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(54) **TARGET SEQUENCE OF RNA VIRUS AND USE THEREOF**

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 CPC *A61K 39/12* (2013.01); *A61K 31/7088* (2013.01); *A61P 31/14* (2018.01); *C07K 14/005* (2013.01); *C12N 7/00* (2013.01); *A61K 2039/5254* (2013.01)

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(57) **ABSTRACT**

The present invention provides a target sequence of an RNA virus. The target sequence is a nucleic acid sequence fragment in the gene sequence in the RNA virus containing 20-40 bases and having not less than 95% similarity to genome sequence of human or related species such as livestock and poultry. The above-mentioned target sequence of the RNA virus is selected from SEQ ID NO. 1 - SEQ ID NO. 615. The present invention also relates to a primer composition for constructing the above-mentioned target sequence, biomaterials such as antisense RNA related to the above-mentioned target sequence, and related uses such as design of a vaccine lacking the target sequence. The virus fragment with the above-mentioned sequence constructed in the present invention has the function of interacting with human genomic DNA and is similar to viral miRNA. Moreover, the effect of overexpression of the target sequence of the RNA virus on the expression level of surrounding genes is verified, and a new concept that the above-mentioned target fragment is an important pathogenic substance of the RNA virus is proposed. The above-mentioned target sequence has important application value for the detection and diagnosis of RNA viruses, drug screening, as well as the treatment of diseases caused by RNA viruses and the design/optimization of vaccines and methods.

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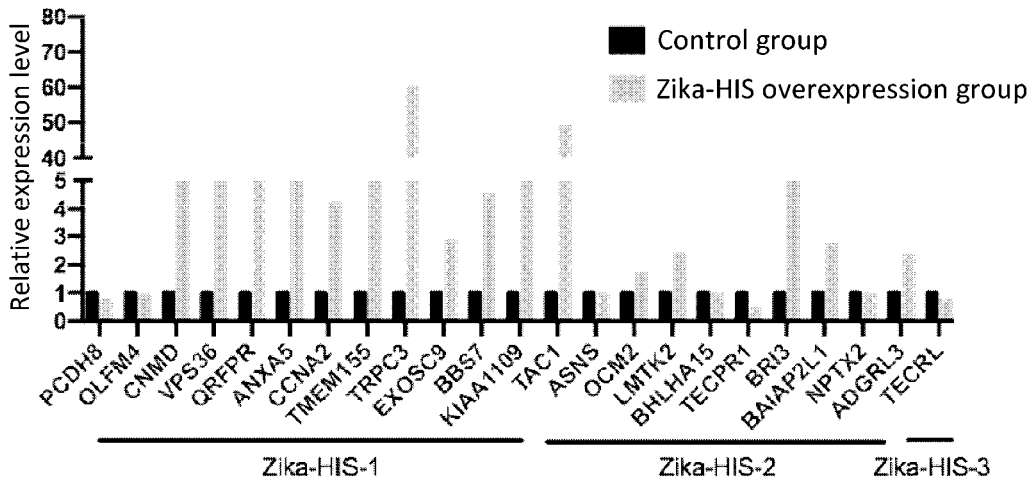
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C12N 7/00 (2006.01)

Specification includes a Sequence Listing.



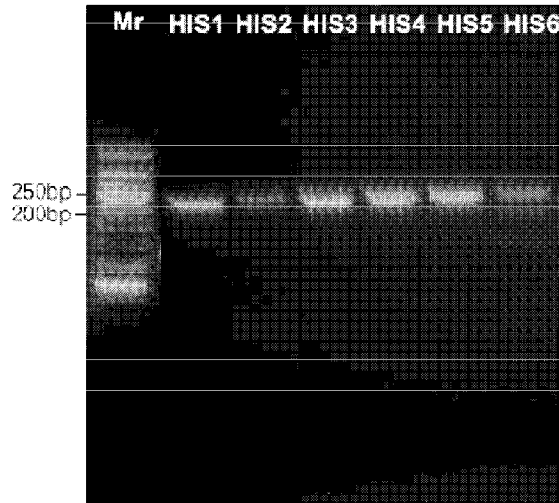


FIG. 1

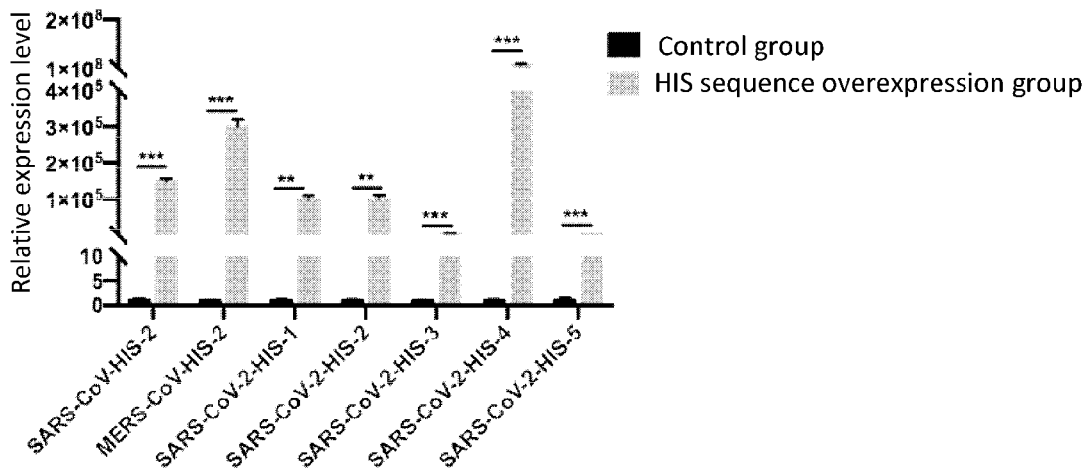


FIG. 2

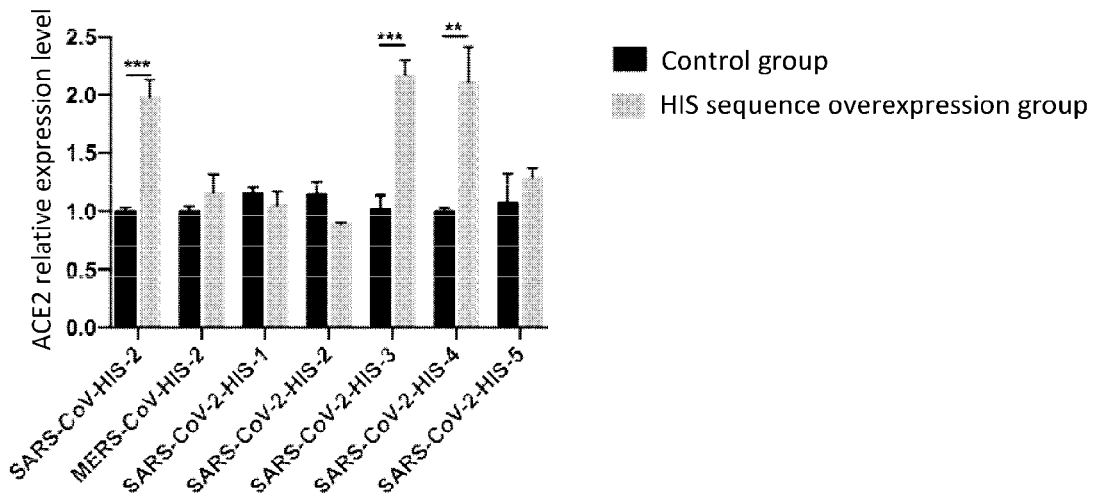


FIG. 3

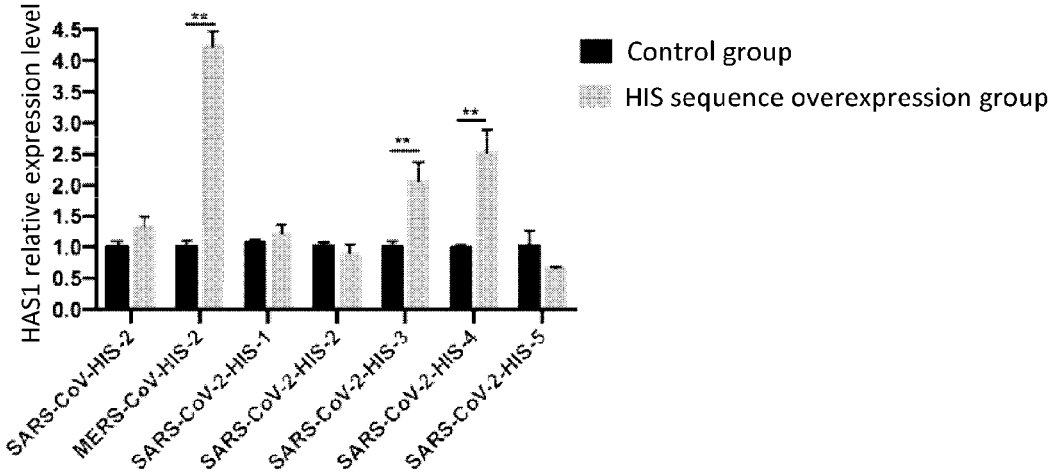


FIG. 4

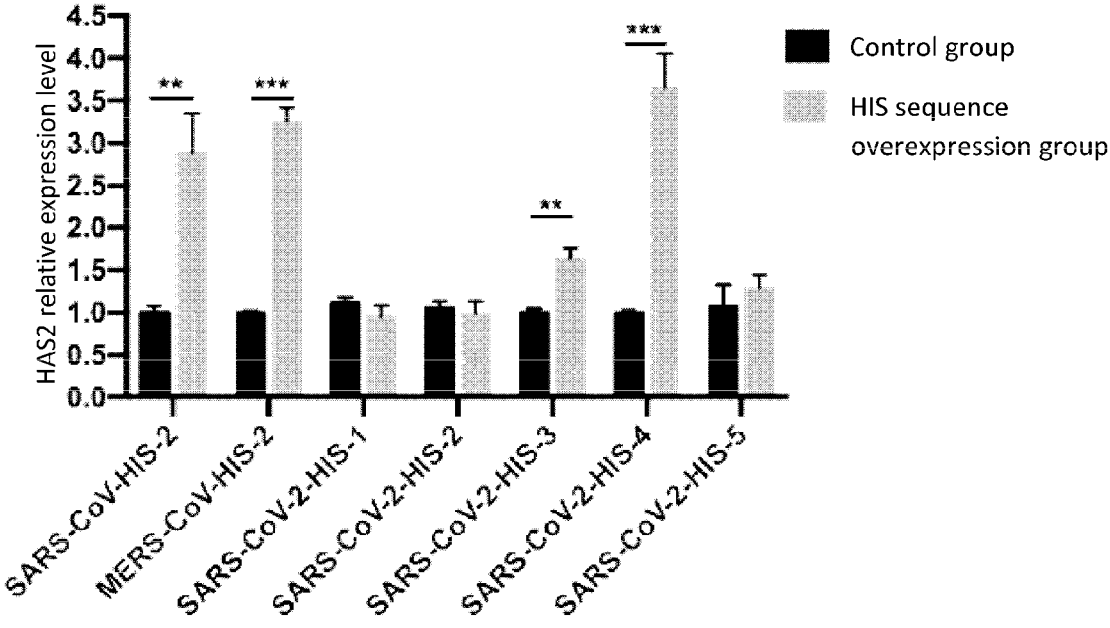


FIG. 5

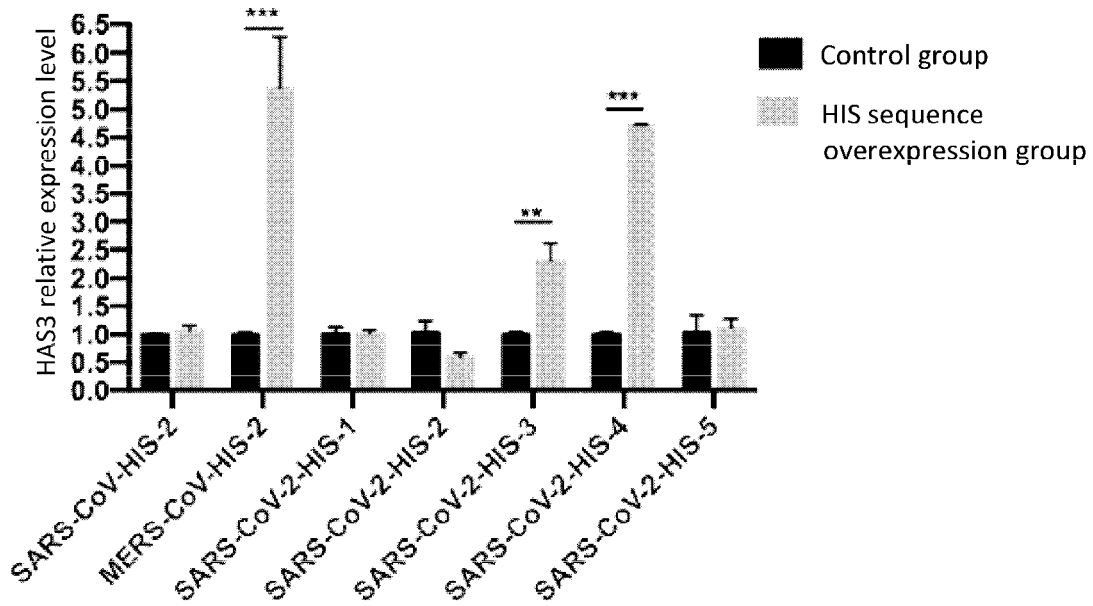


FIG. 6

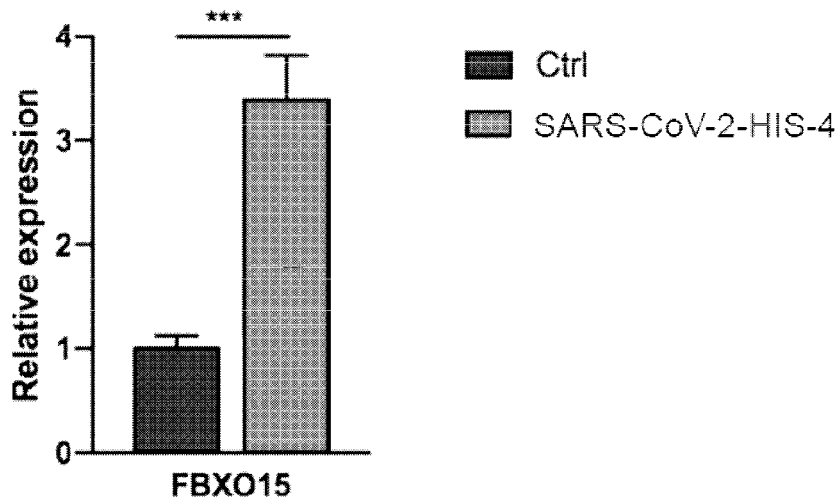


FIG. 7

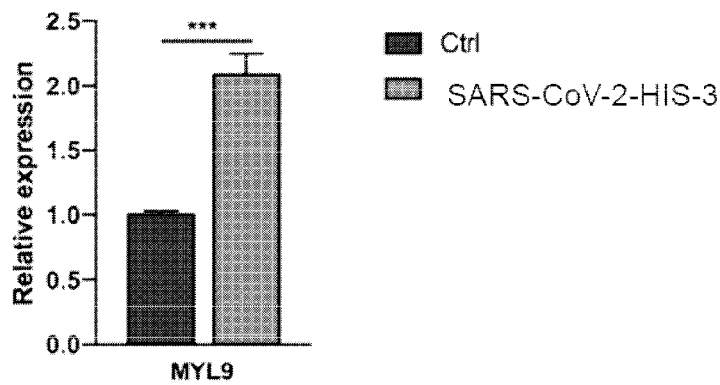


FIG. 8

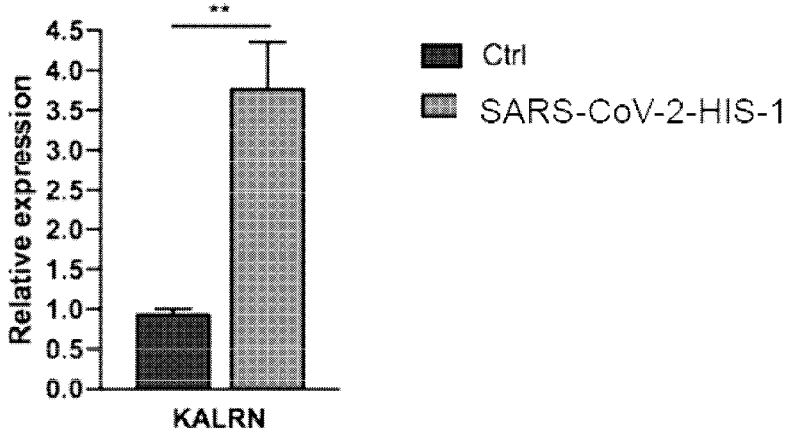


FIG. 9

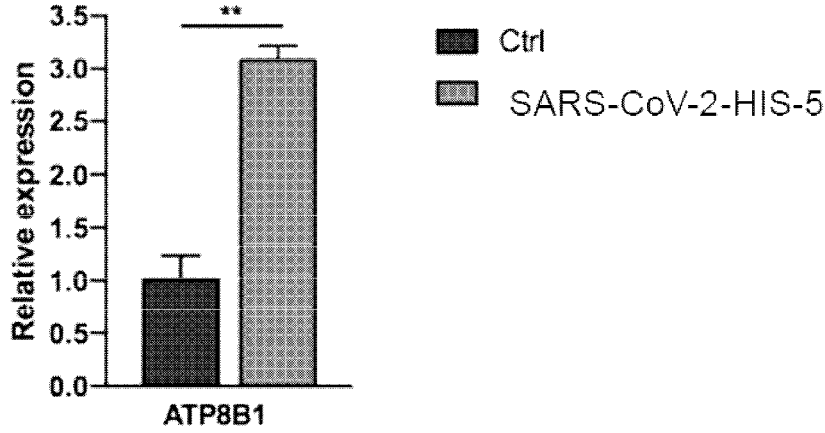


FIG. 10

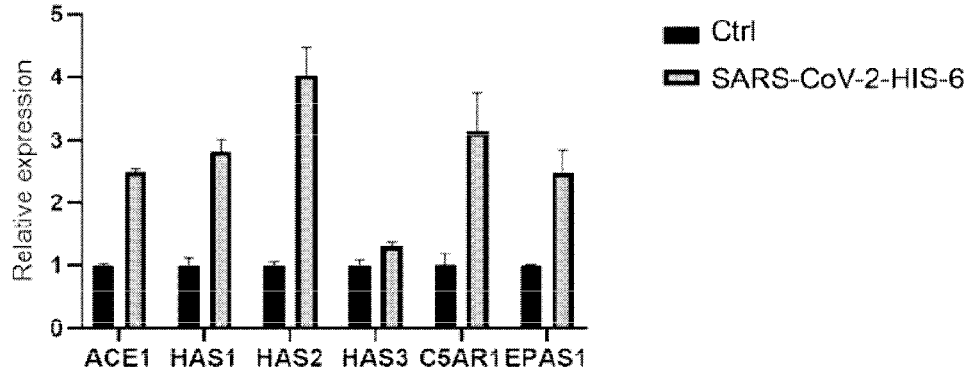


FIG. 11

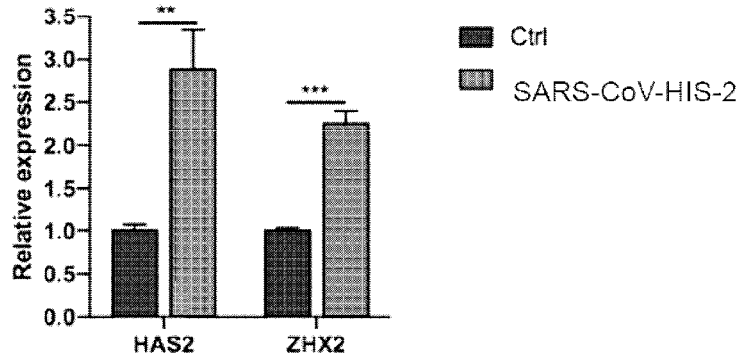


FIG. 12

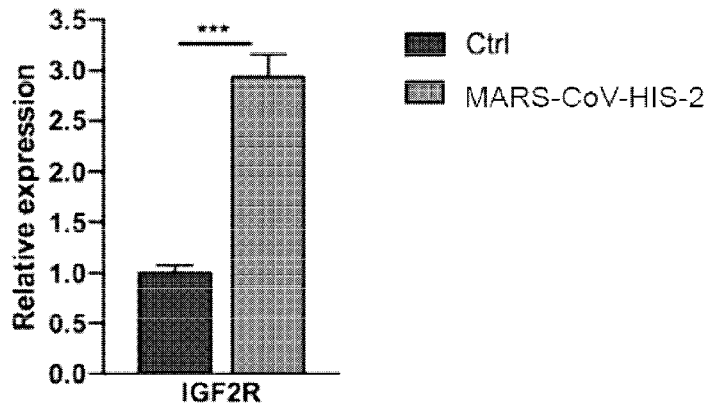


FIG. 13

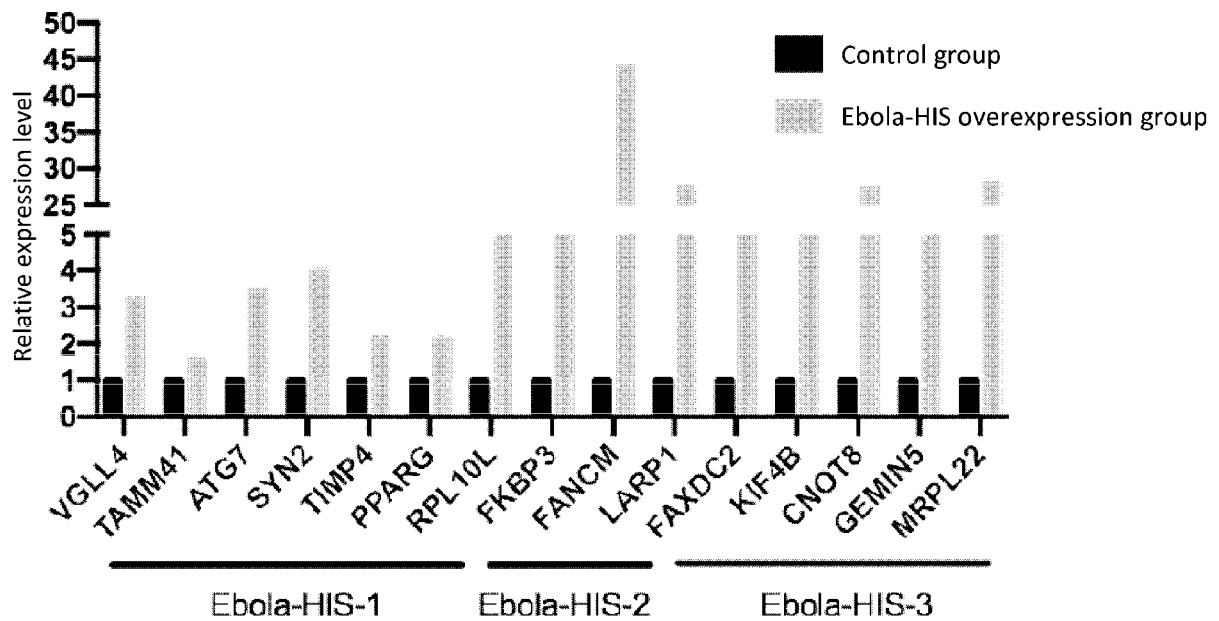


FIG. 14

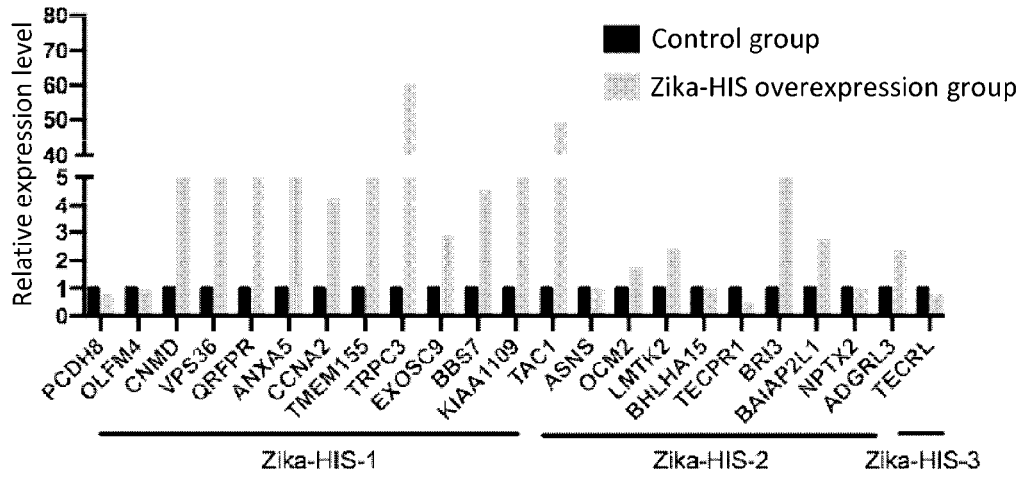


FIG. 15

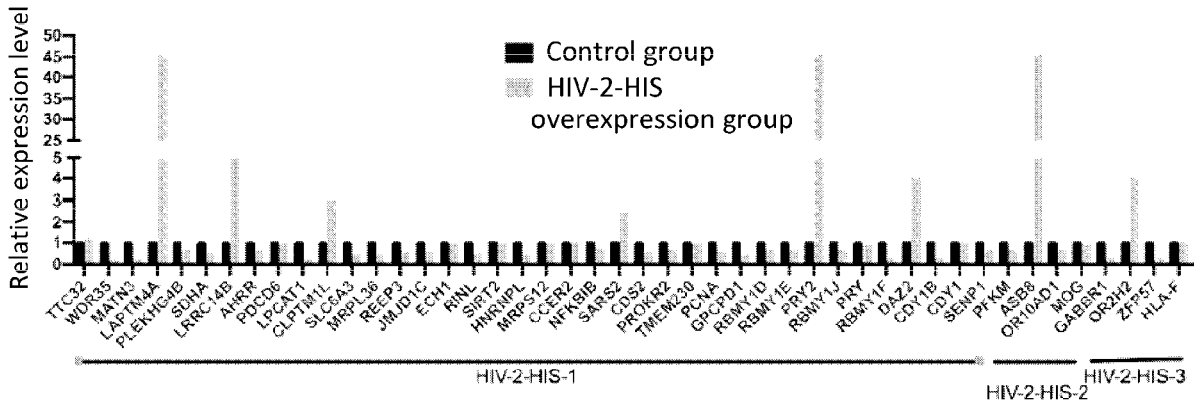


FIG. 16

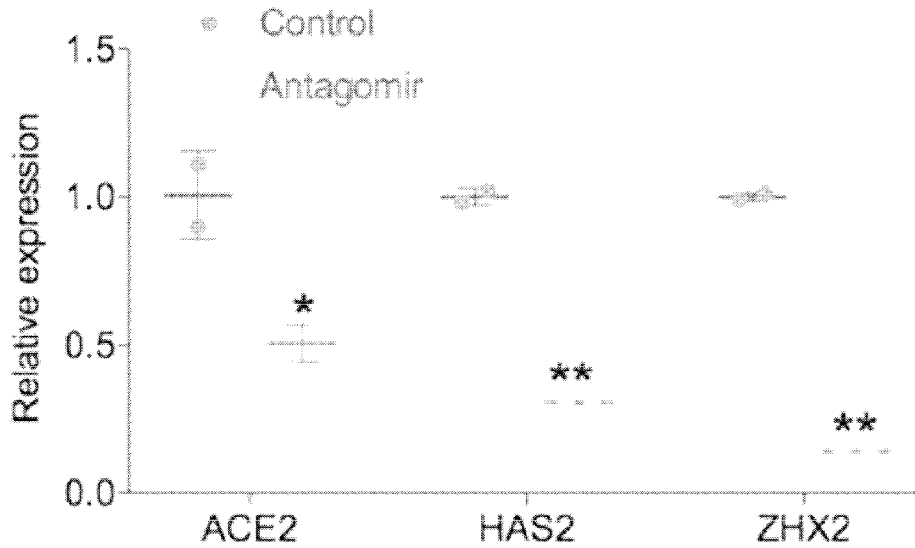


FIG. 17

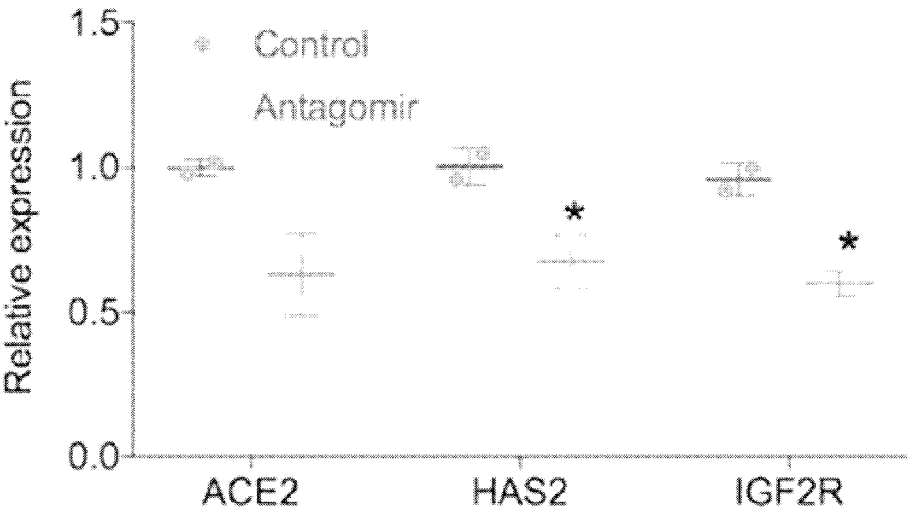


FIG. 18

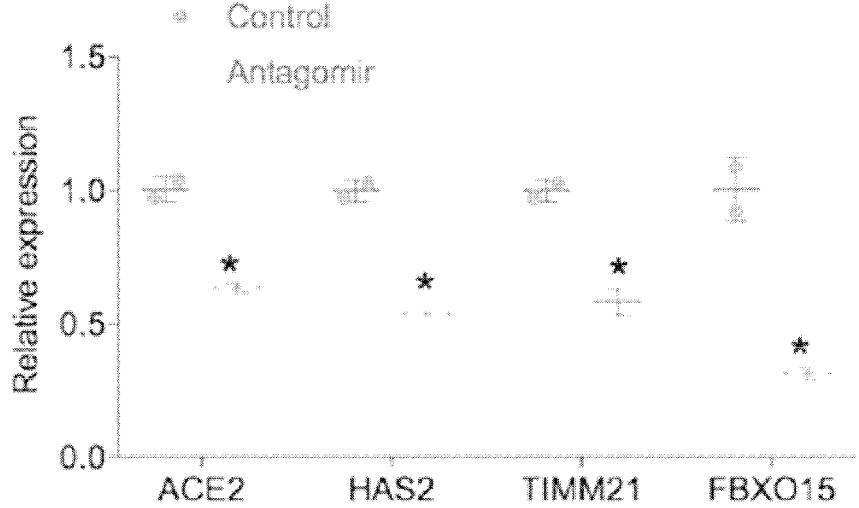


FIG. 19

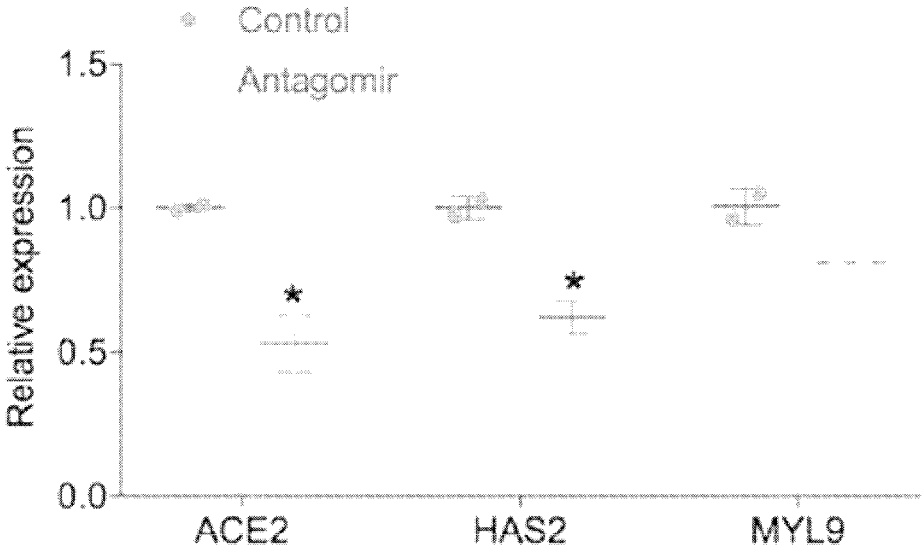


FIG. 20

TARGET SEQUENCE OF RNA VIRUS AND USE THEREOF

REFERENCE TO A SEQUENCE LISTING SUBMITTED ELECTRONICALLY VIA EFS-WEB

[0001] The content of the electronically submitted sequence listing in ASCII text file (Name: 4969_0020000_Seqlisting_ST25; Size: 269,003 bytes; and Date of Creation: Jan. 31, 2022) is herein incorporated by reference in its entirety.

TECHNICAL FIELD

[0002] The present invention relates to the field of biotechnology, in particular to a target sequence of an RNA virus and the use thereof.

BACKGROUND OF THE INVENTION

[0003] RNA viruses are also called RNA-type viruses, which refer to viruses whose genetic material is RNA. In the process of virus RNA replication, the activity of enzymes responsible for the error repair mechanism is very low to almost none, thereby leading to very fast mutation. Furthermore, vaccines are developed based on the stable nucleotides sequence or proteins of viruses, and therefore vaccines against RNA viruses are difficult to develop. The RNA viruses cannot be reproduced by themselves, and can be reproduced only in living cells. Common RNA viruses are: HIV, poliovirus, tobacco mosaic virus, SARS virus, MERS virus, ebola virus, severe acute respiratory syndrome-related coronavirus 2 (2019-nCoV), etc. Coronavirus is a type of unsegmented positive-sense RNA virus with an envelope, can infect a variety of hosts such as mammals and birds, and can cause mild to moderate respiratory diseases especially in humans. In the past two decades, the emergence of two highly pathogenic coronaviruses has appeared in the process of zoonotic infection: severe acute respiratory syndrome-related coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV). Corona Virus Disease 2019, referred to as "COVID-19" briefly, refers to pneumonia caused by the infection of 2019 severe acute respiratory syndrome-related coronavirus 2. COVID-19 is an acute infectious pneumonia. Researchers have discovered that its pathogen is a new type of β -coronavirus that has not previously been found in humans. The virus was subsequently named severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) by the World Health Organization (WHO). The initial symptoms of a patient with COVID-19 are mostly fever, fatigue and dry cough, and they gradually develop severe symptoms such as dyspnea. In some severe cases, acute respiratory distress syndrome, septic shock and even death may occur. As of Jul. 7, 2020, SARS-CoV-2 has continued to spread in 188 countries and regions around the world, causing more than 11.62 million confirmed cases and 538,000 deaths. There is currently no effective target specifically for coronavirus.

[0004] Nucleic acid is an important carrier for the storage and transmission of genetic information in organisms, and also plays an extremely important role in the regulation of biological functions. With people's deepening understanding of the structure and function of the nucleic acid, the value of nucleic acid as a target for drug design has been paid more and more attention by everyone. MicroRNA

(miRNA) is a type of small single-stranded short-sequence RNA with a length of about 22-25 nucleotides, it does not code a protein, but the nucleotides at positions 2-8 from its 5' end can bind to the 3' UTR (3' untranslated region) of homologous mRNA by means of incomplete base pairing. At first, it is believed that only the sequence in one of the strands of the miRNA hairpin structure has a regulatory effect to exert function by negatively regulating gene expression by inducing messenger RNA (mRNA) degradation and post-transcriptional gene silencing, and the other strand would be degraded. However, more and more evidences later show that the upper and lower strands of miRNA can function as an independent miRNA. In addition to negative regulation by miRNA, some cases reported that miRNA can promote gene expression or translation under special circumstances (Vasudevan et al., 2007, Vasudevan and Steitz, 2007, Place et al., 2008). XIAOM et al. found in 2015 that, for example, has-miR-26a-1, has-miR-3179, has-24-1, etc. can bind to an enhancer (the result was published in the journal RNABiology) and activate gene expression at the genome-wide level (XIAO M, LI J, LI W, et al. 2017. MicroRNAs activate gene transcription epigenetically as an enhancer trigger. RNA Biol [J], 14: 1326-1334.). Our previous work has shown that this feature of miRNA is not a single case, but is suitable for many tissues and cells. When studying the epigenetic regulation mechanism of miRNA itself, 1594 miRNA precursors were systematically analyzed in 7 different tissues and cells. It was unexpectedly found that the positions of more than 300 miRNA precursors in the genome highly overlapped with that of the histone modification marker H3K4me1 or H3K27ac of the enhancer. This allowed the inventors to link the two important molecular biological events, i. e., miRNA and enhancer that are both histocyte-specific (Xiao et al., 2017). Based on this, the inventors believe that miRNA is an important bifunctional molecule. When miRNA is located in the cytoplasm, it can act on the 3' UTR region of mRNA, thereby blocking the translation of mRNA and exerting a negative regulatory effect on genes, like a fire extinguisher; in contrast, when miRNA is located in the nucleus, it changes the chromatin state of the enhancer by binding to the enhancer, thereby activating the transcriptional expression of genes, like an igniter. The inventors call the RNA that is located in the nucleus and has an activating effect as NamiRNA (nuclear activating miRNA). Based on this, the inventors propose a NamiRNA-enhancer-target gene network activation model to reveal the function of miRNA in the nucleus. Surprisingly, there is a direct positive regulatory relationship between NamiRNA and target genes, and NamiRNA is also involved in the biological behaviors such as the proliferation, migration and invasion of tumor cells.

[0005] Hyaluronic acid (HA) is one of the main components of glycosaminoglycan (GAG) in proteoglycans, is also one of the components of extracellular matrix (ECM) that has been studied extensively, and plays an important role in the function and development of normal tissues, comprising providing support and anchoring for cells, promoting signaling between cells, and promoting cell movement and migration. HA is synthesized by a type of integral membrane protein called HA synthase (hyaluronic acid synthase, HAS), of which there are three types in vertebrates: HAS1, HAS2 and HAS3. HA is extended by these enzymes which are capable of repeatedly adding glucuronic acid and N-acetylglucosamine to the nascent polysaccharide, and extruded

through the cell membrane to enter the extracellular space. HA is a macromolecular viscous glycosaminoglycan that can be secreted by type II lung epithelial cells, endothelial cells and lung fibroblasts, wherein fibroblasts can be stimulated by pathogenic factors, such as oxygen free radicals, to synthesize large amounts of HA. The basic structure of HA is β -D gluconic acid and 2-acetyl-2-deoxy-D-glucose, which are linear chain molecular polymers of repeating disaccharides connected by β 1.3 and β 2.4 glucosidic bond, respectively, and are the most important glycosaminoglycan. HA is mainly distributed in the interstitium around capillaries and bronchioles in lung tissue, and is widely expressed in the extracellular matrix, and can also be expressed on the cell surface. The greatest function of hyaluronic acid is to absorb and store water. One molecule of hyaluronic acid can absorb 9 molecules of water. The increase of hyaluronic acid will undoubtedly aggravate the increase of local water. Studies have shown that HA can increase local edema and promote the inflammatory cascade, leading to leukocyte migration, proliferation and differentiation.

[0006] Hyaluronic acid synthase inhibitor (4-Methylumbelliferone, 4-MU) is a selective inhibitor of HA synthesis. 4-MU is a derivative of the coumarin family. Other coumarin derivatives, such as Marcumar® and Coumadin®, are mostly used as preventive drugs to reduce the occurrence of cardiovascular disease due to the anticoagulant mechanisms thereof.

[0007] ACE2 is a receptor of severe acute respiratory syndrome-related coronavirus 2, and the expression level thereof is closely related to the course of the diseases caused by severe acute respiratory syndrome-related coronavirus 2.

[0008] HAS1, HAS2, and HAS3 belong to the family of hyaluronic acid synthases, and the increase of their expression level and deposition in the extracellular matrix is closely related to the diseases caused by severe acute respiratory syndrome-related coronavirus 2 and the complications thereof.

[0009] FBXO15 is a member of the F-box protein family, and the expression level thereof is closely related to the inflammatory response.

[0010] MYL9 is myosin light chain 9, and the expression level thereof is closely related to inflammatory response.

[0011] KALRN is a RhoGEF kinase, and the expression level thereof is related to the progression of sarcoidosis and inflammation of multiple organs such as kidney and lung.

[0012] ATP8B1 is a member of the type P cation transport ATPase family, and the expression level thereof is closely related to the inflammatory response.

[0013] IGF2R is a receptor for insulin-like growth factor 2 and mannose 6-phosphate, and the expression level thereof is closely related to the inflammatory response.

[0014] C5AR1 is complement component 5a receptor 1, and the expression level thereof is closely related to the regulation of the inflammatory response.

[0015] EPAS1 is endothelial PAS domain protein 1, and the expression level thereof is closely related to the regulation of the inflammatory response.

[0016] TIMM21 is internal mitochondrial membrane translocase 21, and the expression level thereof is closely related to the regulation of the inflammatory response.

[0017] So far, the mechanism of severe acute respiratory syndrome caused by RNA viruses, especially severe acute

respiratory syndrome-related coronavirus 2, is not clear. There are also many problems in understanding the pathogenic mechanism and designing or producing vaccines of other related RNA viruses. In addition, the diseases caused by RNA viruses lack effective treatment drugs and treatment regimens, and the virus virulence and susceptible populations are difficult to determine. There is an urgent need to study the pathogenic mechanism of RNA viruses, and develop the detection for the pathogenicity and population susceptibility of RNA viruses, seek for specific drugs and treatment regimens for RNA viruses, prepare RNA virus vaccines with high efficiency and low toxicity, and propose practical Chinese solutions for humans to overcome RNA virus infections.

SUMMARY OF THE INVENTION

[0018] The RNA sequence of severe acute respiratory syndrome-related coronavirus 2 has about 30,000 bases. The inventors found that, when comparing severe acute respiratory syndrome-related coronavirus 2 with the human genome in the early stage, the nucleic acid sequence of severe acute respiratory syndrome-related coronavirus 2 contains 5 human genome sequences, ranging in length from 24-28 bp. These 5 sequences are extremely conserved and identical in humans and primates. The conservation of the 5 sequences suggests that they are of great significance. In order to facilitate the research on the function and use of the above-mentioned conservative sequences, the inventors named the above-mentioned conservative sequences as HISs (Human Insert Sequences). Furthermore, the inventors found that there are 3 and 2 human genome sequences (HIS) in the genomes of SARS and MERS viruses, respectively. The location distribution of HIS in the genomes of severe acute respiratory syndrome-related coronavirus 2, SARS, and MERS viruses is mainly in the enhancer region in human, suggesting that HISs are related to gene activation; there are a large number of inflammatory factor genes in the upstream and downstream 200 K range of the enhancer where the HIS in SARS-CoV-2 is located; the RNA region where HIS is located can form a virus derived hairpin structure. It is found from further analysis that HIS can form a hairpin structure with miRNA precursor characteristics; based on HIS, most of target genes in relation to HIS are also related to inflammatory factors by means of bioinformatics analysis and prediction; the HIS target area of SARS virus and severe acute respiratory syndrome-related coronavirus 2 has hyaluronic acid synthase (HAS) genes; According to the NamiRNA-enhancer-gene activation theory (Xiao et al., 2017) discovered and proposed by the inventors in the previous research work, the inventors believe that the HIS sequences of severe acute respiratory syndrome-related coronavirus 2 and SARS virus will activate inflammatory factors after the human body being infected with the viruses, which causes a storm of inflammatory factors and may produce excessive hyaluronic acid by activating hyaluronic acid synthase to cause ground-glass changes in lung and then lead to ARDS. In view of the fact that the HIS sequences in severe acute respiratory syndrome-related coronavirus 2 are an important material basis and an important pathogenesis for the pathogenicity of the coronavirus, the inventors further confirm by experiments that the HIS sequences in SARS-COV-2, SARS-COV and MERS virus, when overexpressed in cells, can activate the expression of

HAS and inflammatory factors, and increase the production of the extracellular hyaluronic acid. More importantly, it is found that the content of hyaluronic acid in the serum of a patient with COVID-19 is closely related to the severity of the patient's condition. The inventors believe that the target sequences of the virus can also cause changes in hematological indicators and can be used for clinical detection of patient's condition combined with clinical data. Therefore, the targets in coronaviruses can be used in clinical diagnosis, drug therapy design against this target and possible design/optimization of vaccines. The development of such targets can be extended to other RNA viruses, and similar results are obtained by verifying with the typical coronaviruses, HIV, zika virus and ebola virus. In particular, the regions where the HIS sequences of other RNA viruses pair with the human genome are mostly related to the pathogenicity and characteristics of such RNA viruses.

[0019] Comparing with the prior art, the above technical solutions are used in the present invention, and the following technical effects are achieved:

[0020] In the present invention, the gene sequence of the RNA virus is aligned with the human genome to screen out multiple target sequences with not less than 95% similarity to the human genome (i.e., more than 95% of complementary pairing) and stable structure, and the successfully constructed virus fragment has the function of interacting with human genomic DNA and is similar to viral miRNA. In addition, the effect of overexpression of the target sequences of the RNA virus on the expression level of surrounding genes has been verified. The above-mentioned screening and verification have good application value in the diagnosis and detection of RNA viruses, screening of drugs for the treatment of conditions caused by RNA viruses, and design/optimization of vaccines.

[0021] The RNA viruses involved in the present invention comprise RNA viruses that infect humans, RNA viruses that infect poultry, livestock, and zoonotic animals. Specifically, the target sequence consistent with the human genome is named HIS (Human Insert Sequence), the target sequence consistent with the chicken genome is named CIS (Chicken Insert Sequence), and the target sequence consistent with the pig genome is named PIS (Pig Insert Sequence), the target sequence consistent with the dog genome is named DIS (Dog Insert Sequence), and the target sequence consistent with mallard genome is named MIS (Mallard Insert Sequence). The specific target sequences of these viruses, as same as that of SARS-COV-2, can activate gene expression through an enhancer, and are closely related to diseases caused by viruses in humans and other species, and then can be used as targets for the determination of virus virulence. The antisense RNA sequences of the specific target sequences can be used for drug development, and deletion of the target sequences is an important strategy for the design of an attenuated vaccine.

[0022] The present invention overcomes the defects in the prior art, provides a target sequence of an RNA virus which has the function of interacting with the human genome, and verifies the effect of overexpression of the target sequence of the RNA virus on the expression level of surrounding genes. The target sequence and the antisense RNA sequence thereof are developed and used for the diagnosis and treatment of RNA viruses and the design/optimization of vaccines.

[0023] In order to achieve the above objective, the following technical solutions are used in the present invention:

[0024] In the first aspect, the present invention provides a target sequence of an RNA virus. The target sequence is a nucleic acid sequence fragment in the nucleotide sequence of the RNA virus containing not less than 20-40 bases and having not less than 95% similarity to human genome sequence (i.e., more than 95% identity or complementary pairing).

[0025] In order to further optimize the above-mentioned target sequence of the RNA virus, the technical measures used in the present invention also comprise:

[0026] further, the RNA virus comprises but is not limited to: severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), severe acute respiratory syndrome-related coronavirus (SARS-CoV), middle east respiratory syndrome coronavirus (MERS-CoV), zika virus, ebola virus, HIV, norwalk virus, alkhurma virus, enterovirus, kemerovo virus, coxsackievirus, hepatitis A virus, dengue virus 2, rubella virus, marburg marburgvirus, poliovirus, respiratory syncytial virus, mumps virus, australian bat lyssavirus, andes virus, powassan virus, langat virus, eyach virus, colorado tick fever virus, lassa virus, omsk hemorrhagic fever virus, machupo virus, junin virus, guanarito virus, sin nombre virus, hantaan virus, puumala virus, dobrava virus, seoul virus, crimean-congo hemorrhagic fever virus, sabia virus, thogoto virus, european bat lyssavirus 1, european bat lyssavirus 2, chapare virus, rotavirus, tai forest ebolavirus, bundibugyo ebolavirus, rift valley fever virus, irkut virus, influenza A virus, bayou virus, kysanur forest disease virus, black creek canal virus, Japanese encephalitis virus, duvnhage lyssavirus, Lujo mammarenavirus, measles morbillivirus, tick-borne encephalitis virus, avian influenza virus, swine influenza virus, Rabies virus, etc.

[0027] Further, the target sequence of the RNA virus is selected from any one or more of SEQ ID NO. 1 - SEQ ID NO. 615. Further, the target sequence of the severe acute respiratory syndrome-related coronavirus 2 comprises SEQ ID NO. 1 - SEQ ID NO. 6; and/or, the target sequence of severe acute respiratory syndrome-related coronavirus comprises SEQ ID NO. 7 - SEQ ID NO. 9; and/or, the target sequence of middle east respiratory syndrome coronavirus comprises SEQ ID NO. 10, SEQ ID NO. 11; and/or, the target sequence of zika virus comprises SEQ ID NO. 12 - SEQ ID NO. 14; and/or, the target sequence of ebola virus comprises SEQ ID NO. 15 - SEQ ID NO. 17; and/or, the target sequence of HIV comprises SEQ ID NO. 18 - SEQ ID NO. 26; and/or, the target sequence of norwalk virus comprises SEQ ID NO. 27; and/or, the target sequence of alkhurma virus comprises SEQ ID NO. 28 - SEQ ID NO. 30; and/or, the target sequence of enterovirus comprises SEQ ID NO. 31, SEQ ID NO. 32; and/or, the target sequence of kemerovo virus comprises SEQ ID NO. 33, SEQ ID NO. 34; and/or, the target sequence of coxsackievirus comprises SEQ ID NO. 35; and/or, the target sequence of hepatitis A virus comprises SEQ ID NO. 36 - SEQ ID NO. 46; and/or, the target sequence of dengue virus 2 comprises SEQ ID NO. 47 - SEQ ID NO. 50; and/or, the target sequence of rubella virus comprises SEQ ID NO. 51; and/or, the target sequence of marburg marburgvirus comprises SEQ ID NO. 52 - SEQ ID NO. 56; and/or, the target sequence of poliovirus comprises SEQ ID NO. 57; and/or, the target sequence of respiratory syncytial virus comprises SEQ ID NO. 58 - SEQ ID NO. 85; and/or, the target

sequence of mumps virus comprises SEQ ID NO. 86; and/or, the target sequence of australian bat lyssavirus comprises SEQ ID NO. 87; and/or, the target sequence of andes virus comprises SEQ ID NO. 88 - SEQ ID NO. 95; and/or, the target sequence of powassan virus comprises SEQ ID NO. 96, SEQ ID NO. 97; and/or, the target sequence of langat virus comprises SEQ ID NO. 98 - SEQ ID NO. 102; and/or, the target sequence of eyach virus comprises SEQ ID NO. 103 - SEQ ID NO. 113; and/or, the target sequence of colorado tick fever virus comprises SEQ ID NO. 114 - SEQ ID NO. 134; and/or, the target sequence of lassa virus comprises SEQ ID NO. 135, SEQ ID NO. 136; and/or, the target sequence of omsk hemorrhagic fever virus comprises SEQ ID NO. 137, SEQ ID NO. 138; and/or, the target sequence of machupo virus comprises SEQ ID NO. 139 - SEQ ID NO. 140; and/or, the target sequence of junin virus comprises SEQ ID NO. 141; and/or, the target sequence of guaranito virus comprises SEQ ID NO. 142 - SEQ ID NO. 147; and/or, the target sequence of sin nombre virus comprises SEQ ID NO. 148 - SEQ ID NO. 152; and/or, the target sequence of hantaan virus comprises SEQ ID NO. 153 - SEQ ID NO. 161; and/or, the target sequence of puumala virus comprises SEQ ID NO. 162 - SEQ ID NO. 173; and/or, the target sequence of dobrava virus comprises SEQ ID NO. 174 - SEQ ID NO. 185; and/or, the target sequence of seoul virus comprises SEQ ID NO. 186 - SEQ ID NO. 199; and/or, the target sequence of crimean-congo hemorrhagic fever virus comprises SEQ ID NO. 200 - SEQ ID NO. 204; and/or, the target sequence of sabia virus comprises SEQ ID NO. 205 - SEQ ID NO. 212; and/or, the target sequence of thogoto virus comprises SEQ ID NO. 213 - SEQ ID NO. 227; and/or, the target sequence of european bat lyssavirus 1 comprises SEQ ID NO. 228 - SEQ ID NO. 232; and/or, the target sequence of european bat lyssavirus 2 comprises SEQ ID NO. 233; and/or, the target sequence of chapare virus comprises SEQ ID NO. 234; and/or, the target sequence of rotavirus comprises SEQ ID NO. 235 - SEQ ID NO. 277; and/or, the target sequence of tai forest ebola-virus comprises SEQ ID NO. 278, SEQ ID NO. 279; and/or, the target sequence of bundibugyo ebolavirus comprises SEQ ID NO. 280; and/or, the target sequence of rift valley fever virus comprises SEQ ID NO. 281; and/or, the target sequence of irkut virus comprises SEQ ID NO. 282 - SEQ ID NO. 285; and/or, the target sequence of influenza A virus comprises SEQ ID NO. 286 - SEQ ID NO. 313; and/or, the target sequence of bayou virus comprises SEQ ID NO. 314 - SEQ ID NO. 327; and/or, the target sequence of kyasaur forest disease virus comprises SEQ ID NO. 328; and/or, the target sequence of black creek canal virus comprises SEQ ID NO. 329 - SEQ ID NO. 334; and/or, the target sequence of japanese encephalitis virus comprises SEQ ID NO. 335 - SEQ ID NO. 337; and/or, the target sequence of duvenhage lyssavirus comprises SEQ ID NO. 338 - SEQ ID NO. 344; and/or, the target sequence of Lujo alkhurma virus comprises SEQ ID NO. 345; and/or, the target sequence of measles morbillivirus comprises SEQ ID NO. 346; and/or, the target sequence of tick-borne encephalitis virus comprises SEQ ID NO. 347; and/or, the target sequence of avian influenza virus comprises SEQ ID NO. 348 - SEQ ID NO. 420; and/or, the target sequence of swine influenza virus comprises SEQ ID NO. 421 - SEQ ID NO. 521; and/or, the target sequence of rabies virus comprises SEQ ID NO. 522 - SEQ ID NO. 615.

[0028] The naming method of each fragment of the above target sequences is the virus name plus HIS or other assigned name plus the fragment number. The specific target sequences are shown in the following table:

TABLE 1

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2)	SARS-CoV--HIS1	5'-UGUCUAUGCUAAUG-GAGG UAAAGGCU-3'	SEQ ID NO. 1
	SARS-CoV-2-HIS-2	5'-UAUAACA-CAUAUAAAAAUACGUGU-3'	SEQ ID NO. 2
	SARS-CoV-2-HIS-3	5'-UUUAUAGC-CUUAUUUCUUAUUU-3'	SEQ ID NO. 3
	SARS-CoV-2-HIS-4	5'-AGGAGAAUGA-CAAAAAA-AAAAAAA-3'	SEQ ID NO. 4
	SARS-CoV-2-HIS-5	5'-UUGUUGCUG-CUAUUUCUUAUUAA-3'	SEQ ID NO. 5
	SARS-CoV-2-HIS-6	5'-CAUGAAGAAA-CAUUUUUAUUUUACUUA-3'	SEQ ID NO. 6
severe acute respiratory syndrome-related coronavirus (SARS-CoV)	SARS-CoV-HIS-1	5'-GAGUUGAGGAAGAA-GAAGAGGAAGACUGG-3'	SEQ ID NO. 7
	SARS-CoV-HIS-2	5'-UAACAUGCUUAG-GAUAAU GGCCUC-3'	SEQ ID NO. 8
	SARS-CoV-HIS-3	5'-AGGAGAAUGA-CAAAAAA-AAAAAAA-3'	SEQ ID NO. 9
Middle East respiratory syndrome coronavirus (MERS-CoV)	MERS-CoV-HIS-1	5'-UUCCAUUUGCACAGA-GUA UCUUUU-3'	SEQ ID NO. 10
	MERS-CoV-HIS-2	5'-UGCUGUAAUUGCU-GUUGUUGCUGCUGUU-3'	SEQ ID NO. 11
Zika virus	Zika-HIS-1	5'-GAAAAAGAGAAAA-GAAAC AAGGG-3'	SEQ ID NO. 12
	Zika-HIS-2	5'-GGGAGGAGGGAG-GAAGAG ACUCC-3'	SEQ ID NO. 13
	Zika-HIS-3	5'-GUUCUAGAGAUG-CAAGAC UUGUG-3'	SEQ ID NO. 14
Ebola virus	Ebola-HIS-1	5'-ACUCAUUCUAC-CAUUUUU UAAAAUUG-3'	SEQ ID NO. 15
	Ebola-HIS-2	5'-AGAUCUGUGACUUCUGG ACUUUU-3'	SEQ ID NO. 16
	Ebola-HIS-3	5'-AAAUAUUUUUUUA-AAAU UUACUU-3'	SEQ ID NO. 17
HIV	HIV-1-HIS-1	5'-ACUUUUUAAAA-	SEQ ID NO. 18

TABLE 1-continued

Target sequence listing of RNA virus				
Virus type	Fragment number	Fragment coding sequence	ID number	
HIV-1	HIS-2	5'-GAAAAGG GGGGA-3'	SEQ ID NO. 19	
	HIS-3	5'-GAAAAGGAAGG-GAAAALTU UCAAA-3'	SEQ ID NO. 20	
	HIS-4	5'-AAAUGACAAGUA-GAUA AUUAG-3'	SEQ ID NO. 21	
	HIS-5	5'-AAAUUUUGGUACCA-GUUA GAGAAA-3'	SEQ ID NO. 22	
	FHS-6	5'-GAAA-GAAAAAAUUAUUUU UAAAA-3'	SEQ ID NO. 23	
	HIS-1	5'-AUUUUCAAGAGC-CAUUU AAAA-3'	SEQ ID NO. 24	
	HIS-2	5'-UAAAACAGGGAC-CAAAAG AACCGU-3'	SEQ ID NO. 25	
	HIS-3	5'-AGAAUCAGAUAA-GUAGAA UUAGA-3'	SEQ ID NO. 26	
	Norwalk virus	HIS	5'-UAUCAAAAAUUUA-GAAA AGGUUA -3'	SEQ ID NO. 27
	Alkhurma virus	HIS-1	5'-GGAUCAGUGGA-GAAAGUG AGGAGGAUGA-3'	SEQ ID NO. 28
		HIS-2	5'-AUGAGAGAU-CUUGGGGGU GGGAC-3'	SEQ ID NO. 29
		HIS-3	5'-GAAAAACUCAAGAU-GAAA GGAU -3'	SEQ ID NO. 30
	Enterovirus	HIS-1	5'-AUUGAUUGG-CUUAAGGAG AAAUA-3'	SEQ ID NO. 31
HIS-2		5'-AAUUGUUUAC-CUAUUUAU UGGUUUUGUG-3'	SEQ ID NO. 32	
Kemerovo virus	HIS-1	5'-CUGUGCUGAACCCAG-GACC AGGA-3'	SEQ ID NO. 33	
	HIS-2	5'-AGAUGAAGCAGUCAC-CAA CCGC-3'	SEQ ID NO. 34	
Coxsackievirus	HIS	5'-AUUAGAUUUAACA-CAGG UGCUACAUC-3'	SEQ ID NO. 35	
Hepatitis A virus	HIS-1	5'-UUGGAAUGUUUUG-CUCCU CUUUA-3'	SEQ ID NO. 36	
	HIS-2	5'-GAAUUUUUUUUUU-UUGU UCAGU-3'	SEQ ID NO. 37	
	HIS-3	5'-UUAGCUAGAUUUA-CAGAU UUGGA-3'	SEQ ID NO. 38	
	HIS-4	5'-AACAAGAGCAGGCCA-GUG UGGUGG-3'	SEQ ID NO. 39	
	HIS-5	5'-UUGAGGAAAAGG-GAACCC UGUACA-3'	SEQ ID NO. 40	
	HIS-6	5'-CCAGGCACUGGGAA-GUCA GUGGCA-3'	SEQ ID NO. 41	
	HIS-7	5'-AAUUAGGAGU-	SEQ ID NO. 42	

TABLE 1-continued

Target sequence listing of RNA virus				
Virus type	Fragment number	Fragment coding sequence	ID number	
Hepatitis A virus	HIS-8	5'-GAUACCUU CACUAA-3'	SEQ ID NO. 43	
	HIS-9	5'-UGAGAAAAAGGCCA-CUGU CCUUA-3'	SEQ ID NO. 44	
	HIS-10	5'-ACAAAUUGGA-GAAAUAGU GAAAA-3'	SEQ ID NO. 45	
	HIS-11	5'-GAAGCAGAGAGAAA-GUAG AGAAG-3'	SEQ ID NO. 46	
	Dengue virus 2	HIS-1	5'-UCAAAAAGGAGAGAA-CAGA UGCGG-3'	SEQ ID NO. 47
		HIS-2	5'-CAAAAGAAGG-CAUUAAAA GAGGA-3'	SEQ ID NO. 48
		HIS-3	5'-GAGAUGGACUUU-GAUUUC UGUGA-3'	SEQ ID NO. 49
		HIS-4	5'-GGAAAUCCAGGGAG-GUUU UGGAA-3'	SEQ ID NO. 50
	Rubella virus	HIS	5'-AAAGGAAGAAUU-GAAAC CCAGA-3'	SEQ ID NO. 51
	Marburg Marburgvirus	HIS-1	5'-GUGGCAGGCCAUUA-CAC CACCA-3'	SEQ ID NO. 52
		HIS-2	5'-AGUUUAAAAUUUA-UCCA AAAUAAAAUUU-3'	SEQ ID NO. 53
HIS-3		5'-AAGAAAA-GAUAAAUAGA ACACAAAGAAUUGA-CAAAAUU U-3'	SEQ ID NO. 54	
Marburg Marburgvirus	HIS-4	5'-UCUAAGCGAAGUAA-CAAC AAGAGU-3'	SEQ ID NO. 55	
	HIS-5	5'-AACAGAAAAG-CAUUU UACAUCAGGCUUCU-3'	SEQ ID NO. 56	
Poliovirus	HIS	5'-UGAUUUUAUUUA-CUGGU AUAAAAUAGU-3'	SEQ ID NO. 57	
	HIS	5'-AACAAACAAACCAGA-GAC ACUAAGGAAAUGCA-3'	SEQ ID NO. 58	
Respiratory syncytial virus	HIS-1	5'-AUACAAUCAAUU-GAAUG GCAU-3'	SEQ ID NO. 59	
	HIS-2	5'-AGAUGACAAUUGU-GAAAU UAAA-3'	SEQ ID NO. 60	
	HIS-3	5'-GUUAUAUUGG-GAAAUGA UGGAAUUUAACA-3'	SEQ ID NO. 61	
	HIS-4	5'-AAAAACUAAGU-GAUUCA ACA-3'	SEQ ID NO. 62	
	HIS-5	5'-AAAUA-CAAAAAUUUACU GAAUACAA-3'	SEQ ID NO. 63	
	HIS-6	5'-UUUACAUCUGGU-CAAC UAUGAAAUGAAA-CUAUUGC-3'	SEQ ID NO. 64	
	HIS-7	5'-CUACAAAAAAUUG-CUAAA AGAA-3'	SEQ ID NO. 64	

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Respiratory syncytial virus-HIS-8	5'-	AUGCUGAACACU- CAAAG AAAA-3'	SEQ ID NO. 65
Respiratory syncytial virus-HIS-9	5'-	AGGAAAGUGAAAA- GAUGG CAAA-3'	SEQ ID NO. 66
Respiratory syncytial virus-HIS-10	5'-	AAUGAGGAAAGU- GAAAAG AUGGCAAAAAGA-3'	SEQ ID NO. 67
Respiratory syncytial virus-HIS-11	5'-	CAAGAAAAAAGAU- GUAU CAU-3'	SEQ ID NO. 68
Respiratory syncytial virus-HIS-12	5'-	CCAUAGAAACAUUU- GAUA ACAAUGAAGAA-3'	SEQ ID NO. 69
Respiratory syncytial virus-HIS-13	5'-	AAAGUAUAUUUAU- GUUA CAACA-3'	SEQ ID NO. 70
Respiratory syncytial virus-HIS-14	5'-	AUGAUACAA- CAAUAAUC UCUUU-3'	SEQ ID NO. 71
Respiratory syncytial virus-HIS-15	5'-	ACUAAUACACAU- GAUAAC AA-3'	SEQ ID NO. 72
Respiratory syncytial virus-HIS-16	5'-	UGAUACAA- CAAUAAUCU CUUUGCUA-3'	SEQ ID NO. 73
Respiratory syncytial virus-HIS-17	5'-	GAAAAGGAAAAGAA- GAUU UCUUG-3'	SEQ ID NO. 74
Respiratory syncytial virus-HIS-18	5'-	AAUGUACAGCAUC- CAAUA AAAA-3'	SEQ ID NO. 75
Respiratory syncytial virus-HIS-19	5'-	UAAUUUUUUU- GAAUGGCC ACCCCAUG-3'	SEQ ID NO. 76
Respiratory syncytial virus-HIS-20	5'-	AAUUUUUUU- GAAUGGCCA CCC-3'	SEQ ID NO. 77
Respiratory syncytial virus-HIS-21	5'-	UCUAUAAAUAUAU- AACU AAA-3'	SEQ ID NO. 78
Respiratory syncytial virus-HIS-22	5'-	UAAAUAUA- GAUAAAUAU ACAUUA-3'	SEQ ID NO. 79
Respiratory syncytial virus-HIS-23	5'-	AAAUGUUU- GUUUAUUAC AUGGAUUAGUA-3'	SEQ ID NO. 80
Respiratory syncytial virus-HIS-24	5'-	AUGGUAAAUA- CAUUGGUU UAAUUUAUA-3'	SEQ ID NO. 81
Respiratory syncytial virus-HIS-25	5'-	AACUAUAUAAAAA- CUUA UGUUAU-3'	SEQ ID NO. 82
Respiratory syncytial virus-HIS-26	5'-	UAUAGAACA- GAAAAAU AAAALTULTUC-3'	SEQ ID NO. 83
Respiratory syncytial virus-HIS-27	5'-	UAGACAAUAUA- CUAUUA UAAAA-3'	SEQ ID NO. 84
Respiratory syncytial virus-HIS-28	5'-	AAUGUUACCAU- GUUAUC UAAUA-3'	SEQ ID NO. 85
Mumps virus	Mumps virus-HIS	5'- AGGUAAAUAUAGA- GAGA GAAUGGAGUU- 3'	SEQ ID NO. 86
Australian bat lyssa	Australian bat lyssavirus-HIS	5'- UAUUUUAAAAGGCA- GAUA AUUAGA-3'	SEQ ID NO. 87

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Andes virus	Andes virus-HIS-1	5'- GGAACUUGGUG- CAUUUUU UUCUA-3'	SEQ ID NO. 88
	Andes virus-HIS-2	5'- AUUUUUUCUGAUUG- CUUU UCAA-3'	SEQ ID NO. 89
	Andes virus-HIS-3	5'- UAUUCUGAAAAUG- GUAUA UUUAA-3'	SEQ ID NO. 90
	Andes virus-HIS-4	5'- AGCCUAUUUCAU- GAUG CCUGA-3'	SEQ ID NO. 91
	Andes virus-HIS-5	5'- UCAACAAAUAUUUA- CAGG CAAAA-3'	SEQ ID NO. 92
	Andes virus-HIS-6	5'- UUAGAAAAAUG- GAAAAGU AUAGA-3'	SEQ ID NO. 93
	Andes virus-HIS-7	5'- AAGAGCUCAA- CAAUAUU UACAG-3'	SEQ ID NO. 94
	Andes virus-HIS-8	5'- UCUAAAUAUUCA- GAAUGC ACUAGAGAAA-3'	SEQ ID NO. 95
Powassan virus	Powassan virus-HIS-1	5'- UGAUGGGGUU- GACGGAG UUGGGGAGU-3'	SEQ ID NO. 96
	Powassan virus-HIS-2	5'- GGGGAUUGGAAAGG- CUCU CUGUG-3'	SEQ ID NO. 97
Langat virus	Langat virus-HIS-1	5'- AAAUGGAGCAGAAA- GAAC ACUCAGG-3'	SEQ ID NO. 98
	Langat virus-HIS-2	5'- UGGCUCGAAGAG- CAUGGA GAGGAA-3'	SEQ ID NO. 99
	Langat virus-HIS-3	5'- AGGAAGGGGAUUGA- GAGA CUCAC-3'	SEQ ID NO. 100
	Langat virus-HIS-4	5'- AAAAUAGACUGGA- GAUGG CCAUGUGGAGAAGC- 3'	SEQ ID NO. 101
	Langat virus-HIS-5	5'- CAGCGCAGGGGAAGA- GUG GGCAGGCAG-3'	SEQ ID NO. 102
Eyach virus	Eyach virus-HIS-1	5'- AAUAAGAAAAGCAA- CAUU GUGAUULTUUAUUUA- 3'	SEQ ID NO. 103
	Eyach virus-HIS-2	5'- UAAAAAAGU- CAAAUUUA UGAUUUA- 3'	SEQ ID NO. 104
	Eyach virus-HIS-3	5'- CUUUGGCAUUUCAGU- GAU UCAGCAAAA-3'	SEQ ID NO. 105
	Eyach virus-HIS-4	5'- AAAUGUGCUC- CUUUC UGGA-3'	SEQ ID NO. 106
	Eyach virus-HIS-5	5'- UUUUAAAAGGAGUG- GUGAA GAAGAAAGA- 3'	SEQ ID NO. 107
	Eyach virus-HIS-6	5'- AAAUAUAUUAAUG- CAUU CAACU-3'	SEQ ID NO. 108
	Eyach virus-HIS-7	5'- GGCAGGUGUGGUUG- CUCA AGCUGUAA-3'	SEQ ID NO. 109
	Eyach virus-HIS-8	5'- UAUAACAUUUCCUG- CUU CCAA-3'	SEQ ID NO. 110

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Colorado tick fever virus	Eyach virus-HIS-9	5'-UCAUUGGAAGAUG-GAGCU CUUU-3'	SEQ ID NO. 111
	Eyach virus-HIS-10	5'-CAGCUUACUCUUCU-CAG AGUUCUUU-3'	SEQ ID NO. 112
	Eyach virus-HIS-11	5'-UUUAUGAAUUCUA-CAGAA AUA AUGAAU-3'	SEQ ID NO. 113
	Colorado tick fever virus-HIS-1	5'-AAAGAUUAUGGAAA-CULTUUCUG -3'	SEQ ID NO. 114
	Colorado tick fever virus-HIS-2	5'-UUGCUGUUUUUC-CAAAACA CUAGA-3'	SEQ ID NO. 115
	Colorado tick fever virus-HIS-3	5'-GUCAAUC-CAAAU AUUGGA AGAAGCAGAA-GUUAU-3'	SEQ ID NO. 116
	Colorado tick fever virus-HIS-4	5'-AUGUGGAGACAUUC-CAGC ACAGAGGAAAC-3'	SEQ ID NO. 117
	Colorado tick fever virus-HIS-5	5'-UCAGGCUCAAGUGAU-CUC UCAUUUCA-3'	SEQ ID NO. 118
	Colorado tick fever virus-HIS-6	5'-UUAAUUGAA-GUUUAUGA AGUUG-3'	SEQ ID NO. 119
	Colorado tick fever virus-HIS-7	5'-AGAAUAGGAAUGU-GUCU GAAA-3'	SEQ ID NO. 120
	Colorado tick fever virus-HIS-8	5'-AAAAGUCAAGAAA-UUUUAU-3'	SEQ ID NO. 121
	Colorado tick fever virus-HIS-9	5'-UAUGCCU-GAUAAUUUUUC ALTUGG-3'	SEQ ID NO. 122
	Colorado tick fever virus-HIS-10	5'-AUAAGGAAAAGU-CAAGA AAALTU-3'	SEQ ID NO. 123
	Colorado tick fever virus-HIS-11	5'-AGAGAGAGAGAAAA-GAAA AUUG-3'	SEQ ID NO. 124
	Colorado tick fever virus-HIS-12	5'-UAUGCCU-GAUAAUUUUUC AUUG-3'	SEQ ID NO. 125
	Colorado tick fever virus-HIS-13	5'-CUGUGUUUCUCCUA-GAA UGUCA-3'	SEQ ID NO. 126
	Colorado tick fever virus-HIS-14	5'-AAAGACAGGAUUU-CAUUA UUUGUA-3'	SEQ ID NO. 127
	Colorado tick fever virus-HIS-15	5'-UGGAUGUGA-GAAAUACUU GGGA-3'	SEQ ID NO. 128
	Colorado tick fever virus-HIS-16	5'-AAAAGACAGGAUUU-CAU AUUU-3'	SEQ ID NO. 129
	Colorado tick fever virus-HIS-17	5'-AAAAGACAGGAUUU-CAU AUUGUAU-3'	SEQ ID NO. 130
	Colorado tick fever virus-HIS-18	5'-GACAGGAUUU-CAUUAUUU' GUAU-3'	SEQ ID NO. 131
Colorado tick fever virus-HIS-19	5'-AGUUCUUUUUGA-CAUUU UGUUC-3'	SEQ ID NO. 132	
Colorado tick fever virus-HIS-20	5'-UGACAUUUUGUU-CUUUCU UUG-3'	SEQ ID NO. 133	
Colorado tick fever virus-HIS-21	5'-GAAA AUGUGUC-	SEQ ID NO. 134	

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Lassa virus	Lassa virus-HIS-1	CAACAA UC CAAUCA-3'	SEQ ID NO. 135
	Lassa virus-HIS-2	5'-GGAAGAAAAGA-CAUUAAA CUAAUU-3'	SEQ ID NO. 136
Omsk hemorrhagic fever virus	Omsk hemorrhagic fever virus-HIS-1	5'-UAAUCUUCUAUAA-GUCUA GUAAA-3'	SEQ ID NO. 137
	Omsk hemorrhagic fever virus-HIS-2	5'-CAGGAAUCCUUGUA-GUGA UGGGAUUGU-3'	SEQ ID NO. 138
Machupo virus	Machupo virus-HIS-1	5'-UAUUUCAUUGG-CAAAAG AAAACAAA-3'	SEQ ID NO. 139
	Machupo virus-HIS-2	5'-AAUGCCUAAUUCU-CAU AAUUUGUUAA-3'	SEQ ID NO. 140
Junin virus	Junin virus-HIS	5'-UAAAUUUAAU-3'	SEQ ID NO. 141
	Guanarito virus-HIS-1	5'-AAACAGUUUCUC-CUUUUC AUAAA-3'	SEQ ID NO. 142
Guanarito virus	Guanarito virus-HIS-2	5'-CAUAGUAUCU-CUUUAAA CCUUUCAUUU-3'	SEQ ID NO. 143
	Guanarito virus-HIS-3	5'-AUAGUAUCU-CUUUAAA CCUUUCAUUU-3'	SEQ ID NO. 144
Guanarito virus	Guanarito virus-HIS-4	5'-UACAAACAUGGG-CAAUUC AAAAUC-3'	SEQ ID NO. 145
	Guanarito virus-HIS-5	5'-GCUCUUCUUUC-CUUAACA AAUGU-3'	SEQ ID NO. 146
Guanarito virus	Guanarito virus-HIS-6	5'-UGUUAAAACACUUU-CUUUC CUUUU-3'	SEQ ID NO. 147
	Sin Nombre virus-HIS-1	5'-AUAGUAUCU-CUUUAAA CCUUUCAUUU-3'	SEQ ID NO. 148
Sin Nombre virus	Sin Nombre virus-HIS-2	5'-ACAACUGAAACAAUG-CAA GGAU-3'	SEQ ID NO. 149
	in Nombre virus-HIS-3	5'-GUUCAAGGGC-CAAUUUA UCACA-3'	SEQ ID NO. 150
Sin Nombre virus	Sin Nombre virus-HIS-4	5'-UAUUAAAUUUUUCU-CAGGU CUAU-3'	SEQ ID NO. 151
	Sin Nombre virus-HIS-5	5'-AGAAAUUCAG-GAAA AUGG AAAA-3'	SEQ ID NO. 152
Hantaan virus	Hantaan virus-HIS-1	5'-CACAAAGCUCAAG-CACGU AUUGU-3'	SEQ ID NO. 153
	Hantaan virus-HIS-2	5'-CUGUUUUUUUUCCU-CUUU CUUUCUG-3'	SEQ ID NO. 154
Hantaan virus	Hantaan virus-HIS-3	5'-UUUCUUUCCUUU-CUUUC UGCUUUUCU-3'	SEQ ID NO. 155
	Hantaan virus-HIS-4	5'-UUUCUUUCCUUU-CUUU CUGCUUUUCU-3'	SEQ ID NO. 156
Hantaan virus	Hantaan virus-HIS-5	5'-UUUCUUUCCUUU-CUUUC UGCUU-3'	SEQ ID NO. 157
	Hantaan virus-HIS-5	5'-UUUCUUUCCUUU-CUUUC UGCUUUCU-3'	SEQ ID NO. 157

TABLE 1-continued

Target sequence listing of RNA virus				
Virus type	Fragment number	Fragment coding sequence	ID number	
Hantaan virus	Hantaan virus-HIS-6	5'- AUAUGGAUGUA- GAUUUCA UUUG-3'	SEQ ID NO. 158	
	Hantaan virus-HIS-7	5'- UUUUCUUUCCUUU- CUUU CUGCUUUCU-3'	SEQ ID NO. 159	
	Hantaan virus-HIS-8	5'- ACAUCUUUACA- GUGGA UAUUUCUC- 3'	SEQ ID NO. 160	
	Hantaan virus-HIS-9	5'- UUCAUACAUCUAAA- CUU AAUCCAGAU-3'	SEQ ID NO. 161	
	Puumala virus	Puumala virus-HIS-1	5'- GACUACAAGAGAAG- GAUG GCAGA-3'	SEQ ID NO. 162
		Puumala virus-HIS-2	5'- AAUGGCAGUUAU- GAAUUA AUUA-3'	SEQ ID NO. 163
		Puumala virus-HIS-3	5'- AAGGUU- GUUUUUUUUUU UAAA-3'	SEQ ID NO. 164
		Puumala virus-HIS-4	5'- CCUUUUCCUUU- CAUCA CUUUUUU-3'	SEQ ID NO. 165
		Puumala virus-HIS-5	5'- CAGGAAAAAUG- GAUAC UAAA-3'	SEQ ID NO. 166
		Puumala virus-HIS-6	5'- AUUUAUUUAUU- CAUUA UCUAUUUA-3'	SEQ ID NO. 167
		Puumala virus-HIS-7	5'- UAUAUAUAUGCAA- GUAGC AUUAUAUA- 3'	SEQ ID NO. 168
		Puumala virus-HIS-8	5'- UGUUAGAUUUCUU- GUCAU UUUUCC-3'	SEQ ID NO. 169
Puumala virus-HIS-9		5'- CCACAGCAACAUG- GUUUC AGUAU-3'	SEQ ID NO. 170	
Puumala virus-HIS-10		5'- CUUGUUAAGUACUU- GAUA UCUGU-3'	SEQ ID NO. 171	
Puumala virus-HIS-11		5'- AUUCUCUUAUUAU- GAAUA AAGCA-3'	SEQ ID NO. 172	
Puumala virus-HIS-12		5'- AGAGAGAAAGAAA- GAGAA UUGGGGAGU- 3'	SEQ ID NO. 173	
Dobrava virus	Dobrava virus-HIS-1	5'- AUAUGGAUGUA- GAUUUCA UUUG-3'	SEQ ID NO. 174	
	Dobrava virus-HIS-2	5'- AACAUUUUUUUC- CUUCU UUUC-3'	SEQ ID NO. 175	
	Dobrava virus-HIS-3	5'- UUUUUAGCCCUUG- CAAAG AACU-3'	SEQ ID NO. 176	
	Dobrava virus-HIS-4	5'- CUUCAUUAAAGU- GUUUUA UCGGAAGUCA-3'	SEQ ID NO. 177	
	Dobrava virus-HIS-5	5'- UGCCUGACUUA- CAGGC CAUUU-3'	SEQ ID NO. 178	
	Dobrava virus-HIS-6	5'- AUUAUCUUAAGAAA- GAUU AAAGAAGAAUUUG-3'	SEQ ID NO. 179	
	Dobrava virus-HIS-7	5'- UCAAGCAAAAUA- GUUC AGAGC-3'	SEQ ID NO. 180	
	Dobrava virus-HIS-8	5'- AACUUUUUAUU- GAUCCAG UGCUCA-3'	SEQ ID NO. 181	

TABLE 1-continued

Target sequence listing of RNA virus				
Virus type	Fragment number	Fragment coding sequence	ID number	
Dobrava virus	Dobrava virus-HIS-9	5'- AGAUUUCUUU- CAAAAAU UUCAA-3'	SEQ ID NO. 182	
	Dobrava virus-HIS-10	5'- AUGCAUACAA- CAAUGGGA AUGUCAUUU-3'	SEQ ID NO. 183	
	Dobrava virus-HIS-11	5'- AUU- GUUUUAUUUUUUU CAUUU-3'	SEQ ID NO. 184	
	Dobrava virus-HIS-12	5'- CAACAUAUUUUU- CAACC AUUUU-3'	SEQ ID NO. 185	
	Seoul virus	Seoul vims-HIS-1	5'- UCCUCUUUUCUUUUC- CUU UCUCUUCUUU- 3'	SEQ ID NO. 186
		Seoul virus-HIS-2	5'- CAGAAAAGCAGUAU- GAGA AGGA-3'	SEQ ID NO. 187
		Seoul virus-HIS-3	5'- UUGCCUGGGGAAAG- GAGG CAGU-3'	SEQ ID NO. 188
		Seoul virus-HIS-4	5'- CAGAAAAGCAGUAU- GAGA AGGA-3'	SEQ ID NO. 189
		Seoul virus-HIS-5	5'- UCUUUUUUUUUC- CUUUCU CCUUCUUU- 3'	SEQ ID NO. 190
		Seoul virus-HIS-6	5'- GUCCUCUUUU- CUUUUCCU UUCUCUUCUUU-3'	SEQ ID NO. 191
		Seoul virus-HIS-7	5'- CUUUUCUUUCCUUU- CUC CUUC-3'	SEQ ID NO. 192
		Seoul virus-HIS-8	5'- CUCUUUUUUUUUC- CUUUC UCCUUCUU-3'	SEQ ID NO. 193
Seoul virus-HIS-9		5'- UUAAUAAGAAUACA- GAUU UAAU-3'	SEQ ID NO. 194	
Seoul virus-HIS-10		5'- UCUCUGAGUUA- GAAAUG AGAAA- 3'	SEQ ID NO. 195	
Seoul virus-HIS-11		5'- CUUUG- CAUUAAAAAUGU GUUUGA-3'	SEQ ID NO. 196	
Seoul virus-HIS-12		5'- UUUUUAUAGUCUA- GAAA CUUAGACUAUA-3'	SEQ ID NO. 197	
Seoul virus-HIS-13		5'- CUACAGGAUGUA- GAUUUU GAAAAUA-3'	SEQ ID NO. 198	
Seoul virus-HIS-14		5'- UCUUUGUAUUCUGG- CUUU CCUUCUUUGGUUG-3'	SEQ ID NO. 199	
Crimean-Congo hemorrhagic fever virus	Crimean-Congo hemorrhagic fever virus-HIS-1	5'- AGAAGACA- CAAAAAAUG UGUUAACAAAAAC- 3'	SEQ ID NO. 200	
	Crimean-Congo hemorrhagic fever virus-HIS-2	5'- UCAGUGUUUUCUGA- CUCC AAAGUU-3'	SEQ ID NO. 201	
	Crimean-Congo hemorrhagic fever virus-HIS-3	5'- UACCAAGAAAAU- GAAGAA GGCUCUUCUGA-3'	SEQ ID NO. 202	
	Crimean-Congo hemorrhagic fever virus-HIS-4	5'- UUUACUUGCUUAU- GUAAC CUUAUUUU-3'	SEQ ID NO. 203	
Crimean-Congo	5'-		SEQ ID	

TABLE 1-continued

Target sequence listing of RNA virus				
Virus type	Fragment number	Fragment coding sequence	ID number	
Sabia virus	hemorrhagic fever virus-HIS-5	UUUCUCUAUUUUCU-CUUG UUUUAAAC-3'	NO. 204	
	Sabia virus-HIS-1	5'-AAGAUGACUAU-CUAAAAU GUCAGG-3'	SEQ ID NO. 205	
	Sabia virus-HIS-2	5'-AUUCACUGCCUU-CUCCCC UCUCA-3'	SEQ ID NO. 206	
	Sabia virus-HIS-3	5'-CUGUCUGCUAACCA-GUAU GAACA-3'	SEQ ID NO. 207	
	Sabia virus-HIS-4	5'-AGAAAGUUCUAU-CAAGUU UUUUU-3'	SEQ ID NO. 208	
	Sabia virus-HIS-5	5'-UUUCAAUUCCUUCU-CAG AAUUC-3'	SEQ ID NO. 209	
	Sabia virus-HIS-6	5'-AUUUUGUACAGAAG-GUUU UCAUAA-3'	SEQ ID NO. 210	
	Sabia virus-HIS-7	5'-AUUGAUUAGAAAU-CAAC UUGGAAAAU-CAAUG-3'	SEQ ID NO. 211	
	Sabia virus-HIS-8	5'-GGAUGUCUUUGU-CUUUCU UUUUCUUUG-3'	SEQ ID NO. 212	
	Thogoto virus	Thogoto virus-HIS-1	5'-ACACCAAAGGGAAA-CUCA CUGACAGAAAAC-3'	SEQ ID NO. 213
		Thogoto virus-HIS-2	5'-GACACAGAUGAA-GAAACU UCCUUU-3'	SEQ ID NO. 214
		Thogoto virus-HIS-3	5'-UACAACCCAAGAGAG-CUU AAAC-3'	SEQ ID NO. 215
		Thogoto virus-HIS-4	5'-AAAGAAUGAA-GUAAAAGGU CAGCA-3'	SEQ ID NO. 216
		Thogoto virus-HIS-5	5'-GUGCUAUUGAUCA-GACUA AUUA-3'	SEQ ID NO. 217
		Thogoto virus-HIS-6	5'-GCUGGACUGUGGU-GACAG CCUC-3'	SEQ ID NO. 218
Thogoto virus-HIS-7		5'-CAACCUCUGCA-CAAAAUG AGCU-3'	SEQ ID NO. 219	
Thogoto virus-HIS-8		5'-ACAAUGGAGCAUG-CAAGG AAGCA-3'	SEQ ID NO. 220	
Thogoto virus-HIS-9		5'-UAGCAGGUAGUAUC-CAAG ACAGAGAC-3'	SEQ ID NO. 221	
Thogoto virus-HIS-10		5'-AAAAUGCUGAG-GAUUUGG GCAA-3'	SEQ ID NO. 222	
Thogoto virus-HIS-11		5'-CAAUAACCAAAGA-GAAAA AAGAA-3'	SEQ ID NO. 223	
Thogoto virus-HIS-12		5'-AAUCAUGGAAGUU-GUUUU CCCCA-3'	SEQ ID NO. 224	
Thogoto virus-HIS-13		5'-AAGCAACCAGGA-GAUUGG UUCA-3'	SEQ ID NO. 225	
Thogoto virus-HIS-14		5'-AUGCAACUGAGAUCA-GAG CAUC-3'	SEQ ID NO. 226	
Thogoto virus-HIS-15		5'-CCAGAGGACAAGAG-CUCU UGUU-3'	SEQ ID NO. 227	
European trinidad rabies virus 1-HIS-1	5'-GAGGACGAGAUGG-GUGGA UCAAGA-3'	SEQ ID NO. 228		

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
dad rabies virus 1	European trinidad rabies virus 1-HIS-2	5'-GAGGACGAGAUGG-GUGGA UCAAGAGGUC-3'	SEQ ID NO. 229
	European bat lyssavirus 1-HIS-3	5'-UUGGCUCAUUCUCU-GUUU UUUUUGUUUUUUU-3'	SEQ ID NO. 230
	European trinidad rabies virus 1-HIS-4	5'-GAGGACGAGAUGG-GUGGA UCAAGAGGUC-3'	SEQ ID NO. 231
	European trinidad rabies virus 1-HIS-5	5'-CUCAUUCUCU-GUUUUUUU UGUUUUUUUU-3'	SEQ ID NO. 232
	European trinidad rabies virus 2-HIS	5'-CUUUUUU-CUAAAAUUAUUU UAAAAU-3'	SEQ ID NO. 233
Chapare virus	Chapare virus-HIS	5'-AUGAGCCCAAGACUU-CUU UUGAU-3'	SEQ ID NO. 234
Rotavirus	Rotavirus A-HIS-1	5'-AAGAAACUGU-GAUUUUA AUACUA-3'	SEQ ID NO. 235
	Rotavirus A-HIS-2	5'-AAGAAUGAUAAAG-CAAAG AAAA-3'	SEQ ID NO. 236
	Rotavirus A-HIS-3	5'-UACUUUUAAAAGAU-CAUG CUUCAUU-3'	SEQ ID NO. 237
	Rotavirus A-HIS-4	5'-UUUAAAAUU-GAUAAAGAA UAAA-3'	SEQ ID NO. 238
	Rotavirus A-HIS-5	5'-AGAAUGAUAAAG-CAAAGA AAAUGUAG-3'	SEQ ID NO. 239
	Rotavirus A-HIS-6	5'-UACUGAUCUCCAACU-CAG AAGA-3'	SEQ ID NO. 240
	Rotavirus A-HIS-7	5'-AAAAUUUGAAA-GAAUGAU AAAGCAA-3'	SEQ ID NO. 241
	Rotavirus A-HIS-8	5'-AAAAUUGAAU-GAAAAUUAU GCAUUCUCUCAA-3'	SEQ ID NO. 242
	Rotavirus A-HIS-9	5'-AAAGCAAGAAAAAU-GAAU GAAAA-3'	SEQ ID NO. 243
	Rotavirus A-HIS-10	5'-CAAGAAAAAUGAAU-GAAA AUAU-3'	SEQ ID NO. 244
	Rotavirus A-HIS-11	5'-AGGAGAAAAUCAAAA-CAAA ACCAU-3'	SEQ ID NO. 245
	Rotavirus A-HIS-12	5'-GCAUUCAAUAAAUA-CAUG CUG-3'	SEQ ID NO. 246
	Rotavirus A-HIS-13	5'-AUGUAAGAACU-GUAAAUA UAA-3'	SEQ ID NO. 247
	Rotavirus A-HIS-14	5'-AAAACAAAAC-CAUAAAAG UAG-3'	SEQ ID NO. 248
	Rotavirus A-HIS-15	5'-AAAGGAGAAAAU-CAAAAACA AAACCAUAAA-3'	SEQ ID NO. 249
	Rotavirus A-HIS-16	5'-UAGGGAGCUCCECA-	SEQ ID NO. 250

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
		CUCC CGUUUUGUGAC-3'	
Rotavirus A-HIS-17		5'- UAUAUAAAAA- GAAAAUGA AAUCAA- 3'	SEQ ID NO. 251
Rotavirus A-HIS-18		5'- GAUUAAAAUUUAU- CAAA AGAAAAUGAA- 3'	SEQ ID NO. 252
Rotavirus A-HIS-19		5'- UAUAUAAAAA- GAAAAUGA AAUCAUA-3'	SEQ ID NO. 253
Rotavirus A-HIS-20		5'- AAAGAAAUGAAU- CAAU AGUUGAGGA-3'	SEQ ID NO. 254
Rotavirus A-HIS-21		5'- UAUAUAAAAA- GAAAAUGA AAUCAUAG-3'	SEQ ID NO. 255
Rotavirus A-HIS-22		5'- AUGACCAAU- GUUAGAU UGAGA-3'	SEQ ID NO. 256
Rotavirus A-HIS-23		5'- UAUAUAAAAA- GAAAAUGA AAUCAUAGUAG- GA-3'	SEQ ID NO. 257
Rotavirus A-HIS-24		5'- UAUAUAAAAA- GAAAAUGA AAUCAUA-3'	SEQ ID NO. 258
Rotavirus A-HIS-25		5'- UUGAAAUAAGAA- GAUUAG AUUUUUUUUU-3'	SEQ ID NO. 259
Rotavirus A-HIS-26		5'- UGAUAUCAUUU- CAAUUA CAUA-3'	SEQ ID NO. 260
Rotavirus A-HIS-27		5'- AAGAAAAAGAA- GAUAGCA AGAA-3'	SEQ ID NO. 261
Rotavirus A-HIS-28		5'- AGCUAAAAGUUUG- GUAGGA AAACAA-3'	SEQ ID NO. 262
Rotavirus A-HIS-29		5'- AAAUCA- GUAAAAUAACA AUAAAUGACAUAC-3'	SEQ ID NO. 263
Rotavirus A-HIS-30		5'- CAUUAAAAUUUAU- CAAAC AAACACAAA- 3'	SEQ ID NO. 264
Rotavirus A-HIS-31		5'- AGCUAAAAGUUUG- GUAGGA AAACAA-3'	SEQ ID NO. 265
Rotavirus A-HIS-32		5'- GAAAUUAC- CAUUAUUUU AUGAUGU-3'	SEQ ID NO. 266
Rotavirus A-HIS-33		5'- AAAUAAGAUCA- GAAUUUU AUUUU-3'	SEQ ID NO. 267
Rotavirus A-HIS-34		5'- AGAAUUUAUUAAU- ACAG UAUA-3'	SEQ ID NO. 268
Rotavirus A-HIS-35		5'- AGCAUUAAAA- CAUUAGAA AUUUUUUUUAAAG-3'	SEQ ID NO. 269
Rotavirus A-HIS-36		5'- AGAAUUUAUUAAU- ACAG UAUAUAGU-3'	SEQ ID NO. 270
Rotavirus A-HIS-37		5'- GAAGAAUUUAUCA- CAUUA AUAA-3'	SEQ ID NO. 271
Rotavirus A-HIS-38		5'- GAAGAACAAA-	SEQ ID NO. 272

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
		CUAUUAAU AAUU-3'	
Rotavirus A-HIS-39		5'- UAAGAUCA- GAAUUUUUU UAUUACUA-3'	SEQ ID NO. 273
Rotavirus A-HIS-40		5'- UAAACCAAA- CAUUUUUCC UUAU-3'	SEQ ID NO. 274
Rotavirus A-HIS-41		5'- AUUUUUAAAAACA- CUUAAAA AUUU-3'	SEQ ID NO. 275
Rotavirus A-HIS-42		5'- CAAUAUUUCUGCU- GUUCA AUUCAUUGG- 3'	SEQ ID NO. 276
Rotavirus A-HIS-43		5'- UUUUUUGGGUUUU- GUUUU UGUUGAUACUUU- GAG-3'	SEQ ID NO. 277
Tai Forest ebolavirus	Tai Forest ebolavirus-HIS-1	5'- GCAAUUUUAU- CUUAAAAU CAAGUACAUA-3'	SEQ ID NO. 278
	Tai Forest ebolavirus-HIS-2	5'- UAACAGACUUG- GAAAAAU ACAUU-3'	SEQ ID NO. 279
Bundibugyo ebolavirus	Bundibugyo ebolavirus-HIS	5'- AUUACCUCAAAAAU- CUA GAACUUUAUUAAUU- CUCAG-3'	SEQ ID NO. 280
Rift Valley fever virus	Rift Valley fever virus-HIS	5'- AAAAUUAAAAA- CAAAAAU GAAAGG-3'	SEQ ID NO. 281
Irkut virus	Irkut virus-HIS-1	5'- CUUAAUUUAUGU- CUUCUU UGUUGUUUUU-3'	SEQ ID NO. 282
	Irkut virus-HIS-2	5'- AUUAAUACAA- CUUAAUU UUUAAUUAAU- CUUUUA-3'	SEQ ID NO. 283
	Irkut virus-HIS-3	5'- AUAAAGAA- GAAUUAUAC AUUGACAUUA-3'	SEQ ID NO. 284
	Irkut virus-HIS-4	5'- UUAUGAAU- GUUUUAUCAU GAUUAAAGAU-3'	SEQ ID NO. 285
Influenza A virus	Influenza A virus-HIS-1	5'- CCCAGCACAGAGAU- GUCA UUGA-3'	SEQ ID NO. 286
	Influenza A virus-HIS-2	5'- AGUGAGAAAUGAU- GAUGU UGAUCAGA-3'	SEQ ID NO. 287
	Influenza A virus-HIS-3	5'- UUCUAAAGGAAAG- CAACCA GAAG-3'	SEQ ID NO. 288
	Influenza A virus-HIS-4	5'- UGAGCAAGAA- GAAAUCCU ACAU-3'	SEQ ID NO. 289
	Influenza A virus-HIS-5	5'- GGAUUGAGAA- GAAAGCUA AAUU-3'	SEQ ID NO. 290
	Influenza A virus-HIS-6	5'- UUAGAAAUGU- CUAAAGCA UUGC-3'	SEQ ID NO. 291
	Influenza A virus-HIS-7	5'- CAGGACAUU- GAAAAUGAA GAGAAG-3'	SEQ ID NO. 292
	Influenza A virus-HIS-8	5'- AAGAGAAAGACCU- GACCA AAGA-3'	SEQ ID NO. 293
	Influenza A virus-HIS-9	5'-	SEQ ID

TABLE 1-continued

Virus type	Target sequence listing of RNA virus		ID number
	Fragment number	Fragment coding sequence	
Influenza A virus-HIS-10		ACUAAGU-CAUAUAAAAUACAAGAAAAA-3'	NO. 294
		5'-AACAAUUUGAGUU-GAUAG ACAAUGAAU-3'	SEQ ID NO. 295
		5'-AUCAUGUUUCAUA-CUUCU AGCCAUUG-3'	SEQ ID NO. 296
		5'-GAAACAUCUAA-GAACAC AGGAA-3'	SEQ ID NO. 297
		5'-UUUCACCAUACCUU-CUC UUCC-3'	SEQ ID NO. 298
		5'-AGGAAG-CAAAUUAAACA GAGAAGAAA-3'	SEQ ID NO. 299
		5'-UGGAAAAUGAAA-GAACUU UGGA-3'	SEQ ID NO. 300
		5'-AAAACAACACUUGG-GUAA AUCAGACA-3'	SEQ ID NO. 301
		5'-GCUGCUGGACAGUCA-GUG GUUU-3'	SEQ ID NO. 302
		5'-GGAUCAAGAAAGAA-GAGU UCUCUGAGA-3'	SEQ ID NO. 303
		5'-GGGGAGACACA-CAAAUUC AGAC-3'	SEQ ID NO. 304
		5'-ACCAAUUGAAAACC-CAGC UCACAAGAGUCA-3'	SEQ ID NO. 305
		5'-AAAUGAGAAUGUG-GAAAC CAUG-3'	SEQ ID NO. 306
		5'-AGAAAUAAAGGAGA-GUUUG GCGC-3'	SEQ ID NO. 307
		5'-AGAAGAGUAGACG-GAAAG UGGA-3'	SEQ ID NO. 308
		5'-GACAUUCUUUGGCUG-GAA AGAGCCUAA-3'	SEQ ID NO. 309
		5'-GAAGAGAGCAGGG-CAAGA AUCAAAACUAGGCU-3'	SEQ ID NO. 310
		5'-AGGGCAAGCUUUC-CAAA UGUC-3'	SEQ ID NO. 311
		5'-GGACAUGAUCCAGA-GAG GAAUGAACAAGGA-CAA-3'	SEQ ID NO. 312
		5'-GGAAUUGU-GAAAAUUCA AUGG-3'	SEQ ID NO. 313
Bayou virus	Bayou virus-HIS-1	5'-GAGUCUACAUCUCA-GUU UUGUC-3'	SEQ ID NO. 314
	Bayou virus-HIS-2	5'-GAGACAGACA-GUAAAGGA AAAU-3'	SEQ ID NO. 315
	Bayou virus-HIS-3	5'-UGAAGAAAA-CUAAAGAA AAAA-3'	SEQ ID NO. 316
	Bayou virus-HIS-4	5'-CCAGACAGCAGACUG-	SEQ ID NO. 317

TABLE 1-continued

Virus type	Target sequence listing of RNA virus		ID number
	Fragment number	Fragment coding sequence	
Bayou virus-HIS-5		GAA GGCA-3'	
		5'-AACAGGAAAU-CAUAUUGA AUUUGU-3'	SEQ ID NO. 318
		5'-AGUAUGCAUGGAAA-GAUU UUCUUAAUG-3'	SEQ ID NO. 319
		5'-CAGAGUUU-GAAUUUUUUGAUCAG-3'	SEQ ID NO. 320
		5'-UGAGGGUAA-CAUUUAAUU UUGGG-3'	SEQ ID NO. 321
		5'-UUUUUUUUUUUGA-GAAA GGGCUUCAU-3'	SEQ ID NO. 322
		5'-AGAAAACAACAGGU-GUUG AUGAG-3'	SEQ ID NO. 323
		5'-UUUUUUUUUUUGA-GAAA GGGCU-3'	SEQ ID NO. 324
		5'-AAAUGAAAAGAUUC-CAGA AAUUG-3'	SEQ ID NO. 325
		5'-ACAACAGAUACAA-CAAAU GCUGGUGAGAAU-3'	SEQ ID NO. 326
		5'-AGUGAUUCAUGCU-GAAAU ACAGU-3'	SEQ ID NO. 327
		5'-AUGAGAGAU-CUUGGGGGU GGGAC-3'	SEQ ID NO. 328
	Black Creek Canal virus-HIS-1	5'-CCAAUGUAUUUAUA-CAUU UACAAGUA-3'	SEQ ID NO. 329
	Black Creek Canal virus-HIS-2	5'-AAGUCAAUGA-GAAAGAG AAUAGAUUUGG-3'	SEQ ID NO. 330
Black Creek Canal virus-HIS-3	5'-UACUUACAUGC-CAAAUCU CAA-3'	SEQ ID NO. 331	
Black Creek Canal virus-HIS-4	5'-AGUCAAUGAGAAA-GAGA AUA-3'	SEQ ID NO. 332	
Black Creek Canal virus-HIS-5	5'-UACAUACUAUUAAU-GUGA UUUU-3'	SEQ ID NO. 333	
Black Creek Canal virus-HIS-6	5'-UUUUGUCCUUC-CAAUUGU GUUG-3'	SEQ ID NO. 334	
Japanese encephalitis virus-HIS-1	5'-GAAGCAGAGAGAAA-GUAG AGAAG-3'	SEQ ID NO. 335	
Japanese encephalitis virus-HIS-2	5'-UCAAAAAGGAGAGAA-CAGA UGCUUGG-3'	SEQ ID NO. 336	
Japanese encephalitis virus-HIS-3	5'-UCCUGGAUGGCAAG-CAG AAGCA-3'	SEQ ID NO. 337	
Duvenhage lyssavirus-HIS	5'-CCUCUAAGUUUC-CUAAGG UUCU-3'	SEQ ID NO. 338	
Human enterovirus D-HIS	5'-AACAAAGCAGGCCA-GUG UGGUG-3'	SEQ ID NO. 339	
Human enterovirus D-HIS	5'-UUGAGGAAAAGG-GAACCC UGUACA-3'	SEQ ID NO. 340	

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
	Human enterovirus D-HIS	5'-CCAGGCACUGGGAA-GUCA GUGGCA-3'	SEQ ID NO. 341
	Human enterovirus D-HIS	5'-AAUUAGGAGU-GAUACCUU CACUAA-3'	SEQ ID NO. 342
	Human enterovirus D-HIS	5'-UGAGAAAAAGGCCA-CUGU CCUUA-3'	SEQ ID NO. 343
	Human enterovirus D-HIS	5'-ACAAUUGGA-GAAUAGU GAAAA-3'	SEQ ID NO. 344
Lujo mam-marenavirus	Lujo mam-marenavirus-HIS	5'-AUUUUAAAAACA-CUUAAAA AUUU-3'	SEQ ID NO. 345
Measles morbillivirus	Measles morbillivirus-HIS	5'-AAAGGAAGAAUU-GAAAC CCAGA-3'	SEQ ID NO. 346
Tick-borne encephalitis virus	Tick-borne encephalitis virus-HIS	5'-GAUGUCAUCA-GAAUGCA GAUGC-3'	SEQ ID NO. 347
Avian influenza virus	Avian influenza virus-CIS-1	5'-ACAAAAGAUGCA-GAAAGA GGCAAG-3'	SEQ ID NO. 348
	Avian influenza virus-CIS-2	5'-AAUGUUAUUGA-GUAUAUA GAGAGA-3'	SEQ ID NO. 349
	Avian influenza virus-CIS-3	5'-CAUUUGAUGAU-CUGGCAU UCCAACU-3'	SEQ ID NO. 350
	Avian influenza virus-CIS-4	5'-GAAGGGAGGCU-GAUCCAG AACAGU-3'	SEQ ID NO. 351
	Avian influenza virus-CIS-5	5'-GGCACAAUGGAGUG-GAG UCUGCU-3'	SEQ ID NO. 352
	Avian influenza virus-CIS-6	5'-CAAAAGAAAAGAAA-GAAG AGCUC-3'	SEQ ID NO. 353
	Avian influenza virus-CIS-7	5'-UCCAAAUUGCUU-CAAAUG AAAA-3'	SEQ ID NO. 354
	Avian influenza virus-CIS-8	5'-AAUUGUACAAAAACCUG AUAC-3'	SEQ ID NO. 355
	Avian influenza virus-CIS-9	5'-AUGAGGAAUGGAGG-GAAU AGCU-3'	SEQ ID NO. 356
	Avian influenza virus-CIS-10	5'-AUUGCUCUUGGCU-GAU GGAU-3'	SEQ ID NO. 357
	Avian influenza virus-CIS-11	5'-UCCAAUCUGAAU-GAUGC AACA-3'	SEQ ID NO. 358
	Avian influenza virus-CIS-12	5'-UAAAAGCUGCAU-CAAUAG GUGU-3'	SEQ ID NO. 359
	Avian influenza virus-CIS-13	5'-GGGAGAUUGAUC-CAAAAC AGCA-3'	SEQ ID NO. 360
	Avian influenza virus-CIS-14	5'-AGGGGAAGCCCA-GAUCC UGGA-3'	SEQ ID NO. 361
	Avian influenza virus-CIS-15	5'-UGCCACAGAGGAGACACA CAAA-3'	SEQ ID NO. 362
	Avian influenza virus-CIS-16	5'-GAGAAAGGAAAGUG-GACA ACA-3'	SEQ ID NO. 363
	Avian influenza virus-	5'-	SEQ ID

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
	CIS-17	5'-CAUAACAACAA-CAAUAAU AACUGAA-3'	SEQ ID NO. 364
	Avian influenza virus-CIS-18	5'-AGGAAGGGAAAAUA-CAAA AAAU-3'	SEQ ID NO. 365
	Avian influenza virus-CIS-19	5'-GAGGAAAUGAGAA-GAAGG CUA-3'	SEQ ID NO. 366
	Avian influenza virus-CIS-20	5'-CUGGAGCUGCUGGAG-CAG CAG-3'	SEQ ID NO. 367
	Avian influenza virus-CIS-21	5'-UCUCAAAUCUGCA-GUUGG UC-3'	SEQ ID NO. 368
	Avian influenza virus-CIS-22	5'-UUGACUAUGGGAGU-GAUG UUU-3'	SEQ ID NO. 369
	Avian influenza virus-CIS-23	5'-AGUUUGAAUU-CAUUGCUG AAG-3'	SEQ ID NO. 370
	Avian influenza virus-CIS-24	5'-GAAAAACAAGAUUU-CUCC CAGUG-3'	SEQ ID NO. 371
	Avian influenza virus-CIS-25	5'-ACAGGGUGAUGGU-GUCCC CC-3'	SEQ ID NO. 372
	Avian influenza virus-MIS-1	5'-AAAUGGACCACAAA-CACA GAAAC-3'	SEQ ID NO. 373
	Avian influenza virus-MIS-2	5'-AUGUCUUCUCAAU-CACU UCAAC-3'	SEQ ID NO. 374
	Avian influenza virus-MIS-3	5'-UACUGCUAAGGAAG-CACA AGAUG-3'	SEQ ID NO. 375
	Avian influenza virus-MIS-4	5'-AAAAUUGAAAC-GAACAA AUUC-3'	SEQ ID NO. 376
	Avian influenza virus-MIS-5	5'-AAUAAAUCAA-CAUUACC CUUU-3'	SEQ ID NO. 377
	Avian influenza virus-MIS-6	5'-AAGCAA-GAUUAAAAGAG AGGA-3'	SEQ ID NO. 378
	Avian influenza virus-MIS-7	5'-UUAGAGCAUCU-GUUGGAA GAAU-3'	SEQ ID NO. 379
	Avian influenza virus-MIS-8	5'-AACAGAGGCUGAA-CAAGA GGA-3'	SEQ ID NO. 380
	Avian influenza virus-MIS-9	5'-UGCAGAAGGAACAG-GAAC GGC-3'	SEQ ID NO. 381
	Avian influenza virus-MIS-10	5'-AUUGUAUGGACA-CAAUUA GAAAC-3'	SEQ ID NO. 382
	Avian influenza virus-MIS-11	5'-AUGAGAAAACGUGCCU-GAG AAACA-3'	SEQ ID NO. 383
	Avian influenza virus-MIS-12	5'-UGUUUUCUUCUGUCU-GAA GA-3'	SEQ ID NO. 384
	Avian influenza virus-MIS-13	5'-CAUAUAAUUGCAU-CACAAU-3'	SEQ ID NO. 385
	Avian influenza virus-MIS-14	5'-ACAAUUCAGCAGUUU-GAA CUGAU-3'	SEQ ID NO. 386
	Avian influenza virus-MIS-15	5'-GAAAGAG-GUAAAUUAAAA AG-3'	SEQ ID NO. 387
	Avian influenza virus-MIS-16	5'-AAGUAGCAGGCUCACUCU GC-3'	SEQ ID NO. 388
	Avian influenza virus-MIS-17	5'-AGAAGGAGAGAAG-	SEQ ID NO. 389

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
		GAAAA UGG-3'	
Avian influenza virus-MIS-18	5'-	ACAAAUACCGCA-GAAAU GC-3'	SEQ ID NO. 390
Avian influenza virus-MIS-19	5'-	AAUGAAUCAACAA-GAAAG AAAA-3'	SEQ ID NO. 391
Avian influenza virus-MIS-20	5'-	AAUGAAUCAACAA-GAAAG AA-3'	SEQ ID NO. 392
Avian influenza virus-MIS-21	5'-	GAGAAUGAAGA-GAAAACU CC-3'	SEQ ID NO. 393
Avian influenza virus-MIS-22	5'-	AUUCAGUGAAAUUG-GAAA AU-3'	SEQ ID NO. 394
Avian influenza virus-MIS-23	5'-	AGAAAUACACCAA-GACCA CAUA-3'	SEQ ID NO. 395
Avian influenza virus-MIS-24	5'-	CUUGAACUUAGAAG-CAGA UAU-3'	SEQ ID NO. 396
Avian influenza virus-MIS-25	5'-	ACAAUGCUAUCAAUUGUA AUC-3'	SEQ ID NO. 397
Avian influenza virus-MIS-26	5'-	ACAAUGCUAUCAAUUGUAU-3'	SEQ ID NO. 398
Avian influenza virus-MIS-27	5'-	GAACUUCAGGACAUA-GAA AAU-3'	SEQ ID NO. 399
Avian influenza virus-MIS-28	5'-	GCCUCCUUUCCA-GAAUG UG-3'	SEQ ID NO. 400
Avian influenza virus-MIS-29	5'-	GAUAUGACUUU-GAAAGGG AG-3'	SEQ ID NO. 401
Avian influenza virus-MIS-30	5'-	AGGGGUUGGAAUGG-CUGC AG-3'	SEQ ID NO. 402
Avian influenza virus-HIS-1	5'-	CAGAGUAGAAUG-CAAUC UCCUCA-3'	SEQ ID NO. 403
Avian influenza virus-HIS-2	5'-	UCCUGCUUUAAC-CAUAAU GACUGA-3'	SEQ ID NO. 404
Avian influenza virus-HIS-3	5'-	UUUCAUAAUGUCAG-CAAA UAUGCA-3'	SEQ ID NO. 405
Avian influenza virus-HIS-4	5'-	GGUCUACAAAACAUA-CUU UGAGAA-3'	SEQ ID NO. 406
Avian influenza virus-HIS-5	5'-	CAAAAUUAGAGAGA-CAGA AAUAGA-3'	SEQ ID NO. 407
Avian influenza virus-HIS-6	5'-	GAAGCAAAACU-GUUUGUG CU-3'	SEQ ID NO. 408
Avian influenza virus-HIS-7	5'-	UUGUUUUUAUGUG-GAGCU AAUCA-3'	SEQ ID NO. 409
Avian influenza virus-HIS-8	5'-	CACAAAGGACAAUAG-GAA AGAAA-3'	SEQ ID NO. 410
Avian influenza virus-HIS-9	5'-	UAAAGAAAUUGAAU-CAGU AAUAA-3'	SEQ ID NO. 411
Avian influenza virus-HIS-10	5'-	AGUGAGACACAGG-GAACA GAGAAA-3'	SEQ ID NO. 412
Avian influenza virus-HIS-11	5'-	CAUAUGAAAGAAU-GUGCA ACAUC-3'	SEQ ID NO. 413
Avian influenza virus-HIS-12	5'-	UCAAUGAAUCAACAAA AAGAAA-3'	SEQ ID NO. 414
Avian influenza virus-HIS-13	5'-	CAGCAGAUAAAA-	SEQ ID NO. 415

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
		GAAUAA UGGAAAUG-3'	
Avian influenza virus-HIS-14	5'-	AGUUGAUAAUAA-CAACUG GUCUGGU-3'	SEQ ID NO. 416
Avian influenza virus-HIS-15	5'-	AGAAGAAGAAAA-GAGGA CUAUUU-3'	SEQ ID NO. 417
Avian influenza virus-HIS-16	5'-	CUUCCAGUUUUGGAGUG UCUGGGAU-3'	SEQ ID NO. 418
Avian influenza virus-HIS-17	5'-	AAUUUUAAUAA-GAAAAU GGAAGAU-3'	SEQ ID NO. 419
Avian influenza virus-HIS-18	5'-	AAUCUAAUGG-GAAUUUAA UAGCUC-3'	SEQ ID NO. 420
Swine influenza virus-PIS-1	5'-	AUGCAGAACUUU-CUUUUU GACUC-3'	SEQ ID NO. 421
Swine influenza virus-PIS-2	5'-	ACAUCUUUUCAU-GUGGG GCAUAA-3'	SEQ ID NO. 422
Swine influenza virus-PIS-3	5'-	CUAGUCAGGCUAGG-CAGA UGGU-3'	SEQ ID NO. 423
Swine influenza virus-PIS-4	5'-	CAAAGCAGAAUGCA-GUUC UCLTCT-3'	SEQ ID NO. 424
Swine influenza virus-PIS-5	5'-	UGCAC-CAUUUAAAUAACA GAUAU-3'	SEQ ID NO. 425
Swine influenza virus-PIS-6	5'-	AGAGUAAGAGACAA-CAUG ACCA-3'	SEQ ID NO. 426
Swine influenza virus-PIS-7	5'-	GGGAAUUGGGA-CAAUGGU GAUG-3'	SEQ ID NO. 427
Swine influenza virus-PIS-8	5'-	AAUGCCUUGUUUCUA-CUA AUAC-3'	SEQ ID NO. 428
Swine influenza virus-PIS-9	5'-	UAAGAGGAUCAG-GAAUGA GAAU-3'	SEQ ID NO. 429
Swine influenza virus-PIS-10	5'-	AUCUCAUUUAAAG-GAAUGA CACA-3'	SEQ ID NO. 430
Swine influenza virus-PIS-11	5'-	AGACAAUGCUAAG-GAAU AGGG-3'	SEQ ID NO. 431
Swine influenza virus-PIS-12	5'-	AAAGCAAUGAAAGA-GUAU GGGGAG-3'	SEQ ID NO. 432
Swine influenza virus-PIS-13	5'-	UUGGUCUGAGGAAU-GUGC CUGCU-3'	SEQ ID NO. 433
Swine influenza virus-PIS-14	5'-	AUCAAUGAACAAA-GAGGA AAUA-3'	SEQ ID NO. 434
Swine influenza virus-PIS-15	5'-	CAGAGAGAGG-CAAUUAA AAAG-3'	SEQ ID NO. 435
Swine influenza virus-PIS-16	5'-	CACAAAUUGAAGAU-GACA GAGA-3'	SEQ ID NO. 436
Swine influenza virus-PIS-17	5'-	AAACAAGAAGUG-CUUUUG AGAG-3'	SEQ ID NO. 437
Swine influenza virus-PIS-18	5'-	ULTUULTUCAAUUG-CAUCU AUCAA-3'	SEQ ID NO. 438
Swine influenza virus-PIS-19	5'-	CAGAAAUCGAA-GAAUA AAAUG-3'	SEQ ID NO. 439
Swine influenza virus-PIS-20	5'-	CAGCCUAAUCAGAC-	SEQ ID NO. 440

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Swine influenza virus-PIS-21		5'-	SEQ ID
		GGACGGAUAAA-GAAAGAA GAGU-3'	NO. 441
Swine influenza virus-PIS-22		5'-	SEQ ID
		UGGAGUU-GAUAAGGGGAA GGA-3'	NO. 442
Swine influenza virus-PIS-23		5'-	SEQ ID
		ACAGAUUU-GAAAUAUUG AAGG-3'	NO. 443
Swine influenza virus-PIS-24		5'-	SEQ ID
		UGCAUGU-GUAAAUGGCUC UUG-3'	NO. 444
Swine influenza virus-PIS-25		5'-	SEQ ID
		CUUUUCCUGAAA-GUGCCA GCA-3'	NO. 445
Swine influenza virus-PIS-26		5'-	SEQ ID
		AAGACAA-GAAAUGGCCAG UAGG-3'	NO. 446
Swine influenza virus-PIS-27		5'-	SEQ ID
		CUGCAUUUGAA-GAUUAAA GAUUG-3'	NO. 447
Swine influenza virus-PIS-28		5'-	SEQ ID
		CCAUAUCCAAGGU-CUA CAAA-3'	NO. 448
Swine influenza virus-PIS-29		5'-	SEQ ID
		UGAGACUCCAAGAU-CAA GAUG-3'	NO. 449
Swine influenza virus-PIS-30		5'-	SEQ ID
		GCAGGAGUGGAUA-GAUUC UACA-3'	NO. 450
Swine influenza virus-PIS-31		5'-	SEQ ID
		AAAGCAAAUUGUA-GAAAA GAUU-3'	NO. 451
Swine influenza virus-PIS-32		5'-	SEQ ID
		UGCAGGGAAGAACA-CAGA UCUC-3'	NO. 452
Swine influenza virus-PIS-33		5'-	SEQ ID
		UCAAUUGCAUGAA-GACAU UCLTCT-3'	NO. 453
Swine influenza virus-PIS-34		5'-	SEQ ID
		AGAAGUUUAAG-GAUGAU GGA-3'	NO. 454
Swine influenza virus-PIS-35		5'-	SEQ ID
		CUGCCCAUCGGU-GAAGC UCC-3'	NO. 455
Swine influenza virus-PIS-36		5'-	SEQ ID
		AAUACCAGCCUUC-CAUUU CAGAAU-3'	NO. 456
Swine influenza virus-PIS-37		5'-	SEQ ID
		AAUGAAUCCAAAU-CAAAG GA-3'	NO. 457
Swine influenza virus-PIS-38		5'-	SEQ ID
		AUGCCUUGUUUCUA-CUAA UAC-3'	NO. 458
Swine influenza virus-PIS-39		5'-	SEQ ID
		UGAGUUGCCAUUCAC-CAU UGA-3'	NO. 459
Swine influenza virus-PIS-40		5'-	SEQ ID
		AUACAUUGAA-GUUUUACA UUU-3'	NO. 460
Swine influenza virus-PIS-41		5'-	SEQ ID
		GUGUGAUGGGAAUG-GUUG GAGUAU-3'	NO. 461
Swine influenza virus-PIS-42		5'-	SEQ ID
		AUAUGCACAAACA-GAAUG UGU-3'	NO. 462
Swine influenza virus-PIS-43		5'-	SEQ ID
		UGGAUUUGUUGC-CAAUUU CA-3'	NO. 463
Swine influenza virus-PIS-44		5'-	SEQ ID
		AUUAUAAAAGGAAG-GUCU CA-3'	NO. 464
Swine influenza virus-	5'-	SEQ ID	

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
PIS-45		5'-	SEQ ID
		CCAAAGAGGGGAAGAC-GAAAG-3'	NO. 465
Swine influenza virus-HIS-1		5'-	SEQ ID
		UAUUAUAAAUGAA-CAGGA ACAU-3'	NO. 466
Swine influenza virus-HIS-2		5'-	SEQ ID
		ACAAUAAAAGUUG-GAGA AACA-3'	NO. 467
Swine influenza virus-HIS-3		5'-	SEQ ID
		AAAGCCAUGGAA-CAAUG GCUG-3'	NO. 468
Swine influenza virus-HIS-4		5'-	SEQ ID
		GGUCUCAAAAACUAU-CUU UGAGAAA-3'	NO. 469
Swine influenza virus-HIS-5		5'-	SEQ ID
		AAUAGUUUACUU-GAAUAA UACA-3'	NO. 470
Swine influenza virus-HIS-6		5'-	SEQ ID
		UUCAAGAUGGA-GAAAGGG AAGA-3'	NO. 471
Swine influenza virus-HIS-7		5'-	SEQ ID
		AAAAGAAAUACAC-CAAAA CAGU-3'	NO. 472
Swine influenza virus-HIS-8		5'-	SEQ ID
		AACCUAAAUUUCCU-CAG ALTUU-3'	NO. 473
Swine influenza virus-HIS-9		5'-	SEQ ID
		ACAACCUACUUUCU-CAGU ACAGA-3'	NO. 474
Swine influenza virus-HIS-10		5'-	SEQ ID
		AAAUUCAAAACAAG-GAGAU CALTU-3'	NO. 475
Swine influenza virus-HIS-11		5'-	SEQ ID
		UGGUCAGGUUAUU-CUGGC ALTUU-3'	NO. 476
Swine influenza virus-HIS-12		5'-	SEQ ID
		CAACCGGAACCU-GAAC CU-3'	NO. 477
Swine influenza virus-HIS-13		5'-	SEQ ID
		CCAGCACUGAGAGG-GUGA CUGU-3'	NO. 478
Swine influenza virus-HIS-14		5'-	SEQ ID
		GAAAUCAACCU-GAAUGGU UU-3'	NO. 479
Swine influenza virus-HIS-15		5'-	SEQ ID
		UUAUCAAAUACUUG-CUAU AUAC-3'	NO. 480
Swine influenza virus-HIS-16		5'-	SEQ ID
		CUUUU-CUUAAAAUUCCA GCGC-3'	NO. 481
Swine influenza virus-HIS-17		5'-	SEQ ID
		AGAGAAGGAUUAU-CUCUG GUC-3'	NO. 482
Swine influenza virus-HIS-18		5'-	SEQ ID
		GGGGAGACACA-CAAAUUC AGAC-3'	NO. 483
Swine influenza virus-HIS-19		5'-	SEQ ID
		UGAUUAUUGCUG-CUAGAA ACAUA-3'	NO. 484
Swine influenza virus-HIS-20		5'-	SEQ ID
		UGAUUAUUGCUG-CUAGAA ACAU-3'	NO. 485
Swine influenza virus-HIS-21		5'-	SEQ ID
		UGGAGAAAGCCAA-CAAGA UAAAA-3'	NO. 486
Swine influenza virus-HIS-22		5'-	SEQ ID
		ACAAAGAACAUG-CAAAAACAAG-3'	NO. 487
Swine influenza virus-HIS-23		5'-	SEQ ID
		AGGGCAAGCUUUC-CAAA UGUCU-3'	NO. 488
Swine influenza virus-HIS-24		5'-	SEQ ID
		AGGGCAAGCUUUC-CAAA UGUC-3'	NO. 489
Swine influenza virus-HIS-25		5'-	SEQ ID
		CCAAAACUACAUA-CUGGU GGA-3'	NO. 490

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Swine influenza virus-HIS-26	5'-	AGGCAAAGUGGUGU-GUGU GUGC-3'	SEQ ID NO. 491
Swine influenza virus-HIS-27	5'-	UCAAGAGAAAGA-CAUGA CCA-3'	SEQ ID NO. 492
Swine influenza virus-HIS-28	5'-	ACUUUGUAAUCCCAU-GAA UCC-3'	SEQ ID NO. 493
Swine influenza virus-HIS-29	5'-	UUUCAGGCAGAAU-GAAUG CAG-3'	SEQ ID NO. 494
Swine influenza virus-HIS-30	5'-	GAAACACAGGGAACA-GAG AAA-3'	SEQ ID NO. 495
Swine influenza virus-HIS-31	5'-	AAGGAAGAUCU-CAUUUGA GGA-3'	SEQ ID NO. 496
Swine influenza virus-HIS-32	5'-	GAUAGUAAGUGGAA-GAGA UGAA-3'	SEQ ID NO. 497
Swine influenza virus-HIS-33	5'-	CAUAUGAAAGAAU-GUGCA ACAU-3'	SEQ ID NO. 498
Swine influenza virus-HIS-34	5'-	AUAAUACUAGUA-GUAAACA GUAA-3'	SEQ ID NO. 499
Swine influenza virus-HIS-35	5'-	UUGACUGAAGAUCCA-GAU GAA-3'	SEQ ID NO. 500
Swine influenza virus-HIS-36	5'-	AAAAAUGAUGAC-CAAUUC UCA-3'	SEQ ID NO. 501
Swine influenza virus-HIS-37	5'-	UAUGGAAUUCUCU-CUUAC UGA-3'	SEQ ID NO. 502
Swine influenza virus-HIS-38	5'-	AAAAACAAGAAU-GAGU AAGA-3'	SEQ ID NO. 503
Swine influenza virus-HIS-39	5'-	AAGCAACCAGGA-GAUUGG UUCA-3'	SEQ ID NO. 504
Swine influenza virus-HIS-40	5'-	CCAGAGGACAAGAG-CUCU UGUU-3'	SEQ ID NO. 505
Swine influenza virus-HIS-41	5'-	GAAAGAACAUU-CUUUUC UGUG-3'	SEQ ID NO. 506
Swine influenza virus-HIS-42	5'-	CUGUAAUGA-GAAUGGAG ACCU-3'	SEQ ID NO. 507
Swine influenza virus-HIS-43	5'-	GGAAAUUGU-GAAAAUUCA AUGG-3'	SEQ ID NO. 508
Swine influenza virus-HIS-44	5'-	UUUUGCUUUGUGUU-GUUU UGCUG-3'	SEQ ID NO. 509
Swine influenza virus-HIS-45	5'-	AGGACUUCGA-GAAAUUG UUGA-3'	SEQ ID NO. 510
Swine influenza virus-HIS-46	5'-	AAACAACAUACAA-CAAC AAUAA-3'	SEQ ID NO. 511
Swine influenza virus-HIS-47	5'-	AAAAUGCUGAG-GAUUUG GCAA-3'	SEQ ID NO. 512
Swine influenza virus-HIS-48	5'-	UUUCACCAUUACCU-CUC UUCC-3'	SEQ ID NO. 513
Swine influenza virus-HIS-49	5'-	UCUUAUUUCUUCAGA-GAC AAUG-3'	SEQ ID NO. 514
Swine influenza virus-HIS-50	5'-	AGAGAAAAUACUU-GAAAA UUGUG-3'	SEQ ID NO. 515
Swine influenza virus-HIS-51	5'-	ACAGAAAUGUCACU-GAGA GGAG-3'	SEQ ID NO. 516

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Swine influenza virus-HIS-52	5'-	AAAGGGGGUAGGGA-CAAU GGUG-3'	SEQ ID NO. 517
Swine influenza virus-HIS-53	5'-	GACUACAGAUUAU-CAUUA AGAU-3'	SEQ ID NO. 518
Swine influenza virus-HIS-54	5'-	GAAAAAGGAGAGU-GAGAG ACAA-3'	SEQ ID NO. 519
Swine influenza virus-HIS-55	5'-	UAGAUUAAAUGU-GAAAG AUUA-3'	SEQ ID NO. 520
Swine influenza virus-HIS-56	5'-	UCAGACAGCUGCCCA-GAG GGCA-3'	SEQ ID NO. 521
Rabies virus	Rabies virus-DIS-1	5'- ACUUACCAGUCUCAU-CUU CUA-3'	SEQ ID NO. 522
	Rabies virus-DIS-2	5'- UUUUCUAUCCCUCA-GAAA AUCC-3'	SEQ ID NO. 523
	Rabies virus-DIS-3	5'- CUUUGAUCUCGGG-CUUGA GA-3'	SEQ ID NO. 524
	Rabies virus-DIS-4	5'- UCUCUCUGCCUUGUA-GUU GG-3'	SEQ ID NO. 525
	Rabies virus-DIS-5	5'- UAUAACUUUAUA-CUUCAGAA-3'	SEQ ID NO. 526
	Rabies virus-DIS-6	5'- AGAAAUCAUUA-CAAAUCC UU-3'	SEQ ID NO. 527
	Rabies virus-DIS-7	5'- UUCAGACAGAUA-GACCU CA-3'	SEQ ID NO. 528
	Rabies virus-DIS-8	5'- AAUAUCCAGAAUG-GUUUC UG-3'	SEQ ID NO. 529
	Rabies virus-DIS-9	5'- AAGUCAACAU-GAAAAAAA CAG-3'	SEQ ID NO. 530
	Rabies virus-DIS-10	5'- UGAAAAAAAACAA-GAUCUU AA-3'	SEQ ID NO. 531
	Rabies virus-DIS-11	5'- GGGGGGUUCUUUUU-GAAAAA-3'	SEQ ID NO. 532
	Rabies virus-DIS-12	5'- GAGAUGGCCAAG-GUGGGA GA-3'	SEQ ID NO. 533
	Rabies virus-DIS-13	5'- UUUUUACCAUAU-GUAGAG GG-3'	SEQ ID NO. 534
	Rabies virus-DIS-14	5'- GUGCUCUCAU-GAAAUGU CUGU-3'	SEQ ID NO. 535
	Rabies virus-DIS-15	5'- UACCACCUUAAAAUA-CAG AG-3'	SEQ ID NO. 536
	Rabies virus-DIS-16	5'- CUCAGCCAUAAAAU-GAA CG-3'	SEQ ID NO. 537
	Rabies virus-DIS-17	5'- AUUGCAGAAAGUUU-CUCC AAAA-3'	SEQ ID NO. 538
	Rabies virus-DIS-18	5'- AGACUGGACCAG-CUAUGG AAUC-3'	SEQ ID NO. 539
	Rabies virus-DIS-19	5'- AUGUAAUCAC-CUUUAUACA UGAAC-3'	SEQ ID NO. 540
	Rabies virus-DIS-20	5'- GGAAGGACUUG-GUAAAGU UC-3'	SEQ ID NO. 541
	Rabies virus-DIS-21	5'- AAAUCCUGAGGCA-CUUCA ACAU-3'	SEQ ID NO. 542

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Rabies virus-DIS-22	5'-	GUCUGUCAUCUCA-CUGGA UC-3'	SEQ ID NO. 543
Rabies virus-DIS-23	5'-	UGGGCACAGUUGUCA-CUG CU-3'	SEQ ID NO. 544
Rabies virus-DIS-24	5'-	AAACAUUGCAGACAG-GAU AG-3'	SEQ ID NO. 545
Rabies virus-DIS-25	5'-	UGUAAUUCUAGCCU-GAGU CU-3'	SEQ ID NO. 546
Rabies virus-DIS-26	5'-	CCAGGAAAGUCUUCAGAG GAU-3'	SEQ ID NO. 547
Rabies virus-DIS-27	5'-	UAAAAGAUCUUU-CUUGU CU-3'	SEQ ID NO. 548
Rabies virus-DIS-28	5'-	AGACAAAUAAGGU-CAGGA GA-3'	SEQ ID NO. 549
Rabies virus-DIS-29	5'-	AGACAACACCCACUC-CUU CU-3'	SEQ ID NO. 550
Rabies virus-DIS-30	5'-	UAGGUUCAAGUCUGC-CAG AUACA-3'	SEQ ID NO. 551
Rabies virus-DIS-31	5'-	CUUACCAGUCUCAU-CUUC UAC-3'	SEQ ID NO. 552
Rabies virus-DIS-32	5'-	GGCCUUGCUCUUCAGAGA GG-3'	SEQ ID NO. 553
Rabies virus-DIS-33	5'-	CAUGCAGCUAGAACAUG AC-3'	SEQ ID NO. 554
Rabies virus-DIS-34	5'-	GGGGAAGAAAAGUG-GUAG GCA-3'	SEQ ID NO. 555
Rabies virus-DIS-35	5'-	ACAGGAUAGAGCA-GAUUU UU-3'	SEQ ID NO. 556
Rabies virus-DIS-36	5'-	UUGAAAAUGAAC-CUUGAU GA-3'	SEQ ID NO. 557
Rabies virus-DIS-37	5'-	CAUGAGCAAGAU-CUUUGU CAA-3'	SEQ ID NO. 558
Rabies virus-DIS-38	5'-	UCUUGUGA-CAUUUUUACC AAU-3'	SEQ ID NO. 559
Rabies virus-DIS-39	5'-	CAGGAACACAAGAAC-CAAAG-3'	SEQ ID NO. 560
Rabies virus-DIS-40	5'-	UUCACAUUAAAAAAGUGA UA-3'	SEQ ID NO. 561
Rabies virus-DIS-41	5'-	CUGUUGGAAUGGC-CAGGA UG-3'	SEQ ID NO. 562
Rabies virus-DIS-42	5'-	AAGGUGGAGAACU-CAGAG UUU-3'	SEQ ID NO. 563
Rabies virus-DIS-43	5'-	GCAUUUGGAAG-GUAUCUU GC-3'	SEQ ID NO. 564
Rabies virus-DIS-44	5'-	CUCUAUUUCUUGCA-CUUG UG-3'	SEQ ID NO. 565
Rabies virus-DIS-45	5'-	AAGAAGAGACCAU-GUGUA GUU-3'	SEQ ID NO. 566
Rabies virus-DIS-46	5'-	AUAAUGCAUUUG-GAAGGU AU-3'	SEQ ID NO. 567
Rabies virus-DIS-47	5'-	CUAUGAAGUCAU-CAAAU AU-3'	SEQ ID NO. 568

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Rabies virus-DIS-48	5'-	UUCUCAUUUUUGUU-GUUU AUUU-3'	SEQ ID NO. 569
Rabies virus-DIS-49	5'-	AUAACAGACCUAUAACUU AU-3'	SEQ ID NO. 570
Rabies virus-DIS-50	5'-	AGAGAGACACAAGG-CUAA GA-3'	SEQ ID NO. 571
Rabies virus-DIS-51	5'-	UUAGUCCAGAGAGCA-GAAAA-3'	SEQ ID NO. 572
Rabies virus-DIS-52	5'-	CACUGCCUCCUUCAGCAA UCA-3'	SEQ ID NO. 573
Rabies virus-DIS-53	5'-	UAUGAAGUCAU-CAAAAUA UU-3'	SEQ ID NO. 574
Rabies virus-DIS-54	5'-	CAUUAAAAAAGU-GAUAGA UA-3'	SEQ ID NO. 575
Rabies virus-DIS-55	5'-	AGAGAGCAUC-CAAAGGA GUG-3'	SEQ ID NO. 576
Rabies virus-DIS-56	5'-	AAAAAUGUACCAG-GUGU GA-3'	SEQ ID NO. 577
Rabies virus-DIS-57	5'-	ACAUGAGCAAGAU-CUUU GU-3'	SEQ ID NO. 578
Rabies virus-DIS-58	5'-	AAUCACAUUCUU-CACCA GAA-3'	SEQ ID NO. 579
Rabies virus-DIS-59	5'-	CCUCACUCUUUUU-CAUC CA-3'	SEQ ID NO. 580
Rabies virus-DIS-60	5'-	CAUUCACUUUGUAG-GAUG CU-3'	SEQ ID NO. 581
Rabies virus-HIS-1	5'-	AUCAGAAAGG-CUUUAUAU GAC-3'	SEQ ID NO. 582
Rabies virus-HIS-2	5'-	UGUAUUUAAAA-GACAA GGU-3'	SEQ ID NO. 583
Rabies virus-HIS-3	5'-	CUCAUUUUUGUU-GUUUAU UU-3'	SEQ ID NO. 584
Rabies virus-HIS-4	5'-	UGCCAAGCUUGUGUU-CAA CA-3'	SEQ ID NO. 585
Rabies virus-HIS-5	5'-	UGGGCUCUGACAG-GAGGC AUG-3'	SEQ ID NO. 586
Rabies virus-HIS-	5'-	AAGUAAUUAC-CUUUACA UU-3'	SEQ ID NO. 587
Rabies virus-HIS-7	5'-	UACUAUGAUGUAU-CUAUC UA-3'	SEQ ID NO. 588
Rabies virus-HIS-8	5'-	AGGAGGUAUUCUUCUGU AU-3'	SEQ ID NO. 589
Rabies virus-HIS-9	5'-	GAACCCAGAG-GAACCC AC-3'	SEQ ID NO. 590
Rabies virus-HIS-10	5'-	CACUGCCUCCUUCAGCAA UCA-3'	SEQ ID NO. 591
Rabies virus-HIS-11	5'-	AGAGCUCAGAAG-GAGAC AA-3'	SEQ ID NO. 592
Rabies virus-HIS-12	5'-	AAGAGGGGCCUCCUUAUG AA-3'	SEQ ID NO. 593
Rabies virus-HIS-13	5'-	UCUACUGCUUAGGU-GAC GU-3'	SEQ ID NO. 594

TABLE 1-continued

Target sequence listing of RNA virus			
Virus type	Fragment number	Fragment coding sequence	ID number
Rabies virus-HIS-14	5'-	AGAUGGGUGGAU-	SEQ ID NO. 595
		CAAGAG GU-3'	
	5'-	AACGGUGACGAGGCU-	SEQ ID NO. 596
Rabies virus-HIS-15	5'-	GAG GA-3'	
		CAGAGGAU-	SEQ ID NO. 597
Rabies virus-HIS-16	5'-	GUAUUUCUG UC-3'	
		CACAUCCACUGCCUC-	SEQ ID NO. 598
Rabies virus-HIS-17	5'-	CUU CA-3'	
		AGGGAUGUCUUGU-	SEQ ID NO. 599
Rabies virus-HIS-18	5'-	GACAU UUUU-3'	
		CUUCGAAAGCAAGU-	SEQ ID NO. 600
Rabies virus-HIS-19	5'-	CAU UCUA-3'	
		UACAUUCAGC-	SEQ ID NO. 601
Rabies virus-HIS-20	5'-	CAUAAA AUG-3'	
		UUACUGAGUG-	SEQ ID NO. 602
Rabies virus-HIS-21	5'-	CAGGGGCC CUGA-3'	
		UCAACUUCCCAACC-	SEQ ID NO. 603
Rabies virus-HIS-22	5'-	CUC CA-3'	
		CAGAGGACAGG-	SEQ ID NO. 604
Rabies virus-HIS-23	5'-	GAGGGA GGU-3'	
		AGUCAGAACUUG-	SEQ ID NO. 605
Rabies virus-HIS-24	5'-	GAAUGA GAU-3'	
		UCAAAGAUAGAGU-	SEQ ID NO. 606
Rabies virus-HIS-25	5'-	CAAC AGA-3'	
		CAUGAACUGG-	SEQ ID NO. 607
Rabies virus-HIS-26	5'-	GUAUACAA GLTU-3'	
		CUGAUGACAUGCUG-	SEQ ID NO. 608
Rabies virus-HIS-27	5'-	GAGA AGA-3'	
		UGGUCACGUGUU-	SEQ ID NO. 609
Rabies virus-HIS-28	5'-	CAAUCU CAU-3'	
		UUAUGAAGACUGUU-	SEQ ID NO. 610
Rabies virus-HIS-29	5'-	CAGG ACU-3'	
		UUAUGAAGACUGUU-	SEQ ID NO. 611
Rabies virus-HIS-30	5'-	CUGGUGGA-	
		GAUAAAACGU	SEQ ID NO. 612
Rabies virus-HIS-31	5'-	ACUGA-3'	
		UUGAUUGUUUUUCU-	SEQ ID NO. 613
Rabies virus-HIS-32	5'-	CAUU UU-3'	
		UGGUUCUGGGGCU-	SEQ ID NO. 614
Rabies virus-HIS-33	5'-	GUGC CUC-3'	
		GAGCCAGGGCAGGA-	SEQ ID NO. 615
Rabies virus-HIS-34	5'-	GACA GC-3	
		GGGUUCUUUUU-	SEQ ID NO. 616
		GAAAAAAA-3'	

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-UCCUCUUACUGUUUUUUUUUUUUUUU-5'	SEQ ID NO. 715
3'-ACAACGACGACGAUAAAAGAUAAAUU-5'	SEQ ID NO. 716
3'-GUACUUCUUUGUUAAAUAUUAAAUGAAU-5'	SEQ ID NO. 717
3'-CUCAACUCCUUCUUCUUCUCCUUCUGACC-5'	SEQ ID NO. 718
3'-AUUGUACGAAUCCUAAUACCGGAG-5'	SEQ ID NO. 719
3'-UCCUCUUACUGUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 720
3'-AAGGUAAAACGGUCUCUAAGAAAA-5'	SEQ ID NO. 721
3'-ACGACAUAAACGACAACAACGACGACAA-5'	SEQ ID NO. 722
3'-CUUUUUUCUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 723
3'-CCCUCUCCUCCUUCUCUGAGG-5'	SEQ ID NO. 724
3'-CAAGAUCUCUACGUUCUGAACAC-5'	SEQ ID NO. 725
3'-UGAGUAAGAUGGUAAAAAAUUUAAAC-5'	SEQ ID NO. 726
3'-UCUAGGACACUGAAGACCUGAAAA-5'	SEQ ID NO. 727
3'-UUUAAUAAAUAUUUUUUUUUUUUUU-5'	SEQ ID NO. 728
3'-UGAAAAUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 729
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 730
3'-UUUACUUGUUAUCUAUUUAAUC-5'	SEQ ID NO. 731
3'-UUUAAUACCAUGGUCAAUCUUUU-5'	SEQ ID NO. 732
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 733
3'-UAAAUAGUUCUCGGUAAAUUUUUU-5'	SEQ ID NO. 734
3'-AUUUUGUCCUGUUUUUUUUUUUU-5'	SEQ ID NO. 735
3'-UCUUAGUCUAUUCAUCUUAAUCU-5'	SEQ ID NO. 736
3'-UCCGUCUCCUUCUACUCCGGUUG-5'	SEQ ID NO. 737
3'-AUAGUUUUUUAAUUCUUUUCCAAU-5'	SEQ ID NO. 738
3'-CCUAGUCACCUUUUACUCCUCCUACU-5'	SEQ ID NO. 739
3'-UACUCUCUAGAACCCCCACCCUG-5'	SEQ ID NO. 740
3'-UUUUUAGAGUUCUACUUUCCUUA -5'	SEQ ID NO. 741
3'-UACUAACCGAAUUCUUCUUUUUU-5'	SEQ ID NO. 742
3'-UUAACAAAUGGAUAAAUAACCAAAACAC-5'	SEQ ID NO. 743
3'-GACACGACUUGGUCCUGGUCCU-5'	SEQ ID NO. 744
3'-UCUACUUCGUCAGUGGUUGGCG-5'	SEQ ID NO. 745
3'-UAAUCUAAAGUUGUGUCCACGAUUGAG-5'	SEQ ID NO. 746
3'-AACCUCUAAAACGAGGAGAAA-5'	SEQ ID NO. 747
3'-UUUAAAUAUAAAACAAAGUCA-5'	SEQ ID NO. 748
3'-AAUCGAUCUAAAUGUCUAAAACCU-5'	SEQ ID NO. 749
3'-UUGUUCUCGUCGUCACACCACC-5'	SEQ ID NO. 750
3'-AACUCCUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 751
3'-GGUCCUGACCCUUCAGUACCCGU-5'	SEQ ID NO. 752
3'-UUAAUCCUACUAUGGAAGUGAUU-5'	SEQ ID NO. 753
3'-ACUCUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 754
3'-UGUUUAACCUUUUAUCACUUUU-5'	SEQ ID NO. 755
3'-CUUCGUCUCUUUUUUUUUUUUUU-5'	SEQ ID NO. 756
3'-AGUUUUCCUUCUUGUCUACGACC-5'	SEQ ID NO. 757
3'-GUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 758
3'-CUCUACCUGAAACUAAAAGACACU-5'	SEQ ID NO. 759
3'-CCUUUAGGUCCUCCAAAACCUU-5'	SEQ ID NO. 760
3'-UUUCCUUCUUUAAACUUUGGGUCU-5'	SEQ ID NO. 761
3'-CACCGUCCGGUAAUUGUGUGGU-5'	SEQ ID NO. 762
3'-UCAAAUUAAAUAUAGGUUUUUUUAAA-5'	SEQ ID NO. 763
3'-UUCUUUUUCUAUUUUAUCUUGUUUCUAAA-5'	SEQ ID NO. 764
3'-AGAUUCGCUCAUUGUUGUUCUCA-5'	SEQ ID NO. 765
3'-UUGUCUUUCUUCGUAUAAUAGUAGUCCGAA-5'	SEQ ID NO. 766
3'-ACUAAAUAUAAAUGACCAUAAUUUAUCA-5'	SEQ ID NO. 767
3'-UUGUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 768
3'-UAUGUUAGUUAAACUUACCGUA-5'	SEQ ID NO. 769
3'-UCUACUGUAAACACUUUAAUUU-5'	SEQ ID NO. 770
3'-CAAUAUAUACCCUUUACUACCUAAUUGU-5'	SEQ ID NO. 771
3'-UUUUUUUAUUCACUAAGUUGU-5'	SEQ ID NO. 772

TABLE 2

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-ACAGAUACGAUACCUCAUUUCCGA-5'	SEQ ID NO. 712
3'-AUUUGUGUAUUUUUUUUGCACA-5'	SEQ ID NO. 713
3'-AAUAUCGGAAUAAAGAAAUGAAA-5'	SEQ ID NO. 714

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-UUUAUGUUUUUUUAUAGACUUAUGUU-5'	SEQ ID NO. 773
3'- AAAUGUAAGGACCAGUUGAUACUUUACUUU- GAU AAC G-5'	SEQ ID NO. 774
3'-GAUGUUUUUUACGAUUUUUCUU-5'	SEQ ID NO. 775
3'-UACGACUUGUUGAUUUUUUUU-5'	SEQ ID NO. 776
3'-UCCUUUCACUUUUUCACCGUUU-5'	SEQ ID NO. 777
3'-UUACUCCUUUCACUUUUUCACCGUUUUUCU- 5'	SEQ ID NO. 778
3'-GUUCUUUUUUUCUAUCAUGUA-5'	SEQ ID NO. 779
3'- GGUAUCUUUGUAAACUAUUGUUACUUCUU-5'	SEQ ID NO. 780
3'-UUUCAUAUUAUACAAGUUGU-5'	SEQ ID NO. 781
3'-UACUAUUGUUGUUAUAGAGAAA-5'	SEQ ID NO. 782
3'-UGAUUAUGUGUACUAUUGUU-5'	SEQ ID NO. 783
3'-ACUAUUGUUGUUAUAGAGAAACGAU-5'	SEQ ID NO. 784
3'-CUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 785
3'-UUACAUGUCGUAAGUUUUUUU-5'	SEQ ID NO. 786
3'-AUUAAUAAAACUACCGGUGGGGUAC-5'	SEQ ID NO. 787
3'-UUAUAAAACUACCGGUGGG-5'	SEQ ID NO. 788
3'-AGAUAAUUUAUUAUUGAUUU-5'	SEQ ID NO. 789
3'-AUUUUAUCUAUUUUUAUUGUAAU-5'	SEQ ID NO. 790
3'- UUUACAACAAAUUAAGUACCUAAUCAU-5'	SEQ ID NO. 791
3'-UACCAAUAUGUAAACAAAUAAAUAU-5'	SEQ ID NO. 792
3'-UUGAUAAUUUUUGAAUACAUA-5'	SEQ ID NO. 793
3'-AUAUCUUGUACUUUUUAAAUUUAAAAG-5'	SEQ ID NO. 794
3'-AUCUGUUUAUUGAUUAAAUUUU-5'	SEQ ID NO. 795
3'-UUACAAGGUAAACAAUAGAUUAU-5'	SEQ ID NO. 796
3'-UCCAUUUAAUACUCUCUACCCUCA-5'	SEQ ID NO. 797
3'-AUAAAUUUUCCGUCUAUUAAUCU-5'	SEQ ID NO. 798
3'-CCUUGAACCCAGUAAAAGAAU-5'	SEQ ID NO. 799
3'-UAAAAGAACUAAACGAAAAGUU-5'	SEQ ID NO. 800
3'-AUAAAGACUUUACCAUAUAAAUU-5'	SEQ ID NO. 801
3'-UCGGAUAAAAGUAAACGAGACU-5'	SEQ ID NO. 802
3'-AGUUGUUUAUAAAUGCCGUUUU-5'	SEQ ID NO. 803
3'-AAUCUUUUUACCUUUUCAUAUCU-5'	SEQ ID NO. 804
3'-UUCUCGAGUUGUUUAUAAAUGUC-5'	SEQ ID NO. 805
3'-AGAUUUAUAAAGUCUACCGUAUCU-5'	SEQ ID NO. 806
3'-ACUACCCCAACUGCCUCAACCCCUCA-5'	SEQ ID NO. 807
3'-CCCUAAACCUUCCGAGAGAC-5'	SEQ ID NO. 808
3'-UUUACCCGCUUUUCUUGGAGUCC-5'	SEQ ID NO. 809
3'-ACCGAGCUUCUCGUACCCUCCUU-5'	SEQ ID NO. 810
3'-UCCUCCCUAACUCUCGAGUG-5'	SEQ ID NO. 811
3'- UUUUUACUGACCUUACCGGUACACCU- CUUCG-5'	SEQ ID NO. 812
3'-GUCGCGUCCCUUCUCACCCGUCGUC-5'	SEQ ID NO. 813
3'- UUAUUCUUUUCGUUGUAACA- CUAAAUAUUAU-5'	SEQ ID NO. 814
3'-AUUUUUUUCAGUUAAAUAUUAU-5'	SEQ ID NO. 815
3'-GAAACCGUAAAGUCACUAAAGUCUUUU-5'	SEQ ID NO. 816
3'-UUUACACGAGGGGAAAGGACCU-5'	SEQ ID NO. 817
3'-AAAUUUUCCUACCCACUUUCUUUCU-5'	SEQ ID NO. 818
3'-UUUAUUUAUUUACGUAAAGUUGA-5'	SEQ ID NO. 819
3'-CCGUCCACCAACGAGUUCGACAUU-5'	SEQ ID NO. 820
3'-AUUUUUAAAAGGACGAAGGUU-5'	SEQ ID NO. 821
3'-AGUAACCUUCUACCCGAGAAA-5'	SEQ ID NO. 822
3'-GUCGAAUGAGAAGGAGUCUAAGAAA-5'	SEQ ID NO. 823
3'- AAAUACUUAAGAUGUCUUUAUUAUUAUAC- 5'	SEQ ID NO. 824
3'-UUUCUAAUACCUUUGAAAAGAC-5'	SEQ ID NO. 825
3'-AACGACAAAAGGUUUGUAUCU-5'	SEQ ID NO. 826
3'- CAGUUAGGUUUUAACCUUCUUCGUCUU- CAUUA-5'	SEQ ID NO. 827
3'-UACACCUCUGUAAGGUCGUGUCUUUUUG- 5'	SEQ ID NO. 828

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-AGUCCGAGUUCACUAGAGAGUAAAGU-5'	SEQ ID NO. 829
3'-AAUUAACUUCAAAUACUUAAC-5'	SEQ ID NO. 830
3'-UCUAUAUCCUUACACAGACUUU-5'	SEQ ID NO. 831
3'-UUUUUUCAGUUCUUUUUUUUUUUUUU-5'	SEQ ID NO. 832
3'-AUACGGACUUAUUAAAAGUAACC-5'	SEQ ID NO. 833
3'-UUAUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 834
3'-UCUCUCUCUUUUUUUUUUUUUU-5'	SEQ ID NO. 835
3'-AUACGGACUUAUUAAAAGUAACC-5'	SEQ ID NO. 836
3'-GACACAAAAGAGGAUCUUACAGU-5'	SEQ ID NO. 837
3'-UUUCUGUCCUAAAAGUAAUAAAACU-5'	SEQ ID NO. 838
3'-ACCUACACUCUUUAUGAACCCU-5'	SEQ ID NO. 839
3'-UUUUCUGUCCUAAAAGUAAUAAA-5'	SEQ ID NO. 840
3'-UUUUCUGUCCUAAAAGUAAUAAAACUA-5'	SEQ ID NO. 841
3'-CUGUCCUAAAAGUAAUAAAACUA-5'	SEQ ID NO. 842
3'-UCAAGAGAAAACUGUAAAACAAG-5'	SEQ ID NO. 843
3'-ACUGUAAAACAAGAAAAGAAC-5'	SEQ ID NO. 844
3'-CUUUUACAACAGGUUGUAGGUUAGUU-5'	SEQ ID NO. 845
3'-CCUUCUUUCUGUAAUUUGAUUAA-5'	SEQ ID NO. 846
3'-AUUAGAAGAUUUCAGAUCAUUU-5'	SEQ ID NO. 847
3'-GUCCUUAGGAACAUCACUACCCUAAACA-5'	SEQ ID NO. 848
3'-AUAAUAGUUACCGUUUUUUUUUUUU-5'	SEQ ID NO. 849
3'-UUACGGAAUUAGAGUCUAUAAAACAAU- 5'	SEQ ID NO. 850
3'-AUAAAACAAUACUUCUUUUUUUUUU-5'	SEQ ID NO. 851
3'-UUGUUCAAAGAGGAUAGUUAUUU-5'	SEQ ID NO. 852
3'- GUAUCAUAGAGAAUUAUAGGAAAAGUAAA-5'	SEQ ID NO. 853
3'-UAUCAUAGAGAAUUAUAGGAAAAGUAAA- 5'	SEQ ID NO. 854
3'-AUGUUUGUACCCGUUAAAGUUUAG-5'	SEQ ID NO. 855
3'-CGAGAAGAAAGGAUUUGUUACA-5'	SEQ ID NO. 856
3'-ACAAUUUGUAGAAAGAAAGGAAA-5'	SEQ ID NO. 857
3'-UAUCAUAGAGAAUUAUAGGAAA-5'	SEQ ID NO. 858
3'-UGUUGACUUUGUACGUUCCUUA-5'	SEQ ID NO. 859
3'-CAAGUCCCGUUAAUUAUGU-5'	SEQ ID NO. 860
3'-AUUUUUAAAAGAGUCCAGUA-5'	SEQ ID NO. 861
3'-UUUUUAAGUCCUUUUACCUUUUU-5'	SEQ ID NO. 862
3'-GUGUUUCGAGUUCGUGCAUACA-5'	SEQ ID NO. 863
3'-GAACAAAAGAAAGGAAAGAAAGAC-5'	SEQ ID NO. 864
3'-AAAAGAAAGGAAAGAAAGACGAAAGA-5'	SEQ ID NO. 865
3'- AAAAGAAAGGAAAGAAAGACGAAAGAGA-5'	SEQ ID NO. 866
3'-AAAGAAAGGAAAGAAAGACGAA-5'	SEQ ID NO. 867
3'-AAAAGAAAGGAAAGAAAGACGAAAGA-5'	SEQ ID NO. 868
3'-UAUACCUACAUCUAAAAGUAAAC-5'	SEQ ID NO. 869
3'-AAAAGAAAGGAAAGAAAGACGAAAGA-5'	SEQ ID NO. 870
3'-UGUAGAAAUGUUAACCUUAAAAGAAAG-5'	SEQ ID NO. 871
3'-AAGUAUGUAAGAUUUUGAAUUAAGGUCUA- 5'	SEQ ID NO. 872
3'-CUGAUGUUCUUCUACCGUCU-5'	SEQ ID NO. 873
3'-UUACCGUAAUACUUUAUUAU-5'	SEQ ID NO. 874
3'-UCCAAACAUAUUUUUUUUUUUU-5'	SEQ ID NO. 875
3'-GGAAGAAAGGAAAGUAGUAAAAAAA-5'	SEQ ID NO. 876
3'-GUCCUUUUUUUACCUAUGAUUU-5'	SEQ ID NO. 877
3'-UAAUAAAUAUUAGUAAUAGAUUAU-5'	SEQ ID NO. 878
3'-AUUAUUAUACGUUACUAGUUAUUAU-5'	SEQ ID NO. 879
3'-ACAAUCUAAAAGAACAGUAAAAGG-5'	SEQ ID NO. 880
3'-GGUGUCGUUUAACAAAGUCAUA-5'	SEQ ID NO. 881
3'-GAACAAUUCUGAACUUAAGACA-5'	SEQ ID NO. 882
3'-UAAGAGAAUUAUACUUUUUCGU-5'	SEQ ID NO. 883
3'-UCUCUCUUUUUUUCUUUACCCUCA-5'	SEQ ID NO. 884
3'-UAUACCUACAUCUAAAAGUAAAC-5'	SEQ ID NO. 885
3'-UUGUAGAAUAAAAGGAAGAAAAG-5'	SEQ ID NO. 886
3'-AAAAUUCGGGAACGUUUCUUGA-5'	SEQ ID NO. 887
3'-GAAGUAAUUCACAAAAUAGCCUUCAGU- 5'	SEQ ID NO. 888
3'-ACGGACUGAAGUGCCGUAAA-5'	SEQ ID NO. 889
3'- UAAUAGAAUUCUUUCUAAUUUCUU-5'	SEQ ID NO. 890

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
CUUAAAC-5'	
3'-AGUUUCGUUUUAUCCAGUCUCG-5'	SEQ ID NO.891
3'-UUGAAAAUAACUAGGUCACGAGU-5'	SEQ ID NO.892
3'-UCUAUAGAAAGUUUUAAAAGUU-5'	SEQ ID NO.893
3'-UACGUUAGUUGUUACCCUUACAGUAAA-5'	SEQ ID NO.894
3'-UAAACAAUUAUAAAUAAAAGUAAA-5'	SEQ ID NO.895
3'-GUUGUAUUUUUAGUUGGUUAA-5'	SEQ ID NO.896
3'-	SEQ ID NO.897
AGGAGAAAAGAAAAGGAAAGAGGAAGAAA-5'	
3'-GUCUUUCGUCUAUACUUCUCCU-5'	SEQ ID NO.898
3'-AACGGACCCUUUCUCCGCUCA-5'	SEQ ID NO.899
3'-GUCUUUCGUCUAUACUUCUCCU-5'	SEQ ID NO.900
3'-AGAAAAGAAAAGGAAAGAGGAAGAAA-5'	SEQ ID NO.901
3'-	SEQ ID NO.902
CAGGAGAAAAGAAAAGGAAAGAGGAAGAAA-5'	
3'-GAAAAGAAAAGGAAAGAGGAAG-5'	SEQ ID NO.903
3'-GAGAAAAGAAAAGGAAAGAGGAAGAA-5'	SEQ ID NO.904
3'-AAUUUUCUUUAUGUCUAAAUA-5'	SEQ ID NO.905
3'-AGAGACUCAAUCUUUUACUCUUUCA-5'	SEQ ID NO.906
3'-GAAACGUAAUUUUUACACAAACU-5'	SEQ ID NO.907
3'-	SEQ ID NO.908
AAAAUAUACAGAUUUUUGAAUCUGU- GAUAU-5'	
3'-GAUGUCCUACAUCUAAAACUUUUUAU-5'	SEQ ID NO.909
3'-	SEQ ID NO.910
AGAAACAUAAGACCGAAAGGAAGAAAC- CAAC-5'	
3'-	SEQ ID NO.911
UCUUCUGUGUUUUUACACAAUUGU- GUUUUG-5'	
3'-AGUCACAAAAGACUGAGGUUCAA-5'	SEQ ID NO.912
3'-AUGGUUUUUUACUUUCGAGAAGACU- 5'	SEQ ID NO.913
3'-AAAUGAACGAAUACAUUGGAAUAAA-5'	SEQ ID NO.914
3'-AAAGAGAUAAAAGAGAACA AAAUUUG-5'	SEQ ID NO.915
3'-UUCUACUGAUAGAUUUUACAGUCC-5'	SEQ ID NO.916
3'-UAAGUGACGGAAGAAGGGAGAGU-5'	SEQ ID NO.917
3'-GACAGACGAUUGGUCUACUUGU-5'	SEQ ID NO.918
3'-UCUUUCAAGAUAGUUCttttt-5'	SEQ ID NO.919
3'-AAAGUUUAAGGAAGAGUCUUAAG-5'	SEQ ID NO.920
3'-UAAAACAUGUCUCCAAAAGUAUU-5'	SEQ ID NO.921
3'-	SEQ ID NO.922
UAACUAAUCUUUAAGUUGAACUUUUUA- GUUAC-5'	
3'-CCUACAGAAACAGAAAGAAAAGAAAC-5'	SEQ ID NO.923
3'-	SEQ ID NO.924
UGUGUUUCCUUUGAGUGACUGUUUUUG- 5'	
3'-CUGUGUCUACUUCUUUGAAGGAAA-5'	SEQ ID NO.925
3'-AUGUUGGGUUCUCUGAAUUUG-5'	SEQ ID NO.926
3'-UUUCUUACUUCUUUCCAGUCGU-5'	SEQ ID NO.927
3'-CACGAUAACUAGUCUGAUAAU-5'	SEQ ID NO.928
3'-CGACCUGACACCACUGUCGGAG-5'	SEQ ID NO.929
3'-GUUGGAGACGUGUUUUACUCGA-5'	SEQ ID NO.930
3'-UGUUACCUCGUACGUUCCUUCGU-5'	SEQ ID NO.931
3'-AUCGUCCAUCUAGGUUCUGUCUCUG-5'	SEQ ID NO.932
3'-UUUUACGACUUAUACCCGUU-5'	SEQ ID NO.933
3'-GUUAUUGGUUUCUUUUUUCUU-5'	SEQ ID NO.934
3'-UUAGUACUUCAACAAAAGGGGU-5'	SEQ ID NO.935
3'-UUCGUUGGUCCUUAACCAAGU-5'	SEQ ID NO.936
3'-UACGUUGACUCUAGUCUGUAG-5'	SEQ ID NO.937
3'-GGUCUCUGUUCUGAGAACA-5'	SEQ ID NO.938
3'-CUCUGUCUACCCACCUAGUUCU-5'	SEQ ID NO.939
3'-CUCUGUCUACCCACCUAGUUCUCCAG-5'	SEQ ID NO.940
3'-	SEQ ID NO.941
AACCGAUAAGAGACAAAAAAA- CAAAAAA-5'	
3'-CUCUGUCUACCCACCUAGUUCUCCAG-5'	SEQ ID NO.942
3'-GAGUAAGAGACAAAAAAAACAAAAAAA- 5'	SEQ ID NO.943

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-GAAAUAGAUAUUUUAUAAAAUUUA-5'	SEQ ID NO.944
3'-UACUCGGGUUCUGAAGAAAACUA-5'	SEQ ID NO.945
3'-UUCUUUGACACUAAAAUUUAUGAAU-5'	SEQ ID NO.946
3'-UUCUUACUAUUUCGUUUUUUU-5'	SEQ ID NO.947
3'-AUGAAAAUUUCUACGUACGAAAGUAA-5'	SEQ ID NO.948
3'-AAAAUUUUUACUAUUCUUUUUU-5'	SEQ ID NO.949
3'-UCUUACUAUUUCGUUUUUUACAUC-5'	SEQ ID NO.950
3'-AUGACUAGAGGUUGAGUCUUCU-5'	SEQ ID NO.951
3'-UUUUAAACUUUCUACUAUUUCGUUU-5'	SEQ ID NO.952
3'-	SEQ ID NO.953
UUUUUACUUAUUUUUAUCGUAAGAGAA- GUUUU-5'	
3'-UUUCGUUUUUUACUUUUUU-5'	SEQ ID NO.954
3'-GUUCUUUUUACUUUUUUUAU-5'	SEQ ID NO.955
3'-UCCUUUUUAGUUUUUUUGGUUAU-5'	SEQ ID NO.956
3'-CGUAAGUUUUUAUGUACGAC-5'	SEQ ID NO.957
3'-UACAUCUUGACAUUUAUU-5'	SEQ ID NO.958
3'-UUUUGUUUUUGGUUUUUCAUC-5'	SEQ ID NO.959
3'-	SEQ ID NO.960
UUUCCUUUUAGUUUUUUUGGUUUUUU-5'	
3'-AUCCUCGAGGGGUGAGGGCAAAACUCG- 5'	SEQ ID NO.961
3'-AUUAGUUUUUUUUACUUUAGUU-5'	SEQ ID NO.962
3'-CUAAUUUUAAUUAUUUUUUUUACUU- 5'	SEQ ID NO.963
3'-AUUAGUUUUUUUUACUUUAGUU-5'	SEQ ID NO.964
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.965
3'-AUUAGUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.966
3'-UACUGUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.967
3'-	SEQ ID NO.968
AUAUAGUUUUUUUUUUUUUUUUUUUUUU- CUCCU-5'	
3'-AUUAGUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.969
3'-	SEQ ID NO.970
AACUUUUUUUUUUUUUUUUUUUUUUUU- 5'	
3'-ACUUAUAGUAAAAGUUUUUUUUUU-5'	SEQ ID NO.971
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.972
3'-UCGAAUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.973
3'-	SEQ ID NO.974
UUUAGUUUUUUUUUUUUUUUUUUUUUU- GUAUG-5'	
3'-GUAUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.975
3'-UCGAAUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.976
3'-CUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.977
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.978
3'-UCUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.979
3'-	SEQ ID NO.980
UCGUUUUUUUUUUUUUUUUUUUUUUU- 5'	
3'-UCUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.981
3'-CUUCUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.982
3'-CUUCUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.983
3'-AUUCUAGUCUUUUUUUUUUUUUUUU-5'	SEQ ID NO.984
3'-AUUUGGUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.985
3'-UAAAAUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.986
3'-GUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.987
3'-	SEQ ID NO.988
AAAAAACCCAAAACAACAACUAUGAAA- CUC-5'	
3'-CGUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.989
3'-AUUGUCUGAACUUUUUUUUUUUU-5'	SEQ ID NO.990
3'-	SEQ ID NO.991
UAAUGGAAGUUUUUUUUUUUUUUUU- GAAUUUUUUUUUUUUUUUUUUUU-5'	
3'-UUUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.992
3'-GAAUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.993
3'-	SEQ ID NO.994
UAAUUUUUUUUUUUUUUUUUUUUUU- GAAAAU-5'	

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-UAAUUUCUUUUAUAAUUGUAACUGUAAU-5'	SEQ ID NO.995
3'-AAUACUUACAAAAUAGUACUAAUUUCUA-5'	SEQ ID NO.996
3'-GGGUCGUGUCUCUACAGUAAACU-5'	SEQ ID NO.997
3'-UCACUCUUUACUACUACAACUAGUCU-5'	SEQ ID NO.998
3'-AAGAUCCUUUCGUUGGUCUUC-5'	SEQ ID NO.999
3'-ACUCGUUCUUUAGGAGUUA-5'	SEQ ID NO.1000
3'-CCUACUCUUUCGUAUUUA-5'	SEQ ID NO.1001
3'-AAUCUUUACGAAUUCGUAACG-5'	SEQ ID NO.1002
3'-GUCCUGUAAUUUACUUCUCUUC-5'	SEQ ID NO.1003
3'-UUCUCUUUCUGGACUGGUUUCU-5'	SEQ ID NO.1004
3'-UGAUUCAGUAUAAUUUUUAGUUCUUUU-5'	SEQ ID NO.1005
3'-UUGUUAACUCAACUACUGUUACUUA-5'	SEQ ID NO.1006
3'-UAGUACAAAGUAUGAAGAUCCGUAAC-5'	SEQ ID NO.1007
3'-UUUUGUAUGAUUCUUGUGUCCU-5'	SEQ ID NO.1008
3'-AAAGUGGUAUUGGAAGAGAAGG-5'	SEQ ID NO.1009
3'-UCCUUCGUUUUAAUUGUCUCUUCUU-5'	SEQ ID NO.1010
3'-ACCUUUUACUUUCUGAAACCU-5'	SEQ ID NO.1011
3'-UUUUGUUGGAACCCAUUAGUCUGU-5'	SEQ ID NO.1012
3'-CGACGACCUGUCAGUACCAAA-5'	SEQ ID NO.1013
3'-CCUAGUUCUUUCUCUACAGAGACUCU-5'	SEQ ID NO.1014
3'-CCCCUCUGUGUUUAAAGUCUG-5'	SEQ ID NO.1015
3'-UGUUUACUUUUGGGUCGAGUUCUCAGU-5'	SEQ ID NO.1016
3'-UUUACUCUACACCCUUUGGUAC-5'	SEQ ID NO.1017
3'-UCUUUUAUCCUCUCAACCCGCG-5'	SEQ ID NO.1018
3'-UCUCUCUACUCGCCUUUACCU-5'	SEQ ID NO.1019
3'-CUGUAAGAAACCCGACCUUUCUGGAU-5'	SEQ ID NO.1020
3'-CUUCUCUGUCCCGUUCUAGUUUGAUCC-GA-5'	SEQ ID NO.1021
3'-UCCCGUUCGAAAAGGGUUUACAG-5'	SEQ ID NO.1022
3'-CCUGUACUAGGUCUCUCCUACUUGUUC-CUGUU-5'	SEQ ID NO.1023
3'-CCUUUAAACUUUUUAGUUACC-5'	SEQ ID NO.1024
3'-CUCAGAUGUAAGAGUCAAAACAG-5'	SEQ ID NO.1025
3'-CUCUGUCUGUCAUUCCUUUA-5'	SEQ ID NO.1026
3'-ACUUCUUUUUGAUUUUUUUU-5'	SEQ ID NO.1027
3'-GGUCUGUCGUCGACCUUCCGU-5'	SEQ ID NO.1028
3'-UUGUCCUUAGUAUAAUUUAAACA-5'	SEQ ID NO.1029
3'-UCAUACGUACUUUCUAAAAGAAUUAC-5'	SEQ ID NO.1030
3'-GUCUCAAAACUUAAAACUAGUC-5'	SEQ ID NO.1031
3'-ACUCCAUUGUAAAUAUAAACCC-5'	SEQ ID NO.1032
3'-AAAAAAGAAAACUCUUCCCGAAGUA-5'	SEQ ID NO.1033
3'-UCUUUUUGUUGUCCACAACUCUC-5'	SEQ ID NO.1034
3'-AAAAAAGAAAACUCUUUCCCGA-5'	SEQ ID NO.1035
3'-UUUACUUUCUAAAGGUCUUUAAAC-5'	SEQ ID NO.1036
3'-UGUUGCUAUGUUGUUUACGACCACUCUA-5'	SEQ ID NO.1037
3'-UCACUAAGUACGACUUUAGUCA-5'	SEQ ID NO.1038
3'-UACUCUCUAGAACCCACCUCUG-5'	SEQ ID NO.1039
3'-GGUUACAUAUUUAGUAAAUGUUCAU-5'	SEQ ID NO.1040
3'-UUCUAGUUACUCUUUCUUUAUACU-5'	SEQ ID NO.1041
3'-AUGAAUGUACGGUUUAGAGUU-5'	SEQ ID NO.1042
3'-UCAAGUUACUCUUUCUUUAU-5'	SEQ ID NO.1043
3'-AUGUAUGAAUUACACUAAAU-5'	SEQ ID NO.1044
3'-AAAACAGGAAGGUUAAACACAAC-5'	SEQ ID NO.1045
3'-CUUCGUCUCUCUUCAUCUCUUC-5'	SEQ ID NO.1046
3'-AGUUUUCUCUCUUGUCUACGACC-5'	SEQ ID NO.1047
3'-AGGGACCUACCGUUCGUCUUCGU-5'	SEQ ID NO.1048
3'-GUCCUGUAACUUUACUUCUCUUC-5'	SEQ ID NO.1049
3'-UUGUUCUCGUCGGUCACACCACC-5'	SEQ ID NO.1050
3'-AACUCUUUCCUUGGGACAUGU-5'	SEQ ID NO.1051
3'-GGUCCGUGACCCUACGACCCGU-5'	SEQ ID NO.1052

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-UUAAUCCUCACUAUGGAAGUGAUU-5'	SEQ ID NO.1053
3'-ACUCUUUUUCCGGUGACAGGAAAU-5'	SEQ ID NO.1054
3'-UGUUUAACCCUUUAUCACUUUU-5'	SEQ ID NO.1055
3'-AUAUUCUUUAUUGUGGAUACU-5'	SEQ ID NO.1056
3'-UUUCCUUUUUAAUUCUUGGGUCU-5'	SEQ ID NO.1057
3'-CUACAGUAGUUCUACGUCUACG-5'	SEQ ID NO.1058
3'-UGUUUUUCACGUCUUUCUCCGUUC-5'	SEQ ID NO.1059
3'-UUACAAUAAACUCAUAUAUCUCUCU-5'	SEQ ID NO.1060
3'-GUAACUACUAGACCGUAAGGUUGA-5'	SEQ ID NO.1061
3'-CUUCCUCCGACUAGGUUCUUGUCA-5'	SEQ ID NO.1062
3'-CCGUGUUGACCUCACCUCAGACGA-5'	SEQ ID NO.1063
3'-GUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO.1064
3'-AGUUUUACGAAGUUUACUUUU-5'	SEQ ID NO.1065
3'-UUAACUUGUUUUUGGGACUAUG-5'	SEQ ID NO.1066
3'-UACUCCUUACCUCCUUUAUCGA-5'	SEQ ID NO.1067
3'-UAACGAGGAAACGACCUACCUA-5'	SEQ ID NO.1068
3'-AAGUUUAGACUUACUACGUUGU-5'	SEQ ID NO.1069
3'-AUUUUCGACGUAUUUACCA-5'	SEQ ID NO.1070
3'-CCUCUAAACUAGGUUUUUGUCU-5'	SEQ ID NO.1071
3'-UCCCCUCCGGGUCUAGGACCU-5'	SEQ ID NO.1072
3'-ACGGUGUCUCCUCUGUGUUU-5'	SEQ ID NO.1073
3'-CUCUUUCCUUCACCUUUGU-5'	SEQ ID NO.1074
3'-GUUUUUGUUUUUUUUUUUUUUUU-5'	SEQ ID NO.1075
3'-UCCUCCUUUUUUGUUUUUUUA-5'	SEQ ID NO.1076
3'-CUCUUUACUCUUCUCCGAU-5'	SEQ ID NO.1077
3'-GACCUCGACGACCUCGUCGUC-5'	SEQ ID NO.1078
3'-AGAGUUUGAACGUCAACCAG-5'	SEQ ID NO.1079
3'-AACUGAUACCCUCACUACAAA-5'	SEQ ID NO.1080
3'-UCAACUUUAGUAACGACUUC-5'	SEQ ID NO.1081
3'-UUUUUUUUUUUAAAGAGGGUCAC-5'	SEQ ID NO.1082
3'-UGUCCACUACACAGGGGG-5'	SEQ ID NO.1083
3'-UUUACCUUGUUGUUGUCUUUG-5'	SEQ ID NO.1084
3'-UACAGAAGAAGUUAGUGAAGUU-5'	SEQ ID NO.1085
3'-AUGACGAUCCUUCGUGUUCUAC-5'	SEQ ID NO.1086
3'-UUUUUAAACUUUGUUGUUUAAG-5'	SEQ ID NO.1087
3'-UUUUUUUUGUUGUAAUUGGGAAA-5'	SEQ ID NO.1088
3'-UUCGUUCUAAUUUUUCUCUCCU-5'	SEQ ID NO.1089
3'-AAUCUCGUAAGACAACCUUCUA-5'	SEQ ID NO.1090
3'-UUGUCUCCGACUUGUUCUCCU-5'	SEQ ID NO.1091
3'-ACGUCUCCUUGUCCUUGCCG-5'	SEQ ID NO.1092
3'-UAACAUACCUUGUUAACUUUG-5'	SEQ ID NO.1093
3'-UACUUUUGCAGGACUUUUUGU-5'	SEQ ID NO.1094
3'-ACAAAAGAAAGACAGACUUCU-5'	SEQ ID NO.1095
3'-GUUAUUAAUCGUAGUGUA-5'	SEQ ID NO.1096
3'-UGUUUAGUCGUAACUUGACUAU-5'	SEQ ID NO.1097
3'-UUUCUCCAUUUUUUUUUU-5'	SEQ ID NO.1098
3'-UUCAUCGUCCGAGUGAGACG-5'	SEQ ID NO.1099
3'-UCUCCUCUCUCCUUUUACC-5'	SEQ ID NO.1100
3'-UGUUUAGGACGUCUUUACG-5'	SEQ ID NO.1101
3'-UUACUUAGUUGUUCUUUUUU-5'	SEQ ID NO.1102
3'-UUACUUAGUUGUUCUUUUUU-5'	SEQ ID NO.1103
3'-CUCUUACUUCUUUUUGAGG-5'	SEQ ID NO.1104
3'-UAAGUCACUUUAAACUUUUU-5'	SEQ ID NO.1105
3'-UCUUUAGUGGUUCUGGUGUAU-5'	SEQ ID NO.1106
3'-GAACUUGAAUUCUUCGUCUAU-5'	SEQ ID NO.1107
3'-UGUUACGAUAGUUAACUUAG-5'	SEQ ID NO.1108
3'-UGUUACGAUAGUUAACUUUA-5'	SEQ ID NO.1109
3'-CUUGAAGUCCUGUAUCUUUU-5'	SEQ ID NO.1110
3'-CGGAAGGAAAGGUCUUACAC-5'	SEQ ID NO.1111
3'-CUAUACUGAAACUUUCCUC-5'	SEQ ID NO.1112
3'-UCCCCAACUUACCCGACGUC-5'	SEQ ID NO.1113
3'-GUCUCAUCUUACGUUAAGAGGAGU-5'	SEQ ID NO.1114
3'-AAGGACGAAAUGGUUUACUGACU-5'	SEQ ID NO.1115
3'-AAAGUAUUACAGUCGUUUUAACGU-5'	SEQ ID NO.1116
3'-CCAGAUGUUUGUAUGAAACUUCU-5'	SEQ ID NO.1117
3'-GUUUUAAUCUCUCUGUCUUUUU-5'	SEQ ID NO.1118
3'-CUUCGUUUUGACAAACAG-5'	SEQ ID NO.1119

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-AACAAAAAUACACCUCGAUUAGU-5'	SEQ ID NO. 1120
3'-GUGUUUCCUGUUAUCCUUUCUUU-5'	SEQ ID NO. 1121
3'-AUUUUUUUAAACUUAGUCAUUUUUU-5'	SEQ ID NO. 1122
3'-UCACUCUGUGUCCUUGUCUUUU-5'	SEQ ID NO. 1123
3'-GUAUACUUUCUACACGUUGUAG-5'	SEQ ID NO. 1124
3'-AAGUUACUUAGUUGUUUUUUUUU-5'	SEQ ID NO. 1125
3'-GUCGUCUUAUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1126
3'-UCAACUUAUUUGUGACCAGACCA-5'	SEQ ID NO. 1127
3'-UCUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1128
3'-GAAGGGUCAAACCCUACACACCCUA-5'	SEQ ID NO. 1129
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1130
3'-UUAGUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1131
3'-UACGUCUUGAAAGAAAAACUGAG-5'	SEQ ID NO. 1132
3'-UGUAAAGAAAGUACACCCGUUUU-5'	SEQ ID NO. 1133
3'-GAUCAGUCCGUAUCGUCUACCA-5'	SEQ ID NO. 1134
3'-GUUUCGUCUUACGUAAGAGAA-5'	SEQ ID NO. 1135
3'-ACGUGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1136
3'-UCUCAUUUCUGUUGUACUGGU-5'	SEQ ID NO. 1137
3'-CCUUUAACCCUUAUACCUAAC-5'	SEQ ID NO. 1138
3'-UUACGGAAACAAAGAUUUUUU-5'	SEQ ID NO. 1139
3'-AUUCUCUAGUCUUACUCUUU-5'	SEQ ID NO. 1140
3'-UAGAGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1141
3'-UCUGUUUACGUAUUUUUUUUU-5'	SEQ ID NO. 1142
3'-UUUCGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1143
3'-AACAGACUCUUUACCGGACGA-5'	SEQ ID NO. 1144
3'-UAGUUACUUGUUUUUUUUUUU-5'	SEQ ID NO. 1145
3'-GUCUCUCUCCGUUUUUUUUUU-5'	SEQ ID NO. 1146
3'-GUGUUUAAUCUACUGUCUCU-5'	SEQ ID NO. 1147
3'-UUUGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1148
3'-AAAAAAGUUUACGUAAGAUUU-5'	SEQ ID NO. 1149
3'-GUCUUUAAGUUUUUUUUUUUUU-5'	SEQ ID NO. 1150
3'-GUCGUAUAGUCUGUUUUUUUU-5'	SEQ ID NO. 1151
3'-CCUGCCUAAUUUUUUUUUUUUU-5'	SEQ ID NO. 1152
3'-ACCUCACUAAUCCCUUUUUUU-5'	SEQ ID NO. 1153
3'-UGUCUAAACUUUUUUUUUUUUU-5'	SEQ ID NO. 1154
3'-ACGUACACAUUACCGAGAAC-5'	SEQ ID NO. 1155
3'-GAAAAGGACUUUACCGGUCGU-5'	SEQ ID NO. 1156
3'-UUCUGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1157
3'-GACGUAACUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1158
3'-GGUAAUAGGUUUCCAGAUUUUU-5'	SEQ ID NO. 1159
3'-ACUCUGAAGGUUUUAGUUUUU-5'	SEQ ID NO. 1160
3'-CGUCCUACCUUUUUUUUUUUUU-5'	SEQ ID NO. 1161
3'-UUUCGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1162
3'-ACGUCCUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1163
3'-AGUUUACGUACUUUUUUUUUUU-5'	SEQ ID NO. 1164
3'-UCUUCAAUUAUUUUUUUUUUU-5'	SEQ ID NO. 1165
3'-GACGGGUUUAACCUUCCGAGG-5'	SEQ ID NO. 1166
3'-UUAUGGUCGGAAGGUAAAGUUU-5'	SEQ ID NO. 1167
3'-UUACUUAGGUUUAGUUUUUU-5'	SEQ ID NO. 1168
3'-UACGGAACAAGAUUUUUUUUU-5'	SEQ ID NO. 1169
3'-ACUCAACGGUAAGUGGUAAAU-5'	SEQ ID NO. 1170
3'-UAUGUAACUUUUUUUUUUUUUU-5'	SEQ ID NO. 1171
3'-CACACUACUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1172
3'-UAUACGUGUUUUUUUUUUUUUU-5'	SEQ ID NO. 1173
3'-ACCUAAACAACGGUUUUUUUUU-5'	SEQ ID NO. 1174
3'-UAAUUAUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1175
3'-GGUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1176
3'-AUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1177
3'-UGUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1178
3'-UUUCGGUACCUUUUUUUUUUUU-5'	SEQ ID NO. 1179
3'-CCAGAUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1180
3'-UUUAACAAAGAAUUUUUUUUUU-5'	SEQ ID NO. 1181
3'-AAGUUCUACCUUUUUUUUUUUU-5'	SEQ ID NO. 1182
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1183
3'-UUGGAUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1184
3'-UGUUGGAUAAAGAGGUCUAAA-5'	SEQ ID NO. 1185
3'-UUUAAGUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1186

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-ACCAGUCCAAUAGACCGUAAA-5'	SEQ ID NO. 1187
3'-GUUGGACCUUGGACCUUGGA-5'	SEQ ID NO. 1188
3'-GGUCGUGACUCUCCACUGACA-5'	SEQ ID NO. 1189
3'-UUUUAGUUGGACUUACAAA-5'	SEQ ID NO. 1190
3'-AAUAGUUUUAUGAACGAUUAUG-5'	SEQ ID NO. 1191
3'-GAAAAGAAUUUUUUAAGGUCGCG-5'	SEQ ID NO. 1192
3'-UCUCUCCUAUAAGAGACCAG-5'	SEQ ID NO. 1193
3'-CCCCUCUGUGUUUAAGUCUG-5'	SEQ ID NO. 1194
3'-ACUAAUAACGACGAUCUUUGAU-5'	SEQ ID NO. 1195
3'-ACUAAUAACGACGAUCUUUGUA-5'	SEQ ID NO. 1196
3'-ACCUCUUUCGGUUCUAUUUUU-5'	SEQ ID NO. 1197
3'-UGUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1198
3'-UCCCGUUCGAAAGGGUUUACAGA-5'	SEQ ID NO. 1199
3'-UCCCGUUCGAAAGGGUUUACAG-5'	SEQ ID NO. 1200
3'-GGUUUUUAUGUAUGACCACCCU-5'	SEQ ID NO. 1201
3'-UCCGUUUACACACACACACAG-5'	SEQ ID NO. 1202
3'-AGUUUCUCUUUCUGUACUGGU-5'	SEQ ID NO. 1203
3'-UGAAACAUAAGGGUACUUAGG-5'	SEQ ID NO. 1204
3'-AAAGUCCGUCUACUUACGU-5'	SEQ ID NO. 1205
3'-UUUUGUGUCCUUGUCUUUU-5'	SEQ ID NO. 1206
3'-UUCUUUCUAGAGUAAACUCCU-5'	SEQ ID NO. 1207
3'-CUAUCUACCUUCUCUACUU-5'	SEQ ID NO. 1208
3'-GUAUACUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1209
3'-UAUUUAUGAUCAUCAUUGUAUU-5'	SEQ ID NO. 1210
3'-AACUGACUUUCUAGGUUACUU-5'	SEQ ID NO. 1211
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1212
3'-UACCUUUAAGAGAGAAUACU-5'	SEQ ID NO. 1213
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1214
3'-UUCGUUGGUUUUUUUUUUUUUU-5'	SEQ ID NO. 1215
3'-GGUCUCCGUUCUCGAGAACA-5'	SEQ ID NO. 1216
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1217
3'-GACAUUACUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1218
3'-CCUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1219
3'-AAAACGAAACAACAACAAACGAC-5'	SEQ ID NO. 1220
3'-UCCUGAAGCUCUUUUUUUUUUUU-5'	SEQ ID NO. 1221
3'-UUUGUUGUAUUUUUUUUUUUUU-5'	SEQ ID NO. 1222
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1223
3'-AAAGUGGUAUUGGAAAGAGAGG-5'	SEQ ID NO. 1224
3'-AGAAUUAAAGAAGUCUCUGUU-5'	SEQ ID NO. 1225
3'-UCUCUUUUUAUGAACUUUUUUUU-5'	SEQ ID NO. 1226
3'-UGUCUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1227
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1228
3'-CUGAUGUCUUAUUGUAUUUUUU-5'	SEQ ID NO. 1229
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1230
3'-AUCUAUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1231
3'-AGUCUGUCGACGGGUCUCCGU-5'	SEQ ID NO. 1232
3'-UGAAUGGUCAGAUAGAAGAU-5'	SEQ ID NO. 1233
3'-AAAAGAUAGGGAGUCUUUUAGG-5'	SEQ ID NO. 1234
3'-GAAACUAGAGCCGAACUCU-5'	SEQ ID NO. 1235
3'-AGAGAGACGGAACAUAACC-5'	SEQ ID NO. 1236
3'-AUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1237
3'-UCUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1238
3'-AAGUCUGUCUAGUCUGGAGU-5'	SEQ ID NO. 1239
3'-UUUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1240
3'-UUCAGUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1241
3'-ACUUUUUUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1242
3'-CCCCCAAGAAAAACUUUUUU-5'	SEQ ID NO. 1243
3'-CUCUACCGGUUCCACCCUCU-5'	SEQ ID NO. 1244
3'-AAAAUUGGUUUUAUCAUCUCC-5'	SEQ ID NO. 1245
3'-CACGAGGAGUACUUUUACAGACA-5'	SEQ ID NO. 1246
3'-AUGGUGGAAUUUUUUUUUUUU-5'	SEQ ID NO. 1247
3'-GAGUCGGUAAUUUUUUUUUUU-5'	SEQ ID NO. 1248
3'-UAACGUCUUUUUUUUUUUUUUUU-5'	SEQ ID NO. 1249
3'-UCUGACCUUGGUCGAUACCUUAG-5'	SEQ ID NO. 1250
3'-UACAUUAGUGGAAUUGUACUU-5'	SEQ ID NO. 1251
3'-CCUUCUGAACCAUUUCAAAG-5'	SEQ ID NO. 1252
3'-UUUAGGACUCCGUAAGUUGUA-5'	SEQ ID NO. 1253

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-CAGACAGUAGAGUGACCUAG-5'	SEQ ID NO. 1254
3'-ACCCGUGUCAACAGUGACGA-5'	SEQ ID NO. 1255
3'-UUUGUAAAGCUCUGUCCUAUC-5'	SEQ ID NO. 1256
3'-ACAUUAAAGAUCCGACUCAGA-5'	SEQ ID NO. 1257
3'-GGUCCUUUCAGAAGUCUCCUA-5'	SEQ ID NO. 1258
3'-AUUUUCUAGAAAAGAACAGA-5'	SEQ ID NO. 1259
3'-UCUGUUUAUCCAGUCCUCU-5'	SEQ ID NO. 1260
3'-UCUGUUGUGGUGAGGAAGA-5'	SEQ ID NO. 1261
3'-AUCCAAGUUCAGACGGUCUAUGU-5'	SEQ ID NO. 1262
3'-GAAUGGUCAGAGUAGAAGAUG-5'	SEQ ID NO. 1263
3'-CCGGAACGAGAAGUCUCUCC-5'	SEQ ID NO. 1264
3'-GUACGUCGAUCUUGGUACUG-5'	SEQ ID NO. 1265
3'-CCCCUUCUUUACCAUCCGU-5'	SEQ ID NO. 1266
3'-UGUCCUAUCUCGUCUAAAAA-5'	SEQ ID NO. 1267
3'-AACUUUUACUUGGAACUACU-5'	SEQ ID NO. 1268
3'-GUACUCGUUCUAGAAACAGUU-5'	SEQ ID NO. 1269
3'-AGAACACUGUAAAAUGGUUA-5'	SEQ ID NO. 1270
3'-GUCCUUGUGUUCUUGGUUUC-5'	SEQ ID NO. 1271
3'-AAGUGUAAAUUUUUACUUAU-5'	SEQ ID NO. 1272
3'-GACAACCUUACCGUCCUAC-5'	SEQ ID NO. 1273
3'-UUCACCUCUUGAGUCUAAA-5'	SEQ ID NO. 1274
3'-CGUAAAACCUCCAUAGAACG-5'	SEQ ID NO. 1275
3'-GAGAUAAAAGAACGUAACAC-5'	SEQ ID NO. 1276
3'-UUCUUCUCUGGUACACAUAUA-5'	SEQ ID NO. 1277
3'-UAUUACGUAACCUUCCAU-5'	SEQ ID NO. 1278
3'-GAUACUUCAGUAGUUUAUA-5'	SEQ ID NO. 1279
3'-AAGAGUAAAAACAACAAUAAA-5'	SEQ ID NO. 1280
3'-UAUUGUCUGGAUAUUGAAUA-5'	SEQ ID NO. 1281
3'-UCUCUCUGUGUCCGAUUCU-5'	SEQ ID NO. 1282
3'-AAUCAGGUCUCGUCUUUU-5'	SEQ ID NO. 1283
3'-GUGACGGAGAAGUCGUUAGU-5'	SEQ ID NO. 1284
3'-AUACUUCAGUAGUUUAUA-5'	SEQ ID NO. 1285
3'-GUAUUUUUUCACUUAUUAU-5'	SEQ ID NO. 1286
3'-UCUCUCGUAGGUUCCUCAC-5'	SEQ ID NO. 1287
3'-UUUUUAACAUGGUCCACACU-5'	SEQ ID NO. 1288
3'-UUGUACUCGUUCUAGAAACA-5'	SEQ ID NO. 1289
3'-UUAGUGUAAAGAAUGGUCUU-5'	SEQ ID NO. 1290
3'-GGAGUGAGAAUAAAGUAGGU-5'	SEQ ID NO. 1291
3'-GUAAGUAGAAACAUCCUACGA-5'	SEQ ID NO. 1292
3'-UAGUCUUCCGAAAUUACUG-5'	SEQ ID NO. 1293
3'-ACAUAAAUUUUUCUGUCCA-5'	SEQ ID NO. 1294
3'-GAGUAAAAACAACAAUAAA-5'	SEQ ID NO. 1295
3'-ACGGUUCGAAACAGUUGU-5'	SEQ ID NO. 1296
3'-ACCCGAGACUGUCCUCGUAC-5'	SEQ ID NO. 1297
3'-UUCAAUUAAUGGAAUUGUA-5'	SEQ ID NO. 1298
3'-AUGAUACUACUAGAUAGAU-5'	SEQ ID NO. 1299
3'-UCCUCCUACAAGAAGACAUA-5'	SEQ ID NO. 1300
3'-CUUGGGUCUCCUUGGGGGUG-5'	SEQ ID NO. 1301
3'-GUGACGGAGGAAGUCGUUAGU-5'	SEQ ID NO. 1302
3'-UCUCGAGUUUCCUCUGUU-5'	SEQ ID NO. 1303
3'-UUCUCCCCGAGGAGAUACUU-5'	SEQ ID NO. 1304
3'-AGAUGACGAAAUCCACUGCA-5'	SEQ ID NO. 1305
3'-UCUACCACCUAGUUCUCCA-5'	SEQ ID NO. 1306
3'-UUGCCACUGCUCGACUCCU-5'	SEQ ID NO. 1307
3'-GUCUCCUACUAAAAGACAG-5'	SEQ ID NO. 1308
3'-GUGUAGGUGACGGAGGAAGU-5'	SEQ ID NO. 1309
3'-UCCUACAGAACACUGUAAAAA-5'	SEQ ID NO. 1310
3'-GAAGUCUUUCGUUCAGUAAGAU-5'	SEQ ID NO. 1311
3'-AUGUAGUUCGGUAUUUUUAC-5'	SEQ ID NO. 1312
3'-AAUGACUCACGUCCCGGGACU-5'	SEQ ID NO. 1313
3'-AGUUAAAAGGGUUGGGAGGU-5'	SEQ ID NO. 1314
3'-GUCUCCUGUCCUCCUCCA-5'	SEQ ID NO. 1315
3'-UCAGUCUUGAACCUUACUCUA-5'	SEQ ID NO. 1316
3'-AGUUUCUAAUCUCAGUUGUCU-5'	SEQ ID NO. 1317
3'-GUACUUGACCCAUUGUUCAA-5'	SEQ ID NO. 1318
3'-GACUACUGUACGACCUUCU-5'	SEQ ID NO. 1319
3'-ACCAGUGCAAGUUAGAGUA-5'	SEQ ID NO. 1320

TABLE 2-continued

Antisense sequence listing of the target of the RNA virus	
Antisense fragment coding sequence	ID number
3'-AAUACUUCUGACAAGUCCUGA-5'	SEQ ID NO. 1321
3'-GACCACCUCUAUUUUGCAUGACU-5'	SEQ ID NO. 1322
3'-AACUAACAAAAAGAGUAAAA-5'	SEQ ID NO. 1323
3'-ACCAAAGACCCCGACACGGAG-5'	SEQ ID NO. 1324
3'-CUCGGUCCCGUCCUCUGUCG-5'	SEQ ID NO. 1325
3'-CCCAAGAAAAACUUUUUUU-5'	SEQ ID NO. 1326

[0029] The second object of the present invention is to provide a primer composition for constructing any of the above-mentioned target sequences of the RNA virus.

[0030] Further, The primer composition of a part of the target sequence of the RNA virus comprises any one or more of the following groups: the primers of the target sequence SEQ ID NO. 1 are SEQ ID NO. 616 - SEQ ID NO. 619; and/or, the primers of the target sequence SEQ ID NO. 2 are SEQ ID NO. 620 - SEQ ID NO. 623; and/or, the primers of the target sequence SEQ ID NO. 3 are SEQ ID NO. 624 - SEQ ID NO. 627; and/or, the primers of the target sequence SEQ ID NO. 4 are SEQ ID NO. 628 - SEQ ID NO. 631; and/or, the primers of the target sequence SEQ ID NO. 5 are SEQ ID NO. 632 - SEQ ID NO. 635; and/or, the primers of the target sequence SEQ ID NO. 7 are SEQ ID NO. 636 - SEQ ID NO. 639; and/or, the primers of the target sequence SEQ ID NO. 8 are SEQ ID NO. 640 - SEQ ID NO. 643; and/or, the primers of the target sequence SEQ ID NO. 10 are SEQ ID NO. 644 - SEQ ID NO. 647; and/or, the primers of the target sequence SEQ ID NO. 11 are SEQ ID NO. 648 - SEQ ID NO. 651; and/or, the primers of the target sequence SEQ ID NO. 12 are SEQ ID NO. 652 - SEQ ID NO. 655; and/or, the primers of the target sequence SEQ ID NO. 13 are SEQ ID NO. 656 - SEQ ID NO. 659; and/or, the primers of the target sequence SEQ ID NO. 14 are SEQ ID NO. 660 - SEQ ID NO. 663; and/or, the primers of the target sequence SEQ ID NO. 15 are SEQ ID NO. 664 - SEQ ID NO. 667; and/or, the primers of the target sequence SEQ ID NO. 16 are SEQ ID NO. 668 - SEQ ID NO. 671; and/or, the primers of the target sequence SEQ ID NO. 17 are SEQ ID NO. 672 - SEQ ID NO. 675; and/or, the primers of the target sequence SEQ ID NO. 18 are SEQ ID NO. 676 - SEQ ID NO. 679; and/or, the primers of the target sequence SEQ ID NO. 19 are SEQ ID NO. 680 - SEQ ID NO. 683; and/or, the primers of the target sequence SEQ ID NO. 20 are SEQ ID NO. 684 - SEQ ID NO. 687; and/or, the primers of the target sequence SEQ ID NO. 21 are SEQ ID NO. 688 - SEQ ID NO. 691; and/or, the primers of the target sequence SEQ ID NO. 22 are SEQ ID NO. 692 - SEQ ID NO. 695; and/or, the primers of the target sequence SEQ ID NO. 23 are SEQ ID NO. 696 - SEQ ID NO. 699; and/or, the primers of the target sequence SEQ ID NO. 24 are SEQ ID NO. 700 - SEQ ID NO. 703; and/or, the primers of the target sequence SEQ ID NO. 25 are SEQ ID NO. 704 - SEQ ID NO. 707; and/or, the primers of the target sequence SEQ ID NO. 26 are SEQ ID NO. 708 - SEQ ID NO. 711.

[0031] Further, The protective base and EcoRI restriction site sequence CGGAATTC are added to 5' end of the upstream primer, and the protective base and BamHI restriction site sequence CGGGATCC are added to 5' end of the downstream primer.

[0032] Further, the specific sequences of the above-mentioned primers are shown in the following table:

TABLE 3

Amplification primer sequence listing of the target sequence of the RNA virus				
Virus type	Fragment number	Primer number	Amplification primer sequence	ID number
Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2)	SARS-CoV-2-HIS-1	F1-23	5'-attctagagctagcgaattctcatcaactgtatgatgtttacaacagtaatagagca-3'	SEQ ID NO. 616
		R1	5'-gaccttctaaccaccattaacaatagtgtacattcgactctgttctctattacgtt-3'	SEQ ID NO. 617
		R2	5'-gtagtttgcacaaagcctttacctccattagcatagacataaaaggacctctacaacca-3'	SEQ ID NO. 618
	SARS-CoV-2-HIS-2	F1-23	5'-attctagagctagcgaattcaacaacattatcaacaatgcaagagatggttggcttc-3'	SEQ ID NO. 620
		R1	5'-aacattagtttgctgctgtgtgtgagggtattatgttcaagggaacacaaccatctc-3'	SEQ ID NO. 621
		R2	5'-gtaccatcacacgtatftttatgtgttagtctgtgtatgacaaccattagittggc-3'	SEQ ID NO. 622
	SARS-CoV-2-HIS-3	F1-23	5'-attctagagctagcgaattccttaacaaggtttagtagtaacactactaactagttaca-3'	SEQ ID NO. 624
		R1	5'-aagaataaaggcatataattagtacaacaacggtttaaacaccgttaactatggtagt-3'	SEQ ID NO. 625
		R2	5'-aatgttacttctagtaaaagtacacaattgtagcaataaagtaaaagataaggcata-3'	SEQ ID NO. 626
	SARS-CoV-2-HIS-4	F1-23	5'-attctagagctagcgaattcggagtagcagatcagtgtagcagaactgtagggaga-3'	SEQ ID NO. 628
R1		5'-actaaaataattttacacattaggctcttccatagtagcagctctccctagcatgtt-3'	SEQ ID NO. 629	
R2		5'-gtcattctcctaagaagctatataaaatcacatgggatagcactactaataaattattt-3'	SEQ ID NO. 630	
SARS-CoV-2-HIS-5	F1-23	5'-attctagagctagcgaattcgttaataaattggttgaagcagtttaataaagtatacctt-3'	SEQ ID NO. 632	
	R1	5'-acaggtgttattaataagaataatagcagcaacaaaaggacacaagtgttaactttaat-3'	SEQ ID NO. 633	
	R2	5'-ctatgatttcacttgaagaagcagtagtttagacatgacatgaacaggtgtattaaa-3'	SEQ ID NO. 634	
severe acute respiratory syndrome-related coronavirus SARS-CoV	SARS-CoV-HIS-1	F1	5'-ctccctctggaatttgctgctcagcgtgaacagttcaggttgaagaagaagaaggga-3'	SEQ ID NO. 636
		R1	5'-tggctcaatctctgattgctcagtagtatcatccagcagctctctctctctt cct-3'	SEQ ID NO. 637
		F2	5'-attctagagctagcgaattcctcctctggaatttgggtgc-3'	SEQ ID NO. 638
SARS-CoV-HIS-2	R2	5'-tccttcgcccgcggatcatggctcaatctgattgtc-3'	SEQ ID NO. 639	
	F1	5'-tatgggttgggattatcacaatgtgacagagccatgctcaacatgcttaggataatgg-3'	SEQ ID NO. 640	
		R1	5'-aagttacagcaagttgatgttggc	SEQ ID

TABLE 3-continued

Amplification primer sequence listing of the target sequence of the RNA virus					
Virus type	Fragment number	Primer number	Amplification primer sequence	ID number	
Middle East respiratory syndrome coronavirus (MERS-CoV)	MERS-CoV-HIS-1	F1	5'-gtgttgctgacctgctgcttaccctcttctgctcttaccattgacacagatattc-3'	SEQ ID NO. 644	
		R1	5'-gaaagaaccttggatgtaaccacaccgttlaacctataaaagatactctgtgcata-3'	SEQ ID NO. 645	
	MERS-CoV-HIS-2	F1	5'-aataaagtaaaaacgtcttttcagattacaccagtgctgttaattgctgtgttgc-3'	SEQ ID NO. 648	
		R1	5'-gtatagaggttaacaagcagatgcacaagctataagaacagcagcaacaacagcaatt-3'	SEQ ID NO. 649	
	Zika virus	Zika-HIS-1	F1	5'-tgagagagagatgcccaggtgtgtgtacacatgatgggaaaagagaaaa-gaaa caa-3'	SEQ ID NO. 652
		Zika-HIS-2	F1	5'-gtgatcaaaaatgggattatgtagtgccatcaccaaggagaggaggagga-gagac-3'	SEQ ID NO. 656
Ebola virus	Ebola-HIS-1	F1	5'-aaactaccacaacagatgatgataagctctaccgactcattctaccatttttaaa-3'	SEQ ID NO. 664	
		R1	5'-ttctgggcattctgatcatgtgcatggttggatttcccaatttaaaaatggtagaa-3'	SEQ ID NO. 665	
		F2	5'-gaagattctagagctagcgaattcctactcaccacaacagatgat-3'	SEQ ID NO. 666	
	Ebola-HIS-2	F1	5'-ttttcaaatccagaagaatgtttttatcgaacttcggagatccttctgacttctggac-3'	SEQ ID NO. 668	
		R1	5'-tctttatgttaaccattctaggtacaccgttagctggaanaagtcagaagtcacagg-3'	SEQ ID NO. 669	
			F2	5'-gaagattctagagctagcgaattcct	SEQ ID

TABLE 3-continued

Amplification primer sequence listing of the target sequence of the RNA virus				
Virus type	Fragment number	Primer number	Amplification primer sequence	ID number
Ebola-HIS-3	R2		ttcataatccagaaaagtg-3'	NO. 670
			5' -cagatccttcgcccgcggatcctc ttcatgtaaccattct-3'	SEQ ID NO. 671
	F1		5' -gaagattctagagctagcgaattcag atctgagagagaaaaatctc-3'	SEQ ID NO. 672
	R1		5' -cagatccttcgcccgcggatccta tttaattgctcattaa - 3'	SEQ ID NO. 673
	F2		5' -agatctgagagagaaaaatctcaggg ttacttaaggagaaaatatttttaaaa ttt- 3'	SEQ ID NO. 674
	R2		5' -tattattaattgctcatttaagataa gtggcagcattcaagtaattttaaaaaa aat-3'	SEQ ID NO. 675
HIV	HIV-1-HIS-1	F1	5' -tftaagaccaatgacttacaaggcag ctgtagatcttagccacttttaaaagaaa agg-3'	SEQ ID NO. 676
		R1	5' -atatctgtctctttgggagtgat tagccctccagctcccctttcttttaa aaa-3'	SEQ ID NO. 677
		F2	5' -gaagattctagagctagcgaattctt taagaccaatgactfaca-3'	SEQ ID NO. 678
HIV-1-HIS-2	R2		5' -cagatccttcgcccgcggatccat atctgtctctttggga-3'	SEQ ID NO. 679
	F1		5' -aagaaaaataaaagcattagtagaa attgtacagagatggaaaagaggga att-3'	SEQ ID NO. 680
	R1		5' -caaactggagatgtatggaatt tcaggeccaattttgaaatttccctcc ttt- 3'	SEQ ID NO. 681
HIV-1-HIS-3	F2		5' -gaagattctagagctagcgaattcaa gaaaaataaaagcatta-3'	SEQ ID NO. 682
			5' -cagatccttcgcccgcggatccca aatactggagattgtat-3'	SEQ ID NO. 683
	F1		5' -ggctctctgctggatgggtaccgac acaaaaggaattggagaaatgaacaagtag ata-3'	SEQ ID NO. 684
	R1		5' -ccatctaaaaatagcttctctgat tcagcactgactaatttactactgttc att- 3'	SEQ ID NO. 685
	F2		5' -gaagattctagagctagcgaattccc tctatctggcatgggtac-3'	SEQ ID NO. 686
	R2		5' -cagatccttcgcccgcggatccccc atctaaaaatagctactt-3'	SEQ ID NO. 687
HIV-1-HIS-4	F1		5' -cctgagtgaggatttgaatacccc tccttagtgaanaattggtaccagttaga gaa-3'	SEQ ID NO. 688
	R1		5' -tgccccatctacatagaaggtttctg ctcctactatgggtttcttactactgtg acc-3'	SEQ ID NO. 689
	F2		5' -gaagattctagagctagcgaattccc tgagtggaggttttaat-3'	SEQ ID NO. 690
HIV-1-HIS-5	R2		5' -cagatccttcgcccgcggatcctg cccctctacatagaagg-3'	SEQ ID NO. 691
	F1		5' -ggagaaatagatcgaatgggaaaaaat tcggttaaggccaggggaaagaaaaaa- ta taa-3'	SEQ ID NO. 692
	R1		5' -gaactgttctagctccctgcttccc atactatagttttaattatattttct ttc-3'	SEQ ID NO. 693
HIV-1-HIS-6	F2		5' -gaagattctagagctagcgaattcgg agaattagatcagatggga-3'	SEQ ID NO. 694
	R2		5' -cagatccttcgcccgcggatccga atcgttctagctccctgc-3'	SEQ ID NO. 695
	F1		5' -cagaagcagggcgaagccaatggac atacaaatatcaagaccattfaaaaa tct-3'	SEQ ID NO. 696
		R1	5' -attagtgtggcaccctcattctg catatttctgttttcagatttttaaatg get- 3'	SEQ ID NO. 697
		F2	5' -gaagattctagagctagcgaattcca gaagcagggcgaaggcca-3'	SEQ ID NO. 698
		R2	5' -cagatccttcgcccgcggatccat tagtgtggcaccctca-3'	SEQ ID NO. 699

TABLE 3-continued

Amplification primer sequence listing of the target sequence of the RNA virus					
Virus type	Fragment number	Primer number	Amplification primer sequence	ID number	
HIV-2-HIS-1	F1		5' -aagtggtcagaagaagtaaccaaac taacatcttagacataaaaacagggacaaa aga-3'	SEQ ID NO. 700	
			5' -cctcaagctttttagaaccgtctta catagctttgaacggtttttgtccct ggt-3'	SEQ ID NO. 701	
	F2		5' -gaagattctagagctagcgaattcaa gtgtgtcagaagtacaa-3'	SEQ ID NO. 702	
	R2		5' -cagatccttcgcccgcggatccccc tcaagcttttgaagacc-3'	SEQ ID NO. 703	
	HIV-2-HIS-2	F1		5' -caaagccaggagtagtagaagcaat gaatcaccacctaagaatcagataagtag aat-3'	SEQ ID NO. 704
		R1		5' -tgccatcagctactattgtttctattg tatttgcctgttcttaattctactatgat- 3'	SEQ ID NO. 705
HIV-2-HIS-3	F2		5' -gaagattctagagctagcgaattcca aagccaggagtagtaga-3'	SEQ ID NO. 706	
			5' -cagatccttcgcccgcggatcctg ccatcagctactattgtt-3'	SEQ ID NO. 707	
	F1		5' -gggtggctgtggaagctagatcag agaactctcaagaaggcaggaagat- ga ggc-3'	SEQ ID NO. 708	
	R1		5' -atcatcatgtctctgtttgtctg ggtgtactaagcagttggccatcttctc ctg-3'	SEQ ID NO. 709	
	F2		5' -gaagattctagagctagcgaattcgg gtggctgtggaagctag-3'	SEQ ID NO. 710	
	R2		5' -cagatccttcgcccgcggatccat catcatgtctgtcttt-3'	SEQ ID NO. 711	

[0033] In the third aspect, the present invention provides an RNA drug against viruses, characterized in that, the RNA drug comprises the reverse complementary sequence of any of the above-mentioned target sequences of the RNA virus, and cholesterol modification and four phosphorothioate backbone modifications are made at the 3' end of the reverse complementary sequence of any of the above-mentioned target sequences of the RNA virus, two phosphorothioate backbone modifications are made at the 5' end, and methoxy modification is made on the whole chain, or, cholesterol modification and four phosphorothioate backbone modifications are made at the 3' end of any of the above-mentioned target sequences of the RNA virus, two phosphorothioate backbone modifications are made at the 5' end, and methoxy modification is made on the whole chain.

[0034] Further, the reverse complementary sequence of the target sequence of the RNA virus comprises reverse complementary RNA sequence or reverse complementary DNA.

[0035] Further, the RNA drug further comprises a pharmaceutically acceptable carrier or excipient.

[0036] Further, the dosage form of the RNA drug comprises powder, tablet, granule, capsule, solution, aerosol, injection, emulsion or suspension.

[0037] In the fourth aspect, the present invention provides a biomaterial related to any of the above-mentioned target sequences of the RNA virus. The biomaterial is selected from one of the following A) - B):

[0038] A) a DNA and/or RNA molecule that is complementary to any of the above-mentioned target sequences of the RNA virus;

[0039] B) an expression cassette, a recombinant vector, a recombinant microorganism, a recombinant cell line containing any of the above-mentioned target sequences of the RNA virus or the DNA molecule described in A).

[0040] It is understandable that the above-mentioned DNA molecule, expression cassette, recombinant vector, recombinant microorganism, and recombinant cell line can all be biomaterials conventionally used in the art, and can all be prepared by conventional methods in the art.

[0041] Further, the biomaterial is a recombinant vector, and the construction steps of the recombinant vector comprise: 1) designing a primer, and amplifying the target sequence of the RNA virus by PCR; 2) digesting the amplified sequence fragment and an expression vector, and ligating a sequence fragment of interest and the expression vector; 3) transferring the ligated product into *Escherichia coli* and cultivating the *Escherichia coli*; 4) after identification, extracting recombinant plasmid and packaging the recombinant plasmid. Specifically, the target sequences of the RNA viruses are shown in Table 1 above, and a part of primer sequences is shown in Table 2 above.

[0042] Further, the expression vector comprises but is not limited to pCDH vector, other vectors such as pCMVp-NEO-BAN vector, pEGFP vector, pEGFP-Actin, pSV2 vector, pCDNA vector, pLVX vector, pAAV vector, pET vector, pDsRed vector, and virus-related recombinant vector backbones for these vectors can be any suitable vectors used in the art.

[0043] Further, the recombinant vector has the function of expressing a virus-related target fragment; wherein, the related target fragment has the function of interacting (binding) with human genome.

[0044] Further, the recombinant vector has target sequences expressing severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), severe acute respiratory syndrome-related coronavirus (SARS-CoV), and middle east respiratory syndrome coronavirus (MERS-CoV). The above-mentioned target sequence fragments can interact (bind) with human genome; specifically, the target sequences comprise but are not limited to: SARS-CoV-2-HIS-1, SARS-CoV-2-HIS-2, SARS-CoV-2-HIS-3, SARS-CoV-2-HIS-4, SARS-CoV-2-HIS-5, SARS-CoV-HIS-1, SARS-CoV-HIS-2, MERS-CoV-HIS-1 and MERS-CoV-HIS-2.

[0045] In the fifth aspect, the present invention provides use of any of the above-mentioned target sequences of the RNA virus. The use is a use in the preparation of an RNA virus detection or diagnostic reagent, a use in the preparation of a drug for preventing or treating a condition caused by an RNA virus, or a use in the preparation of a vaccine against an RNA virus.

[0046] Further, the condition comprises a human disease, an animal disease and zoonosis.

[0047] Further, when the use is a use in the preparation of a drug for preventing or treating a condition caused by the RNA virus, an effective substance that regulates the target sequence is directly screened; alternatively, according to the effect of the gene regulated by the target sequence, an effective substance against the gene and gene product regulated by the target sequence is screened.

[0048] Further, when the use is a use in the preparation of a vaccine against the RNA virus, the target sequence is knocked out during the design process of the vaccine.

[0049] Further, the method for knocking out the target sequence comprises: CRASPER system and/or ribozyme technology.

[0050] CRISPR comes from the immune system of microorganisms. In such engineering editing system, an enzyme is used to cut a small RNA as a guiding tool into DNA, where cut or other changes can be made. Previous studies have shown that CRISPR can make changes or mutations in the genome more efficiently through these interventions, and the efficiency is higher than other gene editing technologies such as TALEN (transcription activator-like effector nucle-ase). Although CRISPR has many advantages, in the human cancer cell line, it may also produce a large number of “accidentally injured targets”, especially the modification of genes that are not desired to be changed.

[0051] Ribozyme technology is a technology by means of a ribozyme, and is mainly used for the design of ribozymes for use. Ribozymes are RNA molecules that can cleave RNA sequence-specifically and can be designed. The designed ribozyme can be used to select specific mRNA fragments, or can bind to specific mRNA to block the expression of mRNA. Therefore, this technology can be used to study the structure of RNA, and can also be used to treat diseases caused by abnormal gene expression.

[0052] Further, the vaccine is a live attenuated vaccine.

[0053] In the sixth aspect, the present invention provides a live attenuated vaccine. The whole genome of the live attenuated vaccine does not contain the above-mentioned target sequences of the RNA virus.

[0054] In the seventh aspect, the present invention provides use of any of the above-mentioned target sequences of the RNA virus in activating related genes at the cellular level and screening therapeutic drugs against the related genes.

[0055] Further, the RNA virus is a coronavirus, specifically severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), severe acute respiratory syndrome-related coronavirus (SARS-CoV), and middle east respiratory syndrome coronavirus (MERS-CoV).

[0056] Further, in the above-mentioned use, the related genes comprise the ACE2 gene, the coding genes of the hyaluronic acid synthase family HAS1, HAS2, and HAS3, and/or genes within 200 k around the fragment. Further, the genes within 200 k around the fragment comprise but are not limited to FBXO15, MYL9, KALRN, ATP8B1, ZHX2, IGF2R, C5AR1, EPAS1 and TIMM21. It is understandable that, depending on the type of RNA virus, the related genes activated thereby are also different.

[0057] Further, the drug comprises a miRNA inhibitor.

[0058] Further, the miRNA inhibitor comprises antagomir inhibitor.

[0059] It is understandable that the above-mentioned drug may also comprise other drugs that can inhibit activated target genes and other drugs that can regulate the level of hyaluronic acid (inhibit the synthesis of hyaluronic acid, reduce the concentration of hyaluronic acid, etc.).

[0060] In the eighth aspect, the present invention provides use of the target sequences of the RNA virus in the study of drug targets against diseases caused by the RNA virus.

[0061] Further, the target sequences of the RNA virus in the cells of the diseases caused by the RNA virus are found, and the drug targets are found within 200 k around the target sequence of the RNA virus or the drug targets are found

beyond 200 k using the prediction software blast 2.2.30 or bedtools 2.29.2.

[0062] In the ninth aspect, the present invention provides a method for virus detection, which detects the above-mentioned target sequences of the RNA virus.

[0063] Further, the detection of the target sequences comprises RCR amplification and nucleotide sequencing.

[0064] Furthermore, the detection of the target sequences of the RNA virus can be used to determine the diagnosis of viral diseases, determine the pathogenicity and test the susceptibility of the population.

BRIEF DESCRIPTION OF THE DRAWINGS

[0065] FIG. 1 is a running gel electropherogram of 6 target viral vectors related to the coronavirus SARS-CoV-2 amplified by PCR in an embodiment of the present invention.

[0066] FIG. 2 is a schematic diagram of the result of the mRNA level after overexpression of the target fragments of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, ***, $p < 0.001$.

[0067] FIG. 3 is a schematic diagram of the result of the mRNA level of the gene ACE2 after overexpression of the target fragments of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$, ***, $p < 0.001$.

[0068] FIG. 4 is a schematic diagram of the result of the mRNA level of the gene HAS1 after overexpression of the target fragments of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$, ***, $p < 0.001$.

[0069] FIG. 5 is a schematic diagram of the result of the mRNA level of the gene HAS2 after overexpression of the target fragments of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$.

[0070] FIG. 6 is a schematic diagram of the result of the mRNA level of the gene HAS3 after overexpression of the target fragments of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$, ***, $p < 0.001$.

[0071] FIG. 7 is a schematic diagram of the result of the mRNA level of the surrounding gene FBXO15 after overexpression of the target fragment SARS-CoV-2-HIS-4 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, ***, $p < 0.001$.

[0072] FIG. 8 is a schematic diagram of the result of the mRNA level of the surrounding gene MYL9 after overexpression of the target fragment SARS-CoV-2-HIS-3 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, ***, $p < 0.001$.

[0073] FIG. 9 is a schematic diagram of the result of the mRNA level of the surrounding gene ATP8B1 after overexpression of the target fragment SARS-CoV-2-HIS-1 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$.

[0074] FIG. 10 is a schematic diagram of the result of the mRNA level of the surrounding gene KALRN after overexpression of the target fragment SARS-CoV-2-HIS-5 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$.

[0075] FIG. 11 is a schematic diagram of the result of the mRNA level of the surrounding genes after overexpression of the target fragment SARS-CoV-2-HIS-6 of coronavirus in

293T cells by qPCR detection in an embodiment of the present invention.

[0076] FIG. 12 is a schematic diagram of the result of the mRNA level of the surrounding genes after overexpression of the target fragment SARS-CoV-HIS-2 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$, ***, $p < 0.001$.

[0077] FIG. 13 is a schematic diagram of the result of the mRNA level of the surrounding gene after overexpression of the target fragment MERS-CoV-HIS-2 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention; wherein, **, $p < 0.01$.

[0078] FIG. 14 is a schematic diagram of the result of the mRNA level of the surrounding genes after overexpression of target fragments of zika virus in 293T cells by qPCR detection in an embodiment of the present invention.

[0079] FIG. 15 is a schematic diagram of the result of the mRNA level of the surrounding genes after overexpression of target fragments of ebola virus in 293T cells by qPCR detection in an embodiment of the present invention.

[0080] FIG. 16 is a schematic diagram of the result of the mRNA level of the surrounding genes after overexpression of HIV-2 target fragments in 293T cells by qPCR detection in an embodiment of the present invention.

[0081] FIG. 17 is a schematic diagram of the result of antagomir on the mRNA level of the surrounding genes after overexpression of the target fragment SARS-CoV-HIS-2 of coronavirus in 293T cells by qPCR detection in an embodiment of the present invention.

[0082] FIG. 18 is a schematic diagram of the result of the inhibitory effect of antagomir on the mRNA level of genes activated by the target fragment MERS-CoV-HIS-2 of coronavirus by qPCR detection in an embodiment of the present invention; wherein, * < 0.05 .

[0083] FIG. 19 is a schematic diagram of the result of the inhibitory effect of antagomir on the mRNA level of genes activated by the target fragment SARS-CoV-2-HIS-4 of coronavirus by qPCR detection in an embodiment of the present invention; wherein, * < 0.05 .

[0084] FIG. 20 is a schematic diagram of the result of the inhibitory effect of antagomir on the mRNA level of genes activated by the target fragment SARS-CoV-2-HIS-3 of coronavirus by qPCR detection in an embodiment of the present invention; wherein, * < 0.05 .

DETAILED DESCRIPTION OF THE INVENTION

[0085] The specific implementations of the present invention will be further described below in conjunction with the drawings and examples. The following examples are only used to illustrate the technical solutions of the present invention more clearly, and cannot be used to limit the scope of protection of the present invention. In experimental methods in the following examples where no specific conditions are indicated, choices can be made according to conventional methods and conditions in the art or commodity instructions; the relevant reagents and biomaterials in the following examples are all commercially available products; The molecular cloning technology in the following examples provides a method for purifying and amplifying specific DNA fragments at the molecular level in the prior art. The coronavirus, zika virus, ebola virus and HIV are mainly used as examples for discussion in the following examples.

Example 1 - Construction of an Overexpression Vector of the Target of the RNA Virus

[0086] This example is the construction of an overexpression vector of the target of the RNA virus, and the steps comprise:

[0087] 1. Sequence acquisition and primer design SARS-CoV-2 gene sequences were found from Nucleotide database Genbank of NCBI, and then the whole genome nucleotide sequences of the virus were Blast-aligned with the whole genome sequence in human, and finally, the virus nucleotide sequence fragments with a similarity of not less than 95% were screened as viral RNA target sequences (hereinafter referred to as targets). 5 sequences that were completely complementary and paired to the human genome and 1 sequence that was not completely complementary to human genes were screened from SARS-CoV-2. For zika virus, ebola virus, HIV, SARS-CoV, MERS-CoV, and other RNA viruses, the same method was used to obtain target sequences. The screened target sequences are shown in Table 1 above. The upstream and downstream primers were determined using primer5 software, respectively, and the protective base and EcoRI restriction site sequence (CGGAATTC) were added to 5' end of the upstream primer, and the protective base and BamHI restriction site sequence (CGGGATCC) were added to 5' end of the downstream primer. The primers were synthesized by Shanghai Sunny Biotechnology Co., Ltd. The primer sequences of some targets are shown in Table 3 above.

[0088] 2. Obtainment of the target fragment sequence of interest of the RNA virus Taking severe acute respiratory syndrome-related coronavirus 2 target sequence as an example, the viral target fragment was artificially synthesized by means of homologous recombination. After the primers of F123 and R1 designed according to the sequence were annealed, two rounds of nested PCR were performed using F123 and R2 and F123 and R3, and the gene fragments of interest were amplified with Q5 enzyme. The amplification system and program were as follows:

PCR system	Total volume 50 μ l
5 \times Reaction buffer	10 μ l
dNTPs (10 mM)	1 μ l
Upstream primer (10 μ M)	2.5 μ l
Downstream primer (10 μ M)	2.5 μ l
cDNA template	1 μ l
Q5 polymerase	0.5 μ l
ddH ₂ O	32.5 μ l

[0089] PCR program: 98° C. for 30 s;

[0090] 98° C. for 10 s, 55-72° C. for 30 s, 72° C. for 30 s/kb, 35 cycles; and 72° C. for 2 min. For severe acute respiratory syndrome-related coronavirus and middle east respiratory syndrome coronavirus, F1 and R1 primers were used to anneal, and then F2 and R2 and the annealed product were subjected to nested PCR to obtain the fragments of interest.

[0091] 3. Recovery, restriction digestion and purification of PCR products The PCR products were detected

by electrophoresis in 1% agarose gel, the gel was cut and recovered, and the fragments of interest were recovered using a ordinary agarose gel DNA recovery kit (Tiangen Biotech Co., Ltd.); the enzyme digestion process referred to the enzyme digestion system on NEB website, and the enzyme digestion was carried out at 37° CoVemight, and a PCR product recovery kit (Tiangen Biotech Co., Ltd.) was used for purification and recovery.

[0092] 4. Ligation The digested PCR product and the digested pCDH vector were ligated with T4 ligase according to the following ligation system at 16° CoVemight.

Ligation system	
Reagents	Volume
PCR product	1 μ l
Digested pCDH vector	1 μ l
T4DNA ligase buffer	1 μ l
T4DNA ligase	1 μ l
H ₂ O	6 μ l
Total	10 μ l

[0093] 5. Transforming and picking monoclonal ligation.

[0094] (1) 10 μ l of ligation product was added to 50 μ l of DH5 α competent cells, and incubated on ice for 30 min.

[0095] (2) The competent cells were heat shocked at 42° C. for 90 s, and then immediately placed on ice for 5 min.

[0096] (3) 300 μ l of LB liquid medium without antibiotics was added on a clean bench, and the bacteria was shaken on a constant temperature shaker at 37° C. for 30 min.

[0097] (4) 1000 μ l of bacterial solution was centrifuged for 5 min and the supernatant was discarded. The remaining 50 μ l of bacterial solution was spread evenly on the LB solid plate supplemented with ampicillin, and the plate was incubated in a constant temperature incubator at 37° CoVemight.

[0098] (5) An appropriate amount of monoclonal colonies was picked from the overnight-cultured plate, and put into EP tubes containing 200 μ l of LB liquid medium supplemented with ampicillin. The bacteria were shaken in a constant temperature shaker at 37° C. for 2 hours, and then subjected to sequencing and identification. Finally, the target band can be obtained by vector PCR (FIG. 1).

[0099] The results showed that: The length of each target-vector is 200-250 bp. FIG. 1 shows the electrophoresis results of the target-vectors containing 6 targets from severe acute respiratory syndrome-related coronavirus 2, respectively. Specifically, HIS1 is the target-vector containing SARS-CoV-2-HIS-1, and HIS2 is the target-vector containing SARS-CoV-2-HIS-2, HIS3 is the target-vector containing SARS-CoV-2-HIS-3, HIS4 is the target-vector containing SARS-CoV-2-HIS-4, HIS5 is the target-vector containing SARS-CoV-2-HIS-5, and HIS6 is the target-vector containing SARS-CoV-2-HIS-6.

[0100] The same operation as above applied to SARS-CoV, MERS-CoV, zika virus, ebola virus and HIV.

[0101] Example 2 The effect of overexpression of the target sequences of the RNA virus in cells on the expression

level of surrounding genes. In this example, the effect of the overexpression of the target sequences of the RNA virus in 293T cells on the expression level of surrounding genes was detected. The steps are briefly described as follows:

[0102] 1. Preparation of lentivirus by liposome method: According to molecular cloning, SARS-CoV-2, SARS-CoV, MERS-CoV overexpression plasmid, virus packaging plasmid psPAX2 and capsid plasmid pMD2.G-VSVG were transferred into 293T cells, and the supernatant was collected after 48 hr and 72 hr, respectively. The cell debris was filtered through a 0.45 μm filter to obtain the lentivirus stock solution.

[0103] 2. Cell infection: 200,000 cells to be infected (lentiviral stock solution) was spread in a 6 cm culture dish in advance, after the cells adhered on the second day, the first infection was carried out, and the infection was repeated again on the third day; on the fourth day, the cells were allowed to recover for one day without adding any stimulation; on the fifth day, drug screening was started to perform based on corresponding markers carried by the plasmid that reduce the potency of the drug.

[0104] 3. Real-time fluorescence quantitative PCR

Total RNA Extraction

[0105] 10^6 - 10^7 cells were prepared, resuspended in PBS, and then centrifuged to remove the supernatant, 1 ml of Trizol was added for lysis at room temperature for 5 min, then 0.2 ml of chloroform was added. The mixture was shaken in a vortex shaker for 15 s, and left to stand at room temperature for 2 min. The mixture was centrifuged in a centrifuge at 4° C. for 15 min at 13,300 rpm. The upper colorless water phase was transferred into another EP tube. An equal volume of isopropanol was added, mixed thoroughly in a vortex shaker, and the mixture was centrifuged in a centrifuge at 4° C. at 13,300 rpm for 10 min. The supernatant was discarded, and 1 ml of 75% ethanol prepared with DEPC water was added, turned upside down until the precipitate was suspended, and centrifuged in a centrifuge at 4° C. at 13,300 rpm for 5 min. The supernatant was aspirated with a pipette, during the period of drying at room temperature for 5-20 min, the morphology of the precipitation was observed. When just being transparent, 40-100 μl of DEPC water was used for dissolution according to the amount of precipitation. 1 μl was taken and the concentration and OD260/OD280 was measured on Nanodrop. The extracted RNA was stored in a refrigerator at -80° C.

Reverse Transcription Synthesis of cDNA

[0106] Takara (D2680A) reverse transcription PCR kit was used, the PCR reaction system and program were as follows:

Reverse transcription PCR system	Total volume 20 μl
5 \times PrimeScript Buffer	4 μl
dNTP Mixture (2.5 mM each)	4 μl
Random 6 mers (100 μM)	
	1 μl
OligodT Primer (50 μM)	1 μl
PrimeScript Reverse Transcriptase (200 U/ μl)	0.5 μl
RNase Inhibitor (40 U/ μl)	0.5 μl
Total RNA	1 μg

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Reverse transcription PCR system	Total volume 20 μl
RNase Freed H2O up to 20 μl	

Reverse transcription PCR program: 42° C. for 10 min, 95° C. for 2 min.

RT-qPCR

[0107] The expression of the gene of interest at the transcription level was detected using Takara real-time fluorescent quantitative PCR kit.

Real-time fluorescence quantitative PCR system	Total volume 10 μl
Sybr Green Mix	5 μl
Forward (10 μM)	1 μl
Reverse (10 μM)	1 μl
cDNA	3 μl

[0108] Experimental results: After overexpression of the target sequence fragment, the expression level of the fragment was up-regulated tens of thousands of times (FIG. 2). Specifically, the ACE2 gene, which is very related to the coronavirus, was activated after overexpression of the SARS-CoV-HIS, SARS-COV-2-HIS-3 and SARS-COV-2-HIS-4 fragments (FIG. 3). The HAS1 (FIG. 4), HAS2 (FIG. 5) and HAS3 (FIG. 6) genes of the hyaluronic acid synthase family related to severe acute respiratory syndrome-related coronavirus 2 were also significantly activated by SARS-CoV-HIS, MERS-CoV-HIS, SARS-COV-2-HIS-3 and SARS-COV-2-HIS-4 fragments. Finally, it can be seen from the detection that the genes within 200 k around the SARS-COV-2-HIS-4 (FIG. 7), SARS-COV-2-HIS-3 (FIG. 8), SARS-COV-2-HIS-1 (FIG. 9) and SARS-COV-2-HIS-5 (FIG. 10) fragments were all significantly activated. The same results were obtained for the fragment SARS-CoV-2-HIS-6, which was not completely complementary (FIG. 11). The specific genes comprised: FBXO15, MYL9, KALRN, ATP8B1, C5AR1, EPAS1, etc. The same results were also obtained for SARS-COV-HIS-2 (FIG. 12) and MERS-COV-HIS-2 (FIG. 13).

[0109] Specifically, the expression of the gene IGF2R around the target fragment of SARS virus was increased, and the expression of the gene IGF2R around the target fragment of MERS virus was increased. In addition, zika virus (FIG. 14), ebola virus (FIG. 15), and HIV-2 (FIG. 16) were also detected in this example, and the results were also the same, specifically: after overexpression of the target fragment of zika virus in 293T cells, the expression of surrounding 16 genes such as CNMD and VPS36 was increased; after overexpression of the target fragment of ebola virus in 293T cells, the expression of surrounding 15 genes such as VGLL4 and TAMM41 was all increased; after overexpression of HIV target fragment in 293T cells, the expression of surrounding genes BMP5, MMP1 and ADCYAP1 was increased; after overexpression of HIV2 target fragment in 293T cells, the expression of surrounding 8 genes such as LAPTM4A and LRRC14B was increased.

[0110] The above results prove that the constructed vector plays a certain function in the expression of miRNA related

to SARS-CoV-2, and provides a research basis for subsequent research.

Example 3 - Inhibitory Effect of miRNA Inhibitor (antagomiR) or Antisense Sequence For the Target of the RNA Virus on Activated Target Genes

[0111] This example verifies the inhibitory effect of the inhibitor antagomir for the target of the RNA virus on activated target genes, and comprises the following steps:

[0112] step one: preparation of the inhibitor antagomir for the viral target: cholesterol modification and four phosphorothioate backbone modifications were made at the 3' end of the reverse complementary sequence of the target sequence of the RNA virus, two phosphorothioate backbone modifications were made at the 5' end, and methoxy modification was made on the whole chain to obtain the corresponding inhibitor antagomir for the target of the virus.

[0113] step two: the virus stock solution was prepared by the method of example 2, and the cells were infected with the virus stock solution. The infected cells were divided into two groups: an experimental group and a control group, wherein the experimental group was: 10 μ M of virus-infected cell solution added with corresponding inhibitor for the viral target; the control group was: 10 μ M of virus-infected cell solution. After 48 hours, the cell solution of the experimental group and the control group were tested according to the method of real-time fluorescent quantitative PCR in example 4.

[0114] The results of the test were shown in FIGS. 18-21. The inhibitor for the viral target can specifically inhibit the replication of the target sequence, and the antagomir can target the target sequence well, so that the surrounding genes activated by SARS-CoV-HIS-2 (FIG. 17), MERS-CoV-HIS-2 (FIG. 18), SARS-CoV-2-HIS-4 (FIG. 19) and SARS-CoV-2-HIS-3 (FIG. 20) shown a significant tendency to decrease, further verifying the therapeutic value of targets in RNA virus.

[0115] This experiment further verified the inhibitory effect of the reverse complementary sequence of the target sequence of the RNA virus (comprising antisense DNA sequence and antisense RNA sequence), as well as cholesterol modification and four phosphorothioate backbone modifications made at the 3' end of the target sequence of the RNA virus, two phosphorothioate backbone modifications made at the 5' end, and methoxy modification made on the whole chain as an inhibitor on the activated target genes was verified. The test results were similar to that of the inhibitor antagomiR. It can be seen that the above-mentioned three inhibitors all had an inhibitory effect on activated target genes. Antisense RNA or antisense DNA of the target sequence of the RNA virus can be used to inhibit RNA virus nucleic acid and block important pathogenic pathways of RNA virus. The different modified or unmodified products of the antisense RNA or antisense DNA provided an important material basis for the treatment of RNA virus diseases. The detailed sequences of the antisense RNA or antisense DNA are shown in Table 2.

Example 4 - The Increase in Hyaluronic Acid Affected by the Target Can Be Reduced by the Hyaluronic Acid Inhibitor 4-MU

[0116] This example verifies that the increase in hyaluronic acid affected by the target can be reduced by the hyaluronic acid inhibitor 4-MU and comprises the following steps:

[0117] the lentivirus and infected cells were prepared by the method of example 2;

[0118] Replacement with the fresh medium was performed, 100 μ M of hyaluronic acid inhibitor 4-MU was added in the experimental group, and DMSO (the solvent for 4-MU) was added in the control group. After 24 hours, the cell supernatant was collected and detected with hyaluronic acid ELISA kit (R&D, DY3614-05). The steps are briefly described as follows:

[0119] 1) Coating ELISA plate: The plate was coated with 100 μ l/well of Capture Reagent overnight.

[0120] 2) Sealing: The Capture Reagent was removed by patting the plate. The plate was washed 3 times with 400 μ l/well of Wash buffer and patted to dryness. The plate was sealed with 100 μ l/well of Dilute Reagent for 1 h.

[0121] 3) Washing the plate and incubating the sample: The plate was washed with 400 μ l/well of Wash buffer 3 times, 100 μ l/well of standard and serum to be tested were added (100 μ l of the serum from patients with mild and severe COVID-19 was diluted with 200 μ l of Dilute Reagent in the kit to a total volume of 300 μ l, 3 replicate wells were made), and incubated at room temperature for 2 h.

[0122] 4) Washing the plate and incubation with the Detect Reagent. The plate was washed with 400 μ l/well of Wash buffer 3 times, 100 μ l/well of Detect Reagent was added and incubated at room temperature for 2 h.

[0123] 5) Washing the plate and incubation with HRP. The plate was washed with 400 μ l/well of Wash buffer 3 times, 100 μ l/well of HRP was added and incubated at room temperature for 20 min.

[0124] 6) Washing the plate and incubation with the substrate. The plate was washed with 400 μ l/well of Wash buffer 3 times, 100 μ l/well of mixed solution of substrates A and B was added and incubated at room temperature for 20 min.

[0125] 7) Stopping color development. 50 μ l/well of stop solution was added.

[0126] Absorbance was read at 450 nm within 15 min. The test results are shown in Table 4 and Table 5: After overexpression of the target sequence of the virus in cell lines 293T and MRC5, the hyaluronic acid content was significantly increased (Table 4). The hyaluronic acid produced due to overexpression of the target sequence can be reduced using hyaluronic acid inhibitor 4-MU (Table 5). This example proves that the target of the virus has scientific research value and 4-MU has the potential to become a therapeutic drug targeting the target and has a therapeutic value for complications related to the target of the RNA virus.

TABLE 4

Determination of hyaluronic acid content in 293T and MRC5 cells in which the target of the virus is overexpressed				
	293T	Hyaluronic acid (ng/ml)		p value
		p value	MRC5	
CTRL	7.39±0.26	-	59.55±4.73	-
HIS-MERS-CoV-2	76.91±2.29	**	106.97±4.69	**
HIS-SARS-CoV-1-2	115.60±18.10	**	116.84±1.52	**
HIS-SARS-CoV-2-3	62.66±7.14	**	72.40±8.75	ns
HIS-SARS-CoV-2-4	113.95±13.14	**	117.44±2.03	**

TABLE 5

Determination of the inhibitory ability of hyaluronic acid inhibitor on hyaluronic acid in the case of overexpression of the target of the virus			
	Hyaluronic acid (ng/ml)		p value
	DMSO	4-MU (100 μM)	
CTRL	7.39±0.26	3.20±0.39	**
HIS-MERS-CoV-2	76.91±2.29	39.72±5.75	**
HIS-SARS-CoV-1-2	115.60±18.10	23.50±3.44	**
HIS-SARS-CoV-2-3	62.68±7.14	30.02±2.00	**
HIS-SARS-CoV-2-4	113.95±13.14	19.76±11.3	*

Example 5 - Detection of Blood Routine Index

[0127] The blood routine index was provided by the hospital, and the hyaluronic acid in the blood was detected using the hyaluronic acid ELISA kit (R&D, DY3614-05). Specifically, the HA content in the serum of a patient with severe COVID-19 was significantly increased compared with that in a patient with mild COVID-19 (Table 6). In addition, the number of lymphocytes in a patient with severe COVID-19 was significantly lower than that in a patient with mild COVID-19, suggesting that the number of the immune cells in a patient was decreased with the disease progressing to severe; furthermore, D-dimer is a fibrin

degradation product, and the increase of D-dimer level indicates the existence of hypercoagulable state and secondary hyperfibrinolysis in the body. Therefore, the mass concentration of D-dimer has diagnostic significance for thrombotic diseases. The content of D-dimer in the serum of a patient with severe COVID-19 was significantly higher than that in a patient with mild COVID-19, indicating that the risk of coagulation in a patient was increased with the condition of COVID-19 progressing to severe, and also indicating that there was a certain feasibility of subsequent anticoagulation therapy.

TABLE 6

Hematological indicators of a patient with mild or severe COVID-19				
	HA (ng/ml)	LYMPH#	CRP (mg/L)	D-D (ug/ml)
		(10 ⁹ /L)		
Mild (n=37)	3.77±2.86	1.79±0.50	0.77±0.68	0.28±0.12
Severe (n=22)	35.41±28.88***	1.40±0.43**	8.49±9.66***	0.49±0.36*

[0128] The above results provide a basis for the changes in hematological indicators caused by the target sequences of the RNA virus to become clinical diagnosis, and reflects the clinical diagnostic value of the targets of the RNA virus. Moreover, the targets have the potential to become a vaccine. In addition, in the process of preparing vaccines, common attenuated live vaccines still have certain risks that need to be further optimized. The pathogenic risk of a vaccine will be greatly reduced by knockout of the targets.

[0129] The specific examples of the present invention are described in detail above and are only for illustration, and the present invention is not limited to the specific examples described above. For a person skilled in the art, any equivalent modifications and alternatives made to the present invention are also within the scope of the present invention. Therefore, all equivalent changes and modifications made without departing from the spirit and scope of the present invention should fall within the scope of the present invention.

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agaugaagca gucaccaacc gc 22

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auuagauuuc aacacaggug cuacauc 27

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uuggaauuu uugcuccucu uua 23

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gaaauuuuau uuuuuuguuc agu 23

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uuagcuagau uuacagauuu gga 23

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uugaggaaaa ggaaccug uaca 24

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ccaggcacug ggaagucagu ggca 24

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ugagaaaaag gccacugucc uuua 24

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acaaaugga gaaauaguga aaa 23

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gaagcagaga gaaaguagag aag 23

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ucaaaaggag agaacagaug cugg 24

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caaaagaagg cauuuaaaga gga 23

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ggaaaaccag ggagguuuug gaa 23

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aaaggaagaa auugaaaccc aga 23

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guggcaggcc cauacacca cca 23

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aguuuaaaau uauauccaaa auaaaauu 28

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ucuaagcgaa gaaacaacaa gagu 24

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auacaaucua auugaauggc au 22

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agaugacaau ugugaaaaua aa 22

<210> SEQ ID NO 60

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<212> TYPE: RNA

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guuuuuuauug ggaaaugaug gaauuaaca 29

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<212> TYPE: RNA
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aaauacaaaa aaauacuga auacaa 26

<210> SEQ ID NO 63
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uuuacauucc uggucaacua ugaaaugaaa cuauugc 37

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cuacaaaaaa augcuaaaag aa 22

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augcugaaca acucuaagaa aa 22

<210> SEQ ID NO 66
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<212> TYPE: RNA
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aggaaaguga aaagauggca aa 22

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aaugaggaaa gugaaaagau ggcaaaaga 29

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caagaaaaa gauaguauca u 21

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ccaugaaac auugauaac aaugaaga 29

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aaaguauaua uuauuuaca aca 23

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augauaaca caauaucuc uuu 23

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acuaauacac augauaaca 20

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ugauaacaac aaauaucucu uugcua 26

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gaaaaggaaa agaagauuuc uug 23

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<212> TYPE: RNA
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<400> SEQUENCE: 75

aauguacagc auccaauaaa aa 22

<210> SEQ ID NO 76
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<400> SEQUENCE: 76

uaauuuuuu gauggccac cccaug 26

<210> SEQ ID NO 77
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aaauuuuug aauggccacc c 21

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uaaaauaga uaaaauac auua 24

<210> SEQ ID NO 80
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<212> TYPE: RNA
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<210> SEQ ID NO 81
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<212> TYPE: RNA
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augguaaau caugguuaa auuuaua 27

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aacuaauua aaaacuuaug uau 23

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<400> SEQUENCE: 83

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<212> TYPE: RNA

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<210> SEQ ID NO 85

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<212> TYPE: RNA

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<400> SEQUENCE: 85

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<210> SEQ ID NO 86

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<212> TYPE: RNA

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<400> SEQUENCE: 86

agguaaaaa augagagaga auggaguu

28

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<211> LENGTH: 24

<212> TYPE: RNA

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<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 87

uauuuuuuuuu ggcagauuuu uaga

24

<210> SEQ ID NO 88

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<400> SEQUENCE: 88

ggaacuuggu gcauuuuuuu cua

23

<210> SEQ ID NO 89

<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<400> SEQUENCE: 89

auuuuuucug auugcuuuuc aa 22

<210> SEQ ID NO 90
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<212> TYPE: RNA
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uaauucugaaa augguauuu uaa 23

<210> SEQ ID NO 91
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agccuauuuu cauugaugcc uga 23

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<400> SEQUENCE: 92

ucaacaaaau uuuacaggca aaa 23

<210> SEQ ID NO 93
<211> LENGTH: 23
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uuagaaaaau ggaaaaguau aga 23

<210> SEQ ID NO 94
<211> LENGTH: 23
<212> TYPE: RNA
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<400> SEQUENCE: 94

aagagcucaa caaaauuuua cag 23

<210> SEQ ID NO 95
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<212> TYPE: RNA
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<400> SEQUENCE: 95

ucuaaaauuu cagaaugcac uagagaaa 28

<210> SEQ ID NO 96
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<212> TYPE: RNA
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ugaugggggu ugacggaguu ggggagu 27

<210> SEQ ID NO 97
<211> LENGTH: 23
<212> TYPE: RNA
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<400> SEQUENCE: 97

ggggauugga aaggcucucu gug 23

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<212> TYPE: RNA
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<400> SEQUENCE: 98

aaauggagca gaaagaacac ucagg 25

<210> SEQ ID NO 99
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<212> TYPE: RNA
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<400> SEQUENCE: 99

uggcucgaag agcauggaga ggaa 24

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<211> LENGTH: 23
<212> TYPE: RNA
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<400> SEQUENCE: 100

aggaagggga uugagagacu cac 23

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<212> TYPE: RNA
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<400> SEQUENCE: 101

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<210> SEQ ID NO 102
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<212> TYPE: RNA
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<400> SEQUENCE: 102

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<210> SEQ ID NO 103
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aaauaagaaaa gcaacauugu gauuuuuuuuu ua 32

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<212> TYPE: RNA
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<400> SEQUENCE: 104

uaaaaaaagu caaauuuauug auua 24

<210> SEQ ID NO 105
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<212> TYPE: RNA
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cuuuggcauu ucagugauuc agcaaaa 27

<210> SEQ ID NO 106
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<212> TYPE: RNA
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<220> FEATURE:
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aaaugugcuc ccuuuuccug ga 22

<210> SEQ ID NO 107
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<400> SEQUENCE: 107

uuuuuaagga guggugaaga agaaaga 27

<210> SEQ ID NO 108
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<212> TYPE: RNA
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<400> SEQUENCE: 108

aaauuuuuaa aaugcauua acu 23

<210> SEQ ID NO 109
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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ggcaggugug guugcucaag cuguuaa 26

<210> SEQ ID NO 110
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<212> TYPE: RNA
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<400> SEQUENCE: 110

uaauacauuu uccugcuucc aa 22

<210> SEQ ID NO 111
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<212> TYPE: RNA
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<400> SEQUENCE: 111

ucauuugaag auggagcucu uu 22

<210> SEQ ID NO 112
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<212> TYPE: RNA
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<400> SEQUENCE: 112

cagcuuacuc uuccucagag uucuuu

26

<210> SEQ ID NO 113

<211> LENGTH: 30

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 113

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30

<210> SEQ ID NO 114

<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 114

aaagauuau gaaacuuuuc ug

22

<210> SEQ ID NO 115

<211> LENGTH: 23

<212> TYPE: RNA

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<220> FEATURE:

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<400> SEQUENCE: 115

uugcuguuu uccaaacacu aga

23

<210> SEQ ID NO 116

<211> LENGTH: 34

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 116

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34

<210> SEQ ID NO 117

<211> LENGTH: 29

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 117

auguggagac auuccagcac agaggaaac

29

<210> SEQ ID NO 118

<211> LENGTH: 26

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 118

ucaggcucaa gugaucucuc auuuca 26

<210> SEQ ID NO 119
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 119

uuauuugaa guuuugaag uug 23

<210> SEQ ID NO 120
<211> LENGTH: 22
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 120

agauauagga augugucuga aa 22

<210> SEQ ID NO 121
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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uauccugau auuuuuucuu ugg 23

<210> SEQ ID NO 123
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<212> TYPE: RNA
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<400> SEQUENCE: 123

auaaaggaaa agucaagaaa auu 23

<210> SEQ ID NO 124
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 124

agagagagag aaaagaaaau ug 22

<210> SEQ ID NO 125
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 125

uaugccugau aauuuuucau ug 22

<210> SEQ ID NO 126
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 126

cuguguuuuc uccuagaaug uca 23

<210> SEQ ID NO 127
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 127

aaagacagga uucauuauu ugua 24

<210> SEQ ID NO 128
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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caggaaaaaa auggauacua aa 22

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auuuuuuuau aucauuuauc uuuuuu 26

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ccacagcaac augguuucag uau 23

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<223> OTHER INFORMATION: Fragment coding sequence

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aacaucuuau uuccuucuu uc 22

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agauaucuuu caaaaaauu caa 23

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cuuuuuuuuu ccuuucuccu uc 22

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cucuuuuuuuu uuccuuuucuc cuuuuu 26

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cuacaggaug uaguuuuuga aaaua 25

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aagaugacua ucuaaaaugu cagg 24

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cugucugcua accaguauga aca 23

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<212> TYPE: RNA

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<210> SEQ ID NO 217
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<212> TYPE: RNA
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gugcuauuga ucagacuaau ua 22

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<400> SEQUENCE: 218

gcuggacugu ggugacagcc uc 22

<210> SEQ ID NO 219
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<210> SEQ ID NO 220
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gaggacgaga uggguggauc aagagguc 28

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gaggacgaga uggguggauc aagagguc 28

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aaagcaagaa aaugaauga aaa 23

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caagaaaaau gaugaaaau au 22

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gauuaaaauu auaucaaaag aaaaugaa 28

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aaagaaaug aaaucaauag uugagga 27

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uauaucaaaa gaaaugaaa ucaauag 27

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augaccaaau guauagauug aga 23

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uauaucaaaa gaaaauugaaa ucaaua 26

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ugauaucauu uucauuuaca ua 22

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aagaaaaaga agauagcaag aa 22

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agcuuaaguu ugguaaggaaa acaa 24

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cauuuuuuuu auacaacaaa acacaaa

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agcuuaaguu ugguaggaaa acaa

24

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gaaauuuacc auuuuuuuuu gaugu

25

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aaauaagauc agauuuuuuu uua

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<400> SEQUENCE: 268

agaauuuuuuu uuuuacagua ua

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auuuuuaaac acuuuuuuuu uu 22

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caauuuuuu gcuguucauu ucaaugg 27

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gcauuuuuu cuuuuuuua aguuacuuu 28

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uaacagacuu ggaauuuuuac aaau 24

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aaaauuuuuuu acaaaaaauga aagg 24

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cuuuuuuuuuu guuuuuuuuuu uuuuuuuuuu 28

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uuuuuuuuuuu uuuuuuuuuuu uuuuuuuuuuu 33

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uuuuuuuuuuu uuuuuuuuuuu uuuuuuuuuuu 28

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cccagcacag agaugucauu ga 22

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agugagaaau gaugauguug aucaga 26

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uucuaaggaa agcaaccaga ag 22

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ugagcaagaa gaaauccuac au 22

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uuagaaaugu cuuaagcauu gc 22

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aagagaaaga ccugaccaa ga 22

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<212> TYPE: RNA

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<212> TYPE: RNA

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<212> TYPE: RNA

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aucauguuuc auacuucua gccaug 26

<210> SEQ ID NO 297

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gaaacauacu aagaacacag gaa 23

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<212> TYPE: RNA

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<220> FEATURE:
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uuucaccauu accuucucuu cc 22

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aggaagcaaa auuaaacaga gaagaaa 27

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aaaacaacac uuggguaaau cagaca 26

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gcugcuggac agucaguggu uu 22

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ggaucaagaa agaagaguuc ucugaga 27

<210> SEQ ID NO 304
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<220> FEATURE:
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ggggagacac acaaaauucag ac 22

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accaaaugaa aaccagcuc acaagaguca 30

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aaaugagaau guggaaacca ug 22

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agaaaauaagg agaguuuggc gc 22

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<400> SEQUENCE: 308

agaagaguag acggaaagug ga 22

<210> SEQ ID NO 309
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agaagaguag acggaaagug ga 22

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gaagagagca gggcaagaau caaaacuagg cu 32

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agggaagcu uucccaaug uc 22

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ggacaugauu ccagagagga augaacaagg acaa 34

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ggaaaugug aaaaucaau gg 22

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gagucuacau ucucaguuuu guc 23

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gagacagaca guaaaggaaa au 22

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ugaagaaaaa cuaaagaaaa aa 22

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ccagacagca gacuggaagg ca 22

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aacaggaaau cauauugaau uugu 24

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aguaugcaug gaaagauuuu cuuaaug 27

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<400> SEQUENCE: 320

cagaguuuga auuuuugau cag 23

<210> SEQ ID NO 321
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<400> SEQUENCE: 321

ugaggguaac auuuuuuuuu ggg 23

<210> SEQ ID NO 322

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<212> TYPE: RNA

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<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 322

uuuuuuuuuu uugagaaagg gcuucau 27

<210> SEQ ID NO 323

<211> LENGTH: 23

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caaaagaaaa gaaagaagag cuc

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auugcuccuu ugcuggaugg au 22

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uuccaaucug aaugaugca ca 22

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aaauggacca caaacacaga aac 23

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augucuucuu caaucacuuc aac 23

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aaauuuuaca acuuuacccu uu 22

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aagcaagauu aaaaagagag ga 22

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<212> TYPE: RNA

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auuguaugga cacaaauaga aac 23

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<212> TYPE: RNA

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uguuuucuuc ugucugaaga 20

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cauauaaaua gcaucacaau 20

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gaaagaggua aaauaaaaag 20

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aaguagcagg cucacucugc 20

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agaaggagag aaggaaaug g 21

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acaaauaccu gcagaaaugc 20

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gagaauaag agaaaacucc 20

<210> SEQ ID NO 394
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auucagugaa auuggaaaau 20

<210> SEQ ID NO 395
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agaaaucac caagaccaca ua 22

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cuugaacuua gaagcagaua u 21

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acaaugcuau caauuguaau c 21

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<212> TYPE: RNA
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<212> TYPE: RNA
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uuucaaaug ucagcaaaaua ugca 24

<210> SEQ ID NO 406
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<212> TYPE: RNA
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<400> SEQUENCE: 407

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<212> TYPE: RNA
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<400> SEQUENCE: 408

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20

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<211> LENGTH: 23

<212> TYPE: RNA

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<220> FEATURE:

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<400> SEQUENCE: 409

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<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 411

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<211> LENGTH: 24

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fragment coding sequence

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agugagacac agggaacaga gaaa

24

<210> SEQ ID NO 413

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<212> TYPE: RNA

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<220> FEATURE:

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<210> SEQ ID NO 414

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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cagcagauaa aagaauaug gaaug 26

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aguugauau aacaacuggu cuggu 25

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cuucccaguu uuggaguguc ugggau 26

<210> SEQ ID NO 419
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uggagaaaagc caacaagaua aaa 23

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agggcaagcu uuccc aaaug uc 22

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<212> TYPE: RNA

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<212> TYPE: RNA

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<212> TYPE: RNA

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<223> OTHER INFORMATION: Fragment coding sequence

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<212> TYPE: RNA

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<223> OTHER INFORMATION: Fragment coding sequence

<400> SEQUENCE: 615

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<212> TYPE: DNA

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<212> TYPE: DNA

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<212> TYPE: DNA

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<210> SEQ ID NO 637
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<212> TYPE: DNA
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<400> SEQUENCE: 637

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<212> TYPE: DNA

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<211> LENGTH: 59

<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 645

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<210> SEQ ID NO 646

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<212> TYPE: DNA

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<220> FEATURE:
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<400> SEQUENCE: 646

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<400> SEQUENCE: 647

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<400> SEQUENCE: 648

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<210> SEQ ID NO 649
<211> LENGTH: 59
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 649

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<400> SEQUENCE: 650

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<400> SEQUENCE: 651

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<210> SEQ ID NO 652
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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 653
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<212> TYPE: DNA
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<400> SEQUENCE: 653

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 655

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<210> SEQ ID NO 656
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 656

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<210> SEQ ID NO 657
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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 658
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 658

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<210> SEQ ID NO 659
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<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 660

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<210> SEQ ID NO 661
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<212> TYPE: DNA
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 662

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<210> SEQ ID NO 663
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<212> TYPE: DNA
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<210> SEQ ID NO 664
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ ID NO 665
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 665

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<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 666

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<210> SEQ ID NO 667
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<210> SEQ ID NO 668
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<212> TYPE: DNA
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<400> SEQUENCE: 668

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<210> SEQ ID NO 669
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<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 671

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<400> SEQUENCE: 674

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<210> SEQ ID NO 675

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 675

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 676

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<212> TYPE: DNA

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<223> OTHER INFORMATION: Primer

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

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<210> SEQ ID NO 681

<211> LENGTH: 59

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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 682
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<220> FEATURE:
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<400> SEQUENCE: 682

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<210> SEQ ID NO 683
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<220> FEATURE:
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<210> SEQ ID NO 685
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<210> SEQ ID NO 686
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<210> SEQ ID NO 687
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<213> ORGANISM: Artificial Sequence
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<210> SEQ ID NO 691
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<212> TYPE: DNA
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cagatccttc gggccgagg atcctgcccc atctacatag aagg 44

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cuuuuuuuuu auuuuuuuuu uca 23

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ucaaauuuuaa auauagguuu uauuuuaa 28

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acuaaaauuaa aaugaccaua uuuuuauca 28

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gauguuuuuu uacgauuuuc uu 22

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27

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auuaaacaau uacuucuuau uuuaauu 27

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<400> SEQUENCE: 872

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<212> TYPE: RNA

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cugauguucu cuuccuaccg ucu 23

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uuaccgucaa uacuuauaau au 22

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22

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23

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23

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23

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<210> SEQ ID NO 949
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guucuuuuua cuuacuuuua ua 22

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uacauucug acauuuauu u 21

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<212> TYPE: RNA

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auauaguuuu cuuuuacuuu aguu

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<212> TYPE: RNA

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cuaauuuuuu uauaguuuuc uuuuacuu

28

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<212> TYPE: RNA
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<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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22

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<211> LENGTH: 21

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21

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<211> LENGTH: 21

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21

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aaggacgaaa ugguuuuacu gacu 24

<210> SEQ ID NO 1116
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aaaguauuac agucguuuau acgu 24

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ccagauguuu uguaugaaac ucuu 24

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<210> SEQ ID NO 1130
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uuuaaaauua uucuuuuacc uucua 25

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<220> FEATURE:
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uuagauuacc cuuaaaauu cgag 24

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<220> FEATURE:
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<220> FEATURE:
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<400> SEQUENCE: 1133

uguaagaaaa guacaccccg uauu 24

<210> SEQ ID NO 1134

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gaucaguccg auccgucuaac ca 22

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<212> TYPE: RNA

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guuucgucuu acgucaagag aa 22

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<220> FEATURE:

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<400> SEQUENCE: 1136

acgugguuaa uuuuaugucu aua 23

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<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<400> SEQUENCE: 1137

ucucauucuc uguuguacug gu 22

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<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 1138

cccuuaaccc uguuaccacu ac 22

<210> SEQ ID NO 1139

<211> LENGTH: 22

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<400> SEQUENCE: 1139

uuacggaaca aagaugauua ug 22

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auucuccuag uccuuacucu ua 22

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uagaguaaa uccuuacugu gu 22

<210> SEQ ID NO 1142
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23

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22

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1. A target sequence of an RNA virus, wherein the target sequence is a nucleic acid sequence fragment in the gene sequence in the RNA virus containing 20-40 bases and having not less than 95% similarity to human genome sequence.

2. The target sequence of the RNA virus according to claim 1, wherein the target sequence is a nucleic acid sequence fragment in the gene sequence in the RNA virus containing 20-28 bases and having 100% similarity to human genome sequence.

3. The target sequence of the RNA virus according to claim 1, wherein the RNA virus comprises severe acute respiratory syndrome-related coronavirus 2, severe acute respiratory syndrome-related coronavirus, middle east respiratory syndrome coronavirus, zika virus, ebola virus, HIV, norwalk virus, alkhumra virus, enterovirus, kemerovo virus, coxsackievirus, hepatitis A virus, dengue virus 2, rubella virus, marburg marburgvirus, poliovirus, respiratory syncytial virus, mumps virus, australian bat lyssavirus, andes virus, powassan virus, langat virus, eyach virus, colorado tick fever virus, lassa virus, omsk hemorrhagic fever virus, machupo virus, junin virus, guanarito virus, sin nombre virus, hantaan virus, puumala virus, dobrava virus, seoul virus, crimean-congo hemorrhagic fever virus, sabia virus, thogoto virus, black creek canal virus, european bat lyssavirus 1, european bat lyssavirus 2, chapare virus, rotavirus, tai forest ebolavirus, bundibugyo ebolavirus, rift valley fever virus, irkut virus, influenza A virus, bayou virus, kysanur forest disease virus, black creek canal virus, japanese encephalitis virus, duvenhage lyssavirus, Lujo mammarenavirus, measles morbillivirus, tick-borne encephalitis virus, avian influenza virus, swine influenza virus and rabies virus.

4. The target sequence of the RNA virus according to claim 1, wherein the target sequence of the RNA virus is selected from any one or more of SEQ ID NO. 1 - SEQ ID NO. 615.

5. The target sequence of the RNA virus according to claim 4, wherein the target sequence of severe acute respiratory syndrome-related coronavirus 2 comprises SEQ ID NO. 1 - SEQ ID NO. 6; and/or, the target sequence of severe acute respiratory syndrome-related coronavirus comprises SEQ ID

NO. 7 - SEQ ID NO. 9; and/or, the target sequence of middle east respiratory syndrome coronavirus comprises SEQ ID NO. 10, SEQ ID NO. 11; and/or, the target sequence of zika virus comprises SEQ ID NO. 12 - SEQ ID NO. 14; and/or, the target sequence of ebola virus comprises SEQ ID NO. 15 - SEQ ID NO. 17; and/or, the target sequence of HIV comprises SEQ ID NO. 18 - SEQ ID NO. 26; and/or, the target sequence of norwalk virus comprises SEQ ID NO. 27; and/or, the target sequence of alkhumra virus comprises SEQ ID NO. 28 - SEQ ID NO. 30; and/or, the target sequence of enterovirus comprises SEQ ID NO. 31, SEQ ID NO. 32; and/or, the target sequence of kemerovo virus comprises SEQ ID NO. 33, SEQ ID NO. 34; and/or, the target sequence of coxsackievirus comprises SEQ ID NO. 35; and/or, the target sequence of hepatitis A virus comprises SEQ ID NO. 36 - SEQ ID NO. 46; and/or, the target sequence of dengue virus 2 comprises SEQ ID NO. 47 - SEQ ID NO. 50; and/or, the target sequence of rubella virus comprises SEQ ID NO. 51; and/or, the target sequence of marburg marburgvirus comprises SEQ ID NO. 52 - SEQ ID NO. 56; and/or, the target sequence of poliovirus comprises SEQ ID NO. 57; and/or, the target sequence of respiratory syncytial virus comprises SEQ ID NO. 58 - SEQ ID NO. 85; and/or, the target sequence of mumps virus comprises SEQ ID NO. 86; and/or, the target sequence of australian bat lyssavirus comprises SEQ ID NO. 87; and/or, the target sequence of andes virus comprises SEQ ID NO. 88 - SEQ ID NO. 95; and/or, the target sequence of powassan virus comprises SEQ ID NO. 96, SEQ ID NO. 97; and/or, the target sequence of langat virus comprises SEQ ID NO. 98 - SEQ ID NO. 102; and/or, the target sequence of eyach virus comprises SEQ ID NO. 103 - SEQ ID NO. 113; and/or, the target sequence of colorado tick fever virus comprises SEQ ID NO. 114 - SEQ ID NO. 134; and/or, the target sequence of lassa virus comprises SEQ ID NO. 135, SEQ ID NO. 136; and/or, the target sequence of omsk hemorrhagic fever virus comprises SEQ ID NO. 137, SEQ ID NO. 138; and/or, the target sequence of machupo virus comprises SEQ ID NO. 139 - SEQ ID NO. 140; and/or, the target sequence of junin virus comprises SEQ ID NO. 141; and/or, the target sequence of guanarito virus comprises SEQ ID NO. 142 - SEQ ID NO.

147; and/or, the target sequence of sin nombre virus comprises SEQ ID NO. 148 - SEQ ID NO. 152; and/or, the target sequence of hantaan virus comprises SEQ ID NO. 153 - SEQ ID NO. 161; and/or, the target sequence of puumala virus comprises SEQ ID NO. 162 - SEQ ID NO. 173; and/or, the target sequence of dobrava virus comprises SEQ ID NO. 174 - SEQ ID NO. 185; and/or, the target sequence of seoul virus comprises SEQ ID NO. 186 - SEQ ID NO. 199; and/or, the target sequence of crimean-congo hemorrhagic fever virus comprises SEQ ID NO. 200 - SEQ ID NO. 204; and/or, the target sequence of sabia virus comprises SEQ ID NO. 205 - SEQ ID NO. 212; and/or, the target sequence of togoto virus comprises SEQ ID NO. 213 - SEQ ID NO. 227; and/or, the target sequence of european bat lyssavirus 1 comprises SEQ ID NO. 228 - SEQ ID NO. 232; and/or, the target sequence of european bat lyssavirus 2 comprises SEQ ID NO. 233; and/or, the target sequence of chapare virus comprises SEQ ID NO. 234; and/or, the target sequence of rotavirus comprises SEQ ID NO. 235 - SEQ ID NO. 277; and/or, the target sequence of tai forest ebolavirus comprises SEQ ID NO. 278, SEQ ID NO. 279; and/or, the target sequence of bundibugyo ebolavirus comprises SEQ ID NO. 280; and/or, the target sequence of rift valley fever virus comprises SEQ ID NO. 281; and/or, the target sequence of irkut virus comprises SEQ ID NO. 282 - SEQ ID NO. 285; and/or, the target sequence of influenza A virus comprises SEQ ID NO. 286 - SEQ ID NO. 313; and/or, the target sequence of bayou virus comprises SEQ ID NO. 314 - SEQ ID NO. 327; and/or, the target sequence of kysanur forest disease virus comprises SEQ ID NO. 328; and/or, the target sequence of black creek canal virus comprises SEQ ID NO. 329 - SEQ ID NO. 334; and/or, the target sequence of japanese encephalitis virus comprises SEQ ID NO. 335 - SEQ ID NO. 337; and/or, the target sequence of duvenhage lyssavirus comprises SEQ ID NO. 338 - SEQ ID NO. 344; and/or, the target sequence of Lujo mammarenavirus comprises SEQ ID NO. 345; and/or, the target sequence of measles morbillivirus comprises SEQ ID NO. 346; and/or, the target sequence of tick-borne encephalitis virus comprises SEQ ID NO. 347; and/or, the target sequence of avian influenza virus comprises SEQ ID NO. 348 - SEQ ID NO. 420; and/or, the target sequence of swine influenza virus comprises SEQ ID NO. 421 - SEQ ID NO. 521; and/or, the target sequence of rabies virus comprises SEQ ID NO. 522 - SEQ ID NO. 615.

6. A primer composition for constructing a target sequence of an RNA virus, characterized in that, the primers of the target sequence SEQ ID NO. 1 are SEQ ID NO. 616 - SEQ ID NO. 619; and/or, the primers of the target sequence SEQ ID NO. 2 are SEQ ID NO. 620 - SEQ ID NO. 623; and/or, the primers of the target sequence SEQ ID NO. 3 are SEQ ID NO. 624 - SEQ ID NO. 627; and/or, the primers of the target sequence SEQ ID NO. 4 are SEQ ID NO. 628 - SEQ ID NO. 631; and/or, the primers of the target sequence SEQ ID NO. 5 are SEQ ID NO. 632 - SEQ ID NO. 635; and/or, the primers of the target sequence SEQ ID NO. 7 are SEQ ID NO. 636 - SEQ ID NO. 639; and/or, the primers of the target sequence SEQ ID NO. 8 are SEQ ID NO. 640 - SEQ ID NO. 643; and/or, the primers of the target sequence SEQ ID NO. 10 are SEQ ID NO. 644 - SEQ ID NO. 647; and/or, the primers of the target sequence SEQ ID NO. 11 are SEQ ID NO. 648 - SEQ ID NO. 651; and/or, the primers of the target sequence SEQ ID NO. 12 are SEQ ID NO. 652 - SEQ ID NO. 655; and/or, the primers of the target sequence SEQ ID NO. 13 are SEQ ID NO. 656 - SEQ ID NO. 659; and/or, the primers of the target sequence SEQ ID

NO. 14 are SEQ ID NO. 660 - SEQ ID NO. 663; and/or, the primers of the target sequence SEQ ID NO. 15 are SEQ ID NO. 664 - SEQ ID NO. 667; and/or, the primers of the target sequence SEQ ID NO. 16 are SEQ ID NO. 668 - SEQ ID NO. 671; and/or, the primers of the target sequence SEQ ID NO. 17 are SEQ ID NO. 672 - SEQ ID NO. 675; and/or, the primers of the target sequence SEQ ID NO. 18 are SEQ ID NO. 676 - SEQ ID NO. 679; and/or, the primers of the target sequence SEQ ID NO. 19 are SEQ ID NO. 680 - SEQ ID NO. 683; and/or, the primers of the target sequence SEQ ID NO. 20 are SEQ ID NO. 684 - SEQ ID NO. 687; and/or, the primers of the target sequence SEQ ID NO. 21 are SEQ ID NO. 688 - SEQ ID NO. 691; and/or, the primers of the target sequence SEQ ID NO. 22 are SEQ ID NO. 692 - SEQ ID NO. 695; and/or, the primers of the target sequence SEQ ID NO. 23 are SEQ ID NO. 696 - SEQ ID NO. 699; and/or, the primers of the target sequence SEQ ID NO. 24 are SEQ ID NO. 700 - SEQ ID NO. 703; and/or, the primers of the target sequence SEQ ID NO. 25 are SEQ ID NO. 704 - SEQ ID NO. 707; and/or, the primers of the target sequence SEQ ID NO. 26 are SEQ ID NO. 708 - SEQ ID NO. 711.

7. An RNA drug against a virus, wherein the RNA drug comprises the reverse complementary sequence of the target sequence of the RNA virus according to claim 1, cholesterol modification and four phosphorothioate backbone modifications are made at the 3' end of the reverse complementary sequence of the target sequence of the RNA virus, two phosphorothioate backbone modifications are made at the 5' end, and methoxy modification is made on the whole chain, or, cholesterol modification and four phosphorothioate backbone modifications are made at the 3' end of the target sequence of the RNA virus, or two phosphorothioate backbone modifications are made at the 5' end, and methoxy modification is made on the whole chain.

8. The RNA drug according to claim 7, wherein the reverse complementary sequence of the target sequence of the RNA virus comprises reverse complementary RNA sequence or reverse complementary DNA sequence.

9. The RNA drug according to claim 7, further comprising a pharmaceutically acceptable carrier or excipient.

10. The RNA drug against the virus according to claim 7, wherein the dosage form of the RNA drug comprises powder, tablet, granule, capsule, solution, aerosol, injection, emulsion or suspension.

11. A biomaterial related to the target sequence of the RNA virus according to claim 1, wherein the biomaterial is :

- A) a DNA and/or RNA molecule that is complementary and paired to the target sequence of the RNA virus according to claim 1; or
- B) an expression cassette, a recombinant vector, a recombinant microorganism, a recombinant cell line containing the target sequence of the RNA virus according to claim 1 or the DNA molecule in A).

12. The biomaterial according to claim 11, wherein the biomaterial is a recombinant vector, and whose construction steps comprise: 1) designing a primer, and amplifying the target sequence of the RNA virus by PCR; 2) digesting the amplified sequence fragment and an expression vector, and ligating a sequence fragment of interest and the expression vector; 3) transferring the ligated product into *Escherichia coli* and cultivating the *Escherichia coli*; and 4) after identification, extracting recombinant plasmid and packaging the recombinant plasmid.

13. The biomaterial according to claim **11**, wherein the recombinant vector has target sequences expressing severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), severe acute respiratory syndrome-related coronavirus (SARS-CoV), or middle east respiratory syndrome coronavirus (MERS-CoV).

14. A method of preventing or treating a condition caused by the RNA virus comprising administering the RNA virus according to claim **1** to a subject in need thereof.

15. The method according to claim **14**, wherein the condition comprise a human disease, an animal disease and zoonosis.

16. The method according to claim **14**, wherein the RNA virus is administered as a vaccine and an effective substance that regulates the target sequence is directly screened; alternatively, according to the effect of the gene regulated by the target sequence, an effective substance against the gene and gene product regulated by the target sequence is screened.

17. The method according to claim **14**, wherein the target sequence is knocked out.

18. The method according to claim **17**, wherein the method for knocking out the target sequence comprises: CRISPR system and/or ribozyme technology.

19. The method according to claim **16**, wherein the vaccine is a live attenuated vaccine.

20. A live attenuated vaccine, wherein the target sequence of the RNA virus according to claim **1** is deleted or mutated in the whole genome of the live attenuated vaccine.

21. A method of activating related genes at the cellular level and screening therapeutic drugs against the related genes comprising contacting the RNA virus according to claim **1** to genes.

22. The method according to claim **21**, wherein the RNA virus is a coronavirus, and the related genes comprise ACE2 gene, the coding genes of the hyaluronic acid synthase family HAS1, HAS2, and HAS3, and/or genes within 200 k around the fragment.

23. (canceled)

24. A method of identifying drug targets against diseases caused by an RNA virus comprising analyzing the target sequence of the RNA virus according to claim **1** which is found in the cells of the diseases caused by the RNA virus, and the drug targets are found within 200 k around the target sequence of the RNA virus or the drug targets are found beyond 200 k using the prediction software blast 2.2.30 or bedtools 2.29.2.

25. The method according to claim **23**, wherein the drug comprises a miRNA antagonist.

26. A method for detecting a virus, comprising detecting the target sequence of the RNA virus according to of claim **1**.

27. The method according to claim **26**, wherein the detection of the target sequence comprises PCR amplification and nucleotide sequencing.

* * * * *