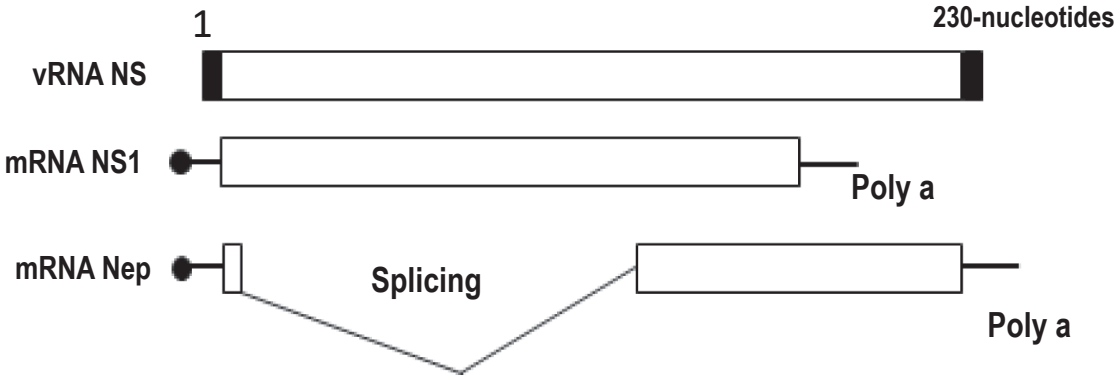
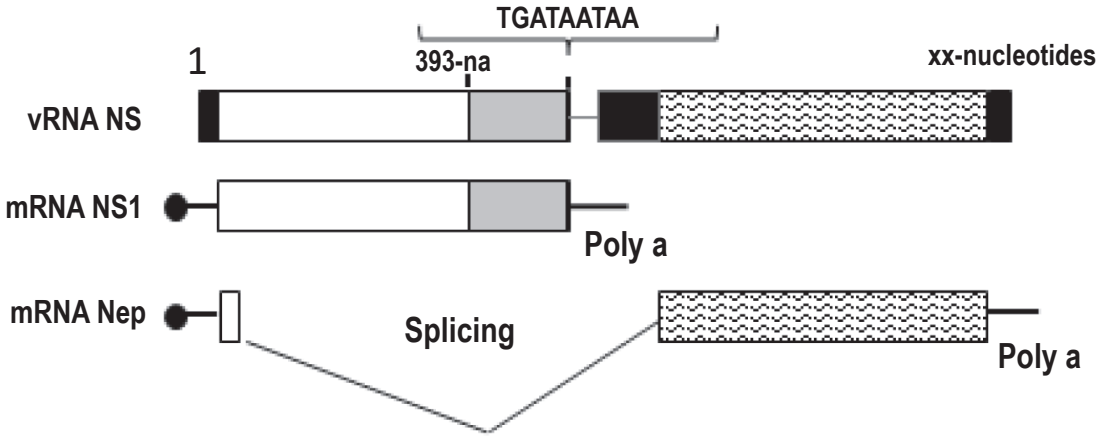
FIG. 1

(A)


1
230-nucleotides
vRNA NS
mRNA NS1
Poly a
mRNA Nep
Splicing
Poly a

(B)


TGATAATAA
1
393-na
xx-nucleotides
vRNA NS
mRNA NS1
Poly a
mRNA Nep
Splicing
Poly a

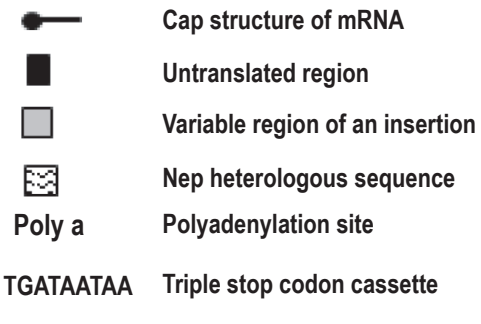

Cap structure of mRNA
Untranslated region
Variable region of an insertion
Nep heterologous sequence
Poly a
Polyadenylation site
TGATAATAA
Triple stop codon cassette

FIG. 2

(A)

AGCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGA
TTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGTGATGCCCCATTC
CTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGCACTCTTGGTCTG
GACATCGAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAA
TCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACCGACA
TGACTCTTGAGGAAATGTCAAGGGAATGGTCCATGCTCATACCCAAGCAGAAAGTGGCAG
GCCCTCTTTGTATCAGAATGGACCAGGCGATCATG**GATAAAAACATCATACTGAAAGCGA**
ACTTCAGTGTGATTTTTGACCGGCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGA
GGGAGCAATTGTTGGCGAAATTTCACCATTGCCTTCTCTTCCAG**GACATACTGCTGAGGAT**
GTCAAAAATGCAGTTGGAGTCCTCATCGGAGGACTTGAATGGAATGATAACACAGTTCG
AGTCTCTGAAACTCTACAGAGATTCGCTTGGAGAAGCAGTAATGAGAATGGGAGACCTC
CACTCACTCCAAAACAGAAACGAGAAATGGCGGGAACAATTAGGTCAGAAGTTTGAAGA
AATAAGATGGTTGATTGAAGAAGTGAGACACAAACTGAAGGTAACAGAGAATAGTTTTG
AGCAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGAA
CTTTCTCATTTCAGCTTATTTAATAATAAAAAACACCCTTGTTTCTACT (SEQ ID NO:1)

(B)

AGCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGA
TTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGTGATGCCCCATTC
CTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGCACTCTTGGTCTG
GACATCGAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAA
TCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACCGACA
TGACTCTTGAGGAAATGTCAAGGGAATGGTCCATGCTCATACCCAAGCAGAAAGTGGCAG
GCCCTCTTTGTATCAGAATGGACCAGGCGATCATG**TGATAATAA**AGTGTGATTTTTGACCG
GCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGAGGGAGCAATTGTTGGCGAAATT
TCACCATTGCCTTCTCTTCCAG**GACATACTAATGAGGATGTCAAAAATGCAATTGGGGTC**
CTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTAAAACTCTACAGAGA
TTCGCTTGGTGAAACAGTAATGAGAATGGGAGACCTCCACTCACTCCAAAACAGAAACG
GAAAATGGCGAGAACAATTAGGTCAAAAGTTCGAAGAAATAAGATGGCTGATTGAAGAA
GTGAGACACAAATTGAAGATAACAGAGAATAGTTTTGAGCAAATAACATTTATGCAAGCC
TTACAGCTACTATTTGAAGTGGAACAAGAGATAAGAACTTTCTCGTTTCAGCTTATTTAAT
AATAAAAAACACCCTTGTTTCTACT (SEQ ID NO:2)

(C)

AGCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGA
TTGCTTTCTTTGGCATGTCCGCAAACGAGTTGCAGACCAAGAACTAGGTGATGCCCCATTC
CTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGCACTCTTGGTCTG
GACATCGAGACAGCCACACGTGCTGGAAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAA
TCCGATGAGGCACTTAAAATGACCATGGCCTCTGTACCTGCGTCGCGTTACCTAACCGACA
TGACTCTTGAGGAAATGTCAAGGGAATGGTCCATGCTCATACCCAAGCAGAAAGTGGCAG
GCCCTCTTTGTATCAGAATGGACCAGGCGATCATG**TGATAATAA**AGTGTGATTTTTGACCG
GCTGGAGACTCTAATATTGCTAAGGGCTTTCACCGAAGAGGGAGCAATTGTTGGCGAAATT
TCACCATTGCCTTCTCTTCCAG**GACATACTAATGAGGATGTCAAAAATGCAATTGGGGTC**
CTCATCGGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTAAAACTCTACAGAGA
TTCGCTTGGAGAAGCAGTAATGAGAATGGGAGACCTCCACTCACTCCAAAACAGAAACG
GAAAATGGCGAGAACAATTAGGTCAAAAGTTCGAAGAAATAAGATGGCTGATTGAAGAA
GTGAGACACAAATTGAAGATAACAGAGAATAGTTTTGAGCAAATAACATTTATACAAGCC
TTACAGCTACTATTTGAAGTGGAACAAGAGATAAGAACTTTCTCGTTTCAGCTTATTTAAT
AATAAAAAACACCCTTGTTTCTACT (SEQ ID NO:3)

FIG. 3

NS124/Nep-Len

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM (SEQ ID NO:4)

NS124-HA2(A)-185

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-GG-**GLFGAIAGFIEGGWTGMIDGWYGYHH QNEQGSGYAADQKSTQNAINGITNKVNTVIEKMNIQFTAVGKEFNKLEKRMENLNKKVDDGFLDIWTYNAELLVLLENERTLDF HDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCDNECMESVRNGTYDYPKYSEESKLNREKVDGVKLESMGIYQ** (SEQ ID NO:5)

NS124-HA2(A)-65-222

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-*GG*-**AVGKEFNKLEKRMENLNKKVDDGFLDI WTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCDNECMESVRNGTYDYPKYSEESKLNREKVDG VKLESMGIYQILAIYSTVASSLVLLVSLGAISFWMCSNGSLQCRICI** (SEQ ID NO:6)

NS124-HA2(A)-23-185

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-GG-**GYHHQNEQGSGYAADQKSTQNAINGI TNKVNTVIEKMNIQFTAVGKEFNKLEKRMENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCDNECMESVRNGTYDYPKYSEESKLNREKVDGVKLESMGIYQ** (SEQ ID NO:7)

NS124-HA2(B)-186

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-GG- **GFFGAIAGFLEGGWEGMIAGWHGYT SHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMNGLHDEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDE HLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFNAGDFSLPTFD** (SEQ ID NO:8)

NS124-Fus(A)-NP

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-*GG*-**GLFGAIAGFIEGGWTGMIDGW**-*GG*-**RESRNPGNA** (SEQ ID NO:9)

NS124-Fus(B)-NP

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-GG- **GFFGAIAGFLEGGWEGMIAGW** -GG-**RESRNPGNA** (SEQ ID NO:10)

NS124-Esat6

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-*GG*-**MTEQQWNFAGIEAAASAIQGNV TSIHSLLDEGKQSLTKLAAAWGGSGSEAYQGVQQKWDATATELNNALQNLARTISEAGQAMASTEGNVTGMFA** (SEQ ID NO:11)

NS124-2A-Esat6

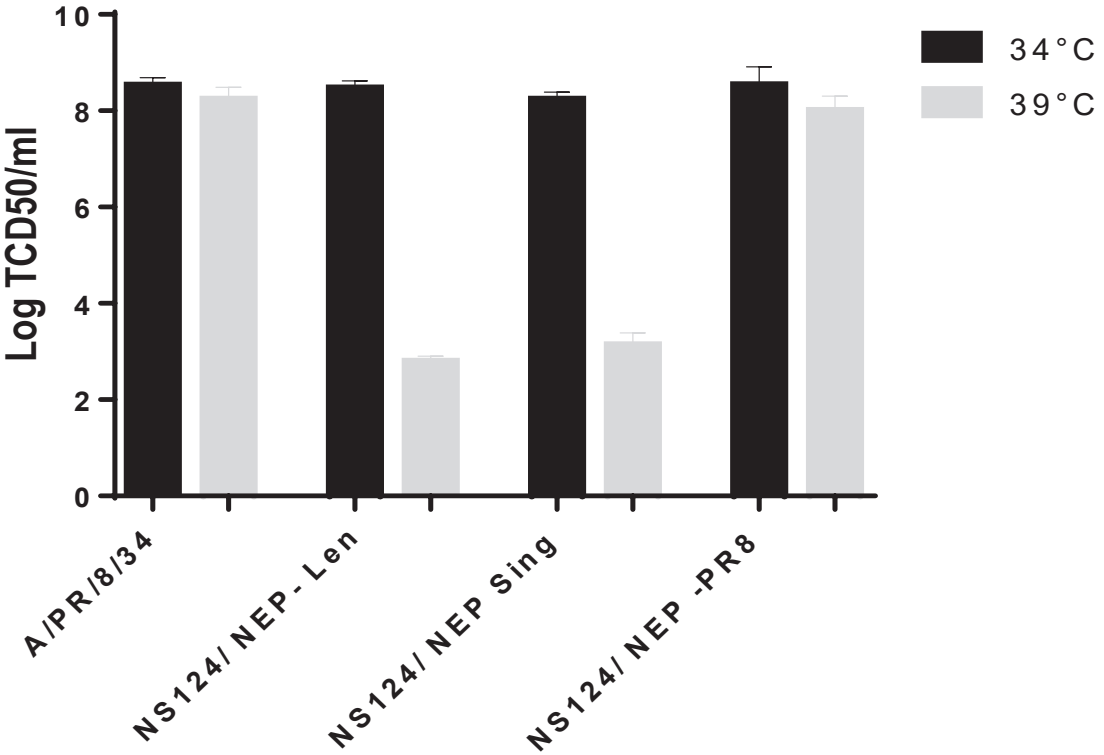
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NS124-HSV-2ASY

MDPNTVSSFQVDCFLWHVRKRVADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILKEESDEALKMTMASVPA SRYLTDMTLEEMSREWSMLIPKQKVAGPLCIRMDQAIM-AAA-**NLLTTPKFT**-AAA-**RMLGDVMAV**-AAA-**NLLTTPKFT**-AAA-**RMLGDVMAV** (SEQ ID NO:13)

FIG. 4

(A)


Log TCD50/ml
10
8
6
4
2
0
34°C
39°C
A/PR/8/34
NS124/NEP-Len
NS124/NEP Sing
NS124/NEP -PR8

(B)

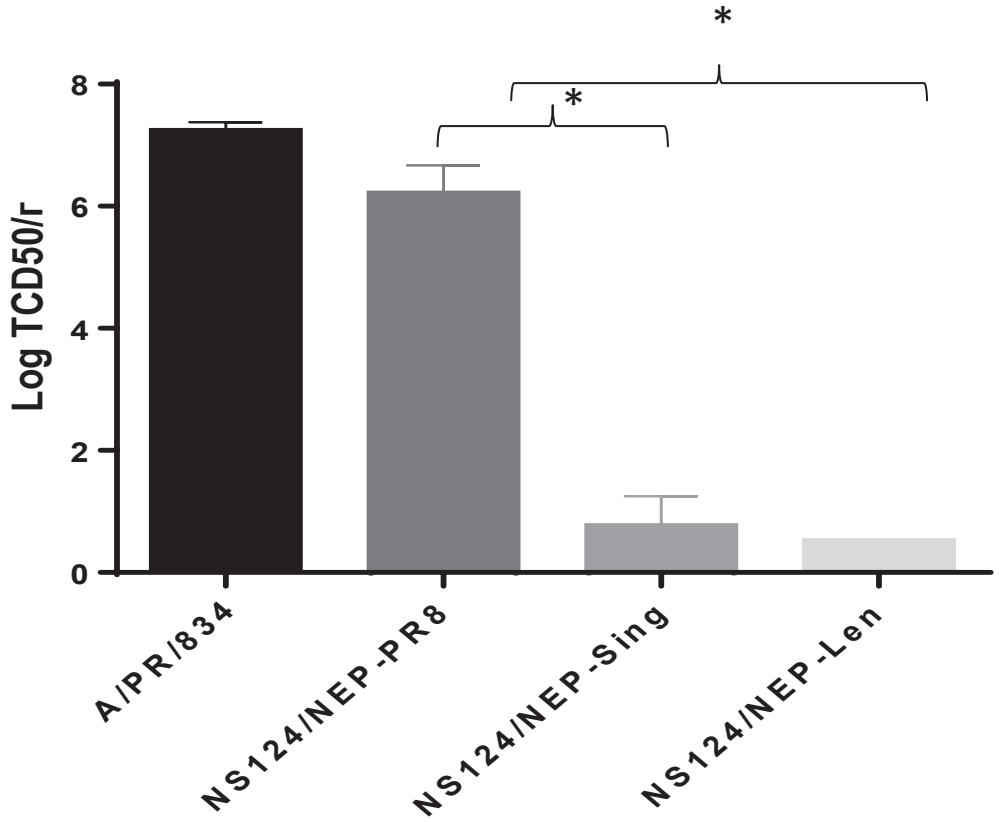
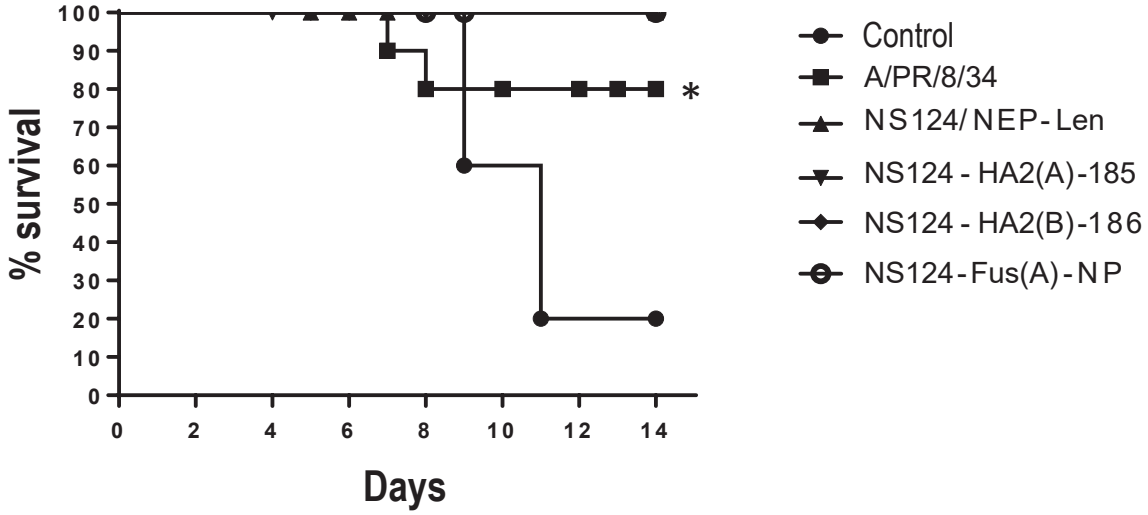

Log TCD50/r
8
6
4
2
0
*
*
A/PR/834
NS124/NEP-PR8
NS124/NEP-Sing
NS124/NEP-Len

FIG. 5

(A)


% survival
Days
*
Control
A/PR/8/34
NS124/NEP-Len
NS124 - HA2(A)-185
NS124 - HA2(B)-186
NS124-Fus(A)-NP

(B)

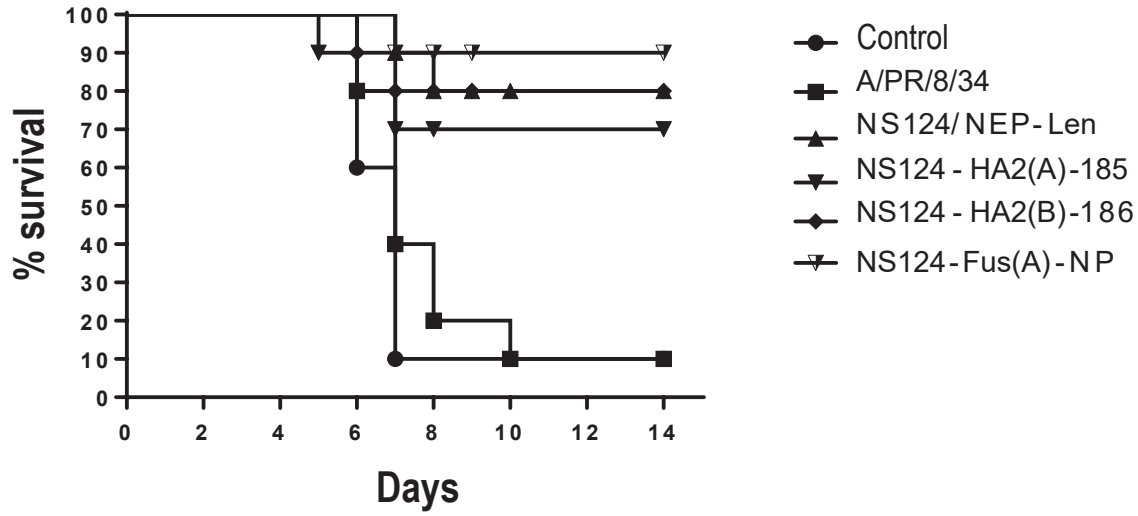
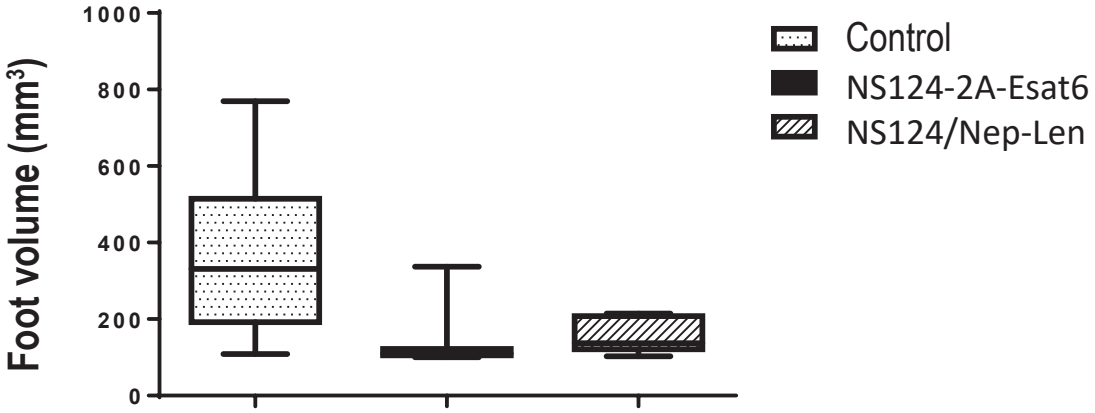

% survival
Days
Control
A/PR/8/34
NS124/NEP-Len
NS124 - HA2(A)-185
NS124 - HA2(B)-186
NS124-Fus(A)-NP

FIG. 6

(A)


1000
800
600
400
200
0
Foot volume (mm3)
Control
NS124-2A-Esat6
NS124/Nep-Len

(B)

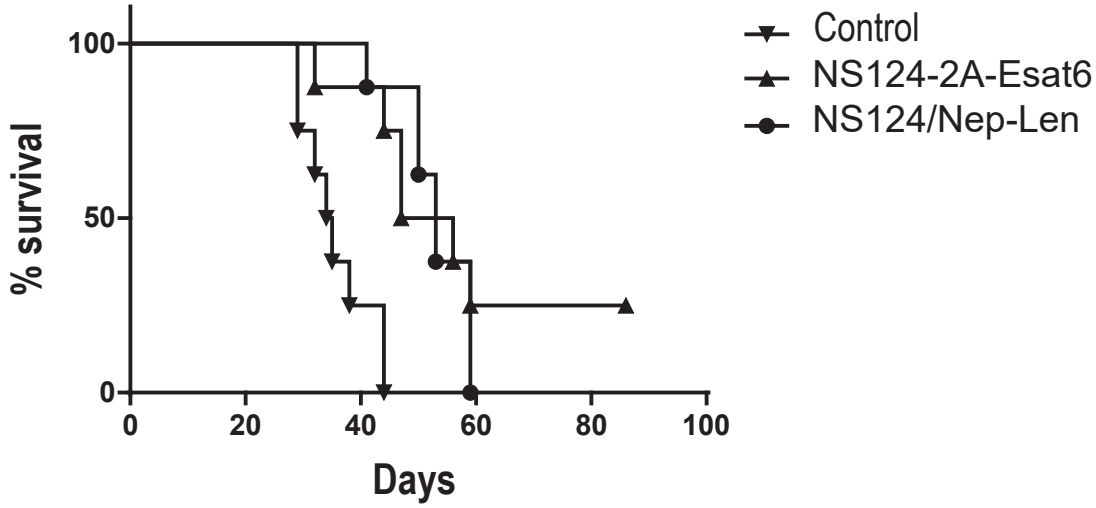

100
50
0
% survival
0
20
40
60
80
100
Days
Control
NS124-2A-Esat6
NS124/Nep-Len

FIG. 7

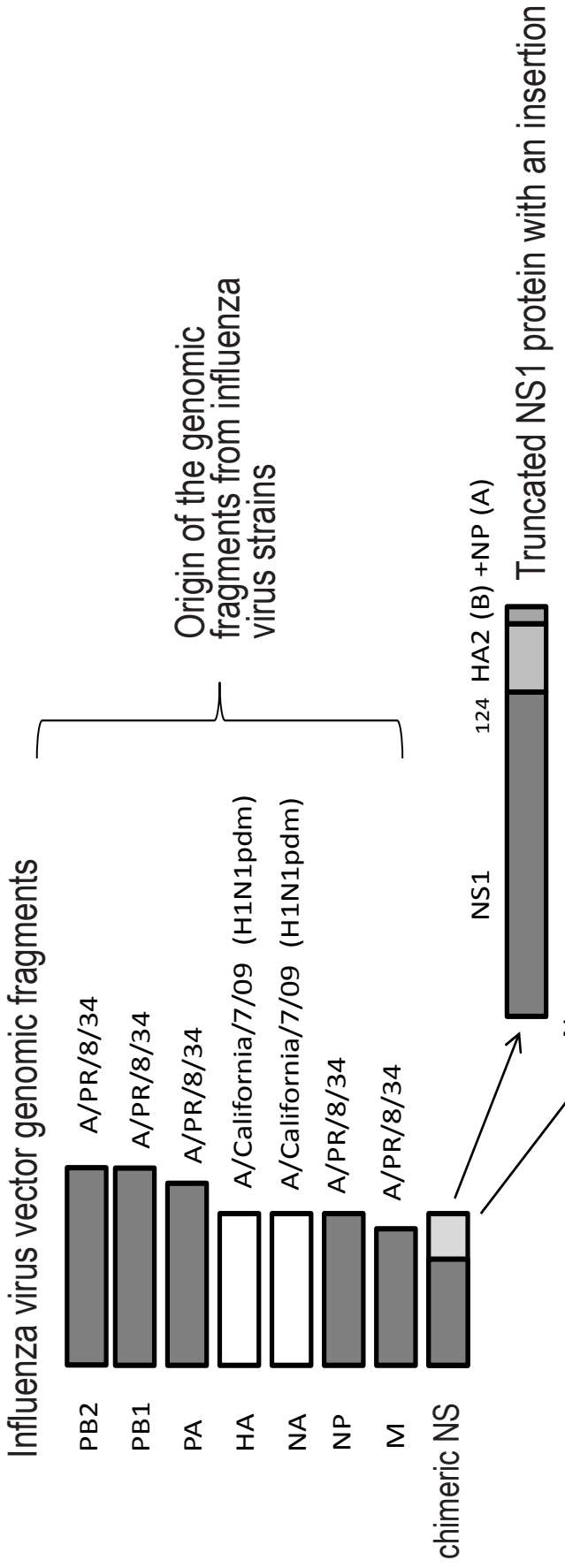

Influenza virus vector genomic fragments
PB2
PB1
PA
HA
NA
NP
M
chimeric NS
A/PR/8/34
A/PR/8/34
A/PR/8/34
A/California/7/09 (H1N1pdm)
A/California/7/09 (H1N1pdm)
A/PR/8/34
A/PR/8/34
Origin of the genomic fragments from influenza virus strains
NS1
124 HA2 (B) +NP (A)
Truncated NS1 protein with an insertion
Nep
Nep protein from H2N2 heterologous strain

FIG. 8

PB2

agcgaaagcaggtcaattatattcaatatggaaagaataaaagaactacgaaatctaatgtcgcagtctcgcacccgcgagatact
cacaaaaaccaccgtggaccatatggccataatcaagaagtacacatcaggaagacaggagaagaacccagcacttaggatga
aatggatgatggcaatgaaatatccaattacagcagacaagaggataacggaaatgattcctgagagaaatgagcaaggacaaa
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catcaatgaactgagcaaccttgcgaaaggagagaaggctaatgtgctaattgggcaaggagacgtggtgttggtaatgaaacgg
aaacgggactctagcatacttactgacagccagacagcgaccaaaagaattcggatggccatcaattagtgtcgaatagtttaaaa
acgaccttgtttctact

SEQ ID NO: 14

PB1

agcgaaagcaggcaaaccatttgaatggatgtcaatccgaccttacttttcttaaaagtgccagcacaaaatgctataagcacaactttcccttatact
ggagaccctccttacagccatgggacaggaacaggatacaccatggatactgtcaacaggacacatcagtactcagaaaagggaagatggacaac
aaacaccgaaactggagcaccgcaactcaacccgattgatgggccactgccagaagacaatgaaccaagtggttatgcccaaacagattgtgtatt
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ctact

SEQ ID NO: 15

FIG. 8 (cont.)

PA

agcgaaagcaggtactgatccaaaatggaagattttgtgcgacaatgcttcaatccgatgattgtcgagcttgcggaaaaaacaatgaaagagtat
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SEQ ID NO: 16

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SEQ ID NO: 17

FIG. 8 (cont.)

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SEQ ID NO: 18

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SEQ ID NO: 19

FIG. 8 (cont.)

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SEQ ID NO: 20

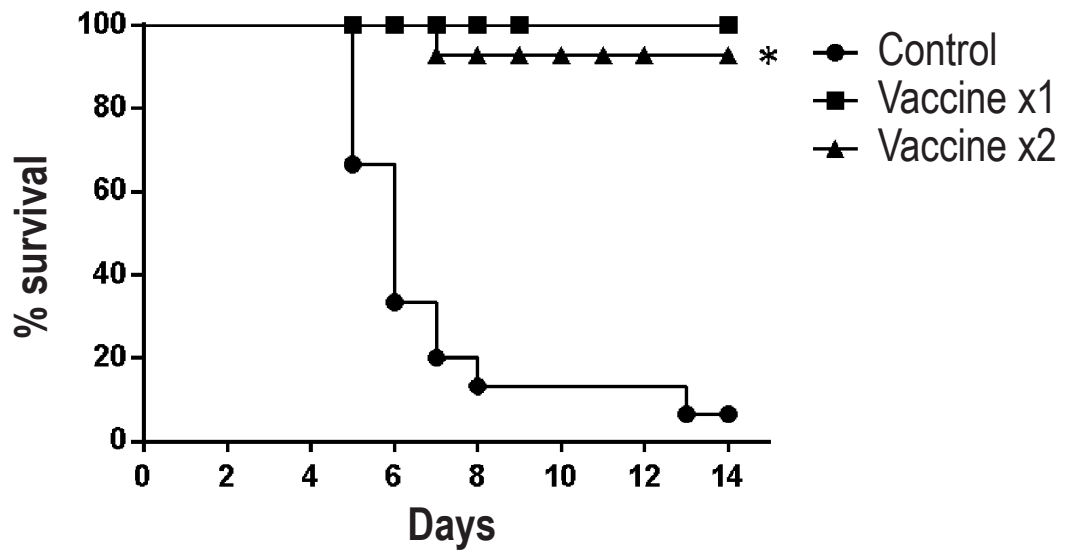
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SEQ ID NO: 21

FIG. 9

(A) A/California/07/09pdm



(B) A/Aichi/2/68 (H3N2)

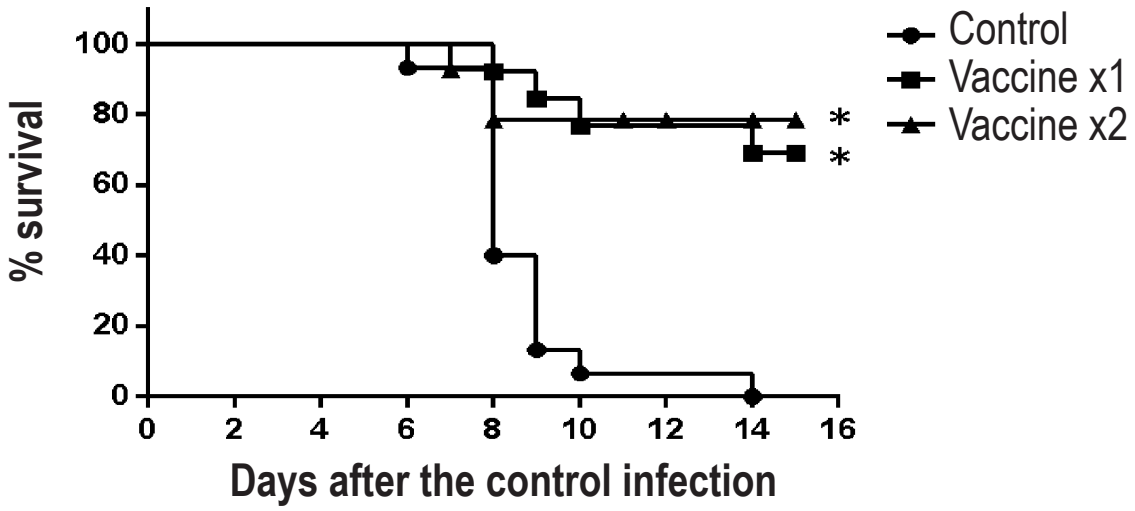
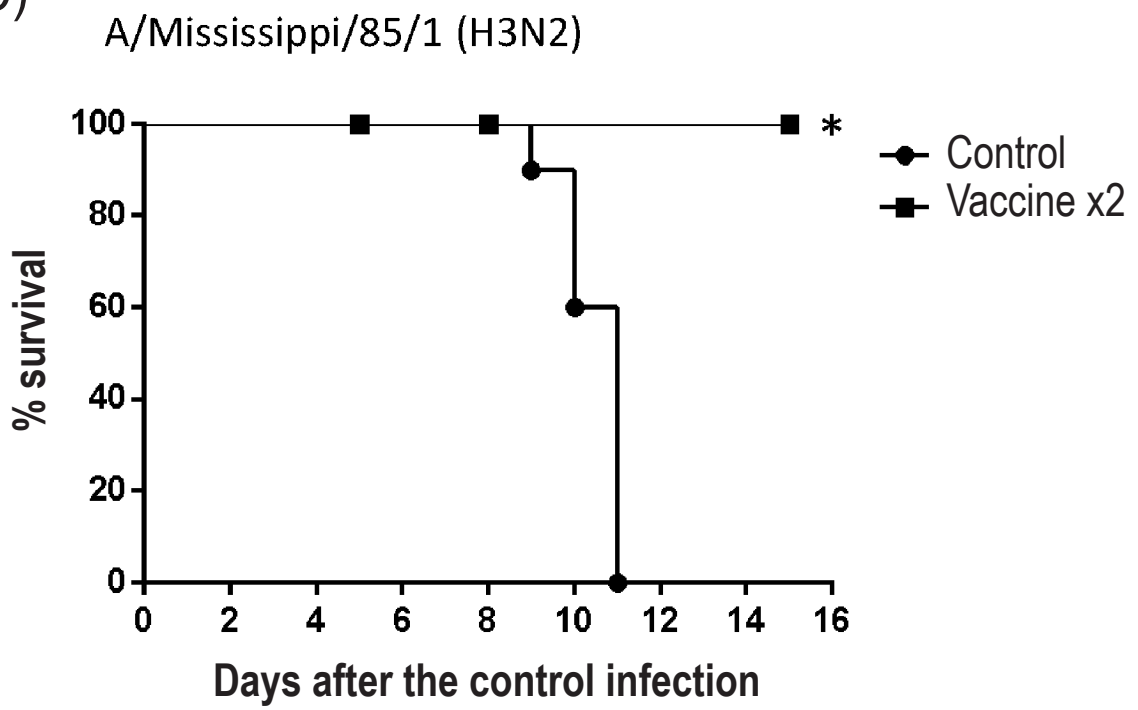


FIG. 9 (cont.)

(C)


A/Mississippi/85/1 (H3N2)
100
80
60
40
20
0
% survival
0
2
4
6
8
10
12
14
16
Days after the control infection
*
Control
Vaccine x2

(D)

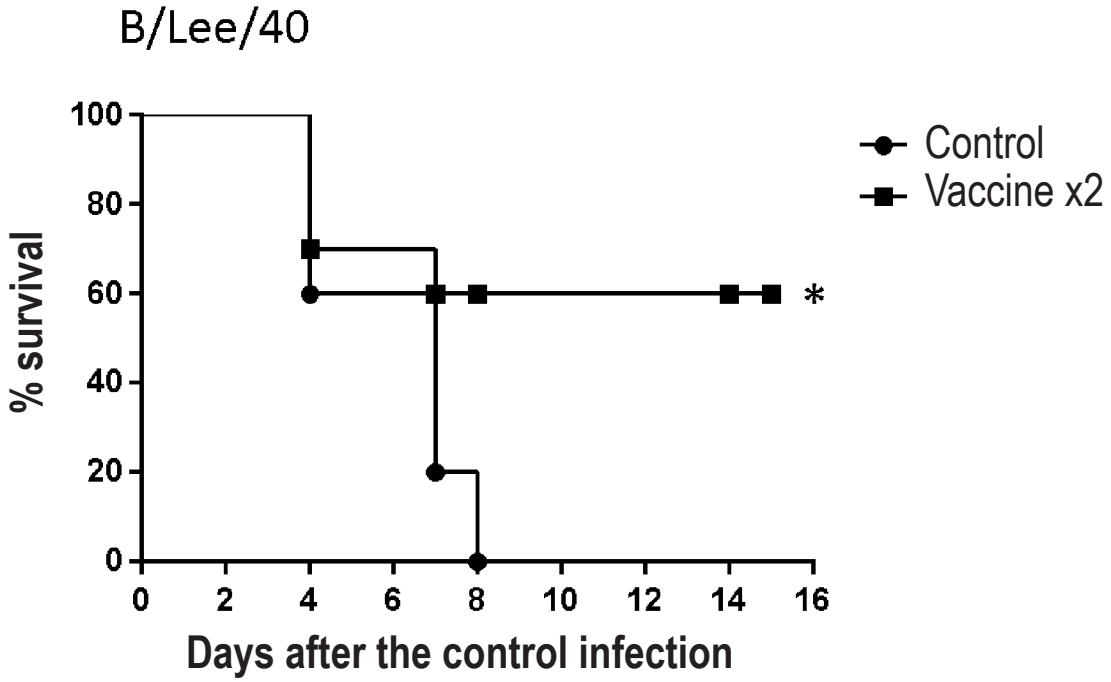
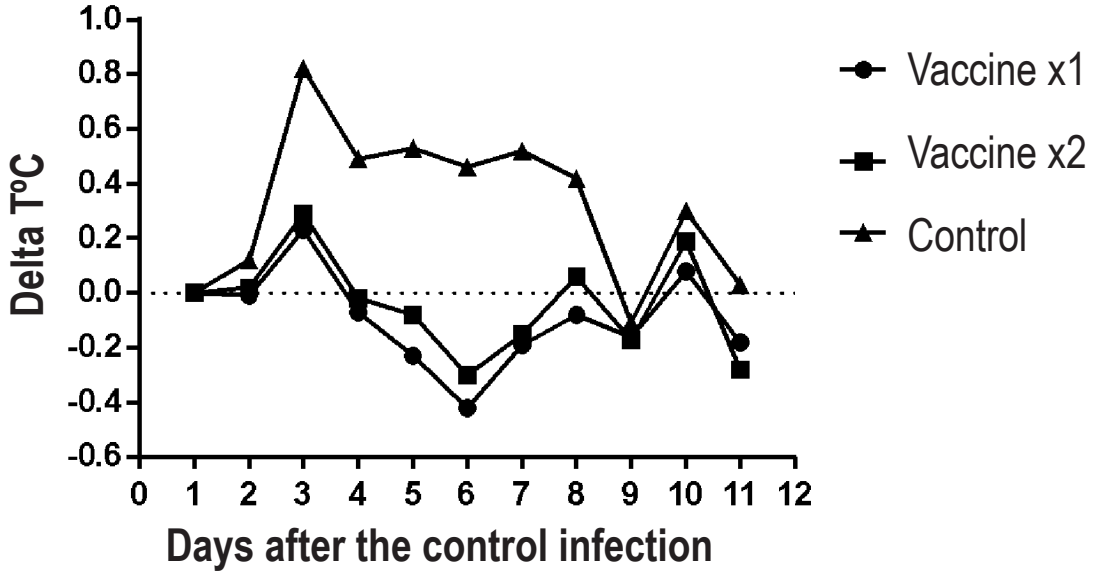
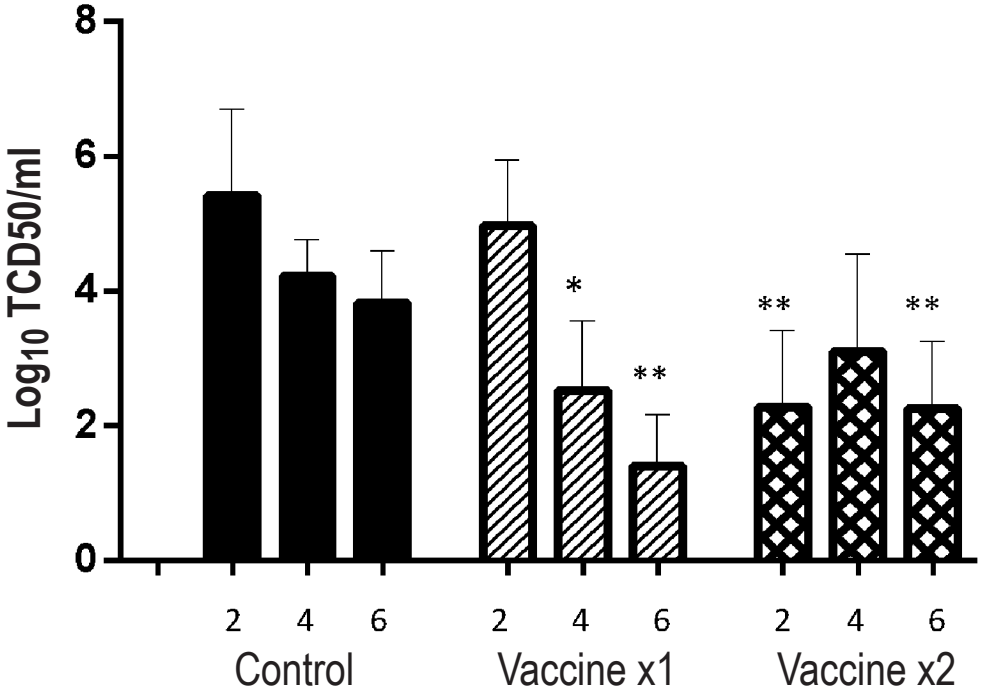

B/Lee/40
100
80
60
40
20
0
% survival
0
2
4
6
8
10
12
14
16
Days after the control infection
*
Control
Vaccine x2

FIG. 10

(A)


1.0
0.8
0.6
0.4
0.2
0.0
-0.2
-0.4
-0.6
Delta T°C
0 1 2 3 4 5 6 7 8 9 10 11 12
Days after the control infection
Vaccine x1
Vaccine x2
Control

(B)


8
6
4
2
0
Log10 TCD50/ml
*
**
**
**
2 4 6 2 4 6 2 4 6
Control
Vaccine x1
Vaccine x2

SEQUENCE LISTING

<110> OBSCHESTVO S OGRANICHENNOI OTVETSTVENNOSTIYU «PHARMENTERPRISES»

<120> ATTENUATED INFLUENZA VECTORS FOR THE PREVENTION AND/OR TREATMENT OF INFECTIOUS DISEASES AND FOR THE TREATMENT OF ONCOLOGICAL DISEASES

<130> 2420-301559RU/061

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<150> 2015147703
<151> 06.11.2015

<150> 2016111907
<151> 30.03.2016

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<170> PatentIn version 3.5

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<213> Influenza A virus

<220>
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<210> 2
<211> 869
<212> DNA
<213> Artificial sequence
<220>
<223> Recombinant NS fragment of influenza A virus with a truncated reading frame of an NS1 protein and a Nep sequence derived from A/Singapore/1/57 (H2N2) virus

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<210> 3
<211> 869
<212> DNA
<213> Artificial sequence

<220>
<223> Recombinant NS fragment of influenza A virus with
a truncated reading frame of an NS1 protei and a Nep sequence
derived from A/Leningrad/134/47/57 (H2N2) virus

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taataataaa aaacaccctt gtttctact 869

<210> 4
<211> 124
<212> PRT
<213> Artificial sequence
<220>
<223> Truncated NS1 protein without insertion of a foreign
sequence

<400> 4
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1 5 10 15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
20 25 30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
35 40 45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
50 55 60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
65 70 75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu

```
                80                  85                  90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
                95                 100                 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
               110                 115                 120
Gln Ala Ile Met
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<210> 5
<211> 311
<212> PRT
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza A virus HA2 subunit fragment

<400> 5

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 1               5                  10                  15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
               20                  25                  30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
               35                  40                  45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
               50                  55                  60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
               65                  70                  75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
               80                  85                  90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
               95                 100                 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
              110                 115                 120
Gln Ala Ile Met Gly Gly Gly Leu Phe Gly Ala Ile Ala Gly Phe
              125                 130                 135
Ile Glu Gly Gly Trp Thr Gly Met Ile Asp Gly Trp Tyr Gly Tyr
              140                 145                 150
His His Gln Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Gln Lys
              155                 160                 165
Ser Thr Gln Asn Ala Ile Asn Gly Ile Thr Asn Lys Val Asn Thr
              170                 175                 180
Val Ile Glu Lys Met Asn Ile Gln Phe Thr Ala Val Gly Lys Glu
              185                 190                 195
Phe Asn Lys Leu Glu Lys Arg Met Glu Asn Leu Asn Lys Lys Val
              200                 205                 210
Asp Asp Gly Phe Leu Asp Ile Trp Thr Tyr Asn Ala Glu Leu Leu
              215                 220                 225
Val Leu Leu Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn
              230                 235                 240
Val Lys Asn Leu Tyr Glu Lys Val Lys Ser Gln Leu Lys Asn Asn
              245                 250                 255
Ala Lys Glu Ile Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys
              260                 265                 270
Asp Asn Glu Cys Met Glu Ser Val Arg Asn Gly Thr Tyr Asp Tyr
              275                 280                 285
Pro Lys Tyr Ser Glu Glu Ser Lys Leu Asn Arg Glu Lys Val Asp
              290                 295                 300
Gly Val Lys Leu Glu Ser Met Gly Ile Tyr Gln
              305                 310
```

<210> 6
<211> 284
<212> PRT
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza A virus HA2 subunit fragment

<400> 6
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
1 5 10 15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
20 25 30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
35 40 45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
50 55 60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
65 70 75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
80 85 90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
95 100 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
110 115 120
Gln Ala Ile Met Gly Gly Ala Val Gly Lys Glu Phe Asn Lys Leu
125 130 135
Glu Lys Arg Met Glu Asn Leu Asn Lys Lys Val Asp Asp Gly Phe
140 145 150
Leu Asp Ile Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu
155 160 165
Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
170 175 180
Tyr Glu Lys Val Lys Ser Gln Leu Lys Asn Asn Ala Lys Glu Ile
185 190 195
Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys
200 205 210
Met Glu Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Lys Tyr Ser
215 220 225
Glu Glu Ser Lys Leu Asn Arg Glu Lys Val Asp Gly Val Lys Leu
230 235 240
Glu Ser Met Gly Ile Tyr Gln Ile Leu Ala Ile Tyr Ser Thr Val
245 250 255
Ala Ser Ser Leu Val Leu Leu Val Ser Leu Gly Ala Ile Ser Phe
260 265 270
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
275 280

<210> 7
<211> 289
<212> PRT
<213> Artificial sequence
<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza A virus HA2 subunit fragment

<400> 7
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu

```
 1               5                  10                  15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
                20                  25                  30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
                35                  40                  45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
                50                  55                  60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
                65                  70                  75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
                80                  85                  90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
                95                 100                 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
               110                 115                 120
Gln Ala Ile Met Gly Gly Gly Tyr His His Gln Asn Glu Gln Gly
               125                 130                 135
Ser Gly Tyr Ala Ala Asp Gln Lys Ser Thr Gln Asn Ala Ile Asn
               140                 145                 150
Gly Ile Thr Asn Lys Val Asn Thr Val Ile Glu Lys Met Asn Ile
               155                 160                 165
Gln Phe Thr Ala Val Gly Lys Glu Phe Asn Lys Leu Glu Lys Arg
               170                 175                 180
Met Glu Asn Leu Asn Lys Lys Val Asp Asp Gly Phe Leu Asp Ile
               185                 190                 195
Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu Asn Glu Arg
               200                 205                 210
Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Glu Lys
               215                 220                 225
Val Lys Ser Gln Leu Lys Asn Asn Ala Lys Glu Ile Gly Asn Gly
               230                 235                 240
Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
               245                 250                 255
Val Arg Asn Gly Thr Tyr Asp Tyr Pro Lys Tyr Ser Glu Glu Ser
               260                 265                 270
Lys Leu Asn Arg Glu Lys Val Asp Gly Val Lys Leu Glu Ser Met
               275                 280                 285
Gly Ile Tyr Gln
```

<210> 8
<211> 294
<212> PRT
<213> Artificial sequence
<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza B virus HA2 subunit fragment

<400> 8

```
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
 1               5                  10                  15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
                20                  25                  30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
                35                  40                  45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
                50                  55                  60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
                65                  70                  75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
```

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

<210> 9
<211> 158
<212> PRT
<213> Artificial sequence
<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza A virus HA2 subunit fragment and a sequence of a B-cell epitope of influenza A virus NP protein

<400> 9

```
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
 1               5                  10                  15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
                20                  25                  30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
                35                  40                  45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
                50                  55                  60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
                65                  70                  75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
                80                  85                  90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
                95                 100                 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
               110                 115                 120
Gln Ala Ile Met Gly Gly Gly Leu Phe Gly Ala Ile Ala Gly Phe
               125                 130                 135
Ile Glu Gly Gly Trp Thr Gly Met Ile Asp Gly Trp Gly Gly Arg
               140                 145                 150
```

Glu Ser Arg Asn Pro Gly Asn Ala
155

<210> 10
<211> 158
<212> PRT
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by a sequence of an influenza A virus HA2 subunit fragment and a sequence of a B-cell epitope of influenza A virus NP protein

<400> 10
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
1 5 10 15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
20 25 30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
35 40 45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
50 55 60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
65 70 75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
80 85 90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
95 100 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
110 115 120
Gln Ala Ile Met Gly Gly Gly Phe Phe Gly Ala Ile Ala Gly Phe
125 130 135
Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp Gly Gly Arg
140 145 150
Glu Ser Arg Asn Pro Gly Asn Ala
155

<210> 11
<211> 221
<212> PRT
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by a sequence of mycobacterium tuberculosis protein Esat6 protein

<400> 11
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
1 5 10 15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
20 25 30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
35 40 45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
50 55 60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
65 70 75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
80 85 90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu

```
                 95                  100                 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
                110                 115                 120
Gln Ala Ile Met Gly Gly Met Thr Glu Gln Gln Trp Asn Phe Ala
                125                 130                 135
Gly Ile Glu Ala Ala Ala Ser Ala Ile Gln Gly Asn Val Thr Ser
                140                 145                 150
Ile His Ser Leu Leu Asp Glu Gly Lys Gln Ser Leu Thr Lys Leu
                155                 160                 165
Ala Ala Ala Trp Gly Gly Ser Gly Ser Glu Ala Tyr Gln Gly Val
                170                 175                 180
Gln Gln Lys Trp Asp Ala Thr Ala Thr Glu Leu Asn Asn Ala Leu
                185                 190                 195
Gln Asn Leu Ala Arg Thr Ile Ser Glu Ala Gly Gln Ala Met Ala
                200                 205                 210
Ser Thr Glu Gly Asn Val Thr Gly Met Phe Ala
                215                 220
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<210> 12
<211> 238
<212> Белок
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by a sequence of self-cleaving 2A peptide and a sequence of mycobacterium tuberculosis protein ESAT-6

<400> 12

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

230 235

<210> 13
<211> 172
<212> PRT
<213> Artificial sequence

<220>
<223> Truncated NS1 protein elongated by sequences of
T-cell epitopes of herpes simplex virus (HSV) types I and II

<400> 13
Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu
1 5 10 15
Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp Ala
20 25 30
Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
35 40 45
Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala
50 55 60
Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu
65 70 75
Ala Leu Lys Met Thr Met Ala Ser Val Pro Ala Ser Arg Tyr Leu
80 85 90
Thr Asp Met Thr Leu Glu Glu Met Ser Arg Glu Trp Ser Met Leu
95 100 105
Ile Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp
110 115 120
Gln Ala Ile Met Ala Ala Ala Asn Leu Leu Thr Thr Pro Lys Phe
125 130 135
Thr Ala Ala Ala Arg Met Leu Gly Asp Val Met Ala Val Ala Ala
140 145 150
Ala Asn Leu Leu Thr Thr Pro Lys Phe Thr Ala Ala Ala Arg Met
155 160 165
Leu Gly Asp Val Met Ala Val
170

<210> 14
<211> 2341
<212> DNA
<213> Influenza A virus/PR/8/34 (H1N1)

<220>
<223> Nucleotide sequence of PB2 genomic fragment

<400> 14
agcgaaagca ggtcaattat attcaatatg gaaagaataa aagaactacg aaatctaatg 60
tcgcagtctc gcacccgcga gatactcaca aaaaccaccg tggaccatat ggccataatc 120
aagaagtaca catcaggaag acaggagaag aacccagcac ttaggatgaa atggatgatg 180
gcaatgaaat atccaattac agcagacaag aggataacgg aaatgattcc tgagagaaat 240
gagcaaggac aaactttatg gagtaaaatg aatgatgccg gatcagaccg agtgatggta 300
tcacctctgg ctgtgacatg gtggaatagg aatggaccaa taacaaatac agttcattat 360
ccaaaaatct acaaaactta ttttgaaaga gtcgaaaggc taaagcatgg aacctttggc 420
cctgtccatt ttagaaacca agtcaaaata cgtcggagag ttgacataaa tcctggtcat 480
gcagatctca gtgccaagga ggcacaggat gtaatcatgg aagttgtttt ccctaacgaa 540
gtgggagcca ggatactaac atcggaatcg caactaacga taaccaaaga gaagaaagaa 600
gaactccagg attgcaaaat ttctcctttg atggttgcat acatgttgga gagagaactg 660
gtccgcaaaa cgagattcct cccagtggct ggtggaacaa gcagtgtgta cattgaagtg 720
ttgcatttga ctcaaggaac atgctgggaa cagatgtata ctccaggagg ggaagtgagg 780
aatgatgatg ttgatcaaag cttgattatt gctgctagga acatagtgag aagagctgca 840

gtatcagcag atccactagc atctttattg gagatgtgcc acagcacaca gattggtgga 900
attaggatgg tagacatcct taggcagaac ccaacagaag agcaagccgt ggatatatgc 960
aaggctgcaa tgggactgag aattagctca tccttcagtt ttggtggatt cacatttaag 1020
agaacaagcg gatcatcagt caagagagag gaagaggtgc ttacgggcaa tcttcaaaca 1080
ttgaagataa gagtgcatga gggatatgaa gagttcacaa tggttgggag aagagcaaca 1140
gccatactca gaaaagcaac caggagattg attcagctga tagtgagtgg gagagacgaa 1200
cagtcgattg ccgaagcaat aattgtggcc atggtatttt cacaagagga ttgtatgata 1260
aaagcagtca gaggtgatct gaatttcgtc aatagggcga atcaacgatt gaatcctatg 1320
catcaacttt taagacattt tcagaaggat gcgaaagtgc tttttcaaaa ttggggagtt 1380
gaacctatcg acaatgtgat gggaatgatt gggatattgc ccgacatgac tccaagcatc 1440
gagatgtcaa tgagaggagt gagaatcagc aaaatgggtg tagatgagta ctccagcacg 1500
gagagggtag tggtgagcat tgaccgtttt ttgagaatcc gggaccaacg aggaaatgta 1560
ctactgtctc ccgaggaggt cagtgaaaca cagggaacag agaaactgac aataacttac 1620
tcatcgtcaa tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa 1680
tggatcatca gaaactggga aactgttaaa attcagtggt cccagaaccc tacaatgcta 1740
tacaataaaa tggaatttga accatttcag tctttagtac ctaaggccat tagaggccaa 1800
tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat 1860
accgcacaga taataaaact tcttcccttc gcagccgctc caccaaagca aagtagaatg 1920
cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc 1980
aattctcctg tattcaacta taacaaggcc acgaagagac tcacagttct cggaaaggat 2040
gctggcactt taactgaaga cccagatgaa ggcacagctg gagtggagtc cgctgttctg 2100
aggggattcc tcattctggg caaagaagac aagagatatg ggccagcact aagcatcaat 2160
gaactgagca accttgcgaa aggagagaag gctaatgtgc taattgggca aggagacgtg 2220
gtgttggtaa tgaaacggaa acgggactct agcatactta ctgacagcca gacagcgacc 2280
aaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac 2340
t 2341

<210> 15
<211> 2288
<212> DNA
<213> Influenza A virus/PR/8/34 (H1N1)

<220>
<223> Nucleotide sequence of PB1 genomic fragment

<400> 15
atggatgtca atccgacctt acttttctta aaagtgccag cacaaaatgc tataagcaca 60
actttccctt atactggaga ccctccttac agccatggga caggaacagg atacaccatg 120
gatactgtca acaggacaca tcagtactca gaaaagggaa gatggacaac aaacaccgaa 180
actggagcac cgcaactcaa cccgattgat gggccactgc cagaagacaa tgaaccaagt 240
ggttatgccc aaacagattg tgtattggag gcgatggctt tccttgagga atcccatcct 300
ggtatttttg aaaactcgtg tattgaaacg atggaggttg ttcagcaaac acgagtagac 360
aagctgacac aaggccgaca gacctatgac tggactctaa atagaaacca acctgctgca 420
acagcattgg ccaacacaat agaagtgttc agatcaaatg gcctcacggc caatgagtct 480
ggaaggctca tagacttcct taaggatgta atggagtcaa tgaacaaaga agaaatgggg 540
atcacaactc attttcagag aaagagacgg gtgagagaca atatgactaa gaaaatgata 600
acacagagaa caatgggtaa aaagaagcag agattgaaca aaaggagtta tctaattaga 660
gcattgaccc tgaacacaat gaccaaagat gctgagagag ggaagctaaa acggagagca 720
attgcaaccc cagggatgca aataaggggg tttgtatact ttgttgagac actggcaagg 780
agtatatgtg agaaacttga acaatcaggg ttgccagttg gaggcaatga gaagaaagca 840
aagttggcaa atgttgtaag gaagatgatg accaattctc aggacaccga actttctttc 900
accatcactg gagataacac caaatggaac gaaaatcaga atcctcggat gtttttggcc 960
atgatcacat atatgaccag aaatcagccc gaatggttca gaaatgttct aagtattgct 1020
ccaataatgt tctcaaacaa aatggcgaga ctgggaaaag ggtatatgtt tgagagcaag 1080
agtatgaaac ttagaactca aatacctgca gaaatgctag caagcatcga tttgaaatat 1140
ttcaatgatt caacaagaaa gaagattgaa aaaatccgac cgctcttaat agaggggact 1200
gcatcattga gccctggaat gatgatgggc atgttcaata tgttaagcac tgtattaggc 1260
gtctccatcc tgaatcttgg acaaaagaga tacaccaaga ctacttactg gtgggatggt 1320
cttcaatcct ctgacgattt tgctctgatt gtgaatgcac ccaatcatga agggattcaa 1380
gccggagtcg acaggtttta tcgaacctgt aagctacttg gaatcaatat gagcaagaaa 1440

aagtcttaca taaacagaac aggtacattt gaattcacaa gtttttttcta tcgttatggg 1500
tttgttgcca atttcagcat ggagcttccc agttttgggg tgtctgggat caacgagtca 1560
gcggacatga gtattggagt tactgtcatc aaaaacaata tgataaacaa tgatcttggt 1620
ccagcaacag ctcaaatggc ccttcagttg ttcatcaaag attacaggta cacgtaccga 1680
tgccatagag gtgacacaca aatacaaacc cgaagatcat ttgaaataaa gaaactgtgg 1740
gagcaaaccc gttccaaagc tggactgctg gtctccgacg gaggcccaaa tttatacaac 1800
attagaaatc tccacattcc tgaagtctgc ctaaaatggg aattgatgga tgaggattac 1860
caggggcgtt tatgcaaccc actgaaccca tttgtcagcc ataaagaaat tgaatcaatg 1920
aacaatgcag tgatgatgcc agcacatggt ccagccaaaa acatggagta tgatgctgtt 1980
gcaacaacac actcctggat ccccaaaaga aatcgatcca tcttgaatac aagtcaaaga 2040
ggagtacttg aggatgaaca aatgtaccaa aggtgctgca atttatttga aaaattcttc 2100
cccagcagtt catacagaag accagtcggg atatccagta tggtggaggc tatggtttcc 2160
agagcccgaa ttgatgcacg gattgatttc gaatctggaa ggataaagaa agaagagttc 2220
actgagatca tgaagatctg ttccaccatt gaagagctca gacggcaaaa atagtgaatt 2280
tagcttgt 2288

<210> 16
<211> 2233
<212> DNA
<213> Influenza A virus/PR/8/34 (H1N1)

<220>
<223> Nucleotide sequence of PA genomic fragment

<400> 16
agcgaaagca ggtactgatc caaaatggaa gattttgtgc gacaatgctt caatccgatg 60
attgtcgagc ttgcggaaaa aacaatgaaa gagtatgggg aggacctgaa aatcgaaaca 120
aacaaatttg cagcaatatg cactcacttg gaagtatgct tcatgtattc agattttcac 180
ttcatcaatg agcaaggcga gtcaataatc gtagaacttg gtgatccaaa tgcacttttg 240
aagcacagat ttgaaataat cgagggaaga gatcgcacaa tggcctggac agtagtaaac 300
agtatttgca acactacagg ggctgagaaa ccaaagtttc taccagattt gtatgattac 360
aaggagaata gattcatcga aattggagta acaaggagag aagttcacat atactatctg 420
gaaaaggcca ataaaattaa atctgagaaa acacacatcc acattttctc gttcactggg 480
gaagaaatgg ccacaaaggc agactacact ctcgatgaag aaagcagggc taggatcaaa 540
accagactat tcaccataag acaagaaatg gccagcagag gcctctggga ttcctttcgt 600
cagtccgaga gaggagaaga gacaattgaa gaaaggtttg aaatcacagg aacaatgcgc 660
aagcttgccg accaaagtct cccgccgaac ttctccagcc ttgaaaattt tagagcctat 720
gtggatggat tcgaaccgaa cggctacatt gagggcaagc tgtctcaaat gtccaaagaa 780
gtaaatgcta gaattgaacc ttttttgaaa acaacaccac gaccacttag acttccgaat 840
gggcctccct gttctcagcg gtccaaattc ctgctgatgg atgccttaaa attaagcatt 900
gaggacccaa gtcatgaagg agagggaata ccgctatatg atgcaatcaa atgcatgaga 960
acattctttg gatggaagga acccaatgtt gttaaaccac acgaaaaggg aataaatcca 1020
aattatcttc tgtcatggaa gcaagtactg gcagaactgc aggacattga gaatgaggag 1080
aaaattccaa agactaaaaa tatgaagaaa acaagtcagc taaagtgggc acttggtgag 1140
aacatggcac cagaaaaggt agactttgac gactgtaaag atgtaggtga tttgaagcaa 1200
tatgatagtg atgaaccaga attgaggtcg ctagcaagtt ggattcagaa tgagtttaac 1260
aaggcatgcg aactgacaga ttcaagctgg atagagctcg atgagattgg agaagatgtg 1320
gctccaattg aacacattgc aagcatgaga aggaattatt tcacatcaga ggtgtctcac 1380
tgcagagcca cagaatacat aatgaagggg gtgtacatca atactgcctt gcttaatgca 1440
tcttgtgcag caatggatga tttccaatta attccaatga taagcaagtg tagaactaag 1500
gagggaaggc gaaagaccaa cttgtatggt ttcatcataa aaggaagatc ccacttaagg 1560
aatgacaccg acgtggtaaa ctttgtgagc atggagtttt ctctcactga cccaagactt 1620
gaaccacata aatgggagaa gtactgtgtt cttgagatag gagatatgct tataagaagt 1680
gccataggcc aggtttcaag gcccatgttc ttgtatgtga gaacaaatgg aacctcaaaa 1740
attaaaatga aatggggaat ggagatgagg cgttgcctcc tccagtcact tcaacaaatt 1800
gagagtatga ttgaagctga gtcctctgtc aaagagaaag acatgaccaa agagttcttt 1860
gagaacaaat cagaaacatg gcccattgga gagtccccca aaggagtgga ggaaagttcc 1920
attgggaagg tctgcaggac tttattagca aagtcggtat tcaacagctt gtatgcatct 1980
ccacaactag aaggattttc agctgaatca agaaaactgc ttcttatcgt tcaggctctt 2040
agggacaacc ttgaacctgg gacctttgat cttgggggggc tatatgaagc aattgaggag 2100

tgcctgatta atgatccctg ggttttgctt aatgcttctt ggttcaactc cttccttaca 2160
catgcattga gttagttgtg gcagtgctac tatttgctat ccatactgtc caaaaaagta 2220
ccttgtttct act 2233

<210> 17
<211> 1027
<212> DNA
<213> Influenza A virus/PR/8/34 (H1N1)

<220>
<223> Nucleotide sequence of NP genomic fragment

<400> 17
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ctctatcatc ccgtcaggcc ccctcaaagc cgagatcgca cagagacttg aagatgtctt 120
tgcagggaag aacactgatc ttgaggttct catggaatgg ctaaagacaa gaccaatcct 180
gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg 240
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caaagaaatc tcactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420
caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga 480
acagattgct gactcccagc atcggtctca taggcaaatg gtgacaacaa ccaatccact 540
aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat 600
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tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa 780
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ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt 1020
ttctact 1027

<210> 18
<211> 1027
<212> DNA
<213> Influenza A virus/PR/8/34 (H1N1)

<220>
<223> Nucleotide sequence of M genomic fragment

<400> 18
agcgaaagca ggtagatatt gaaagatgag tcttctaacc gaggtcgaaa cgtacgtact 60
ctctatcatc ccgtcaggcc ccctcaaagc cgagatcgca cagagacttg aagatgtctt 120
tgcagggaag aacactgatc ttgaggttct catggaatgg ctaaagacaa gaccaatcct 180
gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg 240
aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa 300
catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc 360
caaagaaatc tcactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420
caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga 480
acagattgct gactcccagc atcggtctca taggcaaatg gtgacaacaa ccaatccact 540
aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat 600
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tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa 780
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<210> 19
<211> 1701
<212> DNA
<213> Influenza A virus/California/09-like (H1N1pdm)
<220>
<223> Nucleotide sequence of HA genomic fragment

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gtaacagtaa cacactctgt taaccttcta gaagacaagc ataacgggaa actatgcaaa 180
ctaagagggg tagccccatt gcatttgggt aaatgtaaca ttgctggctg gatcctggga 240
aatccagagt gtgaatcact ctccacagca agttcatggt cctacattgt ggaaacatct 300
agttcagaca atggaacgtg ttacccagga gatttcatca attatgagga gctaagagag 360
caattgagct cagtgtcatc atttgaaagg tttgagatat tccccaaaac aagttcatgg 420
cccaatcatg actcgaacaa aggtgtaacg gcagcatgtc ctcacgctgg agcaaaaagc 480
ttctacaaaa atttaatatg gctagttaaa aaaggaaatt catacccaaa gctcagccaa 540
tcctacatta atgataaagg gaaagaagtc ctcgtgctgt ggggcattca ccatccatct 600
actactgctg accaacaaag tctctatcag aatgcagatg catatgtttt tgtggggaca 660
tcaagataca gcaagaagtt caagccggaa atagcaataa gacccaaagt gagggatcaa 720
gaagggagaa tgaactatta ctggacacta gtagagccgg gagacaaaat aacattcgaa 780
gcaactggaa atctagtggt accgagatat gcattcacaa tggaaagaaa tgctggatct 840
ggtattatca tttcagatac accagtccac gattgcaata caacttgtca gacacccgag 900
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aagctggaat caacaaggat ttaccagatt ttggcgatct attcaactgt cgccagttca 1620
ttggtgctgg tagtctccct gggggcaatc agcttctgga tgtgctctaa tgggtctcta 1680
cagtgtagaa tatgtattta a 1701

<210> 20
<211> 1410
<212> DNA
<213> Influenza A virus/California/09-like (H1N1pdm)

<220>
<223> Nucleotide sequence of NA genomic fragment

<400> 20
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aacttaatat tacaaattgg aaacataatc tcaatatgga ttagccactc aattcaagtt 120
gggaatcaaa gtcagatcga aacatgcaat caaagcgtca ttacttatga aaacaacact 180
tgggtaaatc agacatatgt taacatcagc aacaccaact ttgctgctgg gcagccagtg 240
gtttccgtga aattagcggg caattcctct ctctgccctg ttagtggatg ggctatatac 300
agtaaagaca acagtgtaag agtcggttcc aaggggatg tgtttgtcat aagggaacca 360
ttcatatcat gctccccctt ggaatgcaga accttcttct tgactcaagg ggccttgcta 420
aatgacaaac attccaatgg aaccattaaa gacaggagcc catatcgaac cttaatgagc 480
tgtcctattg gtgaagttcc ctctccatac aactcaagat ttgagtcagt cgcttggtca 540
gcaagtgctt gtcatgatgg catcaattgg ctaacaattg gaatttctgg cccagacagt 600
ggggcagtgg ctgtgttaaa gtacaacggc ataataacag acactatcaa gagttggaga 660
aacgatatat tgagaacaca agagtctgaa tgtgcatgtg taaatggttc ttgctttacc 720
ataatgaccg atggaccaag tgatggacag gcctcataca agatcttcag aatagaaaag 780

ggaaagatag tcaaatcagt cgaaatgaat gcccctaatt atcactatga ggaatgctcc 840
tgttatcctg attctagtga aatcacatgt gtgtgcaggg ataactggca tggctcgaat 900
cgaccgtggg tgtctttcaa ccagaatctg gaatatcaga taggatacat atgcagtggg 960
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agaactaaaa gcattagttc aagaaaaggt tttgagatga tttgggatcc aaatggatgg 1140
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ggatatagcg ggagttttgt tcagcatcca gaactaacag ggctggattg tataagacct 1260
tgcttctggg ttgaactaat cagagggcga cccaaagaga acacaatctg gactagtggg 1320
agcagcatat ccttttgtgg tgtaaacagt gacactgtgg gttggtcttg gccagacggt 1380
gctgagttgc catttaccat tgacaagtaa 1410

<210> 21
<211> 979
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleotide sequence of a chimeric NS fragment gene

<400> 21
agcaaaagca gggtgacaaa gacataatgg atccaaacac tgtgtcaagc tttcaggtag 60
attgctttct ttggcatgtc cgcaaacgag ttgcagacca agaactaggt gatgccccat 120
tccttgatcg gcttcgccga gatcagaaat ccctaagagg aaggggcagc actcttggtc 180
tggacatcga gacagccaca cgtgctggaa agcagatagt ggagcggatt ctgaaagaag 240
aatccgatga ggcacttaaa atgaccatgg cctctgtacc tgcgtcgcgt tacctaaccg 300
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tactatttga agtggaacaa gagataagaa ctttctcgtt tcagcttatt taataataaa 960
aaacaccctt gtttctact 979