Ile Tyr Ser Pro Asp Ser Ser Leu
305                 310                 315                 320


Leu Thr Leu Lys Glu Ala Asp Pro Asn Lys Ile Tyr Arg Leu Leu Lys
                325                 330                 335


Asn Tyr Lys Ser Lys Ser Met Leu Ala Tyr Leu Asn Tyr Asp Ile Asn
            340                 345                 350


Asp Thr Ser Leu
        355


<210>  5
<211>  353
<212>  PRT
<213>  African swine fever virus

<400>  5

Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15


Cys Val Ser Val Asp His Tyr His Ile Leu Lys Cys Cys Gly Leu Trp
            20                  25                  30


Trp His Asn Gly Pro Ile Met Leu His Ile Arg Arg Asn Lys Leu Phe
        35                  40                  45
```

```
Ile Arg Ser Thr Cys Phe Ser Gln Gly Ile Glu Leu Asn Ile Gly Leu
    50                  55                  60

Met Lys Ala Val Lys Glu Asn Asn His Asp Leu Ile Lys Leu Phe Thr
65                  70                  75                  80

Glu Trp Gly Ala Asp Ile Asn Tyr Gly Met Ile Cys Ala Leu Thr Glu
                85                  90                  95

Asn Thr Arg Asp Leu Cys Lys Glu Leu Gly Ala Lys Glu Tyr Leu Glu
            100                 105                 110

Arg Glu Tyr Ile Leu Lys Ile Phe Phe Asp Thr Thr Arg Asp Lys Thr
        115                 120                 125

Ser Ser Asn Ile Ile Phe Cys His Glu Val Phe Ser Asn Asn Pro Asn
    130                 135                 140

Leu Arg Ile Ile Asp Asn Leu Asp Leu Arg Gly Glu Ile Met Trp Glu
145                 150                 155                 160

Leu Arg Gly Leu Met Glu Ile Thr Phe Met Leu Asp His Asp Asp Ser
                165                 170                 175

Phe Ser Thr Val Leu Thr Lys Tyr Trp Tyr Ala Ile Ala Val Asp Tyr
            180                 185                 190

Asp Leu Lys Asp Ala Ile Arg Tyr Phe Tyr Gln Lys Tyr Pro Arg Leu
        195                 200                 205

His Arg Trp Arg Leu Met Cys Ala Leu Phe Tyr Asn Asn Val Phe Asp
    210                 215                 220

Leu His Glu Leu Tyr Glu Ile Glu Arg Val Arg Met Asp Ile Asp Glu
225                 230                 235                 240

Met Met His Ile Ala Cys Ile Gln Asp Tyr Ser Tyr Ser Ala Ile Tyr
                245                 250                 255

Tyr Cys Phe Ile Met Gly Ala Asn Ile Asn Gln Ala Met Leu Val Ser
```

```
            260                 265                 270

Ile Gln Asn Tyr Asn Leu Gly Asn Leu Phe Phe Cys Ile Asp Leu Gly
        275                 280                 285

Ala Asn Ala Phe Glu Glu Gly Lys Ala Leu Ala Glu Gln Lys Glu Asn
    290                 295                 300

Tyr Leu Ile Ala His Ala Leu Ser Leu Lys His Tyr Asn Pro Val Ile
305                 310                 315                 320

Ser Leu Leu Ser Asn Val Met Asp Pro Glu Lys Ile Asn Tyr Met Leu
                325                 330                 335

Lys Asn Tyr His Ser Ile Asn Met Gly Ile Phe Leu Asp Tyr Glu Gln
            340                 345                 350

Arg
```

<210> 6
<211> 350
<212> PRT
<213> African swine fever virus

<400> 6

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Tyr Tyr Asp Leu Trp
            20                  25                  30

Trp Tyr Asn Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
        35                  40                  45

Ser Ser Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Arg Glu Asn Asn Tyr Ser Leu Ile Lys Leu Phe Thr Glu Trp
65                  70                  75                  80
```

```
Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95

Arg Asp Leu Cys Gln Glu Leu Gly Ala Lys Glu Ile Leu Asn Glu Glu
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Leu Lys Leu Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Leu Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Val Arg Tyr Ser Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Met Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Met Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300
```

```
Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Thr Thr Ile Pro Leu
305                 310                 315                 320


Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335


Phe Ser Lys Asn Met Met Ile Phe Leu Ser Tyr Asp Leu Arg
            340                 345                 350
```

<210> 7
<211> 353
<212> PRT
<213> African swine fever virus

<400> 7

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Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15


Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys Tyr Cys Gly
            20                  25                  30


Leu Trp Trp His Asp Ala Pro Leu Lys Leu Cys Met Asp Arg Gly Arg
        35                  40                  45


Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Arg Val
    50                  55                  60


Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80


Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95


Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110


Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Arg Ile Met His Asn
        115                 120                 125


Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
```

```
    130                 135                 140

Pro Met Leu Glu Asn Lys Phe Val Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Val Cys
            180                 185                 190

Lys Asn Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Lys Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Cys Ala Lys Asp Asn Asn Leu Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Val Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Thr Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Lys Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350
```

Leu

<210> 8
<211> 357
<212> PRT
<213> African swine fever virus

<400> 8

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15


Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30


Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Val Phe Ser
        35                  40                  45


Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60


Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80


Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95


Ala Val Tyr Leu Lys Arg Leu Cys Ala Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110


Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asn Leu
        115                 120                 125


Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140


Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160


Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175
```

```
Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn Gln Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys His Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Ala Asp Phe Asp
        275                 280                 285

Arg Ala Gln Leu Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Val Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Met Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350

Ile Ile Val Ile Asp
        355
```

<210> 9
<211> 531
<212> PRT
<213> African swine fever virus

<400> 9

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Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                  10                  15

Leu Pro Glu Phe Phe Asp Asp Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45

Ile Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Gly Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg Tyr
                85                  90                  95

Asn Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Asp Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Ile Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Arg Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys Tyr Thr Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Leu Val His Leu Leu Ile Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Val Cys His Ile Ile
            180                 185                 190

Asp Thr Phe Asp Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205
```

```
Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
    210                 215                 220

His Leu Asp Ile Leu Ile Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Ile Asp Asn Leu Asp Val Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Val Ala Ile Lys Thr Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Gln Lys Ile Ser Gln Tyr Val Ala Thr Phe Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Lys Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Asn Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Glu Arg Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Lys Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Ala Arg Leu Lys His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
```

```
            420                 425                 430

Tyr Glu His Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asn Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495

Asn Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu
            500                 505                 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
        515                 520                 525

Tyr Met Pro
    530
```

<210> 10
<211> 526
<212> PRT
<213> African swine fever virus

<400> 10

```
Met Phe Ser Leu Gln Asp Leu Cys Arg Lys His Leu Phe Ile Leu Pro
1               5                   10                  15

Asp Val Phe Gly Glu His Val Leu Gln Arg Leu Gly Leu Tyr Trp Arg
            20                  25                  30

Cys His Gly Ser Leu Gln Arg Ile Gly Asp Asp His Ile Leu Ile Arg
        35                  40                  45

Arg Asp Leu Ile Leu Ser Thr Asn Glu Ala Leu Arg Met Ala Gly Glu
    50                  55                  60
```

```
Glu Gly Asn Asn Glu Val Val Lys Leu Leu Leu Leu Trp Lys Gly Asn
65                  70                  75                  80

Leu His Tyr Ala Val Ile Gly Ala Leu Gln Gly Asp Gln Tyr Asp Leu
                85                  90                  95

Ile His Lys Tyr Glu Asn Gln Ile Gly Asp Phe His Phe Ile Leu Pro
            100                 105                 110

Leu Ile Gln Asp Ala Asn Thr Phe Glu Lys Cys His Ala Leu Glu Arg
        115                 120                 125

Phe Cys Gly Val Ser Cys Leu Leu Lys His Ala Thr Lys Tyr Asn Met
    130                 135                 140

Leu Pro Ile Leu Gln Lys Tyr Gln Glu Glu Leu Ser Met Arg Ala Tyr
145                 150                 155                 160

Leu His Glu Thr Leu Phe Glu Leu Ala Cys Leu Trp Gln Arg Tyr Asp
                165                 170                 175

Val Leu Lys Trp Ile Glu Gln Thr Met His Val Tyr Asp Leu Lys Ile
            180                 185                 190

Met Phe Asn Ile Ala Ile Ser Lys Arg Asp Leu Thr Met Tyr Ser Leu
        195                 200                 205

Gly Tyr Ile Phe Leu Phe Asp Arg Gly Asn Thr Glu Ala Thr Leu Leu
    210                 215                 220

Thr Gln His Leu Glu Lys Thr Ala Ala Lys Gly Leu Leu His Phe Val
225                 230                 235                 240

Leu Glu Thr Leu Lys Tyr Gly Gly Asn Ile Asp Thr Val Leu Thr Gln
                245                 250                 255

Ala Val Lys Tyr Asn His Arg Lys Leu Leu Asp Tyr Phe Leu Arg Gln
            260                 265                 270

Leu Pro Arg Lys His Ile Glu Lys Leu Leu Leu Leu Ala Val Gln Glu
        275                 280                 285
```

```
Lys Ala Ser Lys Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Tyr
    290                 295                 300

Ser Val Lys Arg Ile Lys Lys Leu Leu Arg Tyr Val Ile Glu Tyr Glu
305                 310                 315                 320

Ser Thr Leu Val Ile Lys Ile Leu Leu Lys Lys Arg Val Asn Leu Ile
                325                 330                 335

Asp Ala Met Leu Glu Lys Met Val Arg Tyr Phe Ser Ala Thr Lys Val
            340                 345                 350

Arg Thr Ile Met Asp Glu Leu Ser Ile Ser Pro Glu Arg Val Ile Lys
        355                 360                 365

Met Ala Ile Gln Lys Met Arg Thr Asp Ile Val Ile His Thr Ser Tyr
    370                 375                 380

Val Trp Glu Asp Asp Leu Glu Arg Leu Thr Arg Leu Lys Asn Met Val
385                 390                 395                 400

Tyr Thr Ile Lys Tyr Glu His Gly Lys Lys Met Leu Ile Lys Val Met
                405                 410                 415

His Gly Ile Tyr Lys Asn Leu Leu Tyr Gly Glu Arg Glu Lys Val Met
            420                 425                 430

Phe His Leu Ala Lys Leu Tyr Val Ala Gln Asn Ala Ala Thr Gln Phe
        435                 440                 445

Arg Asp Ile Cys Lys Asp Cys Tyr Lys Leu Asp Val Ala Arg Phe Lys
    450                 455                 460

Pro Arg Phe Lys Gln Leu Ile Leu Asp Cys Leu Glu Ile Val Thr Lys
465                 470                 475                 480

Lys Ser Cys Tyr Ser Ile Leu Glu Ile Leu Glu Lys His Ile Ile Ser
                485                 490                 495
```

Leu Phe Thr Met Lys Val Met Thr Glu Glu Glu Lys Asn Leu Cys Leu
500 505 510

Glu Ile Leu Tyr Lys Val Ile His Tyr Lys Thr Ile Gln Cys
515 520 525

<210> 11
<211> 254
<212> PRT
<213> African swine fever virus

<400> 11

Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1 5 10 15

Arg Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg
20 25 30

Leu Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala
35 40 45

Asn Thr Lys Glu Leu Glu Asp Phe Leu Arg Ser Asp Gly Gln Ser Glu
50 55 60

Glu Ile Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Cys
65 70 75 80

Pro Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys
85 90 95

Ala Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
100 105 110

Asp Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Lys Lys Val
115 120 125

Arg Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile
130 135 140

Cys His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp
145 150 155 160

```
Phe Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln
                165                 170                 175

Val Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu
            180                 185                 190

Thr Asp Ala Ile Gln Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile
        195                 200                 205

Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala
    210                 215                 220

Pro Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys
225                 230                 235                 240

Lys Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
                245                 250
```

<210> 12
<211> 237
<212> PRT
<213> African swine fever virus

<400> 12

```
Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg Leu
1               5                   10                  15

Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala Asn
            20                  25                  30

Thr Lys Glu Leu Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu Glu
        35                  40                  45

Ile Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
    50                  55                  60

Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys Ala
65                  70                  75                  80

Gly Gln Val Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr Asp
                85                  90                  95
```

```
Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val Arg
            100                 105                 110

Asn Lys Ala Val Glu Leu Tyr Trp Val Phe Arg Ala Ile Asn Met Cys
        115                 120                 125

His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp Phe
    130                 135                 140

Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln Val
145                 150                 155                 160

Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu Thr
                165                 170                 175

Asp Ala Ile Gln Ile Ser Leu Glu Ser Asn Ser Gln Val Gly Ile Cys
            180                 185                 190

Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Arg Ala Pro
        195                 200                 205

Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys Lys
    210                 215                 220

Asp Val Leu Pro Pro His Asp Phe Leu Leu Leu Leu Gln
225                 230                 235
```

<210> 13
<211> 257
<212> PRT
<213> African swine fever virus

<400> 13

```
Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1               5                   10                  15

Lys Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Lys
            20                  25                  30

Leu Lys Asp Leu Thr Pro Pro Gln Arg Ala Val Ala Phe Phe Arg Ala
```

```
        35                  40                  45

Asn Thr Lys Glu Leu Glu Asp Phe Leu Tyr Pro Asp Gly Gln Ser Glu
    50                  55                  60

Glu Leu Leu Pro Gly Leu Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly
65                  70                  75                  80

Ser Ile Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Glu Asn Pro Lys
                85                  90                  95

Ala Gly Arg Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
            100                 105                 110

Asp Ala Asn Ile Tyr Asn Met Leu Ala Arg Leu Arg Pro Glu Leu Val
        115                 120                 125

Arg Asp Lys Ala Ile Glu Leu Tyr Trp Leu Phe Arg Ala Ile Leu Met
    130                 135                 140

Cys His Ser Pro Leu Val Leu Glu Ile Val Arg His Glu Thr Met Asp
145                 150                 155                 160

Phe Ala Glu Thr Ala Phe Ile Cys Ala Ala Tyr Phe Ser Glu Pro Gln
                165                 170                 175

Val Met Tyr Ala Leu Tyr Lys Phe Ile Pro Ile Ser Arg Ala Val Leu
            180                 185                 190

Ala Asp Ala Ile Gln Met Cys Leu Glu Ser Asn Ser Glu Ala Gly Ile
        195                 200                 205

Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Lys Val Pro Gly
    210                 215                 220

Ser Leu Arg Lys Arg Leu Arg Ala Ser Pro Leu Arg Gln Glu Arg Lys
225                 230                 235                 240

Lys Lys Asn Val Leu Pro Pro His Glu Phe Leu Leu Met Leu His Gly
                245                 250                 255
```

Ile

<210> 14
<211> 240
<212> PRT
<213> African swine fever virus

<400> 14

```
Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Lys Leu
1               5                   10                  15


Arg Asp Leu Thr Pro Met Gln Arg Ala Val Ala Phe Phe Arg Val Asn
            20                  25                  30


Thr Lys Glu Leu Glu Asp Phe Leu Tyr Pro Asp Gly Gln Ser Glu Glu
        35                  40                  45


Leu Leu Pro Gly Leu Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
    50                  55                  60


Ile Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Glu Asn Pro Lys Ala
65                  70                  75                  80


Gly Arg Leu Arg Gly Leu Glu Val Lys Leu Leu Glu Arg Leu Tyr Asp
                85                  90                  95


Ala Asn Ile Tyr Asn Met Leu Ala Gln Ile Arg Pro Glu Leu Val Arg
            100                 105                 110


Ile Lys Ala Ile Glu Leu Tyr Trp Leu Phe Arg Ala Ile Leu Met Cys
        115                 120                 125


His Ser Pro Leu Val Leu Glu Ile Val Arg His Glu Thr Met Asp Phe
    130                 135                 140


Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Ser Glu Pro Gln Val
145                 150                 155                 160


Met Tyr Ala Leu Tyr Lys Phe Ile Pro Ile Ser Arg Ala Val Leu Ala
                165                 170                 175
```

```
Asp Ala Ile Glu Met Ser Leu Glu Ser Asn Ser Glu Thr Gly Ile Cys
            180                 185                 190


Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Lys Val Pro Gly Pro
        195                 200                 205


Leu Arg Lys Arg Leu Arg Ala Ser Pro Leu Arg Gln Glu Arg Lys Lys
    210                 215                 220


Lys Asn Val Leu Pro Pro His Glu Phe Leu Leu Met Leu His Gly Ile
225                 230                 235                 240
```

<210> 15
<211> 254
<212> PRT
<213> African swine fever virus

<400> 15

```
Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1               5                   10                  15


Arg Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg
            20                  25                  30


Leu Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala
        35                  40                  45


Asn Thr Lys Glu Leu Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu
    50                  55                  60


Glu Ile Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly
65                  70                  75                  80


Pro Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys
                85                  90                  95


Ala Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
            100                 105                 110


Asp Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val
```

```
        115                 120                 125

Arg Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile
    130                 135                 140

Cys His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp
145                 150                 155                 160

Phe Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln
                165                 170                 175

Val Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu
            180                 185                 190

Thr Asp Ala Ile Arg Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile
        195                 200                 205

Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala
    210                 215                 220

Pro Leu Arg Lys Arg Leu Cys Ala Lys Leu Arg Ser Gln Arg Lys Lys
225                 230                 235                 240

Lys Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
                245                 250
```

<210> 16
<211> 237
<212> PRT
<213> African swine fever virus

<400> 16

```
Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg Leu
1               5                   10                  15

Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala Asn
            20                  25                  30

Thr Lys Glu Val Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu Glu
        35                  40                  45
```

```
Val Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
    50                  55                  60

Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys Ala
65                  70                  75                  80

Gly Gln Val Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr Asp
                85                  90                  95

Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val Arg
            100                 105                 110

Asn Lys Ala Val Glu Leu Tyr Trp Val Phe Arg Ala Ile Asn Met Cys
        115                 120                 125

His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp Phe
    130                 135                 140

Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln Val
145                 150                 155                 160

Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Ser Arg Ala Val Leu Thr
                165                 170                 175

Asp Ala Ile Gln Ile Ser Leu Glu Ser Asn Ser Gln Val Gly Ile Cys
            180                 185                 190

Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Arg Ala Pro
        195                 200                 205

Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys Lys
    210                 215                 220

Asp Val Leu Pro Pro His Asp Phe Leu Leu Leu Leu Gln
225                 230                 235
```

<210> 17
<211> 237
<212> PRT
<213> African swine fever virus

<400> 17

```
Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg Leu
1               5                  10                  15

Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala Asn
            20                  25                  30

Thr Lys Glu Leu Glu Asp Phe Leu Cys Pro Asp Gly Gln Ser Glu Glu
        35                  40                  45

Val Leu Ser Gly Ser Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
    50                  55                  60

Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys Ala
65                  70                  75                  80

Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr Asp
                85                  90                  95

Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val Arg
            100                 105                 110

Asn Lys Ala Val Glu Leu Tyr Trp Val Phe Arg Ala Ile Asn Met Cys
        115                 120                 125

His Ala Pro Leu Val Leu Asp Ile Val Arg Asn Glu Glu Leu Asp Phe
    130                 135                 140

Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln Val
145                 150                 155                 160

Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu Thr
                165                 170                 175

Asp Ala Ile Gln Ile Ser Leu Glu Ser Asn Ser Gln Val Gly Ile Cys
            180                 185                 190

Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Arg Ala Pro
        195                 200                 205

Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys Lys
```

210 215 220

Asp Val Leu Pro Pro His Asp Phe Leu Leu Leu Leu Gln
225 230 235

<210> 18
<211> 254
<212> PRT
<213> African swine fever virus

<400> 18

Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1 5 10 15

Arg Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg
20 25 30

Leu Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala
35 40 45

Asn Thr Lys Glu Leu Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu
50 55 60

Glu Ile Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly
65 70 75 80

Pro Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys
85 90 95

Ala Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
100 105 110

Asp Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val
115 120 125

Arg Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile
130 135 140

Cys His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp
145 150 155 160

```
Phe Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln
                165                 170                 175


Val Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu
            180                 185                 190


Thr Asp Ala Ile Arg Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile
        195                 200                 205


Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala
    210                 215                 220


Pro Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys
225                 230                 235                 240


Lys Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
                245                 250
```

<210> 19
<211> 72
<212> PRT
<213> African swine fever virus

<400> 19

```
Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1               5                   10                  15


Arg Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg
            20                  25                  30


Leu Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala
        35                  40                  45


Asn Thr Lys Glu Leu Glu Asp Phe Leu Arg Ser Asp Gly Gln Ser Glu
    50                  55                  60


Glu Ile Leu Ser Gly Pro Pro Pro
65                  70
```

<210> 20
<211> 153
<212> PRT

<213> African swine fever virus

<400> 20

```
Met Tyr Phe Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1               5                   10                  15


Lys Lys Ile Leu Asp Asp Ser Ser Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30


Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45


Ile Phe Trp Asp Asn Tyr Ile Lys Cys Tyr Arg Asn Asn Asp Lys Met
    50                  55                  60


Phe Tyr Cys Pro Asn Asp Trp Val Gly Tyr Asn Asn Ile Cys Tyr Tyr
65                  70                  75                  80


Phe Ser Asn Gly Ser Phe Ser Lys Asn Tyr Thr Ala Ala Ser Asn Phe
                85                  90                  95


Cys Arg Gln Leu Asn Gly Thr Leu Ala Asn Asn Asp Thr Asn Leu Leu
            100                 105                 110


Asn Leu Thr Lys Ile Tyr Asn Asn Gln Ser Met Tyr Trp Val Asn Asn
        115                 120                 125


Thr Val Ile Leu Arg Gly Asp Asn Lys Tyr Ser Gln Lys Val Asn Tyr
    130                 135                 140


Thr Asp Leu Leu Phe Ile Cys Gly Lys
145                 150
```

<210> 21
<211> 402
<212> PRT
<213> African swine fever virus

<400> 21

```
Met Ile Ile Ile Val Ile Phe Leu Met Cys Leu Lys Ile Val Leu Asn
1               5                   10                  15
```

```
Asn Ile Ile Ile Trp Ser Thr Leu Asn Gln Thr Val Phe Leu Asn Asn
            20                  25                  30

Ile Phe Thr Ile Asn Asp Thr Tyr Gly Gly Leu Phe Trp Asn Thr Tyr
        35                  40                  45

Tyr Asp Asn Asn Arg Ser Asn Phe Thr Tyr Cys Gly Ile Ala Gly Asn
    50                  55                  60

Tyr Cys Ser Cys Cys Gly His Asn Ile Ser Leu Tyr Asn Thr Thr Asn
65                  70                  75                  80

Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Glu Ile Phe Asn Arg
                85                  90                  95

Thr Tyr Glu Leu Val Tyr Leu Asp Lys Lys Ile Asn Tyr Thr Val Lys
            100                 105                 110

Leu Leu Lys Ser Val Asp Ser Pro Thr Ile Thr Tyr Asn Cys Thr Asn
        115                 120                 125

Ser Leu Ile Thr Cys Lys Asn Asn Asn Gly Thr Asn Val Asn Ile Tyr
    130                 135                 140

Leu Ile Ile Asn Asn Thr Ile Val Asn Asp Thr Asn Gly Asp Ile Leu
145                 150                 155                 160

Asn Tyr Tyr Trp Asn Gly Asn Asn Asn Phe Thr Ala Thr Cys Met Ile
                165                 170                 175

Asn Asn Thr Ile Ser Ser Leu Asn Glu Thr Glu Asn Ile Asn Cys Thr
            180                 185                 190

Asn Pro Ile Leu Lys Tyr Gln Asn Tyr Leu Ser Thr Leu Phe Tyr Ile
        195                 200                 205

Ile Ile Phe Ile Val Ser Gly Leu Ile Ile Gly Ile Phe Ile Ser Ile
    210                 215                 220

Ile Ser Val Leu Ser Ile Arg Arg Lys Arg Lys Lys His Val Glu Glu
```

```
225                 230                 235                 240

Ile Glu Ser Pro Pro Pro Ser Glu Ser Asn Glu Glu Asp Ile Ser His
                245                 250                 255

Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285

Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
    290                 295                 300

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320

Pro Cys Pro Pro Pro Lys Pro Cys Ser Pro Pro Lys Pro Cys Arg Pro
                325                 330                 335

Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
            340                 345                 350

Pro Pro Pro Lys Pro Cys Pro Pro Ser Lys Pro Cys Pro Ser Pro Glu
        355                 360                 365

Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu Pro Asn
    370                 375                 380

Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg
385                 390                 395                 400

Ile Ile
```

<210> 22
<211> 392
<212> PRT
<213> African swine fever virus

<400> 22

```
Met Ile Ile Ile Leu Ile Phe Leu Ile Cys Leu Lys Ile Val Leu Asn
1               5                  10                  15

Asn Asn Ile Ile Ile Trp His Thr Leu Asn Glu Thr Ile Phe Leu Asn
            20                  25                  30

Asn Ser Ile Thr Phe Thr Asp Asn Leu Gly Gly Leu Phe Trp Asn Thr
        35                  40                  45

Tyr Tyr Asn Asn Asn His Ser Ile Leu Thr Ser Cys Gly Ile Tyr Gln
    50                  55                  60

Asn Tyr Cys Ser Cys Thr Asn Asn Tyr Ser Thr Ser Leu Tyr Asn Ile
65                  70                  75                  80

Thr Asn Asn Cys Gly Leu Ile Ile Phe Pro Asn Asn Thr Lys Arg Phe
                85                  90                  95

Asn Thr Thr Tyr Glu Leu Val Tyr Leu Asn Asn Ser Thr Lys Tyr Thr
            100                 105                 110

Ile Asn Leu Leu Val Pro Val Thr Pro Pro Asn Ile Thr Tyr Asn Cys
        115                 120                 125

Thr Thr Ser Val Ile Thr Cys Lys Lys Asn Asp Gly Thr Asn Thr Asn
    130                 135                 140

Met Phe Leu Lys Ile Asn Asp Thr Ile Val Lys Ser Ser Asn Glu Ser
145                 150                 155                 160

Val Phe Glu Tyr Ser Trp Asn Ser Thr Asp Leu Asn Asn Asn Phe Thr
                165                 170                 175

Ala Ile Cys Ile Ile Asn Asn Thr Ile Asn Ser Ser Asn Asp Thr Gln
            180                 185                 190

Thr Ile Glu Cys Pro Asn Ile Leu Leu Asn Asn Tyr Leu Asp Phe Phe
        195                 200                 205

Gln Val Thr Ser Tyr Met Phe Tyr Met Ile Ile Phe Ile Val Thr Gly
    210                 215                 220
```

```
Ile Ile Ala Ser Ile Phe Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg
225                 230                 235                 240


Lys Arg Lys Lys His Val Glu Glu Ile Glu Ser Pro Pro Pro Ser Glu
                245                 250                 255


Ser Asn Glu Glu Asp Ile Ser His Asp Asp Thr Thr Ser Ile His Glu
            260                 265                 270


Pro Ser Pro Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln
        275                 280                 285


Tyr Asn Thr Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn
    290                 295                 300


Pro Phe Pro Leu Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro
305                 310                 315                 320


Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
                325                 330                 335


Arg Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
            340                 345                 350


Pro Cys Pro Ser Pro Glu Thr Tyr Ser Pro Pro Lys Pro Leu Pro Asn
        355                 360                 365


Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser
    370                 375                 380


Leu Ile His Val Asp Arg Ile Ile
385                 390
```

<210> 23
<211> 389
<212> PRT
<213> African swine fever virus

<400> 23

```
Met Ile Ile Ile Leu Ile Phe Leu Ile Tyr Leu Lys Leu Val Leu Asn
```

```
1               5                   10                  15

Asn Asn Ile Ile Ile Trp His Pro Thr Leu Asn Glu Thr Ile Phe Leu
            20                  25                  30

Asn Val Thr Thr Ile Gly Asn Ile Ser Gly Leu Phe Trp Asn Thr Tyr
        35                  40                  45

Tyr Asn Asn Asn Arg Ser Glu Leu Thr Lys Cys Gly Ile Tyr Asn Asn
    50                  55                  60

Tyr Cys Ser Cys Asp Ser Leu Asn Thr Ser Leu Tyr Asn Ile Asn Asn
65                  70                  75                  80

Cys Ser Leu Val Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn Thr Ile
                85                  90                  95

Tyr Glu Leu Ile Tyr Ser Gly Asn Gln Thr Asn Tyr Thr Ile Lys Leu
            100                 105                 110

Leu Glu Ser Thr Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Thr Ser
        115                 120                 125

Val Ile Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Phe Leu
    130                 135                 140

Thr Ile Asn Asn Thr Ile Val Asn Ser Thr Asn Glu Asp Val Ile Tyr
145                 150                 155                 160

Tyr Tyr Trp Asn Arg Ser Glu Phe Asn Asn Phe Thr Ala Thr Cys Met
                165                 170                 175

Ile Asn Asn Thr Ile Asn Ser Ser Asn Ile Ser Glu Ile Ile Asp Cys
            180                 185                 190

Thr Asn Thr Leu Leu Leu Asn Ser Tyr Leu Asp Phe Phe Gln Val Ala
        195                 200                 205

Gly Tyr Met Phe Tyr Met Ile Ile Phe Ile Val Thr Gly Ile Thr Val
    210                 215                 220
```

```
Ser Ile Phe Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys
225                 230                 235                 240


Lys His Val Glu Glu Ile Glu Ser Leu Pro Pro Glu Ser Asn Glu Glu
                245                 250                 255


Glu Cys Gln His Asp Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro
            260                 265                 270


Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr
        275                 280                 285


Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro
    290                 295                 300


Leu Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro
305                 310                 315                 320


Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
                325                 330                 335


Lys Pro Cys Pro Pro Pro Glu Ser Cys Ser Ser Pro Glu Ser Cys Ser
            340                 345                 350


Ser Pro Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu
        355                 360                 365


Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His
    370                 375                 380


Val Asp Arg Ile Ile
385
```

<210> 24
<211> 360
<212> PRT
<213> African swine fever virus

<400> 24

```
Met Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile
1               5                   10                  15
```

```
Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile
            20                  25                  30

Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn
        35                  40                  45

Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys
    50                  55                  60

Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys
65                  70                  75                  80

Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln
                85                  90                  95

Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro
            100                 105                 110

Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr
        115                 120                 125

Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn
    130                 135                 140

Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp
145                 150                 155                 160

Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn
                165                 170                 175

Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu
            180                 185                 190

Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile
        195                 200                 205

Pro Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser
    210                 215                 220
```

```
Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu
225                 230                 235                 240


Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His
                245                 250                 255


Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270


Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285


Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
    290                 295                 300


Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320


Pro Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser
                325                 330                 335


Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser
            340                 345                 350


Leu Ile His Val Asp Arg Ile Ile
        355                 360


<210>  25
<211>  375
<212>  PRT
<213>  African swine fever virus

<400>  25

Met Ile Ile Ile Leu Ile Phe Leu Ile Ile Pro Asn Ile Val Leu Ser
1               5                   10                  15


Ile Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn
            20                  25                  30


Ile Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Leu
        35                  40                  45
```

```
Asn Asn Ser Leu Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe
    50                  55                  60

Cys Glu Cys Ser Asn Tyr Ser Thr Ser Leu Tyr Asn Ile Ala His Asn
65                  70                  75                  80

Cys Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Gly Thr Pro Tyr
                85                  90                  95

Gln Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr
            100                 105                 110

Pro Val Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile
        115                 120                 125

Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Ile Ile Tyr Phe Asn Ile
    130                 135                 140

Asn Asp Thr Asn Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn
145                 150                 155                 160

Trp Asn Asn Ser Asn Phe Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn
                165                 170                 175

Asn Thr Ile Asn Ser Ser Asn Asp Thr Gln Thr Ile Asp Cys Ile Asn
            180                 185                 190

Thr Leu Leu Ser Ser Tyr Leu Asp Phe Phe Gln Val Ala Ser Tyr Met
        195                 200                 205

Phe Tyr Met Ile Ile Phe Ile Ala Thr Gly Ile Ile Ala Ser Ile Phe
    210                 215                 220

Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val
225                 230                 235                 240

Glu Glu Ile Glu Ser Pro Ser Pro Ser Glu Ser Asn Glu Glu Glu Gln
                245                 250                 255

Cys Gln His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu
```

```
            260                 265                 270

Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile
        275                 280                 285

Tyr Tyr Met Arg Pro Leu Thr Gln Pro Leu Asn Pro Ser Pro Leu Pro
    290                 295                 300

Lys Leu Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro
305                 310                 315                 320

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Ser Ser Glu Ser
                325                 330                 335

Cys Ser Pro Pro Glu Ser Tyr Ser Leu Pro Lys Pro Leu Pro Asn Ile
            340                 345                 350

Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu
        355                 360                 365

Ile His Val Asp Arg Ile Ile
    370                 375
```

<210> 26
<211> 392
<212> PRT
<213> African swine fever virus

<400> 26

```
Met Ile Ile Lys Leu Ile Phe Leu Ile Cys Phe Lys Ile Val Leu Ser
1               5                   10                  15

Ile Asp Asn Lys Thr Lys Phe Asn Glu Thr Leu Ile Leu Asp Asn Ile
            20                  25                  30

Asp Tyr Trp Val Lys Phe Asn Asp Thr Ile Thr Leu Asp Ser Asn Ile
        35                  40                  45

Thr Ser Glu Ile Glu Ala Val Ser Trp Asn Phe Tyr Asn Asn Thr Phe
    50                  55                  60
```

```
Asn Leu Leu Ala Ile Cys Gly Lys Ala Ser Asn Phe Cys Ser Cys Ser
65                  70                  75                  80

Asn Tyr Ser Thr Ser Phe Phe Asn Ile Thr Asn Asn Cys Ser Leu Thr
                85                  90                  95

Ile Phe Leu Ile Asp Glu Thr Leu Phe Asn Thr Thr Tyr Gln Ile Val
            100                 105                 110

Tyr Ser Thr Asn Ile Ile Asn Tyr Lys Ile Asn Leu Leu Ile Pro Val
        115                 120                 125

Thr Pro Pro Ile Ile Ser Tyr Asn Cys Ala Asn Cys Ser Ile Asn Cys
    130                 135                 140

Lys Lys Ser Asn Gly Thr Asn Thr Asn Ile Phe Leu Ser Ile Asn Asp
145                 150                 155                 160

Thr Ile Val Thr Tyr Thr Asn Glu Ser Ile Leu Asn Tyr Asp Tyr Asn
                165                 170                 175

Cys Ser Ile Leu Asn Asn Asn Phe Thr Val Thr Cys Ile Ile Asn Asn
            180                 185                 190

Thr Ile Ser Thr Ser Asn Thr Thr Glu Phe Ile Asn Cys Thr Asn Ile
        195                 200                 205

Leu Leu Ser Ser Tyr Leu Asp Phe Phe Gln Val Thr Ser Tyr Ile Phe
    210                 215                 220

Tyr Met Ile Ile Phe Ile Val Thr Gly Ile Thr Val Ser Ile Leu Ile
225                 230                 235                 240

Ser Ile Ile Thr Phe Leu Phe Ile Arg Lys Arg Lys His Val Glu Glu
                245                 250                 255

Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Gln Cys His
            260                 265                 270

His Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
        275                 280                 285
```

```
Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
    290                 295                 300

Arg Pro Ser Thr Gln Gln Leu Phe Lys Ser Tyr Ser Leu Pro Lys Pro
305                 310                 315                 320

Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
                325                 330                 335

Lys Pro Cys Pro Pro Ser Lys Pro Cys Pro Pro Pro Glu Pro Tyr Ser
            340                 345                 350

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Tyr Pro Ser Leu Pro Ser
        355                 360                 365

Ile Pro Leu Pro Pro Asp Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser
    370                 375                 380

Leu Ile His Val Asp Arg Ile Ile
385                 390
```

<210> 27
<211> 385
<212> PRT
<213> African swine fever virus

<400> 27

```
Met Ile Ile Lys Leu Ile Phe Leu Ile Ser Phe Lys Met Ile Leu Gly
1               5                   10                  15

Ile Asp Tyr Trp Val Ser Leu Asn Asn Thr Ile Ile Leu Asp Ser Asn
            20                  25                  30

Ile Thr Ile Asn Asn Ile Thr Asn Thr Thr Asn Asn Pro Thr Leu Asn
        35                  40                  45

Gly Ile Phe Trp Asn Ile Tyr Asn Asn Ser Tyr Asn Asn Thr Phe Asn
    50                  55                  60

Leu Leu Thr Thr Cys Gly Asn Thr Tyr Asn Ile Cys Ser Cys Ser Asn
```

```
65                  70                  75                  80

Asn Tyr Asn Thr Ile Leu Phe Asn Tyr Asn Thr Thr Asn Asn Cys Ser
                85                  90                  95

Leu Ile Ile Ser Pro His Asp Glu Lys Ile Phe Asp Thr Met Phe Gln
            100                 105                 110

Ile Ile Tyr Leu Thr Asn Lys Ile Asn Tyr Thr Ile Arg Trp Leu Gln
        115                 120                 125

Pro Val Asp Pro Pro Asn Ile Ser Phe Asn Asp Ser Asn Ser Leu Ile
    130                 135                 140

Lys Cys Glu Lys Asn Asn Gly Thr Asn Thr Glu Ile Tyr Leu Tyr Leu
145                 150                 155                 160

Asn Asp Thr Phe Ile Asn Asn Thr Asn Glu Asn Asp Leu Lys Tyr Tyr
                165                 170                 175

Trp Asn Cys Ser Glu Leu Asn Tyr Asn Ile Thr Ala Thr Cys Ile Ile
            180                 185                 190

Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn Cys Thr
        195                 200                 205

Asn Leu Leu Leu Lys Ser Asp Gln Asn Tyr Phe Leu Lys Asn Ile His
    210                 215                 220

Thr Leu Phe Tyr Ile Ile Ile Phe Ile Val Thr Gly Ile Ile Ile Ser
225                 230                 235                 240

Ile Phe Ile Ala Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys
                245                 250                 255

His Val Glu Glu Ile Glu Ser Pro Ser Pro Glu Ser Asn Glu Glu Glu
            260                 265                 270

Glu Gln Gln His His His Asp Thr Thr Ser Ile His Glu Pro Ser Pro
        275                 280                 285
```

```
Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr
    290                 295                 300

Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Gln Leu Phe Lys Ser Tyr
305                 310                 315                 320

Ser Leu Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
                325                 330                 335

Pro Cys Pro Pro Pro Lys Pro Cys Pro Ser Pro Glu Ser Tyr Pro Ser
            340                 345                 350

Pro Glu Pro Tyr Pro Leu Leu Pro Asn Ile Pro Leu Pro Pro Asn Ile
        355                 360                 365

Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg Ile
    370                 375                 380

Ile
385
```

<210> 28
<211> 382
<212> PRT
<213> African swine fever virus

<400> 28

```
Met Ile Ile Lys Val Ile Phe Leu Val Phe Phe Lys Met Val Leu Ser
1               5                   10                  15

Asn Ile Ile Ile Trp Ser Thr Leu Asn Asn Thr Ile Tyr Leu Asn Ile
            20                  25                  30

Asn Tyr Ser Asp Ser Asn Leu Tyr Thr Gly Leu Phe Trp Asn Lys Tyr
        35                  40                  45

Tyr Asn Asn Thr Arg Asn Asn Phe Thr Thr Cys Val Thr Ser Asn Ser
    50                  55                  60

Ser Tyr Cys Thr Cys Lys Gly His Asn Thr Ser Leu Tyr Asn Ile Thr
65                  70                  75                  80
```

```
Asn Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn
                85                  90                  95

Thr Thr Tyr Glu Leu Val Tyr Leu Asn Asn Lys Ile Asn Tyr Thr Ile
            100                 105                 110

Gln Met Val Gln Pro Val Asp Pro Pro Ile Ile Ile Tyr Asn Asp Thr
        115                 120                 125

Asn Asn Ser Leu Ile Thr Cys Glu Lys Asn Asn Gly Thr Asn Thr Glu
    130                 135                 140

Ile Tyr Leu Tyr Leu Asn Asp Thr Phe Ile Asn Asn Thr Asn Glu Asn
145                 150                 155                 160

Ser Ile Lys Tyr Tyr Trp Asn Cys Ser Glu Leu Asn His Asn Ile Thr
                165                 170                 175

Thr Thr Cys Ile Ile Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys
            180                 185                 190

Val Ile Asn Cys Thr Asn Leu Leu Leu Lys Ser Asp Gln Asn Tyr Phe
        195                 200                 205

Leu Lys Asn Ile His Thr Leu Phe Tyr Ile Ile Ile Phe Ile Val Gly
    210                 215                 220

Gly Thr Leu Ile Ser Ile Ile Ile Ser Ile Ile Thr Phe Leu Ser Leu
225                 230                 235                 240

Arg Lys Arg Lys Lys His Val Glu Glu Ile Glu Ser Pro Pro Pro Ser
                245                 250                 255

Glu Ser Asn Glu Glu Glu His Cys Gln His Asp Asp Thr Thr Ser Ile
            260                 265                 270

His Glu Pro Ser Pro Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg
        275                 280                 285
```

```
Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Pro
    290                 295                 300

Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
305                 310                 315                 320

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
                325                 330                 335

Pro Cys Pro Pro Pro Lys Pro Cys Pro Ser Pro Glu Ser His Ser Pro
            340                 345                 350

Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu
        355                 360                 365

Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg Ile Ile
    370                 375                 380
```

<210> 29
<211> 404
<212> PRT
<213> African swine fever virus

<400> 29

```
Met Phe Ile Thr Leu Ile Phe Leu Ser Tyr Ile Asn Ile Val Leu Ser
1               5                   10                  15

Asn Asn Tyr Trp Ala Arg Leu Asn Glu Thr Ile Thr Leu Asn Ser Asn
            20                  25                  30

Ile Thr Asn Asp Thr Asn Asn Glu Leu Gly Ile Phe Trp Asn Ser Tyr
        35                  40                  45

Asn Asn Thr Tyr Tyr Asn Asn Thr Phe Asn Asn Ile Ala Ile Cys Gly
    50                  55                  60

Lys Lys Gly Ile Phe Cys Glu Cys Asn Ile Asn Tyr Asn Thr Ser Ile
65                  70                  75                  80

Ser Asn Thr Ser Ile Ser Asn Thr Ser Ile Tyr Asn Val Thr Asn Asn
                85                  90                  95
```

```
Cys Ser Leu Thr Ile Phe Leu Tyr Asp Asp Asn Ile Phe Lys Thr Tyr
            100                 105                 110

Gln Leu Val Tyr Gln Asn Tyr Lys Ile Asn Tyr Thr Ile Asn Leu Leu
        115                 120                 125

Leu Pro Val Thr Ser Pro Asn Ile Thr Tyr Asn Cys Thr Asn Ser Leu
    130                 135                 140

Ile Thr Cys Glu Lys Asn Asp Gly Thr Asn Thr Asn Met Phe Leu Ser
145                 150                 155                 160

Ile Asn Asn Ile Thr Ile Asn His Thr Asn Gln Asp Ile Leu Thr Tyr
                165                 170                 175

Tyr Trp Asn Asn Ser Glu Phe Asn Asn Phe Thr Ala Thr Cys Met Ile
            180                 185                 190

Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn Cys Thr
        195                 200                 205

Asn Pro Leu Leu Asn Ser Tyr Gln Asn Tyr Phe Leu Glu Asn Ile His
    210                 215                 220

Thr Leu Phe Tyr Ile Ile Ile Phe Ile Val Ser Gly Leu Ile Ala Ser
225                 230                 235                 240

Ile Phe Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys
                245                 250                 255

His Val Glu Glu Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu
            260                 265                 270

Gln Cys Gln His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg
        275                 280                 285

Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro
    290                 295                 300

Ile Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu
```

305 310 315 320

Pro Asn Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
325 330 335

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
340 345 350

Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Ser Ser
355 360 365

Pro Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu
370 375 380

Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val
385 390 395 400

Asp Arg Ile Ile

<210> 30
<211> 381
<212> PRT
<213> African swine fever virus

<400> 30

Met Ile Ile Lys Leu Ile Phe Leu Ile Cys Phe Lys Ile Val Leu Ser
1 5 10 15

Ile Asn Tyr Trp Val Arg Tyr Asn Asp Thr Val Thr Leu Asn Ser Asn
20 25 30

Ile Asn Ser Glu Thr Glu Gly Ile Phe Trp Asn Phe Tyr Asn Asn Thr
35 40 45

Phe Asn Thr Ile Ala Thr Cys Gly Lys Lys Asn Asn Val Cys Glu Cys
50 55 60

Ser Asn Tyr Asp Lys Ser Leu Tyr Asn Ile Thr Asn Asn Cys Ser Leu
65 70 75 80

```
Thr Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn Thr Thr Tyr Gln Leu
                85                  90                  95

Val Tyr Ser Arg Asn Arg Ile Asn Tyr Thr Ile Asn Leu Leu Leu Pro
            100                 105                 110

Val Thr Ser Pro Ile Ile Thr Tyr Asn Cys Thr Gln Ser Leu Ile Thr
        115                 120                 125

Cys Glu Lys Thr Asn Gly Thr Asn Ile His Leu Phe Leu Asn Leu Asn
    130                 135                 140

Asp Thr Ile Asn Glu Tyr Thr Asn Lys Ser Phe Leu Asn Tyr Tyr Trp
145                 150                 155                 160

Asn Ser Ser Glu Leu Asn Asn Ile Phe Leu Ala Thr Cys Ile Ile Asn
                165                 170                 175

Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn Cys Thr Asn
            180                 185                 190

Pro Leu Leu Lys Ser Tyr Gln Asn Tyr Phe Leu Glu Asn Ile His Thr
        195                 200                 205

Leu Phe Tyr Met Ile Ile Phe Ile Val Ser Gly Ile Thr Ile Ser Ile
    210                 215                 220

Phe Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His
225                 230                 235                 240

Val Glu Glu Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln
                245                 250                 255

Cys Gln His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu
            260                 265                 270

Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile
        275                 280                 285

Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro
    290                 295                 300
```

```
Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro
305                 310                 315                 320


Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro
                325                 330                 335


Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Glu Ser Tyr Ser Pro Pro
            340                 345                 350


Lys Pro Leu Pro Ser Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser
        355                 360                 365


Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg Ile Ile
    370                 375                 380


<210>  31
<211>  402
<212>  PRT
<213>  African swine fever virus

<400>  31

Met Ile Ile Ile Val Ile Phe Leu Met Cys Leu Lys Ile Val Leu Asn
1               5                   10                  15


Asn Ile Ile Ile Trp Ser Thr Leu Asn Gln Thr Val Phe Leu Asn Asn
            20                  25                  30


Ile Phe Thr Ile Asn Asp Thr Tyr Gly Gly Leu Phe Trp Asn Thr Tyr
        35                  40                  45


Tyr Asp Asn Asn Arg Ser Asn Phe Thr Tyr Cys Gly Ile Ala Gly Asn
    50                  55                  60


Tyr Cys Ser Cys Cys Gly His Asn Ile Ser Leu Tyr Asn Thr Thr Asn
65                  70                  75                  80


Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Glu Ile Phe Asn Arg
                85                  90                  95


Thr Tyr Arg Leu Val Tyr Leu Asp Lys Lys Ile Asn Tyr Thr Val Lys
```

```
            100                 105                 110

Leu Leu Lys Ser Val Asp Ser Pro Thr Ile Thr Tyr Asn Cys Thr Asn
        115                 120                 125

Ser Leu Ile Thr Cys Lys Asn Asn Asn Gly Thr Asn Val Asn Ile Tyr
    130                 135                 140

Leu Ile Ile Asn Asn Thr Ile Val Asn Asp Thr Asn Gly Asp Ile Leu
145                 150                 155                 160

Asn Tyr Tyr Trp Asn Gly Asn Asn Asn Phe Thr Ala Thr Cys Met Ile
                165                 170                 175

Asn Asn Thr Ile Ser Ser Leu Asn Glu Thr Glu Asn Ile Asn Cys Thr
            180                 185                 190

Asn Pro Ile Leu Lys Tyr Gln Asn Tyr Leu Ser Thr Leu Phe Tyr Ile
        195                 200                 205

Ile Ile Phe Ile Val Ser Gly Leu Ile Ile Gly Ile Phe Ile Ser Ile
    210                 215                 220

Ile Ser Val Leu Ser Ile Arg Arg Lys Arg Lys Lys His Val Glu Glu
225                 230                 235                 240

Ile Glu Ser Pro Pro Pro Ser Glu Ser Asn Glu Glu Asp Ile Ser His
                245                 250                 255

Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285

Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
    290                 295                 300

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320
```

```
Pro Cys Pro Pro Pro Lys Pro Cys Ser Pro Pro Lys Pro Cys Arg Pro
                325                 330                 335

Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
            340                 345                 350

Pro Pro Pro Lys Pro Cys Pro Pro Ser Lys Pro Cys Pro Ser Pro Glu
        355                 360                 365

Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu Pro Asn
    370                 375                 380

Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg
385                 390                 395                 400

Ile Ile
```

<210> 32
<211> 402
<212> PRT
<213> African swine fever virus

<400> 32

```
Met Ile Ile Ile Val Ile Phe Leu Met Cys Leu Lys Ile Val Leu Asn
1               5                   10                  15

Asn Ile Ile Ile Trp Ser Thr Leu Asn Gln Thr Val Phe Leu Asn Asn
            20                  25                  30

Ile Phe Thr Ile Asn Asp Thr Tyr Gly Gly Leu Phe Trp Asn Thr Tyr
        35                  40                  45

Tyr Asp Asn Asn Arg Ser Asn Phe Thr Tyr Cys Gly Ile Ala Gly Asn
    50                  55                  60

Tyr Cys Ser Cys Cys Gly His Asn Ile Ser Leu Tyr Asn Thr Thr Asn
65                  70                  75                  80

Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Glu Ile Phe Asn Arg
                85                  90                  95
```

```
Thr Tyr Glu Leu Val Asp Leu Asp Lys Lys Ile Asn Tyr Thr Val Lys
            100                 105                 110

Leu Leu Lys Ser Val Asp Ser Pro Thr Ile Thr Tyr Asn Cys Thr Asn
        115                 120                 125

Ser Leu Ile Thr Cys Lys Asn Asn Asn Gly Thr Asn Val Asn Ile Tyr
    130                 135                 140

Leu Ile Ile Asn Asn Thr Ile Val Asn Asp Thr Asn Gly Asp Ile Leu
145                 150                 155                 160

Asn Tyr Tyr Trp Asn Gly Asn Asn Asn Phe Thr Ala Thr Cys Met Ile
                165                 170                 175

Asn Asn Thr Ile Ser Ser Leu Asn Glu Thr Glu Asn Ile Asn Cys Thr
            180                 185                 190

Asn Pro Ile Leu Lys Tyr Gln Asn Tyr Leu Ser Thr Leu Phe Tyr Ile
        195                 200                 205

Ile Ile Phe Ile Val Ser Gly Leu Ile Ile Gly Ile Phe Ile Ser Ile
    210                 215                 220

Ile Ser Val Leu Ser Ile Arg Arg Lys Arg Lys Lys His Val Glu Glu
225                 230                 235                 240

Ile Glu Ser Pro Pro Pro Ser Glu Ser Asn Glu Glu Asp Ile Ser His
                245                 250                 255

Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285

Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
    290                 295                 300
```

```
Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320

Pro Cys Pro Pro Pro Lys Pro Cys Ser Pro Pro Lys Pro Cys Arg Pro
                325                 330                 335

Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
            340                 345                 350

Pro Pro Pro Lys Pro Cys Pro Pro Ser Lys Pro Cys Pro Ser Pro Glu
        355                 360                 365

Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu Leu Pro Asn
    370                 375                 380

Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg
385                 390                 395                 400

Ile Ile
```

<210> 33
<211> 360
<212> PRT
<213> African swine fever virus

<400> 33

```
Met Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile
1               5                   10                  15

Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile
            20                  25                  30

Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn
        35                  40                  45

Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys
    50                  55                  60

Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys
65                  70                  75                  80
```

```
Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Arg
                85                  90                  95

Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro
            100                 105                 110

Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr
        115                 120                 125

Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn
    130                 135                 140

Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp
145                 150                 155                 160

Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn
                165                 170                 175

Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu
            180                 185                 190

Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile
        195                 200                 205

Pro Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser
    210                 215                 220

Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu
225                 230                 235                 240

Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His
                245                 250                 255

Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285

Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
```

```
    290                 295                 300

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320

Pro Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser
                325                 330                 335

Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser
            340                 345                 350

Leu Ile His Val Asp Arg Ile Ile
        355                 360
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<210> 34
<211> 198
<212> PRT
<213> African swine fever virus

<400> 34

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Met Ile Ile Ile Val Ile Phe Leu Met Cys Leu Lys Ile Val Leu Asn
1               5                   10                  15

Asn Ile Ile Ile Trp Ser Thr Leu Asn Gln Thr Val Phe Leu Asn Asn
            20                  25                  30

Ile Phe Thr Ile Asn Asp Thr Tyr Gly Gly Leu Phe Trp Asn Thr Tyr
        35                  40                  45

Tyr Asp Asn Asn Arg Ser Asn Phe Thr Tyr Cys Gly Ile Ala Gly Asn
    50                  55                  60

Tyr Cys Ser Cys Cys Gly His Asn Ile Ser Leu Tyr Asn Thr Thr Asn
65                  70                  75                  80

Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Glu Ile Phe Asn Arg
                85                  90                  95

Thr Tyr Glu Leu Val Tyr Leu Asp Lys Lys Ile Asn Tyr Thr Val Lys
            100                 105                 110
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Leu Leu Lys Ser Val Asp Ser Pro Thr Ile Thr Tyr Asn Cys Thr Asn
        115                 120                 125

Ser Leu Ile Thr Cys Lys Asn Asn Asn Gly Thr Asn Val Asn Ile Tyr
    130                 135                 140

Leu Ile Ile Asn Asn Thr Ile Val Asn Asp Thr Asn Gly Asp Ile Leu
145                 150                 155                 160

Asn Tyr Tyr Trp Asn Gly Asn Asn Asn Phe Thr Ala Thr Cys Met Ile
                165                 170                 175

Asn Asn Thr Ile Ser Ser Leu Asn Glu Thr Glu Asn Ile Asn Cys Thr
            180                 185                 190

Asn Pro Ile Leu Lys Tyr
        195
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<210> 35
<211> 357
<212> DNA
<213> African swine fever virus

<400> 35
atgttggtaa tctttttggg aattcttggc cttctggcca gccaggtctc aagtcaacca 60

gatggacaac ttcgtccaac agaggatcct ccagaagaag aacttaaata ttggtgcacc 120

tacatggaaa gttgccagtt ttgttgggac tgccaagatg gcaattgtat aaacaaagta 180

gatgggtcag tcatttataa aaatgagttt gtgcgaccat gttcagtttc ccgctggatg 240

aataaatgta tgtatgattt aaataagggt atctatcata caatgaattg ttctcagcca 300

cagtcttgga atccctacaa atacttcagg aaggagtgga aaaaagatga actctag 357

<210> 36
<211> 357
<212> DNA
<213> African swine fever virus

<400> 36
atgttggtga tctttttggg aattcttggc cttctggcca gccaggtctc aagtcagcca 60

gttggacaac ttcgtccaac agaggaccct ccagagaatg aactcgaata ttggtgcacc 120

tacatggaaa gttgccagtt ttgctgggac tgtcaagatg gcaattgtat aaacaaagta 180

gatgggtcag tcatttataa aaatgagtat gtgcaaccat gttcagtttc ccgctggcta 240

aataaatgta tgtatgattt agataagggt atctatcata caatgaactg ttctcagcca 300

cggtcttgga atccctacaa atgtttcagg aaggagtgga aaaaagatga actctag 357

<210> 37
<211> 369
<212> DNA
<213> African swine fever virus

<400> 37
atgttggtga tctttttggg aattcttggc cttatggcca gccaggtctt agggctacca 60

tctaatcaac caactggaca acttcgtcca acagaggatc ctccagagga agaactcgaa 120

tactggtgtg cctacatgga aagttgccag ttttgctggg actgccaaga tggcaattgc 180

ataaacaaaa tagatgggtc agtcatttat aaaaatgagt ttgtgcgacc atgttcagtt 240

tcccgctgga tggataaatg tatgtatgat ttaaataagg gtatctatca tacaatgaat 300

tgttctcagc cacagtcttg gaatccctac aaatacttca ggaaggagtg gaaaaaagat 360

gaactctag 369

<210> 38
<211> 357
<212> DNA
<213> African swine fever virus

<400> 38
atgttggtga ccttttttggg aattcttggc cttctggcca gccaggtctc aagtcagctc 60

gttggacaac ttcgtccaac agaggatcct ccagaggaag aactcgaata ctggtgcgcc 120

tacatggaaa gttgccagtt ttgctgggac tgccaagatg gcaattgtat aaacaaaata 180

gatgggtcag tcatttataa aaatgagtat gtgcgaccat gttcagtttc ccgttcgatg 240

gataaatgta tgtatgattt aaataagggt atctaccata gcatgagctg ttctgaccca 300

aaggcctgga atccctacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 39
<211> 357
<212> DNA
<213> African swine fever virus

<400> 39

atgttggtga tctttttggg aattcttggc cttctggcca gccaggtttc aagtcaactc 60

gttggacaac ttcgaccaac agaggatcct ccagaggaag aactcgaata ctggtgcgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagatg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaagcat gtctggtttc ccgttggctg 240

gataaatgta tgtatgattt agataaaggt atctaccata ccatgaattg ttctcagcca 300

tggtcttgga atccttacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 40
<211> 357
<212> DNA
<213> African swine fever virus

<400> 40
atgttggtga tcttcttggg aattcttggc cttctggcca gccaggtttc aagtcagctc 60

gttggacaac ttcgtccaac agaggatcct ccagaggaag aactcgaata ctggtgcgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagatg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaatcat gtctggtttc ccgttggctg 240

gataaatgta tgtatgattt agataaaggt atctaccata ccatgaattg ttctcagcca 300

tggtcttgga atccttacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 41
<211> 357
<212> DNA
<213> African swine fever virus

<400> 41
atgttggtga tcttcttggg aatttttggc cttctggcca gccaggtttc aagtcagctc 60

gttggacaac ttcgtccaac agaggatcct ccagaggaag aactcgaata ctggtgtgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagatg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaatcat gtctggtttc ccgttggctg 240

gataaatgta tgtatgattt agataagggt atctaccata ccatgaattg ttctcagcca 300

tggtcttgga atccttacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 42
<211> 357
<212> DNA

<213> African swine fever virus

<400> 42
atgttggtga tcttcttggg aattcttggc cttctggcca gccaggtttc aagtcagctc 60

gttggacaac ttcgtccaac agaggatcct ccagaggaag aactcgaata ctggtgcgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagatg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaatcat gtctggtttc ccgttggctg 240

gataaatgta tgtatgattt agataaaggt atctaccata ccatgaattg ttctcagcca 300

tggtcttgga atccttacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 43
<211> 357
<212> DNA
<213> African swine fever virus

<400> 43
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gttggacaac ttcgaccaac agaggatcct ccagaggaag aactcgaata ctggtgcgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagatg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaatcat gtctggtttc ccgttggctg 240

gataaatgta tgtatgattt agataaaggt atctaccata ccatgaattg ttctcagcca 300

tggtcttgga atccttacaa atacttcagg aaggaatgga aaaaagatga actctag 357

<210> 44
<211> 375
<212> DNA
<213> African swine fever virus

<400> 44
atgaaggtgc tgattctagt actactgggg gtcgttatcc ttcaggctgc tcctatacgt 60

aaattagaag acctactgcc aacccgtaat cctccccaaa atgagctagt ttactggtgc 120

acctacgcaa accaatgtga cttttgctgg gaatgtgtac acggaatctg ccgaaacaga 180

attcaagcag attggcctgt gattcaccaa aatgactgga ttataaattg caccgtttcc 240

cgctggaatg gtatatgtag gtattatgaa ggacccagag tccatataga tcatgaaatg 300

gactgtgcaa atccaacatc ccatacttat ccacacattg aatacatgaa gatctatgaa 360

agagatgacc tatga 375

<210> 45
<211> 375
<212> DNA
<213> African swine fever virus

<400> 45
atgaaggtgc tgattctagt actactgggg gtcgttatcc ttcaggctgc tcctatacgt 60

aaattagaag acctactgcc aacccgtaat cctccccaaa atgagttagt ttattggtgc 120

acctacgcaa accaatgtga tttttgctgg gaatgtatac acggaatctg ccgaaacaga 180

attcaagcag attggcctgt gattcaccaa aatgactgga ttataaattg caccgtttcc 240

cgctggaatg gtatatgtag gtattatgaa ggacccagag gccatataga tcatgaaatg 300

gactgtgcaa atccaacata ccatacttat ccacacattg aatacatgaa gatttatgta 360

agagatgacc tatga 375

<210> 46
<211> 375
<212> DNA
<213> African swine fever virus

<400> 46
atgaaggtgc tgattctagt actgctggcg gtggttatcc ttcaagccgc tcctatacgt 60

aaattagaag atctactacc aacccgttat cctcctgacc atgagctagt ttattggtgc 120

acctacgcaa accaatgtga cttttgctgg gaatgcgtac acggtatctg ccgaaatagg 180

attcaagcag attggccggt tattcaccaa aatgactgga ttataaattg cacggtttcc 240

cgctggaatg gtatatgtag ttattatgaa ggacccagaa accatacaga tcatcaaatg 300

gactgtgcaa atccaacatc ccatacctat ccacatagag aatacatgaa aatttatgaa 360

agagatgact tataa 375

<210> 47
<211> 381
<212> DNA
<213> African swine fever virus

<400> 47
atgaaggtgc tgattctagt actactgggg gggggggta ttattcttca ggccgctcct 60

atacgtaaat tagaagatct actaccaacc cgttatcctc ctgaacatga gctggtttat 120

tggtgcacct acgcaaacca atgtgacttt tgctgggaat gcgtccacgg tatttgccga 180

aacaggattc aagcagattg gccggttatt catcaaaatg actggattat aaattgcacg 240

gtttcccgct ggaatggcca atgtcattat tatgaaggtt ctcaacaata tctacatcat 300

gaaatggact gtacaaatcc aacatcccat acctatccac atacagaata catgaagatc 360

tatgaaagag atgacttatg a 381

<210> 48
<211> 375
<212> DNA
<213> African swine fever virus

<400> 48
atgaaggtgc taattctagt actactgggg gtggttatcc ttcaggccgc tcctatacgt 60

aaattagaag atctactacc aacccgttat cctcctgaac atgagctagt ttattggtgc 120

acttacgcaa accaatgtga cttttgctgg gaatgcgtcc acggtatctg ccgaaacagg 180

attcaagcag attggccagt tattcatcaa aatgactgga ttataaattg cacggtttcc 240

cgctggaatg gtatatgtag ttattatgaa ggacccagaa accatacaga tcatcaaatg 300

gactgtgcaa atccaacatc ccatacttat ccacatagag aatacatgaa gatctatgaa 360

agagatgact tatga 375

<210> 49
<211> 375
<212> DNA
<213> African swine fever virus

<400> 49
atgaaggtgc taattctagt actactgggg gtggttattc ttcaggccgc tcctatacgt 60

aaattagaag atctactacc aacccgttat cctcctgaac atgagctagt ttattggtgc 120

acttacgcaa accaatgtga cttttgctgg gaatgcgtcc acggtatctg ccgaaacagg 180

attcaagcag attggccagt tattcaccaa aatgactgga ttataaattg cacagtttct 240

cgctggaatg gtatatgtag ttattatgaa ggacccagaa accatacaga tcatcaaatg 300

gactgtgcaa atccaacatc ccatacttat ccacatagag aatacatgaa gatctatgaa 360

agagatgact tatga 375

<210> 50

<211> 375
<212> DNA
<213> African swine fever virus

<400> 50
atgaaggtgc taattctagt actactgggg gtggttattc ttcaggccgc tcctatacgt 60

aaagtagaaa atctactgcc aacccgtaat cctccccaaa atgaattagt ttattggtgc 120

acctatgcaa accaatgtga cttttgctgg gaatgcattc acggcatctg ccgaaacagg 180

attcaagcag attggccagt tattcatcaa aatgactgga ttataaattg cacggtttcc 240

cgctggaatg gccaatgtca ttattatgaa ggttctcaac aatatctgca tcatgaaatg 300

gactgtataa atccaacatc ccatacctat ccacatacag aatacatgaa gatctatgaa 360

agagatgact tatga 375

<210> 51
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 51
ttaccgcaaa ttgtctctca gcgaagaaaa tgaatgaaac gtttctgtat attcataggt 60

tgaaattatt ttacgcactt cactaggttc taatattttc ttatgaagta ttgaatgggg 120

gcttaaaagt cctttcttaa aaagaagttt catcataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccta tttacttcat gattaatgaa 300

acctatcaac gtctctaagg ccgtattgat atttgcgcct aaggcaaaac aatagtatat 360

acccaattta ttttgagggt acatacaagc aagcgacatc atgtcatttg gatctaaacg 420

tatattttcc tgaaaatatg catgatggat ttcatcaaca ttacctaagt atacagccgt 480

ttttaaacgc caataatcta ggtgaggaaa tttcttacta agaaaacgaa taggttttat 540

aagattaaac tctatggcga tcttaaacca aaattttaat acatatgtat tttttatcat 600

tttttctttt tcatctaaat ttaagataaa acgattgtaa ataaagtcta tcaacacgta 660

aaaatcatgg ctatcaaaac tgtcgagaat cgaaatattg tcataataaa tatctatagc 720

taataagacc ttttgttgtt taattagatc aacaaacata ttatacaacc ctacatctaa 780

aaattttgga tcagctccta gttgaataca cagaactttc gtcctttccg tcttggcaca 840

tatgatgcca taattaatgt tggcacccca taaaacaaat aacttgatta gatcagtctg 900

gtttttcttc acagccctca ccaaggctct gtcaagctca tagctgtcaa catcagaaca 960

tgacatagag ccactggtta ccattttaca ttgtttacaa aaacctatgg gtccgttttc 1020

ccaccataat ccaagctgct gtaaaataaa aatatcatcc tcatgataat ttgaaaaagc 1080

cttgttttct atcaagactt tttttgtaag aacctgtaaa gaattcat 1128

<210> 52
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 52
ttaccgcaaa ttgtctctca gcgaagaaaa tgaatgaaac gtttctgtat attcataggt 60

tgaaattatt ttacgcactt cactaggttc taatattttc ttatgaagta ttgaatgggg 120

gcttaaaagt cctttcttaa aaagaagttt catcataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccta tttacttcat gattaatgaa 300

acctatcaac gtctctaagg ccgtattgat atttgcgcct aaggcaaaac aatagtatat 360

acccaattta ttttgagggt acatacaagc aagcgacatc atgtcatttg gatctaaacg 420

tatattttcc tgaaaatatg catgatggat ttcatcaaca ttacctaagt atacagccgt 480

ttttaaacgc caataatcta ggtgaggaaa tttcttacta agaaaacgaa taggttttat 540

aagattaaac tctatggcga tcttaaacca aaattttaat acatatgtat tttttatcat 600

tttttctttt tcatctaaat ttaagataaa acgattgtaa ataaagtcta tcaacacgta 660

aaaatcatgg ctatcaaaac tgtcgagaat cgaaatattg tcataataaa tatctatagc 720

taataagacc ttttgttgtt taattagatc aacaaacata ttatacaacc ctacatctaa 780

aaattttgga tcagctccta gttgaataca cagaactttc gtcctttccg tcttggcaca 840

tatgatgcca taattaatgt tggcacccca taaaacaaat aacttgatta gatcagtctg 900

gtttttcttc acagccctca ccaaggctct gtcaagctca tagctgtcaa catcagaaca 960

tgacatagag ccactggtta ccattttaca ttgtttacaa aaacctatgg gtccgttttc 1020

ccaccataat ccaagctgct gtaaaataaa aatatcatcc tcatgataat ttgaaaaagc 1080

cttgttttct atcaagactt tttttgtaag aacctgtaaa gaattcat 1128

<210> 53
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 53
ttaccgcaaa ttgtctctca gtaaagaaaa tgaatgaaac gtttctgtat attcataggt 60

tgaaattatt ttacgcactt caccaggttc taatattttt ttatgaagta ttgaatgggg 120

gcttaaaagt cctttcttaa aaagaagttt cattataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccta tttacttcat gattaatgaa 300

acctatcaac gtctctaagg cagtattgat atttgcacct aaggcaaaac aatagtatat 360

acctaattta ttctgagggt acatacaagc aagcggcatc atgtcatttg gatctaaacg 420

tatattttcc tgaaaatatg catgatggat ttcatcaaca ttacctaagt atacagccgt 480

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aagattaaac tctatggcga tcttaaacca aaattttaat acatatgtat tttttatcat 600

tttttctttt tcatctaaat ttaagataaa acaattgtaa ataaagtcta tcaacacgta 660

aaaatcatgg ctatcaaacc tgtcgagaat cgaaatatta tcataataaa tatctatagc 720

taataagacc ttttgttgtt taattagatc aacaaacata ttatacaacc ctacatctaa 780

aaattttgga tcagctccta gttgaataca cagagctttc atcctttctg tcttggcgca 840

tatgatgcca taattaatgt tggcacccca taaaacaaat aacttgatta gatcagtctg 900

gtttttcttc acagccctca ccaaggctct gtcaagctca tagctgtcaa cgtcagagca 960

tgacatagcg ccactagtta ccattttaca ttgtttacaa aaacctatgg gaccgttttc 1020

ccaccatagt ccaagctgct gtaaaataaa aatatcatct tcatgatatt ttgaaaaagc 1080

cttgttttct atcaagactt tttttgtaag aacctgtaaa gaattcat 1128

<210> 54
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 54
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gcttaaaagt cctttcttaa aaagaagttt cattataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccta tttacttcat gattaatgaa 300

acctatcaac gtctctaagg cagtattgat atttgcgcct aaggcaaaac aatagtatat 360

acctaattta ttctgagggt acatacaagc aagcgacatc atgtcatttg gatctaaacg 420

tatattttcc tgaaaatatg catgatggat ttcatcaaca ttacctaagt atacagccgt 480

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aagattaaac tctatggcga tcttaaacca aaattttaat acatatgtat tttttatcat 600

tttttctttt tcatctaaat ttaagataaa acaattgtaa ataaagtcta tcaatacgta 660

aaaatcatgg ctatcaaaac tgtcgagaat cgaaatatta tcataataaa tatctatagc 720

taataagacc ttttgttgtt taattagatc aacaaacata ttatacaatc ctacatctaa 780

aaattctgga ttggctccta gttcaataca caggtctttc gtcctttccg tcttggcaca 840

tatgatgcca taattaatgt tggcacccca taaaacaaac aacttgatta gatcagtctg 900

gtttttcttc acagccctta ccaaggctct gtcaagctca tagctgtcaa cgtcagagca 960

tgacatagag ccactggtta ccattttaca ttgtttacaa aaacctatgg ggccattatg 1020

ccaccacaat ccaagctgct gtaaaataaa aatatcatcc tcatgatatt ctgaaaaagc 1080

cttgttttct atcaagactt tttttgtaag aacctgtaaa gaattcat 1128

<210> 55
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 55
ttaccgcaaa ttgtctctca gcaaagaaaa tgaatgaaac gtttccgtat attcataggt 60

tgaaattatt ttacgcactt cactaggttc taatattttc ttatgaagta ttgaatgggg 120

gcttaaaagt cctttcttaa aaagaagttt cattataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccta tttacttcat gattaatgaa 300

acctatcaac gtctctaagg cagtattgat atttgcgcct aaggcaaaac aatagtatat 360

acctaattta ttctgagggt acatacaagc aagcgacatc atgtcatttg gatctaaacg 420

tatattttcc tgaaaatatg catgatggat ttcatcaaca ttacctaagt atacagccgt 480

ttttaaacgc caataatcta gatgaggaaa tttcttacta agaaaacgaa taggttttat 540

aagattaaac tctatggcga tcttaaacca aaattttaat acatatgtat tttttatcat 600

tttttctttt tcatctaaat ttaagataaa acaattgtaa ataaagtcta tcaatacgta 660

aaaatcatgg ctatcaaaac tgtcgagaat cgaaatatta tcataataaa tatctatagc 720

taataagacc ttttgttgtt taattagatc aacaaacata ttatacaatc ctacatctaa 780

aaattctgga ttggctccta gttcaataca caggtctttc gtcctttccg tcttggcaca 840

tatgatgcca taattaatgt tggcacccca taaaacaaac aacttgatta gatcagtctg 900

gtttttcttc acagccctta ccaaggctct gtcaagctca tagctgtcaa cgtcagagca 960

tgacatagag ccactggtta ccattttaca ttgtttacaa aaacctatgg ggccattatg 1020

ccaccacaat ccaagctgct gtaaaataaa aatatcatcc tcatgatatt ctgaaaaagc 1080

cttgttttct atcaagactt tttttgtaag aacctgtaaa gaattcat 1128

<210> 56
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 56
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tgaaattatt ttacgcactt cactaggttc taatattttc ttatgaagta ttgaatgggg 120

gcttaaaagt cctttcctaa aaagaagttt cattataaca ttcttttctt gtctaagaag 180

agtttcttgt attttttttg tataaggatt ggcacccaaa cttatacaaa aatgtacatt 240

actccaaata ccataatttg aaaagaaagt tatttcccca tttacttcat gattaatgta 300

acgtatcaat gtctctaagg cagtattgat atttgcgcct aaggcaaaac aatagtatat 360

acctaattta ttctgagggt acatacaagc aagcggcatc atgtcatttg gatctaaacg 420

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<213> African swine fever virus

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<210> 69
<211> 1071
<212> DNA
<213> African swine fever virus

<400> 69
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atagcaaaga gcacatgtta accaccacgt attcaaatac ttaaaatgtt ggtaaacata 480

agaaatggcc tccctaagat tatcctgcaa tgccacgata aaacagtata tagttaacat 540

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atgtatacac gactttattt ccctttataat gacataggct gaaaagggat tgtcattaaa 660

aaatttaaga cataagataa tattactact agtagtgcta ggatgtatta atttaaagaa 720

tatgtgcata atcttctttt tatccacttg gtgcttggct cctaattccc agcaaaattc 780

tcgaataggt ggcgtattcg cgcaaattaa cccatagttg atgtctgcgc cccaatccgt 840

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<210> 70
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<212> DNA
<213> African swine fever virus

<400> 70
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tgccagggct ttgcctcct caaaggcatc ggcccccagg tctatacaaa agaataagtt 240

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aaaacaataa tatatggtta aaaaattgtt atcttttgtg caggctatcc gcatcatttc 360

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atagcaaaga acacatgtta accaccacgt attcagatac ttaaaatgtt ggtaaacata 480

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aagtttaaga cataagataa tattactact agtagtgcta ggatgtatta atttaaagaa 720

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tcgaacaggt ggcgtattcg cgcaaattaa cccatagttg atgtctgcgc cccaatccgt 840

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atgctgtctg gctagtacct ttttggcgaa ggattgtaag gaaggaaaca t 1071

<210> 71
<211> 1071
<212> DNA
<213> African swine fever virus

<400> 71
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gtctggctta taaatgtcta atgataaacg atgagatatt aaatagtaat tccgttgctc 180

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aaaacaataa tatatagtta aaaaattgtt atcttttgtg caggccatcc gcatcatttc 360

atccacgtcc atgcggatct tttccttttc atacaaatta tgtaggtcaa acagcttatt 420

aaaacaaaga gcacagatta accaccacgt atttagatac ttaaaatgtt ggtaaacata 480

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atatatggat atccttattt cccttataat gacataggct ggaaagggat tatcattaaa 660

aagtttaaga cataagataa tattactgct agtagtgcca ggatgtatta atttaaagaa 720

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tcgaacagac ggcgtattgg cgcaaattaa cccatagttg atgtctgcgc cccattccgt 840

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tggagcctta taccaccata gtccgcaacg ttctaagata acatggtact caatagatac 1020

ttgctgtctg gctagtacct ttttggcgaa ggattgtaag gaaggaaaca t 1071

<210> 72
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 72
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ataaatgtct aatgataaac gatgagatat caaaaagtaa ttccgttgct ctgccagggc 180

ttttgcctct tcaaaggcat cggcccccaa gtctatacaa aagaacaggt tatccatatt 240

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atatatagtt aaaaaattgt tatcttttgt gcaggctatc cgcatcattt catccatgtc 360

catgcggatt ttttcctttt cgtacaaatt atgtaggtca aacagcttat taaaacaaag 420

agcacagatt agccaccacg tattcagata tttaaaatgt tggtaaacat aagaaatggc 480

ctccctaaga ttatcctgca atgccaccat aaaacagtat atcgttaaca tatcaccatc 540

cgaaatatta cttaatacgt cggtgtcttc tactaacttt ttcagcttcc aatatatgga 600

tgactttatt tcccttataa tgacataggc tgaaaagggg ttatcattaa aaagtttaag 660

acataagata atattactgc tagtagtgcc aggatgtatt aatttaaaga acatgtgcat 720

aatcttcttt ttatccacgc ggtacttggc tcctagttcc cagcacaatt ctcgaacagg 780

cggcgtattg gcgcaaatta acccatagtt gatgtctgcg ccccattccg taaacagttt 840

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atctgcaaag cttggcagct ttatcagcat atgtttgcaa tcaagggaaa ttggagcctt 960

ataccaccat agtccgcagc gttctaagat aacatggtaa tcaatagata catgctgtct 1020

ggctagtacc tttttggcga aggattgtaa ggaaggaaac at 1062

<210> 73
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 73
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ataaatgtct aatgataaac gatgagatat caaaaagtaa ttccgttgct ctgccagagc 180

ctttgcctct tcaaaggcgt cggcccccag gtctatacaa aagaacaggt tatccatatt 240

atagaatcgt atggaggcaa tcatggccaa attaatatta gctcctaaga taaaacaata 300

atatatagtt aaaaaattgt tatcttttgt gcaggctatc cgcatcattt catccatgtc 360

catgcggatt ttttcctttt cgtacaaatt atgtaggtca aacagcttat taaaacaaag 420

agcacagatt agccaccaca tattcagata cttaaaatgt tggtaaacat aagaaatggc 480

ctccctaaga ttatcctgca atgccaccat aaaacagtat atcgttaaca tatcaccatc 540

tgaaatatca cttaatacgt cggtgtcttc tactaacttt ctcagcttcc aatatatgga 600

tgactttatt tcccttataa tgacataggc tgaaaagggg ttatcattaa aaagtttaag 660

acataagata atattactgc tagtagtgcc aggatgtatt aatttaaaga acatgtgcat 720

aatcttcttt ttatccacgc ggtacttggc tcctagttcc cagcacaatt ctcgaacagg 780

cggtgtattg gcgcaaatta acccatagtt gatgtctgcg ccccattccg taaacagttt 840

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ataccaccat agtccgcagc gttctaagat aacatggtaa tcaatagata catgctgtct 1020

ggctagtacc tttttggcga aggattgtaa ggaaggaaac at 1062

<210> 74
<211> 1068
<212> DNA
<213> African swine fever virus

<400> 74
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tggactataa atatctattg ataaacgatg atacatcaaa aagtaattcc gctggtctgc 180

cagggctttt gcctcttcaa aggcatcggc tcccaggtct atacaaaaga acaagttatc 240

catattatag aattgtacgc aggcaagcat agcctgatta atattagctc ctaagagaaa 300

acagtaatat atggttaaaa agttgttatc tttagtgcag gctatgcaca tcatttcatc 360

catgtccatg cggatctttt ccttttcata caaatcatgt aggtcaaaca gcttattaaa 420

acaaagagca cagattaacc accacgtatt cagatgctta aaatgttggt aaaaataaga 480

aatggcctcc ctaagattat cctgcaatgc caggataaaa cagtatatag tcaacatatc 540

atcatccgac atattactta atatgtcagt gtcttctact aaccttctca gcttccaata 600

tatagacgac tttatttccc ttataatgac ataggttgga aaaggattat tattaaaaag 660

tttaagacat aagataatat tactactagt agtgccatga tgtattaatt taaaaaacat 720

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aacaggcggc gtattagcgc aaattaatcc atagttgatg tccgcgcccc attccgtaaa 840

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caagccatct gcaaagcttg gcagctttat taacatatgt ttgcaatcaa gtgaaattgg 960

agccttatac caccatagtc cgcaatgttt taagatataa tgataatcaa tggatacatg 1020

atgtctagct aataccttt tggcgaagga ttgtaaagaa ggaaacat 1068

<210> 75
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 75

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gcaatttatt ttttcagggt ccgtaacgat cgacaacaga gaaataaccg gattgtaatg 120

ctttaatgat aaggcatggg ctatcagata attttccttt tgttctgcca aagctttgcc 180

ctcctcaaag gcatcggcac ccaggtctat acaaaagaac aggtttccaa gattatagtt 240

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cctcagatcc agattatcta taatccttaa attggggtta ttggaaaaca cctcgtggca 660

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gagagcacaa atcattccat agttaatatc tgcaccccat tcagtaaaca gctttatcaa 840

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atgccaccac aggccacaac acttcaggac atgatattga tctaccggta tacactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 76
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 76
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atgccaccac aggccacaac acttcaggac atgatattga tctaccggta tacactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 77
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 77
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ctttaatgat aaggcatggg ctatcagata attttccttt tgttctgcca aagctttgcc 180

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atgccaccac aggccacaac acttcaggat atgataatga tccaccgaca cgcactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 78
<211> 1062
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<213> African swine fever virus

<400> 78
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gaggtcatag tccaccgcta tagcatacca gtatttggtt aaaacagtgc taaagctatc 540

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ctctctttct aaatattctt tggctcccag ctctttgcac agatcacggg tattttccgt 780

gagagcacaa atcattccat agttaatatc tgcaccccat tcagtaaaca gctttatcaa 840

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atgccaccac aggccacaac acttcaggat atgataatga tccaccgaca cgcactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 79
<211> 1062
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<213> African swine fever virus

<400> 79
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aaagataata ttgctactgg ttttatcgcg cgtcgtatca aagaaaattt ttaaaatata 720

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atgccaccac aggccacaac acttcaggat atgataatga tccaccgaca cgcactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 80
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 80
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ctttaatgat aaggcattgg ctatcagata atttcccttt tgttctgcca aagctttgcc 180

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cctcagatcc agattatcta taatccttaa attggggtta ttggaaaaca cctcgtggca 660

aaagataata ttgttactgg ttttatcgcg cgttgtatca aagaaaattt ttaaaatata 720

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atgccaccac aggccacaac acttcaggat atgataatga tccaccgaca cgcactgccc 1020

ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 81
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 81
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ctttaatgat aaggcattgg ctatcagata atttcccttt tgttctgcca aagctttgcc 180

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<210> 82
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 82
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<210> 83
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<212> DNA
<213> African swine fever virus

<400> 83
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ggccagtact ttcttcgtga gggattgcag ggaaggcaac at 1062

<210> 84
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<212> DNA
<213> African swine fever virus

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<210> 85
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<212> DNA
<213> African swine fever virus

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<210> 86
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 86
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ggccagcact ttcttggata gggattgcaa ggaaggcaac at 1062

<210> 87
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 87
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ggccagcact tttttggata gggattgcaa ggaaggcaac at 1062

<210> 88
<211> 1053
<212> DNA
<213> African swine fever virus

<400> 88
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<210> 89
<211> 1053
<212> DNA
<213> African swine fever virus

<400> 89
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<210> 90
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<213> African swine fever virus

<400> 90
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<210> 91
<211> 1053
<212> DNA
<213> African swine fever virus

<400> 91
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<210> 92
<211> 1053
<212> DNA
<213> African swine fever virus

<400> 92
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tcctgatttt atttgtattc ggccacgatc catacaaagc ttgagaggag catcatgcca 960

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cgtctttttg acgagggtct gcagagagag cggcaacgac at 1062

<210> 107
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 107
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agaaagcaaa ctatagttga tatttgcgcc ccactctgta aagagcttta tcagactata 840

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cgtctttttg acgagggtct gcagagagag cggcaacgac at 1062

<210> 109
<211> 1062

<212> DNA
<213> African swine fever virus

<400> 109
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tatttggatt ttttccttgt ggtatatatc atgaagctca tatattttgt tataatatag 420

gtaacatttt aatcgccatt cattaagatc cgtatatttc tcatccagaa agcaaatggc 480

atctttataa tcgtattgta ctgctttggc gtaccaatat ttcactagta attcacttaa 540

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ttgtgcagca aatttgtttt ctaaattagg attatttata aatatctcat ggcacaaaat 660

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ctccagagtt tctttggcgc ctagctgtct acacaaatct cggacgtgct tcgtattgat 780

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cgtctttttg acgagggttt gtagagagag cggcgccgac at 1062

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<211> 1062
<212> DNA
<213> African swine fever virus

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gtaacatttt aatcgccatt catcaagatc cgtatatttt tcatccagaa agcaaatggc 480

atctttatga tcgtattgta ctgcattggc gtaccaatat ttcactagta attcgcttaa 540

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gtctagagtt tctttggcgc ctagctgtct acacaaatct cgggcgtgct tcgtattgat 780

agaaagcaga ctatagttga tatatgcgcc ccactctgta aataacttta tcagactata 840

gttattttcc ttaacagcta ttattaatgc cacacaaagg tctatatctt ctcctaggaa 900

tcccgatttt atgtatattc gtccacgatc tatgtaaagc ttgaggggag catcatgcca 960

ccataagcca cagtatttca aaatgtgttc atctatcgac aaacatgatg tactggctac 1020

cgtctttttg acgagggtct gcagagagag cggcgacgac at 1062

<210> 111
<211> 1062
<212> DNA
<213> African swine fever virus

<400> 111
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actaccctct tcaaaggcat taccacccaa atctatacag aaatatatat taccgatgtt 240

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tatttggatt ttttccttgt ggtatatatc atgaagctca tatattttgt tataacatag 420

gtaacatttt aatcaccatt catcaagatc cgtatatttt tcatccagaa agcaaatggc 480

atctttatgg tcgtattgta ctgcattggc gtaccaatat ttcactagca attcgcttaa 540

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tcccgatttt atgtatattc gcccacgatc tatgtaaagc ttgaggggag catcatgcca 960

ccataagcca cagtatttca aaatgtgttc atctatcgac aaacatgatg taccggctac 1020

cgtctttttg acgagggtct gcagagagag cggcgacgac at 1062

<210> 112
<211> 1074
<212> DNA
<213> African swine fever virus

<400> 112
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caaggtcaca tcacggctga aaagctgctt tactaagaaa atgttgctca agttatacat 180

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tttcatcatc agattagggc tgatgcaaat ctctttttca cgacacaact cgtgtatgtc 420

aaaaatgtta ttaaaataaa ggctacaagc tacccgccaa tagaggtgat ttttatgcct 480

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aactgtgtct aaagtggttc tagttacggt ttccaagagt ggattatgac aaaacatgtc 660

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atcctcagaa aaacactgta aatgtttata cgaaaaaact tgcttacaat tgttacatag 960

gtgaatagga cctaaatccc accacaaacc aaaacgctgc aacgtataat catagtcact 1020

tgaaagataa ttgcatgcca caacttttt ggccaacgtt tgtaaagaca acat 1074

<210> 113
<211> 1074
<212> DNA
<213> African swine fever virus

<400> 113
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caaggtcaca tcacggctga aaagctgctt tactaagaaa atgttgctca agttatacat 180

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aaaaatgtta ttaaaataaa ggctacaagc tacccgccaa tagaggtgat ttttatgcct 480

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<211> 1074
<212> DNA

<213> African swine fever virus

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tgaaagataa ttgcatgcca caacctttt ggccaatgtt tgtaaagaca acat 1074

<210> 115
<211> 1074
<212> DNA
<213> African swine fever virus

<400> 115
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<210> 116
<211> 1074
<212> DNA
<213> African swine fever virus

<400> 116
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<210> 117
<211> 1074
<212> DNA
<213> African swine fever virus

<400> 117
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<213> African swine fever virus

<400> 118
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<213> African swine fever virus

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aactgtgtct aaagtggttc tagttacggt ttccaagagt ggattatgac aaaacatgtc 660

ataacccagt agaactcctg cacaggattt taggttggcc acttctttta aaatttccag 720

aagacggggt tcggatacag gcgtcaagcc tcccagttcc gcacacagcc gctttagata 780

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<213> African swine fever virus

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aagacggggt tcggatacag gcgtcaagcc tcccagttcc gcacacagcc gctttagata 780

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tgaaagataa ttgcatgcca caacttttt ggccaacgtt tgtaaagaca acat 1074

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<212> DNA
<213> African swine fever virus

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caagctcaca tcacggctga aaagctgttt tactaaaaaa aggttgctca agttatacat 180

ataaactcta cgcgcaatga gtcgcgccct atcaaagtta gtagccccca aatcaatgca 240

gaaaaatagg tttaaagtat tattgttata gatagataga ttcatgccat aatcaagact 300

agcccctaac atatgacagt aataaatggc tgcataattt tcttcccgca agcaagcaaa 360

tttcatcatc agattagggc taatgcaaat ctctttttta caacacagct catgcaagtc 420

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gtgaatagga cctaaatccc accacaaacc aaaacgctgc agcgtataat cataatcact 1020

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<213> African swine fever virus

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caagctcgca tcacggctga aaagctgttt tactaaaaaa atgttgctca agttatacat 180

ataaactcta tgcgcaatga gtcgcgctct atcaaagtta gtagccccca aatcaataca 240

gaaaaatagg tttaaagtat tattgttata gatagataga ttcatgccat aatcgggact 300

agcccccaac atatgacagt aataaatggc tgcataattt tcttcccgca ggcaagcaaa 360

tttcatcatt agattagggc taatgcaaat ctctttttta gaacacagct catgcaagtc 420

aaaaatatta ttaaaataaa ggctacaagc cagccgccaa tagagctgat ttttatgctt 480

ttcatagaaa tagtgaatcg cttttgtaaa attatgtcgt aatgccaggg caaaccaaaa 540

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ataacccagt agaactcctg cacaggattt cagatcggcc acttctttta aaatttccag 720

aagacgagat tcggagacag gtgttaagcc tcctagttct gtgcacagcc gttttagatc 780

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gtgaatagga cctaaatccc accacaaacc aaaacgctgc agcgtataat catagtcact 1020

tgaaagataa ttgcatgcca caacctttt ggccaacgtt tgtaaagaca acat 1074

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<213> African swine fever virus

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ataaactcta tgcgcaatga gtcgcgctct atcaaagtta gtagccccca aatcaatgca 240

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tttcatcatt agattagggc taatgcaaat ctctttttta gaacacagct catgcaagtc 420

aaaaatgtta ttaaaataaa ggctacaagt tagccgccaa tacagctgat ttttatgttt 480

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aagacgagat tcggagacag gtgttaagcc tcctagttcc gtgcacagcc gttttagatg 780

cacggcagga acacgtataa gtccatattc aggatttgcg ccccaatcca caaacaatcg 840

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gtgaatagga cctaaatccc accacaaacc aaaacgctgc agcgtataat catagtcact 1020

tgaaagataa ttgcacgcca caacttttt ggccaacgtt tgtaaagaca acat 1074

<210> 124
<211> 1071
<212> DNA
<213> African swine fever virus

<400> 124
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acgatttgca ttgatgagga tagccaaata ttgataaaat cggcaagctt caaagaaggc 180

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acccggaacc tttgtcagaa attaggcgca aaggaagctt tgaatgaaag ggatatttta 360

caaatatttt ataaaacacg tcatcttaaa actagcagta atattatttt atataatgaa 420

ttgttttcta ataatctcct tttccaaaat atagagagat tgagtttaat agtttatagg 480

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caaaagaata ataatatatt agtagaaata ttatcattta aaaattatta tagttcaaat 960

acctctcttt tatcaataaa aacgacagat ccggaaaaaa ttaatgcctt attagatgaa 1020

gaaaagtatg agtcaaaaaa tatgttaatg tatgaagaat tatctcattg a 1071

<210> 125
<211> 1071
<212> DNA
<213> African swine fever virus

<400> 125
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tctaaagaac actactttat tttgaaatat tgtggtttat ggtggcatga agcgccgatt 120

acgatttgca ttgatgagga tagccaaata ttgataaaat cggcaagctt caaagaaggc 180

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acccggaacc tttgtcagaa attaggcgca aaggaagctt tgaatgaaag ggatatttta 360

caaatatttt ataaaacacg tcatcttaaa actagcagta atattatttt atataatgaa 420

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caaaagaata ataatatatt agtagaaata ttatcattta aaaattatta tagttcaaat 960

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gaaaagtatg agtcaaaaaa tatgttaatg tatgaagaat tatctcattg a 1071

<210> 126
<211> 1065
<212> DNA
<213> African swine fever virus

<400> 126
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acgatttgca ttgatgagga tagccaaata ttgataaaat cggcaagctt taaagaaggc 180

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<210> 127
<211> 1052
<212> DNA
<213> African swine fever virus

<400> 127
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acccgaaacc tctgtcggga attaggcgcg aaggaagctt tgaatgaaag ggatatttta 360

caaatatttt ataaaacacg tgatattaaa actagcagtc atgttatttt atgccatgaa 420

ttattatcca ataacccccc tttccagaat atagagagaa tgcgttcaat aatttatagg 480

agtctggaaa aactatcaat caactttata ttggatgata tttcatttag tgaaatgtta 540

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aagtatgagt caaaaaatat gttaatgttt ga 1052

<210> 128
<211> 1086
<212> DNA
<213> African swine fever virus

<400> 128
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aagctgttta ccgagtgggg tgcagacatc aactctagct tagtcactgt taatacggag 300

tgtacccgaa acctctgtcg ggaattaggc gcgaaggaag ctttgaatga aagggatatt 360

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gaaaagtatg agtcaaaaaa tatgttaatg tatgatgaat ttgacgcctg tactaataat 1080

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<210> 129
<211> 1086
<212> DNA
<213> African swine fever virus

<400> 129
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<211> 1074
<212> DNA
<213> African swine fever virus

<400> 130
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attaattgta atctaaggag aatatcaatt aactttatat tggatgaaat ttcatttaat 540

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caatatttct atcaaaaata taagcagttt aaagactggc gactaatatg tggacttgct 660

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gcaaaacaac agaatgataa tgaattggta aaggtattat cattgaaaaa ctattacagt 960

ccagatagct ccctttatc attaaaaata acagatccgg aaaaaattaa tatcttatta 1020

gatgatgaaa catatgagtc aaaaaatgag ttaatatatg aagaattaat ataa 1074

<210> 131
<211> 1095
<212> DNA
<213> African swine fever virus

<400> 131
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aataatgtgt ttgatcttca tgaaatatat aacaaagaaa aggttggtat ggatattaat 720

caaatgatag agataacctg tgcatatatg tgtagttatt ccaccattta ctattgtttt 780

gtaatgggag ctgacattaa tcgggcaatg attatctcgg ttacaaaatc ttatacttat 840

aacttgttct tttgtataga tttaggagct actgccttcg aagagtgttt agaaatagca 900

aaacaacaga ataataatga attagtaaaa atattatcat tgaaaaacta ttatagtcca 960

gatagctccc ttatatcatt aaaaataaca gatccggaga aaattaatat cttattagat 1020

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gataagtatc atcatttaga tattcgcatg ctttcaagcc tacaactcct acataaggtg 720

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<211> 1596
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<400> 141

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<213> African swine fever virus

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<211> 1581
<212> DNA
<213> African swine fever virus

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<211> 1554
<212> DNA
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<211> 1569
<212> DNA
<213> African swine fever virus

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<210> 155
<211> 1581
<212> DNA
<213> African swine fever virus

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<211> 1581
<212> DNA
<213> African swine fever virus

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<213> African swine fever virus

<400> 157

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<211> 1575
<212> DNA
<213> African swine fever virus

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gaaaaatgcc acgccttgga acgtttttgt gatgttccat gcctactaga acatgctaca 420

aaacacaaca tgctccctat tctccaaaaa taccaagaag agctgtttat aagagtgtat 480

ctccgcgaaa ccctatttga actagcatgc ctatggcaga ggtatgatat ccttaaatgg 540

atagagcaaa ccatgcatgt ttacgaccta aagattatgt ttaatattgc catctccaag 600

agggatctaa gcatgtactc tttagaatat attctctttt ttaatagagg gaacaccgat 660

gttgcgttag caacgttgct aacgcaacat ctcgagaaga cagcggccaa ggggctcctc 720

cactttgtgc tagaaacgtt aaaatacggc ggtaacataa acatcgtcct ctcccaagcc 780

gtaaaataca atcatagaaa acttttagat tattttctgc gtcaactacc tcgtaaaaat 840

attgaaaaac ttttgttgct ggccgtacag gaaagggctt ctaagaaaac attgaactta 900

ctgttgtctt atttaaacta ctccgtgaaa cgcatcaaaa aactgctgcg ctatgtgata 960

gagcatgagt ccacactggt gataaggatt ttattaaaaa aaagaataaa cctaatagac 1020

gccgtgttgg aaaagactgt aagatatttt tctatgacta aagtgaggac gatcatggat 1080

gagctttcga ttaatccgga aaaagtcatt aaaatggccg tgcagaaaat gagaacggat 1140

atcgtgatcc atacttctta tgtttgggag gatgatctag aaagacttat tcgtcttaaa 1200

aatatgctat acactataaa gtatgagcat ggaaaaaaaa tgctaattaa agtcattcac 1260

ggcatataca aaaacttata cggcgaaaaa gaaaaagtca tgtttaattt ggccaagttc 1320

tatgctgctc aaaacgcggc cacccaattc aaagacactt gtaaagactg ttgcaaactg 1380

gatgtggcgc ggtttaaaca actaatttta gactgtttag acattattac taaaaaaacg 1440

tgcctcagta tcatggaaat cttagaaaat catattattt cgctatttgc tatgaaaatg 1500

atgacggagg atgaaaaaaa cttaggttta gaaatattat ataaagtaat tagttacaaa 1560

atgatatcat attaa 1575

<210> 159
<211> 350
<212> PRT
<213> African swine fever virus

<400> 159

Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1 5 10 15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
20 25 30

Trp His Asp Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
35 40 45

Ser Ala Gly Ile Lys Glu Gly Leu Asn Leu Asn Thr Ala Leu Val Lys
50 55 60

Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65 70 75 80

Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
85 90 95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
100 105 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
115 120 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
130 135 140

Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145 150 155 160

```
Glu Leu Ile Val Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Ser Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320

Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335

Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 160
<211> 350
<212> PRT
<213> African swine fever virus

<400> 160

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                  10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30

Trp His Asp Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
        35                  40                  45

Ser Ala Gly Ile Lys Glu Gly Leu Asn Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80

Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Val Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205
```

```
Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Ser Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320

Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335

Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 161
<211> 350
<212> PRT
<213> African swine fever virus

<400> 161

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30

Trp His Asp Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
        35                  40                  45
```

```
Ser Ala Gly Ile Lys Glu Gly Leu Asn Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80

Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Ser Ser Ile Gln
```

```
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320

Pro Lys Ser Met Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335

Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 162
<211> 350
<212> PRT
<213> African swine fever virus

<400> 162

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30

Trp His Asp Gly Pro Ile Thr Phe Asp His Asn Leu Lys Leu Ile Lys
        35                  40                  45

Ser Ala Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80

Gly Ala Asn Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95
```

```
Arg Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Ala Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Ala Phe Glu Glu Gly Thr Ile Ala Leu Gly Glu Gly Tyr Lys Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320
```

```
Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335


Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350


<210>  163
<211>  350
<212>  PRT
<213>  African swine fever virus

<400>  163

Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15


Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30


Trp His Asp Gly Pro Ile Thr Phe Asp His Asn Leu Lys Leu Ile Lys
        35                  40                  45


Ser Ala Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60


Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80


Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95


Arg Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110


Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125


Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140


Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
```

```
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile Tyr Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Val Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Ala Phe Glu Glu Gly Thr Ile Ala Leu Gly Glu Gly Tyr Lys Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320

Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Val Lys Asn Tyr
                325                 330                 335

Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 164
<211> 350
<212> PRT

<213> African swine fever virus

<400> 164

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                  10                  15


Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30


Trp His Asp Gly Pro Ile Thr Phe Asp His Asn Leu Lys Leu Ile Lys
        35                  40                  45


Ser Ala Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60


Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80


Gly Ala Asn Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95


Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110


Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125


Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140


Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160


Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175


Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190


Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205
```

```
Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Ala Phe Glu Glu Gly Thr Ile Ala Leu Gly Glu Gly Tyr Lys Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro Leu
305                 310                 315                 320

Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335

Val Ser Lys Asn Met Met Ile Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 165
<211> 350
<212> PRT
<213> African swine fever virus

<400> 165

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Tyr Tyr Asp Leu Trp
            20                  25                  30

Trp His Asp Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
```

```
        35                  40                  45

Ser Ala Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Lys Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Ala Glu Trp
65                  70                  75                  80

Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Ser Ser Glu His Thr
                85                  90                  95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Lys
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Ile Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Ile Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile Tyr Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255
```

```
Tyr Met Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300

Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Thr Thr Ile Pro Leu
305                 310                 315                 320

Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335

Phe Ser Lys Asn Met Met Ile Phe Leu Ser Tyr Asp Leu Arg
            340                 345                 350
```

<210> 166
<211> 350
<212> PRT
<213> African swine fever virus

<400> 166

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15

Cys Val Pro Thr Asn Gln His Tyr Leu Leu Lys Tyr Tyr Asp Leu Trp
            20                  25                  30

Trp Tyr Asn Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
        35                  40                  45

Ser Ser Gly Ile Lys Glu Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60

Ala Val Arg Glu Asn Asn Tyr Ser Leu Ile Lys Leu Phe Thr Glu Trp
65                  70                  75                  80

Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95
```

```
Arg Asp Leu Cys Gln Glu Leu Gly Ala Lys Glu Ile Leu Asn Glu Glu
            100                 105                 110

Glu Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Ile Leu Gln
    130                 135                 140

Lys Val Asn Asn Leu Lys Leu Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Leu Leu Ser
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Val Arg Tyr Ser Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile His Met Asp Ile Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Met Tyr Tyr Cys
                245                 250                 255

Tyr Met Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Gly Thr Thr Ala Leu Gly Glu Gly Tyr Glu Leu Ile
    290                 295                 300
```

```
Lys Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Thr Thr Ile Pro Leu
305                 310                 315                 320


Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn Tyr
                325                 330                 335


Phe Ser Lys Asn Met Met Ile Phe Leu Ser Tyr Asp Leu Arg
            340                 345                 350


<210>  167
<211>  349
<212>  PRT
<213>  African swine fever virus

<400>  167

Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1               5                   10                  15


Cys Leu Pro Thr Asp Gln Tyr Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30


Trp Tyr Asp Ser Pro Ile Thr Phe Asp His Asn Leu Gly Leu Ile Lys
        35                  40                  45


Ser Ala Gly Ile Lys Asp Gly Leu Asp Leu Asn Thr Ala Leu Val Lys
    50                  55                  60


Ala Val Arg Glu Asn Asn Tyr Asn Leu Ile Lys Leu Phe Thr Glu Trp
65                  70                  75                  80


Gly Ala Asp Ile Asn Tyr Gly Leu Val Ser Val Asn Thr Glu His Thr
                85                  90                  95


Arg Asp Leu Cys Arg Glu Leu Gly Ala Lys Glu Thr Leu Asn Glu Glu
            100                 105                 110


Glu Ile Leu Arg Ile Phe Ile Asp Leu Lys Phe Tyr Lys Thr Ser Ser
        115                 120                 125


Asn Ile Ile Leu Cys His Glu Val Phe Ser Asn Asn Pro Leu Leu Gln
    130                 135                 140
```

```
Lys Val Asn Asn Leu Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Leu Ile Lys Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Asn
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Val Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile Tyr Met Asp Leu Glu Glu Met Met
225                 230                 235                 240

Arg Val Ala Cys Ile Lys Asp His Asn Leu Ser Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Val Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Ala Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Met Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Val Phe Glu Glu Asn Met Pro Val Gly Glu Gly Tyr Glu Leu Ile Arg
    290                 295                 300

Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ser Thr Ala Pro Leu Pro
305                 310                 315                 320

Lys Asn Thr Asp Pro Glu Ile Ile Asp His Val Leu Lys Asn Tyr Lys
                325                 330                 335

Ser Lys Asn Met Met Thr Phe Leu Ser Tyr Asp Leu Arg
            340                 345
```

<210> 168

<211> 351
<212> PRT
<213> African swine fever virus

<400> 168

Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Gly Gln
1 5 10 15

Cys Leu Pro Glu Asp Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
20 25 30

Trp Asn Asn Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
35 40 45

Ser Ala Gly Leu Gln Glu Gly Leu Asp Leu Asn Met Ala Leu Val Lys
50 55 60

Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu Phe Thr Glu Trp
65 70 75 80

Gly Ala Asn Ile Asn Tyr Gly Leu Ile Ser Val Asn Thr Glu His Thr
85 90 95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Lys Thr Leu Asn Glu Gly
100 105 110

Asp Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe His Lys Thr Ser Ser
115 120 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asp Asn Leu Leu Leu Lys
130 135 140

Lys Val Asn Asn Leu Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145 150 155 160

Glu Ile Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Asn
165 170 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Val Arg Tyr Asn Leu
180 185 190

```
Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile Cys Met Asp Leu Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Ser Leu Ser Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Met Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Ile Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Ala Phe Glu Glu Gly Met Ala Leu Val Gly Gln Glu Gly Tyr Glu Pro
    290                 295                 300

Ile Arg Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro
305                 310                 315                 320

Leu Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Glu Leu Lys Asn
                325                 330                 335

Tyr Phe Ser Lys Asn Met Met Val Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350
```

<210> 169
<211> 351
<212> PRT
<213> African swine fever virus

<400> 169

```
Met Leu Pro Ser Leu Gln Ser Leu Thr Lys Lys Val Leu Ala Arg Gln
1               5                   10                  15

Cys Leu Pro Glu Asp Gln His Tyr Leu Leu Lys Cys Tyr Asp Leu Trp
            20                  25                  30
```

```
Trp Asn Asn Ala Pro Ile Thr Phe Asp His Asn Leu Arg Leu Ile Lys
        35                  40                  45

Leu Ala Gly Ile Gln Glu Gly Leu Asp Leu Asn Met Ala Leu Val Lys
    50                  55                  60

Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu Phe Thr Glu Trp
65                  70                  75                  80

Gly Ala Asn Ile Asn Tyr Gly Leu Ile Ser Val Asn Thr Glu His Thr
                85                  90                  95

Trp Asp Leu Cys Arg Glu Leu Gly Ala Lys Lys Thr Leu Asn Glu Gly
            100                 105                 110

Asp Ile Leu Gln Ile Phe Ile Asp Leu Lys Phe Tyr Lys Thr Ser Ser
        115                 120                 125

Asn Ile Ile Leu Cys His Glu Val Phe Ser Asp Asn Leu Leu Leu Lys
    130                 135                 140

Arg Val Asn Asn Leu Lys Met Arg Ile Glu Ile Phe Trp Glu Leu Arg
145                 150                 155                 160

Glu Ile Ile Glu Lys Thr Asp Leu Leu Asn Asn Glu Phe Ser Leu Asn
                165                 170                 175

Thr Leu Leu Leu Lys Tyr Trp Tyr Ala Ile Ala Val Arg Tyr Asn Leu
            180                 185                 190

Lys Glu Ala Ile Gln Tyr Phe Tyr Gln Lys Tyr Thr His Leu Asn Thr
        195                 200                 205

Trp Arg Leu Thr Cys Ala Leu Cys Phe Asn Asn Val Phe Asp Leu His
    210                 215                 220

Glu Ala Tyr Glu Lys Asp Lys Ile Cys Met Asp Leu Glu Glu Met Met
225                 230                 235                 240

Arg Ile Ala Cys Ile Lys Asp His Asn Leu Ser Thr Ile Tyr Tyr Cys
```

```
                245                 250                 255

Tyr Met Leu Gly Ala Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
            260                 265                 270

Tyr Tyr Asn Ile Glu Asn Ile Phe Phe Cys Met Asp Leu Gly Ala Asp
        275                 280                 285

Ala Phe Glu Glu Gly Met Ala Leu Val Gly Gln Glu Gly Tyr Glu Pro
    290                 295                 300

Ile Arg Asn Ile Leu Ser Leu Lys Ile Tyr Ser Pro Ala Thr Thr Pro
305                 310                 315                 320

Leu Pro Lys Ser Thr Asp Pro Glu Ile Ile Asp His Ala Leu Lys Asn
                325                 330                 335

Tyr Phe Ser Lys Asn Met Met Val Phe Leu Thr Tyr Asp Leu Arg
            340                 345                 350


<210>  170
<211>  353
<212>  PRT
<213>  African swine fever virus

<400>  170

Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Ile Ala
1               5                   10                  15

Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys Tyr Cys Gly
            20                  25                  30

Leu Trp Trp His Asp Ala Pro Leu Lys Leu Cys Met Asp Arg Gly Arg
        35                  40                  45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Arg Val
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80
```

```
Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Gly Leu Leu Ser Ile Asn
                85                  90                  95

Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Arg Ile Met His Asn
        115                 120                 125

Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
    130                 135                 140

Pro Ile Leu Glu Asn Lys Phe Val Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Gly Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Asp Cys
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Glu Asn Ile Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300
```

Leu Ser His Ser Leu Ala Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305 310 315 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asp
325 330 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
340 345 350

Leu

<210> 171
<211> 353
<212> PRT
<213> African swine fever virus

<400> 171

Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Ile Ala
1 5 10 15

Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys Tyr Cys Gly
20 25 30

Leu Trp Trp His Asp Ala Pro Leu Lys Leu Cys Met Asp Arg Gly Arg
35 40 45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Arg Val
50 55 60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65 70 75 80

Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Gly Leu Leu Ser Ile Asn
85 90 95

Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
100 105 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Arg Ile Met His Asn

```
        115                 120                 125

Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
    130                 135                 140

Pro Ile Leu Glu Asn Lys Phe Val Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Gly Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Asp Cys
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Glu Asn Ile Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Ala Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335
```

```
Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350


Leu
```

<210> 172
<211> 353
<212> PRT
<213> African swine fever virus

<400> 172

```
Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15


Asn Gln Ser Leu Ser Ile Asp Glu His Cys Ile Leu Lys His Cys Gly
            20                  25                  30


Leu Trp Trp His Asp Val Pro Leu Lys Leu Cys Met Asp Arg Gly Gln
        35                  40                  45


Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu His Ile
    50                  55                  60


Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80


Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95


Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110


Leu Glu Asp Asp Asp Ile Phe Arg Ile Phe Thr Lys Ile Met His Asn
        115                 120                 125


Lys Thr Ser Gly Ser Ile Ile Leu Cys His Asp Ile Phe Met Asn Asn
    130                 135                 140


Pro Asn Ile Glu Asp Lys Phe Thr Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160
```

```
Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Gly Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Glu Cys
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Glu Asn Ile Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Ala Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350

Leu
```

<210> 173
<211> 353
<212> PRT
<213> African swine fever virus

<400> 173

Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1 5 10 15

Ser Gln Cys Leu Ser Thr Asp Glu His Cys Ile Leu Lys His Cys Gly
20 25 30

Leu Trp Trp His Asp Val Pro Leu Lys Leu Cys Met Asp Arg Gly Gln
35 40 45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu His Ile
50 55 60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65 70 75 80

Phe Thr Glu Trp Gly Ala His Ile Asn Tyr Ser Leu Leu Ser Ile Asn
85 90 95

Thr Glu His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
100 105 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Lys Ile Met His Asn
115 120 125

Lys Thr Ser Gly Arg Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
130 135 140

Pro Asn Ile Glu Asn Lys Phe Thr Ile Gln Leu Arg Gly Leu Ile Cys
145 150 155 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
165 170 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Glu Cys
180 185 190

```
Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Glu Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr His Phe
    290                 295                 300

Leu Ser His Ser Leu Thr Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350

Leu
```

<210> 174
<211> 353
<212> PRT
<213> African swine fever virus

<400> 174

```
Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15
```

```
Ser Gln Cys Leu Ser Thr Asp Glu His Cys Ile Leu Lys His Cys Gly
            20                  25                  30

Leu Trp Trp His Asp Val Pro Leu Lys Leu Cys Met Asp Arg Gly Gln
        35                  40                  45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu His Val
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80

Phe Thr Glu Trp Gly Ala His Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95

Thr Glu His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Lys Thr
            100                 105                 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Lys Ile Met His Asn
        115                 120                 125

Lys Thr Ser Gly Arg Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
    130                 135                 140

Pro Asn Ile Glu Asn Lys Phe Thr Ile Gln Leu Arg Gly Leu Ile Cys
145                 150                 155                 160

Lys Arg Leu Trp Arg Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Glu Cys
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Gly Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220
```

```
Glu Met Tyr His Lys Asp Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240


Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255


Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270


Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285


Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr His Phe
    290                 295                 300


Leu Ser His Ser Leu Ala Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320


Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Gly
                325                 330                 335


Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350


Leu
```

<210> 175
<211> 353
<212> PRT
<213> African swine fever virus

<400> 175

```
Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15


Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys His Cys Gly
            20                  25                  30


Leu Trp Trp His Asp Val Pro Leu Lys Leu Cys Met Asp Arg Gly Gln
        35                  40                  45
```

```
Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu His Ile
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80

Phe Thr Glu Trp Gly Ala His Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95

Thr Glu His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110

Leu Glu Asp Asp Asp Val Phe Arg Ile Phe Thr Lys Ile Met His Asn
        115                 120                 125

Lys Thr Ser Gly Arg Ile Ile Leu Cys His Asp Ile Phe Met Asn Asn
    130                 135                 140

Pro Asn Ile Glu Asn Lys Phe Thr Ile Gln Leu Arg Gly Leu Ile Cys
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Glu Cys
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Glu Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Phe Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Glu Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Ser Thr Lys Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Ile Gln
```

```
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Ala Leu Asp Ile Phe Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Phe Leu Lys Asp
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350

Leu
```

<210> 176
<211> 353
<212> PRT
<213> African swine fever virus

<400> 176

```
Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15

Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys Tyr Cys Gly
            20                  25                  30

Leu Trp Trp His Asp Ala Pro Leu Lys Leu Cys Met Asp Arg Gly Arg
        35                  40                  45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Arg Val
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80
```

```
Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95

Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Arg Ile Met His Asn
        115                 120                 125

Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
    130                 135                 140

Pro Ile Leu Glu Asn Lys Phe Val Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Lys Leu Asn
                165                 170                 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Val Cys
            180                 185                 190

Lys Asn Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Lys Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Cys Ala Lys Asp Asn Asn Leu Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Ser Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300
```

```
Leu Ser His Ser Leu Thr Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350

Leu
```

<210> 177
<211> 353
<212> PRT
<213> African swine fever virus

<400> 177

```
Met Ser Leu Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15

Ser Gln Cys Leu Ser Ile Asp Glu His Cys Ile Leu Lys Tyr Cys Gly
            20                  25                  30

Leu Trp Trp His Asp Ala Pro Leu Lys Leu Cys Met Asp Arg Gly Arg
        35                  40                  45

Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Arg Val
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80

Phe Thr Glu Trp Gly Ala Asn Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95

Thr Lys His Ile Arg Glu Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110

Leu Glu Asp Asn Asp Ile Phe Arg Ile Phe Thr Arg Ile Met His Asn
```

```
        115                 120                 125

Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Met Asn Asn
    130                 135                 140

Pro Met Leu Glu Asn Lys Phe Val Ile Gln Leu Arg Gly Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Trp Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Asn
                165                 170                 175

Asp Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Val Cys
            180                 185                 190

Lys Asn Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Leu Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Glu Met Tyr His Lys Lys Lys Val Gln Ile Asp Val His Asp Met Ile
225                 230                 235                 240

Cys Leu Ala Cys Ala Lys Asp Asn Asn Leu Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Val Gly Asn Ile Phe Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Arg Ala Ile Ala Glu Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Thr Leu Asp Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Lys Ile Ser Ser Leu Leu Lys Asp
                325                 330                 335
```

```
Tyr Lys Ser Lys Asn Leu Ser Ile Ile Trp Glu Tyr Ser His Asn Ile
            340                 345                 350


Leu
```

<210> 178
<211> 353
<212> PRT
<213> African swine fever virus

<400> 178

```
Met Ser Ala Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15


Ser Thr Ser Cys Leu Ser Ile Asp Glu His Ile Leu Lys Tyr Cys Asp
            20                  25                  30


Leu Trp Trp His Asp Ala Pro Leu Lys Leu Tyr Met Asp Arg Gly Arg
        35                  40                  45


Ile Gln Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Cys Val
    50                  55                  60


Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Asn Leu Ile Lys Leu
65                  70                  75                  80


Phe Thr Glu Leu Gly Ala Asn Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95


Thr Lys His Val Arg Asp Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110


Leu Glu Asp Tyr Asp Ile Phe Cys Ile Phe Asn Lys Ile Met His Asn
        115                 120                 125


Lys Thr Ser Gly Ser Val Ile Leu Cys His Glu Ile Phe Ile Asn Asn
    130                 135                 140


Pro Asn Leu Glu Asn Lys Phe Ala Ala Gln Leu Arg Arg Leu Ile Tyr
145                 150                 155                 160
```

```
Lys Arg Leu Cys Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Ser
                165                 170                 175

Glu Leu Leu Val Lys Tyr Trp Tyr Ala Lys Ala Val Gln Tyr Asp Tyr
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asn Glu
        195                 200                 205

Trp Arg Leu Lys Cys Tyr Leu Tyr Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Asp Ile Tyr His Lys Glu Lys Ile Gln Ile Asp Val Asn Glu Met Leu
225                 230                 235                 240

Ser Leu Ala Cys Ile Arg Asp Asn Asn Pro Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Tyr Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Ser Ala Ile Ala Arg Gln Lys Gly Tyr Asn Phe
    290                 295                 300

Leu Ser His Ser Leu Val Leu Asn Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asn
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Leu Asp Tyr Ser His Asn Ile
            340                 345                 350

Leu
```

<210> 179
<211> 353
<212> PRT
<213> African swine fever virus

<400> 179

```
Met Ser Ser Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                  10                  15


Ser Thr Ser Cys Leu Ser Ile Asp Glu His Ile Leu Lys Tyr Cys Gly
            20                  25                  30


Leu Trp Trp His Asp Ala Pro Leu Lys Leu Tyr Ile Asp Arg Gly Arg
        35                  40                  45


Ile Tyr Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Cys Val
    50                  55                  60


Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Leu Ile Lys Leu
65                  70                  75                  80


Phe Thr Glu Trp Gly Ala Tyr Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95


Thr Lys His Ala Arg Asp Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110


Leu Asp Asp Tyr Asp Ile Phe Cys Ile Phe Asn Lys Ile Met His Asn
        115                 120                 125


Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Ile Asn Asn
    130                 135                 140


Pro Lys Leu Glu Asn Asn Phe Ala Ala Gln Leu Arg Arg Leu Ile Tyr
145                 150                 155                 160


Lys Arg Leu Cys Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Ser
                165                 170                 175


Glu Leu Leu Val Lys Tyr Trp Tyr Ala Asn Ala Val Gln Tyr Asp His
            180                 185                 190
```

```
Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asp Glu
        195                 200                 205

Trp Arg Leu Lys Cys Tyr Leu Cys Tyr Asn Lys Ile Tyr Glu Leu His
    210                 215                 220

Asp Ile Tyr His Lys Lys Lys Ile Gln Ile Asp Val Asn Glu Met Leu
225                 230                 235                 240

Ser Leu Ala Cys Ile Arg Asp Asn Asn Leu Leu Thr Ile Tyr Tyr Cys
                245                 250                 255

Tyr Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln
            260                 265                 270

Tyr Tyr Asn Ile Gly Asn Ile Tyr Phe Cys Ile Asp Leu Gly Gly Asn
        275                 280                 285

Ala Phe Glu Glu Gly Ser Ala Ile Ala Arg Gln Asn Gly Tyr Asn Phe
    290                 295                 300

Leu Cys His Ser Leu Ile Leu Asn Ile Tyr Ser Ser Asp Ala Ser Leu
305                 310                 315                 320

Pro Leu Asn Leu Lys Val Pro Glu Glu Ile Ser Ser Leu Leu Lys Asn
                325                 330                 335

Tyr Lys Ser Lys Asn Leu Ser Ile Ile Leu Asp Tyr Ser His Lys Ile
            340                 345                 350

Leu
```

<210> 180
<211> 352
<212> PRT
<213> African swine fever virus

<400> 180

```
Met Ser Ser Pro Leu Ser Leu Gln Thr Leu Val Lys Lys Thr Val Ala
1               5                   10                  15
```

```
Gly Thr Ser Cys Leu Ser Ile Asp Glu His Ile Leu Lys Tyr Cys Gly
            20                  25                  30

Leu Trp Trp His Asp Ala Pro Leu Lys Leu Tyr Ile Asp Arg Gly Arg
        35                  40                  45

Ile Tyr Ile Lys Ser Gly Phe Leu Gly Glu Asp Ile Asp Leu Cys Val
    50                  55                  60

Ala Leu Ile Ile Ala Val Lys Glu Asn Asn Tyr Ser Met Ile Lys Leu
65                  70                  75                  80

Phe Thr Glu Trp Gly Ala Tyr Ile Asn Tyr Ser Leu Leu Ser Ile Asn
                85                  90                  95

Thr Lys His Ala Arg Asp Leu Cys Arg Gln Leu Gly Ala Lys Glu Thr
            100                 105                 110

Leu Asp Asp Tyr Asp Ile Phe Cys Ile Phe Asn Lys Ile Met His Asn
        115                 120                 125

Lys Thr Ser Gly Ser Ile Ile Leu Cys His Glu Ile Phe Ile Asn Asn
    130                 135                 140

Pro Asn Leu Glu Asn Asn Phe Ala Ala Gln Leu Arg Arg Leu Ile Tyr
145                 150                 155                 160

Lys Arg Leu Cys Gly Leu Ile Glu Ile Lys Glu Thr Asp Glu Leu Ser
                165                 170                 175

Glu Leu Leu Val Lys Tyr Trp Tyr Ala Asn Ala Val Gln Tyr Asp His
            180                 185                 190

Lys Asp Ala Ile Cys Phe Leu Asp Glu Lys Tyr Thr Asp Leu Asp Glu
        195                 200                 205

Trp Leu Lys Cys Tyr Leu Cys Tyr Asn Lys Ile Tyr Glu Leu His Asp
    210                 215                 220
```

```
Ile Tyr His Lys Glu Lys Ile Gln Ile Asp Val Asn Glu Met Leu Ser
225                 230                 235                 240


Leu Ala Cys Ile Arg Asp Asn Asn Leu Leu Thr Ile Tyr Tyr Cys Tyr
                245                 250                 255


Ala Leu Gly Gly Asn Ile Asn Gln Ala Met Leu Thr Ser Val Gln Tyr
            260                 265                 270


Tyr Asn Ile Gly Asn Ile Tyr Phe Cys Ile Asp Leu Gly Gly Asn Ala
        275                 280                 285


Phe Glu Glu Gly Ser Ala Ile Ala Arg Gln Asn Gly Tyr Asn Phe Leu
    290                 295                 300


Ser His Ser Leu Val Leu Asn Ile Tyr Ser Ser Asp Ala Ser Leu Pro
305                 310                 315                 320


Leu Asn Leu Lys Asp Pro Glu Glu Ile Ser Ser Leu Leu Lys Asn Tyr
                325                 330                 335


Lys Ser Lys Asn Leu Ser Ile Ile Leu Asp Tyr Ser His Lys Ile Leu
            340                 345                 350


<210>  181
<211>  357
<212>  PRT
<213>  African swine fever virus

<400>  181

Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15


Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30


Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Val Phe Ser
        35                  40                  45


Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60
```

```
Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95

Ala Val Tyr Leu Lys Arg Leu Cys Ala Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Arg Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His His Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys His Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Ala Asp Phe Asp
```

```
        275                 280                 285

Arg Ala Gln Leu Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Val Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350

Ile Ile Val Ile Asp
        355
```

<210> 182
<211> 357
<212> PRT
<213> African swine fever virus

<400> 182

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30

Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Val Phe Ser
        35                  40                  45

Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95
```

```
Ala Val Tyr Leu Lys Arg Leu Cys Ala Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Arg Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His His Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys His Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Ala Asp Phe Asp
        275                 280                 285

Arg Ala Gln Leu Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Val Leu
305                 310                 315                 320
```

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Thr Tyr Thr
325 330 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
340 345 350

Ile Ile Val Ile Asp
355

<210> 183
<211> 357
<212> PRT
<213> African swine fever virus

<400> 183

Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1 5 10 15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
20 25 30

Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Ile Phe Ser
35 40 45

Tyr Lys His Val Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
50 55 60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65 70 75 80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
85 90 95

Ala Val His Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
100 105 110

Val Ser Glu Ser Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Arg Leu
115 120 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn

```
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His His Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Gln Lys Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys Tyr Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Thr Asp Phe Asp
        275                 280                 285

Arg Ala Gln Arg Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Ala Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Ser Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350
```

Ile Ile Val Ile Asp
        355

<210> 184
<211> 357
<212> PRT
<213> African swine fever virus

<400> 184

Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1   5   10   15

Leu Ser Ser Asp Tyr Asp Tyr Met Leu Gln Arg Phe Gly Leu Trp Trp
            20   25   30

Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Ile Phe Ser
        35   40   45

Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50   55   60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65   70   75   80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85   90   95

Ala Val His Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
            100   105   110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Lys Leu
        115   120   125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130   135   140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145   150   155   160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His His Leu Leu
                165   170   175

```
Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Lys Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys Tyr Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Thr Asp Phe Asp
        275                 280                 285

Arg Ala Gln Arg Ile Ala His Lys Thr Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Ala Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Ser Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350

Ile Ile Val Ile Asp
        355
```

<210> 185
<211> 357
<212> PRT
<213> African swine fever virus

<400> 185

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                  10                  15

Leu Ser Ser Asp Tyr Asp Tyr Met Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30

Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Ile Phe Ser
        35                  40                  45

Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60

Ala Leu Val Lys Ala Val Lys Arg Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Cys Val Pro
                85                  90                  95

Thr Val His Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asn Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys Tyr Asn
    130                 135                 140

Pro Leu Leu Glu Thr Ile Thr Arg Thr Thr Leu Asp Thr Val Met Tyr
145                 150                 155                 160

Ser Cys Ser Lys Ile Pro Leu Met Gly Asp Thr Ala His His Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205
```

```
Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys Tyr Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Ser Leu Asn Leu Phe Phe Cys Ile Asp Leu Gly Ala Thr Asp Phe Asp
        275                 280                 285

Arg Ala Gln Arg Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Leu Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Ala Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Arg Leu Lys Ala Tyr Thr
                325                 330                 335

Ser Lys Asn Met Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350

Ile Ile Val Ile Asp
        355
```

<210> 186
<211> 357
<212> PRT
<213> African swine fever virus

<400> 186

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30
```

```
Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Ile Phe Ser
        35                  40                  45

Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95

Ala Val His Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Thr Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Lys Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn His Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240
```

```
Cys Leu Gln Lys Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys Tyr Arg Leu
                245                 250                 255


Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270


Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Thr Asp Phe Asp
        275                 280                 285


Arg Ala Gln His Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300


Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Ala Leu
305                 310                 315                 320


Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Arg Leu Lys Ser Tyr Thr
                325                 330                 335


Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350


Ile Ile Val Ile Asp
        355


<210>  187
<211>  357
<212>  PRT
<213>  African swine fever virus

<400>  187

Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15


Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30


Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Val Phe Ser
        35                  40                  45


Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60
```

```
Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95

Ala Val Tyr Leu Lys Arg Leu Cys Ala Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asn Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn Gln Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys His Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Ala Asp Phe Asp
```

```
        275                 280                 285

Arg Ala Gln Leu Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Val Leu
305                 310                 315                 320

Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Met Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350

Ile Ile Val Ile Asp
        355
```

<210> 188
<211> 357
<212> PRT
<213> African swine fever virus

<400> 188

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30

Asp Leu Gly Pro Ile His Leu Cys Asn Asn Cys Lys Gln Val Phe Ser
        35                  40                  45

Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95
```

```
Ala Val Tyr Leu Lys Arg Leu Cys Ala Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Pro Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asn Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Thr Tyr
145                 150                 155                 160

Thr Cys Ser Asn Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Lys Arg His Lys Asn Gln Leu Tyr Trp Arg Val
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Ile His Glu Leu Cys
    210                 215                 220

Arg Glu Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Lys Asn Tyr Ala Ala Ile Tyr Tyr Cys His Arg Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Met Phe Phe Cys Ile Asp Leu Gly Ala Ala Asp Phe Asp
        275                 280                 285

Arg Ala Gln Leu Ile Ala His Lys Ala Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Thr Leu Val Leu
305                 310                 315                 320
```

```
Asp Val Thr Glu Pro Gln Glu Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335


Ser Lys Asn Met Lys Arg Ala Glu Glu Tyr Leu Thr Ala His Pro Glu
            340                 345                 350


Ile Ile Val Ile Asp
        355
```

<210> 189
<211> 357
<212> PRT
<213> African swine fever virus

<400> 189

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                   10                  15


Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30


Asp Leu Gly Pro Ile His Leu Cys Asn Thr Cys Lys Gln Ile Phe Ser
        35                  40                  45


Tyr Lys His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Glu Ala
    50                  55                  60


Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80


Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95


Ala Val His Leu Lys Arg Leu Cys Met Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110


Val Ser Glu Ser Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asp Leu
        115                 120                 125


Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
```

```
    130                 135                 140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asp Thr Val Met Tyr
145                 150                 155                 160

Thr Arg Ser Lys Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175

Ser Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Glu Lys His Lys Asn Gln Leu Tyr Trp Arg Leu
        195                 200                 205

Thr Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Leu His Glu Leu Cys
    210                 215                 220

Cys Lys Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Glu Asn Tyr Ala Ala Ile Tyr Tyr Cys His Met Leu
                245                 250                 255

Gly Ala Ser Leu Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Leu Phe Phe Cys Ile Asp Leu Gly Ala Thr Asn Phe Asp
        275                 280                 285

Arg Ala Arg Leu Ile Ala Arg Arg Val Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Leu Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Val Ser Leu Ile Leu
305                 310                 315                 320

Asp Leu Thr Glu Pro Gln Ala Ile Tyr Asp Met Leu Asn Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Gln Ala Glu Glu Tyr Phe Thr Ala His Pro Glu
            340                 345                 350
```

Ile Val Val Ile Asp
        355

<210> 190
<211> 357
<212> PRT
<213> African swine fever virus

<400> 190

Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1   5   10   15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20   25   30

Asp Leu Gly Pro Ile His Leu Cys Asn Thr Cys Lys Gln Ile Phe Ser
        35   40   45

Tyr Gln His Leu Gln Cys Phe Ser Glu Asp Asp Leu Cys Leu Asp Ala
    50   55   60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65   70   75   80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85   90   95

Ala Val Asp Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
            100   105   110

Val Ser Glu Ser Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asp Leu
        115   120   125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130   135   140

Pro Leu Leu Glu Thr Val Thr Arg Thr Thr Leu Asn Thr Val Met Tyr
145   150   155   160

Thr Arg Ser Lys Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165   170   175

```
Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Glu Lys His Lys Asn Gln Leu Tyr Trp Arg Leu
        195                 200                 205

Ala Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Leu His Glu Leu Cys
    210                 215                 220

Ser Lys Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Glu Asn Tyr Ala Ala Ile Tyr Tyr Cys His Met Leu
                245                 250                 255

Gly Ala Ser Pro Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Leu Phe Phe Cys Ile Asp Leu Gly Ala Thr Asn Phe Asp
        275                 280                 285

Arg Ala Arg Leu Ile Ala His Arg Val Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Ala Ser Leu Val Leu
305                 310                 315                 320

Asn Ile Thr Glu Pro Gln Ala Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Phe Thr Ala His Pro Glu
            340                 345                 350

Ile Val Val Ile Asp
        355
```

<210> 191
<211> 357
<212> PRT
<213> African swine fever virus

<400> 191

```
Met Leu Ser Leu Gln Thr Leu Ala Lys Lys Val Val Ala Cys Asn Tyr
1               5                  10                  15

Leu Ser Ser Asp Tyr Asp Tyr Thr Leu Gln Arg Phe Gly Leu Trp Trp
            20                  25                  30

Asp Leu Gly Pro Ile His Leu Cys Asn Thr Cys Lys Gln Ile Phe Ser
        35                  40                  45

Tyr Gln His Leu Gln Cys Phe Ser Val Asp Asp Leu Cys Leu Asp Ala
    50                  55                  60

Ala Leu Val Lys Ala Val Lys Ser Asp Asn Leu Glu Leu Ile Arg Leu
65                  70                  75                  80

Phe Val Asp Trp Gly Ala Asn Pro Glu Tyr Gly Leu Ile Arg Val Pro
                85                  90                  95

Ala Val His Leu Lys Arg Leu Cys Thr Glu Leu Gly Gly Leu Thr Pro
            100                 105                 110

Val Ser Glu Ser Arg Leu Leu Glu Ile Leu Lys Glu Val Ala Asp Leu
        115                 120                 125

Lys Ser Cys Ala Gly Val Leu Leu Gly Tyr Asp Met Phe Cys His Asn
    130                 135                 140

Pro Leu Met Glu Thr Val Thr Arg Thr Thr Leu Asn Thr Val Met Tyr
145                 150                 155                 160

Thr Arg Ser Lys Ile Pro Leu Thr Gly Asp Thr Ala His Leu Leu Leu
                165                 170                 175

Thr Lys Phe Trp Phe Ala Leu Ala Leu Arg His Asn Phe Thr Lys Ala
            180                 185                 190

Ile His Tyr Phe Tyr Glu Lys His Lys Asn Gln Leu Tyr Trp Arg Leu
        195                 200                 205
```

```
Thr Cys Ser Leu Tyr Phe Asn Asn Ile Phe Asp Leu His Glu Leu Cys
    210                 215                 220

Ser Lys Lys Glu Ile Cys Ile Ser Pro Asn Leu Met Met Lys Phe Ala
225                 230                 235                 240

Cys Leu Arg Glu Glu Asn Tyr Ala Ala Ile Tyr Tyr Cys His Met Leu
                245                 250                 255

Gly Ala Ser Pro Asp Tyr Gly Met Asn Leu Ser Ile Tyr Asn Asn Asn
            260                 265                 270

Thr Leu Asn Leu Phe Phe Cys Ile Asp Leu Gly Ala Thr Asn Phe Asp
        275                 280                 285

Arg Ala Arg Leu Ile Ala His Arg Val Tyr Met Tyr Asn Leu Ser Asn
    290                 295                 300

Ile Phe Leu Val Lys Gln Leu Phe Ser Arg Asp Ala Ser Leu Val Leu
305                 310                 315                 320

Asn Ile Thr Glu Pro Gln Ala Ile Tyr Asp Met Leu Lys Thr Tyr Thr
                325                 330                 335

Ser Lys Asn Leu Lys Arg Ala Glu Glu Tyr Phe Thr Ala His Pro Glu
            340                 345                 350

Ile Val Val Ile Asp
        355
```

<210> 192
<211> 531
<212> PRT
<213> African swine fever virus

<400> 192

```
Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asn Arg Lys
1               5                   10                  15

Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30
```

```
Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45

Ile Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Thr Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Gln Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys His Arg Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Phe Thr His Leu Leu Ile Glu Lys Ala Cys Lys Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asn Met Ile
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu His Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Arg Phe Ile Tyr Asn Arg Ile Val Pro Asp Lys Tyr His
    210                 215                 220

His Leu Asp Ile Arg Met Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240
```

```
Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Lys Asp Asn Ile Asn Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Ile Tyr Phe Ile Pro Gln Ser Thr His Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Leu Val Ala Ile Lys Ala Lys Ser Ser Arg
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Asn Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser His Tyr Val Ala Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Arg Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Lys Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Leu Lys Ile
    370                 375                 380

Ala Ala Arg Ile Asn Arg Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Val Arg Leu Lys Tyr Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Asp Arg Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460
```

```
Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480


Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495


Asn Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Val Met Gly Val Leu
            500                 505                 510


Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys Gln
        515                 520                 525


Tyr Met Pro
    530


<210>  193
<211>  531
<212>  PRT
<213>  African swine fever virus

<400>  193

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asn Arg Lys
1               5                   10                  15


Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30


Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45


Ile Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Thr Ala
    50                  55                  60


Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80


Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95


Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
```

```
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Gln Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys His Arg Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Phe Thr His Leu Leu Ile Glu Lys Ala Cys Lys Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asn Met Ile
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu His Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Arg Phe Ile Tyr Asn Arg Ile Val Pro Asp Lys Tyr His
    210                 215                 220

His Leu Asp Ile Arg Met Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Lys Asp Asn Ile Asn Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Ile Tyr Phe Ile Pro Gln Ser Thr His Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Leu Val Ala Ile Lys Ala Lys Ser Ser Arg
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Asn Leu
305                 310                 315                 320
```

```
Ile Lys Lys Ile Ser His Tyr Val Ala Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Arg Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Lys Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Leu Lys Ile
    370                 375                 380

Ala Ala Arg Ile Asn Arg Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Val Arg Leu Lys Tyr Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Asp Arg Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495

Asn Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Val Met Gly Val Leu
            500                 505                 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys Gln
        515                 520                 525

Tyr Met Pro
```

530

<210> 194
<211> 531
<212> PRT
<213> African swine fever virus

<400> 194

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1 5 10 15

Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
20 25 30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
35 40 45

Ile Gln Gln His Asn Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
50 55 60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65 70 75 80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
85 90 95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
100 105 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
115 120 125

Arg Gln Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
130 135 140

Lys Phe Arg Val Leu Leu Ser Phe Lys His Arg Leu Arg Asp Asp Leu
145 150 155 160

Pro Phe Thr His Leu Leu Ile Glu Lys Ala Cys Lys Asp His Asn Tyr
165 170 175

```
Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asn Met Ile
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Arg Phe Ile Tyr Asn Arg Ile Val Pro Asp Lys Tyr His
    210                 215                 220

His Leu Asp Ile Arg Met Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Lys Asp Asn Ile Asn Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Ile Tyr Phe Ile Pro Gln Ser Thr His Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Leu Val Ala Ile Lys Thr Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Asn Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser His Tyr Val Ala Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Arg Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Lys Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Leu Lys Ile
    370                 375                 380

Ala Ala Arg Ile Asn Arg Thr Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400
```

```
Val Trp Lys Asn His Ala Val Arg Leu Lys Tyr Leu Lys His Ala Val
                405                 410                 415


His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430


Tyr Asp Arg Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445


Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460


Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480


Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495


Asn Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Val Met Gly Val Leu
            500                 505                 510


Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
        515                 520                 525


Tyr Met Pro
    530


<210>  195
<211>  531
<212>  PRT
<213>  African swine fever virus

<400>  195

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                   10                  15


Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30


Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
```

```
        35                  40                  45

Ile Gln Gln Arg Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Gly Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Ile
        115                 120                 125

Arg Arg Cys Phe Phe Asn Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys His Arg Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Leu Thr His Leu Leu Ile Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Thr Tyr Asp Ile Met
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Glu Tyr His
    210                 215                 220

His Leu Asp Ile Leu Ile Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255
```

```
His Asn Asn Asp Asn Leu Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Phe Ile Pro Gln Leu Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Met Ala Ile Lys Arg Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Thr Leu Ser Ile Glu Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser Gln Tyr Val Val Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Lys Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Met Leu Thr Lys Tyr Val Lys Tyr Ala Ile Phe Asn Lys Tyr Val Val
        355                 360                 365

Arg Cys Met Asp Arg Phe Ser Ile Asn Pro Glu Arg Ile Ile Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Arg Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Ala Arg Leu Lys His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Asp Arg Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Ile Leu Asp Thr Ile Gln Phe Lys Ser Leu Leu Leu
```

```
465                 470                 475                 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495

Asn Ile Val Asn Lys Tyr Ile Gly Asp Leu Phe Ala Met Gly Val Leu
            500                 505                 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
        515                 520                 525

Tyr Met Leu
    530
```

<210> 196
<211> 531
<212> PRT
<213> African swine fever virus

<400> 196

```
Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                   10                  15

Leu Pro Glu Phe Phe Asp Asp Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45

Ile Gln Gln His Thr Leu Ile Pro Ile Asn Glu Ala Leu Arg Thr Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110
```

```
Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Arg Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys Tyr Arg Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Leu Thr His Leu Leu Ile Glu Lys Ala Cys Glu Asn His Asn Tyr
                165                 170                 175

Glu Val Ile Arg Trp Ile Tyr Glu Asn Leu His Ile Tyr Asn Met Ile
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Asn Lys Tyr His
    210                 215                 220

His Ile Asp Ile Leu Ile Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Asn Asp Asn Leu Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Met Val Ala Ile Lys Thr Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser Gln Tyr Val Val Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335
```

```
Ile Gly Ile Leu Ser Met Lys Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Leu Leu Thr Lys Phe Val Lys Asn Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Tyr Met Asp Thr Phe Ser Ile Asn Pro Glu Lys Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Lys Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Ile Trp Lys Asn His Ala Ala Arg Leu Glu His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Glu Tyr Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asn Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495

Asn Ile Val Asn Lys Tyr Ile Asp Asn Leu Phe Ala Met Gly Val Leu
            500                 505                 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
        515                 520                 525

Tyr Met Pro
    530
```

<210> 197
<211> 531
<212> PRT
<213> African swine fever virus

<400> 197

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1 5 10 15

Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
20 25 30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
35 40 45

Ile Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
50 55 60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65 70 75 80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
85 90 95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
100 105 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
115 120 125

Arg Arg Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
130 135 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys Tyr Arg Leu Glu Asn Asp Leu
145 150 155 160

Pro Leu Ala His Leu Leu Ile Lys Lys Ala Cys Glu Asp His Asn Tyr
165 170 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asn Ile Met
180 185 190

```
Asp Thr Phe Gly Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Arg
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
    210                 215                 220

Tyr Leu Asp Val Leu Ile Leu Ser Gly Leu His Leu Leu Tyr Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Asn Asp Asn Leu Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Tyr Ile Pro Gln Leu Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Met Ala Ile Lys Lys Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Lys Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser Gln Tyr Val Ala Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Asn Met Arg Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Lys Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Ile Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Lys Met Leu Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Ala Trp Lys Asn His Ala Ala Arg Leu Lys His Leu Lys His Ala Val
```

405 410 415

Tyr Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Leu Ile
420 425 430

Tyr Asp His Tyr Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
435 440 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
450 455 460

Tyr Asp Cys Cys Leu Leu Asp Thr Ile Arg Phe Lys Asn Leu Leu Leu
465 470 475 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
485 490 495

Thr Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu
500 505 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
515 520 525

Tyr Met Pro
530

<210> 198
<211> 531
<212> PRT
<213> African swine fever virus

<400> 198

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1 5 10 15

Leu Pro Glu Phe Phe Asp Asp Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
20 25 30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
35 40 45

```
Ile Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Gly Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg Tyr
                85                  90                  95

Asn Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Asp Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Ile Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Arg Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys Tyr Thr Leu Glu Asp Asp Leu
145                 150                 155                 160

Pro Leu Val His Leu Leu Ile Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Val Cys His Ile Ile
            180                 185                 190

Asp Thr Phe Asp Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
    210                 215                 220

His Leu Asp Ile Leu Ile Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Ile Asp Asn Leu Asp Val Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270
```

```
Asn His Arg Lys Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Val Ala Ile Lys Thr Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Gln Lys Ile Ser Gln Tyr Val Ala Thr Phe Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Ser Met Lys Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Asn Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Glu Arg Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Lys Met Met Leu Val Lys Lys Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Ala Arg Leu Lys His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Glu His Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asn Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480
```

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
485 490 495

Asn Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu
500 505 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
515 520 525

Tyr Met Pro
530

<210> 199
<211> 531
<212> PRT
<213> African swine fever virus

<400> 199

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1 5 10 15

Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
20 25 30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
35 40 45

Val Gln Gln His Thr Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
50 55 60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65 70 75 80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
85 90 95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
100 105 110

Leu Pro Phe Ile Asp Asn Pro Val Ile Phe His Lys Cys His Ile Met
115 120 125

```
Arg Arg Cys Phe Phe Asp Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys Tyr Arg Leu Glu Asn Asp Leu
145                 150                 155                 160

Pro Leu Ala His Leu Leu Val Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Leu Tyr Glu Asn Leu His Ile Tyr Asn Ile Met
            180                 185                 190

Glu Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Arg
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
    210                 215                 220

Tyr Leu Asp Val Leu Ile Leu Ser Gly Leu His Leu Leu Tyr Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Asn Asp Asn Leu Asp Ile Ile Leu Thr Gln Ala Val Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Tyr Ile Pro Gln Leu Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Met Ala Ile Lys Lys Lys Ser Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Lys Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser Gln Tyr Val Ala Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Gly Ile Leu Asn Met Lys Arg Lys Lys Lys Ile Tyr Leu Asp Ile
```

```
            340                 345                 350

Ile Leu Thr Lys Phe Val Lys Tyr Ala Ile Phe Asn Lys Tyr Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Ile Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Lys Met Leu Leu Val Lys Lys Ile Ser Gln His
385                 390                 395                 400

Ala Trp Lys Asn His Ala Ala Arg Leu Lys His Leu Lys His Ala Val
                405                 410                 415

Tyr Thr Met Lys His Lys Asp Gly Lys Asn Arg Leu Met Asn Leu Ile
            420                 425                 430

Tyr Asp His Tyr Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Leu Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Gly Lys Asn Ala His Asp Ala Thr Asn Ile
                485                 490                 495

Thr Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu
            500                 505                 510

Ser Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His
        515                 520                 525

Tyr Met Pro
    530

<210>  200
<211>  530
<212>  PRT
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<213> African swine fever virus

<400> 200

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Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Arg Lys
1               5                  10                  15


Leu Pro Glu Phe Phe Asp Asp Tyr Val Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30


Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45


Ile Gln Gln His Asn Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60


Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80


Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95


Asn Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110


Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Met Met
        115                 120                 125


Arg Arg Cys Phe Phe Asn Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140


Lys Phe Ser Val Leu Leu Tyr Phe Lys Tyr Ile Leu Lys Glu Asn Leu
145                 150                 155                 160


Pro Leu Val His Ser Leu Ile Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175


Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Glu Ile Met
            180                 185                 190


Asp Thr Phe Lys Cys Ala Ile Ala His Lys Asp Leu His Leu Tyr Ser
        195                 200                 205
```

```
Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
    210                 215                 220

His Leu Asp Ile Arg Ile Leu Ser Arg Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Thr Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Lys Asp Asn Ile Asn Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Asn Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Val Ala Ile Lys Thr Asn Ala Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Val Lys Lys Leu Ser Gln Tyr Val Val Ala Tyr Lys Ser Thr Asn Ile
                325                 330                 335

Ile Ser Ile Leu Ser Met Gln Gln Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Val Val Lys Asn Ala Ile Phe Ile Lys Phe Val Ile
        355                 360                 365

Gly Cys Met Val Thr Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Lys Lys Met Lys Leu Val Lys Asn Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Ala Lys Leu Lys His Leu Lys His Ala Val
                405                 410                 415
```

```
His Thr Met Lys His Gln Glu Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430


Tyr Asp His Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445


Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460


Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480


Asp Cys Ser Tyr Ile Ile Ala Lys Asn Ala His Asp Ala Ser Ile Asn
                485                 490                 495


Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu Ser
            500                 505                 510


Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys Asp Tyr
        515                 520                 525


Met Leu
    530
```

<210> 201
<211> 530
<212> PRT
<213> African swine fever virus

<400> 201

```
Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                   10                  15


Leu Pro Glu Phe Phe Asp Asp Tyr Val Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30


Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45


Ile Gln Gln His Asn Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60
```

```
Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn His His
                85                  90                  95

Asn Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Thr Met
        115                 120                 125

Arg Arg Cys Phe Phe Asn Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Ser Val Leu Leu Tyr Phe Lys Tyr Ile Leu Lys Glu Asn Leu
145                 150                 155                 160

Pro Leu Val His Ser Leu Ile Glu Lys Ala Tyr Lys Tyr His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asp Ile Ile
            180                 185                 190

Asn Thr Phe Lys Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Val Tyr Asn Arg Ile Val Pro Tyr Lys Tyr Tyr
    210                 215                 220

His Leu Asp Ile Arg Ile Leu Leu Arg Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Thr Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Thr Asn Asn Ile Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Asn Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
```

```
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Val Ala Ile Lys Thr Asn Ala Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Val Lys Lys Leu Ser Gln Tyr Val Val Ala Tyr Lys Ser Thr Asn Ile
                325                 330                 335

Ile Ser Ile Leu Ser Arg Gln Gln Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Lys Val Val Lys Asn Ala Val Phe Asn Lys Phe Val Ile
        355                 360                 365

Gly Cys Met Val Thr Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Lys Lys Met Lys Leu Val Lys Asn Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Val Lys Leu Lys Tyr Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Gln Glu Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Asp His Cys Tyr Tyr His Met Gln Glu Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Val Lys Asn Ala His Asp Ala Ser Ile Asn
                485                 490                 495
```

```
Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu Ser
            500                 505                 510


Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys Asp Tyr
        515                 520                 525


Met Leu
    530


<210>  202
<211>  530
<212>  PRT
<213>  African swine fever virus

<400>  202

Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                   10                  15


Leu Pro Glu Phe Phe Asp Asp Tyr Val Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30


Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45


Ile Gln Gln His Asn Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60


Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80


Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg His
                85                  90                  95


Asn Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110


Leu Pro Phe Ile Asp Asp Pro Val Ile Phe His Lys Cys His Ile Met
        115                 120                 125


Arg Arg Cys Phe Phe Asn Cys Met Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140
```

```
Lys Phe Ser Val Leu Leu Tyr Phe Lys Tyr Ile Leu Lys Glu Asn Leu
145                 150                 155                 160

Pro Leu Val His Ser Leu Ile Glu Lys Ala Tyr Lys Tyr His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ile Tyr Asp Ile Ile
            180                 185                 190

Asn Thr Phe Lys Tyr Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Val Tyr Asn Arg Ile Val Pro Tyr Lys Tyr Tyr
    210                 215                 220

His Leu Asp Ile Arg Ile Leu Leu Arg Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Thr Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Thr Asn Asn Ile Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Asn Ile Leu Thr Tyr Phe Ile Pro Gln Ser Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Phe Val Ala Ile Lys Thr Asn Ala Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Val Lys Lys Leu Ser Gln Tyr Val Val Ala Tyr Lys Ser Thr Asn Ile
                325                 330                 335

Ile Ser Ile Leu Ser Met Gln Gln Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350
```

```
Ile Leu Thr Lys Val Val Lys Asn Ala Val Phe Ile Lys Phe Val Ile
        355                 360                 365

Gly Cys Met Val Thr Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Lys Lys Met Lys Leu Val Lys Asn Ile Ser Glu His
385                 390                 395                 400

Val Trp Lys Asn His Ala Ala Lys Leu Lys His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Gln Glu Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430

Tyr Asp His Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Ser Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Ile Leu Asp Thr Ile Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Ser His Ile Ile Ala Lys Asn Ala His Asp Ala Ser Ile Asn
                485                 490                 495

Ile Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu Ser
            500                 505                 510

Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys Tyr Asp
        515                 520                 525

Ile Leu
    530
```

<210> 203
<211> 530
<212> PRT
<213> African swine fever virus

<400> 203

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Met Phe Ser Leu Gln Asn Leu Cys Arg Lys Thr Leu Pro Asp Cys Lys
1               5                  10                  15

Leu Pro Glu Phe Phe Asp Glu Tyr Ile Leu Gln Leu Leu Gly Leu Tyr
            20                  25                  30

Trp Glu Asn His Gly Thr Ile Gln Arg Ala Gly Asn Asn Cys Val Leu
        35                  40                  45

Ile Gln Gln His Asn Leu Ile Pro Val Asn Glu Ala Leu Arg Ile Ala
    50                  55                  60

Ala Ser Glu Glu Asn Tyr Glu Ile Val Ser Leu Leu Leu Ala Trp Glu
65                  70                  75                  80

Gly Asn Leu Tyr Tyr Ala Ile Ile Gly Ala Leu Glu Gly Asn Arg Pro
                85                  90                  95

Asp Leu Ile Arg Lys Tyr Asp Asp Gln Ile Lys Asp His His Glu Ile
            100                 105                 110

Leu Pro Phe Ile Asp Asp Pro Ile Ile Phe His Lys Cys His Ile Met
        115                 120                 125

Arg Arg Cys Phe Phe Asn Cys Ile Leu Tyr Gln Ala Val Lys Tyr Ser
    130                 135                 140

Lys Phe Arg Val Leu Leu Tyr Phe Lys His Arg Leu Gly Asp Asp Leu
145                 150                 155                 160

Pro Leu Thr His Leu Leu Ile Glu Lys Ala Cys Glu Asp His Asn Tyr
                165                 170                 175

Glu Val Ile Lys Trp Ile Tyr Glu Asn Leu His Ser Tyr Asn Ile Met
            180                 185                 190

Asp Thr Phe Glu Cys Ala Ile Ala His Lys Asp Leu Arg Leu Tyr Cys
        195                 200                 205

Leu Gly Tyr Thr Phe Ile Tyr Asn Arg Ile Val Pro Tyr Lys Tyr His
```

```
    210                 215                 220

His Leu Asp Ile Cys Ile Leu Ser Ser Leu Gln Leu Leu His Lys Val
225                 230                 235                 240

Ala Ala Lys Gly Tyr Leu Asp Phe Ile Leu Glu Thr Leu Lys Tyr Asp
                245                 250                 255

His Asn Ile Asn Asn Ile Asp Ile Ile Leu Thr Gln Ala Ala Thr Tyr
            260                 265                 270

Asn His Arg Lys Ile Leu Thr Tyr Phe Ile Pro Gln Leu Thr Tyr Ala
        275                 280                 285

Gln Ile Glu Gln Cys Leu Leu Val Ala Ile Lys Thr Lys Ala Ser Lys
    290                 295                 300

Lys Thr Leu Asn Leu Leu Leu Ser His Leu Asn Leu Ser Ile Lys Leu
305                 310                 315                 320

Ile Lys Lys Ile Ser Gln Tyr Val Val Thr Tyr Asn Ser Thr Asn Ile
                325                 330                 335

Ile Ser Ile Leu Ser Met Arg Arg Lys Lys Lys Ile Tyr Leu Asp Ile
            340                 345                 350

Ile Leu Thr Glu Phe Val Lys Asn Ala Ile Phe Asn Lys Phe Val Val
        355                 360                 365

Arg Cys Met Asp Thr Phe Ser Ile Asn Pro Glu Arg Ile Val Lys Met
    370                 375                 380

Ala Ala Arg Ile Asn Arg Met Met Leu Val Lys Asn Ile Ser Glu Arg
385                 390                 395                 400

Val Trp Lys Asn His Ala Val Lys Leu Lys His Leu Lys His Ala Val
                405                 410                 415

His Thr Met Lys His Gln Glu Gly Lys Asn Arg Leu Met Asn Phe Ile
            420                 425                 430
```

```
Tyr Asp His Cys Tyr Tyr His Met Gln Gly Glu Glu Ile Phe Gly Leu
        435                 440                 445

Ala Arg Phe Tyr Ala Ile His His Ala Pro Lys Leu Phe Asp Val Phe
    450                 455                 460

Tyr Asp Cys Cys Met Leu Asp Ala Thr Arg Phe Lys Ser Leu Leu Leu
465                 470                 475                 480

Asp Cys Pro His Ile Ile Gly Lys Asn Ala Tyr Asp Ala Gly Ile Asn
                485                 490                 495

Leu Val Asn Lys Tyr Ile Gly Asn Leu Phe Ala Met Gly Val Leu Ser
            500                 505                 510

Lys Lys Glu Ile Leu Gln Asp Tyr Pro Ser Ile Tyr Ser Lys His Asp
        515                 520                 525

Met Phe
    530
```

<210> 204
<211> 462
<212> DNA
<213> African swine fever virus

<400> 204
atgtatttta agaaaaaata catcggtctt attgataaga actgtgaaaa aaaaatatta 60

gatgattcta gtacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

atgataactc ttatttataa tttcatattc tgggataatt atataaaatg ttaccgaaat 180

aatgataaaa tgttttactg tcctaatgat tgggttggat ataataatat ttgttactat 240

tttagtaatg gtagtttttc taaaaattat acagctgcta gtaatttttg tagacaatta 300

aatggtacac ttgctaataa tgatactaat ttattaaatc taactaaaat atataataat 360

caatctatgt attgggttaa caatacggta atattacgtg gtgataataa atatagtcaa 420

aaagttaact atacagattt attatttatt tgtggtaaat aa   462

<210> 205
<211> 477

<212> DNA
<213> African swine fever virus

<400> 205
atgttttcta acaaaaagta catcggtctt atcaataaga aggagggttt gaaaaaaaaa 60

atagatgatt atagtatatt aataattgga atattaattg gaactaacat cttaagcctt 120

attataaata taataggaga gattaataaa ccaatatgtt accaaaatga tgataagata 180

ttttattgcc ctaaagattg ggttggatat aataatgttt gttattattt tggcaatgaa 240

gaaaaaaatt ataataatgc aagtaattat tgtaagcaat taaatagtac gcttactaat 300

aataatacta ttttagtaaa tcttactaaa acattaaatc ttactaaaac atataatcac 360

gaatctaatt attgggttaa ttattcttta attaaaaatg agtcagtact attacgtgat 420

agtggatatt acaaaaaaca aaaacatgta agtttattat atatttgtag taaataa 477

<210> 206
<211> 495
<212> DNA
<213> African swine fever virus

<400> 206
atgtattcta agaaaaagta catcggtctt attgacaaga actgtgaaaa aaaaatatta 60

gatgatgcta ctacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

attataactc ttatctataa tttcatattt tgggagaatt atataaaatg tatccaaaat 180

gatgataaga tgttttactg tcctaaagat tgggttgggt ataataatgc gtgttattat 240

tttagtaata acaataaaaa ttatacagat gcaaataatt attgtaaaaa ttcacataat 300

agtacacttg ctaataatga tactaaatta ttaaatctta ctaaattatt aaatctttct 360

aaattatatt acaatgattc tacatattgg gttaaatatt ctttacctaa aaataaagca 420

gtaacattac gtaacagtac ctacaaatat gatagagtta aatctacaga aacatttttt 480

atttgtagta actaa 495

<210> 207
<211> 498
<212> DNA
<213> African swine fever virus

<400> 207
atgtattcta agaaaaagta catcggtctt attgacaaaa gctgtgaaaa aaaaatatta 60

gatgatccta ctacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

attataactc ttatctataa tttcatattt tgggagaatt atataaaatg tatccgaaat 180

gatgataaga tgttttactg ccctaaagat tgggttggat ataataatgt gtgttattat 240

tttagtaacg ataatggaaa aaattatatg aatgcaagta atttttgtaa taaaaaaaat 300

agcacgcttg ctaataatac gactaattta gtaaatctta ctaaaatatt aaattttacc 360

aaacaatata atcatgaatc actttattgg gttaattatt ctttaagtaa taatatgtca 420

ttagcattac agaatagtaa ttttccttct tcaggaagac gtaaatatat ggacttatta 480

tatatatgta gtatataa 498

<210> 208
<211> 462
<212> DNA
<213> African swine fever virus

<400> 208
atgtatttta agaaaaaata catcggtctt attgataaga actgtgaaaa aaaaatatta 60

gatgattcta gtacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

atgataactc ttatttataa tttcatattc tgggataatt atataaaatg ttaccgaaat 180

aatgataaaa tgttttactg tcctaatgat tgggttggat ataataatat ttgttactat 240

tttagtaatg gtagtttttc taaaaattat acagctgcta gtaatttttg tagacaatta 300

aatggtacac ttgctaataa tgatactaat ttattaaatc taactaaaat atataataat 360

caatctatgt attgggttaa caatacggta atattacgtg gtgataataa atatagtcaa 420

aaagttaact atacagattt attatttatt tgtggtaaat aa 462

<210> 209
<211> 477
<212> DNA
<213> African swine fever virus

<400> 209
atgttttcta acaaaaagta catcggtctt atcaataaga aggagggttt gaaaaaaaaa 60

atagatgatt atagtatatt aataattgga atattaattg gaactaacat cttaagcctt 120

attataaata taataggaga gattaataaa ccaatatgtt accaaaatga tgataagata 180

ttttattgcc ctaaagattg ggttggatat aataatgttt gttattattt tggcaatgaa 240

gaaaaaaatt ataataatgc aagtaattat tgtaagcaat taaatagtac gcttactaat 300

aataatacta ttttagtaaa tcttactaaa acattaaatc ttactaaaac atataatcac 360

gaatctaatt attgggttaa ttattcttta attaaaaatg agtcagtact attacgtgat 420

agtggatatt acaaaaaaca aaaacatgta agtttattat atatttgtag taaataa 477

<210> 210
<211> 486
<212> DNA
<213> African swine fever virus

<400> 210
atgttttcta acaaaaagta catcggtctt attgacaagt actgtgaaaa aaaaatatta 60

gatgattcta gtacaataaa aatttgttac atattaattg gaatactgat tggaactaat 120

atgataactc ttatttataa tttcatattt tgggagaatt atataacatg taaccaaaaa 180

gataagacgt tttactgtcc taaagattgg gttggatata ataatgtttg ttattatttt 240

ggcaatgatg aaaaaaatta taataatgca agtaattatt gtaagcaatt aaatagtacg 300

cttactaata ataatactaa tttagtaaat cttactaaaa cattaaatct tactaaaaca 360

tataatcacg aatctaatta ttgggttaat tattctttaa ttaaaaatga gtcagtacta 420

ttacgcaata gtggatatta taaaaaacaa aaacatgtaa gtttattata tatttgtagt 480

aaataa 486

<210> 211
<211> 492
<212> DNA
<213> African swine fever virus

<400> 211
atgttttcta ataaaaagta cattggtctt atcaataaga aggagggatt gaaaaaaaaa 60

atagatgatt atagtatatt aataattgga atattaattg gaactaacat cttaagcctt 120

attataaata taataggaga gattaataaa ccaatatgtt accaaaataa tgataagata 180

ttttattgcc ctaaagattg ggttggatat aataatgttt gttattattt tagtaatgat 240

aatggcaata attatacaac tgcggataat aaatgtaaac aattaaataa tagtacactg 300

gctaataatc ttactgattt attaaatctt acgagtttct taaatcttac taaattatat 360

catcatcatt ctcattattg ggttaattat tctttaaata ataattattc agtaccatta 420

attgatagta aatataattt aaataggaaa aaaagtcact atacagattt actatttatt 480

tgcagcaaat aa 492

<210> 212
<211> 465
<212> DNA
<213> African swine fever virus

<400> 212
atgtatttta agaaaaaata catcggtctt attgataaga actgtgaaaa aaaaatatta 60

gatgattcta gtacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

atgataactc ttatttataa tttcatattc tgggataatt atataaaatg ttaccgaaat 180

aatgataaaa tgttttactg tcctaatgat tgggttggat ataataatgt ttgttactat 240

tttagtaatg gtagtttttt taaaaattat acagatgcta ataattattg taaaaaaata 300

aatagtactc ttgctaataa tgatactaat ttattaagtt taactaaaat atacaataat 360

caatctatgt attgggttaa caatacagta gcattacgtg gtgatagtgt atatgcacaa 420

agaaaagtta ataattcaga tctattattt atttgtagta aataa 465

<210> 213
<211> 465
<212> DNA
<213> African swine fever virus

<400> 213
atgtatttta agaaaaagta catcggtctt attgataaga actgtgaaaa aaaaatatta 60

gatgattgta ctacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

atgataactc ttatttataa tttcatattt tgggatcatt atatgacatg taacaaaaaa 180

gataagatgt tttactgtcc taaagattgg gttggatata ataatgtttg ttattatttt 240

agtaatgata gttttactaa gaattataca tatgcaagta attcttgtaa aaaaataaat 300

agtacacttg ctaataatga tactaattta ctaaatctta ttaaagtata taataatgta 360

tctgagtatt gggttaataa tacagtaaca ttacgtggtg atcataaata cataaataag 420

caaaataatt gtaatacaga atttttattt atttgtagta gatag 465

<210> 214
<211> 471
<212> DNA

<213> African swine fever virus

<400> 214
atgttttcta acaaaaagta tccgagtctt atcgaaaaaa aaatggatga cttgatgact 60

ttaaagtttt gttacatcat tattgcaatc ttgatcatga ctaatatttt tagccttgtt 120

gtgaatatat gggggggggg tgatcgacaa tcttatgaga atgtatttta ttgtcctaaa 180

gattgggttg gatataataa tgcatgttat tattttagta atgatatgaa aaattataca 240

gaagcaagta attattgtaa aaatttatat aatagtacaa ttgttaataa taatactaat 300

atagtaaatc ttactaaaac attaaatctt actaaaatat ataatcatga aagtaattat 360

tgggttaatt attctttaat taataatgag tcattaacat tacgggacag taattttcct 420

tcttcaggaa aacgtacata tatagattta ttatatatat gtagtatata a 471

<210> 215
<211> 468
<212> DNA
<213> African swine fever virus

<400> 215
atgtatttta agaaaaagta catcggtctt attgataaga actgtgaaaa aaaaatatta 60

gatgattgta ctacaataaa aatttgttac atattaattg gaatattgat tggaactaat 120

atgataactc ttatttataa tttcatattt tgggatcatt atatgacatg taacaaaaaa 180

gataagatgt tttactgtcc taaagattgg gttggatata ataatgtttg ttattatttt 240

aataatgata gtaagaatta tacaactgct actaattctt gtaaacaatt aaatagtaca 300

cttgctaata atgatactaa tttattaaat cttactaaag tatatcacca tgataaatta 360

tattgggtta actattcttt aaatgacaat ttttcattat cattacgtaa tagtacatat 420

gaaaaaagat ctaaatattt gccattatta tttatttgca gtaaataa 468

<210> 216
<211> 477
<212> DNA
<213> African swine fever virus

<400> 216
atgtttttga acaaaaagta tccgagtctt atcgaaaaaa aaatggatga tttgatgact 60

ttaaagtttt gttacttaat aatcacattt ttaatcataa ccaatatttt tagccttgct 120

ataaatatat gggggggggg tgatatgata gatcgacaaa gttgtgaaaa tatattttac 180

tgtcctaaag attgggttgg ctataataat gcgtgttatt attttagtaa taacaataaa 240

aattatacag atgcaaataa ttattgtaaa aattcacata atagtacact tgctaataat 300

gatactaaat tattaaatct tactaaatta ttaaatcttt ctaaattata ttacaatgat 360

tctacatatt gggttaaata ttctttacct aaaaataaag cagtaacatt acgtaacagt 420

acctacaaat atgatagagt taaatataca gaaacatttt ttatttgtag taactaa 477

<210> 217
<211> 158
<212> PRT
<213> African swine fever virus

<400> 217

Met Phe Ser Asn Lys Lys Tyr Ile Gly Leu Ile Asn Lys Lys Glu Gly
1 5 10 15

Leu Lys Lys Lys Ile Asp Asp Tyr Ser Ile Leu Ile Ile Gly Ile Leu
20 25 30

Ile Gly Thr Asn Ile Leu Ser Leu Ile Ile Asn Ile Ile Gly Glu Ile
35 40 45

Asn Lys Pro Ile Cys Tyr Gln Asn Asp Asp Lys Ile Phe Tyr Cys Pro
50 55 60

Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe Gly Asn Glu
65 70 75 80

Glu Lys Asn Tyr Asn Asn Ala Ser Asn Tyr Cys Lys Gln Leu Asn Ser
85 90 95

Thr Leu Thr Asn Asn Asn Thr Ile Leu Val Asn Leu Thr Lys Thr Leu
100 105 110

Asn Leu Thr Lys Thr Tyr Asn His Glu Ser Asn Tyr Trp Val Asn Tyr
115 120 125

Ser Leu Ile Lys Asn Glu Ser Val Leu Leu Arg Asp Ser Gly Tyr Tyr
130 135 140

```
Lys Lys Gln Lys His Val Ser Leu Leu Tyr Ile Cys Ser Lys
145                 150                 155


<210>  218
<211>  164
<212>  PRT
<213>  African swine fever virus

<400>  218

Met Tyr Ser Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1               5                   10                  15


Lys Lys Ile Leu Asp Asp Ala Thr Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30


Ile Gly Ile Leu Ile Gly Thr Asn Ile Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45


Ile Phe Trp Glu Asn Tyr Ile Lys Cys Ile Gln Asn Asp Asp Lys Met
    50                  55                  60


Phe Tyr Cys Pro Lys Asp Trp Val Gly Tyr Asn Asn Ala Cys Tyr Tyr
65                  70                  75                  80


Phe Ser Asn Asn Asn Lys Asn Tyr Thr Asp Ala Asn Asn Tyr Cys Lys
                85                  90                  95


Asn Ser His Asn Ser Thr Leu Ala Asn Asn Asp Thr Lys Leu Leu Asn
            100                 105                 110


Leu Thr Lys Leu Leu Asn Leu Ser Lys Leu Tyr Tyr Asn Asp Ser Thr
        115                 120                 125


Tyr Trp Val Lys Tyr Ser Leu Pro Lys Asn Lys Ala Val Thr Leu Arg
    130                 135                 140


Asn Ser Thr Tyr Lys Tyr Asp Arg Val Lys Ser Thr Glu Thr Phe Phe
145                 150                 155                 160


Ile Cys Ser Asn
```

<210> 219
<211> 165
<212> PRT
<213> African swine fever virus

<400> 219

Met Tyr Ser Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Ser Cys Glu
1   5   10   15

Lys Lys Ile Leu Asp Asp Pro Thr Thr Ile Lys Ile Cys Tyr Ile Leu
            20   25   30

Ile Gly Ile Leu Ile Gly Thr Asn Ile Ile Thr Leu Ile Tyr Asn Phe
        35   40   45

Ile Phe Trp Glu Asn Tyr Ile Lys Cys Ile Arg Asn Asp Asp Lys Met
    50   55   60

Phe Tyr Cys Pro Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr
65   70   75   80

Phe Ser Asn Asp Asn Gly Lys Asn Tyr Met Asn Ala Ser Asn Phe Cys
                85   90   95

Asn Lys Lys Asn Ser Thr Leu Ala Asn Asn Thr Thr Asn Leu Val Asn
            100   105   110

Leu Thr Lys Ile Leu Asn Phe Thr Lys Gln Tyr Asn His Glu Ser Leu
        115   120   125

Tyr Trp Val Asn Tyr Ser Leu Ser Asn Asn Met Ser Leu Ala Leu Gln
    130   135   140

Asn Ser Asn Phe Pro Ser Ser Gly Arg Arg Lys Tyr Met Asp Leu Leu
145   150   155   160

Tyr Ile Cys Ser Ile
                165

<210> 220

<211> 153
<212> PRT
<213> African swine fever virus

<400> 220

Met Tyr Phe Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1 5 10 15

Lys Lys Ile Leu Asp Asp Ser Ser Thr Ile Lys Ile Cys Tyr Ile Leu
20 25 30

Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
35 40 45

Ile Phe Trp Asp Asn Tyr Ile Lys Cys Tyr Arg Asn Asn Asp Lys Met
50 55 60

Phe Tyr Cys Pro Asn Asp Trp Val Gly Tyr Asn Asn Ile Cys Tyr Tyr
65 70 75 80

Phe Ser Asn Gly Ser Phe Ser Lys Asn Tyr Thr Ala Ala Ser Asn Phe
85 90 95

Cys Arg Gln Leu Asn Gly Thr Leu Ala Asn Asn Asp Thr Asn Leu Leu
100 105 110

Asn Leu Thr Lys Ile Tyr Asn Asn Gln Ser Met Tyr Trp Val Asn Asn
115 120 125

Thr Val Ile Leu Arg Gly Asp Asn Lys Tyr Ser Gln Lys Val Asn Tyr
130 135 140

Thr Asp Leu Leu Phe Ile Cys Gly Lys
145 150

<210> 221
<211> 158
<212> PRT
<213> African swine fever virus

<400> 221

Met Phe Ser Asn Lys Lys Tyr Ile Gly Leu Ile Asn Lys Lys Glu Gly

```
1               5                   10                  15

Leu Lys Lys Lys Ile Asp Asp Tyr Ser Ile Leu Ile Ile Gly Ile Leu
            20                  25                  30

Ile Gly Thr Asn Ile Leu Ser Leu Ile Ile Asn Ile Ile Gly Glu Ile
        35                  40                  45

Asn Lys Pro Ile Cys Tyr Gln Asn Asp Asp Lys Ile Phe Tyr Cys Pro
    50                  55                  60

Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe Gly Asn Glu
65                  70                  75                  80

Glu Lys Asn Tyr Asn Asn Ala Ser Asn Tyr Cys Lys Gln Leu Asn Ser
                85                  90                  95

Thr Leu Thr Asn Asn Asn Thr Ile Leu Val Asn Leu Thr Lys Thr Leu
            100                 105                 110

Asn Leu Thr Lys Thr Tyr Asn His Glu Ser Asn Tyr Trp Val Asn Tyr
        115                 120                 125

Ser Leu Ile Lys Asn Glu Ser Val Leu Leu Arg Asp Ser Gly Tyr Tyr
    130                 135                 140

Lys Lys Gln Lys His Val Ser Leu Leu Tyr Ile Cys Ser Lys
145                 150                 155


<210>  222
<211>  161
<212>  PRT
<213>  African swine fever virus

<400>  222

Met Phe Ser Asn Lys Lys Tyr Ile Gly Leu Ile Asp Lys Tyr Cys Glu
1               5                   10                  15

Lys Lys Ile Leu Asp Asp Ser Ser Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30
```

```
Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45


Ile Phe Trp Glu Asn Tyr Ile Thr Cys Asn Gln Lys Asp Lys Thr Phe
    50                  55                  60


Tyr Cys Pro Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe
65                  70                  75                  80


Gly Asn Asp Glu Lys Asn Tyr Asn Asn Ala Ser Asn Tyr Cys Lys Gln
                85                  90                  95


Leu Asn Ser Thr Leu Thr Asn Asn Asn Thr Asn Leu Val Asn Leu Thr
            100                 105                 110


Lys Thr Leu Asn Leu Thr Lys Thr Tyr Asn His Glu Ser Asn Tyr Trp
        115                 120                 125


Val Asn Tyr Ser Leu Ile Lys Asn Glu Ser Val Leu Leu Arg Asn Ser
    130                 135                 140


Gly Tyr Tyr Lys Lys Gln Lys His Val Ser Leu Leu Tyr Ile Cys Ser
145                 150                 155                 160


Lys
```

<210> 223
<211> 163
<212> PRT
<213> African swine fever virus

<400> 223

```
Met Phe Ser Asn Lys Lys Tyr Ile Gly Leu Ile Asn Lys Lys Glu Gly
1               5                   10                  15


Leu Lys Lys Lys Ile Asp Asp Tyr Ser Ile Leu Ile Ile Gly Ile Leu
            20                  25                  30


Ile Gly Thr Asn Ile Leu Ser Leu Ile Ile Asn Ile Ile Gly Glu Ile
        35                  40                  45
```

```
Asn Lys Pro Ile Cys Tyr Gln Asn Asn Asp Lys Ile Phe Tyr Cys Pro
    50                  55                  60

Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe Ser Asn Asp
65                  70                  75                  80

Asn Gly Asn Asn Tyr Thr Thr Ala Asp Asn Lys Cys Lys Gln Leu Asn
                85                  90                  95

Asn Ser Thr Leu Ala Asn Asn Leu Thr Asp Leu Leu Asn Leu Thr Ser
            100                 105                 110

Phe Leu Asn Leu Thr Lys Leu Tyr His His His Ser His Tyr Trp Val
        115                 120                 125

Asn Tyr Ser Leu Asn Asn Asn Tyr Ser Val Pro Leu Ile Asp Ser Lys
    130                 135                 140

Tyr Asn Leu Asn Arg Lys Lys Ser His Tyr Thr Asp Leu Leu Phe Ile
145                 150                 155                 160

Cys Ser Lys
```

<210> 224
<211> 154
<212> PRT
<213> African swine fever virus

<400> 224

```
Met Tyr Phe Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1               5                   10                  15

Lys Lys Ile Leu Asp Asp Ser Ser Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30

Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45

Ile Phe Trp Asp Asn Tyr Ile Lys Cys Tyr Arg Asn Asn Asp Lys Met
    50                  55                  60
```

```
Phe Tyr Cys Pro Asn Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr
65                  70                  75                  80


Phe Ser Asn Gly Ser Phe Phe Lys Asn Tyr Thr Asp Ala Asn Asn Tyr
                85                  90                  95


Cys Lys Lys Ile Asn Ser Thr Leu Ala Asn Asn Asp Thr Asn Leu Leu
            100                 105                 110


Ser Leu Thr Lys Ile Tyr Asn Asn Gln Ser Met Tyr Trp Val Asn Asn
        115                 120                 125


Thr Val Ala Leu Arg Gly Asp Ser Val Tyr Ala Gln Arg Lys Val Asn
    130                 135                 140


Asn Ser Asp Leu Leu Phe Ile Cys Ser Lys
145                 150
```

<210> 225
<211> 154
<212> PRT
<213> African swine fever virus

<400> 225

```
Met Tyr Phe Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1               5                   10                  15


Lys Lys Ile Leu Asp Asp Cys Thr Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30


Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45


Ile Phe Trp Asp His Tyr Met Thr Cys Asn Lys Lys Asp Lys Met Phe
    50                  55                  60


Tyr Cys Pro Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe
65                  70                  75                  80


Ser Asn Asp Ser Phe Thr Lys Asn Tyr Thr Tyr Ala Ser Asn Ser Cys
```

```
                85                  90                  95

Lys Lys Ile Asn Ser Thr Leu Ala Asn Asn Asp Thr Asn Leu Leu Asn
            100                 105                 110

Leu Ile Lys Val Tyr Asn Asn Val Ser Glu Tyr Trp Val Asn Asn Thr
        115                 120                 125

Val Thr Leu Arg Gly Asp His Lys Tyr Ile Asn Lys Gln Asn Asn Cys
    130                 135                 140

Asn Thr Glu Phe Leu Phe Ile Cys Ser Arg
145                 150
```

<210> 226
<211> 156
<212> PRT
<213> African swine fever virus

<400> 226

```
Met Phe Ser Asn Lys Lys Tyr Pro Ser Leu Ile Glu Lys Lys Met Asp
1               5                   10                  15

Asp Leu Met Thr Leu Lys Phe Cys Tyr Ile Ile Ile Ala Ile Leu Ile
            20                  25                  30

Met Thr Asn Ile Phe Ser Leu Val Val Asn Ile Trp Gly Gly Gly Asp
        35                  40                  45

Arg Gln Ser Tyr Glu Asn Val Phe Tyr Cys Pro Lys Asp Trp Val Gly
    50                  55                  60

Tyr Asn Asn Ala Cys Tyr Tyr Phe Ser Asn Asp Met Lys Asn Tyr Thr
65                  70                  75                  80

Glu Ala Ser Asn Tyr Cys Lys Asn Leu Tyr Asn Ser Thr Ile Val Asn
                85                  90                  95

Asn Asn Thr Asn Ile Val Asn Leu Thr Lys Thr Leu Asn Leu Thr Lys
            100                 105                 110
```

```
Ile Tyr Asn His Glu Ser Asn Tyr Trp Val Asn Tyr Ser Leu Ile Asn
        115                 120                 125


Asn Glu Ser Leu Thr Leu Arg Asp Ser Asn Phe Pro Ser Ser Gly Lys
    130                 135                 140


Arg Thr Tyr Ile Asp Leu Leu Tyr Ile Cys Ser Ile
145                 150                 155


<210>  227
<211>  155
<212>  PRT
<213>  African swine fever virus

<400>  227

Met Tyr Phe Lys Lys Lys Tyr Ile Gly Leu Ile Asp Lys Asn Cys Glu
1               5                   10                  15


Lys Lys Ile Leu Asp Asp Cys Thr Thr Ile Lys Ile Cys Tyr Ile Leu
            20                  25                  30


Ile Gly Ile Leu Ile Gly Thr Asn Met Ile Thr Leu Ile Tyr Asn Phe
        35                  40                  45


Ile Phe Trp Asp His Tyr Met Thr Cys Asn Lys Lys Asp Lys Met Phe
    50                  55                  60


Tyr Cys Pro Lys Asp Trp Val Gly Tyr Asn Asn Val Cys Tyr Tyr Phe
65                  70                  75                  80


Asn Asn Asp Ser Lys Asn Tyr Thr Thr Ala Thr Asn Ser Cys Lys Gln
                85                  90                  95


Leu Asn Ser Thr Leu Ala Asn Asn Asp Thr Asn Leu Leu Asn Leu Thr
            100                 105                 110


Lys Val Tyr His His Asp Lys Leu Tyr Trp Val Asn Tyr Ser Leu Asn
        115                 120                 125


Asp Asn Phe Ser Leu Ser Leu Arg Asn Ser Thr Tyr Glu Lys Arg Ser
    130                 135                 140
```

```
Lys Tyr Leu Pro Leu Leu Phe Ile Cys Ser Lys
145                 150                 155


<210>  228
<211>  158
<212>  PRT
<213>  African swine fever virus

<400>  228

Met Phe Leu Asn Lys Lys Tyr Pro Ser Leu Ile Glu Lys Lys Met Asp
1               5                   10                  15


Asp Leu Met Thr Leu Lys Phe Cys Tyr Leu Ile Ile Thr Phe Leu Ile
            20                  25                  30


Ile Thr Asn Ile Phe Ser Leu Ala Ile Asn Ile Trp Gly Gly Gly Asp
        35                  40                  45


Met Ile Asp Arg Gln Ser Cys Glu Asn Ile Phe Tyr Cys Pro Lys Asp
    50                  55                  60


Trp Val Gly Tyr Asn Asn Ala Cys Tyr Tyr Phe Ser Asn Asn Asn Lys
65                  70                  75                  80


Asn Tyr Thr Asp Ala Asn Asn Tyr Cys Lys Asn Ser His Asn Ser Thr
                85                  90                  95


Leu Ala Asn Asn Asp Thr Lys Leu Leu Asn Leu Thr Lys Leu Leu Asn
            100                 105                 110


Leu Ser Lys Leu Tyr Tyr Asn Asp Ser Thr Tyr Trp Val Lys Tyr Ser
        115                 120                 125


Leu Pro Lys Asn Lys Ala Val Thr Leu Arg Asn Ser Thr Tyr Lys Tyr
    130                 135                 140


Asp Arg Val Lys Tyr Thr Glu Thr Phe Phe Ile Cys Ser Asn
145                 150                 155


<210>  229
<211>  1083
```

<212> DNA
<213> African swine fever virus

<400> 229
atgataatac ttatttttt aatattttct aacatagttt taagtattga ttattgggtt 60

agttttaata aaacaataat tttagatagt aatattacta atgataataa tgatataaat 120

ggagtatcat ggaatttttt taataattct tttaatacac tagctacatg tggaaaagca 180

ggtaactttt gtgaatgttc taattatagt acatcaatat ataatataac aaataattgt 240

agcttaacta tttttcctca taatgatgta tttgatacaa catatcaagt agtatggaat 300

caaataatta attatacaat aaaattatta acacctgcta ctcccccaaa tatcacatat 360

aattgtacta atttttaat aacatgtaaa aaaaataatg gaacaaacac taatatatat 420

ttaaatataa atgatacttt tgttaaatat actaatgaaa gtatacttga atataactgg 480

aataatagta acattaacaa ttttacagct acatgtataa ttaataatac aattagtaca 540

tctaatgaaa caacacttat aaattgtact tatttaacat tgtcatctaa ctatttttat 600

actttttta aattatatta tattccatta agcatcataa ttgggataac aataagtatt 660

cttcttatat ccatcataac ttttttatct ttacgaaaaa gaaaaaaaca tgttgaagaa 720

atagaaagtc caccacctga atctaatgaa gaagaacaat gtcagcatga tgacaccact 780

tccatacatg aaccatctcc cagagaacca ttacttccta agccttacag tcgttatcag 840

tataatacac ctatttacta catgcgtccc tcaacacaac cactcaaccc atttccctta 900

cctaaaccgt gtcctccacc caaaccatgt ccgccaccca aaccatgtcc tccacctaaa 960

ccatgtcctt cagctgaatc ctattctcca cccaaaccac tacctagtat cccgctacta 1020

cccaatatcc cgccattatc tacccaaaat atttcgctta ttcacgtaga tagaattatt 1080

taa 1083

<210> 230
<211> 1083
<212> DNA
<213> African swine fever virus

<400> 230
atgataatac ttatttttt aatattttct aacatagttt taagtattga ttattgggtt 60

agttttaata aaacaataat tttagatagt aatattacta atgataataa tgatataaat 120

ggagtatcat ggaatttttt taataattct tttaatacac tagctacatg tggaaaagca 180

ggtaactttt gtgaatgttc taattatagt acatcaatat ataatataac aaataattgt 240

agcttaacta tttttcctca taatgatgta tttgatacaa catatcaagt agtatggaat 300

caaataatta attatacaat aaaattatta acacctgcta ctcccccaaa tatcacatat 360

aattgtacta atttttaat aacatgtaaa aaaaataatg gaacaaacac taatatatat 420

ttaaatataa atgatacttt tgttaaatat actaatgaaa gtatacttga atataactgg 480

aataatagta acattaacaa ttttacagct acatgtataa ttaataatac aattagtaca 540

tctaatgaaa caacacttat aaattgtact tatttaacat tgtcatctaa ctatttttat 600

actttttta aattatatta tattccatta agcatcataa ttgggataac aataagtatt 660

cttcttatat ccatcataac ttttttatct ttacgaaaaa gaaaaaaaca tgttgaagaa 720

atagaaagtc caccacctga atctaatgaa gaagaacaat gtcagcatga tgacaccact 780

tccatacatg aaccatctcc cagagaacca ttacttccta agccttacag tcgttatcag 840

tataatacac ctatttacta catgcgtccc tcaacacaac cactcaaccc atttccctta 900

cctaaaccgt gtcctccacc caaaccatgt ccgccaccca aaccatgtcc tccacctaaa 960

ccatgtcctt cagctgaatc ctattctcca cccaaaccac tacctagtat cccgctacta 1020

cccaatatcc cgccattatc tacccaaaat atttcgctta ttcacgtaga tagaattatt 1080

taa 1083

<210> 231
<211> 1170
<212> DNA
<213> African swine fever virus

<400> 231
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agtggtctat tttggaatac atattataat aataatcgta gtgaacttac taagtgcgga 180

atatataata attattgttc atgtgatagt cttaatacat cattgtataa tataaataat 240

tgtagtttag ttatttttcc aaataataca aaaatattta atacaatata tgaattaata 300

tattcaggta atcaaactaa ttatacaata aaattgctag aatctactac tcctccaaat 360

attacatata attgtactac atctgtaata acatgtaaaa aaaataatgg gacaaatact 420

aatatatttt taactataaa taatacgatt gttaattcta ctaatgaaga tgttatttac 480

tactattgga atagaagtga atttaataac tttacagcta catgtatgat taataataca 540

attaattcat caaatatatc agaaattata gactgtacta atacattatt attaaacagt 600

tatttagact tttttcaagt agccggttat atgttttata tgataatttt tattgtaact 660

ggaataacag taagtatttt tatttcaatc ataacttttt tatctttacg aaaaagaaaa 720

aaacatgttg aagaaataga aagtctacca cctgaatcta atgaagaaga atgtcagcat 780

gatgatgaca ccacttccat acatgaacca tcccccagag aaccattact tcctaaacct 840

tacagtcgtt atcagtataa tacacctatt tactacatgc gtccctcaac acaaccactc 900

aacccatttc ccctacctaa accatgccca ccacctaaac cgtgtccgcc acccaaacca 960

tgtcctccac ccaaaccatg cccgccaccc aaaccatgcc cgccacctaa accatgtcct 1020

ccacctgaat catgttcttc acctgaatca tgttcttcac ctgaatcata ttctccaccc 1080

aaaccactac ctagtatccc gctgctaccc aatatcccgc cattatctac acaaaatatt 1140

tcgcttattc atgtagatag aattatttaa 1170

<210> 232
<211> 1221
<212> DNA
<213> African swine fever virus

<400> 232
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aatgaattag gtatattttg gaattcttat aataatactt attataataa tacatttaat 180

aatattgcta tatgtggaaa aaaaggtatt ttttgtgaat gtaatattaa ttataataca 240

tctatatcta atacatctat atctaataca tcaatatata atgtaacaaa taattgtagt 300

ttaacgattt ttctttatga tgataatata tttaaaacat atcaattagt atatcagaat 360

tacaaaatta attatacaat aaacttatta ttacctgtta cttctccaaa tattacatat 420

aattgtacta actctttaat aacatgtgaa aaaaatgatg ggacaaacac taatatgttt 480

ttatctataa ataatataac cattaatcat actaatcaag atattcttac ttactattgg 540

aataatagtg agtttaataa ttttacagct acatgtatga ttaataatac acttaattca 600

gcaaatacca caaaagttat caattgcact aatccattat taaattctta ccaaaattat 660

tttcttgaaa atattcatac attatttttat atcataattt ttattgtgag tggattaata 720

gcaagtattt ttatttcaat tataactttt ttatctttac gaaaaagaaa aaaacatgtt 780

gaagaaatag aaagtccacc acctgaatct aatgaagaag aacaatgtca gcatgatgac 840

accacttcca tacatgaacc atctcccaga gaaccattac ttcctaaacc ttacagtcgt 900

tatcaatata atacacctat ttactacatg cgtccctcaa cacaaccact caacccattt 960

cccctaccta acccatgtcc tccacctaaa ccgtgtcctc cacccaaacc atgcccgcca 1020

cctaaaccat gtcccccacc caaaccatgc ccgccaccta aaccgtgtcc tccacccaaa 1080

ccatgtccac cacctaaacc atgttcttca cctgaatcat attctccacc caaaccacta 1140

cctagtatcc cgctactacc caatatccca ccattatcta cacaaaatat ttcacttatt 1200

catgtagata gaattattta a 1221

<210> 233
<211> 1122
<212> DNA
<213> African swine fever virus

<400> 233
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ggtggtctat tttggaatac atattatgat aataatcgta gtaattttac ttattgtgga 180

atagcaggaa attattgttc atgttgtggt cataacatat cattgtataa tacaacaaat 240

aattgtagtt taattatttt tcctaacaat acagaaatat ttaatagaac atatgaatta 300

gtatatttgg acaaaaaaat taattataca gtaaaactat taaaatctgt tgattcccca 360

actattacat ataattgtac taattcttta ataacatgta aaaataataa tgggacaaat 420

gttaatatat atttaattat taataataca attagttcat tgaatgaaac agaaaatata 480

aattgtacta atccaatatt aaaatatcaa aattatttat ccacattatt ttatatcata 540

atttttattg tgagtggatt aataataggt atttttattt caatcatatc tgtattatct 600

atacgaagaa aaagaaaaaa acatgttgaa gaaatagaaa gtccaccacc ctctgaatct 660

aatgaagaag atatttctca cgatgacacc acttccatac atgaaccatc tcccagagaa 720

ccattacttc ctaagcctta cagtcgttat cagtataata cacctattta ctacatgcgt 780

ccctcaacac aaccactcaa cccatttccc ctacctaaac catgcccgcc acctaaacca 840

tgtcctccac ccaagccatg cccgccaccc aaaccatgtc ctccacctaa accgtgttct 900

ccacccaaac cgtgtcgtcc acctaaacca tgtcctccac ctaaaccatg tcctccacct 960

aaaccatgtc ctccacctaa accatgtcct ccatccaaac catgtccttc acctgaatcc 1020

tattctccac ccaaaccact acctagtatc ccgttactac ccaatatccc gccattatct 1080

acacaaaata tttcgcttat tcatgtagat agaattattt aa 1122

<210> 234
<211> 1209
<212> DNA
<213> African swine fever virus

<400> 234
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tggagtactt taaatcaaac tgtattttta aataatattt ttacaattaa tgatacatat 120

ggtggtctat tttggaatac atattatgat aataatcgta gtaattttac ttattgtgga 180

atagcaggaa attattgttc atgttgtggt cataacatat cattgtataa tacaacaaat 240

aattgtagtt taattatttt tcctaacaat acagaaatat ttaatagaac atatgaatta 300

gtatatttgg acaaaaaaat taattataca gtaaaactat taaaatctgt tgattcccca 360

actattacat ataattgtac taattcttta ataacatgta aaaataataa tgggacaaat 420

gttaatatat atttaattat taacaataca attgttaatg atactaatgg agatatcctt 480

aattattatt ggaatggtaa taataatttt acagctacat gtatgattaa taatacaatt 540

agttcattga atgaaacaga aaatataaat tgtactaatc caatattaaa atatcaaaat 600

tatttatcca cattatttta tatcataatt tttattgtga gtggattaat aataggtatt 660

tttatttcaa tcatatctgt attatctata cgaagaaaaa gaaaaaaaca tgttgaagaa 720

atagaaagtc caccaccctc tgaatctaat gaagaagata tttctcacga tgacaccact 780

tccatacatg aaccatctcc cagagaacca ttacttccta agccttacag tcgttatcag 840

tataatacac ctatttacta catgcgtccc tcaacacaac cactcaaccc atttccccta 900

cctaaaccat gcccgccacc taaaccatgt cctccaccca agccatgccc gccacccaaa 960

ccatgtcctc cacctaaacc gtgttctcca cccaaaccgt gtcgtccacc taaaccatgt 1020

cctccaccta aaccatgtcc tccacctaaa ccatgtcctc cacctaaacc atgtcctcca 1080

tccaaaccat gtccttcacc tgaatcctat tctccaccca aaccactacc tagtatcccg 1140

ttactaccca atatcccgcc attatctaca caaaatattt cgcttattca tgtagataga 1200

attatttaa 1209

<210> 235
<211> 1149
<212> DNA
<213> African swine fever virus

<400> 235
atgataataa aggttatttt tttagttttc tttaaaatgg ttttaagtaa tattataata 60

tggagtactt taaataacac aatatattta aatattaatt attcagatag taatttatat 120

actggtctat tttggaataa atattataat aatactcgta ataattttac tacttgtgta 180

acatcaaata gtagctattg tacatgtaaa ggccataaca catcattgta taatataaca 240

aataattgta gtttaatcat ttttccaaat aatacaaaaa tatttaatac aacatatgaa 300

ttagtatatt taaataataa aattaattat acaatacaaa tggtacaacc tgttgatcct 360

ccaattatta tatataatga tactaataat tctttaataa catgtgaaaa aaataatgga 420

acgaatactg aaatctattt atatttaaat gatacattta ttaataatac taatgaaaat 480

agtattaaat actattggaa ttgtagcgaa ttaaaccata atattacaac tacatgtatt 540

attaataata cacttaattc ggcaaatacc acaaaagtta taaattgcac taatctattg 600

ttaaaatctg accaaaatta ttttcttaaa aatattcata cattatttta tatcataatt 660

tttattgtgg gtggaacatt aataagcatt attatatcaa tcataacttt tttatcttta 720

cgaaaaagaa aaaaacatgt tgaagaaata gaaagtccac caccctctga atctaatgaa 780

gaagaacatt gtcagcatga tgataccact tccatacatg aaccatctcc cagagaacca 840

ttacttccta agccttacag tcgttatcag tataatacac ctatttacta catgcgtccc 900

tcaacacaac cactcaaccc atttccccta cctaaaccat gtcctccacc taaaccgtgt 960

cctccaccca aaccatgtcc tccacctaaa ccgtgtcctc cacctaaacc gtgtccccca 1020

cctaaaccat gtccttcacc tgaatcccat tctccaccca aaccactacc tagtatcccg 1080

ctgctaccca atattccccc attatctaca caaaatattt cgcttattca tgtagataga 1140

attatttaa 1149

<210> 236
<211> 1128
<212> DNA
<213> African swine fever virus

<400> 236
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aatggagtat catggaattt ccttaataat tctcttaata cactagctac atgtggaaaa 180

gcaggtaact tttgtgaatg ctctaattat agtacatcac tatataatat agcacataat 240

tgtagcttaa ctattttccc tcataatgat gtatttggta caccatatca agtagtatgg 300

aatcaaataa ttaattatac aataaaatta ttaacacctg ttactccccc aaatattaca 360

tataattgta ctaatttttt aataacatgt aaaaaaaata atggaacaaa tactattata 420

tatttcaata taaatgatac taatgttaaa tatactaatg aaagtatact tgaatataac 480

tggaataata gtaactttaa caattttaca gctacatgta taattaataa tacaattaat 540

tcatcaaatg atacacaaac tatagactgc atcaatacat tattaagcag ttatttagac 600

ttttttcaag tagccagtta tatgttttat atgataattt ttattgcaac tggaataata 660

gcaagtattt ttatatcaat cataactttt ttatctttac gaaaaagaaa aaaacatgtt 720

gaagaaatag aaagtccatc gccatctgaa tctaatgaag aagaacaatg tcagcatgat 780

gacaccactt ccatacatga accgtctccc agagaaccat tacttcctaa gccttacagt 840

cgatatcagt ataatacacc tatttactat atgcgtccct taacacaacc actcaatcca 900

tctcccctac ccaaactgtg tcctccaccc aaaccgtgtc ctccacccaa accgtgtcct 960

ccacccaaac cgtgtcctcc acccaaaccg tgtccttcat ctgaatcatg ttctccacct 1020

gaatcatatt ctctacccaa accactacct aatatcccgc tactacccaa tatcccgcca 1080

ttatctacac aaaatatctc gcttattcac gtagatagaa ttatttaa 1128

<210> 237
<211> 1158
<212> DNA
<213> African swine fever virus

<400> 237
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actactaata atcctacatt aaatggtata ttttggaata tttataataa tagttataat 180

aatactttta atttacttac cacatgtggg aatacatata atatatgttc ttgttctaat 240

aattataata caatattatt taattataat accacaaata attgtagttt aattatttct 300

cctcatgatg aaaaaatttt tgatacgatg tttcagataa tatatttaac taataaaatt 360

aattatacaa tacgatggtt acaacctgtt gatcccccaa atatttcatt taatgatagt 420

aattctttaa taaaatgtga aaaaaataat ggaacaaata ctgaaatcta tttatattta 480

aatgatacat ttattaataa tactaatgaa aatgatctta aatattattg gaattgtagt 540

gagttaaact ataatattac agctacatgt attattaata atacacttaa ttcggcaaat 600

accacaaaag ttataaattg cactaatcta ttattaaaat ctgaccaaaa ttattttctt 660

aaaaacattc atacattatt ttatatcata atttttattg taactgggat aataataagt 720

atttttatag caatcataac ttttttatct ttacgaaaaa gaaaaaaaca tgttgaagaa 780

atagaaagtc catcgcctga atctaatgaa gaggaagaac aacaacatca tcatgacact 840

acttccatac atgaaccgtc tcccagagaa ccattacttc ctaagcctta cagtcgttat 900

cagtataata cacctattta ttacatgcgt ccctcaacac aacaactatt taaatcatat 960

tctttaccca aaccatgtcc cccacctaaa ccatgtcctc cacctaaacc atgtccccca 1020

cccaaaccat gtccctcacc agaatcatat ccctcacctg aaccatatcc tctactacct 1080

aatatcccac taccacccaa tatcccgcca ttatctacac aaaatatttc gcttattcac 1140

gtagatagaa ttatttaa 1158

<210> 238
<211> 1143
<212> DNA
<213> African swine fever virus

<400> 238
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acaataactt tagatagtaa tattactagt gaaatagaag ctgtatcttg gaatttttat 180

aataatactt ttaatctact tgctacatgt ggaaaagcaa gtaacttttg tagttgttct 240

aattatagta catcattttt taatattaca aataattgta gtttaactat ttttttaata 300

gacgagacgt tatttaatac aacatatcaa atagtatatt caactaatat aattaattat 360

aaaataaact tattaatacc tgttactcct ccaattattt catataattg tactaattgt 420

tctataaatt gtaaaaaaag taatggtaca aatactaata ttttttttatc tataaatgat 480

acaattgtta catatactaa tgaaagtatt cttaattatg attataactg tagtatttta 540

aataataatt ttacagttac atgtataatt aataatacaa ttagtacatc aaatactaca 600

gaatttataa actgcactaa tatattatta agtagttatc tagatttttt tcaagtaact 660

agttatatat tttatatgat aatttttatt gtaactggaa taacagtaag tattcttata 720

tccatcataa ctttcttatt tatacgaaaa agaaaacatg ttgaagaaat agaaagtcca 780

ccgcctgaat ctaatgaaga agaacaacaa tgtcatcatg acaccacttc tatacatgaa 840

ccgtctccca gagaaccatt acttcctaag ccttacagtc gttatcaata taatacacct 900

atttactaca tgcgtccctc aacacaacaa ctatttaaat catattcttt acccaaacca 960

tgtcccccac ctaaaccatg tcctccaccc aaaccatgtc ccccacccaa accatgtcct 1020

ccacccaaac catgtcctcc atccaaacca tatccttcac tacctagtat cccgctacca 1080

cccgatatcc cgccattatc tacacaaaat atttcgctta ttcacgtaga tagaattatt 1140

taa 1143

<210> 239
<211> 1179
<212> DNA
<213> African swine fever virus

<400> 239
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acaataactt tagatagtaa tattactagt gaaatagaag ctgtatcttg gaatttttat 180

aataatactt ttaatctact tgctatatgt ggaaaagcaa gtaacttttg tagttgttct 240

aattatagta catcattttt taatattaca aataattgta gtttaactat ttttttaata 300

gacgagacgt tatttaatac aacatatcaa atagtatatt caactaatat aattaattat 360

aaaataaact tattaatacc tgttactcct ccaattattt catataattg tgctaattgt 420

tctataaatt gtaaaaaaag taatggtaca aatactaata ttttttttatc tataaatgat 480

acaattgtta catatactaa tgaaagtatt cttaattatg attataactg tagtatttta 540

aataataatt ttacagttac atgtataatt aataatacaa ttagcacatc aaatactaca 600

gaatttataa actgcactaa tatattatta agtagttatc tagatttttt tcaagtaact 660

agttatatat tttatatgat aatttttatt gtaactggaa taacagtaag tattcttata 720

tccatcataa ctttcttatt tatacgaaaa agaaaacatg ttgaagaaat agaaagtcca 780

ccgcctgaat ctaatgaaga agaacaacaa tgtcatcatg acaccacttc tatacatgaa 840

ccgtctccca gagaaccatt acttcctaag ccttacagtc gttatcaata taatacacct 900

atttactaca tgcgtccctc aacacaacaa ctatttaaat catattcttt acccaaacca 960

tgtcccccac ctaaaccatg tcctccacct aaaccatgtc ccccacctaa accatgtcct 1020

ccatccaaac catgtcctcc acctgaacca tattctccac ccaaaccatg tcctccaccc 1080

aaaccatatc cttcactacc tagtatcccg ctaccacccg atatcccgcc attatctaca 1140

caaaatattt cgcttattca cgtagataga attatttaa 1179

<210> 240
<211> 1146
<212> DNA
<213> African swine fever virus

<400> 240
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ttttggaatt tttataataa tacttttaat actattgcca catgtggaaa aaaaaataat 180

gtttgtgaat gttctaatta tgataaatcc ttatataata taacaaataa ttgtagttta 240

acaatttttc caaataatac aaaaatattt aatacaacat atcaattagt atattcacgc 300

aatagaatta attacacaat aaatttgtta ttacctgtta catctccaat tattacatat 360

aattgtactc aatctttaat aacatgtgaa aaaactaatg gaacaaatat tcatttattc 420

ttaaatttaa atgatacaat taatgaatat actaacaaaa gttttctcaa ttactattgg 480

aatagtagtg agttaaataa tatttttctt gctacatgta ttattaataa tacacttaat 540

tcagcaaata ctacaaaagt tatcaattgc actaacccat tattaaaatc ttaccaaaat 600

tattttcttg aaaatattca tacattattt tatatgataa tttttattgt atctggaata 660

acaataagta tttttatatc aatcataact tttttatctt tacgaaaaag aaaaaaacat 720

gttgaagaaa tagagagtcc accacctgaa tctaatgaag aagaacaatg tcagcatgat 780

gacaccactt ctatacatga accatctccc agagaaccat tacttcctaa accttacagt 840

cgttatcagt ataatacacc tatttactac atgcgtccct caacacaacc actcaaccca 900

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aaaccatgtc ctccacctga atcatattct ccacccaaac cactacctag tatcccgctg 1080

ctacccaata tcccgccatt atctacacaa aatatttcgc ttattcatgt agatagaatt 1140

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<210> 241
<211> 1182
<212> DNA
<213> African swine fever virus

<400> 241
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aatcttggtg gtctattttg gaatacatat tataataata atcatagtat ccttactagt 180

tgcggaatat atcaaaatta ttgttcatgc actaataatt atagcacatc attatataat 240

ataacaaata attgtggttt aataattttt ccaaataata caaaaagatt taacacaacg 300

tatgaattag tatatttaaa taatagtact aaatatacaa taaacttatt agtacctgtt 360

actcctccaa atattacata taattgtact acatctgtaa taacatgtaa aaaaaatgat 420

ggcacaaata ctaatatgtt tttaaaaata aatgatacaa tcgttaaaag tagtaatgaa 480

agtgtttttg aatactcttg gaatagtact gatttaaata acaattttac ggctatatgt 540

ataattaata atacaattaa ttcatcaaat gacacacaaa ctatagaatg tcccaatata 600

ttattaaaca attatttaga ctttttttcaa gtaactagtt acatgtttta tatgataatt 660

tttattgtaa ctggaataat agcaagtatt tttatttcaa tcataacttt tttatcttta 720

cgaaaaagaa aaaaacatgt tgaagaaata gaaagtccac caccctctga atctaatgaa 780

gaagatattt ctcacgatga caccacttcc atacatgaac catctcccag agaaccatta 840

cttcctaagc cttacagtcg ttatcagtat aatacaccta tttactacat gcgtccctca 900

acacaaccac tcaacccatt tcccctacct aaaccatgcc cgccacctaa accatgcccg 960

ccacccaaac catgtcctcc acctaaaccg tgtcctccac ccaaaccgtg tcgtccacct 1020

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tattctccac ccaaaccact acctaatatc ccgctgctac ccaatatccc gccattatct 1140

acacaaaata tttcgcttat tcacgtagat aggattattt aa 1182

<210> 242
<211> 360
<212> PRT
<213> African swine fever virus

<400> 242

Met Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile
1 5 10 15

Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile
20 25 30

Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn
35 40 45

Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys
50 55 60

Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys
65 70 75 80

Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln
85 90 95

Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro
100 105 110

Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr
115 120 125

Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn
130 135 140

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Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp
145                 150                 155                 160

Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn
                165                 170                 175

Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu
            180                 185                 190

Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe Lys Leu Tyr Tyr Ile
        195                 200                 205

Pro Leu Ser Ile Ile Ile Gly Ile Thr Ile Ser Ile Leu Leu Ile Ser
    210                 215                 220

Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys His Val Glu Glu
225                 230                 235                 240

Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Cys Gln His
                245                 250                 255

Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
            260                 265                 270

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
        275                 280                 285

Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro Lys Pro Cys
    290                 295                 300

Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
305                 310                 315                 320

Pro Cys Pro Ser Ala Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser
                325                 330                 335

Ile Pro Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser
            340                 345                 350

Leu Ile His Val Asp Arg Ile Ile
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<210> 243
<211> 406
<212> PRT
<213> African swine fever virus

<400> 243

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Met Ile Met Phe Ile Thr Leu Ile Phe Leu Ser Tyr Ile Asn Ile Val
1               5                  10                  15


Leu Ser Asn Asn Tyr Trp Ala Arg Leu Asn Glu Thr Ile Thr Leu Asn
            20                  25                  30


Ser Asn Ile Thr Asn Asp Thr Asn Asn Glu Leu Gly Ile Phe Trp Asn
        35                  40                  45


Ser Tyr Asn Asn Thr Tyr Tyr Asn Asn Thr Phe Asn Asn Ile Ala Ile
    50                  55                  60


Cys Gly Lys Lys Gly Ile Phe Cys Glu Cys Asn Ile Asn Tyr Asn Thr
65                  70                  75                  80


Ser Ile Ser Asn Thr Ser Ile Ser Asn Thr Ser Ile Tyr Asn Val Thr
                85                  90                  95


Asn Asn Cys Ser Leu Thr Ile Phe Leu Tyr Asp Asp Asn Ile Phe Lys
            100                 105                 110


Thr Tyr Gln Leu Val Tyr Gln Asn Tyr Lys Ile Asn Tyr Thr Ile Asn
        115                 120                 125


Leu Leu Leu Pro Val Thr Ser Pro Asn Ile Thr Tyr Asn Cys Thr Asn
    130                 135                 140


Ser Leu Ile Thr Cys Glu Lys Asn Asp Gly Thr Asn Thr Asn Met Phe
145                 150                 155                 160


Leu Ser Ile Asn Asn Ile Thr Ile Asn His Thr Asn Gln Asp Ile Leu
                165                 170                 175


Thr Tyr Tyr Trp Asn Asn Ser Glu Phe Asn Asn Phe Thr Ala Thr Cys
```

```
            180                 185                 190

Met Ile Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn
        195                 200                 205

Cys Thr Asn Pro Leu Leu Asn Ser Tyr Gln Asn Tyr Phe Leu Glu Asn
    210                 215                 220

Ile His Thr Leu Phe Tyr Ile Ile Ile Phe Ile Val Ser Gly Leu Ile
225                 230                 235                 240

Ala Ser Ile Phe Ile Ser Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg
                245                 250                 255

Lys Lys His Val Glu Glu Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu
            260                 265                 270

Glu Glu Gln Cys Gln His Asp Asp Thr Thr Ser Ile His Glu Pro Ser
        275                 280                 285

Pro Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn
    290                 295                 300

Thr Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe
305                 310                 315                 320

Pro Leu Pro Asn Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
                325                 330                 335

Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro
            340                 345                 350

Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys
        355                 360                 365

Ser Ser Pro Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro
    370                 375                 380

Leu Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile
385                 390                 395                 400
```

His Val Asp Arg Ile Ile
405

<210> 244
<211> 373
<212> PRT
<213> African swine fever virus

<400> 244

Met Ile Ile Ile Val Ile Phe Leu Met Cys Leu Lys Ile Val Leu Asn
1 5 10 15

Asn Ile Ile Ile Trp Ser Thr Leu Asn Gln Thr Val Phe Leu Asn Asn
20 25 30

Ile Phe Thr Ile Asn Asp Thr Tyr Gly Gly Leu Phe Trp Asn Thr Tyr
35 40 45

Tyr Asp Asn Asn Arg Ser Asn Phe Thr Tyr Cys Gly Ile Ala Gly Asn
50 55 60

Tyr Cys Ser Cys Cys Gly His Asn Ile Ser Leu Tyr Asn Thr Thr Asn
65 70 75 80

Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Glu Ile Phe Asn Arg
85 90 95

Thr Tyr Glu Leu Val Tyr Leu Asp Lys Lys Ile Asn Tyr Thr Val Lys
100 105 110

Leu Leu Lys Ser Val Asp Ser Pro Thr Ile Thr Tyr Asn Cys Thr Asn
115 120 125

Ser Leu Ile Thr Cys Lys Asn Asn Asn Gly Thr Asn Val Asn Ile Tyr
130 135 140

Leu Ile Ile Asn Asn Thr Ile Ser Ser Leu Asn Glu Thr Glu Asn Ile
145 150 155 160

Asn Cys Thr Asn Pro Ile Leu Lys Tyr Gln Asn Tyr Leu Ser Thr Leu
165 170 175

```
Phe Tyr Ile Ile Ile Phe Ile Val Ser Gly Leu Ile Ile Gly Ile Phe
            180                 185                 190

Ile Ser Ile Ile Ser Val Leu Ser Ile Arg Arg Lys Arg Lys Lys His
        195                 200                 205

Val Glu Glu Ile Glu Ser Pro Pro Pro Ser Glu Ser Asn Glu Glu Asp
    210                 215                 220

Ile Ser His Asp Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu
225                 230                 235                 240

Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile
                245                 250                 255

Tyr Tyr Met Arg Pro Ser Thr Gln Pro Leu Asn Pro Phe Pro Leu Pro
            260                 265                 270

Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro
        275                 280                 285

Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Ser Pro Pro Lys Pro
    290                 295                 300

Cys Arg Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
305                 310                 315                 320

Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Ser Lys Pro Cys Pro
                325                 330                 335

Ser Pro Glu Ser Tyr Ser Pro Pro Lys Pro Leu Pro Ser Ile Pro Leu
            340                 345                 350

Leu Pro Asn Ile Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His
        355                 360                 365

Val Asp Arg Ile Ile
    370
```

<210> 245
<211> 385
<212> PRT
<213> African swine fever virus

<400> 245

Met Ile Ile Lys Leu Ile Phe Leu Ile Ser Phe Lys Met Ile Leu Gly
1 5 10 15

Ile Asp Tyr Trp Val Ser Leu Asn Asn Thr Ile Ile Leu Asp Ser Asn
20 25 30

Ile Thr Ile Asn Asn Ile Thr Asn Thr Thr Asn Asn Pro Thr Leu Asn
35 40 45

Gly Ile Phe Trp Asn Ile Tyr Asn Asn Ser Tyr Asn Asn Thr Phe Asn
50 55 60

Leu Leu Thr Thr Cys Gly Asn Thr Tyr Asn Ile Cys Ser Cys Ser Asn
65 70 75 80

Asn Tyr Asn Thr Ile Leu Phe Asn Tyr Asn Thr Thr Asn Asn Cys Ser
85 90 95

Leu Ile Ile Ser Pro His Asp Glu Lys Ile Phe Asp Thr Met Phe Gln
100 105 110

Ile Ile Tyr Leu Thr Asn Lys Ile Asn Tyr Thr Ile Arg Trp Leu Gln
115 120 125

Pro Val Asp Pro Pro Asn Ile Ser Phe Asn Asp Ser Asn Ser Leu Ile
130 135 140

Lys Cys Glu Lys Asn Asn Gly Thr Asn Thr Glu Ile Tyr Leu Tyr Leu
145 150 155 160

Asn Asp Thr Phe Ile Asn Asn Thr Asn Glu Asn Asp Leu Lys Tyr Tyr
165 170 175

Trp Asn Cys Ser Glu Leu Asn Tyr Asn Ile Thr Ala Thr Cys Ile Ile
180 185 190

```
Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn Cys Thr
        195                 200                 205

Asn Leu Leu Leu Lys Ser Asp Gln Asn Tyr Phe Leu Lys Asn Ile His
    210                 215                 220

Thr Leu Phe Tyr Ile Ile Ile Phe Ile Val Thr Gly Ile Ile Ile Ser
225                 230                 235                 240

Ile Phe Ile Ala Ile Ile Thr Phe Leu Ser Leu Arg Lys Arg Lys Lys
                245                 250                 255

His Val Glu Glu Ile Glu Ser Pro Ser Pro Glu Ser Asn Glu Glu Glu
            260                 265                 270

Glu Gln Gln His His His Asp Thr Thr Ser Ile His Glu Pro Ser Pro
        275                 280                 285

Arg Glu Pro Leu Leu Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr
    290                 295                 300

Pro Ile Tyr Tyr Met Arg Pro Ser Thr Gln Gln Leu Phe Lys Ser Tyr
305                 310                 315                 320

Ser Leu Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys
                325                 330                 335

Pro Cys Pro Pro Pro Lys Pro Cys Pro Ser Pro Glu Ser Tyr Pro Ser
            340                 345                 350

Pro Glu Pro Tyr Pro Leu Leu Pro Asn Ile Pro Leu Pro Pro Asn Ile
        355                 360                 365

Pro Pro Leu Ser Thr Gln Asn Ile Ser Leu Ile His Val Asp Arg Ile
    370                 375                 380

Ile
385
```

<210> 246

<211> 380
<212> PRT
<213> African swine fever virus

<400> 246

```
Met Ile Ile Lys Leu Ile Phe Leu Ile Cys Phe Lys Ile Val Leu Ser
1               5                  10                  15


Ile Asp Asn Lys Thr Lys Phe Asn Glu Thr Leu Ile Leu Asp Asn Ile
            20                  25                  30


Asp Tyr Trp Val Lys Phe Asn Asp Thr Ile Thr Leu Asp Ser Asn Ile
        35                  40                  45


Thr Ser Glu Ile Glu Ala Val Ser Trp Asn Phe Tyr Asn Asn Thr Phe
    50                  55                  60


Asn Leu Leu Ala Thr Cys Gly Lys Ala Ser Asn Phe Cys Ser Cys Ser
65                  70                  75                  80


Asn Tyr Ser Thr Ser Phe Phe Asn Ile Thr Asn Asn Cys Ser Leu Thr
                85                  90                  95


Ile Phe Leu Ile Asp Glu Thr Leu Phe Asn Thr Thr Tyr Gln Ile Val
            100                 105                 110


Tyr Ser Thr Asn Ile Ile Asn Tyr Lys Ile Asn Leu Leu Ile Pro Val
        115                 120                 125


Thr Pro Pro Ile Ile Ser Tyr Asn Cys Thr Asn Cys Ser Ile Asn Cys
    130                 135                 140


Lys Lys Ser Asn Gly Thr Asn Thr Asn Ile Phe Leu Ser Ile Asn Asp
145                 150                 155                 160


Thr Ile Val Thr Tyr Thr Asn Glu Ser Ile Leu Asn Tyr Asp Tyr Asn
                165                 170                 175


Cys Ser Ile Leu Asn Asn Asn Phe Thr Val Thr Cys Ile Ile Asn Asn
            180                 185                 190
```

```
Thr Ile Ser Thr Ser Asn Thr Thr Glu Phe Ile Asn Cys Thr Asn Ile
        195                 200                 205

Leu Leu Ser Ser Tyr Leu Asp Phe Phe Gln Val Thr Ser Tyr Ile Phe
    210                 215                 220

Tyr Met Ile Ile Phe Ile Val Thr Gly Ile Thr Val Ser Ile Leu Ile
225                 230                 235                 240

Ser Ile Ile Thr Phe Leu Phe Ile Arg Lys Arg Lys His Val Glu Glu
                245                 250                 255

Ile Glu Ser Pro Pro Pro Glu Ser Asn Glu Glu Glu Gln Gln Cys His
            260                 265                 270

His Asp Thr Thr Ser Ile His Glu Pro Ser Pro Arg Glu Pro Leu Leu
        275                 280                 285

Pro Lys Pro Tyr Ser Arg Tyr Gln Tyr Asn Thr Pro Ile Tyr Tyr Met
    290                 295                 300

Arg Pro Ser Thr Gln Gln Leu Phe Lys Ser Tyr Ser Leu Pro Lys Pro
305                 310                 315                 320

Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Pro
                325                 330                 335

Lys Pro Cys Pro Pro Pro Lys Pro Cys Pro Pro Ser Lys Pro Tyr Pro
            340                 345                 350

Ser Leu Pro Ser Ile Pro Leu Pro Pro Asp Ile Pro Pro Leu Ser Thr
        355                 360                 365

Gln Asn Ile Ser Leu Ile His Val Asp Arg Ile Ile
    370                 375                 380
```

<210> 247
<211> 414
<212> DNA
<213> African swine fever virus

<400> 247

atgctggtga ttatcctggg aattattggc ctgctggcca gtagcaacct ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgaaccccc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacca gcagggtttg gggaaacaac tccacaagta ttattgagaa tgactatgta 240

aaatattgtg aggtttcccg ctggggtgac ctatgtagat atgatgtgga ggagcacatt 300

taccatagca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaaca tcccagaaag gatttgaaaa aagatgaatt ctag 414

<210> 248
<211> 414
<212> DNA
<213> African swine fever virus

<400> 248
atgctggtga ttatcctggg aattattggc ctgctggcca gtagcaacct ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgaaccccc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacca gcagggtttg gggaaacaac tccacaagta ttattgagaa tgactatgta 240

aaatattgtg aggtttcccg ctggggtgac ctatgtagat atgatgtgga ggagcacatt 300

taccatagca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaaca tcccagaaag gatttgaaaa aagatgaatt ctag 414

<210> 249
<211> 414
<212> DNA
<213> African swine fever virus

<400> 249
atgctggtga ttatcctggg agttattggc ctgctggcca gtagcaactt ggtttcatcc 60

tccacttcta ctcggatagg tggacatctt cctctaacat ttgatcctcc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

gtctgtacta gcaggatctg ggggaacaac tccacaagta ttgttgagaa cagctatgta 240

aaatattgtg aagtttcccg ctggggtgac cagtgtagat atgatgtgga ggagcgcatt 300

taccatacca tgaactgttc tgacccaaaa ccctggaatc cttataaaat tacaagggtg 360

gagtggaaaa agaatgaaca tttcagaaag gatttgaaaa aagatgaatt ctag 414

<210> 250
<211> 414
<212> DNA
<213> African swine fever virus

<400> 250
atgctggtga ttatcctggg agttattggc ctgctggcca gtagcaactt ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgatcctcc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

gtctgtacta gcaggatctg ggggaacaac tccacaagta ttgttgagaa cagctatata 240

aaatattgtg aagtttcccg ctggggtgac cagtgtagat atgatgtgga ggagcacatt 300

tactatacca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaaca tttcagaaag gatttgaaaa aagatgaatt ctag 414

<210> 251
<211> 378
<212> DNA
<213> African swine fever virus

<400> 251
atgctggtga ttatcctggg agttattggc ctgctggcca gtagcaactt ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgatcctcc agagaatgaa 120

cttggatact ggtacactta tgtggaaagt tgtcggttct gctgggattg tgaagatggg 180

gtctgtacta gcagggtttg gggaaacaac tccacaagta ttgttgagaa tgactatgta 240

aaatattgtg aggtttctcg ctggggtgac caatgtagat atgatgtgga ggagcacatt 300

tactatacca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaaggaa 360

ggagtggaaa aaggatga 378

<210> 252
<211> 414
<212> DNA
<213> African swine fever virus

<400> 252
atgctggtga ttatcctggg agttattggc ctgctggcca gtagcaactt ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacag aggatcctcc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacta gcagggtttg gggaaacaac tccacaagta ttgttgagaa cgactatgta 240

aaatattgtg aggtttctcg ctggggtgac caatgtagat atgatgtaga ggagcacatt 300

tactatacca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa aggatgaaca ttccagaaag aatttgaaaa aagatgaatt ctag 414

<210> 253
<211> 414
<212> DNA
<213> African swine fever virus

<400> 253
atgctggtga ttatcctggg aattattggc ctgctggcca gtagcaacct ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgatccccc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacca gcagggtttg gggaaacaac tccacaagta ttgttgagaa tgactatgta 240

aaatattgtg aggtttcccg ctggggaaac ctatgtagat atgatgtgga ggagcacatt 300

tactatagca tgaactgttc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaata tctcagaaag gatttgaaaa aagatgaatt ctag 414

<210> 254
<211> 105
<212> DNA
<213> African swine fever virus

<400> 254
atgaactgtt ctgacccaaa gccctggaat ccttataaaa ttgcaaggaa ggagtggaaa 60

aagaatgaac atcccagaaa ggatttgaaa aaagatgaat tctag 105

<210> 255
<211> 414
<212> DNA
<213> African swine fever virus

<400> 255
atgctggtga ttatcctggg aattattggc ctgctggcca gtagcaacct ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgatccccc agagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacca gcagggtttg gggaaacaac tccacaagta ttgttgagaa tgactatgta 240

aaatattgtg aggtttcccg ctggggtaac ctatgtagat atgatgtgga ggagcacatt 300

taccatagca tgaactgctc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaaca tcccagaaag gatttgaaaa aagatgaatt ctag 414

<210> 256
<211> 414
<212> DNA
<213> African swine fever virus

<400> 256
atgctggtga ttatcctggg aattattggc ctgctggcca gtagcaacct ggtttcatcc 60

tccacttcta ctcgggtagg tggacatctt cctctaacat ttgatccccc cgagaatgaa 120

cttggatact ggtgcactta tgtggaaagc tgtcggttct gctgggattg tgaagatggg 180

atttgtacca gcagggtttg gggaaacaac tccacaagta ttgttgagaa tgactatgta 240

aaatattgtg aggtttcccg ctggggtaac ctatgtagat atgatgtgga ggagcacatt 300

taccatagca tgaactgctc tgacccaaag ccctggaatc cttataaaat tgcaaggaag 360

gagtggaaaa agaatgaaca tcccagaaag gatttgaaaa aagatgaatt ctag 414

<210> 257
<211> 1587
<212> DNA
<213> African swine fever virus

<400> 257
atgttctccc tacaggacct ctgtcggaag aacactttct tccttccaaa tgattttagc 60

aagcatactc tacaacggct ggggttgtat tggaaagagc atggatccgt ccatcgaata 120

gaaaaggaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

cttgcaggag aggaggggga cacagatgtg gtacagctct tgttactatg ggagggaaat 240

ctgcattatg ccatcatagg agctttgaag actgagaatt ataatctagt atgtgagtac 300

catagccaaa ttcaggactg gcatattctc ctacccttga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttggatgt gaccttatat gccttctcca acatgctgta 420

aaatgtgata tgctttctat tcttgttaaa tataaggagg atttactaaa tgtaaggatt 480

aggcatcgta cccaatccct gtttgttttg gcatgcgaaa atcggagatt tgagattatt 540

gaatggatag gtcaaaatct gtcaattcct gaacctgagg ccatttttag cattgctatt 600

gttacaaaag atgtagaact gttttcctta ggatataaaa ttatttttga ttacatgcaa 660

agacaaggaa tttttcaatt aaccaatgta gttcgcatgc ttctgctaaa tcgtcatatt 720

ggtatggcaa tagaaaaagg acttttacct tttattctgg aaactttaaa atatggtggt 780

agtgtaaaaa gagctttatc ttatgcagta atagataata aaagaaaaat tatagactat 840

cttgtacgcc atgaaaatat accccgagga actattgaaa gacttttgca tctagctgtg 900

aaaaaacaat cttccaggaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtagatcaca aatccactct tgtgttaaaa 1020

attttattgg aaaaaaagga aaatctagtg gatgctgttt taacaagact tgtaaaacat 1080

tctacatatt tccaggtgag agaatttatc caggagtttt ccatcagccc agaaaaattc 1140

attaaaatag ctgtgcggga aaagaaaaat gtgttaatcg aggctatttc tgaagatatt 1200

tgggaaaatc ccacagaaag aattacttat ctcaaacaga tagtgcacac cataaaatat 1260

gaaagtggaa ggcggttttt gatagacatc attcacagca tttaccaaag ttactcacta 1320

aaacacgaag atattcttaa actggcaaca ttttatgtca aacacaatgc aatcacccat 1380

tttaaagatc tctgcaaata tctttggctg aacagaggaa cagaaagtaa gaaactgttt 1440

ttagagtgct tggaaattgc tgatgagaag gagtttcctg atattaaaaa tattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagct 1560

tatgctttag agtatgacat gtattaa 1587

<210> 258
<211> 1587
<212> DNA
<213> African swine fever virus

<400> 258
atgttctccc tacaggacct ctgtcggaag aacactttct tccttccaaa tgattttagc 60

aagcatactc tacaacggct ggggttgtat tggaaagagc atggatccgt ccatcgaata 120

gaaaaggaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

cttgcaggag aggaggggga cacagatgtg gtacagctct tgttactatg ggagggaaat 240

ctgcattatg ccatcatagg agctttgaag actgagaatt ataatctagt atgtgagtac 300

catagccaaa ttcaggactg gcatattctc ctacccttga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttggatgt gaccttatat gccttctcca acatgctgta 420

aaatgtgata tgctttctat tcttgttaaa tataaggagg atttactaaa tgtaaggatt 480

aggcatcgta cccaatccct gtttgttttg gcatgcgaaa atcggagatt tgagattatt 540

gaatggatag gtcaaaatct gtcaattcct gaacctgagg ccatttttag cattgctatt 600

gttacaaaag atgtagaact gttttcctta ggatataaaa ttatttttga ttacatgcaa 660

agacaaggaa tttttcaatt aaccaatgta gttcgcatgc ttctgctaaa tcgtcatatt 720

ggtatggcaa tagaaaaagg acttttacct tttattctgg aaactttaaa atatggtggt 780

agtgtaaaaa gagctttatc ttatgcagta atagataata aaagaaaaat tatagactat 840

cttgtacgcc atgaaaatat accccgagga actattgaaa gacttttgca tctagctgtg 900

aaaaaacaat cttccaggaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtagatcaca aatccactct tgtgttaaaa 1020

attttattgg aaaaaaagga aaatctagtg gatgctgttt taacaagact tgtaaaacat 1080

tctacatatt tccaggtgag agaatttatc caggagtttt ccatcagccc agaaaaattc 1140

attaaaatag ctgtgcggga aaagaaaaat gtgttaatcg aggctatttc tgaagatatt 1200

tgggaaaatc ccacagaaag aattacttat ctcaaacaga tagtgcacac cataaaatat 1260

gaaagtggaa ggcggttttt gatagacatc attcacagca tttaccaaag ttactcacta 1320

aaacacgaag atattcttaa actggcaaca ttttatgtca aacacaatgc aatcacccat 1380

tttaaagatc tctgcaaata tctttggctg aacagaggaa cagaaagtaa gaaactgttt 1440

ttagagtgct tggaaattgc tgatgagaag gagtttcctg atattaaaag tattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagct 1560

tatgctttag agtatgacat gtattaa 1587

<210> 259
<211> 1578
<212> DNA
<213> African swine fever virus

<400> 259
atgttctccc tacaggacct ctgtcggaag aacattttct tccttccaaa tgattttagc 60

aagcataccc tacaatggct gggattatat tggaaagagc atggatccgt ccatcgagca 120

gaaaaagaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

cttgcaggag aggaggggga cacagatgta gtacagctct tgttattatg ggagggaaat 240

ctgcattatg ccatcatagg agccttgaag actgaaaaat ataacctaat atgtgagtat 300

catagccaaa ttcaggactg gcatattctc ctacccatga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttggatgt gactttattt gccttctcca acatgctgta 420

aaatacaaca tgctttctat tcttgtcaaa tataaggagg atctactaaa tgcaaggatt 480

aggcatcgta tccaatccct gtttgttttg gcatgcgaaa atcggagaat tgaaattatt 540

gattggatag gccaaaatct gccaattcct gaacctgatg ccatttttag cattgctgtt 600

gctacaagag atttagaact gttttcctta gggtacaaga ttatttttga ttacatgcaa 660

agacagggaa tcattcaatt aaccaatgga gttcgcatgg ttgtgctaaa tcgtcacatt 720

agcatggcaa tagataatgg tcttttacct tttgttctgg aaactttaaa acatggtggg 780

aatatacata gagccttatc ttatgcagta acacacaata gaagaaaaat tctggattat 840

cttattcgcc agaaaaatat agcccctaat acaattgaaa gacttttata tctggccgtg 900

aaaaatcaat cttccaggaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtaaatgaga aatccactct tgtgttaaaa 1020

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attaaaatag ctgtgcggga aaagaaaaat gtgttaatcg aggctatttc tgaagatatt 1200

tgggaaaatc ccacagaaag aattacttat ctcaaacaga tagtgcacac cataaaatat 1260

gaaagtggaa ggcgattttt ggtagacatc attcacagca tttaccaaag ttactcacta 1320

aaacacgaag atattcttaa actggcaaca ttttatgtca aacacaatgc aatcacccat 1380

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ttagagtgtt tagaaattgc tgatgagaag gagtttcctg atattaaaag tattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagcc 1560

tatgatgctt tagagtag 1578

<210> 260

<211> 1578
<212> DNA
<213> African swine fever virus

<400> 260
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gaaaaagaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

cttgcaggag aggaggggga cacagatgta gtacagctct tgttattatg ggagggaaat 240

ctgcattatg ccatcatagg agccttgaag actgaaaaat ataacctaat atgtgagtat 300

catagccaaa ttcaggactg gcatattctc ctacccatga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttggatgt gactttattt gccttctcca acatgctgta 420

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aggcatcgta tccaatccct gtttgttttg gcatgcgaaa atcggagaat tgaaattatt 540

gattggatag gccaaaatct gccaattcct gaacctgatg ccatttttag cattgctgtt 600

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agcatggcaa tagataatgg tcttttacct tttgttctgg aaactttaaa acatggtggg 780

aatatacata gagccttatc ttatgcagta acacacaata gaagaaaaat tctggattat 840

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ttagagtgtt tagaaattgc tgatgagaag gagtttcctg atattaaaag tattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagcc 1560

tatgatgctt tagagtag 1578

<210> 261
<211> 1578
<212> DNA
<213> African swine fever virus

<400> 261
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gaaaaggaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacat 180

cttgcaggag aggaggggaa cacagatgta gtacagctct tgttattatg ggagggaaat 240

ctgcattatg ccatcatagg agccttgaag actgagaaat ataacctaat atgtgagtac 300

catagccaaa ttcagaactg gcatgttctc ctccccttga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttggatgt gactttattt gccttctcca acatgctgta 420

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aggcatcgta tccaatccct gtttgttttg gcatgcgaaa atcggagatt tgagattatt 540

gaatggatag gtcaaaatct gccaattcct gaacctgagg ccatttttag cattgctatt 600

gttacaaaag atatagaact gttttcctta gcgtacaagc ttatttttga ttacatgcaa 660

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ggtatggcaa tagaaaaagg acttttaccc tttattctgg aaactttaaa atatggtggt 780

agtgtaaata gagctttatc ttatgcagta atagataata aaagaaaaat tatagactat 840

cttgtacgcc atgaaaatat accccgtgga actattgaaa gacttttgca tctagctgtg 900

aaaaaacaat cttccagaaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtagatcaca actctactct tgtgttaaaa 1020

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tctacatatt tccgggtaag agaatttatc caggagtttt ccatcagccc agaaaaattc 1140

attaaaatag ctgtgcggga aaagaaaaat gtgttaatcg aggctatttc tgaagatatt 1200

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gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagcc 1560

tataatgctt tagagtag 1578

<210> 262
<211> 1557
<212> DNA
<213> African swine fever virus

<400> 262
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aagcataccc tacaatggct ggggttatat tggaaagagc atggatccgt ccatcgagca 120

gaaaaagaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttactg 180

cttgcaggag aggaggggga cacagatgta gtacagctct tgttgctatg ggaaggaaat 240

ctgcattatg ccatcatagg agccttgaag actgagaaat atagcctagt atgtgagtac 300

catagccaaa ttcaggactg gcatgttctc ctccccttga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttgaatgt gactttatat gccttctaca acatgctgta 420

aaatgtgaca tgctttctat tcttgttaaa tataaagagg atctactaaa tgtaaggatt 480

aggcatcgta tccaatccct gtttgttttg gcatgcgaaa atcggagatt tgagattatt 540

gaatggatag gtcaaaatct gccaattcct gaacctgagg ccatttttag cattgctatt 600

gttacaaaag atatagaact gttttcctta ggatacaagc ttatttttga ttacatgcaa 660

agacaaggaa cttttcaatt aaccaatatg gttcgcatgc ttctgctaaa tcgttacatt 720

ggtatggcaa tagaaaaagg ccttttaccc tttatcgtgg aaactttaaa atatggtggt 780

agtgtaaata gagctttatc ttatgcagtc atagataata aaagaaaaat tatagactat 840

cttgtacgtc atgaaaatat accccgtgga actattgaaa gacttttgca tctagctgtg 900

aaaaaacaat cttccagaaa aactttgaac ttgttgctat cttacataaa ctacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtagatcaca actctaccct tgtgttaaaa 1020

attttattgg aaaaaaagga aaatttagtg gatgctgttt taacaagact tgtaaaacat 1080

tctacatatt tccgggtgag agaatttatc caggagtttt ccatcagccc agaaaaattc 1140

attaaaatag ctgtgcggga acagaaaaat gtgttaatcg aggctatttc tgaagatatt 1200

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gaaagtggaa ggcggttttt gatagacatc attcacagca tttaccaaag ttactcacta 1320

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tttaaagatc tctgcaaata tctttggctg aacagaggaa cagaaagtaa gaaactgttt 1440

ttagagtgct tggaaattgc tgatgagaag gagtttcctg atattaaaag cattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacta aggaagaaat catataa 1557

<210> 263
<211> 1581
<212> DNA
<213> African swine fever virus

<400> 263
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aagcataccc tacaacggct ggggttatat tggaaagagc atggatccgt ccatcgagca 120

gaaaaagaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

cttgcaggag aggaggggga cacagatgta gtacagctct tattattatg ggaaggaaat 240

cttcattatg ccatcatagg agccttgaag actgagaaat ataacctaat atatgagtac 300

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gaaaaatgtc atgatttaag ccttgcatgt gactttatat gccttctcca acatgctata 420

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gaatggatag gtcaaaatct gccaattcct gaacctgatg ccatttttag cattgctgtt 600

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agcatggcaa tagataatgg tcttttaccc tttgttctgg aaactttaaa acatggtggg 780

aatatacata gagccttatc ttatgcagta acacacaata aaagaaaaat tctggattat 840

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aaaaatcaat catccagaaa aactttgaac ttgttactat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtaaatgaga aatccactct tgtgttaaaa 1020

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attaaaatag ctgtgcggga aaagaaaaat gtgttgatcg aggctatttc tgaagatatt 1200

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gaaagtggaa ggcgattttt ggtagacatc attcacagca tttaccaaag ttactcacta 1320

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tttaaagatc tctgcaaata tctttggctg aacagaggaa cagaaagtaa aaaactcttt 1440

ttagagtgtt tagaaattgc tgatgagaag gagtttcctg atattaaaag cattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaagc ctatggatgc 1560

tttagagtag ccatgtatta a 1581

<210> 264
<211> 1578
<212> DNA
<213> African swine fever virus

<400> 264
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aagcataccc tacaatggct ggggttatat tggaaagagc atggatccgt ccatcgagca 120

gaaaaagaca gcataatgat acagaatgaa ttggttcttt ctatcaatga tgctttactg 180

cttgcaggag aggaggggga catagatgta gtacagctct tgttattatg ggagggtaat 240

ctgcattatg ccatcatagg agccttgaag actgagaaat ataacctaat atgtgagtac 300

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gaaaaatgtc atgatttaag ccttgcatgt gactttatat gccttctcca acatgctgta 420

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aaaaatcaat cttccaggaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctggt agagcatgta gtaaatgaga aatccactct tgtgttaaaa 1020

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gaaagtggaa gacgattttt gatagagatc attcacagca tttaccaaag ttactcacta 1320

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gaatatatta actacttgtt tactgcagga actattacca aggaagaaat catgcaagcc 1560

tatgatgctt tagagtag 1578

<210> 265
<211> 1578
<212> DNA
<213> African swine fever virus

<400> 265
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aagcataccc tacaatggct ggggttatat tggaaagagc atggatccgt ccatcgagca 120

gaaaaaaaca gcatagtgat acagaatgaa ttggttcttt ctatcaatga tgctttacag 180

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ctgcattatg ccatcatagg agccttgaag actgagaaat ataatctaat atgtgagtac 300

catagccaaa ttcaggactg gcatgttctc ctccccttga ttcaagatcc agaaacattc 360

gaaaaatgtc atgatttaag ccttgcatgt gactttatat gccttctaca acatgctgta 420

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aaaaatcaat cttccaggaa aactttgaac ttgttgctat cttacataaa ttacaaggtg 960

aaaaatgtta aaaagctagt agagcatgta gtaaatgaga aatccactct tgtgttaaaa 1020

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tttaaagatc tctgcaaata tctttggctg aacagaggaa cagaaagtaa gaaactgttt 1440

ttagagtgtt tagaaattgc tgatgagaag gagtttcctg atattaaaag cattgtgagt 1500

gaatatatta actacttgtt tactgcagga gctattacca aggaagaaat catgcaagcc 1560

tatgatgctt tagagtag 1578

<210> 266
<211> 618
<212> DNA
<213> African swine fever virus

<400> 266
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gttggacaac ttcgtccaac agaggagcct ccagaggaag aactcgaata ctggtgtgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagacg gcacttgtat aaacaaaata 180

gatgggtcag taatttacaa gaatgagtat gtgaaatcat gtctggtttc ccgttggctg 240

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gaacttgaat actggtgcac ttatacagaa aactgcaagt tttgctggaa ttgtcaaaat 420

ggcctttgtg agggcaaatt ggagaataca acaattcttg aaaatgagta tgtgcaatca 480

tgtatagttt cccgctggct aaataaatgt atgtatgatc taggacaggg gattcaccat 540

gtaatggcct gttctgaacc aaagccctgg aatccttaca aaatcttaaa gagagagtgg 600

aaagaaaata atagttaa 618

<210> 267
<211> 618
<212> DNA
<213> African swine fever virus

<400> 267
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gttggacaac ttcgtccaac agaggagcct ccagaggaag aactcgaata ctggtgtgcc 120

tacatggaaa gttgccaatt ttgctgggac tgccaagacg gcacttgtat aaacaaaata 180

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gataaatgta tgtatgattt agataagggt atctaccata ccatgaattg caaccaggtc 300

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gaacttgaat actggtgcac ttatacagaa aactgcaagt tttgctggaa ttgtcaaaat 420

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gtaatggcct gttctgaacc aaagccctgg aatccttaca aaatcttaaa gagagagtgg 600

aaagaaaata atagttaa 618

<210> 268
<211> 372
<212> DNA
<213> African swine fever virus

<400> 268
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ggcaaattgg agaatacaac aattcttgaa aatgagtatg tgcaatcatg tatagtttcc 240

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tctgaaccaa agccctggaa tccttacaaa atcttaaaga gagagtggaa aaaaaatgtc 360

agccaaaatt aa 372

<210> 269
<211> 372
<212> DNA
<213> African swine fever virus

<400> 269
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ggcaaattgg agaatacaac aattcttgaa aatgagtatg tgcaatcatg tatagtttcc 240

cgctggctaa ataaatgtat gtatgatcta ggacagggga ttcaccatgt aatgccctgt 300

tctgaaccaa agccctggaa tccttacaaa atcttaaaga aagagtggaa agaaaatgtc 360

agccaaaatt aa 372

<210> 270
<211> 363
<212> DNA
<213> African swine fever virus

<400> 270
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gttggacaac ttcatccaac ggaaaatcct tcagagaatg aacttgaata ctggtgcact 120

tacatggaat gttgccagtt ttgctgggac tgtcaagatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgta tgtatgatct gggtcaaggc attgatcatg taatggtctg ttctcaacca 300

aagtactgga atccttataa aatcttaaag aaagagtgga aagaaaataa cagccaaaat 360

taa 363

<210> 271
<211> 363

<212> DNA
<213> African swine fever virus

<400> 271
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tacatggaat gttgccagtt ttgctgggac tgtcaagatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgca tgtatgatct gggtcaaggc attgatcatg taatggtctg ttctcaacca 300

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taa 363

<210> 272
<211> 366
<212> DNA
<213> African swine fever virus

<400> 272
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gttggacaac ttcatccaac ggaaaatcct tcagagaatg aacttgaata ctggtgcact 120

tacatggaat gttgccagtt ttgctgggac tgtcaaaatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgta tgtatgatct gggtcaaggc attgatcatg taatggtctg ttctcagcca 300

aaatactgga atccttataa aatcttaaag aaagagtgga aagaaaataa cagccaaaat 360

aaataa 366

<210> 273
<211> 357
<212> DNA
<213> African swine fever virus

<400> 273
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gttggacaac ttcatccaac ggaaaatcct tcagagaatg aacttgaata ctggtgcact 120

tacatggaat gttgccagtt ttgctgggac tgtcaaaatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgta tgtatgatct gggtcaaggc attgatcatg taatggtctg ttctcaacca 300

aaatactgga atccttataa aatcttaaag aaagagtgga aagaaaataa tagttaa 357

<210> 274
<211> 366
<212> DNA
<213> African swine fever virus

<400> 274
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gttggacaac ttcatccaac ggaaaatcct tcagagaatg aacttgaata ctggtgcact 120

tacatggaat gttgccagtt ttgctgggac tgtcaaaatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgta tgtacgatct gggtcaaggc attgatcatg taatggtctg ttctcaacca 300

aaatactgga atccttataa aatcttaaag aaagagtgga aagaaaataa cagccaaaat 360

aaataa 366

<210> 275
<211> 366
<212> DNA
<213> African swine fever virus

<400> 275
atgttagtaa tcttcttggg aattcttggc cttctggcca accaggtctc aagccagctc 60

gttggacaac ttcatccaac ggaaaatcct tcagagaatg aacttgaata ctggtgcact 120

tacatggaat gttgccagtt ttgctgggac tgtcaaaatg gcctttgtgt gaataagttg 180

ggaaatacaa caattcttga aaatgagtat gtgcatccat gtatagtttc ccgctggcta 240

aataaatgta tgtacgatct gggtcaaggc attgatcatg taatggtctg ttctcaacca 300

aaatactgga atccttataa aatcttaaag aaagagtgga aagaaaataa cagccaaaat 360

aaataa 366

<210> 276
<211> 312
<212> DNA
<213> African swine fever virus

<400> 276
atgaaggttt ttctaggact tttactaggt tattcaacca tcctcattct tacatatcaa 60

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atggaaaaat ggagggataa gaattggtca atcattataa ggtattattg tttttacctt 180

gtatttagct ttgcatttgc tggttgcgtt gcatttgcga tctgcaaaaa tctacgactg 240

tgtacaacca tgaaattact tatgcttttg aatattttgg ttttgttatc tcagccaatt 300

ttgaataatt ga 312

<210> 277
<211> 360
<212> DNA
<213> African swine fever virus

<400> 277
atgaaggttt ttctaggact tttactaggt tattcaacca tccttattct tacctatcaa 60

tcaccaacaa ccccgtggtg tttttatgaa atatcactta aaatacctaa tcatcatagc 120

atgaaatgtt gttcgtatcc tagactttat gaacatgaaa tgttcatgga aaaatggagg 180

gataagaatt ggccaatcat tataaggtat tattgttttt accttgtatt tagctttgta 240

tttgctggtt gcgttgcatt tgcgatctgc aaaaatctac gactgagtac aaccatgaaa 300

ttacttatgc ttttgagtat tttggttttg ttgttatctc agccaatctt gaataattga 360

<210> 278
<211> 360
<212> DNA
<213> African swine fever virus

<400> 278
atgaaggttt ttctaggact tttactaggt tattcaacca tccttattct tacctatcaa 60

tcaccaacaa ccccgtggtg tttttatgaa atatcactta aaatacctaa tcatcatagc 120

atgaaatgtt gttcgtatcc tagactttat gaacatgaaa tgttcatgga aaaatggagg 180

gataagaatt ggccaatcat tataaggtat tattgttttt accttgtatt tagctttgta 240

tttgctggtt gcgttgcatt tgcgatctgc aaaaatctac gactgagtac aaccatgaaa 300

ttacttatgc ttttgagtat tttggttttg ttgttatctc agccaatctt gaataattga 360

<210> 279
<211> 507
<212> DNA
<213> African swine fever virus

<400> 279
atgaaggttt ttctaggact tttactaggt ttttcaatca tcctcattct tacatatcaa 60

tcaccgacaa ctcagcatcc tcctaaggaa gagcttgcgt actggtgcac ttatgcaaaa 120

tcttgtgact tctgctggga ttgccaaaat gacacttgta taaataaggt aataaatgag 180

tctatttcga taacttcgat tgtaaactgt agagttactc gcgattccca atcctgtttt 240

tatgaaatat cagttaaaat acctaatcat catagcatgg aatgttcata tcctagactt 300

tatgaacatg aaatgtttat ggaaaaatgg agggatgagt attggccaat cattataaaa 360

cagtgttgtt tttaccttgt atttagcatt gcatttgctg gatgcgttgc atttgcgatc 420

tgcaaaaatc tacgactgcg tacaactata aaactactta ttcttttgag tattttggtt 480

tggttgtctc aaccagtctt gaattga 507

<210> 280
<211> 516
<212> DNA
<213> African swine fever virus

<400> 280
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acaccaacaa cccagcatcc tcctaaggag gagcttccat attggtgtac gtatgtaaag 120

aattgcgacc tctgttggga ttgtcaagat agcatctatt ggaacaaggt aataagtgag 180

tctatttcga taaattcgat tataaactgt agagttactt gcgattccca atctcagtcc 240

tgcttttatg aaatattact taaaatacct aatcatcata gcatggaatg ttcttatcct 300

ggatcgtatg aaaatgaaat gttcatggaa aaatggaggg atgagaattg gtcaatcatt 360

ataaaacatt attgttttta ccttgtattt agctttgcat ttgctggttg cgttgcattt 420

gcgatctgca aaaatctacg actgagtaca actatgaaat tacttatgct tttgagtatt 480

ttggtttgct tatctcagcc aatcttgaat aattga 516

<210> 281
<211> 510
<212> DNA
<213> African swine fever virus

<400> 281
atgaaggttt ttctaggact tttactaggt ttttcaatca tcctcattct tacatatcaa 60

tcaccgacaa cccagcatcc tcctaaggaa gagcttgcgt actggtgcac ttatgcaaaa 120

tcttgtgact tctgctggga ttgccaaaat gacacttgta taaataaggt aataaatgag 180

tctatttcga taacttcgat tgtaaactgt agagttactc gcgattccca gtcctgtttt 240

tatgatatat cagttaaaat acctaatcat catagcatgg aatgttcata tcctagactt 300

tatgaacatg aaatgtttat ggaaaaatgg agggatgagt attggccaat cattataaaa 360

cagtgttgtt tttaccttgt atttagcttt gcatttgctg gttgcgttgc atttgcgatc 420

tgcaaaaacc tacgactgcg tacaactata aaactactta ttcttttgag tattttggtt 480

tggttatctc agccaatctt gaataattga 510

<210> 282
<211> 312
<212> DNA
<213> African swine fever virus

<400> 282
atgaaggttt ttctaggact tttactaggt tattcaacca tcctcattct tacatatcaa 60

tcaccaacaa cccagtggtg tttttatgaa atatcactta aaatacttaa tcatcatagc 120

atggaaaaat ggagggataa gaattggtca atcattataa ggtattattg tttttacctt 180

gtatttagct ttgcatttgc tggttgcgtt gcatttgcga tctgcaaaaa tctacgactg 240

tgtacaacca tgaaattact tatgcttttg aatattttgg ttttgttatc tcagccaatt 300

ttgaataatt ga 312

<210> 283
<211> 516
<212> DNA
<213> African swine fever virus

<400> 283
atgaaggttt ttctaggact tttactaggt tattcaacca tcctcattct tacatatcaa 60

tcaccaacaa cccagcatcc tcctaaggaa gagcttgagt attggtgcac ttatgcaaaa 120

acttgtgact tctgctggga ttgccaaaat gacacttgta taaataaggt aataaatgaa 180

tctatttcga tgaattcgat tgtaaactgt agagttactc gcgattccca atcccagtcc 240

tgtttttatg aaatatcact taaaatacct aattatcata gcatggaatg ttcatatcct 300

agactttata aacatttcat gtccatggaa aaatggaggg atgagaattg gccaatcctt 360

ataagacatt attgttttta ccttgtattt agctttgcat ttgctggttg cgttgcattt 420

gcgatctgca aaaatctacg actgcgtaca accatgaaat tacttatgct tttgagtatt 480

ttggttttgt tatctcagcc aatcttgaat aattga 516

<210> 284
<211> 324
<212> DNA
<213> African swine fever virus

<400> 284
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cttacatatc aatcaccgac aacccagtgg tgtttttatg aaatatcact taaaatactt 120

aatcatcata gcatggaaaa atggagggat aagaattggt caatcattat aaggtattat 180

tgtttttacc ttgtgtttag ctttgcattt gccggttgcg ttgcatttgc gatctgcaaa 240

aatctacgac tgtgtacaac catgaaatta cttatgcttt tgggtatttt ggttttgtta 300

tctcagccaa tcttgaataa ttga 324

<210> 285
<211> 354
<212> DNA
<213> African swine fever virus

<400> 285
atgaaggttt ttctaggact tttactaggt tattcaacca tcctcattct tacatatcaa 60

tcaccagcaa cccagtggtg tttttatgaa atatcactta aaatacctaa tcatcatagc 120

atggaatgtt catatcctag actttataaa catttcatat tcatggaaaa atggagggat 180

aagaattggt caatcattat aaggtattat tgtttttacc ttgtatttag ttttgcattt 240

gctggttgca ttgcatttgc gatctgcaaa aatctacgac tgtgtacaac tatgaaatta 300

cttatgcttt tgagtatttt ggttttgtta tctcagccaa tcttgaataa ttga 354

<210> 286
<211> 354
<212> DNA
<213> African swine fever virus

<400> 286
atgaaggttt ttctaggact tttactaggt tattcaacca tcctcattct tacatatcaa 60

tcaccagcaa cccagtggtg tttttatgaa atatcactta aaatacctaa tcatcatagc 120

atggaatgct catatcctag actttataaa catttcatgt tcatgaaaaa atggagggat 180

aagaattggt caatcattat aaggtattat tgtttttacc ttgtatttag ttttgcattt 240

gctggttgca ttgcatttgc gatctgcaaa aatctacgac tgtgtacaac tatgaaatta 300

cttatgcttt tgagtatttt ggttttgtta tctcagccaa tcttgaataa ttga 354

<210> 287
<211> 714
<212> DNA
<213> African swine fever virus

<400> 287
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cctcagcagc gggcagttgc cttctttcga gccaatacta aggagctaga ggacttctta 120

tgctcagatg ggcagtctga ggaggtactg tctggccccc ttcttaaccg tctactagaa 180

ccctcaggcc ctcttgatat tttaaccgga tatcacctat ttcgtcagaa tcccaaggca 240

ggtcagttgc gcggccttga ggtcaagatg cttgaacggt tatacgatgc taatatttac 300

aatatactgt ctcggctgcg gcctgaaaaa gttcgcaaca aggctattga gctatactgg 360

gttttccgag ctatccatat ttgtcatgct cctttagttt tagatattgt acgatatgag 420

gaaccggact ttgctgaact ggcctttatt tgtgctgctt actttggtga acctcaggta 480

atgtatttgc tctacaaata tatgcctctg acccgcgcag ttcttacgga tgccatccgg 540

ataagtcttg agagcaacaa ccaggtaggg atttgctatg cttacttgat gggaggcagc 600

ctcaagggac tagtctccgc cccactgcgt aaacgtctgc gcgccaaact acgctcgcag 660

cgcaaaaaga aggacgttct ttcaccccac gacttcttac tgctgctcca gtag 714

<210> 288
<211> 714
<212> DNA
<213> African swine fever virus

<400> 288
atgttagaaa tagtattggc aacgctgcta ggcgacctgc agcggctccg ggttcttacc 60

cctcagcagc gggcagttgc cttctttcga gccaatacta aggagctaga ggacttctta 120

tgctcagatg ggcagtctga ggaggtactg tctggccccc ttcttaaccg tctactagaa 180

ccctcaggcc ctcttgatat tttaaccgga tatcacctat ttcgtcagaa tcccaaggca 240

ggtcagttgc gcggccttga ggtcaagatg cttgaacggt tatacgatgc taatatttac 300

aatatactgt ctcggctgcg gcctgaaaaa gttcgcaaca aggctattga gctatactgg 360

gttttccgag ctatccatat ttgtcatgct cctttagttt tagatattgt acgatatgag 420

gaaccggact ttgctgaact ggcctttatt tgtgctgctt actttggtga acctcaggta 480

atgtatttgc tctacaaata tatgcctctg acccgcgcag ttcttacgga tgccatccgg 540

ataagtcttg agagcaacaa ccaggtaggg atttgctatg cttacttgat gggaggcagc 600

ctcaagggac tagtctccgc cccactgcgt aaacgtctgc gcgccaaact acgctcgcag 660

cgcaaaaaga aggacgttct ttcaccccac gacttcttac tgctgctcca gtag 714

<210> 289
<211> 219
<212> DNA
<213> African swine fever virus

<400> 289
atgcaaaata aaatcccaaa ttttaacctt ttctttttt ttctatacag gatgttagaa 60

atagtattgg caacgctgct aggcgacctg cagcggctcc gggttcttac ccctcagcag 120

cgggcggttg ccttctttcg agccaatact aaggagctag aggacttctt acgctcagat 180

gggcaatctg aggagatact gtctggcccc cctccttaa 219

<210> 290
<211> 765
<212> DNA
<213> African swine fever virus

<400> 290
atgcaaaata aaatcccaaa ttttaacctt ttctttttt ttctatacag gatgttagaa 60

atagtattgg caacgctgct aggcgacctg cagcggctcc gggttcttac ccctcagcag 120

cgggcggttg ccttctttcg agccaatact aaggagctag aggacttctt acgctcagat 180

gggcaatctg aggagatact gtctggcccc ctccttaacc gtctactaga accctcatgc 240

cctcttgata ttttaaccgg atatcaccta tttcgtcaga atcccaaggc aggtcagttg 300

cgcggccttg aggtcaagat gcttgaacgg ttatacgatg ctaatattta caatatattg 360

tctcggctgc gacctgaaaa agtccgcaac aaggctattg agctatactg ggttttccga 420

gctatccata tttgtcatgc tcctttagtt ttagatattg tacgatatga ggaaccggac 480

tttgctgaac tggcctttat ttgtgctgct tactttggtg aacctcaggt aatgtatttg 540

ctctacaaat atatgcctct gacccgcgca gttcttacgg atgccatcca gataagtctt 600

gagagcaaca accaggtagg gatttgctat gcttacttga tgggaggcag cctcaaggga 660

ctagtctccg ccccactgcg taaacgtctg cgcgccaaac tacgctcgca gcgcaaaaag 720

aaggacgttc tttcacccca cgacttctta ctgctgctcc agtag 765

<210> 291
<211> 765
<212> DNA
<213> African swine fever virus

<400> 291
atgcaaaata aaatcccaaa ttttaacctt ttctttttt ttctatacag gatgttagaa 60

atagtattgg caacgctgct aggcgacctg cagcggctcc gggttcttac ccctcagcag 120

cgggcggttg ccttctttcg agccaatact aaggagctag aggacttctt acgctcagat 180

gggcaatctg aggagatact gtctggcccc ctccttaacc gtctactaga accctcatgc 240

cctcttgata ttttaaccgg atatcaccta tttcgtcaga atcccaaggc aggtcagttg 300

cgcggccttg aggtcaagat gcttgaacgg ttatacgatg ctaatattta caatatattg 360

tctcggctgc gacctaaaaa agtccgcaac aaggctattg agctatactg ggttttccga 420

gctatccata tttgtcatgc tcctttagtt ttagatattg tacgatatga ggaaccggac 480

tttgctgaac tggcctttat ttgtgctgct tactttggtg aacctcaggt aatgtatttg 540

ctctacaaat atatgcctct gacccgcgca gttcttacgg atgccatcca gataagtctt 600

gagagcaaca accaggtagg gatttgctat gcttacttga tgggaggcag cctcaaggga 660

ctagtctccg ccccactgcg taaacgtctg cgcgccaaac tacgctcgca gcgcaaaaag 720

aaggacgttc tttcacccca cgacttctta ctgctgctcc agtag 765

<210> 292
<211> 714
<212> DNA
<213> African swine fever virus

<400> 292
atgttagaaa tagtattggc aacgctgcta ggtgacctgc agcggctccg ggttcttacc 60

cctcagcagc gggcggttgc cttctttcga gccaatacta aggagctaga ggacttttta 120

tgctcagatg ggcagtctga ggagatactg tccggccccc tccttaaccg tctactagaa 180

ccctcaggcc ctcttgatat tttaaccgga tatcacttat ttcgtcagaa tcccaaggca 240

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gtttttcggg ctatcaatat gtgtcatgct cctttagttt tagatattgt acgatatgag 420

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ataagtcttg agagcaacag ccaggtaggg atttgctatg cctacttgat gggaggcagc 600

ctcaagggcc tagtccgtgc cccactacgt aaacgtctgc gcgccaaact acgctcgcag 660

cgcaaaaaga aggacgttct tccaccccat gacttcttac tgctgctcca gtaa 714

<210> 293
<211> 714
<212> DNA
<213> African swine fever virus

<400> 293
atgttagaaa tagtattggc aacgctgcta ggtgacctgc agcggctccg ggttcttacc 60

cctcagcagc gggcggttgc cttctttcga gccaatacta aggaggtaga agacttctta 120

tgctcagatg ggcagtctga ggaggtactg tccggccccc tccttaaccg tctactagaa 180

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gtttttcggg ctatcaatat gtgtcatgct cctttagttt tagatattgt acgatatgag 420

gaaccggact ttgctgaact ggcctttatt tgtgctgctt actttggtga acctcaggta 480

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ctcaagggcc tagtccgtgc cccactacgt aaacgtctgc gcgccaaact acgctcgcag 660

cgcaaaaaga aggacgttct tccaccccac gacttcttac tgctgctcca gtaa 714

<210> 294

<211> 714
<212> DNA
<213> African swine fever virus

<400> 294
atgttagaaa tagtattggc aacgctgcta ggtgacctgc agcggctccg ggttcttacc 60

cctcagcagc gggcggttgc cttctttcga gccaatacta aagagctaga ggacttctta 120

tgtccagatg ggcagtctga ggaggtgctg tctggctccc tccttaaccg tctactagaa 180

ccctcaggcc ctcttgatat tttaactgga tatcacctat ttcgtcagaa tcccaaggca 240

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gtttttcggg ctatcaatat gtgtcatgct cctttagttt tagatattgt acgaaatgag 420

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ctcaagggac tagtccgtgc cccgctacgt aaacgtctgc gcgccaaact acgctcgcag 660

cgcaaaaaga aggatgttct tccaccccac gacttcttac tgctgctcca gtaa 714

<210> 295
<211> 774
<212> DNA
<213> African swine fever virus

<400> 295
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atagtattgg caacgctgct gggtgatctg cagcaactta aggatcttac acctaagcag 120

cgggccgtag ctttcttccg agccaacacc aaagagctag aggactttct ctaccccgat 180

gggcagactg aggagttact ccctggattt cttcttaacc atttactaga accctcaggc 240

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cgaggccttg aggtgaaaat gcttgaacgg ttatatgatg ctaatattta caatatgctg 360

gctcggctac ggcctgagtt ggttcgtgac aaggctgttg agctatattg gctttttcga 420

gctattttaa tatgtcatgg tcccttggtt ttggagattg tacgacatga gacgttggac 480

tttgcagaaa ccgcctttat ctgtgctgct tactttagtg aacctcaggt aatgtacgct 540

ctttataact ttataccacc cactcatgca gtccttgctg atgccatcca gatgtgtctt 600

gagagcaaca gcgaggcagg gatttgctat gtctacctaa tgggaggtaa cctcaagggc 660

aaggtgcccg gctcgctgcg caaacgtctg cgtgccagtc cacttcggca agaacgcaaa 720

aagaaaaacg tccttccgcc ccacgaattc ctactcctgc tccacgggat ttaa 774

<210> 296
<211> 774
<212> DNA
<213> African swine fever virus

<400> 296
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atagtattgg ccacgctgct aggtgatctg cagaaactta aggatcttac acctccgcag 120

cgggctgtgg ctttctttcg agccaacacc aaagagctag aggactttct ctaccccgat 180

gggcagtctg aggagttact ccctggactt ctccttaacc gtttactaga accttcaggt 240

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cgaggccttg aggtgaaaat gcttgaacgg ttatatgatg ctaatattta caatatgctg 360

gctcggctac ggcctgagtt ggttcgtgac aaggctattg agctatattg gctctttcgg 420

gctattttaa tgtgtcatag tcccttagtt ttggagattg tacgacatga gacaatggat 480

tttgcagaaa ccgcctttat ctgtgccgct tactttagtg aacctcaggt aatgtacgct 540

ctttataaat ttatacctat ctctcgtgca gtccttgctg atgccattca gatgtgtctt 600

gagagcaaca gcgaggcggg gatttgctat gcttacctaa tgggggggtag cctcaagggc 660

aaggtgcctg gctcgctgcg caaacgtctg cgtgccagtc cacttcggca agagcgcaaa 720

aagaaaaacg tcctcccgcc ccatgaattc ctactcatgc tccatgggat ttaa 774

<210> 297
<211> 765
<212> DNA
<213> African swine fever virus

<400> 297
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atagtattgg caacgctgct aggtgacctg cagcggctcc gggttcttac ccctcagcag 120

cgggcggttg ccttctttcg agccaatact aaggagctag aggacttctt atgctcagat 180

gggcagtctg aggagatact gtccggcccc ctccttaacc gtctactaga accctcaggc 240

cctcttgata ttttaaccgg atatcactta tttcgtcaga atcccaaggc aggtcagttg 300

cgcggtcttg aggtcaagat gcttgaacgg ttatacgatg ctaatattta caatatattg 360

tctcggctgc gacctgaaaa agttcgcaac aaggctattg agctatactg ggttttccga 420

gctatccata tttgtcatgc tcctttagtt ttagatattg tacgatatga ggaaccggac 480

tttgctgaac tggcctttat ttgtgctgct tactttggtg aacctcaggt aatgtatttg 540

ctctacaaat atatgcctct gacccgcgca gttcttacgg atgccatccg gataagtctt 600

gagagtaaca accaggtagg gatttgctat gcttacttga tgggaggcag cctcaaggga 660

ctagtctccg ccccactgcg taaacgtctg cgcgccaaac tacgctcaca gcgcaaaaag 720

aaagacgttc tttcacccca cgacttctta ctgctgctcc agtaa 765

<210> 298
<211> 765
<212> DNA
<213> African swine fever virus

<400> 298
atgcaaaata aaatcccaaa ttttaacctt ttctttttt ttctatacag gatgttagaa 60

atagtattgg caacgctgct aggcgacctg cagcggctcc gggttcttac ccctcagcag 120

cgggcggttg ccttctttcg agccaatact aaggagctag aggacttctt atgctcagat 180

gggcagtctg aggagatact atctggcccc cttcttaacc gtctactaga accctcaggc 240

cctcttgata ttttaactgg atatcaccta tttcgtcaga accccaaggc aggtcagtta 300

cgcggccttg aggtcaagat gcttgaacgg ttatacgatg ctaatattta caatatattg 360

tctcggctgc gacctgaaaa agttcgcaac aaggctattg agctttactg ggttttttcga 420

gctatccata tttgtcatgc tcctttagtt ttagatattg tacgatatga ggaaccggac 480

tttgctgaac tggcctttat ttgtgctgct tactttggtg aacctcaggt aatgtatttg 540

ctctacaaat atatgcctct gacccgcgca gttcttacgg atgccatccg gataagtctt 600

gagagtaaca accaggtagg gatttgctat gcttacttga tgggaggcag cctcaaggga 660

ctagtctccg ccccactgcg taaacgtctg tgcgccaaac tacgctcgca gcgcaaaaag 720

aaggacgttc tttcacccca cgacttctta ctgctgctcc agtaa 765

<210> 299
<211> 774
<212> DNA
<213> African swine fever virus

<400> 299
atgcaaaata aaatcccaaa ttttaacctt ttctttttt ttctatacaa gatgttagaa 60

atagtattgg caacgctgct aggtgatctg cagaaactta aagatcttac acctatgcag 120

cgggctgtgg ctttctttcg agccaacact aaagagctag aggacttcct ctgccccgat 180

gggcagtctg aggagttact ccctggactt ctccttaacc gtttattaga accttcaggt 240

cctattgaca ttttaaccgg ttaccaccta tttcgtgaga atccgaaggc aggtcggctg 300

cgtggccttg aggtcaagct gcttgaacgg ttatatgatg ctaacatcta caatatattg 360

gcccagctac ggcctgagtt ggttcgcaat aaggctgttg agttatattg gctctttcgg 420

gctattttga tgtgtcatgg tcccttagtt ttggagattg tacgacatga gacaatggat 480

tttgcagaat tagcctttat ctgtgctgct tactttagtg aacctcaggt aatgtacgct 540

atttataaat ttatacctat ctcttgcgca gtccttgctg atgccattca gatgtgtctt 600

gagagtaaca gcgaggcggg gatttgctat gcttacctaa tgggggggtag cctcaagggc 660

aaggtgcctg gcgcgctgcg caaacgtctg cgtgccagtc cacttcggca agagcgcaaa 720

aagaaaaacg ttcttccacc ccatgaattc ctactcatgc ttcatgggat ttaa 774

<210> 300
<211> 723
<212> DNA
<213> African swine fever virus

<400> 300
atgttagaaa tagtattggc aacgctgcta ggtgatctgc agaagcttag ggatcttaca 60

cctatgcagc gggctgtggc tttctttcga gtcaacacta aagagctaga ggacttcctc 120

taccccgatg ggcagtctga ggagttgctc cctggacttc tccttaaccg tttactagaa 180

ccttcaggcc ctattgacat tttaaccggt taccacctat ttcgtgagaa cccaaaggca 240

ggtcggctgc gtggccttga ggttaagctg cttgaacggt tatatgatgc taacatctac 300

aatatgttgg cccaaatacg acctgagttg gttcgtatca aggctattga gttatattgg 360

ctctttcggg ctattttaat gtgtcatagt cccttagttt tggagattgt acgacatgag 420

acaatggatt ttgcagaatt agcctttatc tgtgctgctt actttagtga acctcaggta 480

atgtacgctc tttataaatt tatacctatt tctcgcgcag tccttgctga tgccatcgag 540

atgtctcttg agagcaacag cgagacgggg atttgctatg cctacctaat ggggggtagc 600

ctcaagggca aggtgcccgg cccgctgcgc aaacgtctgc gtgccagtcc acttcggcaa 660

gagcgcaaaa agaaaaacgt ccttccgccc catgaatttc tactcatgct ccatgggatt 720

taa 723

<210> 301
<211> 237
<212> PRT
<213> African swine fever virus

<400> 301

Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg Leu
1 5 10 15

Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala Asn
20 25 30

Thr Lys Glu Leu Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu Glu
35 40 45

Val Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
50 55 60

Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys Ala
65 70 75 80

Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr Asp
85 90 95

Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val Arg
100 105 110

Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile Cys
115 120 125

His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp Phe
130 135 140

```
Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln Val
145                 150                 155                 160


Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu Thr
                165                 170                 175


Asp Ala Ile Arg Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile Cys
            180                 185                 190


Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala Pro
        195                 200                 205


Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys Lys
    210                 215                 220


Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
225                 230                 235


<210>  302
<211>  237
<212>  PRT
<213>  African swine fever virus

<400>  302

Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg Leu
1               5                   10                  15


Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala Asn
            20                  25                  30


Thr Lys Glu Leu Glu Asp Phe Leu Cys Ser Asp Gly Gln Ser Glu Glu
        35                  40                  45


Val Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly Pro
    50                  55                  60


Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys Ala
65                  70                  75                  80


Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr Asp
                85                  90                  95
```

```
Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val Arg
            100                 105                 110

Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile Cys
        115                 120                 125

His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp Phe
    130                 135                 140

Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln Val
145                 150                 155                 160

Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu Thr
                165                 170                 175

Asp Ala Ile Arg Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile Cys
            180                 185                 190

Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala Pro
        195                 200                 205

Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys Lys
    210                 215                 220

Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
225                 230                 235


<210>  303
<211>  257
<212>  PRT
<213>  African swine fever virus

<400>  303

Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1               5                   10                  15

Lys Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Lys
            20                  25                  30

Leu Lys Asp Leu Thr Pro Met Gln Arg Ala Val Ala Phe Phe Arg Ala
```

```
        35                  40                  45

Asn Thr Lys Glu Leu Glu Asp Phe Leu Cys Pro Asp Gly Gln Ser Glu
    50                  55                  60

Glu Leu Leu Pro Gly Leu Leu Leu Asn Arg Leu Leu Glu Pro Ser Gly
65                  70                  75                  80

Pro Ile Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Glu Asn Pro Lys
                85                  90                  95

Ala Gly Arg Leu Arg Gly Leu Glu Val Lys Leu Leu Glu Arg Leu Tyr
            100                 105                 110

Asp Ala Asn Ile Tyr Asn Ile Leu Ala Gln Leu Arg Pro Glu Leu Val
        115                 120                 125

Arg Asn Lys Ala Val Glu Leu Tyr Trp Leu Phe Arg Ala Ile Leu Met
    130                 135                 140

Cys His Gly Pro Leu Val Leu Glu Ile Val Arg His Glu Thr Met Asp
145                 150                 155                 160

Phe Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Ser Glu Pro Gln
                165                 170                 175

Val Met Tyr Ala Ile Tyr Lys Phe Ile Pro Ile Ser Cys Ala Val Leu
            180                 185                 190

Ala Asp Ala Ile Gln Met Cys Leu Glu Ser Asn Ser Glu Ala Gly Ile
        195                 200                 205

Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Lys Val Pro Gly
    210                 215                 220

Ala Leu Arg Lys Arg Leu Arg Ala Ser Pro Leu Arg Gln Glu Arg Lys
225                 230                 235                 240

Lys Lys Asn Val Leu Pro Pro His Glu Phe Leu Leu Met Leu His Gly
                245                 250                 255
```

Ile

<210> 304
<211> 257
<212> PRT
<213> African swine fever virus

<400> 304

```
Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1               5                  10                  15


Lys Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Gln
            20                  25                  30


Leu Lys Asp Leu Thr Pro Lys Gln Arg Ala Val Ala Phe Phe Arg Ala
        35                  40                  45


Asn Thr Lys Glu Leu Glu Asp Phe Leu Tyr Pro Asp Gly Gln Thr Glu
    50                  55                  60


Glu Leu Leu Pro Gly Phe Leu Leu Asn His Leu Leu Glu Pro Ser Gly
65                  70                  75                  80


Pro Ile Glu Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys
                85                  90                  95


Ala Gly Arg Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
            100                 105                 110


Asp Ala Asn Ile Tyr Asn Met Leu Ala Arg Leu Arg Pro Glu Leu Val
        115                 120                 125


Arg Asp Lys Ala Val Glu Leu Tyr Trp Leu Phe Arg Ala Ile Leu Ile
    130                 135                 140


Cys His Gly Pro Leu Val Leu Glu Ile Val Arg His Glu Thr Leu Asp
145                 150                 155                 160


Phe Ala Glu Thr Ala Phe Ile Cys Ala Ala Tyr Phe Ser Glu Pro Gln
                165                 170                 175
```

Val Met Tyr Ala Leu Tyr Asn Phe Ile Pro Pro Thr His Ala Val Leu
            180   185   190

Ala Asp Ala Ile Gln Met Cys Leu Glu Ser Asn Ser Glu Ala Gly Ile
        195   200   205

Cys Tyr Val Tyr Leu Met Gly Gly Asn Leu Lys Gly Lys Val Pro Gly
    210   215   220

Ser Leu Arg Lys Arg Leu Arg Ala Ser Pro Leu Arg Gln Glu Arg Lys
225   230   235   240

Lys Lys Asn Val Leu Pro Pro His Glu Phe Leu Leu Leu Leu His Gly
                245   250   255

Ile

<210> 305
<211> 254
<212> PRT
<213> African swine fever virus

<400> 305

Met Gln Asn Lys Ile Pro Asn Phe Asn Leu Phe Phe Phe Phe Leu Tyr
1   5   10   15

Arg Met Leu Glu Ile Val Leu Ala Thr Leu Leu Gly Asp Leu Gln Arg
            20   25   30

Leu Arg Val Leu Thr Pro Gln Gln Arg Ala Val Ala Phe Phe Arg Ala
        35   40   45

Asn Thr Lys Glu Leu Glu Asp Phe Leu Arg Ser Asp Gly Gln Ser Glu
    50   55   60

Glu Ile Leu Ser Gly Pro Leu Leu Asn Arg Leu Leu Glu Pro Ser Cys
65   70   75   80

Pro Leu Asp Ile Leu Thr Gly Tyr His Leu Phe Arg Gln Asn Pro Lys

```
                85                  90                  95

Ala Gly Gln Leu Arg Gly Leu Glu Val Lys Met Leu Glu Arg Leu Tyr
            100                 105                 110

Asp Ala Asn Ile Tyr Asn Ile Leu Ser Arg Leu Arg Pro Glu Lys Val
        115                 120                 125

Arg Asn Lys Ala Ile Glu Leu Tyr Trp Val Phe Arg Ala Ile His Ile
    130                 135                 140

Cys His Ala Pro Leu Val Leu Asp Ile Val Arg Tyr Glu Glu Pro Asp
145                 150                 155                 160

Phe Ala Glu Leu Ala Phe Ile Cys Ala Ala Tyr Phe Gly Glu Pro Gln
                165                 170                 175

Val Met Tyr Leu Leu Tyr Lys Tyr Met Pro Leu Thr Arg Ala Val Leu
            180                 185                 190

Thr Asp Ala Ile Gln Ile Ser Leu Glu Ser Asn Asn Gln Val Gly Ile
        195                 200                 205

Cys Tyr Ala Tyr Leu Met Gly Gly Ser Leu Lys Gly Leu Val Ser Ala
    210                 215                 220

Pro Leu Arg Lys Arg Leu Arg Ala Lys Leu Arg Ser Gln Arg Lys Lys
225                 230                 235                 240

Lys Asp Val Leu Ser Pro His Asp Phe Leu Leu Leu Leu Gln
                245                 250
```

<210> 306
<211> 123
<212> PRT
<213> African swine fever virus

<400> 306

```
Met Leu Val Ile Phe Leu Gly Leu Leu Gly Leu Leu Ala Asn Gln Val
1               5                   10                  15
```

```
Leu Gly Leu Pro Asn Gln Pro Ala Gly Gln Leu His Pro Thr Asp Asn
            20                  25                  30

Pro Pro Lys Glu Glu Leu Gly Tyr Trp Cys Thr Tyr Thr Glu Ser Cys
        35                  40                  45

Lys Phe Cys Trp Asn Cys Gln Asn Gly Leu Cys Glu Gly Lys Leu Glu
    50                  55                  60

Asn Thr Thr Ile Leu Glu Asn Glu Tyr Val Gln Ser Cys Ile Val Ser
65                  70                  75                  80

Arg Trp Leu Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His
                85                  90                  95

Val Met Ala Cys Ser Glu Pro Lys Pro Trp Asn Pro Tyr Lys Ile Leu
            100                 105                 110

Lys Arg Glu Trp Lys Lys Asn Val Ser Gln Asn
        115                 120
```

<210> 307
<211> 123
<212> PRT
<213> African swine fever virus

<400> 307

```
Met Leu Val Ile Phe Leu Gly Leu Leu Gly Leu Leu Ala Asn Gln Val
1               5                   10                  15

Leu Gly Leu Pro Asn Gln Pro Ala Gly Gln Leu His Pro Thr Asp Asn
            20                  25                  30

Pro Pro Lys Glu Glu Leu Gly Tyr Trp Cys Thr Tyr Thr Glu Ser Cys
        35                  40                  45

Lys Phe Cys Trp Asn Cys Gln Asn Gly Leu Cys Glu Gly Lys Leu Glu
    50                  55                  60

Asn Thr Thr Ile Leu Glu Asn Glu Tyr Val Gln Ser Cys Ile Val Ser
65                  70                  75                  80
```

```
Arg Trp Leu Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile His His
                85                  90                  95


Val Met Pro Cys Ser Glu Pro Lys Pro Trp Asn Pro Tyr Lys Ile Leu
            100                 105                 110


Lys Lys Glu Trp Lys Glu Asn Val Ser Gln Asn
        115                 120


<210>  308
<211>  120
<212>  PRT
<213>  African swine fever virus

<400>  308

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Asn Gln Val
1               5                   10                  15


Ser Ser Gln Leu Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20                  25                  30


Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35                  40                  45


Trp Asp Cys Gln Asp Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50                  55                  60


Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65                  70                  75                  80


Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85                  90                  95


Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
            100                 105                 110


Trp Lys Glu Asn Asn Ser Gln Asn
        115                 120


<210>  309
<211>  120
```

<212> PRT
<213> African swine fever virus

<400> 309

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Asn Gln Val
1   5   10   15

Ser Ser Gln Leu Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20   25   30

Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35   40   45

Trp Asp Cys Gln Asp Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50   55   60

Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65   70   75   80

Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85   90   95

Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
            100   105   110

Trp Lys Glu Asn Asn Ser Gln Asn
        115   120

<210> 310
<211> 121
<212> PRT
<213> African swine fever virus

<400> 310

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Asn Gln Val
1   5   10   15

Ser Ser Gln Leu Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20   25   30

Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35   40   45

```
Trp Asp Cys Gln Asn Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50                  55                  60

Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65                  70                  75                  80

Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85                  90                  95

Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
            100                 105                 110

Trp Lys Glu Asn Asn Ser Gln Asn Lys
        115                 120
```

<210> 311
<211> 118
<212> PRT
<213> African swine fever virus

<400> 311

```
Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Val Asn Gln Val
1               5                   10                  15

Ser Ser Gln Pro Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20                  25                  30

Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35                  40                  45

Trp Asp Cys Gln Asn Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50                  55                  60

Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65                  70                  75                  80

Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85                  90                  95

Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
```

```
            100                 105                 110


Trp Lys Glu Asn Asn Ser
        115


<210>  312
<211>  121
<212>  PRT
<213>  African swine fever virus

<400>  312

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Asn Gln Val
1               5                   10                  15


Ser Ser Gln Leu Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20                  25                  30


Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35                  40                  45


Trp Asp Cys Gln Asn Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50                  55                  60


Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65                  70                  75                  80


Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85                  90                  95


Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
            100                 105                 110


Trp Lys Glu Asn Asn Ser Gln Asn Lys
        115                 120


<210>  313
<211>  121
<212>  PRT
<213>  African swine fever virus

<400>  313

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Asn Gln Val
```

```
1               5                   10                  15

Ser Ser Gln Leu Val Gly Gln Leu His Pro Thr Glu Asn Pro Ser Glu
            20                  25                  30

Asn Glu Leu Glu Tyr Trp Cys Thr Tyr Met Glu Cys Cys Gln Phe Cys
        35                  40                  45

Trp Asp Cys Gln Asn Gly Leu Cys Val Asn Lys Leu Gly Asn Thr Thr
    50                  55                  60

Ile Leu Glu Asn Glu Tyr Val His Pro Cys Ile Val Ser Arg Trp Leu
65                  70                  75                  80

Asn Lys Cys Met Tyr Asp Leu Gly Gln Gly Ile Asp His Val Met Val
                85                  90                  95

Cys Ser Gln Pro Lys Tyr Trp Asn Pro Tyr Lys Ile Leu Lys Lys Glu
            100                 105                 110

Trp Lys Glu Asn Asn Ser Gln Asn Lys
        115                 120
```

<210> 314
<211> 205
<212> PRT
<213> African swine fever virus

<400> 314

```
Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Ser Gln Val
1               5                   10                  15

Ser Ser Gln Leu Val Gly Gln Leu Arg Pro Thr Glu Glu Pro Pro Glu
            20                  25                  30

Glu Glu Leu Glu Tyr Trp Cys Ala Tyr Met Glu Ser Cys Gln Phe Cys
        35                  40                  45

Trp Asp Cys Gln Asp Gly Thr Cys Ile Asn Lys Ile Asp Gly Ser Val
    50                  55                  60
```

```
Ile Tyr Lys Asn Glu Tyr Val Lys Ser Cys Leu Val Ser Arg Trp Leu
65                  70                  75                  80


Asp Lys Cys Met Tyr Asp Leu Asp Lys Gly Ile Tyr His Thr Met Asn
                85                  90                  95


Cys Asn Gln Val Leu Gly Leu Pro Asn Gln Pro Ala Gly Gln Leu His
            100                 105                 110


Pro Thr Asp Asn Pro Pro Gln Glu Glu Leu Glu Tyr Trp Cys Thr Tyr
        115                 120                 125


Thr Glu Asn Cys Lys Phe Cys Trp Asn Cys Gln Asn Gly Leu Cys Glu
    130                 135                 140


Gly Lys Leu Glu Asn Thr Thr Ile Leu Glu Asn Glu Tyr Val Gln Ser
145                 150                 155                 160


Cys Ile Val Ser Arg Trp Leu Asn Lys Cys Met Tyr Asp Leu Gly Gln
                165                 170                 175


Gly Ile His His Val Met Ala Cys Ser Glu Pro Lys Pro Trp Asn Pro
            180                 185                 190


Tyr Lys Ile Leu Lys Arg Glu Trp Lys Glu Asn Asn Ser
        195                 200                 205


<210>  315
<211>  205
<212>  PRT
<213>  African swine fever virus

<400>  315

Met Leu Val Ile Phe Leu Gly Ile Leu Gly Leu Leu Ala Ser Gln Val
1               5                   10                  15


Ser Ser Gln Leu Val Gly Gln Leu Arg Pro Thr Glu Glu Pro Pro Glu
            20                  25                  30


Glu Glu Leu Glu Tyr Trp Cys Ala Tyr Met Glu Ser Cys Gln Phe Cys
        35                  40                  45
```

```
Trp Asp Cys Gln Asp Gly Thr Cys Ile Asn Lys Ile Asp Gly Ser Val
    50                  55                  60

Ile Tyr Lys Asn Glu Tyr Val Lys Ser Cys Leu Val Ser Arg Trp Leu
65                  70                  75                  80

Asp Lys Cys Met Tyr Asp Leu Asp Lys Gly Ile Tyr His Thr Met Asn
                85                  90                  95

Cys Asn Gln Val Leu Gly Leu Pro Asn Gln Pro Ala Gly Gln Leu His
            100                 105                 110

Pro Thr Asp Asn Pro Pro Gln Glu Glu Leu Glu Tyr Trp Cys Thr Tyr
        115                 120                 125

Thr Glu Asn Cys Lys Phe Cys Trp Asn Cys Gln Asn Gly Leu Cys Glu
    130                 135                 140

Gly Lys Leu Glu Asn Thr Thr Ile Leu Glu Asn Glu Tyr Val Gln Ser
145                 150                 155                 160

Cys Ile Val Ser Arg Trp Leu Asn Lys Cys Met Tyr Asp Leu Gly Gln
                165                 170                 175

Gly Ile His His Val Met Ala Cys Ser Glu Pro Lys Pro Trp Asn Pro
            180                 185                 190

Tyr Lys Ile Leu Lys Arg Glu Trp Lys Glu Asn Asn Ser
        195                 200                 205
```

<210> 316
<211> 103
<212> PRT
<213> African swine fever virus

<400> 316

```
Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln Trp Cys Phe Tyr Glu Ile Ser
            20                  25                  30
```

```
Leu Lys Ile Leu Asn His His Ser Met Glu Lys Trp Arg Asp Lys Asn
        35                  40                  45

Trp Ser Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe
    50                  55                  60

Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu
65                  70                  75                  80

Cys Thr Thr Met Lys Leu Leu Met Leu Leu Asn Ile Leu Val Leu Leu
                85                  90                  95

Ser Gln Pro Ile Leu Asn Asn
            100
```

<210> 317
<211> 119
<212> PRT
<213> African swine fever virus

<400> 317

```
Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Pro Trp Cys Phe Tyr Glu Ile Ser
            20                  25                  30

Leu Lys Ile Pro Asn His His Ser Met Lys Cys Cys Ser Tyr Pro Arg
        35                  40                  45

Leu Tyr Glu His Glu Met Phe Met Glu Lys Trp Arg Asp Lys Asn Trp
    50                  55                  60

Pro Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe Val
65                  70                  75                  80

Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu Ser
                85                  90                  95

Thr Thr Met Lys Leu Leu Met Leu Leu Ser Ile Leu Val Leu Leu Leu
```

```
            100                 105                 110


Ser Gln Pro Ile Leu Asn Asn
        115


<210>  318
<211>  119
<212>  PRT
<213>  African swine fever virus

<400>  318

Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15


Leu Thr Tyr Gln Ser Pro Thr Thr Pro Trp Cys Phe Tyr Glu Ile Ser
            20                  25                  30


Leu Lys Ile Pro Asn His His Ser Met Lys Cys Cys Ser Tyr Pro Arg
        35                  40                  45


Leu Tyr Glu His Glu Met Phe Met Glu Lys Trp Arg Asp Lys Asn Trp
    50                  55                  60


Pro Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe Val
65                  70                  75                  80


Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu Ser
                85                  90                  95


Thr Thr Met Lys Leu Leu Met Leu Leu Ser Ile Leu Val Leu Leu Leu
            100                 105                 110


Ser Gln Pro Ile Leu Asn Asn
        115


<210>  319
<211>  168
<212>  PRT
<213>  African swine fever virus

<400>  319

Met Lys Val Phe Leu Gly Leu Leu Leu Gly Phe Ser Ile Ile Leu Ile
```

```
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln His Pro Pro Lys Glu Glu Leu
            20                  25                  30

Ala Tyr Trp Cys Thr Tyr Ala Lys Ser Cys Asp Phe Cys Trp Asp Cys
        35                  40                  45

Gln Asn Asp Thr Cys Ile Asn Lys Val Ile Asn Glu Ser Ile Ser Ile
    50                  55                  60

Thr Ser Ile Val Asn Cys Arg Val Thr Arg Asp Ser Gln Ser Cys Phe
65                  70                  75                  80

Tyr Glu Ile Ser Val Lys Ile Pro Asn His His Ser Met Glu Cys Ser
                85                  90                  95

Tyr Pro Arg Leu Tyr Glu His Glu Met Phe Met Glu Lys Trp Arg Asp
            100                 105                 110

Glu Tyr Trp Pro Ile Ile Ile Lys Gln Cys Cys Phe Tyr Leu Val Phe
        115                 120                 125

Ser Ile Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu
    130                 135                 140

Arg Leu Arg Thr Thr Ile Lys Leu Leu Ile Leu Leu Ser Ile Leu Val
145                 150                 155                 160

Trp Leu Ser Gln Pro Val Leu Asn
                165
```

<210> 320
<211> 171
<212> PRT
<213> African swine fever virus

<400> 320

```
Met Lys Val Phe Leu Ala Leu Leu Leu Gly Tyr Leu Thr Ile Leu Ile
1               5                   10                  15
```

```
Leu Thr Tyr Gln Thr Pro Thr Thr Gln His Pro Pro Lys Glu Glu Leu
            20                  25                  30

Pro Tyr Trp Cys Thr Tyr Val Lys Asn Cys Asp Leu Cys Trp Asp Cys
        35                  40                  45

Gln Asp Ser Ile Tyr Trp Asn Lys Val Ile Ser Glu Ser Ile Ser Ile
    50                  55                  60

Asn Ser Ile Ile Asn Cys Arg Val Thr Cys Asp Ser Gln Ser Gln Ser
65                  70                  75                  80

Cys Phe Tyr Glu Ile Leu Leu Lys Ile Pro Asn His His Ser Met Glu
                85                  90                  95

Cys Ser Tyr Pro Gly Ser Tyr Glu Asn Glu Met Phe Met Glu Lys Trp
            100                 105                 110

Arg Asp Glu Asn Trp Ser Ile Ile Ile Lys His Tyr Cys Phe Tyr Leu
        115                 120                 125

Val Phe Ser Phe Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys
    130                 135                 140

Asn Leu Arg Leu Ser Thr Thr Met Lys Leu Leu Met Leu Leu Ser Ile
145                 150                 155                 160

Leu Val Cys Leu Ser Gln Pro Ile Leu Asn Asn
                165                 170


<210>  321
<211>  169
<212>  PRT
<213>  African swine fever virus

<400>  321

Met Lys Val Phe Leu Gly Leu Leu Leu Gly Phe Ser Ile Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln His Pro Pro Lys Glu Glu Leu
            20                  25                  30
```

```
Ala Tyr Trp Cys Thr Tyr Ala Lys Ser Cys Asp Phe Cys Trp Asp Cys
        35                  40                  45

Gln Asn Asp Thr Cys Ile Asn Lys Val Ile Asn Glu Ser Ile Ser Ile
    50                  55                  60

Thr Ser Ile Val Asn Cys Arg Val Thr Arg Asp Ser Gln Ser Cys Phe
65                  70                  75                  80

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

Tyr Pro Arg Leu Tyr Glu His Glu Met Phe Met Glu Lys Trp Arg Asp
            100                 105                 110

Glu Tyr Trp Pro Ile Ile Ile Lys Gln Cys Cys Phe Tyr Leu Val Phe
        115                 120                 125

Ser Phe Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu
    130                 135                 140

Arg Leu Arg Thr Thr Ile Lys Leu Leu Ile Leu Leu Ser Ile Leu Val
145                 150                 155                 160

Trp Leu Ser Gln Pro Ile Leu Asn Asn
                165
```

<210> 322
<211> 103
<212> PRT
<213> African swine fever virus

<400> 322

```
Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln Trp Cys Phe Tyr Glu Ile Ser
            20                  25                  30

Leu Lys Ile Leu Asn His His Ser Met Glu Lys Trp Arg Asp Lys Asn
        35                  40                  45
```

```
Trp Ser Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe
    50                  55                  60

Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu
65                  70                  75                  80

Cys Thr Thr Met Lys Leu Leu Met Leu Leu Asn Ile Leu Val Leu Leu
                85                  90                  95

Ser Gln Pro Ile Leu Asn Asn
            100
```

<210> 323
<211> 171
<212> PRT
<213> African swine fever virus

<400> 323

```
Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1               5                   10                  15

Leu Thr Tyr Gln Ser Pro Thr Thr Gln His Pro Pro Lys Glu Glu Leu
            20                  25                  30

Glu Tyr Trp Cys Thr Tyr Ala Lys Thr Cys Asp Phe Cys Trp Asp Cys
        35                  40                  45

Gln Asn Asp Thr Cys Ile Asn Lys Val Ile Asn Glu Ser Ile Ser Met
    50                  55                  60

Asn Ser Ile Val Asn Cys Arg Val Thr Arg Asp Ser Gln Ser Gln Ser
65                  70                  75                  80

Cys Phe Tyr Glu Ile Ser Leu Lys Ile Pro Asn Tyr His Ser Met Glu
                85                  90                  95

Cys Ser Tyr Pro Arg Leu Tyr Lys His Phe Met Ser Met Glu Lys Trp
            100                 105                 110

Arg Asp Glu Asn Trp Pro Ile Leu Ile Arg His Tyr Cys Phe Tyr Leu
```

115 120 125

Val Phe Ser Phe Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys
130 135 140

Asn Leu Arg Leu Arg Thr Thr Met Lys Leu Leu Met Leu Leu Ser Ile
145 150 155 160

Leu Val Leu Leu Ser Gln Pro Ile Leu Asn Asn
165 170

<210> 324
<211> 107
<212> PRT
<213> African swine fever virus

<400> 324

Met Asn Ala Thr Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser
1 5 10 15

Thr Ile Leu Ile Leu Thr Tyr Gln Ser Pro Thr Thr Gln Trp Cys Phe
20 25 30

Tyr Glu Ile Ser Leu Lys Ile Leu Asn His His Ser Met Glu Lys Trp
35 40 45

Arg Asp Lys Asn Trp Ser Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu
50 55 60

Val Phe Ser Phe Ala Phe Ala Gly Cys Val Ala Phe Ala Ile Cys Lys
65 70 75 80

Asn Leu Arg Leu Cys Thr Thr Met Lys Leu Leu Met Leu Leu Gly Ile
85 90 95

Leu Val Leu Leu Ser Gln Pro Ile Leu Asn Asn
100 105

<210> 325
<211> 117
<212> PRT
<213> African swine fever virus

<400> 325

Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1   5   10   15

Leu Thr Tyr Gln Ser Pro Ala Thr Gln Trp Cys Phe Tyr Glu Ile Ser
            20   25   30

Leu Lys Ile Pro Asn His His Ser Met Glu Cys Ser Tyr Pro Arg Leu
        35   40   45

Tyr Lys His Phe Ile Phe Met Glu Lys Trp Arg Asp Lys Asn Trp Ser
    50   55   60

Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe Ala Phe
65   70   75   80

Ala Gly Cys Ile Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu Cys Thr
                85   90   95

Thr Met Lys Leu Leu Met Leu Leu Ser Ile Leu Val Leu Leu Ser Gln
            100   105   110

Pro Ile Leu Asn Asn
        115

<210> 326
<211> 117
<212> PRT
<213> African swine fever virus

<400> 326

Met Lys Val Phe Leu Gly Leu Leu Leu Gly Tyr Ser Thr Ile Leu Ile
1   5   10   15

Leu Thr Tyr Gln Ser Pro Ala Thr Gln Trp Cys Phe Tyr Glu Ile Ser
            20   25   30

Leu Lys Ile Pro Asn His His Ser Met Glu Cys Ser Tyr Pro Arg Leu
        35   40   45

```
Tyr Lys His Phe Met Phe Met Lys Lys Trp Arg Asp Lys Asn Trp Ser
    50                  55                  60

Ile Ile Ile Arg Tyr Tyr Cys Phe Tyr Leu Val Phe Ser Phe Ala Phe
65                  70                  75                  80

Ala Gly Cys Ile Ala Phe Ala Ile Cys Lys Asn Leu Arg Leu Cys Thr
                85                  90                  95

Thr Met Lys Leu Leu Met Leu Leu Ser Ile Leu Val Leu Leu Ser Gln
            100                 105                 110

Pro Ile Leu Asn Asn
        115
```

<210> 327
<211> 210
<212> PRT
<213> African swine fever virus

<400> 327

```
Met Ile Ile Ile Leu Ile Phe Leu Ile Cys Leu Lys Ile Val Leu Asn
1               5                   10                  15

Asn Asn Ile Ile Ile Trp His Thr Leu Asn Glu Thr Ile Phe Leu Asn
            20                  25                  30

Asn Ser Ile Thr Phe Thr Asp Asn Leu Gly Gly Leu Phe Trp Asn Thr
        35                  40                  45

Tyr Tyr Asn Asn Asn His Ser Ile Leu Thr Ser Cys Gly Ile Tyr Gln
    50                  55                  60

Asn Tyr Cys Ser Cys Thr Asn Asn Tyr Ser Thr Ser Leu Tyr Asn Ile
65                  70                  75                  80

Thr Asn Asn Cys Gly Leu Ile Ile Phe Pro Asn Asn Thr Lys Arg Phe
                85                  90                  95

Asn Thr Thr Tyr Glu Leu Val Tyr Leu Asn Asn Ser Thr Lys Tyr Thr
            100                 105                 110
```

Ile Asn Leu Leu Val Pro Val Thr Pro Pro Asn Ile Thr Tyr Asn Cys
        115   120   125

Thr Thr Ser Val Ile Thr Cys Lys Lys Asn Asp Gly Thr Asn Thr Asn
    130   135   140

Met Phe Leu Lys Ile Asn Asp Thr Ile Val Lys Ser Ser Asn Glu Ser
145   150   155   160

Val Phe Glu Tyr Ser Trp Asn Ser Thr Asp Leu Asn Asn Asn Phe Thr
                165   170   175

Ala Ile Cys Ile Ile Asn Asn Thr Ile Asn Ser Ser Asn Asp Thr Gln
            180   185   190

Thr Ile Glu Cys Pro Asn Ile Leu Leu Asn Asn Tyr Leu Asp Phe Phe
        195   200   205

Gln Val
    210

<210> 328
<211> 207
<212> PRT
<213> African swine fever virus

<400> 328

Met Ile Ile Ile Leu Ile Phe Leu Ile Tyr Leu Lys Leu Val Leu Asn
1   5   10   15

Asn Asn Ile Ile Ile Trp His Pro Thr Leu Asn Glu Thr Ile Phe Leu
            20   25   30

Asn Val Thr Thr Ile Gly Asn Ile Ser Gly Leu Phe Trp Asn Thr Tyr
        35   40   45

Tyr Asn Asn Asn Arg Ser Glu Leu Thr Lys Cys Gly Ile Tyr Asn Asn
    50   55   60

Tyr Cys Ser Cys Asp Ser Leu Asn Thr Ser Leu Tyr Asn Ile Asn Asn
65   70   75   80

```
Cys Ser Leu Val Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn Thr Ile
                85                  90                  95


Tyr Glu Leu Ile Tyr Ser Gly Asn Gln Thr Asn Tyr Thr Ile Lys Leu
            100                 105                 110


Leu Glu Ser Thr Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Thr Ser
        115                 120                 125


Val Ile Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Phe Leu
    130                 135                 140


Thr Ile Asn Asn Thr Ile Val Asn Ser Thr Asn Glu Asp Val Ile Tyr
145                 150                 155                 160


Tyr Tyr Trp Asn Arg Ser Glu Phe Asn Asn Phe Thr Ala Thr Cys Met
                165                 170                 175


Ile Asn Asn Thr Ile Asn Ser Ser Asn Ile Ser Glu Ile Ile Asp Cys
            180                 185                 190


Thr Asn Thr Leu Leu Leu Asn Ser Tyr Leu Asp Phe Phe Gln Val
        195                 200                 205


<210>  329
<211>  211
<212>  PRT
<213>  African swine fever virus

<400>  329

Met Ile Ile Lys Val Ile Phe Leu Val Phe Phe Lys Met Val Leu Ser
1               5                   10                  15


Asn Ile Ile Ile Trp Ser Thr Leu Asn Asn Thr Ile Tyr Leu Asn Ile
            20                  25                  30


Asn Tyr Ser Asp Ser Asn Leu Tyr Thr Gly Leu Phe Trp Asn Lys Tyr
        35                  40                  45


Tyr Asn Asn Thr Arg Asn Asn Phe Thr Thr Cys Val Thr Ser Asn Ser
```

```
    50                  55                  60

Ser Tyr Cys Thr Cys Lys Gly His Asn Thr Ser Leu Tyr Asn Ile Thr
65                  70                  75                  80

Asn Asn Cys Ser Leu Ile Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn
                85                  90                  95

Thr Thr Tyr Glu Leu Val Tyr Leu Asn Asn Lys Ile Asn Tyr Thr Ile
            100                 105                 110

Gln Met Val Gln Pro Val Asp Pro Pro Ile Ile Ile Tyr Asn Asp Thr
        115                 120                 125

Asn Asn Ser Leu Ile Thr Cys Glu Lys Asn Asn Gly Thr Asn Thr Glu
    130                 135                 140

Ile Tyr Leu Tyr Leu Asn Asp Thr Phe Ile Asn Asn Thr Asn Glu Asn
145                 150                 155                 160

Ser Ile Lys Tyr Tyr Trp Asn Cys Ser Glu Leu Asn His Asn Ile Thr
                165                 170                 175

Thr Thr Cys Ile Ile Asn Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys
            180                 185                 190

Val Ile Asn Cys Thr Asn Leu Leu Leu Lys Ser Asp Gln Asn Tyr Phe
        195                 200                 205

Leu Lys Asn
    210


<210>  330
<211>  205
<212>  PRT
<213>  African swine fever virus

<400>  330

Met Ile Ile Lys Leu Ile Phe Leu Ile Cys Phe Lys Ile Val Leu Ser
1               5                   10                  15
```

```
Ile Asn Tyr Trp Val Arg Tyr Asn Asp Thr Val Thr Leu Asn Ser Asn
            20                  25                  30

Ile Asn Ser Glu Thr Glu Gly Ile Phe Trp Asn Phe Tyr Asn Asn Thr
        35                  40                  45

Phe Asn Thr Ile Ala Thr Cys Gly Lys Lys Asn Asn Val Cys Glu Cys
    50                  55                  60

Ser Asn Tyr Asp Lys Ser Leu Tyr Asn Ile Thr Asn Asn Cys Ser Leu
65                  70                  75                  80

Thr Ile Phe Pro Asn Asn Thr Lys Ile Phe Asn Thr Thr Tyr Gln Leu
                85                  90                  95

Val Tyr Ser Arg Asn Arg Ile Asn Tyr Thr Ile Asn Leu Leu Leu Pro
            100                 105                 110

Val Thr Ser Pro Ile Ile Thr Tyr Asn Cys Thr Gln Ser Leu Ile Thr
        115                 120                 125

Cys Glu Lys Thr Asn Gly Thr Asn Ile His Leu Phe Leu Asn Leu Asn
    130                 135                 140

Asp Thr Ile Asn Glu Tyr Thr Asn Lys Ser Phe Leu Asn Tyr Tyr Trp
145                 150                 155                 160

Asn Ser Ser Glu Leu Asn Asn Ile Phe Leu Ala Thr Cys Ile Ile Asn
                165                 170                 175

Asn Thr Leu Asn Ser Ala Asn Thr Thr Lys Val Ile Asn Cys Thr Asn
            180                 185                 190

Pro Leu Leu Lys Ser Tyr Gln Asn Tyr Phe Leu Glu Asn
        195                 200                 205
```

<210> 331
<211> 203
<212> PRT
<213> African swine fever virus

<400> 331

```
Met Ile Ile Leu Ile Phe Leu Ile Phe Ser Asn Ile Val Leu Ser Ile
1               5                  10                  15

Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn Ile
            20                  25                  30

Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Phe Asn
        35                  40                  45

Asn Ser Phe Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe Cys
    50                  55                  60

Glu Cys Ser Asn Tyr Ser Thr Ser Ile Tyr Asn Ile Thr Asn Asn Cys
65                  70                  75                  80

Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Asp Thr Thr Tyr Gln
                85                  90                  95

Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr Pro
            100                 105                 110

Ala Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile Thr
        115                 120                 125

Cys Lys Lys Asn Asn Gly Thr Asn Thr Asn Ile Tyr Leu Asn Ile Asn
    130                 135                 140

Asp Thr Phe Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn Trp
145                 150                 155                 160

Asn Asn Ser Asn Ile Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn Asn
                165                 170                 175

Thr Ile Ser Thr Ser Asn Glu Thr Thr Leu Ile Asn Cys Thr Tyr Leu
            180                 185                 190

Thr Leu Ser Ser Asn Tyr Phe Tyr Thr Phe Phe
        195                 200
```

<210> 332

<211> 204
<212> PRT
<213> African swine fever virus

<400> 332

```
Met Ile Ile Ile Leu Ile Phe Leu Ile Ile Pro Asn Ile Val Leu Ser
1               5                  10                  15


Ile Asp Tyr Trp Val Ser Phe Asn Lys Thr Ile Ile Leu Asp Ser Asn
            20                  25                  30


Ile Thr Asn Asp Asn Asn Asp Ile Asn Gly Val Ser Trp Asn Phe Leu
        35                  40                  45


Asn Asn Ser Leu Asn Thr Leu Ala Thr Cys Gly Lys Ala Gly Asn Phe
    50                  55                  60


Cys Glu Cys Ser Asn Tyr Ser Thr Ser Leu Tyr Asn Ile Ala His Asn
65                  70                  75                  80


Cys Ser Leu Thr Ile Phe Pro His Asn Asp Val Phe Gly Thr Pro Tyr
                85                  90                  95


Gln Val Val Trp Asn Gln Ile Ile Asn Tyr Thr Ile Lys Leu Leu Thr
            100                 105                 110


Pro Val Thr Pro Pro Asn Ile Thr Tyr Asn Cys Thr Asn Phe Leu Ile
        115                 120                 125


Thr Cys Lys Lys Asn Asn Gly Thr Asn Thr Ile Ile Tyr Phe Asn Ile
    130                 135                 140


Asn Asp Thr Asn Val Lys Tyr Thr Asn Glu Ser Ile Leu Glu Tyr Asn
145                 150                 155                 160


Trp Asn Asn Ser Asn Phe Asn Asn Phe Thr Ala Thr Cys Ile Ile Asn
                165                 170                 175


Asn Thr Ile Asn Ser Ser Asn Asp Thr Gln Thr Ile Asp Cys Ile Asn
            180                 185                 190
```

```
Thr Leu Leu Ser Ser Tyr Leu Asp Phe Phe Gln Val
        195                 200
```