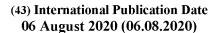
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(57) Abstract: Probe sets capable of detecting pathogen nucleic acids in a sample are described. The probe set can be provided on a solid support, such as a microarray. Methods of detecting pathogen nucleic acids in a sample using the probe set are also provided. In some examples, the probes and methods are capable of detecting one or more RNA viruses, one or more DNA viruses, one or more bacterial nucleic acids, and/or one or more protozoan nucleic acids in a sample.

METHODS AND COMPOSITIONS FOR DETECTING TRANSFUSION-TRANSMITTED PATHOGENS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 62/799,482, filed January 31, 2019, which is incorporated herein by reference in its entirety.

FIELD

This disclosure relates to compositions and methods for detecting pathogens in a sample, particularly probes and microarrays and methods of their use.

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This invention was made with Government support under project number Z01 CL002068-28 by the National Institutes of Health, Clinical Center. The Government has certain rights in the invention.

BACKGROUND

Each year millions of blood donations are collected globally and millions of blood components are transfused to patients. Though screening of these blood units using serologic and nucleic acid testing (NAT) has greatly reduced the risk of some transfusion-transmitted infections (TTIs), the vast majority of bloodborne agents are not screened (Alter *et al.*, *Semin. Hematol.* 44:32-41, 2007; Glynn *et al.*, *Transfusion* 53:438-454, 2013; Leveton *et al.*, *Transfusion* 36:919-927, 1996). The U.S. Food and Drug Administration-licensed methods for infectious disease screening of donor blood include: 1) nucleic acid testing (NAT) for Hepatitis B virus (HBV), Hepatitis C virus (HCV), HIV-1 and -2, Babesia, West Nile virus (WNV) and Zika virus (ZIKV); and 2) immunoassays for HBV, HCV, HIV-1 and -2, cytomegalovirus (CMV), human T-cell lymphotropic virus I and II (HTLV), Treponema pallidum (syphilis), and Trypanosoma cruzi (Chagas). HTLV, syphilis, and Chagas antibody testing fail to detect these pathogens during a window period and Chagas is screened only once on samples from first-time blood donors (Duncan *et al.*, *Exp. Rev. Mol. Diagn.* 16:83-95, 2016).

The American Association of Blood Banks Transfusion-Transmitted Diseases Committee produced a list of over 30 pathogens of concern for transmission via blood that included bacteria, parasites, prions and viruses (Stramer *et al.*, *Transfusion* 49:1S-29S, 2009). Only prions cannot be detected by currently available technology. Nearly all the other agents currently require individual qPCR or serologic testing and it is logistically impractical and cost prohibitive to test all known and potential agents individually (Stramer *ISBT Science Series* 9:30-37, 2014; Atrey *et al.*, *Transfusion* 51:1855-1871, 2011).

Multiplex PCR-based devices for testing blood-borne pathogens are limited. FDA-approved blood donor screening assays that use transcription-mediated amplification for multiplex detection of HBV, HCV,

and HIV 1 and 2 include the cobas TaqScreen MPX Test (Roche Molecular Systems, Inc.) and the Procleix Ultrio Plus (Gen-Probe, Inc.) (Duncan *et al.*, *Exp. Rev. Mol. Diagn.* 16:83-95, 2016).

SUMMARY

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A multiplex assay capable of detecting many, most, or all known pathogens of concern in a single small blood sample with high sensitivity and specificity could significantly increase the safety of the blood supply. Further, to counter emerging pathogens, the platform should be adaptable for rapid addition and validation of probes to detect new agents. Microarray-based technology offers the advantage of multiplex detection in a miniaturized format with high adaptability.

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Disclosed herein are probe sets that include probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, or at least 99% identity) with the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769, or subsets thereof. In some examples, the probe set includes probes with the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769, or a subset thereof. In some embodiments, the probe set includes one or more probes (such as 30 or more probes) for one or more RNA viruses, such as one or more of Chikungunya virus, Dengue virus type 1, Dengue virus type 2, Dengue virus type 3, Dengue virus type 4, Hepatitis A virus, Hepatitis C virus type 1, Hepatitis C virus type 2, Hepatitis C virus type 3, Hepatitis E virus, Human immunodeficiency virus type 1, Human immunodeficiency virus type 2, Human T-lymphotropic virus type 1, Human immunodeficiency virus type 2, Human T-lymphotropic virus type 1, West Nile virus, and Zika virus.

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In other embodiments, the probe set includes one or more probes for one or more DNA viruses, such as one or more of cytomegalovirus (CMV, also known as HHV-5), Epstein Barr virus (EBV, also known as HHV-4, for example subtype B95-8 and/or AG876)), human herpes virus 8 (HHV-8), Hepatitis B virus (such as one or more of Hepatitis B virus subtype adw, subtype adw, subtype adr, and subtype ayr), human parvovirus B19, and human papillomavirus (HPV, such as one or more of type 6, 11, 16, and 18). In some embodiments, the probe set includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, or at least 99% identity) with the nucleic acid sequences of SEQ ID NOs: 1770-2647, or a subset thereof. In some examples, the probe set includes probes with the nucleic acid sequences of SEQ ID NOs: 1770-2647, or a subset thereof.

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Further disclosed are probe sets that include one or more probes for one or more bacterial or protozoan pathogens, such as one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi Leishmania major, Babesia microti, Plasmodium falciparum, and Plasmodium vivax.* In some embodiments, the probe set includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, or at least 99% identity) with the nucleic acid sequences of SEQ ID NOs: 2648-3207, or a subset thereof. In some examples, the probe set includes probes with the nucleic acid sequences of SEQ ID NOs: 2648-3207, or a subset thereof.

In some embodiments, the disclosed probe sets include at least one negative control probe and/or at least one positive control probe. In some examples the negative control probe is a probe with at least 90% identity (such as at least 90%, at least 95%, at least 98%, or at least 99% identity) with the nucleic acid sequences of any one of SEQ ID NOs: 1571-1690. In other examples the control probe is a probe with at least 90% identity (such as at least 90%, at least 95%, at least 98%, or at least 99% identity) with the nucleic acid sequences of any one of SEQ ID NOs: 3208-3628.

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In one non-limiting embodiment, the probe set is a set of probes including each of SEQ ID NOs: 1-1769. In another non-limiting embodiment, the probe set is a set of probes including each of SEQ ID NOs: 1770-2647 and 3208-3628, each of SEQ ID NOs: 2648-3628, or each of SEQ ID NOs: 1770-3628. In a further non-limiting embodiment, the microarray includes probes including each of SEQ ID NOs: 1-3628.

Also disclosed are microarrays that include a probe set described herein, for example, wherein the probes are covalently linked to a solid support. In one non-limiting example, the microarray includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, at least 99%, or at least 100% identity) with the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769, or subsets thereof. In another non-limiting example, the microarray includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, at least 99%, or at least 100% identity) with the nucleic acid sequences of SEQ ID NOs: 1770-2647, or subsets thereof. In a further non-limiting example, the microarray includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, at least 99%, or at least 100% identity) with the nucleic acid sequences of SEQ ID NOs: 2648-3207, or subsets thereof. In yet another non-limiting embodiment, the microarray includes probes with at least 90% identity (such as at least 90%, at least 95%, at least 98%, at least 99%, or at least 100% identity) with the nucleic acid sequences of SEQ ID NOs: 1770-3207, or subsets thereof. The microarray may further include negative and/or positive control probes. In one non-limiting embodiment, the microarray includes probes including each of SEQ ID NOs: 1-1769. In other non-limiting embodiments, the microarray includes probes including each of SEQ ID NOs: 1770-2647 and 3208-3628, each of SEQ ID NOs: 2648-3628, each of SEQ ID NOs: 1770-3628. In a further non-limiting embodiment, the microarray includes probes including each of SEO ID NOs: 1-3628.

Disclosed herein are methods of detecting one or more pathogen nucleic acids in a sample. In some examples, the methods include detecting nucleic acids from one or more RNA viruses, such as one or more of Chikungunya virus, Dengue virus type 1, Dengue virus type 2, Dengue virus type 3, Dengue virus type 4, Hepatitis A virus, Hepatitis C virus type 1, Hepatitis C virus type 2, Hepatitis C virus type 3, Hepatitis E virus, Human immunodeficiency virus type 1, Human immunodeficiency virus type 2, Human T-lymphotropic virus type II, West Nile virus, and Zika virus in a sample. In other examples, the methods include detecting nucleic acids from one or more DNA viruses, such as one or more of cytomegalovirus, Epstein Barr virus, human herpes virus 8, Hepatitis B virus, human parvovirus B19, and human papillomavirus.

Also disclosed are methods of detecting one or more bacterial and/or protozoan nucleic acids in a sample. In some examples, the methods include detecting nucleic acids from one or more of *Treponema* pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum, and Plasmodium vivax.

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In some examples, the methods include contacting a sample with a disclosed probe set or microarray under conditions sufficient to allow hybridization of pathogen nucleic acids present in the sample to the probes of the probe set or microarray and measuring hybridization of the sample to one or more of the probes, thereby detecting one or more nucleic acids in the sample. The sample may be a blood, serum, or plasma sample, or nucleic acids (such as RNA or cDNA) isolated from the sample. In particular examples, the sample is a blood donation sample or nucleic acids isolated from a blood donation sample. In particular examples, nucleic acids (such as RNA or cDNA) from the sample are labeled prior to contacting the probe set or microarray with the nucleic acids. In one example, the method includes preparing cDNA from the sample and labeling the cDNA. In some examples, the method does not include amplifying RNA from the sample prior to preparing the cDNA.

The foregoing and other features of the disclosure will become more apparent from the following detailed description, which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1C are a series of panels showing pathogen chip design (FIG. 1A), sample preparation work flow (FIG. 1B), and analysis strategy (FIG. 1C) for pathogen detection microarrays.

FIGS. 2A-2C are a series of graphs showing amplification method and Pathogen Chip assay performance assessed using positive control viral RNAs. FIG. 2A shows SPIA amplification vs. standard (STD) method. cDNA concentration after amplification for four representative viral RNAs is shown. Starting RNA concentration was <10 ng/μl each. FIG. 2B shows Pathogen chip assay performance 1. Bars are the mean of Cy3 signal for the Chikungunya and West Nile probes hybridized to test samples positive for CHIKV and WNV and a negative plasma sample. Only probes specific to target showed a specific hybridization signal. No signal was detected for negative plasma. FIG. 2C shows Pathogen chip assay performance 2. Detection responses of four representative samples (Dengue-4) were measured over a dilution series from 10,000 to 10 genomic copies per sample. Bars are the mean of Cy3 signals for all probes to the indicated viruses hybridized to test samples.

SEQUENCE LISTING

Any nucleic acid and amino acid sequences listed herein or in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases and amino acids, as defined in 37 C.F.R. § 1.822. In at least some cases, only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand.

In the accompanying sequence listing: SEO ID NOs: 1-110 are Hepatitis C virus genotype 1 probes SEQ ID NOs: 111-210 are Hepatitis C virus genotype 2 probes SEQ ID NOs: 211-310 are Hepatitis C virus genotype 3 probes 5 SEO ID NOs: 311-400 are Human Immunodeficiency virus 1 probes SEQ ID NOs: 401-510 are Human Immunodeficiency virus 2 probes SEQ ID NOs: 511-570 are Human T-lymphotropic virus I probes SEQ ID NOs: 571-660 are Human T-lymphotropic virus II probes SEQ ID NOs: 661-760 are West Nile virus NY99 probes 10 SEQ ID NOs: 761-870 are West Nile virus 956 probes SEO ID NOs: 871-900 are Chikungunya virus probes SEQ ID NOs: 901-1000 are Dengue virus 1 probes SEQ ID NOs: 1001-1100 are Dengue virus 2 probes SEQ ID NOs: 1101-1199 are Dengue virus 3 probes 15 SEQ ID NOs: 1200-1300 are Dengue virus 4 probes SEQ ID NOs: 1301-1390 are GB virus C/Hepatitis G virus probes SEQ ID NOs: 1391-1500 are Hepatitis A virus probes SEO ID NOs: 1501-1570 are Hepatitis E virus probes SEQ ID NOs: 1571-1580 are White clover cryptic virus 1 probes 20 SEQ ID NOs: 1581-1620 are Broad bean wilt virus 1 probes SEO ID NOs: 1621-1690 are Lettuce necrotic vellows virus probes SEO ID NOs: 1691-1700 are Zika virus isolate Brazil-ZKV2015 probes SEQ ID NOs: 1701-1710 are Zika virus strain PRVABC59 probes SEQ ID NOs: 1711-1720 are Zika virus isolate Z1106033 probes 25 SEQ ID NOs: 1721-1730 are Zika virus isolate SSABR1 probes SEO ID NOs: 1731-1769 are Zika virus strain ZikaSPH2015 probes SEQ ID NOs: 1770-1852 are Cytomegalovirus probes SEQ ID NOs: 1853-1917 are Epstein Barr virus B95-8 probes SEQ ID NOs: 1918-2023 are Epstein Barr virus AG876 probes 30 SEQ ID NOs: 2024-2108 are Human herpesvirus 8 probes SEQ ID NOs: 2109-2192 are Human papillomavirus subtype 6b probes SEQ ID NOs: 2193-2271 are Human papillomavirus subtype 11 probes SEQ ID NOs: 2272-2342 are Human papillomavirus subtype 16 probes SEQ ID NOs: 2343-2419 are Human papillomavirus subtype 18 probes 35 SEQ ID NOs: 2420-2470 are Hepatitis B virus subtype adw probes SEQ ID NOs: 2471-2520 are Hepatitis B virus subtype ayw probes

SEQ ID NOs: 2521-2556 are Hepatitis B virus subtype adr probes

SEQ ID NOs: 2557-2602 are Hepatitis B virus subtype ayr probes

SEQ ID NOs: 2603-2647 are Human parvovirus B19 probes

SEQ ID NOs: 2648-2751 are Treponema pallidum probes

SEQ ID NOs: 2752-2852 are Ehrlichia chaffeensis probes

SEQ ID NOs: 2853-2861 are Ehrlichia ewingii probes

SEQ ID NOs: 2862-2922 are Ehrlichia muris probes

SEQ ID NOs: 2923-3001 are Borrelia burgdorferi probes

SEQ ID NOs: 3002-3085 are Coxiella burnetii probes

SEQ ID NOs: 3086-3097 are Trypanosoma brucei probes

SEQ ID NO: 3098 is a *Trypanosoma cruzi* probe

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SEQ ID NOs: 3099-3113 are *Leishmania major* probes

SEQ ID NOs: 3114-3154 are Babesia microti probes

SEQ ID NOs: 3155-3185 are *Plasmodium falciparum* probes

SEQ ID NOs: 3186-3207 are Plasmodium vivax probes

SEQ ID NOs: 3208-3301 are human ACTB probes

SEQ ID NOs: 3302-3385 are human ARL1 probes

SEQ ID NOs: 3386-3519 are human CCDN1 probes

SEQ ID NOs: 3520-3557 are Aedes albopictus densovirus 2 probes

SEQ ID NOs: 3558-3598 are Maize streak virus probes

SEQ ID NOs: 3599-3628 are Tomato pseudo-curly top virus probes

DETAILED DESCRIPTION

Disclosed herein are customized sets of probes, including microarray-based pathogen chips, for simultaneous detection of nucleic acids from RNA viruses, DNA viruses, and/or bacteria or protozoan pathogens in blood samples (such as human plasma) that are designed to have the flexibility to expand to detect emerging agents in a relatively short time frame. The presence of multiple probes per target represents an advantage in comparison to traditional NAT or EIA assays since the pathogen(s) can be detected even in the case of failure of one of the probes due to mutation (Petrik *Vox Sanguinis* 80:1-11, 2001). The flexibility and high-throughput capability of microarrays hold great potential for pathogen detection and identification, but historically have had limitations in detecting the presence of the low viral levels (Chen *et al.*, *J. Vis. Exp.* 50:e2536, 2011; Wang *et al.*, *Proc. Natl. Acad. Sci. USA* 99:15687-15692, 2002; Eckburg *et al.*, *Clin. Infect. Dis.* 43:e71-e76, 2006). Disclosed herein are probe sets and microarray assays that include: 1) a platform design that simultaneously detects and distinguishes multiple pathogens and closely related strains or subtypes; and 2) a combination of amplification and labeling protocols to detect multiple targets present at low levels in a sample.

I. Terms

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Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in *Lewin's Genes X*, ed. Krebs *et al.*, Jones and Bartlett Publishers, 2009 (ISBN 0763766321); Kendrew *et al.* (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Publishers, 1994 (ISBN 0632021829); Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by Wiley, John & Sons, Inc., 1995 (ISBN 0471186341); and George P. Rédei, *Encyclopedic Dictionary of Genetics, Genomics, Proteomics and Informatics*, 3rd Edition, Springer, 2008 (ISBN: 1402067534), and other similar references.

Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. The singular terms "a," "an," and "the" include plural referents unless the context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. Hence "comprising A or B" means including A, or B, or A and B. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description.

Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including explanations of terms, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

In order to facilitate review of the various embodiments of the disclosure, the following explanations of specific terms are provided:

Array or Microarray: An arrangement of nucleic acids (such as DNA or RNA) or proteins (such as antibodies) in assigned locations on a matrix or substrate. In some examples, the nucleic acid molecules or proteins are attached covalently to the matrix or substrate.

Babesia: A tick-borne protozoan parasite that infects vertebrate red blood cells. In humans, *Babesia* species may cause asymptomatic infection or babesiosis, characterized by flu-like symptoms. Most cases of transmission between humans are attributed to a tick vector; however, it may also be transmitted through blood transfusion or organ donation. The most common pathogenic species in humans are *Babesia divergens* and *Babesia microti*. *Babesia* sequences are publicly available, and include GenBank Accession Nos. ASM107745v2 (*Babesia divergens*) and ASM69194v2 and ASM165006v1 (*Babesia microti*), which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Borrelia: A genus of tick-borne spirochete bacteria that cause Lyme disease. The major species of Borrelia that cause Lyme disease include Borrelia burgdorferi, Borrelia afzelii, Borrelia garinii, and Borrelia mayonii. Borrelia has been identified in blood stored for donation, though there is currently no evidence of Lyme disease linked to blood transfusion. Borrelia sequences are publicly available, and

include GenBank Accession Nos. ASM868v2 (*Borrelia burgdorferi*), ASM30473v1 (*Borrelia afzelii*), ASM192254v1 (*Borrelia garinii*), and ASM194566v1 (*Borrelia mayonii*), which are incorporated by reference in their entirety as present in GenBank on January 30, 2020).

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Chikungunya virus (CHIKV): A positive-sense single-stranded RNA virus of the alphavirus genus in the family *Togaviridae*. This virus is primarily transmitted by *Aedes* mosquitoes, particularly *A. albopictus* and *A. aegypti*. The symptoms of CHIKV infection include rash, high fever and joint pain. CHIKV was first isolated in Tanzania in 1952 and re-emerged in Kenya in 2004. The evolution and spread of this virus into new geographic areas, and the disease severity resulting from CHIKV infection, present a serious public health concern. CHIKV sequences are publicly available, and include GenBank Accession No. NC_004162 (gi|27754751)), which is incorporated by reference in its entirety as present in GenBank on January 30, 2019.

Coxiella burnetii: A Gram-negative bacteria that causes Q fever. Symptoms are typically flu-like and may be mild or severe, and a small percentage of infected individuals develop chronic Q fever. The bacteria infects livestock (such as cows, sheep, and goats) and is transmitted to humans by contact with feces, urine, milk, or other products from an infected animal, typically by breathing dust contaminated with the bacteria. Coxiella burnetii sequences are publicly available, and includes GenBank Accession No. ASM776v2, which is incorporated by reference in its entirety as present in GenBank on January 30, 2020.

Cytomegalovirus (CMV): Also known as human herpesvirus 5. A common virus that infects up to 50% of adults by the age of 40. Most people show no symptoms of infection or only mild symptoms; however, babies born with congenital CMV infection may have long-term health problems. CMV is transmitted by body fluids, including blood transfusions. CMV sequences are publicly available, and include GenBank Accession No. NC_006273, which is incorporated by reference in its entirety as present in GenBank on January 30, 2020.

Dengue virus (DEN): An RNA virus of the family *Flaviviridae*, genus *Flavivirus*. There are four serotypes of dengue virus, referred to as DEN1, DEN2, DEN3 and DEN4. All four serotypes can cause the full spectrum of dengue disease. Infection with one serotype can produce lifelong immunity to that serotype. However, severe complications can occur upon subsequent infection by a different serotype. Dengue virus is primarily transmitted by *Aedes* mosquitoes, particularly *A. aegypti*. Symptoms of dengue virus infection include fever, headache, muscle and joint pain and a skin rash similar to measles. In a small percentage of cases, the infection develops into a life-threatening dengue hemorrhagic fever, typically resulting in bleeding, low platelet levels and blood plasma leakage, or into dengue shock syndrome, characterized by dangerously low blood pressure. DEN sequences are publicly available, and include GenBank Accession Nos. NC_001477 (gi|9626685) (DEN1), NC_001474 (gi|158976983) (DEN2), NC_001475 (gi|163644368) (DEN3), and NC_002640 (gi|12084822) (DEN4), which are incorporated by reference in their entirety as present in GenBank on January 30, 2019.

Epstein-Barr virus (EBV): Also known as human herpesvirus 4. EBV is a common virus that is spread primarily through saliva, though it can also be spread by sexual contact, blood transfusion, and organ

transplantation. EBV causes infectious mononucleosis, characterized by fatigue, fever, swollen lymph nodes, and sore throat; however, EBV infection may also be asymptomatic. EBV sequences are publicly available, and include GenBank Accession Nos. AJ278309 (EBV strain B95-8), DQ279927 (EBV strain AG876), and NC_009334, all of which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

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Ehrlichia: A genus of tick-borne bacteria that causes ehrlichiosis. In some cases, *Ehrlichia* has been transmitted through blood transfusion or organ transplantation. Symptoms can include rash, fever, headache, muscle aches, nausea, vomiting, and diarrhea. Severe, late stage illness can include neural damage, respiratory failure, and organ failure. Disease causing species include *Ehrlichia chaffeensis*, *Ehrlichia ewingii*, and *Ehrlichia muris*. *Ehrlichia* sequences are publicly available, and include GenBank Accession Nos. NC_007799 (*E. chaffeensis*) and NC_023063 (*E. muris*), which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Hepatitis A virus (HAV): A single-stranded RNA virus in the order *Picornavirales*, family *Picornaviridae*. The virus is transmitted through fecal-oral and blood routes. HAV causes symptoms such as nausea, vomiting, diarrhea, jaundice, fever, and abdominal pain and typically lasts about 8 weeks. Acute liver failure may occur in some cases. HAV sequences are publicly available, and include GenBank Accession No. NC_001489 (gi|9626732), which is incorporated by reference in its entirety as present in GenBank on January 30, 2019.

Hepatitis B virus (HBV): A DNA virus of the *Hepadnaviridae* family. HBV is transmitted through blood or bodily fluids and new infections are frequently asymptomatic in healthy adults. Immunosuppressed adults and children less than 5 years of age more commonly exhibit symptoms, including flu-like symptoms and jaundice. HBV sequences are publicly available and include GenBank Accession Nos. AY518556 (subtype adw), NC_003977 (subtype ayw), AY123041 (subtype adr), and X04615 (subtype ayr), all of which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Hepatitis C virus (HCV): A single-stranded positive sense RNA virus of the family *Flaviviridae*. HCV is transmitted primarily through blood and acute infection typically causes mild or no symptoms. However, chronic infection frequently leads to liver disease, including cirrhosis, liver failure, and/or hepatocellular carcinoma. HCV type 1 sequences are publicly available, and include GenBank Accession No. NC_004102 (gi|22129792). HCV type 2 sequences are also publicly available, and include GenBank Accession No. NC_009823 (gi|157781212). HCV type 3 sequences are also publicly available, and include GenBank Accession No. NC_009824 (gi|157781216). Each of these sequences are incorporated by reference in their entirety as present in GenBank on January 30, 2019.

Hepatitis E virus (HEV): A single-stranded positive sense RNA virus that is currently classified in the *Hepeviridae* family, genus *Orthohepevirus*. HEV causes liver inflammation, and is typically an acute and self-limiting infection. However, it can cause chronic hepatitis in individuals with weakened immune systems, particularly organ transplant recipients. HEV sequences are publicly available, and include

GenBank Accession No. NC_001434 (gi|9626440), which is incorporated by reference in its entirety as present in GenBank on January 30, 2019.

Human Immunodeficiency virus (HIV): A single-stranded positive-sense RNA virus (retrovirus) that causes HIV infection and acquired immunodeficiency syndrome (AIDS). HIV is transmitted by blood or sexual contact. HIV type 1 sequences are publicly available, and include GenBank Accession No. NC_001802 (gi|9629357). HIV type 2 sequences are also publicly available and include GenBank Accession No. NC_001722 (gi|9628880). Each sequence is incorporated by reference in their entirety as present in GenBank on January 30, 2019

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Human Herpesvirus 8 (HHV-8): Also known as Kaposi sarcoma-associated herpesvirus. HHV-8 is associated with Kaposi sarcoma and other cancers, including some lymphomas. It is transmitted through bodily fluids, including blood, saliva, and sexual contact. HHV-8 sequences are publicly available and include GenBank Accession No. NC_009333, which is incorporated by reference in its entirety as present in GenBank on January 30, 2020.

Human parvovirus: A single-stranded DNA virus of the *Parvoviridae* family. Parvovirus B19 is the only parvovirus known to infect humans. B19 primarily causes disease in children, and causes what is sometimes called "fifth disease," a mild rash. Parvovirus B19 can be transmitted via respiratory secretions or through blood or blood products. Human parvovirus B19 sequences are publicly available and include GenBank Accession No. NC_000883, which is incorporated by reference in its entirety as present in GenBank on January 30, 2020.

Human papillomavirus (HPV): A DNA virus of the family *Papillomaviridae*. HPV is a common sexually transmitted virus that can cause warts and cancers, including cervical cancer and head and neck cancer, in some individuals. HPV DNA can be detected in the blood in some cases; however, it is not clear whether it can be transmitted by blood transfusion. There are over 100 known types of HPV to date. HPV sequences are publicly available, and include GenBank Accession Nos. HG793809 (type 6), HE574701 (type 11), NC_001526 (type 16), and NC_001357 (type 18), each of which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Human T-lymphotropic virus (HTLV): A group of positive-sense RNA retroviruses that are implicated in cancer (for example, T-cell lymphomas) and myelopathy. HTLV type I sequences are publicly available, and include GenBank Accession Nos. AF033817 and NC_001436 (gi|9626453). HTLV type II sequences are also publicly available and include GenBank Accession No. NC_001488 (gi|9626726). Each sequence is incorporated by reference in their entirety as present in GenBank on January 30, 2019

Leishmania major: A trypanosomatid parasite transmitted by sand flies. *L. major* causes cutaneous leishmaniosis. *L. major* sequences are publicly available, and include GenBank Accession No. ASM272v2, incorporated by reference in its entirety as present in GenBank on January 30, 2020.

Plasmodium: A genus of mosquito-transmitted protozoan parasites that causes malaria in humans. The two major malaria causing *Plasmodium* species in humans are *P. falciparum* and *P. vivax. P. falciparum* is also associated with Burkitt's lymphoma. *Plasmodium* can be transmitted by blood

transfusion, causing transfusion-transmitted malaria. *Plasmodium* sequences are publicly available and include GenBank Accession No. ASM276v2 (*P. falciparum*) and ASM241v2 (*P. vivax*), which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Probe: A probe typically comprises an isolated nucleic acid (for example, at least 10 or more nucleotides in length, such as 10-60, 15-50, 20-40, 20-50, 25-50, or 30-60 nucleotides in length). In some examples, a probe includes a detectable label, while in other examples a probe does not include a detectable label.

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Sample (or biological sample): A biological specimen containing nucleic acids (for example, DNA, RNA, and/or mRNA), proteins, or combinations thereof, obtained from a subject. Examples include, but are not limited to, peripheral blood, serum, plasma, urine, saliva, tissue biopsy, fine needle aspirate, surgical specimen, and autopsy material. In some examples, a sample includes blood, serum, or plasma.

Subject: A living multi-cellular vertebrate organism, a category that includes human and non-human mammals. In one example, a subject is a blood donor.

Treponema: A genus of spirochete bacteria. The major pathogenic species in humans is *Treponema pallidum*, of which subspecies *T. pallidum pallidum* causes syphilis. The bacteria is transmitted primarily by sexual contact. Nucleic acid sequences for *T. pallidum pallidum* are publicly available and include GenBank Accession Nos. NC_016844 and NC_00919, which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

Trypanosoma: A genus of protozoan parasites transmitted by blood-feeding insects. *T. brucei* is transmitted by infected tsetse flies and causes sleeping sickness (trypanosomiasis) in humans. There are two types of trypanosomiasis: East African trypanosomiasis, caused by *Trypanosoma brucei rhodesiense* and West African trypanosomiasis, caused by *Trypanosoma brucei gambiense*. *Trypanosoma brucei brucei* infects primarily cattle, and does not normally infect humans. *T. cruzi* causes Chagas disease and is transmitted by triatomine bugs. *Trypanosoma* sequences are publicly available and include GenBank Accession Nos. ASM21029v1 (*T. brucei gambiense*), and ASM20906v1 (*T. cruzi*), each of which are incorporated by reference in their entirety as present in GenBank on January 30, 2020.

West Nile virus (WNV): A member of the virus family *Flaviviridae* and the genus *Flavivirus*. WNV was first isolated from a woman in the West Nile district of Uganda in 1937. The virus was later identified in birds in the Nile delta region in 1953. Human infections attributable to WNV have been reported in many countries for over 50 years. In 1999, a WNV circulating in Israel and Tunisia was imported into New York, producing a large and dramatic outbreak that spread throughout the continental United States in the following years. Human infection is most often the result of bites from infected mosquitoes, but may also be transmitted through contact with other infected animals, their blood or other tissues. Infection with WNV is asymptomatic in about 80% of infected people, but about 20% develop West Nile fever. Symptoms include fever, headache, fatigue, body aches, nausea, vomiting, swollen lymph glands and in some cases, a skin rash. Approximately 1 in 150 of infected individuals develop severe, neuroinvasive disease, such as encephalitis, meningitis, or poliomyelitis. WNV sequences are publicly

available, and include GenBank Accession Nos. NC_009942 (gi|158516887) (NY99, lineage 1) and NC_001563 (gi|11528013) (956, lineage 2), which are incorporated by reference in their entirety as present in GenBank on January 30, 2019.

Zika virus (ZKV or ZikV): A member of the virus family *Flaviviridae* and the genus *Flavivirus*. ZikV is spread by the daytime-active mosquitoes *Aedes aegypti* and *A. albopictus*. This virus was first isolated from a *Rhesus* macaque from the Zika Forest of Uganda in 1947. Since the 1950s, ZikV has been known to occur within a narrow equatorial belt from Africa to Asia. The virus spread eastward across the Pacific Ocean in 2013-2014, resulting in ZikV outbreaks in Oceania to French Polynesia, New Caledonia, the Cook Islands, and Easter Island. In 2015, ZkV spread to Mexico, Central America, the Caribbean and South America, where ZkV has reached pandemic levels. Infection by ZikV generally causes either no symptoms or mild symptoms, including mild headache, maculopapular rash, fever, malaise, conjunctivitis and joint pain. However, ZkV infection has been linked to the birth of microcephalic infants following maternal infection. Reports have also indicated that ZikV has the potential for human blood-borne and sexual transmission. ZikV sequences are publicly available, and include GenBank Accession Nos. KU497555 (gi|985578255) (isolate Brazil-Zk2015), KU501215 (gi|984874581) (strain PRVABC59), KU312312 (gi|973447404) (isolate Z1106033), KU707826 (gi|992324757) (isolate SSABR1), and KU321639 (strain ZikaSPH2015), which are incorporated by reference in their entirety as present in GenBank on January 30, 2019.

20 II. Probes and Microarrays

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Disclosed herein is a nucleic acid probe set capable of detecting nucleic acid molecules from one or more RNA viruses, including Chikungunya virus (CHIKV), Dengue virus types 1, 2, 3, or 4, (DEN1, DEN2, DEN3, DEN4), Hepatitis A virus (HAV), Hepatitis C virus (HCV) types 1, 2, or 3, Hepatitis E virus (HEV), Human Immunodeficiency virus (HIV) types 1 or 2, Human T-lymphotropic virus (HTLV) types I or II, West Nile virus (WNV), and Zika virus (ZKV). In some embodiments, the probe set includes 30 or more probes for one or more of the viruses (such as 30 or more, 50 or more, 60 or more, 70 or more, 80 or more, 90 or more, 100 or more, 110 or more, or 120 or more), for example 30-120 probes, 50-100 probes, or 70-110 probes for one or more of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1, HIV type 2, HTLV type 1, HTLV type 2, WNV, and ZIKV.

In some embodiments, the probe set includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In other embodiments, the probe set includes a subset of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In some examples, the subset includes at least one probe for each of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1,

HIV type 2, HTLV type 1, HTLV type 2, WNV, and ZKV, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each virus. In some examples, the subset includes at least 40 probes (such as at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, or at least 110 probes) for one or more of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1, HIV type 2, HTLV type 1, HTLV type 2, WNV, and ZKV.

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In one non-limiting example, the probe set includes or consists of each of the probes of SEQ ID NOs: 1-1769. In another non-limiting example, the probe set includes or consists of each of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In another example, the probe set includes or consists of each of the probes of SEQ ID NOs: 1-1300 and 1391-1769. In other embodiments, the probe set includes a subset of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769 or a subset of the probes of SEQ ID NOs: 1-1300 and 1391-1769.

Also disclosed herein is a nucleic acid probe set capable of detecting nucleic acid molecules from one or more DNA viruses, including one or more of cytomegalovirus, Epstein Barr virus (*e.g.*, one or more of EBV subtype B95-8 and EBV subtype AG876), human herpes virus 8, Hepatitis B virus (*e.g.*, one or more of HBV subtypes adw, ayw, adr, and ayr), human parvovirus B19, and human papillomavirus (*e.g.*, one or more of HPV types 6, 11, 16, and 18). In some embodiments, the probe set includes 10 or more probes for one or more of the viruses (such as 15 or more, 20 or more, 30 or more, 50 or more, 60 or more, 70 or more, 80 or more, 90 or more, 100 or more, 110 or more, or 120 or more), for example 10-50 probes, 30-120 probes, 50-100 probes, or 70-110 probes for one or more of cytomegalovirus, Epstein Barr virus, human herpes virus 8, Hepatitis B virus, human parvovirus B19, and human papillomavirus.

In some embodiments, the probe set includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1770-2647. In other embodiments, the probe set includes a subset of the probes of SEQ ID NOs: 1770-2647, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 1770-2647. In some examples, the subset includes at least one probe for each of CMV, EBV subtype B95-8, EBV subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, HPV type 6, HPV type 11, HPV type 16, and HPV type 18, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each virus. In some examples, the subset includes at least 10 probes (such as at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, or at least 110 probes) for one or more of CMV, EBV subtype B95-8, EBV subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, HPV type 6, HPV type 11, HPV type 16, and HPV type 18. In one non-limiting example, the probe set includes or consists of each of the probes of SEQ ID NOs: 1770-2647.

Further disclosed herein is a nucleic acid probe set capable of detecting nucleic acid molecules from one or more bacterial and/or protozoan pathogens, including one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum,* and *Plasmodium vivax*. In some embodiments, the probe set includes 10 or more probes for one or more of the viruses (such as 10 or more, 20 or more, 30 or more, 50 or more, 60 or more, 70 or more, 80 or more, 90 or more, 100 or more, 110 or more, or 120 or more), for example 30-120 probes, 50-100 probes, or 70-110 probes for one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Leishmania major, Babesia microti, Plasmodium falciparum*, and *Plasmodium vivax*

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In some embodiments, the probe set includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 2648-3207. In other embodiments, the probe set includes a subset of the probes of SEQ ID NOs: 2648-3207, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 50%, at least 97%, at least 98%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 2648-3207. In some examples, the subset includes at least one probe for each of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii*, *Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum*, and *Plasmodium vivax*, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each pathogen. In some examples, the subset includes at least 10 probes (such as at least 20, at least 30, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, or at least 110 probes) for one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Leishmania major, Babesia microti, Plasmodium falciparum*, and *Plasmodium vivax*. In one non-limiting example, the probe set includes or consists of each of the probes of SEQ ID NOs: 2648-3207.

In further embodiments, one or more of the disclosed probe sets are combined. Thus, some embodiments, the probe set includes probes for detecting at least one RNA virus, at least one DNA virus, at least one bacterial pathogen, at least one protozoan pathogen, or combinations of two or more thereof. In one example, a probe set includes probes capable of detecting nucleic acid molecules from one or more DNA viruses and one or more bacterial and/or protozoan pathogens. In one non-limiting example, a probe set includes probes including or consisting of each of the probes of SEQ ID NOs: 1770-3207. In another example, a probe set includes probes capable of detecting nucleic acid molecules from one or more RNA viruses, one or more DNA viruses, and one or more bacterial and/or protozoan pathogens. In a non-limiting example, the probe set includes probes including or consisting of each of the probes of SEQ ID NOs: 1-1300, SEQ ID NOs: 1391-1570, SEQ ID NOs: 1691-1769, and SEQ ID NOs: 1770-3207.

In additional embodiments, a disclosed probe set further includes one or more control probes, such as one or more positive and/or negative control probes. For testing for validity of the run, intra-array

reproducibility control and normalization. positive control probes may include one or more of: 1) one or more reference probes for intensity normalization, 2) one or more internal standards of known concentrations, and 3) one or more probes that are homologous to an internal control included in the hybridization mix. In some embodiments, positive control probes include one or more (such as 1, 10, 25, 50, 96, or more) ERCC probes (External RNA Controls Consortium) and one or more (such as 1, 10, 25, 50, 96, 250, 500, 900, or more) biological replicates targeting human genome sequences (for example, to define possible host contaminant).

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Negative control probes may include one or more probes for a virus that is known not to be present in human or mammalian subjects. In some non-limiting examples, negative control probes are specific for a plant virus. In other examples, negative control probes can be a structural negative probe, such as a sequence that forms a hairpin and does not hybridize with nucleic acids from any species.

In some examples, the probe set includes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, or at least 120 control probes. In some examples, the control probes are for one or more one or more different negative control viruses (such as 1, 2, 3, 4, 5, or more negative control viruses). In some examples, the probe set includes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, at least 120, or more negative control probes. In some examples, the negative control probes are probes for one or more of White clover cryptic virus 1 (*e.g.* SEQ ID NOs: 1571-1580), Broad bean wilt virus 1 (*e.g.*, SEQ ID NOs: 1582-1620), Lettuce necrotic yellows virus (*e.g.*, SEQ ID NOs: 1621-1690), Aedes albopictus densovirus 2 (*e.g.*, SEQ ID NOs: 3520-3557), Maize streak virus (*e.g.*, SEQ ID NOs: 3558-3598), and/or Tomato pseudo-curly top virus (*e.g.*, SEQ ID NOs: 3599-3628). In additional examples, the probe set includes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 110, at least 120, or more positive control probes. In some examples, the positive control probes are probes for one or more housekeeping genes, such as one of more of ACTB (*e.g.*, SEQ ID NOs: 3208-3301), ARL1 (*e.g.*, SEQ ID NOs: 3302-3385), and/or CCDN1 (*e.g.*, SEQ ID NOs: 3386-3519).

In some embodiments, the disclosed probes are between 30 and 80 nucleotides in length (for example 30-50, 40-60, 50-70, or 60-80 nucleotides in length). In some examples, the probes are 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 nucleotides in length and are capable of hybridizing to the disclosed pathogen (*e.g.*, viral, bacterial, or protozoan) nucleic acid molecules. In some examples, the probes are 60 nucleotides in length. In some examples, each of the probes in the probe set has a Tm between about 72-89°C, such as about 74-88°C, about 75-85°C, or about 76-82°C. In one specific example, each of the probes in the probe set has a Tm between 74.4 and 87.8°C. Tm ranges for exemplary RNA virus probes are shown in Table 1.

In other embodiments the disclosed probe sets, or a subset thereof, are linked to a solid support. In some examples, the disclosed probe sets, or a subset thereof, are included on a microarray. In other examples, the solid support is a bead or plurality of beads, a microplate, column, or microfluidic device.

In some embodiments, the microarray is a solid support or substrate including the probe set (or subset thereof) covalently linked to the support or substrate. Within an array, each arrayed probe is addressable, in that its location can be reliably and consistently determined within at least two dimensions of the array. Addressable arrays usually are computer readable, in that a computer can be programmed to correlate a particular address on the array with information about the sample at that position (such as hybridization or binding data, including for instance signal intensity).

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The microarray can include any of the probe sets described above, individually, or in combination. In some embodiments, the microarray includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In another embodiment, the microarray includes or consists of nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1-1300 and 1391-1769. In one non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In a further non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In a further non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1-1300 and 1391-1769.

In another embodiment, the microarray includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1770-2647. In one non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1770-2647. In another non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1170-2647 and 3250-3628.

In another embodiment, the microarray includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 2648-3207. In one non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 2648-3207. In another non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 2648-3519.

In a further embodiment, the microarray includes nucleic acid probes that are at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the nucleic acid sequences of SEQ ID NOs: 1770-3207. In one non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1770-3207. In a further non-limiting example, the microarray includes or consists of each of the probes of SEQ ID NOs: 1770-3628.

In other embodiments, the microarray includes a subset of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769. In some examples, the microarray includes at least one probe for each of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1, HIV type 2, HTLV type 1, HTLV type 2,

WNV, and ZKV, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each virus. In some examples, the microarray includes at least 40 probes (such as at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, or at least 110 probes) for one or more of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1, HIV type 2, HTLV type 1, HTLV type 2, WNV, and ZKV.

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In other embodiments, the microarray includes a subset of the probes of SEQ ID NOs: 1770-2647, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 1770-2647. In some examples, the microarray includes at least one probe for each of CMV, EBV subtype B95-8, EBV subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, HPV type 6, HPV type 11, HPV type 16, and HPV type 18, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each virus. In some examples, the microarray includes at least 10, or at least 110 probes) for one or more of CMV, EBV subtype B95-8, EBV subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayr, Hepatitis B virus subtype adr, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, HPV type 6, HPV type 11, HPV type 16, and HPV type 18.

In other embodiments, the microarray includes a subset of the probes of SEQ ID NOs: 2648-3207, such as at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 99%, or at least 99.9% of the probes of SEQ ID NOs: 2648-3207. In some examples, the microarray includes at least one probe for each of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum*, and *Plasmodium vivax*, such as at least 1, at least 2, at least 5, at least 10, at least 20, at least 30, or more probes for each virus. In some examples, the microarray includes at least 10 probes (such as at least 30, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, or at least 110 probes) for one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Leishmania major, Babesia microti, Plasmodium falciparum*, and *Plasmodium vivax*.

In additional embodiments, the microarray includes one or more control probes, such as one or more positive and/or negative control probes. In some examples, the microarray includes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, or at least 120 negative control probes. In some examples, the microarray includes one or more negative control probes selected from SEQ ID NOs: 1571-1580, SEQ ID NOs: 1582-1620, SEQ ID NOs: 1621-1690, and SEQ ID NOs: 3520-3628. In additional examples, the microarray includes at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 110, or at least 120

positive control probes. In some examples, the microarray includes one or more positive control probes selected from SEQ ID NOs: 3208-3519.

The solid support or substrate of the array can be formed from an organic polymer. Suitable materials for the solid support include, but are not limited to: polypropylene, polyethylene, polybutylene, polybutylene

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A wide variety of array formats can be employed in accordance with the present disclosure. One example includes a two-dimensional pattern of discrete cells (such as 4096 squares in a 64 by 64 array). Other array formats including, but not limited to slot (rectangular) and circular arrays are equally suitable for use. In some examples, the array is a multi-well plate. In one example, the array is formed on a polymer medium, which is a thread, membrane or film. An example of an organic polymer medium is a polypropylene sheet having a thickness on the order of about 1 mil. (0.001 inch) to about 20 mil., although the thickness of the film is not critical and can be varied over a fairly broad range. The array can include biaxially oriented polypropylene (BOPP) films, which in addition to their durability, exhibit low background fluorescence.

The array formats of the present disclosure can be included in a variety of different types of formats. A "format" includes any format to which the solid support can be affixed, such as microtiter plates (*e.g.*, multi-well plates), test tubes, inorganic sheets, dipsticks, and the like. For example, membranes can be affixed to glass slides. The particular format is, in and of itself, unimportant. All that is necessary is that the solid support can be affixed thereto without affecting the functional behavior of the solid support or any biopolymer absorbed thereon, and that the format (such as the slide) is stable to any materials into which the device is introduced (such as clinical samples and hybridization solutions).

The arrays of the present disclosure can be prepared by a variety of approaches. In one example, oligonucleotides (*e.g.*, probes) are synthesized separately and then attached to a solid support (see U.S. Patent No. 6,013,789). In another example, probes are synthesized directly onto the support to provide the desired array (see U.S. Patent No. 5,554,501). Suitable methods for covalently coupling oligonucleotides to a solid support and for directly synthesizing oligonucleotides on the support are known; a summary of suitable methods can be found in Matson *et al.*, *Anal. Biochem.* 217:306-10, 1994. In one example, the oligonucleotides are synthesized onto the support using conventional chemical techniques for preparing oligonucleotides on solid supports (such as PCT applications WO 85/01051 and WO 89/10977, or U.S. Patent No. 5,554,501).

The oligonucleotides can be bound to the support or substrate by either the 3' end of the oligonucleotide or by the 5' end of the oligonucleotide. In one example, the oligonucleotides are bound to

the solid support by the 3' end. In general, the internal complementarity of an oligonucleotide probe in the region of the 3' end and the 5' end determines binding to the support.

III. Methods of Detecting Viral Nucleic Acids

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Disclosed herein are methods of detecting one or more pathogen nucleic acids (such as one or more viral, bacterial, and/or protozoan nucleic acids) in a sample from a subject. In some embodiments, the methods include preparing or isolating nucleic acids (such as DNA, RNA, or cDNA) from a sample, labeling the nucleic acids, and contacting the probe set, or a microarray including the probe set, with the labeled nucleic acids under conditions sufficient to allow pathogen nucleic acids present in the sample to hybridize with one or more of the probes. The presence and/or identity of pathogen nucleic acids in the sample is determined by detecting hybridization. In one example, hybridization is detected by measuring presence of labeled nucleic acid at an addressable location in an array.

In particular embodiments, the methods include detecting one or more nucleic acids from RNA viruses in a sample, including one or more of CHIKV, DEN1, DEN2, DEN3, DEN4, HAV, HCV type 1, HCV type 2, HCV type 3, HEV, HIV type 1, HIV type 2, HTLV type I, HTLV type II, WNV, and ZKV. In other embodiments, the methods include detecting one or more nucleic acids from DNA viruses, including one or more of CMV, EBV subtype B95-8, EBV subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, HPV type 6, HPV type 11, HPV type 16, and HPV type 18. In still other embodiments, the methods include detecting one or more nucleic acids from bacteria and/or protozoans, including one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum, and Plasmodium vivax. In further embodiments, the methods include detecting nucleic acids from at least one RNA virus, DNA virus, bacteria, and protozoan, such as at least one of the RNA viruses, DNA viruses, bacteria, and protozoans disclosed herein, or any combination thereof.*

Exemplary samples include peripheral blood, serum, plasma, cerebrospinal fluid, urine, saliva, feces, mucus, nasal wash, tissue biopsy, fine needle aspirate, surgical specimen, placenta, autopsy material, semen, vaginal fluid or tissue, and environmental samples. In particular examples, the sample is a blood sample, such as plasma. In non-limiting examples, the sample is blood or plasma from a blood donor. Thus, in some examples, the methods disclosed herein are used to screen donated blood for one or more pathogens potentially present and/or transmitted through blood transfusions.

In some embodiments, the methods include isolating nucleic acids (such as RNA, cDNA, or a combination thereof) from the sample and contacting the probe set or microarray with the isolated nucleic acids. Methods of isolating RNA (*e.g.*, viral RNA) from a sample are known and include commercially available kits, such as QIAGEN® RNeasy® mini-columns, MASTERPURE® Complete DNA and RNA Purification Kit (EPICENTRE® Madison, Wis.), Paraffin Block RNA Isolation Kit (Ambion, Inc.), and

RNA Stat-60 (Tel-Test). cDNA is then prepared from the isolated RNA, and optionally labeled. In some examples, the methods include amplifying RNA prior to cDNA preparation and labeling, for example, using Quick Amp WT labeling kit (Agilent). Other methods of amplifying RNA include commercially available kits such as Ovation® RNA Amplification kit (Nugen), ArcturusTM RiboAmpTM HS kit (ThermoFisher), and Complete Whole Transcriptome Amplification Kit (WTA2, Sigma-Aldrich).

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In some embodiments, the methods do not include isolating and/or amplifying RNA from a sample prior to labeling. In some examples, the methods include generating amplified cDNA from a sample, followed by labeling the cDNA (for example with a fluorescent label, such as Cy3). In one non-limiting example, amplified cDNA is prepared from the sample using single-primer isothermal amplification (for example, Ribo-SPIA, NuGen) prior to labeling. Methods of labeling cDNA are known and include commercially available kits, such as Genomic DNA Enzymatic Labeling Kit (Agilent). In some examples, the methods generate amplified and labeled cDNA from about 250 pg of target viral RNA (such as about 500 pg, about 750 pg, about 1 ng, about 2 ng, or more of target viral RNA).

In other examples, the methods include isolating DNA from the sample and contacting the probe set or microarray with the isolated DNA. Methods of isolating DNA (such as viral DNA, bacterial DNA, or protozoan DNA) from a sample are known and include commercially available kits. In some examples, the methods include isolating viral DNA from a sample using a viral nucleic acid isolation kit. In one non-limiting example, the viral DNA is isolated using Dynabeads SILANE viral NA kit (Invitrogen). In other examples, bacterial or protozoan DNA is isolated from a sample using a DNA isolation kit. In one non-limiting example, bacterial or protozoan DNA is isolated using QIAamp DNA Blood Mini kit (Qiagen). One of ordinary skill in the art can select appropriate methods or kits to isolate pathogen DNA from samples, for example, blood or plasma samples.

The sample (such as nucleic acids isolated and/or amplified from a sample) can be labeled with any suitable label. Generally, the label will be selected based on the intended use of the sample or the desired readout. In some examples, the sample or nucleic acids from the sample is labelled with a fluorescent or chemiluminescent compound. In other examples, the label is an enzyme, a fluorophore, or a radioactive isotope. In one specific non-limiting example, the label is CyTM3 or CyTM5.

Fluorophores suitable for use with the methods disclosed herein, include, but are not limited to, 6-carboxyfluorescein (FAM), tetrachlorofluorescein (TET), tetramethylrhodamine (TMR), hexachlorofluorescein (HEX), JOE, ROX, CAL FluorTM, PulsarTM, QuasarTM, Texas RedTM, CyTM3 and CyTM5. Other examples of fluorophores that can be used with the methods provided herein include 4-acetamido-4'-isothiocyanatostilbene-2,2'disulfonic acid, acridine and derivatives such as acridine and acridine isothiocyanate, 5-(2'-aminoethyl)amino-naphthalene-1-sulfonic acid (EDANS), 4-amino-N-[3-vinylsulfonyl)phenyl]-naphthalimide-3,5 disulfonate (Lucifer Yellow VS), N-(4-anilino-1-naphthyl)-maleimide, anthranilamide, Brilliant Yellow, coumarin and derivatives such as coumarin, 7-amino-4-methylcoumarin (AMC, Coumarin 120), 7-amino-4-trifluoromethylcouluarin (Coumaran 151); cyanosine; 4',6-diaminidino-2-phenylindole (DAPI); 5', 5"-dibromopyrogallol-sulfonephthalein (Bromopyrogallol Red);

7-diethylamino-3-(4'-isothiocyanatophenyl)-4-methylcoumarin; diethylenetriamine pentaacetate; 4,4'diisothiocyanatodihydro-stilbene-2,2'-disulfonic acid; 4,4'-diisothiocyanatostilbene-2,2'-disulfonic acid; 5-[dimethyl-amino]naphthalene-1-sulfonyl chloride (DNS, dansyl chloride); 4-(4'-dimethylaminophenylazo)benzoic acid (DABCYL); 4-dimethylaminophenylazophenyl-4'-isothiocyanate (DABITC); eosin and derivatives such as eosin and eosin isothiocyanate; erythrosin and derivatives such as erythrosin B and erythrosin isothiocyanate; ethidium; fluorescein and derivatives such as 5-carboxyfluorescein (FAM), 5-(4,6-dichlorotriazin-2-vl)aminofluorescein (DTAF), 2'7'-dimethoxy-4'5'-dichloro-6-carboxyfluorescein (JOE), fluorescein, fluorescein isothiocyanate (FITC), and QFITC (XRITC); fluorescamine; IR144; IR1446; Malachite Green isothiocyanate; 4-methylumbelliferone; ortho cresolphthalein; nitrotyrosine; pararosaniline; Phenol Red; B-phycoerythrin; o-phthaldialdehyde; pyrene and derivatives such as pyrene, pyrene butyrate and succinimidyl 1-pyrene butyrate; Reactive Red 4 (Cibacron .RTM. Brilliant Red 3B-A); rhodamine and derivatives such as 6-carboxy-X-rhodamine (ROX), 6-carboxyrhodamine (R6G), lissamine rhodamine B sulfonyl chloride, rhodamine (Rhod), rhodamine B, rhodamine 123, rhodamine X isothiocyanate, sulforhodamine B, sulforhodamine 101 and sulfonyl chloride derivative of sulforhodamine 101 (Texas Red); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); tetramethyl rhodamine; tetramethyl rhodamine isothiocyanate (TRITC); riboflavin; rosolic acid and terbium chelate derivatives.

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Other fluorophores that can be used include thiol-reactive europium chelates that emit at approximately 617 nm (Heyduk and Heyduk, *Analyt. Biochem.* 248:216-27, 1997; *J. Biol. Chem.* 274:3315-22, 1999). Other fluorophores that can be used include cyanine, merocyanine, styryl, and oxonyl compounds, such as those disclosed in U.S. Patent Nos. 5,627,027; 5,486,616; 5,569,587; and 5,569,766, and in published PCT application no. US98/00475, each of which is incorporated herein by reference. Specific examples of fluorophores disclosed in one or more of these patent documents include CyTM3 and CyTM5, for instance, and substituted versions of these fluorophores. Additional fluorophores that can be used include GFP, LissamineTM, diethylaminocoumarin, fluorescein chlorotriazinyl, naphthofluorescein, 4,7-dichlororhodamine and xanthene (as described in U.S. Patent No. 5,800,996 to Lee *et al.*, herein incorporated by reference) and derivatives thereof. Other fluorophores are commercially available from known sources.

The methods include contacting the sample (such as labeled nucleic acids from a sample) with a probe set disclosed herein (or subset thereof), or a microarray including the probe set (or subset thereof), under conditions sufficient to allow hybridization of pathogen nucleic acids present in the sample to one or more probes and detecting presence of pathogen nucleic acids hybridized to the probe set or microarray.

Presence of one or more pathogen nucleic acids in the sample can be detected using any suitable means. For example, detection of hybridization can be accomplished by detecting nucleic acid molecules (such as RNA) using nucleic acid amplification methods (such as real-time RT-PCR) or array analysis. In a specific embodiment of the microarray technique, labeled cDNA prepared from a sample is applied to an array including a probe set disclosed herein. Labeled cDNA from the sample can hybridize specifically to one or more probes on the array. After washing to remove non-specifically bound probes, the chip is

scanned by confocal laser microscopy or by another detection method, such as a CCD camera. Quantitation of hybridization of sample to each arrayed element allows for assessment of corresponding RNA abundance (e.g., if cDNA is analyzed). Microarray analysis can be performed by commercially available equipment, following manufacturer's protocols, such as are supplied with Affymetrix GeneChip® technology (Affymetrix, Santa Clara, CA), or Agilent's microarray technology (Agilent Technologies, Santa Clara, CA).

In some examples, a sample is determined to contain nucleic acids from a particular pathogen by detecting hybridization between the sample (nucleic acid) and one or more probes of the pathogen-specific probe set. In some examples, a sample is determined to be positive for a pathogen when the log ratio between the signal intensity mean for the pathogen-specific probe set and the mean of a control group probe set is ≥ 1.5 . In other examples, a sample is determined to be negative for a pathogen when the log ratio between the signal intensity mean for the pathogen-specific probe set and the mean of a control group probe set is <1. In further examples, the sample is determined to be borderline for the pathogen when the log ratio between the signal intensity mean for the pathogen-specific probe set and the mean of a control group probe set is ≥ 1.0 to ≤ 1.5 . In some examples, a sample that is determined to be borderline for one or more pathogens is retested (for example, retested with the assay disclosed herein and/or tested using a virusspecific nucleic acid based test). In other examples, a sample that is determined to be borderline is discarded (e.g., not administered to a subject). In additional examples, a sample is determined to be positive for a particular pathogen when $\geq 50\%$ of the individual probes for the particular pathogen have a log ratio of ≥ 1.5 . In some examples, a sample is determined to be positive for a particular pathogen when $\geq 50\%$ of the individual probes for the particular pathogen have a log ratio of >1.5 and the log ratio between the signal intensity mean for the pathogen-specific probe set and the mean of a control group probe set is ≥ 1.5 .

EXAMPLES

The following examples are provided to illustrate certain particular features and/or embodiments. These examples should not be construed to limit the disclosure to the particular features or embodiments described.

Example 1

Materials and Methods

Microarray-based platform design

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Selection of transfusion-transmitted RNA viruses: Sequences of 16 RNA viruses of concern for transmission to blood recipients (released by AABB Transfusion-Transmitted Diseases Committee (Stramer et al., Transfusion 49:1S-29S, 2009)) were downloaded from GenBank at NCBI (available on the World Wide Web at ncbi.nlm.nih.gov/genbank).

The complete genome for each RNA virus was uploaded in FASTA format using Agilent eArray software (available on the World Wide Web at earray.chem.agilent.com/earray/, Agilent Technologies Inc.,

Santa Clara, CA). Design settings were chosen to select 60-mer sense probes with 3' bias from each viral gene, according to the base composition methodology, which considers fusion temperature, GC% and cross-hybridization potential for probes. To get the best quality level probes for viral genome detection the "best probe" (BP) was selected. The probes were checked for vector and low complexity masking. Entire viral genome sequences were covered to the extent possible with all available Agilent-designed probes. The microarray was supplemented with additional predesigned GE (gene expression) array probes for 906 genes from the human genome (replicated 10 times), ERCC probes (replicated 45 times) and probes covering plant virus sequences (negative control). The selected probes and their characteristics are provided in Table 1.

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Oligonucleotide probe selection and methodology: Oligonucleotide probes were synthesized in situ from 3'-end base by base with Agilent SurePrint inkjet technology according to the manufacturer's protocol (Wolber *et al.*, *Meth. Enzymol.* 410:28-57, 2006). The microarrays were manufactured with 60-mer oligonucleotides synthesized in 15,000 features on eight replicate arrays per slide.

Sample collection and processing: Specimens positive for CHIKV, DENV1-4, HIV1-2, WNV strain NY99, and ZIKV were prepared, validated, and supplied by the FDA Center for Biologics Evaluation and Research (CBER) (Dong *et al.*, *J. Appl. Microbiol.* 120:1119-1129, 2016).

HCV genotypes 1a, 2a, and 3, and HEV RNA-positive plasma were purchased from Sera Care (Sera Care, Milford, MA). All positive specimens were diluted in negative plasma (Basematrix diluent, Sera Care) to create a range of concentrations. HAV RNA was obtained from Dr. Patrizia Farci, (National Institutes of Health, Bethesda, MD). HTLV types I and II NATtrol (Nucleic Acid Testing Control) were purchased from ZeptoMetrix (ZeptoMetrix, Buffalo, NY) (Table 2).

Table 1. Selected viral probes

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%	L%	2% C	PolyX
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	243	1	09	66	85. 97	0	36.6	18.3	20	25	55	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	194	2	09	148	86.	0	26.6	28.3	20	25	55	5
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	193	3	09	149	86.	0	25	30	20	25	55	5
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	173	4	09	169	86. 33	0	28.3	26.6	20	25	55	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	172	5	09	170	85. 49	0	28.3	25	21.6	25	53.3 3	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	171	9	09	171	84. 8	0	28.3	25	21.6	25	53.3 3	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	170	7	09	172	84. 8	0	28.3	25	21.6	25	53.3 3	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	169	8	09	173	85. 38	0	26.6	26.6	21.6	25	53.3 3	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	168	6	09	174	.98 09	0	26.6	28.3	21.6	23.3 3	55	3
5 UTR	Hepatitis C genotype 1	gi 22129792:1- 341	167	10	09	175	86. 62	0	26.6	28.3	23.3 3	21.6	55	3
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	488	11	09	86	83. 62	0	16.6	33.3 3	13.3 3	36.6 7	50	3
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	487	12	09	87	83. 16	0	16.6	33.3 3	15	35	50	3
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	486	13	09	88	83. 16	0	18.3	31.6	15	35	50	3
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	485	14	09	68	83. 23	0	18.3	31.6	15	35	50	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	V%	L%	5% C	PolyX
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	484	15	09	06	82. 5	0	20	30	15	35	50	ĸ.
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	483	16	09	91	83. 08	0	18.3	31.6	15	35	50	r,
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	482	17	09	92	83. 48	0	20	31.6	15	33.3 3	51.6	ĸ.
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	481	18	09	93	83. 48	0	21.6	30	15	33.3 3	51.6	ĸ.
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	480	19	09	94	83. 47	0	21.6	30	15	33.3 3	51.6	3
core protein	Hepatitis C genotype 1	gi 22129792:342 -914	479	20	09	56	83. 15	0	21.6	28.3	16.6	33.3 3	50	ĸ
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	342	21	09	239	81. 42	0	25	20	25	30	45	æ
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	341	22	09	240	81. 39	0	25	20	25	30	45	3
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	340	23	09	241	80. 98	0	25	20	25	30	45	3
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	339	24	09	242	80. 98	0	23.3 3	21.6	25	30	45	3
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	504	25	09	77	86. 03	0	35	20	15	30	55	4
E1 protein	Hepatitis C genotype 1	gi 22129792;915 -1494	203	26	09	82	84. 91	0	35	18.3	15	31.6	53.3 3	4
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	505	27	09	62	84. 78	0	33.3 3	18.3	16.6	31.6	51.6	4
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	501	28	09	80	84. 88	0	33.3 3	20	16.6	30	53.3 3	4
E1 protein	Hepatitis C	gi 22129792.915	500	29	09	81	85.	0	35	20	16.6	28.3	55	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5 %	3%	V %	L%	5% C	PolyX
	genotype 1	-1494					73				7	3		
E1 protein	Hepatitis C genotype 1	gi 22129792:915 -1494	379	30	09	202	85. 79	0	35	20	20	25	55	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	703	31	09	387	80. 23	0	25	20	28.3	26.6	45	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	702	32	09	388	80. 23	0	23.3	21.6	28.3	26.6	45	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	701	33	09	389	80. 33	0	23.3 3	21.6	28.3	26.6 7	45	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	700	34	09	390	79. 75	0	21.6	23.3	28.3	26.6	45	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	669	35	09	391	80. 57	0	23.3 3	21.6	28.3	26.6	45	4
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2 <i>5</i> 79	697	36	09	393	80. 57	0	23.3	21.6	28.3	26.6	45	3
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	969	37	09	394	79. 86	0	21.6	21.6	28.3	28.3	43.3 3	3
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	695	38	09	395	79. 16	0	20	21.6	28.3	30	41.6	3
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	694	39	09	396	79. 16	0	18.3	23.3	28.3	30	41.6	3
E2 protein	Hepatitis C genotype 1	gi 22129792:149 1-2579	693	40	09	397	79. 61	0	20	23.3	26.6	30	43.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	56	41	09	134	85. 66	0	33.3 3	21.6	6.67	38.3 3	55	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	55	42	09	135	85. 02	0	31.6	23.3	6.67	38.3 3	55	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	54	43	09	136	84.	0	31.6	21.6	6.67	40	53.3	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	₩%	%T	S%	PolyX
p7 protein	Hepatitis C genotype 1	gi 22129792;258 0-2768	53	44	09	137	84. 15	0	33,3 3	20	29'9	40	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	52	45	09	138	84. 01	0	35	18.3	29.9	40	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	51	46	09	139	84. 59	0	33,3 3	20	29'9	40	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792;258 0-2768	50	47	09	140	84. 59	0	33.3 3	20	8.33	38.3 3	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	49	48	09	141	84	0	31.6	21.6	8,33	38.3 3	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	48	49	09	142	84. 14	0	31.6	21.6	8.33	38.3 3	53.3 3	3
p7 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	47	50	09	143	84. 72	0	30	23.3	8.33	38.3 3	53.3 3	ю
NS2 protein	Hepatitis C genotype 1	gi 22129792:258 0-2768	366	51	09	286	81. 87	0	23.3	21.6	26.6	28.3 3	45	4
NS2 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	194	52	09	458	80. 3	0	16.6	28.3	21.6	33.3 3	45	3
NS2 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	193	53	09	459	79. 57	0	15	28.3	23.3	33.3 3	43.3	8
NS2 protein	Hepatitis C genotype 1	gi 22129792;276 9-3419	192	54	09	460	79. 57	0	13.3	30	23.3	33.3 3	43.3 3	3
NS2 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	191	55	09	461	79. 55	0	13.3	30	23.3	33.3 3	43.3 3	3
NS2 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	190	56	09	462	78. 99	0	15	28.3	23.3	33.3 3	43.3	3
NS2 protein	Hepatitis C genotype 1	gi 22129792:276 9-3419	189	57	09	463	79. 66	0	15	28.3	23.3	33.3 3	43.3	3
NS2 protein	Hepatitis C	gi 22129792:276	188	58	09	464	79.	0	15	30	23.3	31.6	45	3

V ₀	3 7		3 7 45 3	33.3 45	33.3 45 3 21.6 45	33.3 45 33.3 45 7 45 7 45 7 45	33.3 45 33.3 45 21.6 45 7 45 28.3 45	33.3 45 33.3 45 21.6 45 7 28.3 45 3 21.6 53.3 7	33.3 45 33.3 45 21.6 45 7 28.3 45 3 21.6 53.3 7 28.3 45 3 21.6 53.3 7 28.3 55	33.3 45 33.3 45 21.6 45 7 28.3 45 3 21.6 53.3 7 20 55 20 55	33.3 45 33.3 45 21.6 45 7 28.3 45 3 21.6 53.3 7 20 55 20 55 28.3 51.6 3 7	33.3 45 33.3 45 21.6 45 7 28.3 45 3 21.6 53.3 7 20 55 20 55 28.3 51.6 3 7 28.3 51.6 3 7 28.3 51.6 3 7 28.3 51.6 3 7 5 5 5 5 5 5 5 5 5 5 5 5 5	21.0 45 33.3 45 21.6 45 7 28.3 45 3 28.3 45 3 21.6 53.3 7 20 55 20 55 21.6 53.3 7 21.6 53.3 7 21.6 53.3 7 21.6 53.3 3 21.6 53.3 5 20 55 21.6 53.3 3 21.6 53.3 5 21.6 53.3 21.6 53.3	21.0 45 33.3 45 33.3 45 21.6 45 7 45 28.3 45 3 45 3 45 3 7 20 55 21.6 53.3 20 55 21.6 55 23.3 55 3 55 20 55 20 55 20 55	21.0 45 33.3 45 33.3 45 21.6 45 7 45 28.3 45 3 45 21.6 53.3 20 55 28.3 51.6 3 7 21.6 55 23.3 55 20 55 20 55 20 55 20 55 21.6 51.6 7 7 7 7 7 7
	ε.	16.6 28.3 23.3 7 3 3		16.6 28.3 21.6 7 3 7	28.3	28.3 3 30 30 7	28.3 3 30 26.6 7	28.3 30 30 7 7 25 35	28.3 30 30 7 7 25 25 35 35 33	28.3 30 30 7 7 26.6 7 35 35 35	28.3 30 30 26.6 7 35 35 35 35 7	28.3 30 30 26.6 7 35 35 35 36.6 7 30	28.3 30 30 26.6 7 26.6 7 30 33.3 33.3	28.3 30 30 26.6 7 35 35 35 36 37 37 38 33 33 33 35 35 36 37 38 38 38 38 38 38 38 38 38 38 38 38 38	28.3 30 30 30 35 35 35 35 35 35 36.6 7 7 26.6 7 26.6 7 30 30 30 30 30 30 30 30 30 30 30 30 30
		0	81. 0 1 7		81. 0 1 47	0	0 0 0	0 0 0	0 0 0 0	0 0 0 0 0	0 0 0 0 0				
92 465 80.			466 81	82 81	-	274 80	, v	\$	\$	\$	80				
09	09		09	09	_	09	09	09	09 09	09 09 09	09 09 09	09 09 09 09	09 09 09 09 09	09 09 09 09 09	09 09 09 09 09 09
187 59			186 60	1812 61		1620 62		0 4	0 4 7		 				
		9-3419	gi 22129792:276 9-3419	gi 22129792:342 0-5312	gi 22129792:342			9792:342	9792:342 9792:342 9792:342	 		 			
genotype 1		Hepatitis C genotype 1	Hepatitis C genotype 1	Hepatitis C genotype 1	Hepatitis C genotype 1		Hepatitis C genotype 1	Hepatitis C genotype 1 Hepatitis C genotype 1	Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C genotype 1	Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C genotype 1	Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C genotype 1 Hepatitis C	Hepatitis C genotype 1	Hepatitis C genotype 1	Hepatitis C genotype 1	Hepatitis C genotype 1
		NS2 protein	NS2 protein	NS3 protease/ helicase	NS3 protease/	licase	S3 protease/	S3 protease/ elicase S3 protease/ elicase	S3 protease/ elicase S3 protease/ elicase S3 protease/ elicase	NS3 protease/ helicase NS3 protease/ helicase NS3 protease/ helicase NS3 protease/ helicase	NS3 protease/ helicase NS3 protease/ helicase NS3 protease/ helicase helicase helicase helicase helicase	NS3 protease/ helicase NS3 protease/ helicase NS3 protease/ helicase helicase NS3 protease/ helicase helicase helicase helicase	NS3 protease/ helicase helicase helicase	NS3 protease/ helicase	NS3 protease/ helicase NS3 protease/ helicase helicase NS3 protease/ helicase helicase helicase NS3 protease/ helicase helicase helicase helicase helicase NS3 protease/ helicase helicase

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	V%	L%	S%C	PolyX
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	101	73	09	62	83	0	31.6	18.3	28.3	21.6	50	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	001	74	09	63	82. 48	0	31.6	18.3	30	20	50	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	66	22	09	64	82. 45	0	31.6	18.3	30	20	50	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	86	92	09	99	82. 74	0	33.3 3	18.3	28.3	20	51.6	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	26	LL	09	99	83. 4	0	33.3 3	18.3	28.3	20	51.6	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	96	78	09	29	84.	0	33.3 3	20	26.6	20	53.3 3	æ
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	95	62	09	89	84. 37	0	33.3 3	21.6	25	20	55	3
NS4A protein	Hepatitis C genotype 1	gi 22129792:531 3-5474	94	80	09	69	84.	0	31.6	21.6	25	21.6	53.3 3	3
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	133	81	09	651	81. 1	0	26.6	18.3	28.3	26.6	45	3
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	723	82	09	61	85. 12	0	26.6	28.3	23.3	21.6	55	3
NS4B protein	Hepatitis C genotype 1	gi 22129792;547 5-6257	702	83	09	82	85. 36	0	23.3	31.6	25	20	55	3
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	456	84	09	328	85. 9	0	28.3	26.6	21.6	23.3	55	4
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	416	85	09	368	86.	0	35	20	20	25	55	3
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	226	86	09	558	85. 23	0	16.6	35	23.3	25	51.6	4
NS4B protein	Hepatitis C	gi 22129792:547	204	87	09	580	86.	0	21.6	33.3	18.3	26.6	55	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5%	2%	W%	L%	ر د د	PolyX
	genotype 1	5-6257					8		7	3	3	7		
NS4B protein	Hepatitis C genotype 1	gi 22129792;547 5-62 <i>5</i> 7	182	88	09	602	86. 58	0	25	30	18.3	26.6	55	4
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	162	68	09	622	84.	0	28.3 3	25	21.6	25	53.3 3	3
NS4B protein	Hepatitis C genotype 1	gi 22129792:547 5-6257	113	06	09	671	84. 31	0	26.6	25	26.6	21.6	51.6	3
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	402	91	09	943	82. 2	0	16.6	28.3	28.3	26.6	45	5
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	1138	92	09	207	85. 98	0	20	35	23.3	21.6	55	3
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	1078	93	09	267	86. 55	0	20	35	23.3	21.6	55	4
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	974	94	09	371	85. 27	0	26.6 7	28.3	26.6	18.3	55	5
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	826	95	09	619	85. 49	0	36.6	18.3	23.3	21.6	55	3
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	578	96	09	191	85. 27	0	23.3	31.6	25	20	55	3
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	515	26	09	830	85. 03	0	30	25	23.3	21.6	55	4
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	342	86	09	1003	84.	0	38.3 3	16.6	25	20	55	5
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	214	66	09	1131	85. 18	0	31.6	23.3	23.3	21.6	55	4
NS5A protein	Hepatitis C genotype 1	gi 22129792:625 8-7601	154	100	09	1611	84. 43	0	26.6 7	25	28.3	20	51.6	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 1	gi 22129792:760 2-9374	1560	101	09	214	81. 13	0	18.3	26.6	35	20	45	3

PolyX	E.	m	ю	n	4	т	n	5	5	3	3	ĸ	m	ĸ	†
S%G	43.3	41.6	43.3	45	45	45	45	45	45	55	55	53.3	53.3	53.3	,
L%	21.6	21.6	21.6	20	25	31.6	31.6	30	30	25	26.6	26.6	26.6	26.6	, , ,
V %	35	36.6	35	35	30	23.3	23.3	25	25	20	18.3	20	20	20	
2%C	25	25	26.6	28.3 3	30	23.3	23.3	25	25	18.3	28.3 3	26.6	26.6	26.6	,
9%	18.3	16.6	16.6	16.6	15	21.6	21.6	20	20	36.6	26.6	26.6	26.6	26.6	
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	08	79. 91	80. 32	81. 05	81. 64	80.	81. 12	81. 8	82. 09	86. 27	86. 34	85.	8 8	8 8	,
End Distance	215	216	217	218	383	490	491	542	543	80	150	151	152	153	
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:	102	103	104	105	901	107	108	109	110	1111	112	113	114	115	
BP Start	1559	1558	1557	1556	1391	1284	1283	1232	1231	242	172	171	170	169	
Target ID	gi 22129792:760 2-9374	gi 157781212:1- 321	1.01000001												
Virus	Hepatitis C genotype 1	Hepatitis C genotype 2													
Product	NS5B RNA- dependent RNA polymerase	5 UTR													

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	V%	L%	2% C	PolyX
	genotype 2													
5 UTR	Hepatitis C genotype 2	gi 157781212:1- 321	<i>L</i> 91	211	09	155	86. 1	0	25	30	20	25	55	3
5 UTR	Hepatitis C genotype 2	gi 157781212:1- 321	991	811	09	156	86. 64	0	25	30	21.6	23.3	55	3
5 UTR	Hepatitis C genotype 2	gi 157781212:1- 321	163	611	09	159	85. 77	0	25	30	21.6	23.3	55	3
5 UTR	Hepatitis C genotype 2	gi 157781212:1- 321	162	120	09	160	85. 03	0	26.6	28.3	21.6	23.3	55	3
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	98	121	09	550	82	0	15	30	43.3 3	11.6	45	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	35	122	09	551	81. 31	0	13.3	30	45	11.6	43.3	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	34	123	09	552	80. 33	0	11.6	30	45	13.3	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	33	124	09	553	79. 71	0	11.6	30	45	13.3	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	32	125	09	554	80. 36	0	11.6	30	45	13.3	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	31	126	09	555	80. 76	0	11.6	30	45	13.3	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	30	127	09	556	80. 73	0	11.6	30	46.6	11.6	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	67	128	09	557	80. 23	0	11.6	30	48.3 3	10	41.6	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	28	129	09	558	80. 17	0	10	30	99	10	40	5
core protein	Hepatitis C genotype 2	gi 157781212:32 2-906	13	130	09	573	80. 76	0	13.3	30	46.6	10	43.3	5

Virus		Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	L%	S%G	PolyX
Hepatitis C genotype 2	(1)	gi 157781212:92 1-1498	495	131	09	84	85. 82	0	30	25	13.3	31.6	55	8
Hepatitis C genotype 2	() ()	gi 157781212:92 1-1498	459	132	09	120	86. 52	0	31.6	23.3	15	30	55	4
Hepatitis C genotype 2	() 8	gi 157781212:92 1-1498	439	133	09	140	85. 78	0	31.6	23.3	16.6	28.3	55	4
Hepatitis C genotype 2	() 8	gi 157781212:92 1-1498	419	134	09	160	85. 1	0	30	25	18.3	26.6	55	4
Hepatitis C genotype 2	() 8	gi 157781212:92 1-1498	362	135	09	217	86. 77	0	28.3	26.6	23.3	21.6	55	8
Hepatitis C genotype 2	() 8	gi 157781212:92 1-1498	342	136	09	237	84.	0	26.6	26.6	25	21.6	53.3	3
Hepatitis C genotype 2	(1)	gi 157781212:92 1-1498	322	137	09	257	85. 97	0	21.6	33.3	23.3	21.6	55	3
Hepatitis C genotype 2	() ()	gi 157781212:92 1-1498	296	138	09	283	85. 94	0	20	35	18.3	26.6	55	ς.
Hepatitis C genotype 2	() ()	gi 157781212:92 1-1498	276	139	09	303	86. 01	0	20	33.3 3	21.6	25	53.3 3	n
Hepatitis C genotype 2	() ()	gi 157781212:14 92-2540	24	140	09	555	85. 87	0	23.3 3	31.6	23.3	21.6	55	2
Hepatitis C genotype 2	() ()	gi 157781212:92 1-1498	944	141	09	106	81. 03	0	15	30	30	25	45	4
Hepatitis C genotype 2	() ()	gi 157781212:14 92-2540	943	142	09	107	81	0	15	28.3	31.6	25	43.3	4
Hepatitis C genotype 2	() ()	gi 157781212:14 92-2540	941	143	09	109	79. 92	0	13.3	30	33.3	23.3	43.3	4
Hepatitis C genotype 2	(1)	gi 157781212:14 92-2540	940	144	09	110	80. 58	0	13.3 3	30	33.3 3	23.3	43.3	4
Hepatitis C	7)	gi 157781212:14	939	145	09	111	81.	0	13.3	30	35	21.6	43.3	4

80. 0 28.3 66. 0 3 80. 0 28.3 77. 0 7 79. 0 26.6 81. 0 7 86. 0 33.3 86. 0 33.3 87. 0 33.3 87. 0 33.3	80. 0 66. 0 1 1 0 80. 0 81. 0 86. 0 86. 0 83. 0 85. 0	324 80. 0 325 80. 0 326 81. 0 327 81. 0 69 86. 0 109 83. 0 224 85. 0	80. 0 66 0 1 1 0 81. 0 81. 0 86. 0 83. 0	146 60 324 80. 0 147 60 325 80. 0 148 60 326 79. 0 149 60 327 79. 0 150 60 328 79. 0 151 60 69 86. 0 83 86. 0 88. 0	146 60 324 80. 0 147 60 325 80. 0 148 60 326 79. 0 149 60 327 79. 0 150 60 328 79. 0 151 60 69 86. 0
	80. 1 1. 1 2. 1 1. 1 2. 1 3. 1 3. 1 3. 1 3. 1 3. 1 3. 1 4. 1 5. 1	325 80. 326 81. 327 81. 328 81. 69 86. 109 83. 184 85. 224 85. 13	60 325 80. 60 326 81. 60 327 81. 60 328 81. 60 69 86. 60 69 83. 60 109 83.	147 60 325 80. 148 60 326 79. 149 60 327 79. 150 60 328 81. 151 60 69 86.	725 147 60 325 80. 724 148 60 326 79. 723 149 60 327 79. 722 150 60 328 79. 524 151 60 69 86.
	29. 42. 88. 88. 88. 88. 88. 88. 88. 88. 88. 8	326 79. 327 79. 328 81. 69 86. 109 83. 184 85. 224 85. 13	60 326 79. 60 327 81 60 328 79. 60 69 86. 60 69 86. 60 109 83. 60 83.	148 60 326 79. 149 60 327 79. 150 60 328 79. 151 60 69 86. 183 83.	724 148 60 326 79. 723 149 60 327 81 722 150 60 328 81 524 151 60 69 86.
	79. 81. 86. 86. 87. 83. 83.	327 79. 328 81 69 86. 109 83. 184 85. 224 85.	60 327 79. 60 328 79. 60 69 86. 60 109 83. 60 109 83.	149 60 327 79. 150 60 328 79. 151 60 69 86. 151 86. 83.	723 149 60 327 79. 722 150 60 328 79. 524 151 60 69 86.
	29. 86. 83. 87. 87. 88. 87. 87. 87.	328 79. 69 86. 109 83. 184 85. 224 85.	60 328 79. 60 69 86. 60 109 83.	150 60 328 79. 151 60 69 86. 153 83	722 150 60 328 79. 524 151 60 69 86.
0 0	86. 0 42 0 83. 0 87 0 85. 0	69 86. 0 109 83. 0 184 85. 0 224 85. 0	60 69 86. 0 42 0 60 109 83. 0	151 60 69 86. 0	524 [15] 60 69 86. 0
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	85. 0 33 85	184 85. 0 224 85. 0		$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	60 109 83. 0
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86. 0 30 25	0 30	394 86. 0 30		156 60 354 86. 0	60 354 86 0 28.3
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	354		09		
409 153 369 154 281 155	gil57781212:27 281	gi 157781212:27 77-3368		genotype 2 Hepatitis C genotype 2 Hepatitis C genotype 2 Hepatitis C	

Target ID	a	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%C	V ₀ / ₀	L%	2 S%	PolyX
gi 157781212:27 77-3368	21		160	60	572	85. 42	0	25	30	18.3	26.6	55	5
gi 157781212:27 992 77-3368	992		161	09	257	80. 97	0	25	20	35	20	45	5
gi 157781212:35 991 12-4759	166		162	09	258	79. 98	0	23.3 3	20	35	21.6	43.3 3	S
gi 157781212:35 990 12-4759	066		163	09	259	79. 94	0	23.3 3	18.3	35	23.3	41.6	S
gi 157781212:35 989	686		164	09	260	79. 58	0	23.3 3	20	35	21.6	43.3 3	5
gi 157781212:35 988 12-4759	886		165	09	261	79. 13	0	23.3	18.3	35	23.3	41.6	S
gi 157781212:35 987	786		166	09	262	79. 21	0	23.3	18.3	35	23.3	41.6	S
gi 157781212:35 986 12-4759	986		167	09	263	79. 3	0	23.3	18.3	33.3 3	25	41.6	5
gi 157781212:35 985 12-4759	586		168	09	264	78. 66	0	21.6	20	33.3 3	25	41.6	5
gi157781212:35 984	984		169	09	265	79. 21	0	21.6	20	33.3 3	25	41.6	5
gi 157781212:35 983 12-4759	983		170	09	266	79. 51	0	21.6	21.6	31.6	25	43.3 3	5
gi 157781212:53 119 24-5501	119		171	09	09	84. 4	0	35	18.3	21.6	25	53.3 3	4
gi 157781212:53 118 24-5501	118		172	09	19	84. 4	0	36.6	16.6	21.6	25	53.3 3	4
gi 157781212:53 24-5501	117		173	09	62	84. 65	0	38.3 3	16.6	21.6	23.3	55	4
gi 157781212:53 116	116		174	09	63	84.	0	38.3	16.6	21.6	23.3	55	4

Ta	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5%	3%C	%A	L%	2 9%	PolyX
24-5501						5		3	7	7	3		
gi 157781212:53 24-5501		1115	175	09	64	84. 5	0	36.6	18.3	21.6	23.3 3	55	4
gi 157781212:53 24-5501		114	176	09	65	84. 65	0	36.6	18.3	21.6	23.3	55	4
gi 157781212:53 24-5501	–	113	177	09	99	84.	0	36.6	18.3	21.6	23.3	55	4
gi 157781212:53 1 24-5501	_	112	178	09	<i>L</i> 9	84. 64	0	36.6	18.3	21.6	23.3 3	55	4
gi 157781212:53 1 24-5501	_	111	179	09	89	84. 45	0	35	18.3	21.6	25	53.3 3	4
gi 157781212:53 124-5501		110	180	09	69	84. 41	0	33.3 3	18.3	21.6	26.6	51.6	4
gi 157781212:55 88 31-6115	88	}	181	09	498	81. 45	0	20	25	33.3 3	21.6	45	3
gi 157781212:55 87 31-6115	8	7	182	09	499	81. 54	0	20	25	33.3 3	21.6	45	3
g 157781212:55 31-6115	_	13	183	09	573	81. 76	0	16.6	28.3	36.6	18.3	45	3
gi 157781212:55 31-6115		12	184	09	574	81. 76	0	15	30	36.6	18.3 3	45	3
gi 157781212:55 31-6115		8	185	09	578	82. 24	0	15	30	38.3 3	16.6	45	3
gi 157781212:55 31-6115		7	186	09	579	81. 73	0	15	30	38.3	16.6	45	3
gi 157781212:55 31-6115	. •	9	187	09	580	81. 06	0	16.6	28.3 3	38.3 3	16.6	45	3
gi 157781212:55 31-6115		5	188	09	581	80.	0	16.6	26.6	38.3	18.3	43.3	3

	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	Э%С	8 %	L%	c C	PolyX
NS4B protein	Hepatitis C genotype 2	gi 157781212:55 31-6115	4	189	09	582	80.	0	16.6	26.6	38.3	18.3	43.3	8
NS4B protein	Hepatitis C genotype 2	gi 157781212:55 31-6115	ю	190	09	583	81. 64	0	18.3	26.6	36.6	18.3	45	3
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	54	191	09	1352	82. 47	0	15	30	26.6	28.3	45	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	46	192	09	1360	80. 77	0	13.3	30	31.6	25	43.3	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	45	193	09	1361	80. 86	0	13.3	30	31.6	25	43.3	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	43	194	09	1363	80. 94	0	13.3	30	33.3 3	23.3	43.3	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	42	195	09	1364	80. 21	0	13.3	30	33.3 3	23.3	43.3	8
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	41	961	09	1365	80. 37	0	13.3	30	33.3 3	23.3	43.3	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	40	197	09	1366	80. 16	0	11.6	30	33.3	25	41.6	5
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	39	198	09	1367	79. 46	0	11.6	28.3	33.3	26.6	40	δ.
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	38	199	09	1368	78. 76	0	11.6	26.6	33.3 3	28.3 3	38.3	\$
NS5A protein	Hepatitis C genotype 2	gi 157781212:62 66-7670	37	200	09	1369	78. 05	0	13.3	25	33.3 3	28.3 3	38.3	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1389	201	09	191	82. 16	0	16.6	28.3	26.6	28.3	45	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1388	202	09	162	81. 45	0	16.6	28.3	26.6	28.3	45	5
NS5B RNA-	Hepatitis C	gi 157781212:76	1387	203	09	163	81.	0	16.6	26.6	28.3	28.3	43.3	5

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%C	₩%	L%	5% C	PolyX
dependent RNA polymerase	genotype 2	64-9212					29		7	7	3	3	3	
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1386	204	09	164	81. 01	0	16.6	26.6	26.6 7	30	43.3 3	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1385	205	09	165	80. 66	0	16.6	28.3	25	30	45	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1384	206	09	166		0	16.6	28.3	25	30	45	3
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1383	207	09	167	81.	0	16.6	26.6	26.6	30	43.3 3	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1382	208	60	168	80. 73	0	16.6	28.3	25	30	45	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1381	209	09	169	80. 73	0	16.6	28.3	25	30	45	5
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 2	gi 157781212:76 64-9212	1380	210	09	170	80. 73	0	16.6	28.3	25	30	45	5
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	245	211	09	95	86. 03	0	35	20	16.6	28.3 3	55	3
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	244	212	09	96	86. 01	0	35	20	18.3	26.6	55	3
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	242	213	60	86	85. 18	0	36.6 7	18.3	20	25	55	3
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	241	214	09	66	85. 09	0	36.6 7	18.3	20	25	55	3
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	192	215	09	148	86. 22	0	23.3 3	31.6	23.3	21.6	55	5
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	191	216	90	149	86. 22	0	21.6	33.3 3	23.3	21.6	55	5
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	170	217	09	170	86. 32	0	28.3	26.6	21.6	23.3	55	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	8 %	%T	S%G	PolyX
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	691	218	09	171	85. 62	0	28.3	26.6	21.6	23.3 3	55	4
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	168	219	09	172	85. 62	0	28.3	26.6	21.6	23.3 3	55	4
5 UTR	Hepatitis C genotype 3	gi 157781216:1- 339	191	220	09	173	86. 2	0	26.6	28.3 3	21.6	23.3 3	55	4
Core protein	Hepatitis C genotype 3	gi 157781216;34 0-912	486	221	09	88	82. 34	0	16.6	28.3	15	40	45	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	485	222	09	68	82. 06	0	16.6	28.3	15	40	45	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	484	223	09	06	81. 52	0	16.6	28.3	16.6	38.3 3	45	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	483	224	09	91	81. 43	0	16.6	28.3	16.6	38.3 3	45	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	514	225	09	09	80.	0	11.6	31.6	11.6	45	43.3	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	513	226	09	19	80. 29	0	11.6	31.6	11.6	45	43.3	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	512	227	09	62	80. 37	0	11.6	31.6	11.6	45	43.3	4
Core protein	Hepatitis C genotype 3	gi 157781216;34 0-912	502	228	09	72	80. 32	0	11.6	30	10	48.3 3	41.6	4
Core protein	Hepatitis C genotype 3	gi 157781216:34 0-912	501	229	09	73	80. 39	0	13.3	30	10	46.6 7	43.3 3	4
Core protein	Hepatitis C genotype 3	gi 157781216:91 3-1488	499	230	09	75	81. 25	0	16.6	28.3	8.33	46.6 7	45	4
E1 protein	Hepatitis C genotype 3	gi 157781216:34 0-912	37	231	09	540	81. 72	0	21.6	23.3	28.3	26.6 7	45	2
E1 protein	Hepatitis C	gi 157781216:91	36	232	09	541	80.	0	21.6	23.3	26.6	28.3	45	2

3 7 3 C	5		6 26.6 30 43.3 2	26.6 30 43.3 7 3 45 25 30 45	26.6 30 43.3 25 30 45 25 30 45	26.6 30 43.3 25 30 45 25 30 45 25 30 45 23.3 31.6 45	26.6 30 43.3 25 30 45 25 30 45 25 30 45 23.3 31.6 45 23.3 31.6 45 3 7 45	26.6 30 43.3 25 30 45 25 30 45 23.3 31.6 45 23.3 31.6 45 3 7 45 23.3 31.6 45 3 7 45	26.6 30 43.3 7 30 45 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 31.6 45 3 7 45 25 30 45	26.6 30 43.3 7 30 45 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 7 45 23.3 7 45 25 30 45 25 31.6 43.3 25 7 3	26.6 30 43.3 25 30 45 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 31.6 45 25 30 45 25 31.6 43.3 28.3 26.6 45	26.6 30 43.3 7 30 45.3 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 31.6 45 25 30 45 25 31.6 45 28.3 26.6 45 33 7 45 28.3 26.6 45 20 35 45	26.6 30 43.3 7 30 43.3 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 31.6 45 25 30 45 25 31.6 45 28.3 26.6 45 20 35 45 20 35 45	26.6 30 43.3 7 30 43.3 25 30 45 23.3 31.6 45 23.3 7 45 23.3 31.6 45 25 30 45 25 31.6 45 26 7 3 28.3 26.6 45 20 35 45 20 35 45 20 35 45	26.6 30 43.3 7 30 43.3 25 30 45 23.3 31.6 45 23.3 31.6 45 23.3 31.6 45 25 30 45 26 31.6 45 28 3.6 45 20 35 45 20 35 45 20 36.6 43.3 20 36.6 43.3
7	/ 3	21.6 21.6 26.6 7 7		21.6 23.3 25	23.3	23.3 23.3 3 3 23.3 3	23.3 23.3 3 23.3 3 21.6	23.3 23.3 3 23.3 3 7 7 23.3 3 23.3	23.3 23.3 3 23.3 3 21.6 7 7 23.3 3 3 23.3 3	23.3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	23.3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 3 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3	23.3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 3 23.3 3 3 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3	23.3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3	23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 3 23.3 3 3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 3 3 3 3 3 3 3 3 3 3 3 3	23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 23.3 3 3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 13.3 3 3 3 3 3 3 3 3 3 3 3 3 3
80. 0 21.	0		80. 0 21.		80. 0 21. 7	0 0	0 0 0	0 0 0	0 0 0 0	0 0 0 0 0	0 0 0 0 0	0 0 0 0 0 0	0 0 0 0 0 0 0		
542 80.			543 80.		544 80										
		99	, 09		09										
		233	234	325	552	236	236	235 236 237 238	235 236 237 238 239	235 236 237 238 239 240	235 236 237 239 240 240	235 236 237 239 240 241 242	235 236 237 239 240 241 242 243	235 236 237 239 240 241 242 243 244	235 236 237 239 240 241 242 243 244 245
<u> </u>		91 35	91 34	91 33											
00+1-0		gi 157781216:91 3-1488	gi 157781216:91 3-1488	gi 157781216:91 3-1488	0011	gi 157781216:91 3-1488	gi 157781216:91 3-1488 gi 157781216:91 3-1488	gi[157781216:91] 3-1488 gi[157781216:91] 3-1488 gi[157781216:91] 3-1488	gi[157781216:91] 3-1488 gi[157781216:91] 3-1488 gi[157781216:91] 3-1488 gi[157781216:91] 3-1488	gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488	gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488	gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:14 89-2544	gi 5778 216:91 3-1488 gi 5778 216:91 3-1488 gi 5778 216:91 3-1488 gi 5778 216:91 3-1488 gi 5778 216:91 3-1488 gi 5778 216:14 89-2544 gi 5778 216:14	gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:14 89-2544 gi 157781216:14 89-2544 gi 157781216:14 89-2544 gi 157781216:14	gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:91 3-1488 gi 157781216:14 89-2544
gemotype 3		Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C	Servery Pe	Hepatitis C genotype 3	Hepatitis C genotype 3 Hepatitis C genotype 3	Hepatitis C genotype 3 Hepatitis C genotype 3 Hepatitis C genotype 3 Hepatitis C	Hepatitis C genotype 3 Hepatitis C genotype 3 Hepatitis C genotype 3 Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3 Hepatitis C	Hepatitis C genotype 3	Hepatitis C genotype 3 Hepatitis C	Hepatitis C genotype 3 Hepatitis C
	1	E1 protein	E1 protein	E1 protein		nic	oin ein	ein ein	ein ein ein	ein ein ein ein	ein ein ein ein	ein ein ein	E1 protein E1 protein E1 protein E1 protein E2/NS1 protein protein E2/NS1 protein E2/NS1	E1 protein E1 protein E1 protein E1 protein E1 protein E2/NS1 protein E2/NS1 protein E2/NS1 protein E2/NS1	E1 protein E1 protein E1 protein E1 protein E1 protein E2/NS1 protein E2/NS1 protein E2/NS1 protein E2/NS1 protein E2/NS1

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5 %	2%C	W%	L%	5% C	PolyX
E2/NS1 protein	Hepatitis C genotype 3	gi 157781216:14 89-2544	732	247	09	325	79. 81	0	31.6	10	21.6	36.6	41.6	3
E2/NS1 protein	Hepatitis C genotype 3	gi 157781216:25 45-3375	731	248	09	326	79. 81	0	31.6	10	21.6	36.6	41.6	3
E2/NS1 protein	Hepatitis C genotype 3	gi 157781216:14 89-2544	730	249	09	327	80. 59	0	31.6	10	21.6	36.6 7	41.6	3
E2/NS1 protein	Hepatitis C genotype 3	gi 157781216:14 89-2544	729	250	09	328	80. 31	0	31.6	10	21.6	36.6 7	41.6	3
NS2	Hepatitis C genotype 3	gi 157781216:14 89-2544	724	251	09	801	81. 33	0	23.3	21.6	30	25	45	4
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	710	252	09	122	81. 32	0	18.3	26.6	30	25	45	£.
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	708	253	09	124	80. 65	0	20	25	31.6	23.3 3	45	£.
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	707	254	09	125	80. 51	0	20	23.3	33.3 3	23.3	43.3 3	3
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	706	255	09	126	08	0	20	23.3	33.3	23.3	43.3	3
NS2	Hepatitis C genotype 3	gi 157781216;25 45-3375	705	256	09	127	80. 1	0	20	23.3	33.3 3	23.3 3	43.3 3	8
NS2	Hepatitis C genotype 3	gi 157781216;25 45-3375	704	257	09	128	80. 54	0	20	23.3	33.3 3	23.3 3	43.3 3	3
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	703	258	09	129	80. 09	0	20	25	31.6	23.3	45	3
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	702	259	09	130	80. 47	0	20	23.3	31.6	25	43.3 3	3
NS2	Hepatitis C genotype 3	gi 157781216:25 45-3375	701	260	09	131	80. 09	0	21.6	23.3	31.6	23.3	45	3
NS3 protease/	Hepatitis C	gi 157781216:33	1684	261	09	270	80.	0	16.6	28.3	28.3	26.6	45	3

PolyX		3	3	n	r.	r.	m	4	4	4	m	m	ro .	m	,
S%		45	45	45	45	45	45	45	45	43.3	48.3	48.3	46.6	46.6	46.6
L%	7	25	25	26.6	25	25	25	31.6	33.3 3	33.3 3	20	20	20	18.3	18.3
₩	3	30	30	28.3	30	30	30	23.3	21.6	23.3	31.6	31.6	33.3 3	35	1
3%C	3	28.3 3	28.3	28.3	30	28.3 3	26.6	25	25	23.3	20	18.3	18.3	18.3	
9%	7	16.6	16.6	16.6	15	16.6	18.3	20	20	20	28.3	30	28.3 3	28.3	26.6
X-Hyb Pot		0	0	0	0	0	0	0	0	0	0	0	0	0	(
Tm	7	80. 77	80.	80.	80. 24	80. 24	80. 98	80. 9	80. 39	80. 33	81. 66	81. 66	81. 97	81. 46	81.
End Distance		272	277	278	280	281	283	309	310	311	09	61	62	63	
Probe Length		09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:		262	263	264	265	266	267	268	269	270	271	272	273	274	t
BP Start		1682	1677	1676	1674	1673	1671	1645	1644	1643	103	102	101	100	9
Target ID	76-5328	gi 157781216:33 76-5328	gi 157781216:53 29-5490	gi 157781216:53 29-5490	gi 157781216:53 29-5490	gi 157781216:53 29-5490	gi 157781216:53								
Virus	genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C genotype 3	Hepatitis C
Product	helicase	NS3 protease/ helicase	NS4A protein	NS4A protein	NS4A protein	NS4A protein									

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	J%	₩%	L%	S% C	PolyX
NS4A protein	Hepatitis C genotype 3	gi 157781216:53 29-5490	86	276	09	\$9	81. 96	0	28.3	20	33.3 3	18.3	48.3	3
NS4A protein	Hepatitis C genotype 3	gi 157781216:53 29-5490	26	277	09	99	81. 96	0	28.3	20	33.3 3	18.3	48.3	3
NS4A protein	Hepatitis C genotype 3	gi 157781216:53 29-5490	96	278	09	29	82. 6	0	28.3 3	20	33.3 3	18.3	48.3	3
NS4A protein	Hepatitis C genotype 3	gi 157781216:53 29-5490	95	279	09	89	82. 63	0	28.3	20	33.3 3	18.3	48.3	3
NS4A protein	Hepatitis C genotype 3	gi 157781216:53 29-5490	94	280	09	69	81. 96	0	28.3	20	33.3 3	18.3	48.3	3
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	237	281	09	547	81. 84	0	15	30	25	30	45	9
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	236	282	09	548	84	0	15	30	23.3	31.6	45	9
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	133	283	09	651	81. 96	0	26.6	18.3	26.6	28.3	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	132	284	09	652	82. 25	0	26.6	18.3	26.6	28.3	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	130	285	09	654	81. 23	0	26.6	18.3	28.3	26.6	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	129	286	09	655	81. 95	0	28.3	16.6	28.3	26.6	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	118	287	09	999	82. 5	0	25	20	28.3 3	26.6	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	117	288	09	667	81. 99	0	25	20	30	25	45	4
NS4B protein	Hepatitis C genotype 3	gi 157781216:54 91-6273	116	289	09	668	81. 65	0	23.3	20	30	26.6	43.3	4
NS4B protein	Hepatitis C	gi 157781216:54	115	290	09	699	81.	0	25	20	28.3	26.6	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	W%	L%	2% C	PolyX
	genotype 3	91-6273			b		37				3	7		
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	513	291	09	844	80. 76	0	20	25	23.3	31.6	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	512	292	09	845	80. 32	0	20	25	23.3	31.6	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	511	293	09	846	80. 22	0	20	25	23.3	31.6	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	510	294	09	847	80. 15	0	20	25	25	30	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	609	295	09	848	80. 05	0	20	25	25	30	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	508	296	09	849	80. 05	0	20	25	26.6	28.3	45	4
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	507	297	09	850	79. 39	0	21.6	23.3 3	26.6	28.3	45	3
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	506	867	09	851	79. 19	0	21.6	21.6	26.6	30	43.3	3
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	505	299	09	852	78. 49	0	21.6	20	26.6	31.6	41.6	3
NS5A protein	Hepatitis C genotype 3	gi 157781216:62 74-7629	504	300	09	853	78. 59	0	23.3 3	18.3 3	26.6	31.6	41.6	3
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 3	gi 157781216:76 30-9402	1548	301	09	226	82. 27	0	20	25	30	25	45	4
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 3	gi 157781216:76 30-9402	1373	302	09	401	81. 84	0	16.6	28.3 3	28.3	26.6	45	3
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 3	gi 157781216:76 30-9402	1350	303	09	424	79. 41	0	16.6	26.6	26.6	30	43.3	3
NS5B RNA- dependent RNA polymerase	Hepatitis C genotype 3	gi 157781216:76 30-9402	1330	304	09	444	81. 36	0	20	25	23.3	31.6	45	4

PolyX	5	5	e.	3	3	2	4	4	4	9	9	4	5	4	4	2	9	
S%	43.3 3	45	45	43.3 3	45	45	43.3	40	43.3	41.6	36.6	35	45	36.6 7	38.3 3	43.3 3	45	
L%	33.3 3	30	20	28.3 3	21.6	26.6	23.3	20	23.3	15	23.3 3	21.6	21.6	25	25	21.6	28.3 3	
V %	23.3 3	25	35	28.3 3	33.3 3	28.3 3	33.3 3	40	33.3 3	43.3 3	40	43.3 3	33.3 3	38.3 3	36.6 7	35	26.6 7	
2%C	30	26.6	18.3	18.3	21.6	25	8.33	11.6	20	13.3	15	16.6	21.6	15	11.6	18.3	18.3	
9%	13.3	18.3	26.6	25	23.3	20	35	28.3	23.3	28.3	21.6	18.3	23.3	21.6	26.6	25	26.6	
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	80.	85.	80.	79.	80.	79. 91	80.	77.	80. 91	79. 33	78. 04	74. 91	81. 58	77.	77.	79. 82	81. 78	
End Distance	491	512	1102	1248	1627	1675	29	144	204	295	355	450	546	909	999	726	209	
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	
BP Start	1283	1262	672	526	147	66	4241	4164	4104	4013	3953	3858	3762	3702	3642	3582	1295	
Target ID	gi 157781216:76 30-9402	gi 9629357:336- 4642	gi 9629357;336- 4642	gi 9629357:336- 4642	gi 9629357:336- 4642	gi 9629357:336- 4642	gi 9629357;336- 4642	gi 9629357:336- 4642	gi 9629357:336- 4642	gi 9629357:336- 4642	gi 9629357;336- 1838	gi 9629357;336- 4642	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0					
Virus	Hepatitis C genotype 3	HIV 1																
Product	NS5B RNA- dependent RNA polymerase	Gag-Pol	gag															

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3% C	₩%	L%	2 %	PolyX
gag	HIV 1	gi 9629357:336- 1838	1162	323	09	342	82. 47	0	28.3 3	16.6 7	33.3 3	21.6	45	3
gag	I AIH	gi 9629357:336- 1838	1102	324	09	402	78. 85	0	20	18.3 3	43.3	18.3 3	38.3 3	4
gag	HIV 1	gi 9629357:336- 1838	959	325	09	545	79. 58	0	21.6	20	31.6	26.6 7	41.6	4
gag	I AIH	gi 9629357:336- 1838	668	326	09	905	78. 28	0	21.6	16.6	43.3	18.3	38.3	9
gag	HIV 1	gi 9629357:336- 1838	837	327	09	299	80. 04	0	21.6	23.3 3	36.6	18.3	45	3
gag	I AIH	gi 9629357:336- 1838	750	328	09	754	75. 62	0	18.3 3	16.6	40	25	35	4
gag	HIV 1	gi 9629357:336- 1838	690	329	09	814	80. 67	0	26.6 7	18.3	38.3 3	16.6	45	4
gag	HIV 1	gi 9629357:336- 1838	601	330	09	903	81. 87	0	28.3 3	16.6	36.6 7	18.3 3	45	4
Vif	I AIH	gi 9629357:4587 -5165	466	331	09	114	78. 8	0	21.6	20	40	18.3	41.6	9
Vif	HIV 1	gi 9629357.4587 -5165	426	332	09	154	77. 98	0	13.3 3	25	43.3	18.3	38.3 3	9
Vif	HIV 1	gi 9629357:4587 -5165	386	333	09	194	78. 39	0	23.3	18.3	33.3 3	25	41.6	3
Vif	I AIH	gi 9629357:4587 -5165	346	334	09	234	77. 97	0	21.6	18.3	31.6	28.3	40	3
Vif	I AIH	gi 9629357:4587 -5165	304	335	09	276	75. 46	0	13.3 3	21.6	28.3	36.6	35	5
Vif	HIV 1	gi 9629357.4587 -5165	264	336	09	316	78. 46	0	20	20	45	15	40	5
Vif	I AIH	gi 9629357:4587 -5165	224	337	09	356	79. 26	0	33.3 3	10	38.3 3	18.3 3	43.3	5
Vif	HIV 1	gi 9629357:5105 -5396	184	338	09	396	78. 73	0	28.3 3	13.3 3	33.3 3	25	41.6	4
Vif	HIV 1	gi 9629357:4587 -5165	144	339	09	436	77. 87	0	20	20	38.3 3	21.6	40	4
Vif	I AIH	gi 9629357:4587 -5165	104	340	09	476	77. 27	0	21.6	18.3 3	35	25	40	4
vpr	I AIH	gi 9629357:4587 -5165	215	341	09	78	81. 1	0	30	15	35	20	45	3
vpr	HIV 1	gi 9629357:5105 -5396	195	342	09	86	79. 56	0	21.6	20	26.6	31.6	41.6	4
vpr	HIV 1	gi 9629357:5105 -5396	175	343	09	118	78.	0	18.3	20	30	31.6	38.3	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%A	L%	%G	PolyX
vpr	HIV 1	gi 9629357:5105 -5396	155	344	09	138	.62 69	0	21.6	18.3	31.6	28.3 3	40	3
vpr	HIV 1	gi 9629357:5105 -5396	135	345	09	158	78. 79	0	26.6 7	13.3	33.3 3	26.6	40	4
ıdı	HIV 1	gi 9629357:5105 -5396	109	346	09	184	81.	0	28.3 3	16.6	26.6	28.3 3	45	4
vpr	HIV 1	gi 9629357:5105 -5396	68	347	09	204	78. 58	0	20	20	25	35	40	4
vpr	HIV 1	gi 9629357:5105 -5396	69	348	09	224	79. 94	0	28.3 3	15	26.6	30	43.3 3	4
vpr	HIV 1	gi 9629357:5105 -5396	49	349	09	244	77. 34	0	26.6	13.3	31.6	28.3	40	4
ıda	HIV 1	gi 9629357:5105 -5396	29	350	09	264	79. 95	0	28.3 3	9.91	38.3 3	16.6	45	4
tat	HIV 1	gi 9629357:5377 -7970	2504	351	09	16	80. 29	0	18.3 3	26.6	30	25	45	3
tat	HIV 1	gi 9629357:5377 -7970	2377	352	09	218	77.	0	28.3 3	29.9	33.3 3	31.6	35	3
tat	HIV 1	gi 9629357:5377 -7970	2310	353	09	285	76. 51	0	15	20	48.3 3	16.6	35	4
tat	HIV 1	gi 9629357:5377 -7970	2250	354	09	345	79. 94	0	26.6	15	38.3 3	20	41.6	3
tat	HIV 1	gi 9629357:5377 -7970	2190	355	09	405	80 80	0	21.6	21.6	26.6	30	43.3	4
tat	HIV 1	gi 9629357:5377 -7970	2023	356	09	572	82. 24	0	28.3 3	9.91	28.3	26.6	45	3
tat	HIV 1	gi 9629357.5377 -7970	1903	357	09	692	81. 72	0	35	10	30	25	45	9
tat	HIV 1	gi 9629357:5377 -7970	1771	358	09	824	79. 96	0	30	15	35	20	45	3
tat	HIV 1	gi 9629357:5377 -7970	1711	359	09	884	77. 23	0	25	13.3	35	26.6	38.3 3	3
tat	HIV 1	gi 9629357:5377 -7970	1651	360	09	944	77. 7	0	16.6 7	18.3	45	20	35	4
rev	HIV 1	gi 9629357:5516 -8199	2625	361	09	09	78. 01	0	25	9.91	35	23.3 3	41.6	3
rev	HIV 1	gi 9629357:5516 -8199	2551	362	09	134	80. 4	0	23.3 3	21.6	23.3	31.6	45	2
rev	HIV 1	gi 9629357:5516 -8199	2454	363	09	231	80. 23	0	31.6	13.3	38.3 3	16.6	45	2
rev	HIV 1	gi 9629357;5516 -8199	2365	364	09	320	80. 29	0	18.3	26.6	30	25	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	%C	8 %	L%	S%G	PolyX
rev	HIV 1	gi 9629357:5516 -8199	2238	398	09	447	77. 17	0	28.3 3	6.67	33.3 3	31.6	35	3
rev	HIV 1	gi 9629357;5516 -8199	2171	998	09	514	76. 51	0	15	20	48.3 3	16.6	35	4
rev	HIV 1	gi 9629357:5516 -8199	2111	298	09	574	79. 94	0	26.6 7	15	38.3 3	20	41.6	3
rev	HIV 1	gi 9629357:5516 -8199	2051	89£	09	634	80. 08	0	21.6	21.6	26.6 7	30	43.3 3	4
rev	HIV 1	gi 9629357:5516 -8199	1884	698	09	801	82. 24	0	28.3 3	16.6	28.3 3	26.6 7	45	3
rev	HIV 1	gi 9629357:5516 -8199	1764	370	09	921	81. 72	0	35	10	30	25	45	9
nda	HIV 1	gi 9629357;5608 -5856	136	371	09	114	78. 38	0	30	11.6	41.6	16.6	41.6	3
vpu	HIV 1	gi 9629357:5608 -5856	189	372	09	61	85. 51	0	40	13.3 3	18.3 3	28.3 3	53.3 3	5
nda	HIV 1	gi 9629357:5608 -5856	188	373	09	62	85. 89	0	40	15	16.6	28.3 3	55	5
nda	HIV 1	gi 9629357:5608 -5856	186	374	09	64	86. 58	0	40	15	18.3 3	26.6 7	55	5
nda	HIV I	gi 9629357;5608 -5856	184	375	09	99	86. 64	0	40	15	18.3 3	26.6 7	55	5
nda	HIV 1	gi 9629357:5608 -5856	183	376	09	29	86. 64	0	40	15	20	25	55	5
nda	HIV 1	gi 9629357:5608 -5856	182	277	09	89	85. 92	0	40	15	18.3 3	26.6 7	55	5
nda	HIV 1	gi 9629357:5608 -5856	181	378	09	69	85. 79	0	38.3 3	15	20	26.6 7	53.3 3	5
vpu	HIV 1	gi 9629357;5608 -5856	180	379	09	70	85. 81	0	38.3 3	15	21.6	25	53.3 3	5
vpu	HIV 1	gi 9629357:5608 -5856	179	380	09	71	85. 37	0	38.3 3	15	21.6	25	53.3 3	5
asp	HIV 1	gi 9629357:6919 -7488	478	381	09	93	82. 24	0	28.3 3	16.6	28.3 3	26.6 7	45	3
asp	HIV 1	gi 9629357:6919 -7488	361	382	09	210	81. 72	0	35	10	30	25	45	9
asp	HIV 1	gi 9629357:6919 -7488	315	383	09	256	80. 7	0	26.6 7	16.6	41.6	15	43.3 3	5
asp	HIV 1	gi 9629357:6919 -7488	212	384	09	359	80. 63	0	30	15	35	20	45	2
asp	HIV 1	gi 9629357:6919 -7488	182	385	09	389	76.	0	21.6	13.3	38.3	26.6	35	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	%A	%T	S%C	PolyX
asp	HIV 1	gi 9629357:6919 -7488	152	386	09	419	79. 95	0	18.3 3	23.3 3	30	28.3 3	41.6	4
asp	HIV I	gi 9629357:6919 -7488	122	387	09	449	80. 68	0	21.6	20	38.3 3	20	41.6	4
asp	HIV 1	gi 9629357:6919 -7488	92	388	09	479	78. 34	0	16.6 7	20	46.6 7	16.6	36.6	4
asp	HIV 1	gi 9629357:6919 -7488	62	389	09	609	79. 23	0	16.6	23.3 3	43.3 3	16.6	40	4
asp	HIV 1	gi 9629357:6919 -7488	32	390	09	539	77. 8	0	25	13.3 3	36.6 7	25	38.3 3	3
nef	HIV 1	gi 9629357:8343 -8963	443	391	09	179	80. 47	0	25	20	38.3 3	16.6	45	3
nef	HIV 1	gi 9629357:8343 -8963	423	392	09	199	79. 2	0	28.3 3	15	41.6 7	15	43.3 3	3
nef	HIV 1	gi 9629357:8343 -8963	402	393	09	220	79. 81	0	23.3 3	20	31.6 7	25	43.3	3
nef	HIV 1	gi 9629357:8343 -8963	322	394	09	300	79. 39	0	16.6	28.3 3	28.3 3	26.6 7	45	3
nef	HIV 1	gi 9629357:8343 -8963	302	395	09	320	80. 05	0	15	28.3 3	33.3 3	23.3 3	43.3 3	3
nef	I AIH	gi 9629357:8343 -8963	274	396	09	348	80. 65	0	26.6 7	16.6 7	40	16.6 7	43.3	9
nef	HIV 1	gi 9629357:8343 -8963	254	397	09	368	79. 99	0	23.3 3	18.3 3	35	23.3	41.6	9
nef	HIV 1	gi 9629357:8343 -8963	234	398	09	388	80. 05	0	26.6 7	15	35	23.3	41.6	6
nef	HIV 1	gi 9629357:8343 -8963	214	399	09	408	78. 88	0	16.6	25	28.3 3	30	41.6	5
nef	HIV 1	gi 9629357:8343 -8963	105	400	09	517	81. 69	0	21.6	23.3 3	38.3 3	16.6	45	5
5'LTR	HIV 2	gi 9628880:1- 855	701	401	09	155	79. 1	0	18.3 3	25	25	31.6	43.3	3
5'LTR	HIV 2	gi 9628880:1- 855	513	402	09	343	79. 71	0	20	23.3 3	21.6 7	35	43.3 3	3
5'LTR	HIV 2	gi 9628880:1- 855	384	403	09	472	79. 15	0	25	18.3 3	41.6	15	43.3	3
5'LTR	HIV 2	gi 9628880:1- 855	354	404	09	502	77. 55	0	21.6 7	16.6 7	45	16.6	38.3 3	3
5'LTR	HIV 2	gi 9628880:1- 855	324	405	09	532	79. 96	0	28.3 3	13.3 3	43.3 3	15	41.6	4
5'LTR	HIV 2	gi 9628880:1- 855	209	406	09	647	81. 97	0	28.3	16.6	33.3 3	21.6	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	%A	L%	%G	PolyX
5'LTR	HIV 2	gi 9628880:1- 855	141	407	09	715	80. 36	0	26.6 7	18.3	36.6 7	18.3 3	45	2
5'LTR	HIV 2	gi 9628880:1- 855	89	408	09	882	78. 77	0	23.3 3	18.3	33.3 3	25	41.6	3
5' LTR	HIV 2	gi 9628880:1- 855	38	409	09	818	75. 67	0	20	16.6	43.3 3	20	36.6 7	5
5'LTR	HIV 2	gi 9628880:1- 855	8	410	09	848	75. 56	0	26.6 7	11.6	41.6	20	38.3 3	5
gag polyprotein	HIV 2	gi 9628880:1103 -2668	1137	411	09	430	82. 46	0	30	15	38.3 3	16.6 7	45	3
gag polyprotein	HIV 2	gi 9628880:1103 -2668	066	412	09	277	80. 03	0	25	20	36.6 7	18.3 3	45	4
gag polyprotein	HIV 2	gi 9628880:1103 -2668	930	413	09	637	81. 88	0	16.6 7	28.3 3	41.6 7	13.3 3	45	6
gag polyprotein	HIV 2	gi 9628880:1103 -2668	870	414	09	269	81. 02	0	21.6 7	21.6	40	16.6	43.3 3	4
gag polyprotein	HIV 2	gi 9628880:1103 -2668	810	415	09	757	79. 55	0	21.6	20	41.6	16.6 7	41.6	4
gag polyprotein	HIV 2	gi 9628880:1103 -2668	750	416	09	817	80. 48	0	23.3 3	21.6	36.6 7	18.3 3	45	4
gag polyprotein	HIV 2	gi 9628880:1103 -2668	909	417	09	1961	80. 93	0	25	20	38.3 3	16.6 7	45	3
gag polyprotein	HIV 2	gi 9628880:1103 -2668	546	418	09	1021	79. 57	0	20	20	31.6 7	28.3 3	40	3
gag polyprotein	HIV 2	gi 9628880:1103 -2668	473	419	09	1094	81. 5	0	31.6 7	13.3	33.3 3	21.6 7	45	4
gag polyprotein	HIV 2	gi 9628880:1103 -2668	348	420	09	1219	80. 48	0	20	25	45	10	45	4
gag-pol	HIV 2	gi 9628880:1103 -5754	4593	421	09	09	77. 83	0	20	21.6	35	23.3 3	41.6	4
gag-pol	HIV 2	gi 9628880:1103 -5754	4533	422	09	120	79. 05	0	18.3 3	23.3	35	23.3 3	41.6	5
gag-pol	HIV 2	gi 9628880:1103 -5754	4473	423	09	081	79. 42	0	23.3 3	20	36.6 7	20	43.3 3	5
gag-pol	HIV 2	gi 9628880:1103 -5754	4388	424	09	265	80. 72	0	23.3 3	21.6	33.3 3	21.6	45	4
gag-pol	HIV 2	gi 9628880:1103 -5754	4273	425	09	380	78. 61	0	28.3 3	15	43.3 3	13.3 3	43.3 3	4
gag-pol	HIV 2	gi 9628880:1103 -5754	4173	426	09	480	80. 85	0	28.3 3	16.6	33.3 3	21.6	45	3
gag-pol	HIV 2	gi 9628880:1103 -5754	4096	427	09	557	76. 38	0	11.6	23.3	50	15	35	3

X																					
PolyX	4	3	ε	4	4	4	3	4	4	S	5	S	4	9	9	9	9	9	9	9	٧
2% C	41.6	38.3	45	43.3	43.3	41.6	40	43.3 3	41.6	43.3	38.3 3	41.6	45	45	43.3	43.3	45	45	45	45	15
L%	25	16.6	23.3	16.6	25	28.3	31.6	21.6	26.6 7	23.3	15	20	16.6	23.3	23.3	23.3	23.3	23.3	25	25	26.6
W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-	33.3 3	45	31.6	40	31.6	30	28.3	35	31.6	33.3 3	46.6	38.3 3	38.3 3	31.6	33.3 3	33.3 3	31.6	31.6	30	30	28.3
2%	11.6	15	18.3	25	30	13.3	21.6	25	23.3 3	23.3	16.6	20	18.3	15	15	15	16.6	16.6	16.6	16.6	9.91
9%	30	23.3	26.6	18.3	13.3 3	28.3	18.3	18.3 3	18.3	20	21.6	21.6	26.6	30	28.3	28.3	28.3	28.3	28.3	28.3	28.3
X-Hyb Pot																					
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	79.	76.	81. 32	79	80. 96	80°.	78. 94	80. 21	79. 16	3 %	78.	79.	80.	81. 55	81. 42	81. 16	80.	81. 28	81. 53	81.	8
End Distance	617	703	764	209	261	311	341	372	402	432	464	494	591	120	121	122	123	124	126	127	001
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	9
	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	
SEQ ID NO:	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	077
BP Start	4036	3950	3889	440	388	338	308	277	247	217	185	155	58	223	222	221	220	219	217	216	31.0
Target ID	gi 9628880:1103 -5754	gi 9628880:1103 -5754	gi 9628880:1103 -5754	gi 9628880:5423 -6070	gi 9628880:5898 -6239	gi 9628880:5898 -6239	gi 9628880;5898 -6239	gi 9628880:5898 -6239	gi 9628880:5898 -6239	gi 9628880:5898 -6239	gi 9628880:5898 -6239	gi 9628880:5898									
Virus	HIV 2	HIV ?																			
Product	gag-pol	gag-pol	gag-pol	gp2-vif protein	gp3-vpx Protein	gp3-vpx															

214 449 60 129 80. 0 7 7 213 450 60 130 80. 0 26 166 151 450 60 114 81. 0 25 76 151 451 60 114 81. 0 183 266 150 452 60 115 80. 0 183 266 149 453 60 116 80. 0 183 266 144 455 60 117 80. 0 183 26 144 456 60 119 80. 0 183 26 144 456 60 119 45. 0 183 25 144 456 60 121 80. 0 183 25 145 45 60 122 79. 0 183 25 144	N.	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	Э%	%	L%	ر 3%	PolyX
gl9628880:3898 113 450 60 130 80 0 25 166 gl962880:538 151 451 60 114 81. 0 183 266 gl962880:623 150 452 60 115 80. 0 183 266 gl962880:623 149 453 60 116 80. 0 183 266 gl962880:623 148 454 60 117 80. 0 183 266 gl962880:623 147 455 60 117 80. 0 183 266 gl962880:623 147 455 60 120 45 0 183 266 gl962880:623 145 457 60 120 45 0 183 266 gl962880:623 145 457 60 122 35 0 183 26 gl962880:623 145 450 60 122	\geq	2	gi 9628880:5898 -6239	214	449	09	129	99	0	26.6	16.6	28.3 3	28.3 3	43.3	5
gl962880:6239 151 451 60 114 81. 0 18.3 266 gl962880:6239 150 452 60 115 80. 0 18.3 266 gl962880:6239 149 453 60 116 80. 0 18.3 266 gl962880:6239 148 454 60 117 80. 0 18.3 266 gl962880:6239 147 455 60 117 80. 18.3 266 gl962880:6239 147 455 60 119 80. 0 18.3 266 gl962880:6239 145 456 60 120 45 0 18.3 266 gl962880:6239 144 456 60 120 45 0 18.3 266 gl962880:6239 144 458 60 120 45 0 18.3 25 gl962880:6239 145 460 60 121	≥	. 2	gi 9628880:5898 -6239	213	450	09	130	80. 29	0	25	16.6	28.3	30	41.6	5
gi9628880:6239 150 452 60 115 80. 0 18.3 266 gi9628880:6239 149 453 60 116 80. 0 18.3 266 gi9628880:6239 148 454 60 117 80. 0 18.3 266 gi9628880:6239 147 455 60 118 80. 0 18.3 266 gi9628880:6239 146 456 60 119 80. 0 18.3 266 gi9628880:6239 145 457 60 120 70. 18.3 266 gi9628880:6239 144 458 60 120 70. 0 18.3 266 gi9628880:6239 142 460 60 121 70. 0 21.6 3.3 25 gi9628880:6402 234 460 60 124 70. 0 21.6 3.3 25 gi9628880:6402 233		7.2	gi 9628880:6239 -6502	151	451	09	114	81. 27	0	18.3	26.6	38.3	16.6 7	45	4
gj9628880:6239 148 453 60 116 80. 0 18.3 26.6 6502 6502 148 454 60 117 80. 0 18.3 26.6 6502 6502 147 455 60 118 80. 0 18.3 26.6 gj9628880:6239 147 456 60 119 80. 0 18.3 26.6 gj9628880:6239 145 457 60 120 79. 0 18.3 26.6 gj9628880:6239 143 459 60 121 83 0 18.3 26.6 gj9628880:6239 142 460 60 121 79. 0 18.3 26.6 gj9628880:6402 2314 459 60 122 79. 0 21.6 33.3 26.6 gj9628880:6402 2314 462 60 124 79. 0 216 33.3 26.6 33.3	🗀	V 2	gi 9628880:6239 -6502	150	452	09	115	99	0	18.3	26.6	36.6	18.3	45	4
gi9628880:6239 148 454 60 117 80. 0 18.3 25 gi9628880:6239 147 455 60 118 80. 0 18.3 266 gi9628880:6239 146 456 60 119 80. 0 18.3 266 gi9628880:6239 146 456 60 120 46 0 18.3 26 gi9628880:6239 144 458 60 120 46 0 18.3 25 gi9628880:6239 142 459 60 122 54 0 20 3 gi9628880:6402 142 460 60 122 54 0 21 2 gi9628880:6402 233 461 60 174 79 0 21 2 10 gi9628880:6402 2131 462 60 243 75 0 2 10 gi9628880:6402 2131 464 <td< td=""><td></td><td>12</td><td>gi 9628880:6239 -6502</td><td>149</td><td>453</td><td>09</td><td>116</td><td>80.</td><td>0</td><td>18.3</td><td>26.6</td><td>36.6</td><td>18.3</td><td>45</td><td>4</td></td<>		12	gi 9628880:6239 -6502	149	453	09	116	80.	0	18.3	26.6	36.6	18.3	45	4
gij9628880:6239 147 455 60 118 80. 0 18.3 26.6 6502 4502 60 119 80. 0 18.3 26.6 6502 4502 60 120 45 0 18.3 26.6 6502 450 60 120 46 120 18.3 26.6 gij9628880:6239 144 458 60 121 88 0 18.3 25 gij9628880:6239 143 459 60 122 79. 0 20.3 3 gij9628880:6402 2343 461 60 123 80. 0 21.3 25 10 8957 2857 60 243 75. 0 26.6 18.3 3 3 3 3 4 1 4 4 6 174 14 6 174 14 14 14 4 1 1 14 1	I ⊑	V 2	gi 9628880:6239 -6502	148	454	09	117	80.	0	18.3	25	36.6	20	43.3	4
gij9628880:6239 146 456 60 119 80. 0 18.3 26.7 4502 457 60 120 45 0 18.3 25.4 4502 457 60 120 45 0 18.3 25 4502 458 60 121 78. 0 18.3 25 gi9628880:6239 144 458 60 121 78. 0 18.3 25 gi9628880:623 142 459 60 122 79. 0 21.6 23.3 gi9628880:6402 2383 461 60 174 79. 0 21.6 18.3 8957 8957 60 243 76. 0 76. 18.3 8957 8957 60 426 60 426 80. 60 16.6 18.3 8957 8957 80 16.6 18.2 9. 16.6 18.3	l	V 2	gi 9628880:6239 -6502	147	455	09	118	80. 37	0	18.3	26.6	35	20	45	4
gij962880:6239 145 457 60 120 79. 0 18.3 25 6502 26302 144 458 60 121 78. 0 18.3 25 6502 26302 143 459 60 122 79. 0 18.3 25 gij962880:6239 142 460 60 123 80. 0 20. 33.3 gij962880:6402 2383 461 60 174 79. 0 21.6 23.3 gij962880:6402 2314 462 60 243 75. 0 21.6 18.3 gij962880:6402 2192 463 60 243 76. 0 26.6 18.3 gij962880:6402 2191 465 60 510 80. 7 3 gij9628880:6402 1938 466 60 510 81. 0 26.6 18.3 gij9628880:6402 1762 467 <td>1</td> <td>V 2</td> <td>gi 9628880:6239 -6502</td> <td>146</td> <td>456</td> <td>09</td> <td>611</td> <td>80. 45</td> <td>0</td> <td>18.3 3</td> <td>26.6</td> <td>36.6 7</td> <td>18.3 3</td> <td>45</td> <td>4</td>	1	V 2	gi 9628880:6239 -6502	146	456	09	611	80. 45	0	18.3 3	26.6	36.6 7	18.3 3	45	4
gi/9628880:6239 144 458 60 121 78. 0 18.3 25 gi/9628880:6239 143 459 60 122 79. 0 21.6 23.3 gi/962880:6239 142 460 60 123 80. 0 21.6 23.3 gi/962880:6402 2314 462 60 174 79. 0 21.6 23.3 gi/9628880:6402 2314 462 60 243 75. 0 21.6 10 gi/9628880:6402 2131 464 60 426 80. 7 3 gi/9628880:6402 2131 464 60 426 80. 7 3 gi/9628880:6402 2047 465 60 510 81. 0 26.6 18.3 gi/9628880:6402 1762 467 60 795 81. 0 26.6 18.3 gi/9628880:6402 1762 467 60 795 <td>_</td> <td>V 2</td> <td>gi 9628880:6239 -6502</td> <td>145</td> <td>457</td> <td>09</td> <td>120</td> <td>79. 46</td> <td>0</td> <td>18.3 3</td> <td>25</td> <td>36.6 7</td> <td>20</td> <td>43.3 3</td> <td>4</td>	_	V 2	gi 9628880:6239 -6502	145	457	09	120	79. 46	0	18.3 3	25	36.6 7	20	43.3 3	4
gi/962880:6239 143 459 60 122 79. 0 20. 23.3 -6502 460 60 123 80. 0 21.6 3.3 -6502 23880:6402 2383 461 60 174 79. 0 21.6 23.3 -8957 2895 2314 462 60 24.3 75. 0 25 10 -8957 2192 463 60 365 3.6 3.6 16.6 18.3 -8957 2131 464 60 426 80. 0 7 3 -8957 2131 464 60 510 81. 0 7 3 -8957 2152 465 60 510 81. 0 7 3 -8957 216. 60 795 81. 0 7 3 3 11.6 2 1 1 4 1 3 2	_	V 2	gi 9628880:6239 -6502	144	458	09	121	78. 83	0	18.3	25	36.6	20	43.3 3	4
gil962880:6239 142 460 60 123 80. 0 21.6 23.3 6502 2383 461 60 174 79. 0 21.6 23.3 gl962880:6402 2314 462 60 243 75. 0 21.6 10 gl962880:6402 2192 463 60 365 76. 0 7.5 10 gl962880:6402 2131 464 60 426 80. 0 26.6 18.3 gl962880:6402 2047 465 60 510 81. 0 26.6 18.3 gl962880:6402 1938 466 60 510 82. 0 26.6 18.3 gl962880:6402 1762 467 60 795 81. 0 7 3 gl9628880:6402 1762 467 60 795 81. 0 26.6 18.3 gl9628880:6402 1762 467 60 <td></td> <td>V 2</td> <td>gi 9628880:6239 -6502</td> <td>143</td> <td>459</td> <td>09</td> <td>122</td> <td>79. 54</td> <td>0</td> <td>20</td> <td>23.3</td> <td>36.6 7</td> <td>20</td> <td>43.3 3</td> <td>4</td>		V 2	gi 9628880:6239 -6502	143	459	09	122	79. 54	0	20	23.3	36.6 7	20	43.3 3	4
gil9628880:6402 2383 461 60 174 79. 0 21.6 20 8957 2314 462 60 243 75. 0 25 10 8957 2192 463 60 365 3. 0 25 10 8957 2192 463 60 426 80. 0 7 3 8957 2047 465 60 510 81. 0 7 3 8957 2047 465 60 510 82. 0 7 3 8957 2047 465 60 510 82. 0 7 3 8957 1762 467 60 795 81. 0 7 3 8957 28957 170 468 60 795 81. 0 7 3 8957 28957 1895 1 7 3 1 6 </td <td></td> <td>IV 2</td> <td>gi 9628880:6239 -6502</td> <td>142</td> <td>460</td> <td>09</td> <td>123</td> <td>80. 24</td> <td>0</td> <td>21.6</td> <td>23.3 3</td> <td>35</td> <td>20</td> <td>45</td> <td>3</td>		IV 2	gi 9628880:6239 -6502	142	460	09	123	80. 24	0	21.6	23.3 3	35	20	45	3
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		IV 2	gi 9628880:6402 -8957	2383	461	09	174	79. 14	0	21.6	20	23.3	38	41.6	9
gi 9628880:6402 2192 463 60 365 76. 0 16.6 18.3 -8957 2131 464 60 426 80. 0 7 3 8957 2131 464 60 426 93 0 26.6 18.3 8957 2047 465 60 510 81. 0 26.6 18.3 8957 1762 467 60 795 81. 0 26.6 18.3 8957 28957 469 60 795 81. 0 7 3 8957 319628880:6402 1762 469 60 855 78. 0 7 3 8957 319628880:6402 1579 469 60 978 81. 0 25 16.6 8957 3133 11.6 33.3 11.6 33.3 11.6		V 2	gi 9628880:6402 -8957	2314	462	09	243	75. 32	0	25	10	35	30	35	3
gi 9628880:6402 2131 464 60 426 80. 0 26.6 18.3 -8957 2047 465 60 510 81. 0 7.6 18.3 -8957 2047 465 60 619 82. 0 7.6 18.3 -8957 466 60 619 82. 0 7.0 3 -8957 1762 467 60 795 81. 0 16.6 28.3 -8957 1702 468 60 855 13 0 25 16.6 -8957 1579 469 60 978 81. 0 33.3 11.6		IV 2	gi 9628880:6402 -8957	2192	463	09	365	76. 3	0	16.6	18.3 3	48.3 3	16.6 7	35	4
gi 9628880:6402 2047 465 60 510 81. 0 26.6 18.3 8957 465 60 619 82. 0 7 3 8957 8957 466 60 619 82. 0 76.6 18.3 8957 1762 467 60 795 81. 0 16.6 28.3 8957 1702 468 60 855 13 0 25 16.6 8957 1579 469 60 978 81. 0 33.3 11.6		V 2	gi 9628880:6402 -8957	2131	464	09	426	80. 93	0	26.6	18.3	33.3 3	21.6	45	5
gi 9628880:6402 1938 466 60 619 82. 0 26.6 18.3 8957 1160 <td< td=""><td></td><td>V 2</td><td>gi 9628880:6402 -8957</td><td>2047</td><td>465</td><td>09</td><td>510</td><td>81. 51</td><td>0</td><td>26.6</td><td>18.3</td><td>31.6</td><td>23.3 3</td><td>45</td><td>4</td></td<>		V 2	gi 9628880:6402 -8957	2047	465	09	510	81. 51	0	26.6	18.3	31.6	23.3 3	45	4
gi 9628880:6402 1762 467 60 795 81. 1 0 16.6 7 28.3 3 gi 9628880:6402 1702 468 60 855 78. 13 0 25 76. 7 gi 9628880:6402 1579 469 60 978 81. 81. 0 33.3 11.6 11.6		V 2	gi 9628880:6402 -8957	1938	466	09	619	82. 14	0	26.6 7	18.3	38.3 3	16.6 7	45	3
gi 9628880:6402 - 8957 1702 468 60 855 13 0 25 7 7 10 0 1579 469 60 978 81. 0 33.3 11.6 11.6 16.6 1	_	V 2	gi 9628880:6402 -8957	1762	467	09	562	81. 1	0	16.6	28.3	35	20	45	3
$\begin{vmatrix} g_1 \\ g_2 \\ g_3 \\ g_4 \\ g_5 \\ g_5 \\ g_6 \\ g_7 \\ g_7 \\ g_8 \\ g_1 \\ g_1 \\ g_1 \\ g_2 \\ g_3 \\ g_1 \\ g_2 \\ g_3 \\ g_4 \\ g_1 \\ g_2 \\ g_3 \\ g_4 \\ g_4 \\ g_5 \\ g_4 \\ g_5 \\ g_5 \\ g_5 \\ g_6 \\ g_6 \\ g_6 \\ g_7 \\ g_8 \\ g_$	'	V 2	gi 9628880:6402 -8957	1702	468	09	855	78. 13	0	25	16.6	35	23.3 3	41.6	3
02 3 7		.V 2	gi 9628880:6402 -8957	1579	469	09	826	81. 02	0	33.3 3	11.6	30	25	45	5

Target ID
gl/9628880:6402 -8957 1519 470
gi 9628880:6628 2355 471
gi 9628880:6628 2157 472 -9102
gi 9628880:6628 2088 473 -9102
gi 9628880:6628 1966 474 -9102
gi 9628880:6628 1905 475 -9102
gi 9628880:6628 1821 476 -9102
gi 9628880:6628 1712 477
gi 9628880:6628 1536 478 -9102
gi 9628880:6628 1476 479 -9102
gi 9628880:6628 1353 480 -9102
gi 9628880:6704 2279 481 -9286
gi 9628880:6704 2081 482 -9286
gi 9628880:6704 2012 483 -9286
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gi 9628880:6704 1829 485 -9286
gi 9628880:6704 1745 486 -9286
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gi 9628880:6704 1460 488 -9286
gi 9628880:6704 1400 489 -9286
gi 9628880:6704 1277 490 -9286

181 81. 0	96	492 60 181 81. 0	8880.9120 594 492 60 181 81. 0	8880:9120
$\begin{vmatrix} 181 & 81 & 0 \\ 97 & 97 & 0 \end{vmatrix}$		$ 492 60 181 \frac{81}{2} 0$	8880.9120 594 492 60 181 $81.$ 0	gi 9628880:9120 50, 100 101 81. 5
	60 181 81.	1.6		-9893
249	80. 36 0	493 60 249 80. 0	8880:9120 526 493 60 249 80. 0	8880:9120 526 493 60 249 80. 0
50 322 78 0 23.3	0 78. 0	494 60 322 78. 0	453 494 60 322 78. 0	8880:9120 453 494 60 322 78. 0
352	75. 0	495 60 352 75. 0	60 352 75. 0	8880:9120 423 495 60 352 75. 0
382	75. 0	496 60 382 75. 0	8880:9120 393 496 60 382 75. 0	8880:9120 393 496 60 382 75. 0
416	0 69	497 60 416 77. 0	60 416 77. 0	359 497 60 416 $\frac{77}{69}$ 0
467	76. 0	498 60 467 76. 0	60 467 76. 0	8880:9120 308 498 60 467 76. 0
497	79. 0	499 60 497 79. 0	278 499 60 497 79 . 0	278 499 60 497 79 . 0
527	77. 0	500 60 527 77. 0	248 500 60 527 77. 0	248 500 60 527 77. 0
155	79. 0 18.3	501 60 155 79. 0 18.3	60 155 79. 0 18.3	501 60 155 79. 0 18.3
$\begin{vmatrix} 343 & 79. & 0 & 20 \end{vmatrix}$	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$
472 79. 0 25	79. 0 25 18.3	503 60 472 79. 0 0 25 18.3 3	60 472 79. 0 25 18.3 3	503 60 472 79. 0 0 25 18.3 3
502 77. 0 21.6 16.6	60 507 77. 0 21.6 16.6	\$ 15 0 3 3 4 16.6	\$ 15 0 3 3 4 16.6	504 60 502 77. 0 21.6 16.6
0	0 09	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	354 504 60 502
502 1.1.0 21.0	0.17 0 .// 20.0	504 50 503 71.0 51.0	504 50 503 71.0 51.0	354 504 60 502 77 0 21.0
472 79. 0	60 472 79. 0	503 60 472 79. 0 504 60 503 77. 0	503 60 472 79. 0 504 60 503 77. 0	384 503 60 472 79 0 354 504 60 502 77 0
527 26 165 19. 343 79. 472 79. 502 77.	60 527 77. 60 155 1 60 343 79. 60 472 79. 60 472 15. 60 502 77.	500 60 527 77 501 60 155 79 502 60 343 79 503 60 472 79 504 60 472 79 503 60 472 77	248 500 60 527 77 701 501 60 155 1 513 502 60 343 79 384 503 60 472 79 354 503 60 472 77	Exponential 248 500 60 527 77 -9893 701 501 60 155 79 513 502 60 343 71 384 503 60 472 79 354 504 60 502 77
410 467 497 527 155 143 472 502	60 467 60 497 60 527 60 155 60 343 60 472	498 60 467 498 60 467 499 60 497 500 60 527 501 60 155 502 60 343 503 60 472 504 60 502	8880:9120 308 498 60 467 8880:9120 278 499 60 497 8880:9120 248 500 60 527 701 501 60 155 513 502 60 343 384 503 60 472	9893 359 497 00 410 gi 962880:9120 308 498 60 467 -9893 278 499 60 497 gi 9628880:9120 248 500 60 497 -9893 701 501 60 155 513 502 60 343 384 503 60 472
382 382 416 467 497 527 527 155 143 472	60 382 60 416 60 467 60 497 60 527 60 155 60 343 60 472	496 60 382 497 60 416 498 60 467 499 60 497 500 60 527 501 60 155 503 60 472 503 60 472	359 496 60 382 359 496 60 416 308 498 60 467 278 499 60 497 248 500 60 497 701 501 60 155 313 502 60 343 384 503 60 472 503 60 503	gi 962880:9120 393 496 60 382 -9893 496 60 416 -9893 497 60 416 -9893 497 60 467 -9893 498 60 467 -9893 278 499 60 497 gi 9628880:9120 278 499 60 497 gi 9628880:9120 248 500 60 527 -9893 701 501 60 155 343 502 60 472 354 504 60 507
	09 09 09 09 09 09	495 60 496 60 497 60 499 60 500 60 501 60 503 60 504 60	423 495 60 393 496 60 359 497 60 308 498 60 278 499 60 248 500 60 701 501 60 513 502 60 384 503 60 554 504 60	gi/92880:9120 393 495 60 -9893 496 60 -9893 496 60 -9893 497 60 -9893 499 60 -9893 21862880:9120 278 499 60 -9893 248 500 60 -9893 701 501 60 334 502 60 334 503 60
		494 495 496 497 499 500 500 503	526 493 453 494 423 495 393 496 359 497 278 499 248 500 701 501 513 502 384 503	gi]9628880:9120 453 494 -9893 453 494 -9893 494 453 494 -9893 495 496 498 gi]9628880:9120 359 496 -9893 369628880:9120 378 498 gi]9628880:9120 278 499 -9893 218 500 gi]9628880:9120 248 500 -9893 499 gi]9628880:9120 248 500 -9893 384 503

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5%	2%	₩%		5% 2	PolyX
gag	HTLV 1	gb AF033817.1 : 450-1739	926	512	09	365	81. 2	0	21.6	23.3	36.6	18.3	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	925	513	09	366	69	0	21.6	23.3	38.3 3	16.6	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	924	514	09	367	80. 69	0	20	25	38.3 3	16.6	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	923	515	09	368	81. 23	0	20	25	40	15	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	922	516	09	369	81. 51	0	20	25	40	15	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	921	517	09	370	81. 54	0	20	25	41.6	13.3	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	917	518	09	374	81. 41	0	18.3	26.6	40	15	45	5
gag	HTLV 1	gb AF033817.1 : 450-1739	916	519	09	375	81. 36	0	16.6	26.6	41.6	15	43.3	5
gag	HTLV 1	gb AF033817.1 : 450-1739	516	520	09	376	81. 36	0	16.6	26.6	40	16.6	43.3	5
pro	HTLV 1	gb AF033817.1 : 1718-2404	609	521	09	62	81. 5	0	16.6	28.3	35	20	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	809	522	09	80	81. 38	0	15	28.3 3	36.6 7	20	43.3	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	209	523	09	81	80. 97	0	16.6	28.3	36.6	18.3	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	909	524	09	82	80. 97	0	18.3	26.6	36.6	18.3	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	909	525	09	83	81. 28	0	18.3	25	38.3 3	18.3 3	43.3	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	604	526	09	84	80. 99	0	18.3	26.6	36.6	18.3 3	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	603	527	09	85	80. 99	0	16.6	28.3	36.6 7	18.3 3	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	602	528	09	86	81.	0	18.3	26.6	36.6	18.3 3	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	583	529	09	105	81. 26	0	16.6	28.3	38.3 3	16.6	45	9
pro	HTLV 1	gb AF033817.1 : 1718-2404	285	530	09	106	81. 26	0	15	30	38.3 3	16.6	45	9
Pol	HTLV 1	gi 9626453:2245 -4836	2376	531	09	217	81. 86	0	20	25	28.3 3	26.6 7	45	3
Pol	HTLV 1	gi 9626453:2245 -4836	2262	532	09	331	81. 66	0	13.3	30	38.3	18.3	43.3	4

Product	Virus	Target ID	BP	SEQ ID	Probe Lenoth	End Distance	Tm	X-Hyb Pot	5%	3%	₩%	L%	5% 5	PolyX
Pol	HTLV 1	gi 9626453:2245 -4836	2202	533	09	391	77.	0	11.6	28.3	31.6	28.3	04	3
Pol	HTLV 1	gi 9626453:2245 -4836	2051	534	09	542	79. 82	0	11.6	30	31.6	26.6	41.6	3
Pol	HTLV 1	gi 9626453:2245 -4836	1984	535	09	609	81. 28	0	18.3	26.6	30	25	45	3
Pol	HTLV 1	gi 9626453:2245 -4836	1914	536	09	629	80. 45	0	18.3	26.6	26.6	28.3	45	4
Pol	HTLV 1	gi 9626453:2245 -4836	1475	537	09	1118	79. 19	0	11.6	30	25	33.3 3	41.6	3
Pol	HTLV 1	gi 9626453:2245 -4836	1333	538	09	1260	81. 34	0	15	30	26.6	28.3	45	5
Pol	HTLV 1	gi 9626453:2245 -4836	1242	539	09	1351	81. 27	0	16.6	28.3 3	21.6	33.3 3	45	4
Pol	HTLV 1	gi 9626453:2245 -4836	1182	540	09	1411	79. 74	0	16.6	25	33.3 3	25	41.6	5
rex	HTLV 1	gi 9626453:4773 -8008	3128	541	60	109	81. 24	0	18.3 3	26.6	35	20	45	5
rex	HTLV 1	gi 9626453:4773 -8008	3068	542	09	169	76. 49	0	29.9	30	26.6 7	36.6	36.6 7	4
rex	HTLV 1	gi 9626453:4773 -8008	2975	543	09	262	77.	0	6.67	30	30	33.3 3	36.6	3
rex	HTLV 1	gi 9626453:4773 -8008	2758	544	09	479	81. 27	0	15	30	26.6	28.3	45	4
rex	HTLV 1	gi 9626453:4773 -8008	2160	545	09	1077	80. 71	0	18.3	26.6	21.6	33.3 3	45	4
rex	HTLV 1	gi 9626453:4773 -8008	1489	546	09	1748	78. 44	0	8.33	30	35	26.6	38.3 3	3
rex	HTLV 1	gi 9626453:4773 -8008	1251	547	09	1986	77. 3	0	11.6	28.3 3	30	30	40	9
rex	HTLV 1	gi 9626453:4773 -8008	1146	548	09	2091	82. 63	0	18.3	26.6	36.6 7	18.3	45	5
rex	HTLV 1	gi 9626453:4773 -8008	1086	549	09	2151	78. 28	0	16.6	21.6	40	21.6	38.3 3	3
rex	HTLV 1	gi 9626453:4773 -8008	721	550	09	2516	81. 15	0	16.6	28.3	20	35	45	2
tax	HTLV 1	gi 9626453.4829 -8008	3072	551	09	109	81. 24	0	18.3	26.6	35	20	45	5
tax	HTLV 1	gi 9626453:4829 -8008	3012	552	09	169	76. 49	0	6.67	30	26.6	36.6 7	36.6	4
tax	HTLV 1	gi 9626453:4829 -8008	2919	553	09	262	77.	0	6.67	30	30	33.3 3	36.6	3

gl/9626453:4829 2702 554 -8008
gi 9626453:4829 2104 555 -8008
gi 9626453:4829 1433 556 -8008
gi 9626453:4829 1195 557 -8008
gi 9626453:4829 1090 558 -8008
gi 9626453:4829 1030 559 -8008
gi 9626453:4829 665 560 -8008
gi 9626453:4829 1192 561 -6295
gi 9626453:4829 1152 562 -6295
gi 9626453:4829 1085 563 -6295
gi 9626453:4829 1045 564 -6295
gi 9626453:4829 662 565 -6295
gi 9626453:4829 621 566 -6295
gi 9626453:4829 454 -6295
gi 9626453:4829 388 -6295
gi 9626453:4829 297 -6295
gi 9626453:4829 257 -6295
gi 9626726:1- 763
gi 9626726:1- 763
gi 9626726:1- 260 763
gi 9626726:1- 258 763

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25 23.3 3 21.6 7 7 20
0 0 0
78. 0 88 0 77. 0 51 0
60 513
52
-21

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%A	L%	S%C	PolyX
gs1	HTLV 2	gi 9626726:316- 8751	6864	969	09	1573	80. 03	0	13.3 3	30	30	26.6 7	43.3 3	3
gs1	HTLV 2	gi 9626726:316- 8751	6510	597	09	1927	80. 81	0	13.3 3	30	43.3 3	13.3 3	43.3 3	4
gs1	HTLV 2	gi 9626726:316- 8751	6302	869	09	2135	81. 49	0	15	30	31.6 7	23.3 3	45	4
gs1	HTLV 2	gi 9626726:316- 8751	6038	599	09	2399	81. 19	0	16.6	28.3 3	30	25	45	2
gs1	HTLV 2	gi 9626726:316- 8751	5942	009	09	2495	81. 23	0	20	25	36.6 7	18.3 3	45	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	4170	601	09	212	82. 08	0	20	25	28.3 3	26.6 7	45	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	4051	602	09	331	81. 97	0	18.3 3	26.6	33.3 3	21.6	45	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	3988	603	09	394	77. 04	0	8.33	30	36.6 7	25	38.3 3	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	3878	604	09	504	78. 39	0	9.11	30	30	28.3 3	41.6	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	3759	605	09	623	81 .	0	20	25	30	25	45	5
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	3580	909	09	802	81. 24	0	15	30	31.6	23.3 3	45	3
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	3276	209	09	1106	80. 47	0	13.3 3	30	26.6 7	30	43.3	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	2797	809	09	1585	79. 64	0	15	30	30	25	45	3
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	2698	609	09	1684	81. 71	0	16.6	28.3	28.3 3	26.6 7	45	4
Gag-Pro-Pol	HTLV 2	gi 9626726:807- 5187	2471	610	09	1161	80. 7	0	20	25	31.6	23.3 3	45	3
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	927	611	09	376	81. 37	0	15	30	43.3 3	11.6	45	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	924	612	09	379	82. 65	0	15	30	43.3 3	11.6	45	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	923	613	09	380	82. 37	0	15	30	41.6	13.3 3	45	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	910	614	09	393	80. 15	0	9.11.6	30	38.3 3	20	41.6	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	909	615	09	394	79. 59	0	11.6	30	38.3 3	20	41.6	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	806	616	09	395	79. 44	0	11.6	30	38.3 3	20	41.6	6

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	%C	8 %	L%	%G	PolyX
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	904	617	09	399	80. 74	0	13.3 3	30	36.6	20	43.3	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	903	618	09	400	81. 46	0	13.3 3	30	36.6	20	43.3	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	902	619	09	401	81. 46	0	13.3 3	30	38.3 3	18.3 3	43.3	9
gp2-gag polyprotein	HTLV 2	gi 9626726:807- 2108	901	620	09	402	81. 02	0	13.3 3	30	40	16.6	43.3	9
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	2053	621	09	167	78. 63	0	10	30	30	30	40	9
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	2003	622	09	541	80. 11	0	13.3 3	30	30	26.6	43.3	9
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	1705	623	09	683	80. 81	0	13.3 3	30	43.3 3	13.3 3	43.3	4
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	1488	624	09	1056	79. 23	0	11.6	30	31.6	26.6	41.6	3
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	1219	625	09	1325	80. 73	0	20	23.3	28.3 3	28.3 3	43.3	3
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	1132	626	09	1412	81. 46	0	18.3	25	38.3 3	18.3	43.3	S
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	1092	627	09	1452	79. 8	0	13.3	30	38.3 3	18.3	43.3	5
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	089	628	09	1864	80. 7	0	20	25	26.6	28.3	45	3
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	455	629	09	2089	80. 18	0	15	28.3	28.3	28.3 3	43.3	3
gp4-rex 26 kD protein	HTLV 2	gi 9626726:5121 -7663	293	630	09	2251	80. 81	0	18.3	26.6	35	20	45	9
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	2967	631	09	09	78. 34	0	20	20	33.3 3	26.6	40	4
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	2836	632	09	161	78. 82	0	10	30	30	30	40	5
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	2743	633	09	284	80. 73	0	13.3 3	30	30	26.6	43.3	4
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	2603	634	09	424	80. 42	0	20	25	35	20	45	4
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	2000	635	09	1027	80. 03	0	13.3 3	30	30	26.6 7	43.3	3
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	1646	636	09	1381	80. 81	0	13.3 3	30	43.3 3	13.3 3	43.3	4
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	1438	637	09	1589	81. 49	0	15	30	31.6	23.3 3	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	V %	%T	2 %G	PolyX
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	1174	638	09	1853	81. 19	0	16.6	28.3 3	30	25	45	2
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	1078	639	09	1949	81. 23	0	20	25	36.6 7	18.3 3	45	4
gp5-tax protein	HTLV 2	gi 9626726:5180 -8205	624	640	09	2403	80. 99	0	20	25	25	30	45	3
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	1402	641	09	09	79. 45	0	11.6	30	38.3	20	41.6	4
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	1160	642	09	302	80. 73	0	20	23.3	28.3	28.3 3	43.3 3	3
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	1073	643	09	389	81. 46	0	18.3 3	25	38.3 3	18.3 3	43.3 3	5
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	1033	644	09	429	79. 8	0	13.3 3	30	38.3 3	18.3 3	43.3 3	5
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	621	645	09	841	80. 7	0	20	25	26.6	28.3 3	45	3
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	599	646	09	863	80. 06	0	13.3 3	30	33.3 3	23.3 3	43.3 3	4
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	396	647	09	1066	80. 18	0	15	28.3	28.3	28.3 3	43.3 3	3
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	375	648	09	1087	80. 45	0	20	25	28.3	26.6 7	45	3
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	234	649	09	1228	80. 81	0	18.3 3	26.6	35	20	45	9
gp6-env peptide	HTLV 2	gi 9626726:5180 -6640	9	650	09	1456	79. 38	0	11.6	30	21.6	36.6 7	41.6	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	262	651	09	502	80. 91	0	28.3 3	16.6	36.6	18.3 3	45	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	261	652	09	503	80. 27	0	26.6 7	18.3 3	36.6 7	18.3 3	45	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	260	653	09	504	80. 93	0	26.6 7	18.3 3	36.6 7	18.3 3	45	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	258	654	09	506	81	0	28.3 3	16.6	36.6	18.3 3	45	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	257	655	09	507	80. 3	0	26.6 7	16.6	36.6	20	43.3 3	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	256	656	09	508	80. 17	0	25	16.6	36.6 7	21.6 7	41.6	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	255	657	09	509	79. 64	0	25	16.6	38.3 3	20	41.6	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	254	658	09	510	78. 94	0	23.3	16.6	40	20	40	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%A	L%	5% C	PolyX
3 LTR	HTLV 2	gi 9626726:8190 -8952	253	659	09	511	78.	0	21.6	16.6	41.6	20	38.3	4
3 LTR	HTLV 2	gi 9626726:8190 -8952	251	099	09	513	77. 51	0	20	16.6	41.6	21.6	36.6	4
anchored capsid protein C	66KN ANW	gi 158516887:97 -465	299	661	09	71	81. 86	0	26.6 7	18.3	41.6	13.3	45	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	298	662	09	72	81. 77	0	26.6 7	18.3	40	15	45	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	297	£99	09	73	81. 13	0	26.6 7	18.3 3	40	15	45	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	296	664	09	74	81. 13	0	28.3 3	16.6	40	15	45	4
anchored capsid protein C	66KN ANM	gi 158516887:97 -465	295	665	09	75	80. 86	0	26.6 7	16.6	41.6	15	43.3	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	294	999	09	92	80. 86	0	28.3 3	15	41.6	15	43.3	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	586	<i>L</i> 99	09	84	81. 58	0	28.3 3	15	43.3 3	13.3 3	43.3	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	282	899	09	88	81. 3	0	26.6 7	16.6	43.3 3	13.3 3	43.3	4
anchored capsid protein C	66AN ANM	gi 158516887:97 -465	281	699	09	68	81. 38	0	26.6 7	18.3	43.3 3	11.6	45	4
anchored capsid protein C	WNV NY99	gi 158516887:97 -465	279	029	09	91	82. 19	0	28.3 3	16.6	41.6	13.3	45	4
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	355	671	09	147	81. 75	0	28.3 3	16.6	30	25	45	5
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	354	672	09	148	81. 23	0	28.3 3	16.6	30	25	45	5
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	353	673	09	149	80. 51	0	28.3 3	16.6	30	25	45	5
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	352	674	09	150	80. 31	0	26.6 7	16.6	31.6	25	43.3	5
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	351	675	09	151	80. 31	0	25	18.3	31.6	25	43.3	5
membrane glycoprotein precursor prM	WNV NY99	gi 158516887:46 6-966	350	929	09	152	80.	0	25	20	31.6	23.3	45	5

WNV NY99 gj 188516887-46 349 677 60 153 80. 65 9 25 20 31.6 3.3 45 WNV NY99 g.9168516887-46 346 678 60 154 23. 0 25 20 31.5 15 3.3 45 WNV NY99 gj 188516887-46 347 679 60 156 80. 0 25 18.3 35 21.6 45 WNV NY99 gj 188516887-96 346 689 60 156 80. 0 25 18.3 35 21.6 45 WNV NY99 gj 188516887-96 880 682 60 624 81. 0 25 18.3 45 45 WNV NY99 gj 188516887-96 850 683 60 634 81.0 624 81.0 62 52 18.3 31.5 45 45 WNV NY99 gj 188516887-96 850 683 60 634		Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%	L%	S%G	PolyX
gi188516887-46 348 678 60 154 81. 0 25 20 31.6 31.6 33.3 4.5 gi188516887-46 347 679 60 155 81. 0 25 18.3 31.6 37.6 45.3 gi188516887-36 1168 681 60 155 81. 0 25 18.3 35. 11.6 45.3 gi188516887-36 1168 681 60 524 81. 0 25 18.3 35. 11.6 45.3 gi188516887-36 1168 681 60 624 81. 0 26. 16. 26. 18.3 45. gi188516887-36 880 682 60 624 31. 6 22. 13.3 11.6 83.3 45. gi188516887-36 880 682 60 664 10 26. 18.3 31.6 33.3 45. gi188516887-36 882 <t< td=""><td>\geq</td><td>00 NV NY</td><td>gi 158516887:46 6-966</td><td>349</td><td>677</td><td>09</td><td>153</td><td>80. 66</td><td>0</td><td>25</td><td>20</td><td>31.6</td><td>23.3</td><td>45</td><td>5</td></t<>	\geq	00 NV NY	gi 158516887:46 6-966	349	677	09	153	80. 66	0	25	20	31.6	23.3	45	5
gil38516887.46 347 679 60 155 81 0 25 20 3.3 21.6 45.9 gil38516887.46 346 680 60 156 80 20 25 18.3 3 21.6 43.3 gil38516887.36 1168 681 60 624 81. 0 26 36 18.3 3.5 1.6 43.3 gil38516887.96 880 682 60 624 81. 0 26 166 26. 30. 43.3 47. gil38516887.96 880 682 60 624 31. 0 26. 166 26. 33.3 41.6 43.3 gil38516887.96 880 683 60 684 80. 684 80. 11.1 79. 26. 18.3 41.6 gil38516887.96 895 686 60 909 81. 9 26. 18.3 41.6 gil38516887.96 <td> ⊳</td> <td>66 KN VN/</td> <td>gi 158516887:46 6-966</td> <td>348</td> <td>878</td> <td>09</td> <td>154</td> <td>81. 23</td> <td>0</td> <td>25</td> <td>20</td> <td>31.6</td> <td>23.3</td> <td>45</td> <td>5</td>	⊳	66 KN VN/	gi 158516887:46 6-966	348	878	09	154	81. 23	0	25	20	31.6	23.3	45	5
gil38316887:46 346 680 156 80. 65. 65. 18.3 55. 11. 43.3 45. 45.	⊳	96 AN AN/	gi 158516887:46 6-966	347	629	09	155	81. 23	0	25	20	33.3 3	21.6	45	5
gil38516887:96 1168 681 600 634 82. 60 62 5 5 5 6 18.3 45 gil388516887:96 880 682 60 624 25 0 76 166 266 166 266 18.3 43.3 gil388516887:96 850 683 60 684 80. 0 28.3 13.3 30 28.3 41.6 gil388516887:96 820 684 60 684 80. 0 28.3 13.3 30 28.3 41.6 gil38516887:96 820 684 60 716 82. 0 28.3 3.1 45 41.6 gil38516887:96 395 686 60 909 81. 0 26. 18.3 45 45 gil38516887:96 395 688 60 1111 43 0 26. 18.3 45 45 gil38516887:94 396	>	96 AN ANA	gi 158516887:46 6-966	346	089	09	156	80. 53	0	25	18.3	35	21.6	43.3 3	5
gils8516887;96 880 682 60 624 81. 0 266 166 266 30 43.3 7-2469 850 683 60 654 79. 70 7		96YN VNV	gi 158516887:96 7-2469	1168	681	09	336	82. 12	0	20	25	36.6	18.3	45	3
gil18816887-96 850 683 60 654 79. 71. 10 35 23.3 41.6 gil18816887-96 820 684 80. 684 28. 13.3 30 28.3 41.6 gil18816887-96 788 685 60 716 82. 0 28.3 1.6 28.3 41.6 gil18816887-96 788 686 60 909 81. 0 26.6 18.3 25 30 45 gil18816887-96 395 686 60 1111 79. 0 26. 18.3 31.6 45 gil18816887-96 365 686 60 1111 79. 0 26. 18.3 45 gil18816887-96 368 60 1144 79. 0 26. 18.3 45 gil18816887-96 36 60 1144 79. 0 26. 18.3 45 gil18816887-94 396 <t< td=""><td>></td><td>66KN ANA</td><td>gi 158516887:96 7-2469</td><td>088</td><td>682</td><td>09</td><td>624</td><td>81. 25</td><td>0</td><td>26.6 7</td><td>16.6 7</td><td>26.6 7</td><td>30</td><td>43.3 3</td><td>3</td></t<>	>	66KN ANA	gi 158516887:96 7-2469	088	682	09	624	81. 25	0	26.6 7	16.6 7	26.6 7	30	43.3 3	3
gil58516887:96 684 60 684 80 28.3 13.3 30 28.3 41.0 gil58516887:96 788 685 60 716 82. 0 23.3 21.6 25 30 45 gil58516887:96 595 686 60 909 81. 0 26.6 18.3 3.16 25 30 45 gil58516887:96 393 687 60 1111 79. 0 26.6 18.3 3.16 25 43.3 gil58516887:96 363 688 60 1141 79. 0 21.6 30 45 gil58516887:96 319 688 60 1144 79. 0 20.6 18.3 41.6 gil58516887:96 30 690 60 1414 79. 0 26.6 18.3 45 gil58516887:24 371 691 60 1414 79. 0 26.6 18.3 45 <td> ></td> <td>66KN ANA</td> <td>gi 158516887:96 7-2469</td> <td>850</td> <td>683</td> <td>09</td> <td>654</td> <td>79. 31</td> <td>0</td> <td>31.6</td> <td>10</td> <td>35</td> <td>23.3 3</td> <td>41.6</td> <td>5</td>	>	66KN ANA	gi 158516887:96 7-2469	850	683	09	654	79. 31	0	31.6	10	35	23.3 3	41.6	5
gil38516887:96 788 685 60 716 82. 6. 23.3 21.6 25 30 45 7-2469 995 81. 0 26.6 18.3 25 30 45 7-2469 995 88. 60 1111 79. 0 26. 18.3 31.6 25 45.3 7-2469 363 688 60 1141 78. 0 25 3.3 7 3.3 45 gil38516887:96 319 688 60 1141 78. 0 25 31.6 25 3.4 45 gil38516887:96 319 689 60 1141 79. 0 20 25 31.6 3.3 45 gil38516887:24 97 690 60 1414 79. 0 26.6 18.3 45 45 gil38516887:24 596 699 60 459 82 0 26.6 18.3		66KN VNV	gi 158516887:96 7-2469	820	684	09	684	80. 21	0	28.3 3	13.3 3	30	28.3 3	41.6	4
		66AN ANA	gi 158516887:96 7-2469	788	685	09	716	82. 63	0	23.3 3	21.6	25	30	45	4
	_	96YN VNW	gi 158516887:96 7-2469	595	989	09	606	81. 01	0	26.6	18.3	25	30	45	3
gil38516887:96 363 688 60 1141 78. 0 21.6 40 18.3 41.6 7-2469 319 689 60 1185 82. 0 20 25 31.6 23.3 45 gil38516887:96 90 690 60 1414 79. 0 26.6 18.3 31.6 23.3 45 gil38516887:24 971 691 60 459 86 81. 0 30 15 36.6 18.3 45 gil38516887:24 566 693 60 459 82. 0 33.3 11.6 30 25 45 70-3525 56 693 60 491 88. 0 23.3 11.6 30 54 5 70-3525 51 54 60 540 54 6 53.3 16 15 36.6 18.3 45 gil158516887:24 426 695 <td< td=""><td></td><td>WNV NY99</td><td>gi 158516887:96 7-2469</td><td>393</td><td>289</td><td>09</td><td>11111</td><td>79. 43</td><td>0</td><td>25</td><td>18.3</td><td>31.6</td><td>25</td><td>43.3</td><td>5</td></td<>		WNV NY99	gi 158516887:96 7-2469	393	289	09	11111	79. 43	0	25	18.3	31.6	25	43.3	5
gil188516887:96 319 689 60 1185 82. 0 20 25 31.6 23.3 45 2469 90 690 60 1414 79. 0 26.6 18.3 31.6 23.3 45 2469 7-2469 60 1414 7 0 26.6 18.3 31.6 23.3 45 2469 7-2469 80 80 81. 0 30 15 36.6 18.3 45 24158516887:24 598 692 60 459 82. 0 33.3 11.6 30. 25 45 24158516887:24 566 693 60 491 88. 0 23.3 21.6 31.6 33.6 45 24158516887:24 517 694 60 540 80. 0 25.3 20. 36.6 18.3 45 24158516887:24 426 695 696 631 631		96YN VNV	gi 158516887;96 7-2469	363	889	09	1141	78. 97	0	21.6	20	40	18.3 3	41.6	3
gi 158516887:24 90 690 60 1414 79 0 26.6 18.3 31.6 23.3 45 gi 158516887:24 971 691 60 86 81. 0 30 15 7 3 7 3 45 gi 158516887:24 598 692 60 459 82. 0 33.3 11.6 30 25 45 gi 158516887:24 566 693 60 491 81. 0 23.3 21.6 31.6 31.6 31.6 33.3 45 gi 158516887:24 517 694 60 540 80. 0 23.3 21.6 31.6 33.3 45 gi 158516887:24 426 695 60 540 80. 0 25 20 36.6 18.3 45 gi 158516887:24 426 695 60 631 81. 0 30 15 33.3 17 45 <td></td> <td>WNV NY99</td> <td>gi 158516887:96 7-2469</td> <td>319</td> <td>689</td> <td>09</td> <td>1185</td> <td>82. 37</td> <td>0</td> <td>20</td> <td>25</td> <td>31.6</td> <td>23.3 3</td> <td>45</td> <td>3</td>		WNV NY99	gi 158516887:96 7-2469	319	689	09	1185	82. 37	0	20	25	31.6	23.3 3	45	3
gil188516887:24 971 691 60 86 81. 3.1 0 30 15 36.6 7 18.3 7 45 gil188516887:24 70-3525 582 60 459 82. 08 0 33.3 3 11.6 7 30 25 45 gil188516887:24 70-3525 566 693 60 491 81. 68 0 23.3 3 7 7 7 3 45 gil188516887:24 70-3525 517 694 60 540 80. 7 0 25 20 36. 7 18.3 7 45 gil188516887:24 70-3525 426 695 60 631 81. 55 0 30 15 33.6 3 45 45		WNV NY99	gi 158516887:96 7-2469	06	069	09	1414	79. 7	0	26.6	18.3	31.6	23.3 3	45	2
gi 158516887:24 598 692 60 459 82. big 0 33.3 big 11.6 big 30 25 45 gi 158516887:24 big 566 693 60 491 81. big 0 23.3 big 77 77 31.6 big 45 45 gi 158516887:24 big 517 694 60 540 80. big 25 20 36.6 big 18.3 big 45 gi 158516887:24 big 426 695 60 631 81. big 30 15 23.3 big 7 45		96YN VNV	gi 158516887:24 70-3525	971	691	09	98	81. 31	0	30	15	36.6 7	18.3 3	45	4
gi 158516887:24 566 693 60 491 81. 68 0 23.3 7 21.6 7 31.6 7 23.3 7 45 45 gi 158516887:24 70-3525 517 694 60 540 80. 7 0 25 20 36.6 7 18.3 3 45 gi 158516887:24 70-3525 426 695 60 631 81. 55 0 30 15 23.3 3 31.6 7 45		66KN ANA	gi 158516887;24 70-3525	869	692	09	459	82. 08	0	33.3 3	11.6	30	25	45	3
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	>	66AN ANA	gi 158516887:24 70-3525	999	693	09	491	81. 68	0	23.3	21.6	31.6	23.3 3	45	3
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	\sim	66 KN ANA	gi 158516887:24 70-3525	517	694	09	540	80.	0	25	20	36.6 7	18.3	45	2
		WNV NY99	gi 158516887:24 70-3525	426	695	09	631	81. 55	0	30	15	23.3 3	31.6	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	V%	L%	2% 5%	PolyX
nonstructural protein NS1	66AN ANA	gi 158516887:24 70-3525	357	969	09	700	81. 52	0	21.6	21.6	28.3 3	28.3 3	43.3 3	4
nonstructural protein NS1	WNV NY99	gi 158516887:24 70-3525	325	269	09	732	79. 8	0	28.3	13.3 3	33.3 3	25	41.6	5
nonstructural protein NS1	WNV NY99	gi 158516887;24 70-3525	130	869	09	927	80. 43	0	26.6	18.3 3	31.6	23.3 3	45	3
nonstructural protein NS1	WNV NY99	gi 158516887:24 70-3525	97	669	09	096	80. 83	0	18.3	25	40	16.6	43.3	3
nonstructural protein NS1	WNV NY99	gi 158516887:24 70-3525	54	700	09	1003	80. 82	0	26.6	18.3 3	30	25	45	3
nonstructural protein NS2A	WNV NY99	gi 158516887:35 26-4218	584	701	09	110	80. 91	0	20	25	33.3 3	21.6	45	9
nonstructural protein NS2A	WNV NY99	gi 158516887;35 26-4218	501	702	09	193	81. 59	0	31.6	13.3 3	23.3 3	31.6	45	2
nonstructural protein NS2A	WNV NY99	gi 158516887:35 26-4218	413	703	09	281	81. 21	0	21.6	23.3 3	30	25	45	3
nonstructural protein NS2A	66AN ANA	gi 158516887:35 26-4218	393	704	09	301	81. 07	0	25	20	28.3 3	26.6 7	45	2
nonstructural protein NS2A	66AN ANA	gi 158516887:35 26-4218	313	705	09	381	81. 95	0	21.6	20	18.3 3	40	41.6	4
nonstructural protein NS2A	MNV NY99	gi 158516887:35 26-4218	293	706	09	401	81. 59	0	26.6 7	16.6 7	21.6	32	43.3 3	4
nonstructural protein NS2A	WNV NY99	gi 158516887:35 26-4218	265	707	09	429	80. 89	0	26.6 7	16.6	26.6 7	30	43.3 3	4
nonstructural protein NS2A	MNV NY99	gi 158516887:35 26-4218	243	708	09	451	81. 2	0	23.3 3	21.6	30	25	45	3
nonstructural protein NS2A	WNV NY99	gi 158516887:35 26-4218	147	709	09	547	81. 37	0	25	20	21.6	33.3 3	45	5
nonstructural protein NS2A	WNV NY99	gi 158516887:35 26-4218	106	710	09	588	80. 63	0	26.6 7	18.3 3	16.6	38.3 3	45	5
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	334	711	09	09	80. 85	0	20	25	28.3 3	26.6 7	45	4
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	249	712	09	145	81. 64	0	25	20	31.6	23.3 3	45	3
nonstructural protein NS2B	MNV NY99	gi 158516887:42 19-4611	246	713	09	148	81. 54	0	25	20	31.6	23.3 3	45	3
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	245	714	09	149	81. 54	0	25	20	33.3 3	21.6 7	45	3
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	242	715	09	152	81. 58	0	25	20	31.6 7	23.3 3	45	3
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	240	716	09	154	81. 58	0	26.6	18.3	30	25	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	%C	% V ₀ A	1%	%G	PolyX
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	239	717	09	155	81. 11	0	26.6 7	18.3 3	31.6 7	23.3 3	45	3
nonstructural protein NS2B	MNV NY99	gi 158516887:42 19-4611	238	718	09	156	80. 29	0	28.3 3	16.6	31.6	23.3 3	45	3
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	237	719	09	157	80. 67	0	26.6 7	16.6	31.6 7	25	43.3 3	3
nonstructural protein NS2B	WNV NY99	gi 158516887:42 19-4611	236	720	09	158	80. 7	0	26.6 7	16.6	31.6	25	43.3 3	3
nonstructural protein NS3	MNV NY99	gi 158516887:46 12-6468	1721	721	09	137	80. 84	0	30	15	38.3 3	16.6	45	3
nonstructural protein NS3	WNV NY99	gi 158516887:46 12-6468	1651	722	09	267	81. 55	0	26.6 7	18.3 3	28.3 3	26.6	45	9
nonstructural protein NS3	WNV NY99	gi 158516887:46 12-6468	1512	723	09	346	80. 83	0	25	20	33.3 3	21.6	45	4
nonstructural protein NS3	WNV NY99	gi 158516887:46 12-6468	1217	724	09	641	81. 63	0	26.6 7	18.3 3	33.3 3	21.6	45	5
nonstructural protein NS3	WNV NY99	gi 158516887:46 12-6468	1157	725	09	701	79. 88	0	28.3 3	15	36.6 7	20	43.3 3	4
nonstructural protein NS3	MNV NY99	gi 158516887:46 12-6468	2601	726	09	761	81. 94	0	26.6 7	18.3 3	31.6	23.3 3	45	4
nonstructural protein NS3	MNV NY99	gi 158516887:46 12-6468	096	727	09	868	81. 24	0	15	30	30	25	45	3
nonstructural protein NS3	WNV NY99	gi 158516887:46 12-6468	LSL	728	09	1101	81. 77	0	23.3 3	21.6	25	30	45	3
nonstructural protein NS3	MNV NY99	gi 158516887:46 12-6468	009	729	09	1258	80. 94	0	23.3 3	21.6	43.3 3	11.6	45	3
nonstructural protein NS3	MNV NY99	gi 158516887:46 12-6468	428	730	09	1430	82. 18	0	26.6 7	18.3 3	28.3 3	26.6	45	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69-6834	091	731	09	207	81. 11	0	23.3 3	21.6	18.3 3	36.6 7	45	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69-6834	159	732	09	208	81. 05	0	21.6 7	21.6	20	36.6 7	43.3 3	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69-6834	158	733	09	209	80. 67	0	21.6 7	23.3 3	18.3 3	36.6 7	45	3
nonstructural protein NS4A	MNV NY99	gi 158516887:64 69 - 6834	151	734	09	210	80. 32	0	21.6	21.6	20	36.6 7	43.3 3	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69 - 6834	951	735	09	211	80. 23	0	21.6 7	21.6	20	36.6 7	43.3 3	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69-6834	155	736	09	212	80. 69	0	21.6 7	21.6 7	21.6 7	35	43.3 3	3
nonstructural protein NS4A	WNV NY99	gi 158516887:64 69-6834	154	737	09	213	80. 32	0	21.6	23.3	20	35	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	%	L%	%G	PolyX
nonstructural protein NS4A	MNV NY99	gi 158516887:64 69-6834	153	738	09	214	80. 69	0	21.6	21.6	20	36.6 7	43.3 3	3
nonstructural protein NS4A	66AN ANA	gi 158516887;64 69-6834	152	739	09	215	80. 26	0	21.6 7	21.6	20	36.6	43.3 3	3
nonstructural protein NS4A	MNV NY99	gi 158516887:64 69-6834	151	740	09	216	79. 62	0	21.6	21.6	20	36.6 7	43.3 3	3
nonstructural protein NS4B	66AN ANA	gi 158516887:69 16-7680	703	741	09	63	76. 76	0	15	20	43.3 3	21.6	35	5
nonstructural protein NS4B	66AN ANA	gi 158516887:69 16-7680	683	742	09	83	80. 89	0	23.3 3	20	98	26.6 7	43.3 3	5
nonstructural protein NS4B	WNV NY99	gi 158516887:69 16-7680	506	743	09	260	80. 89	0	30	15	26.6 7	28.3	45	3
nonstructural protein NS4B	MNV NY99	gi 158516887:69 16-7680	480	744	09	286	81. 85	0	21.6	23.3 3	35	20	45	3
nonstructural protein NS4B	WNV NY99	gi 158516887:69 16-7680	185	745	09	581	79. 07	0	11.6	30	35	23.3 3	41.6	3
nonstructural protein NS4B	MNV NY99	gi 158516887:69 16-7680	165	746	09	601	78. 17	0	11.6	26.6	35	26.6	38.3 3	3
nonstructural protein NS4B	66AN ANA	gi 158516887:69 16-7680	140	747	09	626	81. 65	0	15	30	31.6	23.3	45	3
nonstructural protein NS4B	MNV NY99	gi 158516887:69 16-7680	48	748	09	718	80. 6	0	31.6	11.6	26.6 7	30	43.3 3	3
nonstructural protein NS4B	WNV NY99	gi 158516887:69 16-7680	28	749	09	738	79. 4	0	30	10	35	25	40	3
nonstructural protein NS4B	WNV NY99	gi 158516887:69 16-7680	8	750	09	758	80. 52	0	33.3 3	10	31.6 7	25	43.3	3
nonstructural protein NS5	66AN ANA	gi 158516887:76 81-10395	2656	157	09	09	77. 17	0	23.3 3	16.6	36.6 7	23.3	40	3
nonstructural protein NS6	WNV NY99	gi 158516887:76 81-10395	2596	752	09	120	80. 17	0	26.6 7	18.3	36.6 7	18.3	45	4
nonstructural protein NS7	WNV NY99	gi 158516887:76 81-10395	2480	753	09	236	81. 19	0	26.6 7	18.3 3	40	15	45	4
nonstructural protein NS8	WNV NY99	gi 158516887:76 81-10395	2161	754	09	555	81. 66	0	31.6	13.3	31.6 7	23.3	45	3
nonstructural protein NS9	66AN ANA	gi 158516887:76 81-10395	2101	257	09	615	81. 92	0	21.6	23.3	25	30	45	4
nonstructural protein NS10	MNV NY99	gi 158516887:76 81-10395	1353	952	09	1363	81. 34	0	28.3 3	15	41.6 7	15	43.3 3	9
nonstructural protein NS11	WNV NY99	gi 158516887:76 81-10395	1255	757	09	1461	82. 15	0	33.3 3	11.6	35	20	45	4
nonstructural protein NS12	WNV NY99	gi 158516887:76 81-10395	1195	758	09	1521	81. 38	0	30	15	33.3 3	21.6	45	3

Product	Virus	Target ID	BP Start	SEQ ID	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	₩%	1%	ر 3% 2	PolyX
nonstructural protein NS13	66KN ANM	gi 158516887:76 81-10395	720	759	09	1996	80. 61	0	28.3	16.6	41.6	13.3	45	9
nonstructural protein NS14	66KN ANM	gi 158516887:76 81-10395	365	760	09	2351	81. 09	0	28.3	16.6	25	30	45	2
anchored capsid protein C	956 ANW	gi 11528013:97- 465	256	761	09	114	82. 17	0	20	25	46.6	8.33	45	4
anchored capsid protein C	WNV 956	gi 11528013:97- 465	254	762	09	116	82. 17	0	20	25	46.6	8.33	45	4
anchored capsid protein C	956 ANM	gi 11528013.97- 465	253	763	09	117	82. 17	0	20	25	46.6	8.33	45	4
anchored capsid protein C	956 ANM	gi 11528013:97- 465	249	764	09	121	82. 23	0	18.3	26.6	41.6	13.3	45	4
anchored capsid protein C	956 ANW	gi 11528013:97- 465	232	765	09	138	80. 98	0	20	25	33.3 3	21.6	45	3
anchored capsid protein C	956 ANM	gi 11528013:97- 465	231	992	09	139	80. 13	0	20	23.3	35	21.6	43.3 3	3
anchored capsid protein C	956 ANM	gi 11528013:97- 465	230	192	09	140	79. 56	0	18.3 3	25	35	21.6	43.3 3	3
anchored capsid protein C	956 ANM	gi 11528013:97- 465	229	768	09	141	79. 71	0	20	23.3 3	35	21.6	43.3 3	3
anchored capsid protein C	WNV 956	gi 11528013:97- 465	228	692	09	142	08	0	20	21.6	36.6	21.6	41.6	3
anchored capsid protein C	WNV 956	gi 11528013:97- 465	227	770	09	143	80. 14	0	20	23.3 3	35	21.6	43.3	3
membrane glycoprotein precursor prM	956 ANM	gi 11528013:466 -966	417	771	09	85	82. 64	0	25	20	25	30	45	3
membrane glycoprotein precursor prM	956 ANA	gi 11528013:466 -966	335	772	09	167	80. 7	0	25	20	40	15	45	4
membrane glycoprotein precursor prM	956 ANM	gi 11528013:466 -966	334	773	09	168	80. 01	0	25	18.3 3	40	16.6	43.3	4
membrane glycoprotein precursor prM	956 ANM	gi 11528013:466 -966	333	774	09	691	80. 01	0	26.6	16.6	40	16.6	43.3 3	4
membrane glycoprotein precursor prM	956 ANA	gi 11528013:466 -966	332	775	09	170	80. 7	0	28.3 3	16.6	38.3 3	16.6	45	4
membrane glycoprotein precursor prM	956 ANM	gi 11528013:466 -966	331	776	09	171	81. 21	0	28.3	16.6	36.6	18.3	45	4

Virus		Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	Э%C	V %	L%	2% C	PolyX
WN	WNV 956	gi 11528013:466 -966	330	777	60	172	80.	0	28.3	16.6	35	20	45	4
MW	WNV 956	gi 11528013:466 -966	329	8//	09	173	80.	0	26.6	18.3 3	35	20	45	4
M	956 ANW	gi 11528013:466 -966	327	6LL	09	175	81. 55	0	26.6	18.3 3	38	20	45	4
≸	956 ANW	gi 11528013:466 -966	320	08/	09	182	81. 69	0	28.3	16.6	38.3 3	16.6	45	4
[≨	WNV 956	gi 11528013:742 -966	141	781	09	85	82. 64	0	25	20	25	30	45	3
\geqslant	WNV 956	gi 11528013:742 -966	59	782	09	167	80.	0	25	20	40	15	45	4
≽	WNV 956	gi 11528013:742 -966	58	783	09	168	010	0	25	18.3	40	16.6	43.3	4
≽	WNV 956	gi 11528013:742 -966	57	784	09	169	80. 01	0	26.6	16.6	40	16.6	43.3	4
≽	956 ANM	gi 11528013:742 -966	56	582	09	170	80. 7	0	28.3	16.6 7	38.3 3	16.6	45	4
⊳	956 ANW	gi 11528013:742 -966	55	786	09	171	81. 21	0	28.3	16.6	36.6 7	18.3	45	4
📂	WNV 956	gi 11528013.742 -966	54	187	09	172	80. 8	0	28.3	16.6	35	20	45	4
📂	WNV 956	gi 11528013:742 -966	53	788	09	173	80 80	0	26.6	18.3	35	20	45	4
📂	WNV 956	gi 11528013:742 -966	51	682	09	175	81. 55	0	26.6	18.3	35	20	45	4
📂	WNV 956	gi 11528013.742 -966	44	062	09	182	81. 69	0	28.3	16.6	38.3 3	16.6	45	4
📂	956 ANM	gi 11528013.967 -2457	1312	162	09	180	81. 01	0	25	20	25	30	45	4
≽	956 ANW	gi 11528013:967 -2457	885	79Z	09	209	81. 26	0	21.6	23.3 3	31.6 7	23.3 3	45	4
≽	WNV 956	gi 11528013:967 -2457	813	793	09	629	81. 49	0	31.6	13.3	33.3 3	21.6	45	3
\geqslant	956 ANW	gi 11528013:967 -2457	869	794	09	794	82	0	23.3	21.6	30	25	45	3
≯	956 ANW	gi 11528013:967 -2457	597	795	09	895	81. 01	0	26.6	18.3	21.6	33.3 3	45	3

8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Larget ID	Start	NO:	Length	End Distance	Tm	X-Hyb Pot	5%	2%C	%	L%	ဗ လ လ	PolyX
	gi 11528013:967 -2457	483	962	09	1009	81. 24	0	25	20	28.3	26.6	45	3
WNV 956 89	gi 11528013:967 -2457	397	797	09	1095	81. 7	0	23.3	21.6	28.3	26.6	45	4
WNV 956 gi	gi 11528013;967 -2457	337	798	09	1155	81. 72	0	23.3	21.6	33.3 3	21.6	45	60
WNV 956 gi	gi 11528013:967 -2457	123	799	09	1369	82. 3	0	25	20	31.6	23.3	45	4
WNV 956 89	gi 11528013:967 -2457	63	800	09	1429	80. 88	0	25	18.3	33.3 3	23.3	43.3 3	4
18 8 8 8	gi 11528013:245 8-3513	829	801	09	228	81. 52	0	21.6	23.3	31.6	23.3	45	8
18 956 WW	gi 11528013:245 8-3513	827	802	09	230	80. 95	0	21.6	23.3	33.3 3	21.6	45	8
8 8	gi 11528013:245 8-3513	826	803	09	231	80. 85	0	23.3	21.6	33.3 3	21.6	45	3
g 956 NNW 88	gi 11528013:245 8-3513	825	804	09	232	80. 95	0	23.3	21.6	31.6	23.3	45	3
g 956 VNW	gi 11528013.245 8-3513	824	805	09	233	80. 26	0	21.6	21.6	31.6	25	43.3	3
18 956 VNW	gi 11528013:245 8-3513	823	908	09	234	80. 1	0	20	21.6	33.3 3	25	41.6	33
g 88	gi 11528013:245 8-3513	822	807	09	235	79. 64	0	21.6	21.6	33.3 3	23.3	43.3	3
18 956 VNW	gi 11528013:245 8-3513	821	808	09	236	79. 35	0	20	21.6	35	23.3	41.6	3
18 956 WNW	gi 11528013:245 8-3513	820	608	09	237	78. 71	0	21.6	20	35	23.3	41.6	8
18 956 WW	gi 11528013;245 8-3513	819	810	09	238	79. 27	0	21.6	20	35	23.3	41.6	33
WNV 956 gi	gi 11528013:351 4-4206	556	811	09	138	80. 91	0	20	23.3	40	16.6	43.3	9
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	gi 11528013:351 4-4206	536	812	09	158	80. 41	0	26.6	15	41.6	16.6	41.6	9
WNV 956 gi	gi 11528013:351 4-4206	516	813	09	178	62	0	26.6	13.3	33.3 3	26.6	40	9
WNV 956 gi	gi 11528013:351 4-4206	496	814	09	198	78. 54	0	25	13.3	26.6	35	38.3	4
WNV 956 8	gi 11528013:351 4-4206	476	815	09	218	79. 47	0	20	20	25	35	40	4
WNV 956 8	gi 11528013:351 4-4206	401	816	09	293	80. 68	0	16.6	28.3 3	25	30	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5%	3%C	V %	L%	2% C	PolyX
nonstructural protein NS2A	956 ANM	gi 11528013:351 4-4206	345	817	09	349	81. 37	0	25	20	25	30	45	4
nonstructural protein NS2A	956 ANA	gi 11528013;351 4-4206	325	818	09	369	81. 68	0	21.6	23.3 3	23.3 3	31.6 7	45	3
nonstructural protein NS2A	WNV 956	gi 11528013:351 4-4206	305	819	09	389	81. 52	0	20	23.3 3	23.3 3	33.3 3	43.3	4
nonstructural protein NS2A	WNV 956	gi 11528013:351 4-4206	279	820	09	415	82. 2	0	25	20	23.3 3	31.6 7	45	5
nonstructural protein NS2B	MNV 956	gi 11528013:420 7-4599	249	821	09	145	82. 27	0	26.6	18.3 3	98	25	45	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	248	822	09	146	81. 44	0	28.3 3	16.6 7	30	25	45	4
nonstructural protein NS2B	WNV 956	gi 11528013:420 7-4599	247	823	09	147	81. 44	0	28.3 3	9'91 2	30	25	45	4
nonstructural protein NS2B	WNV 956	gi 11528013:420 7-4599	246	824	09	148	81. 83	0	26.6	16.6	30	26.6 7	43.3 3	4
nonstructural protein NS2B	WNV 956	gi 11528013:420 7-4599	245	825	09	149	81. 83	0	26.6	16.6 7	31.6	25	43.3	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	244	978	09	150	81. 44	0	28.3 3	9'91 2	98	25	45	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	243	827	09	151	81. 25	0	26.6 7	9'9I 2	98	26.6 7	43.3 3	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	242	828	09	152	81. 16	0	25	9'9I 2	31.6	26.6 7	41.6	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	241	678	09	153	81. 48	0	26.6	9'91 2	98	26.6 7	43.3 3	4
nonstructural protein NS2B	956 ANA	gi 11528013:420 7-4599	240	0£8	09	154	81. 99	0	26.6 7	9'91 2	98	26.6 7	43.3 3	4
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1798	831	09	09	80. 56	0	21.6	21.6	33.3 3	23.3 3	43.3 3	4
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1729	832	09	129	80. 67	0	30	15	36.6 7	18.3 3	45	3
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1668	833	09	190	81. 8	0	21.6	23.3 3	31.6	23.3 3	45	3
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1597	834	09	261	81. 8	0	20	25	26.6 7	28.3 3	45	3
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1437	835	09	421	81. 85	0	21.6	23.3 3	31.6	23.3 3	45	3
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1212	836	09	646	81. 8	0	23.3 3	21.6	33.3 3	21.6 7	45	4
nonstructural protein NS3	956 ANA	gi 11528013:460 0-6456	1150	837	09	208	80. 26	0	25	20	36.6 7	18.3	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	Э%	%A	L%	5% C	PolyX
nonstructural protein NS3	956 ANM	gi 11528013:460 0-6456	1073	838		785	81. 88	0	26.6	18.3	25	30	45	4
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	1013	839	09	845	80. 16	0	28.3	9.91	35	20	45	3
nonstructural protein NS3	WNV 956	gi 11528013:460 0-6456	608	840	09	1049	81. 46	0	15	30	30	25	45	4
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	206	841	09	173	80. 63	0	33.3 3	11.6	28.3	26.6 7	45	3
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	205	842	09	174	80. 57	0	31.6	11.6	28.3 3	28.3 3	43.3	3
nonstructural protein NS4A	WNV 956	gi 11528013:645 7-6834	204	843	09	175	80. 16	0	31.6	11.6	26.6	30	43.3	4
nonstructural protein NS4A	WNV 956	gi 11528013;645 7-6834	203	844	09	176	79. 45	0	30	11.6	26.6	31.6	41.6	5
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	202	845	09	177	79. 39	0	28.3	11.6	26.6 7	33.3 3	40	9
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	201	846	09	178	79. 81	0	30	11.6	25	33.3 3	41.6	9
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	200	847	09	179	80. 32	0	30	11.6	25	33.3 3	41.6	9
nonstructural protein NS4A	WNV 956	gi 11528013;645 7-6834	199	848	09	180	80. 02	0	31.6	11.6	25	31.6	43.3	9
nonstructural protein NS4A	956 ANW	gi 11528013;645 7-6834	198	849	09	181	80. 49	0	31.6	01	25	33.3 3	41.6	9
nonstructural protein NS4A	956 ANM	gi 11528013:645 7-6834	197	850	09	182	80. 65	0	33.3 3	01	25	31.6 7	43.3 3	9
nonstructural protein NS4B	956 ANW	gi 11528013:690 4-7671	517	851	09	252	81. 84	0	25	20	26.6 7	28.3 3	45	3
nonstructural protein NS4B	956 ANW	gi 11528013;690 4-7671	513	852	09	256	80. 86	0	26.6 7	18.3 3	28.3 3	26.6 7	45	9
nonstructural protein NS4B	956 ANM	gi 11528013;690 4-7671	512	853	09	257	80. 6	0	26.6 7	9'9I 2	30	26.6 7	43.3 3	9
nonstructural protein NS4B	956 ANM	gi 11528013:690 4-7671	511	854	09	258	80. 69	0	26.6	16.6 7	30	26.6 7	43.3	9
nonstructural protein NS4B	956 ANW	gi 11528013:690 4-7671	510	855	09	259	81. 56	0	28.3 3	9'91 2	30	25	45	9
nonstructural protein NS4B	956 ANW	gi 11528013:690 4-7671	509	856	09	260	82. 07	0	28.3 3	9'91 2	28.3 3	26.6 7	45	9
nonstructural protein NS4B	956 ANM	gi 11528013;690 4-7671	508	857	09	261	81. 53	0	28.3 3	9'9I 2	28.3 3	26.6 7	45	9
nonstructural protein NS4B	WNV 956	gi 11528013:690 4-7671	507	858	09	262	81. 63	0	28.3	16.6	28.3 3	26.6 7	45	6

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	V %	L%	5% C	PolyX
nonstructural protein NS4B	WNV 956	gi 11528013.690 4-7671	506	658	09	263	81. 53	0	28.3	16.6	28.3 3	26.6 7	45	9
nonstructural protein NS4B	MNV 956	gi 11528013:690 4-7671	505	098	09	264	80. 96	0	28.3 3	9'91	28.3 3	26.6 7	45	9
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	2656	861	09	09	79. 85	0	30	15	26.6 7	28.3 3	45	4
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	2596	862	09	120	78. 8	0	28.3 3	13.3 3	33.3 3	25	41.6	4
nonstructural protein NS5	MNV 956	gi 11528013:767 2-10386	2495	863	09	221	81. 04	0	31.6	13.3	31.6	23.3	45	3
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	2116	864	09	009	81. 29	0	21.6	23.3 3	28.3 3	26.6 7	45	3
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	2048	865	60	899	81. 48	0	18.3 3	26.6 7	35	20	45	3
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	1908	998	09	808	81. 66	0	31.6 7	13.3 3	35	20	45	5
nonstructural protein NS5	MNV 956	gi 11528013:767 2-10386	1555	<i>L</i> 98	09	1161	81. 68	0	28.3 3	16.6 7	33.3 3	21.6	45	3
nonstructural protein NS5	MNV 956	gi 11528013:767 2-10386	1354	898	09	1362	81. 41	0	30	51	40	15	45	3
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	1241	698	09	1475	82. 03	0	28.3 3	16.6 7	38	20	45	4
nonstructural protein NS5	WNV 956	gi 11528013:767 2-10386	1170	870	09	1546	81. 44	0	26.6 7	18.3 3	33.3 3	21.6	45	4
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	7323	871	90	103	81. 63	0	20	25	26.6 7	28.3	45	3
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	7262	872	09	164	80. 48	0	33.3 3	11.6	33.3 3	21.6	45	3
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	7166	873	09	260	81. 9	0	28.3 3	16.6	38.3 3	16.6	45	5
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	7088	874	90	338	81. 53	0	25	20	26.6 7	28.3 3	45	4
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	7016	875	09	410	81. 53	0	30	15	33.3 3	21.6	45	2
gp1- nonstructural polyprotein	Chikungunya	gi 27754751:77- 7501	6874	876	09	552	80.	0	13.3	30	28.3	28.3	43.3	3

Section of the continue of t	Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	L%	2 S%	PolyX	
Chikungunya gi27754751.75 6885 878 600 741 80 91 91 91 91 91 91 91 9	tural	Chikungunya	gi 27754751:77- 7501	6745	877	60	681	80. 36	0	30	15	21.6	33.3 3	45	4	
Chikangamya gi2775475177- 6468 880 600 958 81. 0 18.3 2.66 18.3 3.66 18.3 4.5 3.61 3.51 3.51	tural ein	Chikungunya	gi 27754751:77- 7501	6685	878	60	741	80. 26	0	20	21.6	28.3	30	41.6	4	
Chikungunya Gi27754751.75 6468 880 60 958 80 0 7 7 3 56 18.3 45 18 18 18 18 18 18 18 1	tural ein	Chikungunya	gi 27754751:77- 7501	6617	879	09	608	81. 32	0	18.3	26.6 7	26.6	28.3 3	45	3	
ral Chikungunya gil27754751.756 3441 881 60 307 80. 65 25 26 3.33 2.66 4.5 ral Chikungunya gil27754751.756 3.46 882 60 372 80. 25 20 3.33 2.66 4.5 ral Chikungunya gil27754751.756 3.109 883 60 639 81. 0 216 2.33 30 25 4.5 ral Chikungunya gil27754751.756 2945 884 60 933 81. 0 216 2.33 30 25 4.5 ral Chikungunya gil27754751.756 285 60 938 82. 0 216 23.3 35 26 4.5 ral Chikungunya gil27754751.756 235 888 60 1196 81. 0 21. 33.3 21. 4.5 ral Chikungunya gil27754751.756 235	tural	Chikungunya	gi 27754751:77- 7501	6468	088	09	856	80. 67	0	26.6	18.3 3	36.6	18.3	45	es.	
ral Chikungunya gl[27754751756] 33.7 88.2 60 372 82. 0 25 20 33.3 21.6 45 ral Chikungunya gl[27754751756] 3109 88.3 60 639 49. 0 71.6 33.3 21.6 33.3 21.6 45 ral Chikungunya gl[27754751776] 2945 88.4 60 933 81. 0 71.6 33.3 30. 25. 45 ral Chikungunya gl[27754751776] 288.5 60 938 82. 0 71.6 33.3 45 45 ral Chikungunya gl[27754751776] 286 60 938 82. 0 71.6 33.3 45 ral Chikungunya gl[27754751776] 255 888 60 1186 88. 0 71.6 33.3 71.6 45 ral Chikungunya gl[277547517756] 252 889 60 <td>ctural</td> <td>Chikungunya</td> <td>gi 27754751:756 7-11313</td> <td>3441</td> <td>881</td> <td>09</td> <td>307</td> <td>80.</td> <td>0</td> <td>25</td> <td>20</td> <td>28.3</td> <td>26.6</td> <td>45</td> <td>3</td> <td></td>	ctural	Chikungunya	gi 27754751:756 7-11313	3441	881	09	307	80.	0	25	20	28.3	26.6	45	3	
rall Chikungunya gi27754751756 199 883 60 639 81. 0 21.6 23.3 30 25 45 rall Chikungunya gi27754751756 2945 884 60 933 81. 0 71.6 23.3 30 25 45 rall Chikungunya gi27754751756 2815 885 60 933 82. 0 71.6 23.3 30 25 45 rall Chikungunya gi27754751756 285 60 938 82. 0 71.6 23.3 35 25 45 rall Chikungunya gi27754751756 2552 887 60 1196 81. 0 71.6 23.3 25. 45 rall Chikungunya gi27754751756 2552 888 60 1389 82. 0 71.6 33.3 21.6 45 rall Chikungunya gi27754751756 25.3 889	ctural tein	Chikungunya	gi 27754751:756 7-11313	3376	882	09	372	82. 09	0	25	20	33.3 3	21.6	45	3	
rall Chikungunya gil.7754751.756 2945 884 60 803 81. 0 21.6 23.3 30 25 45 rall Chikungunya gil.7754751.756 2815 885 60 933 81. 0 15 30 31.6 23.3 45 rall Chikungunya gil.7754751.756 252 886 60 998 82. 0 21.6 23.3 35 20 45 rall Chikungunya gil.7754751.756 235 887 60 1196 88. 0 16. 23.3 28. 26 45 rall Chikungunya gil.27754751.756 235 888 60 1696 88. 0 16. 23.3 28. 45 rall Chikungunya gil.27754751.756 1733 899 60 1696 88. 0 21.6 23.3 21.6 45 rall Chikungunya gil.27754751.756	ictural tein	Chikungunya	gi 27754751:756 7-11313	3109	883	09	689	81. 49	0	21.6	23.3	30	25	45	4	
ral Chikungunya gi[27754751756] 2815 60 933 81. 0 15 30 31.6 23.3 45 ral Chikungunya gi[27754751756] 286 60 998 81. 0 7 3.3 35 20 45 ral Chikungunya gi[27754751756] 2552 887 60 1196 81. 0 16.6 28.3 28.3 26.6 45 ral Chikungunya gi[27754751756] 2359 888 60 1896 81. 0 7 3.3 26.6 45 ral Chikungunya gi[27754751756] 2359 889 60 1696 80. 7 3.3 17. 3.3 45 ral Chikungunya gi[27754751756] 2359 891 60 116 82. 0 21.6 23.3 18.3 45 ral Chikungunya gi[27754751756] 1733 892 60 <t< td=""><td>ictural tein</td><td>Chikungunya</td><td>gi 27754751:756 7-11313</td><td>2945</td><td>884</td><td>09</td><td>803</td><td>81. 59</td><td>0</td><td>21.6</td><td>23.3</td><td>30</td><td>25</td><td>45</td><td>4</td><td></td></t<>	ictural tein	Chikungunya	gi 27754751:756 7-11313	2945	884	09	803	81. 59	0	21.6	23.3	30	25	45	4	
ral Chikungunya gi[27754751:756] 2750 886 60 998 82. 0 21.6 23.3 35 20 45 ral Chikungunya gi[27754751:756] 2552 887 60 1196 82. 0 7.6 3.3 28.3 28.3 26.6 45 ral Chikungunya gi[27754751:756] 2359 888 60 1696 80. 7.6 3.3 1.6 45 45 ral Chikungunya gi[27754751:756] 2052 889 60 1696 80. 21.6 23.3 18.3 36.6 45 ral Chikungunya gi[27754751:756] 1733 890 60 2015 82. 0 21.6 23.3 31.6 45 ral Chikungunya gi[27754751:756] 1733 891 60 142 82. 0 21.6 23.3 31.6 45 ral Chikungunya gi[27754751:756]	ictural tein	Chikungunya	gi 27754751:756 7-11313	2815	885	09	933	81. 13	0	15	30	31.6	23.3 3	45	3	
ral Chikungunya gi[27754751:756 2552 887 600 1196 88. 60 6 7 7 3 3 28.3 26.6 45 7 11313	octural tein	Chikungunya	gi 27754751:756 7-11313	2750	988	09	866	82. 28	0	21.6	23.3 3	35	20	45	4	
ral Chikungunya gil27754751.756 2359 888 60 1389 82. 0 21.6 23.3 21.6 33.3 45 ral Chikungunya gil27754751.756 2052 889 60 1696 80. 2015 82 0 21.6 23.3 18.3 36.6 45 ral Chikungunya gil27754751.756 2052 899 60 2015 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 2052 892 60 423 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 49 0 25 10 38.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 1631 894 60 844 82 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gil27754751.756 153 83.3 21.6 85 85 85 85 85 85 85 85 85 85 85 85 85	ctural tein	Chikungunya	gi 27754751:756 7-11313	2552	887	09	9611	81. 58	0	16.6	28.3 3	28.3	26.6 7	45	4	
ral Chikungunya gi[27754751:756] 2052 889 60 1696 80, 80, 2016 23.3 18.3 36.6 45 ral Chikungunya gi[27754751:756] 2359 891 60 2015 82	ctural ein	Chikungunya	gi 27754751:756 7-11313	2359	888	09	1389	82. 61	0	21.6	23.3 3	21.6	33.3 3	45	9	
ral Chikungunya gi[27754751:756] 1733 890 60 2015 82. https://propersized.com/and/and/and/and/and/and/and/and/and/and	ctural ein	Chikungunya	gi 27754751:756 7-11313	2052	889	60	9691	80. 13	0	21.6	23.3 3	18.3 3	36.6 7	45	3	
ed Chikungunya gi[27754751.756] 2359 891 60 116 82. 0 21.6 23.3 21.6 33.3 45 ed Chikungunya gi[27754751.756] 2052 892 60 423 82. 0 21.6 23.3 33.3 21.6 45 ed Chikungunya gi[27754751.756] 1631 894 60 844 82. 0 75. 0 21.6 23.3 33.3 21.6 45 ed Chikungunya gi[27754751.756] 1631 894 60 844 82. 0 75. 0 21.6 23.3 33.3 21.6 45 ed Chikungunya gi[27754751.756] 2052 895 60 907 75. 0 25 10 38.3 20.6 35	ctural	Chikungunya	gi 27754751:756 7-11313	1733	068	09	2015	82. 38	0	21.6	23.3 3	33.3 3	21.6 7	45	5	
ed Chikungunya gi[27754751.756] 2052 892 60 423 80. 80. 9 21.6 23.3 18.3 36.6 45 ed Chikungunya gi[27754751.756] 153 893 60 742 82. 9 7 3 3 3 3 21.6 45 ed Chikungunya gi[27754751.756] 1631 894 60 844 82. 97 75 10 38.3 21.6 45 ed Chikungunya gi[27754751.756] 1568 895 60 907 75. 9 25 10 38.3 26.6 35	cated ein	Chikungunya	gi 27754751:756 7-10040	2359	891	09	911	82. 61	0	21.6	23.3 3	21.6	33.3 3	45	9	
ed Chikungunya gi[27754751.756] 1733 893 60 742 82. 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gi[27754751.756] 1631 894 60 844 82. 0 21.6 23.3 33.3 21.6 45 cd Chikungunya gi[27754751.756] 1568 895 60 907 75. 0 25 10 38.3 26.6 35	ncated tein	Chikungunya	gi 27754751:756 7-10040	2052	892	09	423	80. 13	0	21.6	23.3 3	18.3 3	36.6 7	45	3	
ed Chikungunya gi[27754751.756] 1631 894 60 844 82. 0 21.6 23.3 33.3 21.6 45 T-10040 T-10040 T-10040 T-10040 T-10040 T-10040	icated ein	Chikungunya	gi 27754751:756 7-10040	1733	893	60	742	82. 38	0	21.6	23.3 3	33.3 3	21.6	45	5	
ed Chikungunya gi[27754751.756 1568 895 60 907 75. 0 25 10 38.3 26.6 35	ncated ein	Chikungunya	gi 27754751:756 7-10040	1631	894	09	844	82. 49	0	21.6	23.3 3	33.3 3	21.6 7	45	5	
	ncated	Chikungunya	gi 27754751:756 7-10040	1568	895	09	200	75. 74	0	25	10	38.3	26.6	35	3	

PolyX																			
	3	3	8	κ	3	4	4	4	4	4	4	4	4	4	4	5	S	v	2
%G C	45	45	45	45	45	43.3	36.6	38.3	45	43.3	40	40	43.3	45	45	45	43.3	43.3	41.6
L%	21.6	23.3 3	21.6	21.6	25	21.6	21.6	21.6	28.3	25	31.6	31.6	30	23.3	26.6 7	31.6	31.6	31.6	31.6
V%	33.3 3	31.6	33.3 3	33.3 3	30	35	41.6	40	26.6 7	31.6	28.3	28.3	26.6 7	31.6	28.3 3	23.3 3	25	25	26.6
3%C	16.6	25	16.6	28.3	25	21.6	11.6	13.3 3	13.3 3	21.6	23.3	23.3	18.3 3	18.3	20	26.6	25	25	25
9%	28.3 3	20	28.3 3	16.6	20	21.6	25	25	31.6	21.6	16.6	16.6	25	26.6	25	18.3	18.3	18.3	16.6
X-Hyb Pot																			
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tm	79. 99	81. 55	81. 89	80. 92	80. 51	80. 16	77. 96	78. 45	81. 44	98 98	78. 55	78. 65	80. 84	82.	81. 07	81. 61	80.	80. 15	79. 96
End Distance	1181	1251	1341	1487	1576	77	107	127	150	178	198	218	238	262	286	09	61	62	63
e th																			
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	968	268	868	668	006	901	902	903	904	905	906	200	806	606	910	911	912	913	914
BP Start	1294	1224	1134	886	668	266	236	216	193	165	145	125	105	81	57	439	438	437	436
Target ID	gi 27754751:756 7-10040	gi 9626685:95- 436	gi 9626685;95- 436	gi 9626685;95- 436	gi 9626685:95- 436	gi 9626685:95- 436	gi 9626685:95- 436	gi 9626685:437- 934	gi 9626685:437- 934	gi 9626685:437- 934	gi 9626685:437- 934								
Virus	Chikungunya	Chikungunya	Chikungunya	Chikungunya	Chikungunya	DEN 1	DEN I	DEN 1	DEN I	DEN 1	DEN 1	DEN I	DEN 1						
Product	gp3-truncated polyprotein	anchored capsid protein C	membrane glycoprotein precursor M	membrane glycoprotein precursor M	membrane glycoprotein precursor M	membrane glycoprotein precursor M													

yX																		
PolyX	5	5	5	5	5	v	κ	4	4	v	4	κ	v	9	κ	9	κ	3
ر د د	40	41.6	43.3	41.6	40	40	45	45	45	45	45	45	35	45	43.3	36.6	43.3	45
L%	31.6	30	30	30	31.6	30	28.3	33.3 3	20	21.6	23.3	23.3	23.3	15	21.6	28.3	18.3	20
%W	28.3	28.3 3	26.6 7	28.3 3	28.3 3	30	26.6	21.6	35	33.3 3	31.6	31.6	41.6	40	35	35	38.3 3	35
3%C	25	25	25	23.3 3	21.6	21.6	23.3	11.6	15	18.3	25	16.6	15	18.3	23.3	11.6	16.6	25
9%	15	16.6	18.3 3	18.3 3	18.3	18.3	21.6	33.3 3	30	26.6	20	28.3	20	26.6 7	20	25	26.6	20
X-Hyb Pot																		
Tm Y	79. 0 82 0	79. 0	80. 0	79. 0	79. 0	79. 0	80. 9	81. 01	81. 0	81. 0	80. 95 0	81. 0 36 0	77. 0	81. 0	79. 0 51 0	77. 0	80. 02	81. 0
					, ,					-								
End Distance	64	99	99	<i>L</i> 9	89	69	105	167	323	404	532	594	999	752	812	936	09	160
oe gth																		
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	915	916	917	918	616	920	921	922	923	924	925	926	927	928	929	930	931	932
BP Start	435	434	433	432	431	430	1381	1319	1163	1082	954	892	820	734	674	550	766	897
Target ID	gi 9626685:437- 934	gi 9626685:935- 2419	gi 9626685:2420 -3475	gi 9626685:2420 -3475														
Virus	DEN I	DEN 1	DEN 1	DEN I	DEN I	DEN I	DEN 1	DEN 1										
Product	membrane glycoprotein precursor M	envelope protein E	nonstructural protein NS1	nonstructural protein NSI														

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V%	L%	2% C	PolyX
nonstructural protein NS1	DEN I	gi 9626685:2420 -3475	837	933	09	220	80. 04	0	28.3 3	15	26.6 7	30	43.3 3	3
nonstructural protein NS1	DEN I	gi 9626685:2420 -3475	777	934	09	280	80. 92	0	23.3	18.3	30	28.3 3	41.6	4
nonstructural protein NS1	DEN I	gi 9626685:2420 -3475	717	935	09	340	78. 4	0	20	21.6	40	18.3 3	41.6	3
nonstructural protein NS1	DEN 1	gi 9626685:2420 -3475	959	936	09	401	81. 84	0	21.6	23.3	35	20	45	4
nonstructural protein NSI	DEN I	gi 9626685:2420 -3475	969	937	09	461	79. 88	0	30	15	35	20	45	4
nonstructural protein NS1	DEN I	gi 9626685:2420 -3475	496	938	09	561	81. 72	0	21.6	23.3	28.3	26.6 7	45	3
nonstructural protein NS1	DEN I	gi 9626685:2420 -3475	436	939	09	621	79. 19	0	25	13.3 3	36.6	25	38.3 3	4
nonstructural protein NS1	DEN 1	gi 9626685:2420 -3475	359	940	09	869	81. 74	0	16.6	28.3 3	40	15	45	4
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	592	941	09	63	78. 19	0	18.3 3	20	36.6 7	25	38.3 3	4
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	517	942	09	138	79. 52	0	10	30	25	38	40	9
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	477	943	09	178	78. 48	0	16.6	23.3	25	38	40	3
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	437	944	09	218	79. 02	0	16.6	21.6	25	36.6 7	38.3 3	5
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	397	945	09	258	78. 42	0	18.3 3	20	23.3	38.3 3	38.3 3	4
nonstructural protein NS2A	DEN 1	gi 9626685:3476 -4129	357	946	09	298	80. 78	0	31.6	13.3	28.3	26.6 7	45	4
nonstructural protein NS2A	DEN 1	gi 9626685:3476 -4129	309	947	09	346	79. 96	0	25	18.3 3	25	31.6 7	43.3 3	3
nonstructural protein NS2A	DEN 1	gi 9626685:3476 -4129	269	948	09	386	77. 34	0	21.6	18.3 3	23.3 3	36.6 7	40	3
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	131	949	09	524	80. 68	0	28.3 3	16.6	30	25	45	3
nonstructural protein NS2A	DEN I	gi 9626685:3476 -4129	98	950	09	695	80. 86	0	23.3	20	28.3	28.3 3	43.3 3	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	331	951	09	09	80. 85	0	23.3	20	31.6	25	43.3 3	5
nonstructural protein NS2B	DEN 1	gi 9626685:4130 -4519	330	952	09	61	81. 14	0	23.3 3	21.6	30	25	45	5
nonstructural protein NS2B	DEN 1	gi 9626685:4130 -4519	329	953	09	62	81. 59	0	21.6	21.6	31.6	25	43.3	5

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	3%C	%A	%T	S%C	PolyX
nonstructural protein NS2B	DEN 1	gi 9626685:4130 -4519	328	954	09	63	80. 89	0	21.6	21.6 7	30	26.6 7	43.3	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	327	955	09	64	80. 81	0	20	21.6	31.6	26.6 7	41.6	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	326	956	09	9	80. 02	0	20	21.6	30	28.3 3	41.6	5
nonstructural protein NS2B	DEN 1	gi 9626685:4130 -4519	325	957	09	99	80. 02	0	21.6	20	30	28.3	41.6	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	324	958	09	29	80. 72	0	23.3	20	28.3	28.3	43.3	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	323	959	09	89	81. 42	0	25	20	26.6 7	28.3 3	45	5
nonstructural protein NS2B	DEN I	gi 9626685:4130 -4519	321	960	09	70	82. 09	0	25	20	26.6 7	28.3 3	45	5
nonstructural protein NS3	DEN 1	gi 9626685:4520 -6376	1475	961	09	383	80. 94	0	15	30	35	20	45	5
nonstructural protein NS3	DEN I	gi 9626685:4520 -6376	1415	962	09	443	80. 76	0	23.3 3	21.6	35	20	45	3
nonstructural protein NS3	DEN I	gi 9626685:4520 -6376	1213	963	09	645	81. 42	0	23.3 3	21.6	35	20	45	3
nonstructural protein NS3	DEN I	gi 9626685:4520 -6376	1153	964	09	705	77. 27	0	18.3 3	18.3 3	46.6 7	16.6 7	36.6	9
nonstructural protein NS3	DEN I	gi 9626685:4520 -6376	1093	965	09	765	80. 34	0	26.6	15	38.3 3	20	41.6	3
nonstructural protein NS3	DEN 1	gi 9626685:4520 -6376	1033	996	09	825	81. 37	0	23.3 3	21.6	25	30	45	4
nonstructural protein NS3	DEN 1	gi 9626685:4520 -6376	973	967	09	885	80. 25	0	21.6	21.6	36.6 7	20	43.3 3	3
nonstructural protein NS3	DEN I	gi 9626685:4520 -6376	845	968	09	1013	81. 43	0	21.6	23.3 3	30	25	45	4
nonstructural protein NS3	DEN 1	gi 9626685:4520 -6376	785	969	09	1073	80. 31	0	16.6	28.3 3	21.6 7	33.3 3	45	3
nonstructural protein NS3	DEN 1	gi 9626685:4520 -6376	725	970	09	1133	80. 39	0	30	15	36.6 7	18.3 3	45	3
nonstructural protein NS4A	DEN I	gi 9626685:6377 -6757	302	971	09	08	80. 8	0	21.6	23.3 3	18.3 3	36.6 7	45	4
nonstructural protein NS4A	DEN I	gi 9626685:6377 -6757	231	972	09	151	81. 8	0	21.6	23.3 3	25	30	45	5
nonstructural protein NS4A	DEN 1	gi 9626685:6377 -6757	208	973	09	174	81. 34	0	23.3 3	21.6 7	23.3 3	31.6	45	5
nonstructural protein NS4A	DEN 1	gi 9626685:6377 -6757	154	974	09	228	80. 81	0	28.3	16.6	21.6	33.3 3	45	3

	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%	V %	L%	5% C	PolyX
	DEN I	gi 9626685:6377 -6757	134	975	09	248	80. 32	0	21.6	21.6	31.6 7	25	43.3 3	3
	DEN I	gi 9626685:6377 -6757	113	926	09	269	80. 12	0	18.3	26.6	40	15	45	4
nonstructural protein NS4A	DEN I	gi 9626685:6377 -6757	86	226	09	296	80. 09	0	21.6	21.6	38.3 3	18.3	43.3 3	4
	DEN 1	gi 9626685:6377 -6757	99	8/6	09	316	80. 57	0	25	20	33.3 3	21.6	45	4
nonstructural protein NS4A	DEN I	gi 9626685:6377 -6757	23	626	09	359	81. 64	0	20	25	38.3 3	16.6	45	3
nonstructural protein NS4A	DEN 1	gi 9626685:6377 -6757	3	086	09	379	78. 87	0	20	21.6	36.6	21.6	41.6	3
nonstructural protein NS4B	DEN I	gi 9626685:6827 -7573	685	981	09	63	79. 97	0	30	15	26.6 7	28.3	45	4
nonstructural protein NS4B	DEN 1	gi 9626685:6827 -7573	634	982	09	114	80. 33	0	23.3 3	18.3	31.6 7	26.6	41.6	5
nonstructural protein NS4B	DEN 1	gi 9626685:6827 -7573	909	883	09	242	81. 11	0	18.3 3	25	28.3 3	28.3 3	43.3 3	3
nonstructural protein NS4B	DEN I	gi 9626685:6827 -7573	466	984	09	282	79. 24	0	23.3 3	15	31.6 7	30	38.3 3	5
nonstructural protein NS4B	DEN I	gi 9626685:6827 -7573	424	586	09	324	80. 65	0	23.3 3	20	30	26.6	43.3	5
nonstructural protein NS4B	DEN I	gi 9626685:6827 -7573	383	986	09	365	79. 43	0	20	21.6	48.3 3	10	41.6	9
nonstructural protein NS4B	DEN 1	gi 9626685:6827 -7573	336	<i>L</i> 86	09	412	81. 34	0	23.3 3	21.6	98	25	45	4
nonstructural protein NS4B	DEN 1	gi 9626685:6827 -7573	224	886	09	524	79. 92	0	26.6 7	16.6	31.6	25	43.3 3	3
nonstructural protein NS4B	DEN I	gi 9626685:6827 -7573	184	686	09	564	80. 18	0	21.6	21.6	31.6 7	25	43.3 3	3
nonstructural protein NS4B	DEN 1	gi 9626685:6827 -7573	144	066	09	604	79. 98	0	13.3 3	28.3 3	38.3 3	20	41.6	4
nonstructural protein NS5	DEN 1	gi 9626685:7574 -10270	2637	166	09	61	80. 76	0	25	20	9.9£ 7	18.3 3	45	5
nonstructural protein NS5	DEN I	gi 9626685:7574 -10270	2577	766	09	121	79. 62	0	21.6	20	38.3 3	20	41.6	3
nonstructural protein NS5	DEN I	gi 9626685:7574 -10270	2508	866	09	190	80. 76	0	26.6 7	18.3 3	38	20	45	5
nonstructural protein NS5	DEN I	gi 9626685:7574 -10270	2425	766	09	273	81. 21	0	33.3 3	11.6	31.6 7	23.3 3	45	4
nonstructural protein NS5	DEN 1	gi 9626685:7574 -10270	2276	995	09	422	81. 23	0	26.6 7	18.3	28.3 3	26.6	45	3

PolyX																			
Pol	С	4	8	9	4	2	2	2	2	2	2	2	2	2	2	4	4	к	4
2 %	45	41.6	43.3	45	45	45	43.3	43.3	43.3	43.3	43.3	43.3	43.3	45	43.3	41.6	43.3	45	45
1%	28.3 3	15	25	15	20	26.6	26.6 7	26.6 7	25	25	25	25	25	25	26.6 7	30	25	25	21.6
W %	26.6 7	43.3 3	31.6	40	35	28.3	30	30	31.6	31.6	31.6	31.6	31.6	30	30	28.3 3	31.6	30	33.3 3
3%C	23.3 3	13.3 3	18.3	18.3 3	23.3	18.3	18.3 3	20	20	20	20	20	21.6	21.6	20	30	26.6	23.3	20
9%	21.6	28.3 3	25	26.6	21.6	26.6	25	23.3 3	23.3 3	23.3	23.3	23.3	21.6	23.3	23.3	11.6	16.6	21.6	25
X-Hyb Pot																			
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tm	82. 36	79. 94	80. 73	82. 27	81. 36	.08 98 98	80. 25	80. 25	80. 78	80. 38	80. 28	80. 28	80. 28	80. 62	80. 99	80. 14	80.	82. 19	81.
End Distance	596	959	716	622	841	62	63	64	99	99	29	89	69	70	71	09	08	133	165
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	966	266	866	666	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014
BP Start	2102	2042	1982	1919	1857	281	280	279	278	277	276	275	274	273	272	439	419	366	334
Target ID	gi 9626685:7574 -10270	gi 9626685:7574 -10270	gi 9626685:7574 -10270	gi 9626685:7574 -10270	gi 9626685.7574 -10270	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:97 -438	gi 158976983:43 9-936	gi 158976983:43 9-936	gi 158976983:43 9-936	gi 158976983:43 9-936
Virus	DEN 1	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2				
Product	nonstructural protein NS5	anchored capsid protein C	anchored capsid protein C	membrane glycoprotein precursor M	membrane glycoprotein precursor M	membrane glycoprotein precursor M	membrane glycoprotein precursor M												

X																		
PolyX	4	9	9	4	4	4	ε	4	т	9	3	S	9	4	ε	3	ε	ŗ
C C	45	45	45	45	43.3 3	41.6	45	40	45	45	45	45	38.3	45	36.6	45	41.6	4
L%	16.6	16.6	18.3	25	18.3 3	16.6	33.3 3	25	28.3	23.3	18.3	15	30	20	23.3	20	21.6	21.6
%	38.3 3	38.3 3	36.6	30	38.3 3	41.6	21.6	35	26.6 7	31.6	36.6	40	31.6	35	40	35	36.6	33.3
Э%С	18.3	15	16.6	18.3	13.3	18.3	13.3	21.6	25	15	18.3	25	16.6	20	11.6	25	16.6	35
9%	26.6	30	28.3 3	26.6	30	23.3	31.6	18.3	20	30	26.6	20	21.6	25	25	20	25	00
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U
Tm	81. 32	81. 44	81. 21	81. 29	79. 83	80. 03	81. 37	78. 25	81. 06	82. 18	89	80. 32	77. 43	80.	77.	81. 36	90	81.
End Distance	185	245	270	439	459	479	64	124	200	300	360	420	480	540	009	099	09	141
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	1015	9101	1017	8101	6101	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032
BP Start	314	254	229	09	40	20	1422	1362	1286	1186	1126	1066	1006	946	988	826	766	916
Target ID	gi 158976983:43 9-936	gi 158976983:93 7-2421	gi 158976983:24 22-3477	gi 158976983:24														
Virus	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2	DEN 2					
Product	membrane glycoprotein precursor M	envelope protein E	nonstructural protein NS1	nonstructural														

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	1%	2% C	PolyX
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	827	1033	09	230	80. 58	0	31.6	13.3	30	25	45	3
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	792	1034	09	290	80. 38	0	23.3	21.6	36.6	18.3 3	45	3
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	707	1035	09	350	79. 7	0	20	21.6	35	23.3 3	41.6	3
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	647	1036	09	410	81. 28	0	18.3	26.6	33.3 3	21.6	45	5
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	587	1037	09	470	79. 06	0	26.6	15	36.6	21.6	41.6	3
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	520	1038	09	537	81. 45	0	20	25	38.3 3	16.6 7	45	4
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	460	1039	09	297	76. 37	0	21.6	13.3 3	38.3 3	26.6 7	35	4
nonstructural protein NS1	DEN 2	gi 158976983:24 22-3477	362	1040	09	969	80. 24	0	15	30	31.6	23.3 3	45	5
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	550	1041	09	105	79. 5	0	15	25	38.3 3	21.6	40	9
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	508	1042	09	147	82. 33	0	15	30	30	25	45	9
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	468	1043	09	187	80. 48	0	26.6	15	35	23.3 3	41.6	4
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	428	1044	09	227	80. 44	0	20	21.6	30	28.3 3	41.6	3
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	388	1045	09	267	78. 32	0	26.6	13.3	35	25	40	4
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	346	1046	09	309	81. 33	0	23.3	21.6	26.6	28.3 3	45	3
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	306	1047	09	349	79. 47	0	16.6	28.3 3	30	25	45	3
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	266	1048	09	389	77. 78	0	23.3 3	18.3 3	31.6	26.6 7	41.6	3
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	219	1049	09	436	81. 39	0	15	30	23.3	31.6	45	4
nonstructural protein NS2A	DEN 2	gi 158976983:34 78-4131	119	1050	09	536	80. 56	0	31.6	13.3	26.6	28.3 3	45	3
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	328	1051	09	63	81. 92	0	23.3	21.6	33.3 3	21.6	45	3
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	327	1052	09	64	81. 92	0	23.3 3	21.6	31.6	23.3 3	45	4
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	326	1053	09	65	81. 41	0	23.3	21.6	30	25	45	5

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	W%	L%	S%C	PolyX
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	325	1054	09	99	81. 34	0	23.3	21.6	30	25	45	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	324	1055	09	<i>L</i> 9	81. 85	0	23.3	21.6	30	25	45	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	306	1056	09	85	81. 85	0	21.6	23.3	25	30	45	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	298	1057	09	93	81. 68	0	21.6	23.3	28.3	26.6 7	45	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	297	1058	09	94	80. 89	0	21.6	23.3	26.6	28.3	45	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	296	1059	09	95	80. 04	0	21.6	21.6	26.6	30	43.3	5
nonstructural protein NS2B	DEN 2	gi 158976983:41 32-4521	295	1060	09	96	79. 95	0	20	21.6	28.3	30	41.6	5
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1795	1061	60	60	80. 58	0	25	18.3	35	21.6	43.3	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1735	1062	09	120	80. 15	0	31.6	10	40	18.3 3	41.6	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1675	1063	09	180	79. 61	0	28.3	13.3 3	40	18.3 3	41.6	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1590	1064	09	265	79. 93	0	26.6	18.3	31.6	23.3	45	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1509	1065	09	346	82. 18	0	26.6	18.3	31.6	23.3	45	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1449	1066	09	406	81. 01	0	21.6	23.3	40	15	45	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1389	1067	09	466	77. 78	0	21.6	15	45	18.3	36.6	9
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1246	1068	09	609	81. 33	0	21.6	23.3	35	20	45	4
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1186	1069	09	699	80. 44	0	25	18.3	31.6	25	43.3	3
nonstructural protein NS3	DEN 2	gi 158976983:45 22-6375	1126	1070	09	729	76. 54	0	25	11.6	40	23.3	36.6	5
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	312	1071	60	70	76. 19	0	16.6	18.3	26.6	38.3 3	35	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	311	1072	60	71	76. 49	0	18.3 3	18.3 3	25	38.3 3	36.6	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	310	1073	60	72	76. 83	0	16.6	18.3	25	40	35	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	309	1074	09	73	76. 49	0	16.6	20	25	38.3	36.6	9

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	%C	W%	%T	S%G	PolyX
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	308	1075	09	74	76. 29	0	16.6	18.3	26.6	38.3	35	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	307	1076	09	75	76. 29	0	16.6	18.3	26.6	38.3 3	35	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	306	1077	09	92	76. 77	0	16.6	18.3	26.6	38.3	35	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	305	1078	09	77	76. 54	0	16.6	20	25	38.3	36.6	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	304	1079	09	78	77.	0	15	21.6	25	38.3	36.6	9
nonstructural protein NS4A	DEN 2	gi 158976983:63 76-6756	303	1080	09	79	77. 52	0	16.6	21.6	23.3	38.3	38.3 3	9
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	682	1081	09	63	79. 89	0	18.3	23.3	31.6	26.6	41.6	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	632	1082	09	113	80. 07	0	28.3	15	23.3	33.3 3	43.3 3	5
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	532	1083	09	213	80. 39	0	28.3	16.6	23.3	31.6	45	3
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	491	1084	09	254	80. 55	0	25	18.3 3	28.3 3	28.3 3	43.3 3	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	451	1085	09	294	78. 5	0	20	18.3	36.6 7	25	38.3 3	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	332	1086	09	413	81. 51	0	18.3	25	31.6	25	43.3 3	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	287	1087	09	458	79. 87	0	15	28.3 3	25	31.6	43.3 3	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	168	1088	09	577	80. 18	0	16.6	25	33.3 3	25	41.6	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	128	1089	09	617	78. 77	0	18.3	20	33.3 3	28.3	38.3 3	4
nonstructural protein NS4B	DEN 2	gi 158976983:68 26-7569	9	1090	09	739	81. 65	0	26.6	18.3	36.6	18.3	45	6
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2641	1091	09	60	79. 36	0	30	13.3	38.3 3	18.3	43.3	4
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2581	1092	60	120	76. 91	0	15	20	46.6	18.3	35	3
RNA- dependent RNA	DEN 2	gi 158976983:75 70-10269	2505	1093	09	196	81. 55	0	28.3	16.6	33.3 3	21.6	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	L%	S%	PolyX
pol. NS5														
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2440	1094	09	261	81. 5	0	28.3	16.6	38.3	16.6	45	4
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2379	1095	09	322	81. 11	0	23.3	21.6	35	20	45	6
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2152	1096	09	549	81. 62	0	26.6	18.3	31.6	23.3	45	E
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2092	1097	09	609	80. 4	0	21.6	21.6	28.3	28.3	43.3	3
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	2032	1098	09	699	77. 57	0	20	16.6	43.3	20	36.6 7	3
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	1969	1099	09	732	81. 46	0	30	15	28.3	26.6	45	3
RNA- dependent RNA pol. NS5	DEN 2	gi 158976983:75 70-10269	1894	1100	09	807	81. 59	0	25	20	36.6	18.3	45	4
anchored capsid protein C	DEN 3	gi 163644368:95 -436	283	1101	09	09	82. 23	0	18.3	26.6	31.6	23.3	45	5
anchored capsid protein C	DEN 3	gi 163644368.95 -436	282	1102	09	61	81. 79	0	18.3	26.6	33.3 3	21.6	45	5
anchored capsid protein C	DEN 3	gi 163644368:95 -436	281	1103	09	62	80. 67	0	18.3 3	25	33.3 3	23.3	43.3	5
anchored capsid protein C	DEN 3	gi 163644368:95 -436	280	1104	09	63	80. 51	0	16.6	25	35	23.3 3	41.6	5
anchored capsid protein C	DEN 3	gi 163644368:95 -436	279	1105	09	64	80.	0	16.6	26.6	35	21.6	43.3	5

20 45	20 45 5 21.6 43.3 5 7 3 5 7 3 5 31.6 43.3 4 7 3 4 33.3 43.3 4	45. 45. 43.3 43	45. 43.3 4	45 43.3 43	45 43.3 43.3 45	45. 45. 43.3 45. 45. 45. 45. 45. 45. 45. 45.	45 45 43.3 45 45 45 45 45 45 45 45 45 45
25 35 2	35 3 35 6 25 6 23.3	35 35 35 35 35 35 35 35 35 35 35 35 35 3	35 35 35 35 35 35 35 35 35 35 35 35 35 3	35 35 35 35 35 35 35 35 35 35 35 35 35 3	35 35 35 35 35 35 35 35 35 35 35 35 35 3	35 35 35 35 35 35 35 35 35 35	35 35 35 35 35 35 35 35 35 35
	20 3 18.3 25 3 16.6 7 7 7 7 7						
80. 55 0	80. 0 55 0 72 0 80. 0 2 0						
89	09 19	62 61 60	60 69 69 69	60 60 61 60 60 60 60 60 60 60 60 60 60 60 60 60	60 60 61 60 60 63 62 61 60 60 60 60 60 60 60 60 60 60 60 60 60	69 69 69 69	69 69 69 69 69
09	09 09	09 09 09	09 09 09 09	09 09 09 09 09	09 09 09 09 09	09 09 09 09 09	09 09 09 09 09 09
	1110 1110						
	368:43 439 368:43 438						
gi 163644368:95 -436 gi 163644368:95 -436	gi 163644368:43 7-934 gi 163644368:43 7-934	gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934	gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934	gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934	gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 7-934	gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934 gi 163644368:43 7-934	gi 163644368:43 7-934
	DEN 3 DEN 3	DEN 3 DEN 3 DEN 3	DEN 3 DEN 3 DEN 3 DEN 3 DEN 3	DEN 3 DEN 3 DEN 3 DEN 3 DEN 3 DEN 3	DEN 3	DEN 3	DEN 3
DEN 3 DEN 3				ZE ZE ZE ZE ZE ZE ZE ZE		M M Seine Se	glycoprotein precursor M membrane glycoprotein

	Virus	Target ID	BP Start	SEQ ID	Probe Lenoth	End	Tm	X-Hyb Pot	9%	Э%	%A	L%	5% 9%	PolyX
	DEN 3	gi 163644368:93 5-2413	1359	1122	09	121	77. 5	0	21.6	15	35	28.3	36.6	9
	DEN 3	gi 163644368:93 5-2413	1296	1123	09	184	88	0	26.6	18.3	23.3	31.6	45	3
	DEN 3	gi 163644368:93 5-2413	1137	1124	09	343	88.	0	30	15	36.6	18.3	45	4
	DEN 3	gi 163644368:93 5-2413	1077	1125	09	403	80.	0	30	15	28.3	26.6	45	4
	DEN 3	gi 163644368:93 5-2413	994	1126	09	486	81. 55	0	23.3	21.6	35	20	45	4
	DEN 3	gi 163644368:93 5-2413	926	1127	09	554	83.	0	28.3	16.6	38.3	16.6	45	4
	DEN 3	gi 163644368:93 5-2413	866	1128	09	614	80. 1	0	28.3 3	13.3 3	33.3 3	25	41.6	4
	DEN 3	gi 163644368:93 5-2413	805	1129	09	912	81. 01	0	25	20	35	20	45	4
	DEN 3	gi 163644368:93 5-2413	719	1130	09	761	82. 39	0	26.6 7	18.3 3	38.3 3	16.6	45	9
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	266	1131	09	09	78. 87	0	25	16.6	38.3 3	20	41.6	3
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	628	1132	09	178	81. 3	0	28.3	16.6	35	20	45	3
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	816	1133	09	241	81. 09	0	26.6	18.3 3	31.6	23.3	45	3
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	711	1134	09	346	79. 82	0	18.3 3	26.6 7	35	20	45	3
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	651	1135	09	406	81. 24	0	20	25	33.3 3	21.6	45	S
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	591	1136	09	466	80. 52	0	26.6	16.6 7	40	16.6	43.3	5
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	492	1137	09	565	81. 04	0	18.3	26.6	35	20	45	3
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	380	1138	09	229	82. 15	0	16.6	28.3 3	35	20	45	4
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	320	1139	09	737	80. 86	0	26.6 7	16.6	41.6	15	43.3 3	5
nonstructural protein NS1	DEN 3	gi 163644368:24 14-3469	256	1140	09	801	81. 32	0	30	15	33.3 3	21.6	45	4
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	592	1141	09	63	79. 26	0	16.6	25	26.6 7	31.6	41.6	5
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	511	1142	09	144	82. 49	0	25	20	25	30	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	L%	S%C	PolyX
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	463	1143	09	192	82. 44	0	21.6	23.3	25	30	45	5
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	423	1144	09	232	78. 41	0	15	21.6	30	33.3 3	36.6	5
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	383	1145	09	272	8 0. 03	0	21.6	21.6	30	26.6	43.3	4
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	301	1146	09	354	81. 71	0	26.6	16.6	28.3	28.3	43.3	3
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	260	1147	09	395	76. 4	0	25	10	28.3	36.6	35	5
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	220	1148	09	435	78. 21	0	13.3	23.3	25	38.3 3	36.6	5
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	117	1149	09	538	81. 23	0	21.6	23.3	30	25	45	3
nonstructural protein NS2A	DEN 3	gi 163644368:34 70-4123	92	1150	09	625	80. 06	0	21.6	18.3	23.3 3	36.6 7	40	4
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	325	1151	09	99	81. 62	0	13.3 3	30	30	26.6 7	43.3	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	324	1152	09	29	81. 05	0	13.3	30	30	26.6	43.3	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	323	1153	09	89	81. 76	0	15	28.3	30	26.6	43.3	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	322	1154	09	69	82. 46	0	16.6	28.3	28.3	26.6	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	321	1155	09	70	82. 91	0	16.6	28.3	28.3	26.6	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	319	1156	60	72	82. 81	0	16.6	28.3	26.6	28.3	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	318	1157	60	73	82. 78	0	16.6	28.3 3	26.6	28.3 3	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	317	1158	60	74	82. 5	0	16.6	28.3	25	30	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	313	1159	09	78	81. 4	0	18.3	26.6	23.3	31.6	45	5
nonstructural protein NS2B	DEN 3	gi 163644368:41 24-4513	312	1160	60	62	80. 7	0	16.6	26.6	25	31.6	43.3	5
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1767	1161	09	16	81. 61	0	21.6	23.3	30	25	45	9
nonstructural protein NS3	DEN 3	gi 163644368;45 14-6370	1698	1162	09	160	79. 32	0	28.3 3	10	40	21.6	38.3 3	4
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1638	1163	09	220	77. 1	0	21.6	15	41.6	21.6	36.6	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%A	%T	2% C	PolyX
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1493	1164	09	365	80. 49	0	21.6	23.3 3	38.3 3	16.6 7	45	3
nonstructural protein NS3	DEN 3	gi 163644368;45 14-6370	1402	1165	09	954	81. 65	0	20	25	36.6 7	18.3 3	45	3
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1260	1166	09	869	80. 54	0	25	20	36.6 7	18.3	45	3
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1200	1167	60	859	80. 82	0	28.3	15	30	26.6 7	43.3	5
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1137	1168	09	721	75. 78	0	20	15	43.3 3	21.6	35	9
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1077	1169	09	781	81. 42	0	25	18.3	33.3 3	23.3	43.3	9
nonstructural protein NS3	DEN 3	gi 163644368:45 14-6370	1016	1170	09	842	82. 06	0	23.3 3	21.6	35	20	45	4
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	322	1171	09	09	79. 18	0	25	16.6 7	30	28.3 3	41.6	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	321	1172	09	19	79. 47	0	26.6 7	16.6 7	28.3 3	28.3 3	43.3 3	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	320	1173	09	62	80. 12	0	25	18.3 3	28.3 3	28.3 3	43.3 3	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	319	1174	09	63	80. 12	0	25	18.3 3	26.6 7	30	43.3 3	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	318	1175	09	64	80. 19	0	25	18.3 3	26.6 7	30	43.3 3	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	317	1176	09	59	80. 4	0	25	20	25	30	45	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	316	1177	60	99	80. 4	0	26.6	18.3	25	30	45	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	315	1178	60	<i>L</i> 9	81. 04	0	25	20	25	30	45	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	314	1179	60	89	81. 45	0	25	20	23.3 3	31.6 7	45	9
nonstructural protein NS4A	DEN 3	gi 163644368:63 71-6751	313	1180	09	69	81. 42	0	25	20	23.3 3	31.6 7	45	9
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	685	1181	09	09	78. 06	0	25	11.6	31.6	31.6 7	36.6 7	5
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	621	1182	09	124	81. 1	0	23.3 3	21.6	26.6 7	28.3 3	45	5
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	655	1183	09	981	81. 35	0	21.6	23.3 3	30	25	45	3
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	492	1184	09	253	82. 36	0	23.3	21.6	25	30	45	5

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	V %	L%	2 9%	PolyX
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	426	1185	09	319	75. 02	0	21.6	13.3	36.6	28.3 3	35	3
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	350	1186	09	395	82. 01	0	23.3 3	21.6	36.6 7	18.3	45	4
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	290	1187	09	455	80. 53	0	16.6	28.3 3	26.6 7	28.3 3	45	4
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	208	1188	09	537	82. 23	0	28.3 3	16.6	33.3 3	21.6	45	5
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	148	1189	09	297	79. 33	0	18.3 3	25	33.3 3	23.3 3	43.3 3	3
nonstructural protein NS4B	DEN 3	gi 163644368:68 21-7564	37	1190	09	708	80. 91	0	28.3 3	16.6	21.6	33.3 3	45	3
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2626	1191	09	75	80. 29	0	30	15	35	20	45	2
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2516	1192	09	185	80. 9	0	25	20	31.6	23.3 3	45	3
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2456	1193	09	245	78. 2	0	20	18.3 3	40	21.6	38.3 3	4
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2390	1194	09	311	81. 46	0	25	20	26.6	28.3 3	45	3
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2300	1195	09	401	81. 03	0	9.9I 7	28.3 3	31.6	23.3 3	45	2
nonstructural protein NS5	DEN 3	gi 163644368;75 65-10264	2198	1196	09	503	81. 02	0	28.3 3	16.6	38.3 3	16.6	45	3
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2137	1197	09	564	81. 38	0	26.6	18.3 3	30	25	45	4
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	2048	1198	09	653	82. 17	0	28.3 3	16.6	35	20	45	3
nonstructural protein NS5	DEN 3	gi 163644368:75 65-10264	1963	1199	09	738	81. 85	0	30	15	31.6	23.3 3	45	5
nonstructural protein NS5	DEN 4	gi 163644368:75 65-10264	1903	1200	09	798	80. 9	0	26.6 7	18.3 3	40	15	45	4
anchored capsid protein C	DEN 4	gi 12084822:102 -440	278	1201	09	62	81. 5	0	25	20	30	25	45	5
anchored capsid protein C	DEN 4	gi 12084822:102 -440	277	1202	09	63	80. 77	0	23.3 3	20	31.6	25	43.3 3	5
anchored capsid protein C	DEN 4	gi 12084822:102 -440	276	1203	09	64	80. 77	0	21.6	21.6	31.6	25	43.3 3	5
anchored capsid protein C	DEN 4	gi 12084822:102 -440	275	1204	09	99	81. 31	0	21.6	21.6	33.3 3	23.3 3	43.3 3	5
anchored capsid protein C	DEN 4	gi 12084822:102 -440	274	1205	09	99	81. 31	0	21.6	21.6	33.3 3	23.3	43.3	5

$^{\%}T$ $^{\%}G$ PolyX	23.3 45 5	23.3 45 5	23.3 45 5	23.3 45 5	5 43.3 5	43.3	3 3	3 45	£ 45 45	45 45 45	45 45 45 45	45 45 45 45	45 45 45 45 45 45 45 45 45 45 45 45 45 4	45 45 45 45 43.3 3	45 45 45 45 45 45 45 45 45	45 45 45 45 45 45 45 45 45 45 45 45 45 4
	$\begin{array}{c c} 31.6 & 23 \\ 7 & 3 \end{array}$	31.6 23 7 3	31.6 23 7 3	31.6 23 7 3	$\frac{31.6}{7}$ 25	$25 \begin{vmatrix} 31.6 \\ 7 \end{vmatrix}$		25 30	9							
	$\begin{array}{c c} 21.6 & 3 \\ 7 & 7 \end{array}$	21.6	23.3 3	21.6	20	20 2	1	18.3					 	 		
9%	23.3	23.3	21.6	23.3	23.3	23.3		26.6	26.6	26.6 7 25 26.6	26.6 7 25 26.6 7 26.6	26.6 7 25 26.6 7 7 16.6	26.6 7 25 26.6 7 7 16.6 7 25	26.6 7 25 25 7 7 16.6 7 7 25 25	26.6 7 25 25 7 7 7 7 7 7 7 25 25 25 25 25 25 26.6 7 26.6 7 25 25 26.6 7 26.6 7 26.6 7 26.6 7 27 27 27 27 27 27 27 27 27 27 27 27 2	26.6 7 25 25 7 7 7 7 7 7 7 7 25 25 25 25 25 33 33 3
X-Hyb Pot	0	0	0	0	0	0		0	0 0	0 0						
Tm	81. 62	81. 61	80. 97	81. 12	81. 5	79. 82		81. 54	81. 54 81.	81. 54. 81. 97. 80.	81. 54. 81. 80. 6	81. 81. 81. 80. 6 6 81. 81.	81. 881. 80. 80. 6 6 6 81. 81. 81.	81. 81. 80. 81. 81. 81. 81. 81. 81. 81. 81	81. 81. 81. 82. 83. 84. 84. 84. 84. 85. 86. 87. 88. 88. 88. 88. 88. 88. 88	81. 881. 881. 881. 881. 881. 881. 881.
End Distance	<i>L</i> 9	89	69	70	71	77		26	97	97 119 218	97 119 218 240	97 119 218 359	97 119 240 359 403	97 119 240 359 403	97 119 240 359 403 449	97 119 240 359 403 449 473
Probe Length	09	09	09	09	09	09		09	09	09	09 09	09 09 09	09 09 09 09	09 09 09 09	09 09 09 09 09	09 09 09 09 09
SEQ ID NO:	1206	1207	1208	1209	1210	1211		1212	1212	1212	1212 1213 1214 1215	1212 1213 1214 1215 1216	1212 1213 1214 1215 1216 1217	1212 1213 1214 1215 1216 1217	1212 1213 1214 1215 1216 1217 1218	1212 1213 1214 1215 1216 1217 1219 1220
BP Start	273	272	271	270	269	422		402	402	402 380 281	402 380 281 259	402 380 281 259 140	402 380 281 259 140	402 380 281 259 140 96	402 380 281 259 140 96 73	402 380 281 259 140 96 96 50
Target ID	gi 12084822:102 -440	gi 12084822:102 -440	gi 12084822:102 -440	gi 12084822:102 -440	gi 12084822:102 -440	gi 12084822:441 -938		gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938	gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938 gi 12084822:441 -938
Virus	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4		DEN 4	DEN 4 DEN 4	DEN 4 DEN 4 DEN 4	DEN 4 DEN 4 DEN 4 DEN 4	DEN 4 DEN 4 DEN 4 DEN 4 DEN 4	DEN 4 DEN 4 DEN 4 DEN 4 DEN 4 DEN 4	DEN 4	DEN 4	DEN 4
Product	anchored capsid protein C	capsid	capsid	capsid		e ein M	memhrane	ii A	ü A ü A	VII. VII. VII.	#	A in A in A in A	Z II. Z II. Z II. Z II.			

DEN 4 gil 1208482 2423 DEN 4 gil 1208482 2423 DEN 4 gil 1208482 DEN 4 gil 1208482 DEN 4 gil 1208482		Start	NO:	Length	Distance	!	Pot))	170,	101	_	
		1345	1222	09	141	.08	0	33.3	11.6	21.6	33.3	45	
			7771	3	1111	03		т	7	7	3,5	; ;	
		1285	1223	09	201	80 98	0	25	16.6	25	33.3 3	41.6	5
		1216	1224	09	270	82. 36	0	28.3 3	16.6	26.6	28.3 3	45	4
		1156	1225	09	330	81. 57	0	25	20	28.3	26.6 7	45	3
		1096	1226	09	390	80. 71	0	25	20	33.3 3	21.6	45	9
		1026	1227	09	460	82. 09	0	21.6	23.3	33.3 3	21.6	45	5
		996	1228	09	520	80.	0	30	15	33.3 3	21.6	45	4
DEN 4 gi 1208 ² -2423		906	1229	09	580	80. 85	0	26.6	15	38.3	20	41.6	4
DEN 4 gi 12084		846	1230	09	640	78. 53	0	26.6	13.3	35	25	40	3
non-structural DEN 4 gi 1208/ protein NS1 4-3479	gi 12084822:242 4-3479	993	1231	09	64	80. 92	0	31.6	13.3	36.6	18.3	45	5
non-structural DEN 4 gi 12084 protein NS1 4-3479	4822:242	823	1232	09	234	81. 36	0	25	20	35	20	45	4
DEN 4 gi 1208-4-3479	4822:242	710	1233	09	347	82. 19	0	16.6	28.3	30	25	45	5
non-structural DEN 4 gi 1208/ protein NS1 4-3479	4822:242	638	1234	09	419	81. 84	0	21.6	23.3	33.3 3	21.6	45	4
non-structural DEN 4 gi 1208/ protein NS1 4-3479	gi 12084822:242 4-3479	570	1235	09	487	81. 23	0	26.6	18.3	33.3 3	21.6	45	9
non-structural DEN 4 gi 12084 protein NS1 4-3479		510	1236	09	547	80. 05	0	26.6	15	35	23.3	41.6	3
non-structural DEN 4 gi 12084 protein NS1 4-3479	1822:242	450	1237	09	209	80. 03	0	26.6	16.6	30	26.6 7	43.3 3	3
non-structural DEN 4 gi 1208/ protein NS1 4-3479	4822:242	390	1238	09	299	81. 13	0	20	25	35	20	45	5
non-structural DEN 4 gi 1208/ protein NS1 4-3479		330	1239	09	727	79. 15	0	20	18.3	45	16.6	38.3 3	5
non-structural DEN 4 gi 1208/ protein NS1 4-3479		509	1240	09	848	80. 26	0	25	20	33.3 3	21.6	45	3
DEN 4 gi 12084 0-4133		576	1241	09	62	80.	0	16.6	28.3	31.6	23.3	45	3
non-structural DEN 4 gi 12084 protein NS2A 0-4133	gi 12084822:348 0-4133	536	1242	09	119	80. 42	0	20	23.3	33.3 3	23.3	43.3	5

Virus	20	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5 %	3%	8%	L%	S%	PolyX
DEN	4	gi 12084822:348 0-4133	496	1243	09	159	82. 34	0	23.3	21.6	16.6	38.3 3	45	33
DEN	4	gi 12084822:348 0-4133	456	1244	09	199	80. 91	0	25	16.6	23.3	35	41.6	3
DEN	4	gi 12084822:348 0-4133	416	1245	09	239	79. 77	0	15	26.6	30	28.3 3	41.6	3
DEN 4	4	gi 12084822:348 0-4133	376	1246	09	279	77. 78	0	18.3	18.3	38.3	25	36.6	5
DEN 4	4	gi 12084822:348 0-4133	336	1247	09	319	77. 31	0	16.6	20	28.3	35	36.6	4
DEN 4	4	gi 12084822:348 0-4133	296	1248	09	359	81. 43	0	21.6	23.3	33.3 3	21.6	45	3
DEN	4	gi 12084822:348 0-4133	256	1249	09	399	78. 89	0	25	15	31.6	28.3	40	5
DEN 4	4	gi 12084822:348 0-4133	06	1250	09	565	80. 72	0	23.3	21.6	21.6	33.3 3	45	3
DEN 4	4	gi 12084822:413 4-4523	331	1251	09	09	80. 94	0	20	23.3	35	21.6	43.3	4
DEN	4	gi 12084822:413 4-4523	330	1252	09	61	81. 23	0	20	25	33.3 3	21.6	45	4
DEN 4	4	gi 12084822:413 4-4523	329	1253	09	62	81. 69	0	18.3	25	35	21.6	43.3 3	4
DEN 4	4	gi 12084822:413 4-4523	328	1254	09	63	81.	0	18.3	25	33.3 3	23.3	43.3	4
DEN	4	gi 12084822:413 4-4523	327	1255	09	64	81. 46	0	18.3	26.6	31.6	23.3 3	45	4
DEN 4	4	gi 12084822:413 4-4523	326	1256	09	65	81. 36	0	18.3	26.6	30	25	45	4
DEN 4	4	gi 12084822:413 4-4523	325	1257	09	99	81. 29	0	18.3	26.6	30	25	45	4
DEN	4	gi 12084822:413 4-4523	324	1258	09	29	81. 2	0	18.3	26.6	28.3	26.6 7	45	4
DEN 4	4	gi 12084822:413 4-4523	323	1259	09	89	81. 2	0	20	25	28.3	26.6 7	45	4
DEN 4	4	gi 12084822:413 4-4523	311	1260	09	08	81. 14	0	18.3 3	26.6	25	30	45	4
DEN	4	gi 12084822:452 4-6377	1780	1261	09	75	81. 8	0	28.3	16.6	25	30	45	4
DEN 4	4	gi 12084822:452 4-6377	1679	1262	09	176	78. 8	0	30	10	40	20	40	4
DEN 4	4	gi 12084822:452 4-6377	1591	1263	09	264	80. 87	0	33.3 3	11.6	28.3	26.6	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%	L%	2% C	PolyX
non-structural protein NS3	DEN 4	gi 12084822:452 4-6377	1513	1264	09	342	82. 25	0	25	20	31.6	23.3 3	45	9
non-structural protein NS3	DEN 4	gi 12084822:452 4-6377	1442	1265	09	413	81. 19	0	20	25	35	20	45	3
non-structural protein NS3	DEN 4	gi 12084822:452 4-6377	1210	1266	09	645	81. 26	0	30	51	28.3 3	26.6 7	45	5
non-structural protein NS3	DEN 4	gi 12084822:452 4-6377	1150	1267	09	705	79. 28	0	23.3 3	20	38.3 3	18.3 3	43.3 3	5
non-structural protein NS3	DEN 4	gi 12084822.452 4-6377	1088	1268	09	191	78. 17	0	25	9.11.6	41.6	21.6	36.6 7	4
non-structural protein NS3	DEN 4	gi 12084822.452 4-6377	1027	1269	09	828	81. 6	0	28.3 3	16.6 7	30	25	45	4
non-structural protein NS3	DEN 4	gi 12084822:452 4-6377	840	1270	09	1015	80. 76	0	25	20	26.6 7	28.3 3	45	3
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	322	1271	09	09	76. 92	0	18.3 3	18.3 3	35	28.3 3	36.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	321	1272	09	61	76. 3	0	16.6	20	35	28.3 3	36.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	320	1273	09	62	76. 92	0	15	21.6	35	28.3 3	36.6 7	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	319	1274	09	63	77. 77	0	16.6 7	21.6	33,3 3	28.3 3	38.3 3	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	318	1275	09	64	78. 47	0	18.3 3	21.6	31.6	28.3 3	40	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	317	1276	09	99	78. 69	0	18.3 3	23.3 3	30	28.3 3	41.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	316	1277	09	99	79. 4	0	20	21.6	30	28.3 3	41.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	315	1278	09	29	79. 82	0	20	21.6	30	28.3 3	41.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	314	1279	09	89	79. 54	0	20	21.6	28.3 3	30	41.6	9
non-structural protein NS4A	DEN 4	gi 12084822:637 8-6758	313	1280	09	69	79. 51	0	20	21.6	28.3 3	30	41.6	9
non-structural protein NS4B	DEN 4	gi 12084822:682 8-7562	657	1281	09	62	81. 5	0	26.6 7	18.3 3	26.6 7	28.3 3	45	5
non-structural protein NS4B	DEN 4	gi 12084822:682 8-7562	536	1282	09	200	81. 85	0	23.3 3	21.6	25	30	45	3
non-structural protein NS4B	DEN 4	gi 12084822:682 8-7562	506	1283	09	230	80. 7	0	25	20	21.6	33.3 3	45	3
non-structural protein NS4B	DEN 4	gi 12084822:682 8-7562	475	1284	09	261	79. 88	0	23.3	18.3	31.6	26.6	41.6	4

PolyX			_	_				_												
%G F	36.6 4	38.3 5	43.3 4	38.3 4	45 5	36.6 6	43.3 4	45 4	43.3 3	45 3	45 3	45 5	43.3 3	43.3 4	43.3 3	45 4	45 3	45 5	45 5	
L%	23.3	20	23.3	30	25	21.6	25	31.6	21.6	20	25	26.6	20	13.3	23.3	18.3	26.6	26.6	28.3	316
₩%	40	41.6	33.3 3	31.6	30	41.6	31.6	23.3	35	35	30	28.3 3	36.6	43.3	33.3 3	36.6	28.3	28.3 3	26.6	23.3
J%	18.3	20	21.6	25	23.3	13.3	15	18.3	20	26.6	16.6	25	8.33	16.6	25	26.6	25	18.3	21.6	
9%	18.3	18.3	21.6	13.3	21.6	23.3	28.3	26.6	23.3	18.3	28.3	20	35	26.6	18.3	18.3	20	26.6	23.3	
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	76. 31	76. 94	81. 05	78. 06	81. 8	78. 65	79. 06	.08	79. 7	81. 8	81. 03	81. 4	80. 94	80. 84	80. 34	81. 94	81. 82	81. 13	81. 07	8
End Distance	291	322	410	440	669	729	09	191	251	322	548	809	9//	836	968	666	418	837	1318	
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	
BP Start	445	414	326	296	37	7	2641	2510	2450	2379	2153	2093	1925	1865	1805	1702	8205	7786	7305	
Target ID	gi 12084822:682 8-7562	gi 12084822:756 3-10262	gi 9628705:459- 9080	gi 9628705:459- 9080	gi 9628705:459- 9080	oi 9628705·459-														
Virus	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	DEN 4	GB virus C/Hepatitis G	GB virus C/Hepatitis G	GB virus C/Hepatitis G	GB virus					
Product	non-structural protein NS4B	non-structural protein NS5	polyprotein precursor	polyprotein precursor	polyprotein precursor	nolvnrotein														

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	Э%	8 %	1%	C C C	PolyX
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	0689	1305	09	1733	81. 81	0	25	20	23.3	31.6	45	κ
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	8638	1306	09	1985	81. 93	0	20	25	26.6	28.3	45	4
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	5864	1307	09	2759	81. 52	0	21.6	23.3	28.3	26.6	45	ĸ
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	5551	1308	09	3072	81. 18	0	21.6	23.3	25	30	45	æ
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	5488	1309	09	3135	81. 21	0	18.3	26.6	23.3	31.6	45	2
polyprotein precursor	GB virus C/Hepatitis G	gi 9628705:459- 9080	3943	1310	09	4680	80.	0	30	15	26.6	28.3	45	4
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	545	1311	09	536	9.	0	26.6	18.3	25	30	45	8
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	1021	1312	09	09	85. 53	0	33.3 3	21.6	18.3	26.6	55	m
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	964	1313	09	117	86. 53	0	28.3 3	26.6	10	35	55	4
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	924	1314	09	157	85. 28	0	23.3	31.6	20	25	55	5
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	628	1315	09	202	86. 76	0	28.3 3	26.6	25	20	55	4
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	783	1316	09	298	86. 37	0	38.3 3	16.6	16.6	28.3	55	5
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	737	1317	09	344	86. 91	0	30	25	15	30	55	5
putative E1 protein	GB virus C/Hepatitis G	gi 9628705:459- 1538	644	1318	09	437	86. 26	0	35	20	16.6	28.3	55	3
putative E1	GB virus	gi 9628705:459-	601	1319	09	480	87.	0	28.3	26.6	15	30	55	5

	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%С	% A	L%	2 5%	PolyX
gi 9628705:2475 -3233	2475	532	1334	09	228	87. 2	0	33.3 3	21.6	16.6	28.3	55	5
gi 9628705:2475 -3233	475	502	1335	09	258	82. 78	0	31.6	16.6	16.6	35	48.3 3	5
gi 9628705:2475 -3233	175	472	1336	09	288	85. 07	0	28.3	25	20	26.6	53.3 3	3
gi 9628705;2475 -3233	57.5	350	1337	09	410	86. 51	0	35	20	8.33	36.6	55	3
gi 9628705:2475 -3233	75	320	1338	09	440	86. 19	0	33.3 3	21.6	8.33	36.6	55	3
gi 9628705:2475 -3233	75	286	1339	09	474	96	0	33.3	21.6	11.6	33.3	55	ю
gi 9628705:2475 -3233	52	194	1340	09	999	85. 08	0	38.3	16.6	25	20	55	4
gi 9628705:3234 -5111	4	1168	1341	09	711	80.	0	30	15	26.6	28.3	45	4
gi 9628705:3234 -5111	4	1162	1342	09	717	80.	0	30	15	25	30	45	4
gi 9628705:3234 -5111	4.	1156	1343	09	723	80.	0	28.3 3	16.6	28.3	26.6	45	4
gi 9628705:3234 -5111	48	1155	1344	09	724	80. 66	0	26.6	18.3	28.3 3	26.6	45	4
gi 9628705:3234 -5111	34	1154	1345	09	725	80. 56	0	26.6	18.3	28.3 3	26.6	45	4
gi 9628705:3234 -5111	34	1153	1346	09	726	79. 99	0	26.6	18.3	28.3 3	26.6	45	4
gi 9628705:3234 -5111	334	1152	1347	09	727	80. 56	0	26.6	18.3	28.3 3	26.6	45	4
gi 9628705:3234	34	1146	1348	09	733	80.	0	30	15	28.3	26.6	45	6

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	₩%	L%	2% C	PolyX
proteinase/ATP ase/helicase	C/Hepatitis G	-5111			0		43				3	7		
NS3 proteinase/ATP ase/helicase	GB virus C/Hepatitis G	gi 9628705:3234 -5111	1145	1349	09	734	79. 79	0	28.3	16.6	28.3	26.6	45	9
NS3 proteinase/ATP ase/helicase	GB virus C/Hepatitis G	gi 9628705:3234 -5111	1144	1350	09	735	80. 52	0	28.3 3	16.6	28.3	26.6	45	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	45	1351	09	154	85. 13	0	36.6	18.3	23.3	21.6	55	3
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	44	1352	09	155	84. 45	0	36.6	18.3	23.3	21.6	55	3
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	43	1353	09	156	84. 45	0	36.6	18.3	23.3	21.6	55	3
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	42	1354	09	157	85. 11	0	36.6	18.3	23.3	21.6	55	3
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	16	1355	09	183	85. 51	0	31.6	23.3	20	25	55	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	13	1356	09	186	84. 95	0	31.6	23.3 3	20	25	55	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	12	1357	09	187	84. 28	0	31.6	23.3	20	25	55	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	11	1358	09	188	84. 95	0	31.6	23.3	20	25	55	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	9	1359	09	193	85. 09	0	31.6	23.3	20	25	55	9
putative NS4A protein	GB virus C/Hepatitis G	gi 9628705:5112 -5309	5	1360	09	194	85. 03	0	31.6	23.3 3	20	25	55	9
putative NS4B protein	GB virus C/Hepatitis G	gi 9628705:5310 -6152	002	1361	09	144	81. 18	0	21.6	23.3	25	30	45	3
putative NS4B protein	GB virus	gi 9628705:5310 -6152	669	1362	09	145	80.	0	21.6	23.3	25	30	45	3

Virus T.	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	%A	L%	ر 3%	PolyX
l ≌ =	gi 9628705:5310 -6152	869	1363	09	146	80.	0	21.6	23.3 3	25	30	45	3
1 35 7	gi 9628705:5310 -6152	969	1364	09	148	81. 51	0	21.6	23.3	26.6	28.3	45	3
≘-:=	gi 9628705:5310 -6152	695	1365	09	149	80. 72	0	21.6	23.3	26.6	28.3	45	6
9 7	gi 9628705:5310 -6152	694	1366	09	150	80. 02	0	20	23.3	26.6	30	43.3	3
6 1	gi 9628705:5310 -6152	693	1367	09	151	80. 1	0	20	23.3	26.6	30	43.3	3
<u>@</u> :	gi 9628705:5310 -6152	692	1368	09	152	. 80	0	20	25	25	30	45	3
gi 962; -6152	gi 9628705:5310 -6152	169	1369	09	153	80.	0	20	25	25	30	45	3
gi 962 -6152	gi 9628705:5310 -6152	069	1370	09	154	80. 39	0	20	23.3	25	31.6	43.3	3
<u>6</u> 86	gi 9628705:6153 -7388	1174	1371	09	63	81. 64	0	30	15	28.3	26.6	45	3
<u> </u>	gi 9628705:6153 -7388	1173	1372	09	64	81. 57	0	28.3	16.6	28.3	26.6	45	3
6.6	gi 9628705:6153 -7388	1155	1373	09	82	82. 61	0	33.3 3	11.6	23.3 3	31.6	45	3
<u>e</u> v	gi 9628705:6153 -7388	1154	1374	09	83	82. 19	0	33.3 3	11.6	21.6	33.3 3	45	3
I = 1	gi 9628705:6153 -7388	1153	1375	09	84	82. 12	0	31.6	13.3 3	21.6	33.3 3	45	3
	gi 9628705:6153 -7388	944	1376	09	293	81. 93	0	20	25	26.6	28.3	45	4

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%C	V%	L%	ر د د	PolyX
dependent RNA														
pol.														
putative NS5B	GB virus													
RNA-	C/Hepatitis G	gi 9628705:7389	, 1	t 0 c 1	Ş	0171	80.	c	23.3	21.6	ý	Ç	Ų	ų
dependent RNA		-9077	3/2	138/	09	1318	32	o	г	7	52	30		o
pol.														
putative NS5B	GB virus													
RNA-	C/Hepatitis G	gi 9628705:7389	į	9	Ç	•	80	(23.3	21.6		(i,	ı
dependent RNA		-2077	37.1	1388	09	1319	9/	0	3	7	25	30	5	n
pol.														
putative NS5B	GB virus													
RNA-	C/Hepatitis G	gi 9628705:7389	·			,	80	,	!	(23.3	31.6		,
dependent RNA		-2007	74	1389	09	9191	79	0	25	20	3	7	45	κ
pol.														
putative NS5B	GB virus													
RNA-	C/Hepatitis G	gi 9628705:7389	í	000	Ç		80.	C	Ü	ć	23.3	31.6	Ų	,
dependent RNA		-2077	7/3	1390	09	/191/	23	0	25	70	3	7	45	33
pol.														
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	8£L	1681	09	89	81. 03	0	23.3	21.6	23.3 3	31.6	45	4
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	169	1392	09	115	75. 84	0	18.3	16.6	30	35	35	5
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	895	1393	09	238	80. 5	0	21.6	21.6	23.3	33.3 3	43.3	3
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	513	1394	09	293	81. 47	0	26.6	18.3	20	35	45	3
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	466	1395	09	340	80. 79	0	21.6	21.6	31.6	25	43.3	5
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	426	96£1	09	380	80. 48	0	33.3 3	11.6	26.6	28.3 3	45	3
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	378	1397	09	428	80. 46	0	25	20	28.3 3	26.6 7	45	4
1A VP4b mature peptide	Hepatitis A virus	gi 9626732:1- 805	338	1398	09	468	80. 54	0	21.6	23.3	20	35	45	4

X,																					
PolyX	4	S	4	ю	κ	ε	9	ю	4	S	ε	4	4	3	ε	κ	т	4	5	9	۳
د د %9	45	38.3 3	35	35	35	35	45	38.3 3	35	36.6 7	45	38.3 3	35	38.3 3	41.6	41.6	41.6	36.6 7	35	35	35
L%	26.6 7	40	38.3	31.6	31.6	40	30	31.6	36.6 7	30	31.6	38.3	38.3 3	38.3	26.6	35	25	41.6	43.3 3	30	36.6
% A	28.3 3	21.6	26.6	33.3 3	33.3 3	25	25	30	28.3 3	33.3 3	23.3	23.3	26.6	23.3	31.6	23.3	33.3 3	21.6	21.6	35	28.3
2%	15	21.6	18.3	15	20	16.6	23.3 3	13.3 3	15	16.6	23.3	16.6	20	23.3	16.6	21.6	20	13.3 3	15	23.3	0,0
- 5%	30	9.91	9.91	20	15	18.3	21.6	25	20	20	21.6	21.6	15	15	25	20	21.6	23.3	20	11.6	7
X-Hyb Pot																					
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	_
Tm	81. 35	77. 38	76. 15	75. 88	77. 16	76.	80. 84	79. 36	77.	77.	81. 32	78. 29	77. 07	77.	80. 34	79. 49	79. 56	77.	77.	76.	76.
End Distance	520	647	61	121	181	270	338	398	464	524	585	645	09	120	180	240	300	360	423	493	554
Probe Length		_	_	_		_	_	_	_							_			_	_	
	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	07
SEQ ID NO:	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419
BP Start	286	159	909	546	486	397	329	269	203	143	82	22	629	619	559	499	439	379	316	246	185
Target ID	gi 9626732:1- 805	gi 9626732:1- 805	gi 9626732:804- 1469	gi 9626732:1470 -2207	gi 9626732:1470																
Virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Honotitic A viens
Product	1A VP4b mature peptide	1A VP4b mature peptide	1B VP2 mature peptide	1C VP3 mature peptide	1C VP3																

5 40	3.3 43.3 4	۲٦	40	35	3 40 35 36.6	35 35 36.6 7 40	3 40 35 36.6 7 40 45	3 40 35 36.6 7 7 40 40 40	3 40 35 36.6 7 40 40 40	35 36.6 7 7 40 40 40 40 40 35 35 36.6 36.6 40 40 40 40 40 40 40 40 40 40 40 40 40	35 36.6 7 7 40 40 40 40 35 38.3	35 36.6 7 7 40 40 40 40 40 35 38.3 35 35	3 40 40 40 40 40 40 40 40 40 40	3 40 40 40 40 40 40 40 40 40 40	3 40 40 40 40 40 40 40 40 40 40	3 40 40 40 40 40 40 40 40 40 40	3 40 40 40 40 40 40 40 40 40 40	35 36.6 40 40 40 40 40 40 35 35 35 36.6 40 40 40 40 40 40 40 40 40 40 40 40 40	35 36.6 40 40 40 40 40 40 40 35 35 36.6 40 40 40 40 40 35 36.6 40 40 40 40 40 40 40 40 40 40 40 40 40	35 36.6 40 40 40 40 40 40 40 40 40 40
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	33 3		7 3 3 21.6 35 25	35 35 7	3 35 31.6 7 7	33 35 31.6 7 7 7 7 36.6	33 35 31.6 7 7 7 7 7 7 7 7 7 7 7 36.6 7 7 36.6 7 3 3.5 3 3.5 3 3.5 3 3.5 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	35 35 31.6 7 7 7 7 7 7 7 7 7 7 7 36.6 7 7 23.3 3	33 35 31.6 7 7 7 7 7 7 7 7 7 7 7 7 23.3 36.6 25 25	33 35 31.6 7 7 7 7 7 7 7 7 7 7 7 7 23.3 3 6.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 7 7 7 7 7 7 23.3 3 6.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 36.6 7 7 25 25 25 7 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 36.6 7 7 25 25 25 7 7 7 7 36.6 7 7 36.6 7 36.6 7 7 36.6 7 7 36.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 36.6 7 7 7 7 7 7 7 36.6 7 7 36.6 7 7 36.6 7 36.6 7 7 36.6 7 7 36.6 7 7 7 36.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 36.6 7 7 7 36.6 7 7 36.6 36.6 7 7 36.6 7 7 37 36.6 7 7 36.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 7 36.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	35 35 31.6 7 7 21.6 7 36.6 7 7 7 7 7 7 7 36.6 7 7 7 36.6 7 7 7 36.6 7 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 7 7 36.6 7 7 7 7 8 3 8 7 8 7 8 7 8 7 8 7 8 7 8 7	35 35 31.6 7 7 21.6 7 36.6 7 7 7 7 7 36.6 7 7 36.6 7 7 36.6 7 7 36.6 7 36.6 7 36.6 7 36.6 7 36.6 7 36.6 7 36.6 7 36.6 7 36.6 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	35 35 31.6 7 7 21.6 7 36.6 7 7 7 7 7 7 7 30 30 30 30 30 30 30 30 30 30 30 30 30	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
0 7 3	0 31.6 1.7 7	10.2		3 3 20	23.3	20 23.3 3 3 3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	20 20 23.3 3 7 7 7	20 23.3 3 21.6 7 7 23.3 3 23.3	20 23.3 3 3 23.3 7 7 7 7 7 7 7 7 7 7 7 7 7 10	20 20 23.3 3 3 7 7 7 7 7 7 7 7 7 7 7 10	20 20 23.3 3 3 7 7 7 7 7 7 10 10	20 20 23.3 3 3 3 7 7 7 7 7 7 7 10 10 16.6	20 20 23.3 3 3 3 4 7 7 7 7 7 7 10 10 16.6 7 7 7 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	20 20 23.3 3 3 3 23.3 3 3 16.6 16.6 7 7 7 7 7 7 7 7 7 7 7 8 3 3 3 3 3 3 3 3	20 20 23.3 3 3 3 16.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	20 20 23.3 3 3 3 16.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	20 20 20 23.3 3 3 3 3 16.6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	20 20 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	20 20 20 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	20 20 23.3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
78.	57.	79.	76	76. 59	77. 15	77. 15 79. 08	70. 77. 15. 79. 80. 80.	76. 77. 79. 80. 80. 54. 78. 63.	70. 77. 79. 80. 80. 80. 78. 63. 78.	70. 70. 70. 70. 70. 70. 70. 70.	77. 173. 174. 175. 176. 177. 176. 177. 176. 177. 176. 177. 176. 176	76. 77. 79. 80. 80. 80. 80. 80. 73. 74. 78. 63. 63. 63. 64. 77. 78. 63. 77. 78. 64. 77. 78. 65. 77. 77. 77. 77. 77. 77. 77. 7	76. 77. 78. 80. 80. 80. 80. 73. 74. 75. 66. 66. 67. 76. 68. 77. 78. 69. 77. 78. 78. 79. 79. 70. 70. 70. 70. 70. 70. 70. 70	7.7.	76. 17. 17. 18. 18. 18. 18. 18. 18. 18. 18. 18. 18	66 77. 78. 80. 80. 80. 80. 80. 80. 73. 74. 75. 90. 90. 77. 76. 77. 77. 77. 77. 77. 77	66 77. 78. 80. 80. 80. 66. 67. 77. 77. 77. 77. 76. 77. 76. 77. 77	66 70 71 72 73 74 75 76 76 77 77 77 76 76 76 76 76	66 77 77 77 76 76 77 77 77 76 77 77	66 77 77 77 76 76 77 77 77 76 76
09 09		60 120	60 247		90 307															
841 1421 6 781 1422 6	1422		654 1423 (594 1424 (534 1425 (1425	1425 1426 1427	1425 1426 1427 1428	1425 1426 1427 1428 1429	1425 1426 1427 1428 1429 1430	1425 1426 1427 1428 1429 1430	1425 1426 1427 1428 1429 1430 1431	1425 1426 1427 1428 1429 1430 1431 1431	1425 1426 1427 1428 1429 1430 1431 1431 1433	1425 1426 1427 1428 1429 1430 1431 1431 1435	1425 1426 1427 1428 1429 1430 1431 1432 1433 1435 1435	1425 1426 1427 1428 1429 1430 1431 1433 1433 1434 1435 1435 1435	1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1435 1435 1435	1425 1426 1427 1428 1429 1430 1431 1433 1435 1435 1436 1436 1436 1437
gi 9626732:2208 84	/OTC_	<u> </u>			╙															
+	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus															
	ID VP1 H						eptide					 								

PolyX	5	5	5	5	5	5	5	5	5	3	3	3	3	3	3	3	3	3	4	4	
ر 2% 2	43.3	45	45	43.3	43.3	43.3	41.6	41.6	41.6	40	38.3 3	38.3 3	36.6	36.6	35	36.6	38.3 3	40	40	35	416
L%	38.3 3	36.6	36.6 7	38.3	36.6	35	35	36.6	36.6	23.3	25	25	26.6	25	26.6	25	25	25	25	35	283
₩%	18.3	18.3	18.3	18.3	20	21.6	23.3 3	21.6	21.6	36.6	36.6	36.6	36.6	38.3 3	38.3 3	38.3 3	36.6	35	35	30	
3%C	18.3 3	20	18.3 3	18.3	18.3 3	18.3	18.3 3	18.3 3	18.3 3	18.3 3	18.3 3	18.3 3	16.6 7	16.6	51	15	15	51	51	15	18 3
9%	25	25	26.6 7	25	25	25	23.3	23.3	23.3	21.6	20	20	20	20	20	21.6	23.3	25	25	20	23.3
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	81. 63	81. 68	81. 4	81. 28	81. 25	80. 74	80. 68	79. 89	79. 1	77.	78. 06	77. 53	77. 19	76. 75	76. 4	76. 59	77. 29	77. 59	78. 22	77.	70
End Distance	132	133	140	141	142	143	144	145	146	09	61	62	63	64	\$9	99	29	89	69	06	
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	
BP Start	91	06	83	82	81	80	62	78	77	232	231	230	229	228	227	226	225	224	223	568	
Target ID	gi 9626732:5001 -5222	gi 9626732:5001 -5291	gi 9626732:5001 -5291	gi 9626732;5001 -5291	gi 9626732:5001 -5291	gi 9626732:5001 -5291	gi 9626732:5001 -5291	gi 9626732;5001 -5291	gi 9626732:5001 -5291	gi 9626732:5001 -5291	gi 9626732:5001 -5291	gi 9626732:5292 -5948	919626732-5292								
Virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	
Product	3A mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3B (VPg) mature peptide	3C mature peptide	3C mature								

PolyX	4	5	4	4	4	3	3	3	4	4	9	4	3	4	3	3	4	4	3	8	5
ر 9%	45	38.3 3	41.6	43.3	35	40	35	36.6 7	35	35	35	35	43.3	35	35	35	43.3 3	35	45	45	45
L%	23.3	20	25	23.3	33.3 3	38.3 3	41.6	36.6 7	38.3 3	36.6 7	28.3 3	35	23.3	43.3	40	41.6	28.3 3	46.6 7	38.3 3	31.6	35
V %	31.6	41.6	33.3 3	33.3 3	31.6	21.6	23.3 3	26.6	26.6 7	28.3 3	36.6 7	30	33.3 3	21.6	25	23.3	28.3 3	18.3 3	16.6	23.3	20
J%	11.6	15	18.3	16.6	16.6	15	15	13.3	11.6	11.6	11.6	15	23.3	11.6	20	20	23.3	13.3 3	20	25	16.6
9%	33.3 3	23.3	23.3	26.6	18.3	25	20	23.3	23.3	23.3	23.3	20	20	23.3	15	15	20	21.6	25	20	28.3
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tm	81. 56	77. 18	79. 04	81. 22	75. 69	78. 44	76. 48	78. 48	75. 79	77. 16	77. 77	76. 15	80. 71	75.	76. 5	75. 91	80. 51	75. 88	81. 49	81. 26	81. 52
End Distance	214	262	302	345	388	428	468	547	99	175	235	295	355	459	568	631	169	758	192	514	889
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503
BP Start	444	396	356	313	270	230	190	111	1403	1293	1233	1173	1113	1009	006	837	777	710	4891	4569	4395
Target ID	gi 9626732:5292 -5948	gi 9626732:5949 -7415	gi 9626440:4- 5085	gi 9626440:4- 5085	gi 9626440:4- 5085																
Virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis A virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus
Product	3C mature peptide	3D mature peptide	ORF 1- polyprotein	ORF 1- polyprotein	ORF 1- polyprotein																

PolyX	5	4	5	3	3	4	3	4	4	3	3	3	3	3	4	3	3	4	4	4	
9% C	45	45	45	45	45	45	45	43.3	50	55	55	50	55	55	55	55	55	53.3	51.6	51.6	
L%	23.3	30	33.3 3	25	26.6	35	30	33.3 3	28.3	30	31.6	21.6	26.6	28.3	33.3 3	26.6	28.3	28.3	26.6	28.3	,
V %	31.6	25	21.6	30	28.3 3	20	25	23.3	21.6	15	13.3	28.3 3	18.3	16.6	11.6	18.3	16.6	18.3	21.6	20	;
2%C	21.6	20	25	25	23.3	26.6	23.3 3	30	31.6	31.6	30	30	20	28.3	31.6	31.6	28.3	25	23.3	25	
9%	23.3	25	20	20	21.6	18.3	21.6	13.3	18.3	23.3	25	20	35	26.6	23.3 3	23.3	26.6	28.3	28.3	26.6	
X-Hyb Pot	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Tm	81.	81. 02	82. 77	81. 07	81. 77	79. 59	80. 53	80. 72	84. 17	85. 34	85. 66	83. 02	86. 2	86. 55	85. 53	86. 83	87. 13	85. 09	83. 94	84. 32	
End Distance	945	1243	1489	2292	2535	2953	3872	944	09	133	309	369	433	550	610	692	844	09	08	100	
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	
SEQ ID NO:	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	
BP Start	4138	3840	3594	2791	2548	2130	1211	15	668	826	650	590	526	409	349	190	115	431	411	391	
Target ID	gi 9626440:4- 5085	gi 9626440:100- 1057	gi 9626440;100- 1057	gi 9626440:100- 1057	gi 9626440:100- 1057	gi 9626440:1294 -1783	gi 9626440:1294 -1783	gi 9626440:1294 -1783													
Virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	Hepatitis E virus	
Product	ORF 1- polyprotein	Viral methyl- transferase	Peptidase C41	Peptidase C41	Peptidase C41																

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%C	W %	L%	5% C	PolyX
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	207	1545	09	288	81. 52	0	28.3 3	16.6	21.6	33.3 3	45	5
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	205	1546	09	290	80. 94	0	28.3 3	16.6	20	35	45	5
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	204	1547	09	291	80. 23	0	26.6	16.6	20	36.6	43.3	5
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	203	1548	09	292	80.	0	25	16.6	20	38.3	41.6	5
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	202	1549	09	293	79. 73	0	26.6	16.6	20	36.6	43.3	5
RNA dependent RNA pol.	Hepatitis E virus	gi 9626440:4191 -4684	201	1550	09	294	80. 02	0	25	16.6	21.6	36.6	41.6	5
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	135	1551	09	211	85. 04	0	18.3	35	20	26.6	53.3	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	134	1552	09	212	84. 93	0	18.3	33.3 3	20	28.3	51.6	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	133	1553	09	213	85. 04	0	20	33.3 3	18.3 3	28.3	53.3	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	132	1554	09	214	85. 22	0	21.6	33.3 3	16.6	28.3	55	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	131	1555	09	215	85. 04	0	21.6	31.6	16.6	30	53.3 3	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	130	1556	09	216	85. 04	0	23.3 3	30	16.6	30	53.3 3	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	129	1557	09	217	85. 75	0	25	30	15	30	55	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	142	8551	09	204	85. 2	0	15	40	20	25	55	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	141	6551	09	205	85. 22	0	15	40	20	25	55	4
ORF 3- hypo- thetical protein	Hepatitis E virus	gi 9626440:5109 -5453	140	1560	09	206	85. 92	0	16.6	38.3 3	20	25	55	4
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1661	1991	09	323	80. 69	0	20	25	30	25	45	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1660	1562	09	324	80. 56	0	18.3	25	31.6	25	43.3	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%C	∀ %	L%	2 9%	PolyX
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1659	1563	09	325	80. 31	0	18.3	25	31.6	25	43.3	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1658	1564	09	326	80. 37	0	18.3	26.6	30	25	45	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1657	1565	09	327	80. 47	0	18.3	26.6	30	25	45	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1656	1566	09	328	80. 12	0	16.6	26.6	30	26.6 7	43.3	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1655	1567	09	329	.6 <i>7</i> 78	0	16.6 7	28.3 3	28.3 3	26.6 7	45	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1654	1568	09	330	80. 15	0	15	28.3	30	26.6 7	43.3 3	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1653	1569	09	331	79. 86	0	15	28.3	30	26.6 7	43.3 3	3
ORF 2-capsid protein	Hepatitis E virus	gi 9626440:5123 -7105	1652	1570	09	332	79. 5	0	16.6	28.3 3	30	25	45	3
RNA dependent RNA pol.	WCCV1 RNA1	gi 52220883:75- 1925	1783	1571	09	69	81. 65	0	20	25	31.6	23.3 3	45	3
RNA dependent RNA pol.	WCCV1 RNA1	gi 52220883:75- 1925	1722	1572	09	130	80. 78	0	11.6	30	31.6	26.6	41.6	4
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1638	1573	09	214	80. 92	0	23.3	21.6	20	35	45	3
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1410	1574	09	442	80. 83	0	20	25	28.3 3	26.6 7	45	3
RNA dependent RNA pol.	WCCVI RNA1	gi 52220883:75- 1925	1350	1575	09	502	76. 41	0	11.6	23.3 3	35	30	35	3
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1290	1576	09	562	77. 91	0	16.6	21.6	28.3 3	33.3 3	38.3 3	3
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1230	1577	09	622	80. 63	0	13.3 3	30	20	36.6 7	43.3 3	3
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1170	1578	09	682	79. 55	0	15	26.6 7	23.3 3	35	41.6	3
RNA dependent RNA pol.	WCCVI RNAI	gi 52220883:75- 1925	1087	1579	09	292	81. 34	0	20	25	23.3 3	31.6 7	45	5
RNA dependent RNA pol.	WCCV1 RNA1	gi 52220883:75- 1925	666	1580	09	853	80. 88	0	15	30	26.6	28.3 3	45	4
Putative protease cofactor	BBWV I RNA I	gi 39163640:201 -1154	875	1581	09	80	81. 54	0	26.6	18.3	18.3	36.6	45	5
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	815	1582	09	140	81. 22	0	25	20	21.6 7	33.3 3	45	4
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	731	1583	09	224	80. 72	0	20	25	15	40	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	5%	2%C	₩	L%	5% C	PolyX
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	671	1584	09	284	81. 98	0	26.6	16.6	20	36.6	43.3	3
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640;201 -1154	609	1585	09	346	83. 3	0	30	15	30	25	45	9
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640;201 -1154	546	1586	09	409	82. 71	0	23.3 3	21.6	18.3 3	36.6 7	45	5
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	479	1587	09	476	81. 05	0	20	25	21.6	33.3 3	45	3
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	419	1588	09	536	79. 88	0	20	21.6	28.3	30	41.6	3
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640.201 -1154	330	1589	09	625	81. 68	0	28.3 3	16.6	26.6	28.3	45	4
putative pro- tease cofactor	BBWV 1 RNA 1	gi 39163640:201 -1154	252	1590	09	703	81. 33	0	20	25	23.3 3	31.6	45	2
NTP-binding protein	BBWV 1 RNA 1	gi 39163640:115 5-2924	1694	1591	09	LL	81. 2	0	25	20	15	40	45	4
NTP-binding protein	BBWV 1 RNA 1	gi 39163640:115 5-2924	1623	1592	09	148	82. 13	0	25	20	15	40	45	4
NTP-binding protein	BBWV 1 RNA 1	gi 39163640.115 5-2924	1553	1593	09	218	81 . 07	0	25	20	30	25	45	3
NTP-binding protein	BBWV I RNA I	gi 39163640;115 5-2924	1493	1594	09	278	80. 23	0	28.3	15	25	31.6	43.3	5
NTP-binding protein	BBWV 1 RNA 1	gi 39163640;115 5-2924	1431	1595	09	340	80. 25	0	28.3	16.6	31.6	23.3	45	5
NTP-binding protein	BBWV 1 RNA 1	gi 39163640:115 5-2924	1371	1596	09	400	79. 53	0	28.3 3	11.6	30	30	40	4
NTP-binding protein	BBWV 1 RNA 1	gi 39163640.115 5-2924	1310	1597	09	461	82. 34	0	21.6	23.3	28.3	26.6	45	5
NTP-binding protein	BBWV 1 RNA 1	gi 39163640:115 5-2924	1250	1598	09	521	79. 93	0	20	21.6	33.3 3	25	41.6	3
NTP-binding protein	BBWV 1 RNA 1	gi 39163640;115 5-2924	1113	1599	09	859	80. 52	0	21.6	21.6	26.6 7	30	43.3 3	3
NTP-binding protein	BBWV 1 RNA 1	gi 39163640:115 5-2924	1053	1600	09	718	81. 13	0	23.3 3	21.6	28.3 3	26.6	45	4
cysteine protease	BBWV 1 RNA 1	gi 39163640.300 3-3629	512	1601	09	116	80. 72	0	35	8.33	28.3	28.3	43.3	3
cysteine protease	BBWV I RNA I	gi 39163640:300 3-3629	466	1602	09	162	80. 95	0	28.3 3	15	26.6 7	30	43.3	2
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	426	1603	09	202	79. 43	0	23.3 3	18.3	28.3	30	41.6	4
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	335	1604	09	293	79. 61	0	20	20	30	30	40	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	J%	W%	L%	5% C	PolyX
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	295	1605	09	333	78. 88	0	15	23.3	26.6	35	38.3 3	4
cysteine protease	BBWV 1 RNA 1	gi 39163640;300 3-3629	251	1606	09	377	81. 6	0	21.6	23.3	25	30	45	4
cysteine protease	BBWV 1 RNA 1	gi 39163640;300 3-3629	211	1607	09	417	80. 36	0	15	26.6	28.3	30	41.6	4
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	171	1608	09	457	77.	0	25	10	33.3 3	31.6	35	3
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	131	1609	09	497	79. 67	0	30	13.3	31.6	25	43.3	3
cysteine protease	BBWV 1 RNA 1	gi 39163640:300 3-3629	91	1610	09	537	78. 55	0	25	15	28.3	31.6	40	9
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	2038	1611	09	09	79. 2	0	21.6	16.6	26.6	35	38.3 3	5
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1978	1612	09	120	79. 34	0	23.3 3	16.6	25	35	40	3
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1918	1613	09	180	77.	0	16.6	18.3	28.3	36.6	35	4
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1858	1614	09	240	79. 94	0	25	16.6	36.6	21.6	41.6	5
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1798	1615	09	300	80. 36	0	25	18.3	26.6	30	43.3 3	5
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1738	1616	09	360	78. 03	0	20	16.6	36.6	26.6	36.6	4
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1678	1617	09	420	80. 67	0	25	16.6	35	23.3	41.6	4
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1588	1618	09	510	81. 16	0	25	20	26.6	28.3	45	3
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1525	1619	09	573	81.	0	25	20	33.3 3	21.6	45	4
RNA- dependent RNA pol.	BBWV 1 RNA 1	gi 39163640:363 0-5726	1362	1620	09	736	81. 66	0	31.6	11.6	31.6	25	43.3	4
nucleocapsid	LNYV	gi 83659771:1-	1525	1621	09	66	77.	0	20	15	36.6	28.3	35	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%	W%	L%	ر د د	PolyX
protein		1623					34				7	3		
nucleocapsid protein	LNYV	gi 83659771:1- 1623	1465	1622	09	159	79. 32	0	31.6	10	30	28.3	41.6	3
nucleocapsid protein	TNAA	gi 83659771:1- 1623	1398	1623	09	226	82. 08	0	18.3 3	26.6 7	31.6	23.3	45	5
nucleocapsid protein	AANT	gi 83659771:1- 1623	1313	1624	09	311	80. 47	0	23.3 3	21.6	26.6 7	28.3 3	45	2
nucleocapsid protein	AANT	gi 83659771:1- 1623	1253	1625	09	371	76. 59	0	20	16.6	35	28.3 3	36.6	4
nucleocapsid protein	AANT	gi 83659771:1- 1623	1193	1626	09	431	79. 43	0	31.6	13.3 3	33.3 3	21.6	45	3
nucleocapsid protein	TNYV	gi 83659771:1- 1623	1125	1627	09	499	80. 41	0	31.6	13.3 3	28.3 3	26.6 7	45	3
nucleocapsid protein	TNYV	gi 83659771:1- 1623	1065	1628	09	655	81. 55	0	15	30	23.3	31.6	45	3
nucleocapsid protein	TNYV	gi 83659771:1- 1623	686	1629	09	635	81. 41	0	26.6 7	18.3	28.3	26.6 7	45	4
nucleocapsid protein	TNYV	gi 83659771:1- 1623	901	1630	09	723	81. 28	0	23.3 3	21.6 7	25	30	45	3
phospoprotein	TNYV	gi 83659771:163 1-2712	993	1631	09	06	74. 7	0	23.3 3	11.6	31.6	33.3 3	35	3
phospoprotein	AANT	gi 83659771:163 1-2712	933	1632	09	150	78. 41	0	25	15	31.6	28.3 3	40	2
phospoprotein	LNYV	gi 83659771:163 1-2712	873	1633	09	210	79. 22	0	25	15	31.6	28.3	40	4
phospoprotein	LNYV	gi 83659771:163 1-2712	738	1634	09	345	81. 57	0	20	25	41.6	13.3	45	4
phospoprotein	LNYV	gi 83659771:163 1-2712	652	1635	09	431	81. 09	0	23.3	21.6	31.6	23.3	45	3
phospoprotein	AANT	gi 83659771:163 1-2712	655	1636	09	524	80. 06	0	25	20	28.3	26.6 7	45	3
phospoprotein	TNYV	gi 83659771:163 1-2712	491	1637	09	592	78. 34	0	30	10	40	20	40	5
phospoprotein	TNYV	gi 83659771:163 1-2712	431	1638	09	652	80. 68	0	26.6 7	16.6	36.6 7	20	43.3 3	3
phospoprotein	LNYV	gi 83659771:163 1-2712	371	1639	09	712	77. 31	0	20	16.6 7	23.3	40	36.6	3
phospoprotein	AANT	gi 83659771:163 1-2712	311	1640	09	772	80. 9	0	25	20	26.6	28.3 3	45	2
gene"4b	LNYV	gi 83659771:272 0-3765	786	1641	09	09	80. 04	0	26.6 7	13.3 3	28.3	31.6	40	4
gene"4b	LNYV	gi 83659771;272	927	1642	09	120	80.	0	28.3	9'91	23.3	31.6	45	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	J%	₩%	L%	S%	PolyX
		0-3765					16		3	7	3	7		
gene"4b	TNYV	gi 83659771:272 0-3765	867	1643	09	180	79. 39	0	30	13.3	40	16.6	43.3	3
gene"4b	AANT	gi 83659771:272 0-3765	794	1644	09	253	81. 24	0	25	20	43.3 3	11.6	45	3
gene"4b	TNYV	gi 83659771.272 0-3765	734	1645	09	313	78. 57	0	21.6	18.3	35	25	40	3
gene"4b	AKNT	gi 83659771:272 0-3765	674	1646	09	373	74. 79	0	16.6	18.3 3	31.6	33.3 3	35	3
gene"4b	AANT	gi 83659771:272 0-3765	613	1647	09	434	80. 65	0	31.6	13.3 3	30	25	45	4
gene"4b	AKNT	gi 83659771:272 0-3765	553	1648	09	494	79. 78	0	23.3 3	20	23.3 3	33.3 3	43.3	3
gene"4b	AANT	gi 83659771:272 0-3765	491	6491	09	556	80. 43	0	0ε	15	30	25	45	4
gene"4b	AANT	gi 83659771.272 0-3765	431	1650	09	616	81. 19	0	21.6	23.3	30	25	45	3
matrix protein	TNYV	gi 83659771:377 3-4403	554	1651	09	78	77. 42	0	23.3 3	13.3	30	33.3 3	36.6	5
matrix protein	AANT	gi 83659771:377 3-4403	514	1652	09	118	80. 98	0	52	18.3 3	31.6	25	43.3 3	5
matrix protein	AANT	gi 83659771:377 3-4403	438	1653	09	194	78. 92	0	28.3 3	15	31.6	25	43.3	3
matrix protein	TNYV	gi 83659771:377 3-4403	391	1654	09	241	76. 19	0	23.3	11.6	38.3 3	26.6	35	3
matrix protein	LNYV	gi 83659771:377 3-4403	351	1655	09	281	79. 78	0	25	18.3	28.3	28.3	43.3	4
matrix protein	AKNT	gi 83659771:377 3-4403	308	9591	09	324	80. 81	0	23.3 3	21.6	20	35	45	4
matrix protein	AANT	gi 83659771:377 3-4403	244	<i>L</i> \$91	09	388	80. 6	0	23.3 3	21.6	30	25	45	4
matrix protein	AANT	gi 83659771:377 3-4403	203	8591	09	429	75. 23	0	20	15	33.3 3	31.6	35	4
matrix protein	AANT	gi 83659771:377 3-4403	163	6591	09	469	79. 2	0	21.6	18.3 3	18.3 3	41.6	40	4
matrix protein	AKNT	gi 83659771:377 3-4403	51	1660	09	581	81. 35	0	21.6	23.3	31.6	23.3 3	45	3
gene G	AANT	gi 83659771:441 2-6247	1777	1991	09	09	78. 09	0	26.6 7	11.6	38.3 3	23.3 3	38.3 3	4
gene G	LNYV	gi 83659771:441 2 - 6247	1717	1662	09	120	78. 28	0	25	15	26.6	33.3 3	40	2
gene G	LNYV	gi 83659771:441	1657	1663	09	180	79.	0	18.3	25	36.6	20	43.3	2

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	3%	V %	L%	5% C	PolyX
		2-6247					75		3		7		3	
gene G	LNYV	gi 83659771:441 2-6247	1597	1664	09	240	79. 25	0	21.6	16.6	46.6	15	38.3	4
gene G	LNYV	gi 83659771:441 2-6247	1531	1665	09	306	81. 5	0	23.3 3	21.6	21.6	33.3 3	45	3
gene G	LNYV	gi 83659771.441 2-6247	1448	1666	09	389	81. 56	0	25	20	30	25	45	4
gene G	LNYV	gi 83659771:441 2-6247	1365	1667	09	472	80. 43	0	26.6	18.3	38.3 3	16.6	45	3
gene G	LNYV	gi 83659771:441 2-6247	1236	1668	09	601	81. 23	0	25	20	30	25	45	4
gene G	LNYV	gi 83659771:441 2-6247	1160	1669	09	229	80. 45	0	35	8.33	30	26.6 7	43.3 3	3
gene G	LNYV	gi 83659771:441 2-6247	1100	1670	09	737	79. 98	0	21.6	20	26.6	31.6	41.6	3
RNA- dependent RNA pol.	TNAA	gi 83659771:627 8-12613	6101	1671	09	236	75. 47	0	18.3	16.6	31.6	33.3 3	35	3
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	6041	1672	09	296	80. 36	0	21.6	21.6	20	36.6	43.3	3
RNA- dependent RNA pol.	TNAA	gi 83659771:627 8-12613	5949	1673	09	388	81. 57	0	31.6	13.3	20	35	45	5
RNA- dependent RNA pol.	TNAA	gi 83659771:627 8-12613	2887	1674	09	450	80. 33	0	26.6	18.3	33.3 3	21.6	45	3
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	5827	1675	09	510	78. 62	0	26.6	16.6	30	26.6 7	43.3	4
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	5767	1676	09	570	77.	0	16.6	21.6	31.6	30	38.3	4
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	5707	1677	60	630	78. 97	0	21.6	18.3	36.6	23.3 3	40	3
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	5573	1678	60	764	81. 66	0	28.3 3	16.6	36.6	18.3	45	3
RNA- dependent RNA pol.	LNYV	gi 83659771:627 8-12613	5513	1679	09	824	77.	0	30	10	28.3	31.6	40	5

X																			
PolyX	c	ď	S	S	S	S	S	5	v	S	ď	4	S	5	4	4	ю	2	5
2% C	43.3 3	36.6	38.3 3	36.6 7	36.6 7	35	35	35	35	35	36.6 7	45	45	45	45	45	43.3	45	45
L%	21.6	45	43.3	45	45	45	45	43.3 3	41.6	40	38.3 3	21.6	20	26.6	26.6 7	15	33.3 3	26.6	23.3
V %	35	18.3	18.3	18.3	18.3	20	20	21.6	23.3	25	25	33.3 3	35	28.3	28.3	40	23.3	28.3	31.6
3%C	15	11.6	13.3	13.3	13.3	11.6	11.6	11.6	11.6	11.6	11.6	21.6	20	15	25	16.6	16.6	13.3	21.6
9%	28.3	25	25	23.3	23.3	23.3	23.3	23.3	23.3	23.3	25	23.3	25	30	20	28.3 3	26.6	31.6	23.3 3
X-Hyb Pot																			
Tm X	79. 0 84 0	77. 0	77. 0	77 0	76. 0	76. 0	76. 0	75. 0 88	76. 0	76. 0 29 0	76. 0	80. 0	81. 0	80. 0	82. 0	81. 0	81. 0 31 0	81. 0	81. 0
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End Distance	914	09	61	62	63	64	65	73	74	75	92	498	559	632	872	1080	1140	1284	1350
e th																			
Probe Length	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09	09
SEQ ID NO:	1680	1681	1682	1683	1684	1685	1686	1687	1688	1689	1690	1691	1692	1693	1694	1695	1696	1697	1698
BP Start	5423	128	127	126	125	124	123	115	114	113	112	1029 6	1023 5	1016 2	9922	9714	9654	9510	9444
Target ID	gi 83659771:627 8-12613	gi 83659771:126 21-12807	gi 985578255 gb KU497555.1	gi 985578255 gb KU497555.1	gi 985578255 gb KU497555.1	gi 985578255 gb KU497555.1	gi 985578255 gb KU497555.1												
Virus	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	LNYV	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015	Zika Brazil- ZKV2015
Product	RNA- dependent RNA pol.	5' trailer RNA	NS5 protein	NS5 protein	NS5 protein	NS5 protein	NS5 protein	NS5 protein	NS5 protein	NS5 protein									

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	%G	%C	%A	%T	2% C	PolyX
NS5 protein	Zika Brazil- ZKV2015	gi 985578255 gb KU497555.1	9383	1699	09	1411	78. 37	0	23.3 3	15	43.3 3	18.3	38.3 3	5
NS5 protein	Zika Brazil- ZKV2015	gi 985578255 gb KU497555.1	9288	1700	09	1506	81. 82	0	25	20	36.6	18.3	45	3
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	1034 0	1701	09	336	81. 2	0	26.6	18.3	26.6	28.3	45	3
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	1027 7	1702	09	399	81. 27	0	25	20	33.3 3	21.6	45	4
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	1016 8	1703	09	809	80. 62	0	30	15	28.3 3	26.6 7	45	5
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	8266	1704	09	748	82. 48	0	20	25	28.3 3	26.6 7	45	4
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	9720	1705	09	956	81. 39	0	28.3 3	16.6	40	15	45	4
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	0996	1706	09	1016	81. 31	0	26.6 7	16.6 7	23.3 3	33.3 3	43.3 3	3
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	9156	1707	09	1160	81. 05	0	31.6	13.3 3	28.3 3	26.6 7	45	2
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	9450	1708	09	1226	81. 53	0	23.3 3	21.6	31.6	23.3 3	45	5
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	6886	1709	09	1287	78. 37	0	23.3 3	15	43.3 3	18.3	38.3 3	5
NS5 protein	Zika PRVABC59	gi 984874581 gb KU501215.1	9295	1710	09	1381	81. 05	0	26.6 7	18.3 3	36.6 7	18.3 3	45	3
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	1027 4	1711	09	101	81. 2	0	26.6 7	18.3 3	26.6	28.3 3	45	3
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	$1021 \\ 1$	1712	09	164	81. 27	0	25	20	33.3 3	21.6	45	4
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	1010 2	1713	09	273	80. 62	0	30	15	28.3 3	26.6 7	45	5
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	7986	1714	09	513	82. 48	0	20	25	28.3 3	26.6 7	45	4
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	9654	1715	09	721	81. 39	0	28.3 3	16.6	40	15	45	4
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	9594	1716	09	781	81. 31	0	26.6 7	16.6	23.3 3	33.3 3	43.3 3	3
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	9450	1717	09	925	81. 05	0	31.6 7	13.3 3	28.3 3	26.6 7	45	2
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	9384	1718	09	991	81. 53	0	23.3	21.6	31.6	23.3	45	5

Product	Virus	Target ID	BP	SEQ ID	Probe	End	Tm	X-Hyb	9%	%C	%A	1%	9%	PolvX
NS5 protein	Zika Z1106033	gi 973447404 gb	Start 9323	NO:	Length	Distance 1052	78.	F01	23.3	15	43.3	18.3	38.3	
Inchipid Cevi		KU312312.1	7367	1/17	8	7601	37		8		8	3	6	
NS5 protein	Zika Z1106033	gi 973447404 gb KU312312.1	9229	1720	09	1146	81. 05	0	26.6 7	18.3 3	36.6 7	18.3 3	45	3
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	1027 4	1721	09	375	80. 74	0	23.3 3	21.6 7	33.3 3	21.6	45	4
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	1013 9	1722	09	510	80. 62	0	28.3 3	16.6	30	25	45	5
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	0066	1723	09	749	82. 48	0	20	25	28.3 3	26.6 7	45	4
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9695	1724	09	957	81. 39	0	28.3 3	16.6	40	15	45	4
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9632	1725	09	1017	81. 31	0	26.6 7	16.6	23.3 3	33.3 3	43.3 3	3
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9488	1726	09	1161	81. 05	0	31.6	13.3	28.3 3	26.6 7	45	2
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9422	1727	09	1227	81. 53	0	23.3	21.6	31.6	23.3 3	45	5
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9361	1728	09	1288	78. 37	0	23.3 3	15	43.3 3	18.3 3	38.3 3	5
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9596	1729	09	1353	82. 74	0	21.6	23.3 3	38.3 3	16.6	45	5
NS5 protein	Zika SSABR1	gi 992324757 gb KU707826.1	9190	1730	09	1459	80. 12	0	30	15	31.6	23.3 3	45	2
SUTR	ZikaSPH2015	gb KU321639.1 : 1-105	46	1731	09	09	78. 39	0	25	15	30	30	40	4
SUTR	ZikaSPH2015	gb KU321639.1 : 1-105	37	1732	09	69	78. 43	0	26.6 7	11.6	35	26.6 7	38.3 3	4
capsid	ZikaSPH2015	gb KU321639.1 : 106-480	232	1733	09	144	77. 34	0	21.6	13.3 3	41.6	23.3 3	35	3
capsid	ZikaSPH2015	gb KU321639.1 : 106-480	216	1734	09	160	79. 12	0	28.3 3	11.6	41.6	18.3 3	40	9
propeptide	ZikaSPH2015	gb KU321639.1 : 478-750	100	1735	09	174	80. 99	0	23.3 3	21.6	28.3 3	26.6 7	45	3
propeptide	ZikaSPH2015	gb KU321639.1 : 478-750	91	1736	09	183	78. 98	0	23.3 3	16.6	31.6	28.3 3	40	2
membrane protein	ZikaSPH2015	gb KU321639.1 : 751-975	162	1737	09	64	81. 94	0	20	25	31.6	23.3 3	45	5
membrane protein	ZikaSPH2015	gb KU321639.1 : 751-975	148	1738	09	78	80. 99	0	25	20	26.6 7	28.3 3	45	5
envelope protein	ZikaSPH2015	gb KU321639.1 : 976-2490	1442	1739	09	74	80. 57	0	25	20	16.6	38.3	45	5

•	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	2%	V%	L%	ر 3% د	PolyX
Ń	ZikaSPH2015	gb KU321639.1 : 976-2490	1322	1740	09	194	81. 61	0	26.6	15	26.6 7	31.6	41.6	5
ΙŻ	ZikaSPH2015	gb KU321639.1 : 976-2490	1069	1741	09	447	80.	0	21.6	23.3	33.3 3	21.6	45	4
Z	ZikaSPH2015	gb KU321639.1 : 976-2490	556	1742	09	096	79. 05	0	23.3	18.3	23.3	35	41.6	4
Ϊ́	ZikaSPH2015	gb KU321639.1 : 976-2490	318	1743	09	1198	82. 15	0	26.6	18.3	28.3	26.6	45	5
Ż	ZikaSPH2015	gb KU321639.1 : 2491-3576	1023	1744	09	64	79. 96	0	21.6	21.6	31.6	25	43.3	2
Z	ZikaSPH2015	gb KU321639.1 : 2491-3576	648	1745	09	439	80. 43	0	26.6	16.6	38.3 3	18.3	43.3	4
Ϊ́	ZikaSPH2015	gb KU321639.1 : 2491-3576	479	1746	09	809	77. 05	0	26.6	13.3	26.6 7	33.3 3	40	3
Ž	ZikaSPH2015	gb KU321639.1 : 2491-3576	221	1747	09	998	81. 68	0	28.3	16.6	31.6	23.3	45	5
Z	ZikaSPH2015	gb KU321639.1 : 3577-4230	507	1748	09	148	80. 85	0	25	20	28.3	26.6	45	4
Z	ZikaSPH2015	gb KU321639.1 : 3577-4230	503	1749	09	152	80. 03	0	25	18.3	28.3	28.3 3	43.3	4
Z	ZikaSPH2015	gb KU321639.1 : 3577-4230	204	1750	09	451	80. 55	0	23.3	21.6	25	30	45	3
Ż	ZikaSPH2015	gb KU321639.1 : 4231-4662	146	1751	09	287	81. 46	0	28.3	16.6	40	15	45	5
Z	ZikaSPH2015	gb KU321639.1 : 4231-4662	141	1752	09	292		0	28.3	15	40	16.6	43.3	5
Z	ZikaSPH2015	gb KU321639.1 : 4231-4662	136	1753	09	297	81. 32	0	30	15	36.6 7	18.3	45	5
Z	ZikaSPH2015	gb KU321639.1 ; 4663-6471	8191	1754	09	192	81. 23	0	26.6 7	18.3 3	36.6 7	18.3	45	3
Z	ZikaSPH2015	gb KU321639.1 ; 4663-6471	1415	1755	09	395	.08 79	0	15	30	28.3 3	26.6 7	45	3
Z	ZikaSPH2015	gb KU321639.1 : 4663-6471	1013	95/1	09	797	82. 73	0	28.3 3	9.91 7	28.3 3	26.6 7	45	5
Z	ZikaSPH2015	gb KU321639.1 : 4663-6471	629	1321	09	1131	81. 83	0	18.3 3	26.6 7	33.3 3	21.6	45	3
Z	ZikaSPH2015	gb KU321639.1 : 6472-6912	961	85/1	09	246	81. 88	0	33.3 3	9.11.6	23.3 3	31.6	45	5
Z	ZikaSPH2015	gb KU321639.1 ; 6472-6912	238	65/1	09	204	87. 21	0	33.3 3	21.6	18.3 3	26.6 7	55	4
Z	ZikaSPH2015	gb KU321639.1 : 6472-6912	59	1760	09	383	86. 35	0	28.3	26.6	28.3 3	16.6	55	3

Product	Virus	Target ID	BP Start	SEQ ID NO:	Probe Length	End Distance	Tm	X-Hyb Pot	9%	J%	W%	L%	С 9%	PolyX
NS4B protein	ZikaSPH2015	gb KU321639.1 : 6913-8418	1395	1761	09	112	80. 14	0	23.3 3	21.6	33.3 3	21.6	45	5
NS4B protein	ZikaSPH2015	gb KU321639.1 : 6913-8418	889	1762	09	819	80. 74	0	23.3 3	21.6	28.3 3	26.6	45	3
NS4B protein	ZikaSPH2015	gb KU321639.1 : 6913-8418	425	1763	09	1082	80. 52	0	26.6	16.6	33.3 3	23.3	43.3 3	3
NS4B protein	ZikaSPH2015	gb KU321639.1 : 6913-8418	1	1764	09	1506	80. 98	0	31.6	13.3 3	38.3 3	16.6	45	3
NS5 protein	ZikaSPH2015	gb KU321639.1 : 8419-10374	1883	1765	09	74	80. 74	0	23.3	21.6	33.3 3	21.6	45	4
NS5 protein	ZikaSPH2015	gb KU321639.1 : 8419-10374	1241	1766	09	716	81. 31	0	26.6	16.6	23.3	33.3 3	43.3	3
NS5 protein	ZikaSPH2015	gb KU321639.1 : 8419-10374	582	1767	09	1172	79. 51	0	30	15	35	20	45	3
3UTR	ZikaSPH2015	gb KU321639.1 : 10378-10676	239	1768	09	61	84. 45	0	40	15	25	20	55	4
3UTR	ZikaSPH2015	gb KU321639.1 : 10378-10676	230	1769	09	02	84. 24	0	33.3 3	21.6	23.3 3	21.6	55	4

 \overline{WCCV} - White clover cryptic virus; BBWV - Broad bean wilt virus; LNYV - Lettuce necrotic yellows virus

Table 2. Viral pathogens used in testing the Pathogen Chip

Virus	Type/Strain	Source	References
CHIKV	R91064	FDA/CBER Lot Release Panels*	
HAV	SD11	Dr. Farci Lab	
HCV	Genotype 1b	Sera Care (Sera Care, Milford, MA)	
HCV	Genotype 2a	Sera Care (Sera Care, Milford, MA)	
HCV	Genotype 3	Sera Care (Sera Care, Milford, MA)	
HEV	Genotype 3a	WHO Standard	
HIV-1	Group M, Subtype B	FDA/CBER Lot Release Panels	1,2
HIV-2	Subtype B	FDA/CBER Lot Release Panels	3
DENGUE	Serotype 1, 2, 3 and 4	Aedes albopictus C6/36 cell culture	4
HTLV-I		ZeptoMetrix	
HTLV-II		ZeptoMetrix	
WEST	NY99	Cell culture	5
NILE			
ZIKA	PRVABC62	FDA/CBER Lot Release Panels	
ZIKA	FSS13025	FDA/CBER Lot Release Panels	

^{*} The FDA Center for Biologics Evaluation and Research (CBER), Division of Emerging and Transfusion Transmitted Diseases produces and makes available to blood donor screening test manufacturers panels which are sets of vialed human plasma containing virus particles that are carefully quantified for evaluating virus detection devices. Each set has several vials each one a different virus concentration and some with virus-free plasma. These panels are also used to test each new lot of a licensed blood donor screening device for release to the public, hence they are called Lot Release Panels. There are separate panels prepared for each type of virus.

- 1) Davis et al., J Virol Methods, 107:37-44 (2003)
- 2) Lee et al., J Virol Methods, 137:287-291 (2006)
- 3) Lee et al., J Virol Methods, 137:287-291 (2005).
- 4) Dong et al., J Appl Microbiol, 120:1119-1129 (2016).
- 5) Grinev et al., J Virol Methods, 154:27-40 (2008).

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Nucleic acids from positive plasma and from NATtrol were extracted using the DynabeadsTM
SILANE Viral NA Kit (ThermoFisher Scientific, Waltham, MA) according to the manufacturer's protocol.
cDNA from random-primed, reverse-transcribed total RNA was performed with the Ovation Pico
WTA System (NuGEN, San Carlos, CA) using the manufacturer's recommended protocols and input
amounts. For this study, the Agilent SureTag Labeling Kit was used for generating Cy3 labeled cDNA
targets. Labeled cDNA was purified with SureTag Kit spin columns and specific activities (degree of
labeling) were calculated for use in hybridization reactions. A master mix containing 10X blocking agent
and 2X GE hybridization buffer HI-RPM, was added to 3-5 μg of labeled cDNA, denatured, and hybridized
to arrays under 8-chamber gasket slides at 65°C with 20-rpm rotation for 24 hours in an Agilent

hybridization oven. Arrays were processed using wash procedure A and scanned on an Agilent SureScan G4900DA microarray scanner using 5-µm resolution.

Microarray-based platform data analysis: After scanning, microarray images were analyzed using Agilent Feature Extraction software (Agilent Technologies, Inc., Santa Clara, CA) with default protocols and settings. Average pixel intensity and subtraction of local background for each feature was calculated. Images were manually examined to note any arrays affected by high background, scratches, or other technical artifacts. Probe sets associated with low signal intensity or bad quality features were considered unreliable and excluded from the analysis. Feature intensities for Cy3 channels were imported into the Partek Genomics Suite (Partek Inc., St. Louis, MO, USA).

First, microarray analysis was performed by ranking the highest signal intensity probes by the mean of the set of probes defining each pathogen on the platform. Next, an experimental threshold was defined as a log ratio of signal intensity mean for the set of probes defining each pathogen and the mean of the Agilent control probes set. The threshold was applied to all the arrays tested to define the final parameters for test validation.

15 RT-qPCR Validation

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Altona RT-qPCR: CHIKV, DENV 1-4 and ZIKV positive specimens were quantified using the Altona RealStar RT-qPCR kit (Altona Diagnostic GmbH., Hamburg, Germany) according to the manufacturer's instructions. The positive control and the internal control were provided by the manufacturer. Serial dilutions of CHIKV (ATCC VR-3246SD), DENV (ATCC VR-3231SD), and ZIKV (ATCC VR-1843DQ) quantitative genomic RNA (specification range: 1x10⁵ - 1x10⁶ copies/μL) obtained from ATCC (American Type Culture Collection Manassas, VA) were prepared to generate a standard curve for copy number quantification.

Primer Design (Genesig) RT-qPCR: HAV (target/5' NCR), HCV (5'UTR), HEV (ORF2), HIV-1 (target/POL), HIV-2 (target/POL), HTLVI (target/POL), HTLVII (target/POL), and WNV (5'UTR) positive specimens were quantified using the Primer Design Genesig kit (Primerdesign Ltd, United Kingdom) according to the manufacturer's protocol (OneStep RT-qPCR protocol). Each kit contained a positive control template for the PCR set up and for copy number determination (generated serial dilutions for the standard curve).

The RT-qPCR assays were performed on a ViiA7 Applied Biosystems real-time PCR system (Thermo Fisher Scientific Inc., Waltham, MA, USA). Each sample was tested in duplicate and the mean C_{q} value was calculated.

Example 2

Microarray Design, Specificity, and Validation

Microarray design: The pathogen chip design strategy was to cover all high priority blood-borne RNA viruses (retroviruses and both positive- and negative-strand RNA viruses) using multiple probes to independent targets sites in the genome of each species. In total, 1,769 unique viral oligonucleotides derived

from 16 distinct viral genomes (Table 1) were included that allowed discrimination of pathogens at the level of species, subtypes and genotypes. The microarray was supplemented with an additional number of predesigned GE array probes for 906 genes from the human genome, 84 ERCC probes and 120 probes specific for plant viruses representing negative controls (Table 3).

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Table 3. Probe distribution on pathogen chip

Probe group type	Number of targets	Number of probes	Purpose
All spot	1010	14,716	RNA pathogens coverage and internal controls
Pathogen Specific (not replicated)	17	1,769	Probes intensity analysis of pathogen specific genes
Internal Control (replicated 10 times)	902	902	Agilent requirement for probes normalization
ERCC probes (replicated 45 times)	84	84	Determination of intra-probe variance
Negative Control (not replicated)	3	120	Determination of probes cross reactivity

The design included multiple gene targets for each pathogen genome in order to select the best probes for the final platform design. The design strategy was to balance the number of probes for each pathogen with a final count of 90-110 probes each. Probes selected in the final design generated a more intense signal and produced higher percentage coverage of the specific genome across the different experiments (FIG. 1A).

Microarray specificity: One of the challenges impacting the sensitivity of microarray based multipathogen nucleic acid detection in blood specimens is the relatively small concentration of target nucleic acids compared to a high background concentration of human DNA. A novel workflow was designed, combining two different applications (Agilent and Nugen), that had not been previously combined, to address this challenge. Typically, the Agilent amplification WT kit (Oligo dT) is used to amplify total RNA, with a minimum nucleic acid requirement of 25 nanograms, and produces a cRNA final product that is labelled with Cy3 fluorophore. The workflow was modified using a method that generates amplified cDNA from as little as 500 picograms of target viral RNA. One single-primer isothermal amplification using Nugen Ribo-SPIA technology was combined with the Agilent Genomic DNA Enzymatic Labeling Kit for generating Cy3 labeled cDNA. This kit was not previously developed for single color RNA probes and produces 300% the amplified product compared to the standard methodology (FIG. 1B, FIG. 2A). Nearly all samples were detected on the platform and all probes generated a strong signal specific for each positive plasma specimen analyzed. No specific signal was produced by negative control plasma (FIG. 2B). Random non-specific intensity signal was produced in only a few arrays. This indicated that the generation of cDNA instead of amplified RNA followed by Cy3 labelling and hybridization based on a DNA application was successful (FIG. 2C).

Analysis strategies: Quality of signals generated by probes for each species was assessed according to two experimental criteria: 1) defining a threshold able to distinguish a true signal from its background; and 2) defining true positives only when 50% of probes generated a signal above the set threshold. These two levels of data analysis were needed to detect positive probes in the presence of multipathogen testing at the same time and at different concentrations.

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The threshold was defined as the log ratio between the signal intensity mean for each pathogen specific probe set and the mean of the Agilent control group probe set. After comparing the results of the same set of probes across different arrays and selecting the probes showing an inter-array reproducibility, an experimental threshold value was defined as follows: Log Ratio ≤ 1 negative; Log Ratio ≥ 1.0 to ≤ 1.5 borderline; Log Ratio ≥ 1.5 positive.

Data analysis at the individual probe level was also performed to assess if the tested samples were false positives. Only when at least 50% of specific probes had Log Ratio >1.5 was the test considered valid (FIG. 1C).

For nearly all borderline results, only 20-25% of the specific probes showed mean intensity in the correct range, so the test was defined negative. For positive results (Log Ratio >1.5) more than 50% of the specific probes set were in the correct range. One example was an HCV 1a positive plasma samples test that was detected by 110 out of 110 probes at a concentration of 10⁵ copies/mL, 90 out of 110 probes at a concentration of 10⁴ copies/mL, and 70 out of 110 probes at a concentration of 10³ copies/mL. On average, at 10² copies/mL more than 50% of the probes were generating a fluorescence signal above the set threshold.

Data from more than 168 tested samples (one or multiple targets per array) showed consistent results. The mean of the probes specific for any positive plasma sample was always at least 10-fold higher than the mean of internal control probes (background), showing a wide probe population range of intensity. As shown in Table 4 and Table 5, the Log Ratio was above 1.5 for all the pathogens tested at a concentration of 10^2 copies/mL and there were no cross reactions with other probes across the platform.

Microarray sensitivity: HAV, CHIKV, DENV1-4, HCV Genotypes 1a, 2b, and 3, HIV-1,2 and WNV strain NY99 had 10² copies/mL limits of detection. The lowest detectable level for HEV was 10⁴ copies/mL. The analytical sensitivity for each assay was determined using a concentration range based on the clinical requirement for pathogen detection. There were no false negatives or false positives when testing the positive plasma. In the presence of very low pathogen concentrations, the log ratio was at the borderline level so the results were qualified according to double level analysis (at least 50% of the probes generated a fluorescence signal above the set threshold). In the presence of negative plasma samples, the log ratio value was always negative (Table 4).

A mix of different positive plasma samples at different concentrations was simultaneously tested in a single experiment. Four different combinations were generated. The multi-pathogens-mixes were composed of 8 (CHIKV, DEN3, DEN1, HAV, HCV1a, HEV, WNV and ZIKV), 4 (CHIKV, DEN1, ZKV, WNV), 4 (DENV3, HAV HCV1a HEV) and 3 (CHIKV, DEN1, ZIKV) different pathogens, respectively at a concentration range from 10⁵ to 10³ copies/mL. (Table 6).

Table 4. Test results based on Log ratio

	ž	DEN1	DEN2	DEN3	DEN4	НАУ	HCV1a	HCV2a	HCV3	HEV	HIV-1	HIV-2	HTLVI	HTLVII	NN/	ZKV	2020/ S
Ç	2.42	-1.15	-1.22	-0.04	-0.28	-0.50	-0.24	-0.35	-0.56	-0.02	-0.99	-0.68	-0.42	96:0-	-0.97	-0.20	96.0-
DEN1	-0.12	1.60	-0.33	60.0	0.14	-0.08	-0.20	-0.31	-0.52	0.46	-0.76	-0.55	-0.28	-0.76	-0.53	00.00	98.0-
DEN2	-0.24	-0.82	1.84	-0.30	-0.25	-0.24	-0.17	-0.28	-0.49	-0.11	-1.13	-0.89	-0.52	-0.84	-1.00	-0.28	-1.01
DEN3	0.03	-0.19	-0.02	1.62	-0.24	-0.28	-0.24	-0.34	-0.55	0.01	-0.95	-0.81	-0.56	-0.91	-0.22	0.05	-0.96
DEN4	0.07	-0.31	-0.64	0.18	1.80	-0.64	-0.17	-0.28	-0.49	-0.20	-1.02	-0.80	-0.66	-1.05	-0.30	-0.36	-1.07
НАУ	-0.06	-0.97	-1.24	-0.25	-0.34	2.97	-0.21	-0.31	-0.52	0.35	-0.78	-0.47	-0.35	-0.71	-1.22	-0.04	-0.69
HCV1	0.46	-0.53	-0.55	0.63	95.0	0.26	2.91	2.80	2.59	0.79	-0.30	0.94	0.44	-0.05	-0.43	09:0	-0.37
HCV2	0.47	-0.60	-0.72	99.0	0.31	60.0	2.16	2.85	1.84	92.0	-0.53	0.65	-0.10	-0.37	-0.05	0.50	-0.32
HCV3	0.39	-0.73	-0.77	90.0	90.0	-0.07	2.63	2.53	2.32	0.34	-0.28	0.92	0.02	-0.51	-0.68	0.28	-0.46
HEV	0.41	-0.62	-0.63	0.23	0.35	1.06	-0.14	-0.24	-0.45	1.89	-0.31	-0.17	0.10	-0.04	-0.51	0.54	-0.39
HIV1	96.0	0.55	0.08	0.77	95.0	0.01	0.05	-0.06	-0.27	1.07	1.89	0.46	-0.22	90.0	0.13	0.92	0.23
HIV2	-0.13	-0.90	-0.94	0.02	-0.29	-0.07	-0.09	-0.20	-0.41	0.23	0.91	1.68	-0.07	-0.44	-0.75	60.0	-0.66
HTLVI	-0.57	-1.29	-1.43	-0.35	-0.55	-0.51	-0.06	-0.17	-0.38	-0.21	-1.08	-0.87	2.67	0.88	-1.47	-0.15	-0.99
HTLVII	-0.21	-1.11	-1.19	-0.45	-0.40	-0.21	0.19	0.08	-0.13	-0.09	-0.92	-0.59	0.38	3.30	-1.13	-0.10	-0.86
NNN	0.10	-0.50	-0.70	0.21	-0.34	-0.33	-0.19	-0.29	-0.51	0.25	-0.62	-0.52	-0.40	-0.64	2.24	00.00	-0.82
ZKV	-0.29	-0.64	-0.92	-0.49	-0.41	-0.45	0.12	0.26	0.32	0.68	96.0-	-0.68	-0.52	-0.78	0.16	2.07	-0.83
																	J'17

CK, Chikungunya virus; DEN, dengue; HAV, hepatitis A virus; HCV, hepatitis C virus; HEV, hepatitis E virus; HIV, human immunodeficiency virus; HTLV, Human T-cell lymphotropic

virus; WNV, West Nile Virus; ZKV, Zika Virus; NC, negative control.

Table 5. Multi-pathogen mix test results based on Log ratio

	MPM1	MPM2	MPM3	MPM4
CHIKV	3.42	3.37	0.24	2.25
DEN1	3.14	3.10	1.80	2.45
DEN2	1.11	1.10	-0.23	0.35
DEN3	2.72	1.19	3.00	0.51
DEN4	1.31	1.19	0.83	0.59
HAV	1.33	0.12	2.18	-1.13
HCV-1a	2.53	0.61	2.72	-0.59
HCV-2a	2.16	0.66	2.44	-0.65
HCV-3	2.45	0.65	2.60	-0.72
HEV	1.64	0.67	1.21	-0.71
HIV-1	1.05	1.24	1.11	-0.36
HIV-2	0.13	0.24	0.17	-0.81
HTLV-I	-0.17	0.06	-0.07	-1.37
HTLV-II	-0.02	0.12	-0.09	-1.07
WNV	1.63	1.65	0.11	-0.03
ZKV	3.09	3.04	0.30	1.98
		HCV-1a, H	EV, DEN3, I	DEN1,
ZKV, WNV				
		I, ZKV, WN		
MPM3 = H.	AV, HEV, D	EN3, HCV-1	a	
MPM4= CH	IIKV, ZKV,	DEN1		

Table 6. Pathogen Chip performance based plasma panel test results

Pathogen	Copies/mL	pos/total	qPCR Validation
Chikungunya	10^3	1/1	Y
Chikungunya	10^2	4/4	Y
Denguel	10^3	3/3	Y
Dengue1	10^2	2/2	Y
Dengue1	10^1	0/1	Y
Dengue2	10^3	3/3	Y
Dengue2	10^2	3/3	Y
Dengue2	10^1	0/1	Y
Dengue3	10^3	3/3	Y
Dengue3	10^2	3/3	Y
Dengue3	10^1	0/1	Y
Dengue4	10^3	3/3	Y
Dengue4	10^2	3/3	Y
Dengue4	10^1	0/1	Y
HAV	10^3	2/2	Y
HAV	10^2	2/2	Y
HCV-1a	10^3	3/3	Y
HCV-1a	10^2	3/3	Y

Pathogen	Copies/mL	pos/total	qPCR Validation
HCV-2a	10^2	2/2	Y
HCV-3	10^2	2/2	Y
HEV	10^4	3/3	Y
HEV	10^3	0/2	Y
HEV	10^2	0/2	NA
HIV-1	10^3	2/2	У
HIV-1	10^2	2/2	У
HIV-2	10^3	3/3	У
HIV-2	10^2	3/3	У
HTLV-I	10^3	2/2	у
HTLV-I	10^2	2/2	у
HTLV-II	10^3	2/2	У
HTLV-II	10^2	2/2	У
WNV (NY99)	10^5	1/1	у
WNV (NY99)	10^4	1/1	у
WNV (NY99)	10^3	3/3	у
WNV (NY99)	10^2	4/4	у
WNV (NY99)	10^1	0/2	NA
ZIKA PRVABC60	10^3	3/3	Y
ZIKA PRVABC61	10^2	3/3	Y
ZIKA PRVABC62	10^1	0/2	Y
ZIKV FSS13025	10^3	3/3	Y
ZIKV FSS13025	10^2	3/3	Y
ZIKV FSS13025	10^1	0/2	Y
MPM1	10^5 -10^3	3/3	у
MPM2	10^5 -10^3	3/3	у
MPM3	10^5 -10^3	3/3	у
MPM4	10^5 -10^3	3/3	у
NA= not applicable	·		

Among the 99 positive samples tested at a concentration ranking from 10⁵ to 10² copies/mL, 92 out 92 samples were correctly detected. Only HEV testing resulted correct detection in 3 out of 7 positive samples (42%) at a final concentration of 10⁴ copies/mL. No specific signal was detected below this value. There were 21 positive samples that were not detected because the concentration was below the limit of detection of the platform (<10² copies/mL). In all four mix combinations all pathogens were detected without interference among the targets.

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All of the samples tested (single or multiple pathogens at the same time) were performed at least 3 times each, with at least a week interval between the experiments, in order to test the reproducibility of the results. The consistency of positive results across the different arrays confirmed that the array design together with the double level analysis model performed well.

Validation of the limit of microarray data by RT-qPCR: Microarray-based pathogen chip results were confirmed by RT-qPCR of the RNA aliquots used for testing. All positive results were confirmed and the copy numbers for each pathogen were calculated to define the limit of the detection for each species on the array (Table 7).

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Table 7. Validation of Pathogen Chip detection results

Virus	Pathogen Chip Results	qPCR Ct Value	Virus Copy No.
CHIKV	POS	26.9	3.1×10^3
CHIKV	POS	31.6	1.4×10^{2}
CHIKV	POS	31.5	1.6×10^2
CHIKV	POS	29.4	6.3×10^2
CHIKV	POS	29.7	5.8×10^2
DENGUE-1	POS	31.1	2.3×10^{3}
DENGUE-1	POS	34.4	3.0×10^2
DENGUE-1	NEG	38.7	41
DENGUE-2	POS	29.1	8.4×10^3
DENGUE-2	POS	35.9	1.2×10^2
DENGUE-2	NEG	38.9	18
DENGUE-3	POS	29.3	7.1×10^3
DENGUE-3	POS	32.7	8.4×10^2
DENGUE-3	NEG	37.3	31
DENGUE-4	POS	30.3	3.3×10^3
DENGUE-4	POS	34.2	2.6×10^2
DENGUE-4	NEG	37.0	79
HAV	POS	28.4	3.2×10^3
HAV	POS	39.1	2.8×10^3
HAV	POS	29.2	8.2×10^{2}
HAV	POS	32.2	1.2×10^2
HCV-1a	POS	26.2	4.1×10^3
HCV-1a	POS	31.4	1.6×10^2
HCV-2a	POS	27.4	3.8×10^3
HCV-2a	POS	32.1	1.8×10^{2}
HCV-3	POS	33.1	1.4×10^2
HEV	POS	25.4	1.9×10^4
HEV	NEG	28.4	1.8×10^3
HIV-1	POS	27.3	4.6×10^3
HIV-1	POS	32.8	1.6×10^2
HIV-2	POS	27.4	$4.3x10^3$
HIV-2	POS	30.7	1.8×10^2
HTLV-I	POS	28.7	3.9×10^3
HTLV-I	POS	28.3	2.9×10^{2}
HTLV-II	POS	25.574	$2.7x10^3$
HTLV-II	POS	29.289	2.4×10^2
WNV (NY99)	POS	21.5	1.9×10^5
WNV (NY99)	POS	24.5	1.5×10^4
WNV (NY99)	POS	27.6	2.1×10^{3}
WNV (NY99)	POS	31.4	1.0×10^{2}
ZIKA PRVABC60	POS	26.2	1.5×10^3
ZIKA PRVABC60	POS	30.1	1.2×10^{2}
ZIKA PRVABC60	NEG	31.8	41

Virus	Pathogen Chip Results	qPCR Ct Value	Virus Copy No.
ZIKA FSS13025	POS	25.3	2.4×10^3
ZIKA FSS13025	POS	29.1	1.3×10^2
ZIKA FSS13025	NEG	33.0	17

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Example 3 Microarray for Detection of DNA Viruses, Bacteria, and Protozoan Pathogens.

A microarray for DNA viruses, bacteria, and protozoan pathogens was developed. The design included multiple gene targets for each pathogen genome in order to select the best probes for the final platform design. The design strategy was to choose the probes with the best "scores" (homology, thermodynamics, secondary structure and sequence complexity) balancing the cross-hybridization with the host genome and with other pathogens' genomes. The second design strategy was to balance the number of probes for each pathogen with a final count of 50-110 probes each. Probes selected in the final design generated a more intense signal and produced higher percentage coverage of the specific genome across the different experiments.

The final design was supplemented with predesigned DNA array probes (577 control probes, 225 replicates, and 11,620 backbone) specific for the reagents and the assay performance. These are used specifically for image orientation, to assess whether the samples are labeled, for the orientation of the platform during the scan process, and for measuring on element background. These probes form a hairpin and do not hybridize well with labeled sample of any species. In addition, 312 probes specific for three human housekeeping genes (ACTB, ARL1, CCDN1) and 109 probes specific for one Mosquito-specific virus and two plant viruses (Aedes albopictus densovirus 2, Maize streak virus, Tomato pseudo-curly top virus) were added to the design.

The microarray includes probes for cytomegalovirus (CMV; also known as HHV-5), Epstein Barr virus (EBV; also known as HHV-4), human herpesvirus 8 (HHV-8), human papilloma virus (HPV) type 6b HPV6, HPV11, HPV 16, HPV 17, hepatitis B virus (HBV) subtype adw, HBV subtype ayw, HBV subtype adr, HBV subtype ayr, and human parvovirus B19. Exemplary probes provided in Table 8 and include SEQ ID NOs: 1770-1852 (CMV), SEQ ID NOs: 1853-1917 (EBV B95-8), SEQ ID NOs: 1918-2023 (EBV AG876), SEQ ID NOs: 2024-2108 (HHV-8), SEQ ID NOs: 2109-2192 (HPV 6b), SEQ ID NOs: 2193-2271 (HPV 11), SEQ ID NOs: 2272-2342 (HPV 16), SEQ ID NOs: 2343-2419 (HPV 18), SEQ ID NOs: 2420-2470 (HBV subtype adw), SEQ ID NOs: 2471-2520 (HBV subtype ayw), SEQ ID NOs: 2521-2556 (HBV subtype adr), SEQ ID NOs: 2557-2602 (HBV subtype ayr), and SEQ ID NOs: 2603-2647 (human parvovirus B19).

The microarray also includes probes for *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi, Leishmania major, Babesia microti, Plasmodium falciparum, and Plasmodium vivax.* Exemplary probes provided in Table 9 and include SEQ ID NOs: 2648-2751 (*Treponema pallidum*), SEQ ID NOs: 2752-2852 (*Ehrlichia chaffeensis*), SEQ ID NOs: 2853-2861 (*Ehrlichia ewingii*), SEQ ID NOs: 2862-2922 (*Ehrlichia*)

muris), SEQ ID NOs: 2923-3001 (Borrelia burgdorferi), SEQ ID NOs: 3002-3085 (Coxiella burnetii), SEQ ID NOs: 3086-3097 (Trypanosoma brucei), SEQ ID NO: 3098 (Trypanosoma cruzi), SEQ ID NOs: 3099-3113 (Leishmania major), SEQ ID NOs: 3114-3154 (Babesia microti), SEQ ID NOs: 3155-3185 (Plasmodium falciparum), and SEQ ID NOs: 3186-3207 (Plasmodium vivax).

Finally, the microarray includes housekeeping and negative control probes (Table 10). Exemplary probes include SEQ ID NOs: 3208-3301 (housekeeping gene ACTB), SEQ ID NOs: 3302-3385 (housekeeping gene ARL1), SEQ ID NOs: 3386-3519 (housekeeping gene CCDN1), SEQ ID NOs: 3557 (Aedes albopictus densovirus 2), SEQ ID NO: 3558-3598 (Maize streak virus), and SEQ ID NOs: 3599-3628 (Tomato pseudo-curly top virus).

For sample analysis, viral DNA from plasma specimens was extracted with the Invitrogen Dynabeads SILANE viral NA kit. The kit is designed for highly predictable and consistent isolation of viral nucleic acids. Beads and buffers are optimized for sensitive isolation of viral DNA. DNA from bacteria and protozoans was extracted from whole blood with the QIAamp DNA Blood Mini kit (Qiagen) according to the manufacturer's protocol.

SureTag Labeling Kit (Agilent technology) was used to enzymatically label DNA from plasma and blood. A modified protocol was developed and optimized for efficient sample fragmentation, enzymatic labeling, and clean up. A master mix containing 10X aCGH blocking agent and 2X HI-RPM hybridization buffer, was added to 2.5-3 µg of labeled DNA, denatured, and hybridized to arrays under 8-chamber gasket slides at 67°C with 20-rpm rotation for 24 hours in an Agilent hybridization oven. Arrays were processed using wash procedure A and scanned on an Agilent SureScan G4900DA microarray scanner using 5-µm resolution.

CMV, Trypanosoma, Parvovirus B19, HBV, EBV (HHV-4), Treponema, Babesia, Leishmania, Coxiella, Borrelia, Papilloma Virus (HPV 6, 11, 16, 18), and P. falciparum had 10⁴-10³copies/mL limits of detection. There were no false negatives or false positives when testing the positive plasma. All the results were confirmed by RT-qPCR of the DNA aliquots used for testing. All positive results were confirmed and the copy numbers for each pathogen were calculated to define the limit of the detection for each species on the array.

Table 8. Exemplary DNA virus probes

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ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST_P10000630	45812	45860	1770	CMV (HHV-5) Cytomegalovirus	UL34	protein
CUST_P10000631	45872	45916	1771	CMV (HHV-5) Cytomegalovirus	UL34	protein
CUST_P10000638	46336	46384	1772	CMV (HHV-5) Cytomegalovirus	UL34	protein
CUST_P10001082	78547	78591	1773	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST_P10001099	79469	79514	1774	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST P10001109	80183	80227	1775	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST_P10001111	80253	80301	1776	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST_P10001120	80933	80979	1777	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep

			SEQ			
ProbeID	Start	End	ID NO:	Virus	Genomic Region	Product
CUST P10001123	81072	81116	1778	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST P10001126	81245	81289	1779	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST P10001131	81599	81643	1780	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST P10001132	81738	81782	1781	CMV (HHV-5) Cytomegalovirus	UL54	DNA rep
CUST P10001140	82327	82375	1782	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST P10001146	82856	82901	1783	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST P10001152	83347	83399	1784	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST P10001154	83475	83525	1785	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001155	83645	83701	1786	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001156	83677	83724	1787	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001158	83744	83797	1788	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001160	83961	84012	1789	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001161	83993	84052	1790	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001162	84021	84073	1791	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001164	84223	84275	1792	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001165	84398	84442	1793	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001169	84665	84716	1794	CMV (HHV-5) Cytomegalovirus	UL55	envelop
CUST_P10001175	85014	85071	1795	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001177	85085	85132	1796	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001179	85221	85272	1797	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001183	85645	85693	1798	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001189	86404	86461	1799	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001198	87249	87308	1800	CMV (HHV-5) Cytomegalovirus	UL56	encapsi
CUST_P10001603	117602	117650	1801	CMV (HHV-5) Cytomegalovirus	UL80	capsid
CUST_P10001618	118112	118156	1802	CMV (HHV-5) Cytomegalovirus	UL80	capsid
CUST_P10001622	118567	118615	1803	CMV (HHV-5) Cytomegalovirus	UL80	capsid
CUST_P10001664	121437	121483	1804	CMV (HHV-5) Cytomegalovirus	UL83	tegumen
CUST_P10001665	121470	121522	1805	CMV (HHV-5) Cytomegalovirus	UL83	tegumen
CUST_P10001666	121493	121543	1806	CMV (HHV-5) Cytomegalovirus	UL83	tegumen
CUST_P10001675	122579	122623	1807	CMV (HHV-5) Cytomegalovirus	UL83	tegumen
CUST_P10001945	141984	142028	1808	CMV (HHV-5) Cytomegalovirus	UL97	core
CUST_P10001948	142100	142144	1809	CMV (HHV-5) Cytomegalovirus	UL97	core
CUST_P10001960	142742	142789	1810	CMV (HHV-5) Cytomegalovirus	UL97	core
CUST_P10001965	143122	143180	1811	CMV (HHV-5) Cytomegalovirus	UL97	core
CUST_P10001966	143159	143203	1812	CMV (HHV-5) Cytomegalovirus	UL97	core
CUST_P10002353	170852	170896	1813	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002359	171207	171256	1814	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002362	171393	171444	1815	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002371	171811	171858	1816	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002377	172241	172300	1817	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002378	172286	172345	1818 1819	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002379	172307	172366	1019	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge

			SEQ ID		Genomic	
ProbeID	Start	End	NO:	Virus	Region	Product
CUST_P10002381	172506	172559	1820	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002382	172633	172678	1821	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002384	172987	173046	1822	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002385	173023	173082	1823	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002386	173044	173097	1824	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002389	173134	173193	1825	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002390	173156	173215	1826	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002391	173191	173239	1827	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002392	173374	173433	1828	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002393	173395	173454	1829	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002394	173432	173489	1830	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002395	173456	173514	1831	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002396	173503	173553	1832	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002397	173520	173579	1833	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002398	173555	173613	1834	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002399	173596	173649	1835	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002400	173621	173679	1836	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002401	173674	173731	1837	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002402	173693	173746	1838	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002403	173735	173780	1839	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002404	173766	173812	1840	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002406	174051	174095	1841	CMV (HHV-5) Cytomegalovirus	UL122	Beta Ge
CUST_P10002407	174065	174109	1842	CMV (HHV-5) Cytomegalovirus	UL123	Prot E
CUST_P10002408	174215	174259	1843	CMV (HHV-5) Cytomegalovirus	UL123	Prot E
CUST_P10002411	174671	174726	1844	CMV (HHV-5) Cytomegalovirus	UL124	Prot E
CUST_P10002466	178473	178527	1845	CMV (HHV-5) Cytomegalovirus	UL132	Glyco
CUST_P10002470	178801	178851	1846	CMV (HHV-5) Cytomegalovirus	UL132	Glyco
CUST_P10002471	178825	178870	1847	CMV (HHV-5) Cytomegalovirus	UL132	Glyco
CUST_P10002474	178926	178974	1848	CMV (HHV-5) Cytomegalovirus	UL132	Glyco
CUST_P10002475	178954	179000	1849	CMV (HHV-5) Cytomegalovirus	UL132	Glyco
CUST_P10002927	211545	211592	1850	CMV (HHV-5) Cytomegalovirus	US17	protein
CUST_P10002930	211944	211988	1851	CMV (HHV-5) Cytomegalovirus	US17	protein
CUST_P10002934	212083	212127	1852	CMV (HHV-5) Cytomegalovirus	US17	protein
CUST D10002272	1	60	1853	Human harnogrinus 4 (EDV) D05 9	IMD 24	transmembrane
CUST_P10003273 CUST_P10003278	444	503	1854	Human herpesvirus 4 (EBV), B95-8 Human herpesvirus 4 (EBV), B95-8	LMP-2A	protein transmembrane protein
CUST P10003289	1435	1487	1855	Human herpesvirus 4 (EBV), B95-8	LMP-2A	transmembrane protein
CUST_P10003301	2062	2106	1856	Human herpesvirus 4 (EBV), B95-8	BNFR1	tegument protein
CUST_P10003303	2221	2265	1857	Human herpesvirus 4 (EBV), B95-8	BNFR1	tegument protein
CUST_P10003307	2620	2664	1858	Human herpesvirus 4 (EBV), B95-8	BNFR1	tegument protein
CUST_P10003313	3104	3148	1859	Human herpesvirus 4 (EBV), B95-8	BNFR1	tegument protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
Gride Discourse	2020	2052	1860		D) ''ED 1	tegument
CUST_P10003322	3928	3972		Human herpesvirus 4 (EBV), B95-8	BNFR1	protein tegument
CUST_P10003342	5201	5245	1861	Human herpesvirus 4 (EBV), B95-8	BNFR1	protein
CLIST D10002240	5834	5893	1862	Human hamagring 4 (EDV) B05 8	BNFR1	tegument
CUST_P10003349	3634	3693	1062	Human herpesvirus 4 (EBV), B95-8	DINTKI	protein Nuclear
CUST_P10003351	5931	5985	1863	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003352	6010	6069	1864	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
COS1_1 10003332	0010	0007	1865	Titilian herpesvitus 4 (LBV), B75-6	LDIVA-1	Nuclear
CUST_P10003367	7289	7347	1803	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003369	7409	7468	1866	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
_			1867	• ` ` ` ` `		Nuclear
CUST_P10003372	7520	7579	1007	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST P10003375	7605	7664	1868	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
			1869			Nuclear
CUST_P10003376	7635	7694		Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003377	7706	7765	1870	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CHICE DIAGONALE	5521	5500	1871		TD) I I	Nuclear
CUST_P10003378	7731	7790		Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003379	7786	7845	1872	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CLICE PLOOSSO	7001	7000	1873	11 1 1 1 TO A (EDV) DOS 0	EDMA 1	Nuclear
CUST_P10003380	7821	7880		Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003381	7871	7930	1874	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003382	7901	7960	1875	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
CUS1_F10003382	7901	7900	1076	Titilian herpesvirus 4 (EBV), B93-8	EDINA-1	Nuclear
CUST_P10003383	7941	8000	1876	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003384	8000	8051	1877	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
_	0000		1878	Titiman nerpes virus v (2B v), 2 > 0		Nuclear
CUST_P10003390	8236	8291	1070	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST_P10003398	8631	8690	1879	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
			1880			Nuclear
CUST_P10003399	8659	8716		Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003400	8690	8737	1881	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CLICT DIOCOMANA	0006	00.62	1882	Harris hamanina 4 (EDV), DOS 8	EDNIA 1	Nuclear
CUST_P10003404	9006	9063	1000	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003405	9052	9111	1883	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003406	9110	9166	1884	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
CUS1_F10003400	9110	9100	1005	Titilian herpesvirus 4 (EBV), B93-8	EDINA-1	Nuclear
CUST_P10003408	9301	9350	1885	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003409	9349	9399	1886	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
2001_110003107	2512	,,,,	1887	• • • • • • • • • • • • • • • • • • • •		Nuclear
CUST_P10003412	9759	9811	100/	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003413	9788	9841	1888	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
_			1889	•		Nuclear
CUST_P10003418	9961	10012		Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen Nuclear
CUST_P10003427	10915	10966	1890	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
		11046	1891			Nuclear
CUST_P10003429	10994	11046	<u> </u>	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			1892			Nuclear
CUST_P10003432	11304	11362	10,2	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CUST P10003721	35383	35442	1893	Human herpesvirus 4 (EBV), B95-8	EBNA-1	Nuclear antigen
	32303	55.1.2	1004	11411411 11415 1 (22 1), 23 0		Nuclear
CUST_P10003725	35654	35708	1894	Human herpesvirus 4 (EBV), B95-8	EBNA-1	antigen
CLICT D10005257	150676	152720	1895	Human hamagrinus 4 (EDV) B05 8	DALES	Binding Protein
CUST_P10005257	152676	152720		Human herpesvirus 4 (EBV), B95-8	BALF5	Binding
CUST_P10005266	153637	153681	1896	Human herpesvirus 4 (EBV), B95-8	BALF5	Protein
			1897			Binding
CUST_P10005267	153658	153702	10,,	Human herpesvirus 4 (EBV), B95-8	BALF5	Protein
CUST P10005275	154346	154393	1898	Human herpesvirus 4 (EBV), B95-8	BALF5	Binding Protein
2001_110003273	13 13 10	13 1373	1000	Truman nerpestrus (BB1), B33 6	Bill 5	Binding
CUST_P10005279	154462	154516	1899	Human herpesvirus 4 (EBV), B95-8	BALF5	Protein
CLICT D10005201	155210	155262	1900	Harmon harmonicon 4 (EDV) DOS 9	DALES	Binding Protein
CUST_P10005291	155318	155362		Human herpesvirus 4 (EBV), B95-8	BALF5	Binding
CUST_P10005293	155583	155627	1901	Human herpesvirus 4 (EBV), B95-8	BALF5	Protein
			1902			Binding
CUST_P10005300	155914	155958		Human herpesvirus 4 (EBV), B95-8	BALF5	Protein Binding
CUST P10005304	156254	156306	1903	Human herpesvirus 4 (EBV), B95-8	BALF5	Protein
<u> </u>	130231	150500	1004	Transactive States (BBV), By 5	Bi IBi 3	Binding
CUST_P10005325	157914	157963	1904	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein
CLICE DIOOS227	150073	150121	1905	Haman hamanina 4 (EDV) D05 8	DALE4	Binding
CUST_P10005327	158072	158121		Human herpesvirus 4 (EBV), B95-8	BALF4	Protein Binding
CUST_P10005329	158133	158183	1906	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein
			1907			Binding
CUST_P10005332	158230	158286	170,	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein Binding
CUST P10005334	158408	158453	1908	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein
	200100		1909	(= -), =		Binding
CUST_P10005335	158572	158625	1909	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein
CUST P10005336	158595	158644	1910	Human herpesvirus 4 (EBV), B95-8	BALF4	Binding Protein
COS1_110005550	136373	130044	1011	Truman nerpesvirus + (LB V), B75-6	DALIT	Binding
CUST_P10005340	158865	158916	1911	Human herpesvirus 4 (EBV), B95-8	BALF4	Protein
GUIGE PIOCOSSES	160406	160545	1912		DATE	Binding
CUST_P10005355	160486	160545		Human herpesvirus 4 (EBV), B95-8	BALF4	Protein Binding
CUST P10005356	160515	160574	1913	Human herpesvirus 4 (EBV), B95-8	BALF3	Protein
_			1914	•		Binding
CUST_P10005367	161267	161318	1717	Human herpesvirus 4 (EBV), B95-8	BALF3	Protein
CUST P10005380	162040	162086	1915	Human herpesvirus 4 (EBV), B95-8	BALF3	Binding Protein
	102040	102000	1016	Transact temperatures + (EBV), B33 6	Brief 5	Binding
CUST_P10005381	162117	162161	1916	Human herpesvirus 4 (EBV), B95-8	BALF3	Protein
CLICT D10005292	160000	162266	1917	Haman hamanina 4 (EDV) DOS 9	DALE2	Binding
CUST_P10005382	162322	162366		Human herpesvirus 4 (EBV), B95-8	BALF3	Protein latency and B
CUST_P10005496	1	60	1918	Human herpesvirus 4 (EBV),AG876	LMP-2B	cell survival
_			1919	-		latency and B
CUST_P10005503	903	961		Human herpesvirus 4 (EBV),AG876	LMP-2B	cell survival
CUST P10005506	1162	1221	1920	Human herpesvirus 4 (EBV),AG876	LMP-2B	latency and B cell survival
	-102		1921	-		latency and B
CUST_P10005507	1290	1345	1921	Human herpesvirus 4 (EBV),AG876	LMP-2B	cell survival
CUST P10005515	1658	1717	1922	Human herpesvirus 4 (EBV),AG876	LMP-2B	latency and B cell survival
COST_F10003313	1030	1/1/	1022	Truman nerpesviius + (ED v),AG6/6	LIVIF -2D	DNA
CUST_P10005567	5833	5892	1923	Human herpesvirus 4 (EBV),AG876	EBER-1	replication

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST P10005568	5869	5928	1924	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST_P10005571	6014	6073	1925	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST P10005581	6584	6635	1926	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
_			1927	-		DNA
CUST_P10005585	6912	6967		Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005589	7293	7348	1928	Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005592	7417	7476	1929	Human herpesvirus 4 (EBV),AG876	EBER-1	replication
CUST_P10005593	7470	7529	1930	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST P10005594	7520	7579	1931	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST_P10005595	7590	7649	1932	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST P10005596	7615	7674	1933	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
_			1934	, , , , ,		DNA
CUST_P10005597	7645	7704		Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005598	7701	7760	1935	Human herpesvirus 4 (EBV),AG876	EBER-1	replication
CUST P10005599	7740	7799	1936	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST P10005600	7770	7829	1937	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
			1938	•		DNA
CUST_P10005601	7799	7858		Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005602	7835	7894	1939	Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005604	7910	7969	1940	Human herpesvirus 4 (EBV),AG876	EBER-1	replication
CUST P10005605	7940	7999	1941	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
_			1942	• • • • • • • • • • • • • • • • • • • •		DNA
CUST_P10005606	7972	8031	1042	Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005617	8432	8486	1943	Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005619	8501	8560	1944	Human herpesvirus 4 (EBV),AG876	EBER-1	replication
CUST_P10005620	8536	8590	1945	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST P10005622	8614	8673	1946	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
			1947	•		DNA
CUST_P10005623	8647	8706		Human herpesvirus 4 (EBV),AG876	EBER-1	replication DNA
CUST_P10005626	8996	9052	1948	Human herpesvirus 4 (EBV),AG876	EBER-1	replication
CUST_P10005627	9041	9100	1949	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST_P10005628	9096	9149	1950	Human herpesvirus 4 (EBV),AG876	EBER-1	DNA replication
CUST_P10005635	9782	9837	1951	Human herpesvirus 4 (EBV),AG876	BCRF1	Early protein
CUST_P10005640	9942	9995	1952	Human herpesvirus 4 (EBV),AG876	BCRF1	Early protein
CUST_P10005641	10139	10194	1953	Human herpesvirus 4 (EBV),AG876	BCRF1	Early protein
CUST_P10005654	11289	11348	1954	Human herpesvirus 4 (EBV),AG876	BCRF1	Early protein
CUST_P10005661	11661	11720	1955	Human herpesvirus 4 (EBV),AG876	IR1	Repeat Sequence
CUST_P10005662	11765	11824	1956	Human herpesvirus 4 (EBV),AG876	IR1	Repeat Sequence

			SEQ ID		Genomic	
ProbeID	Start	End	NO:	Virus	Region	Product
CUST P10005663	11948	11999	1957	Human herpesvirus 4 (EBV),AG876	IR1	Repeat Sequence
			1958			Nuclear
CUST_P10005933	35619	35674	1,50	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen Nuclear
CUST P10005934	35650	35709	1959	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen
			1960			Nuclear
CUST_P10005935	35773	35832		Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen Nuclear
CUST_P10005941	36221	36277	1961	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen
CLICT D10005042	26201	26260	1962	Haman hamanima 4 (EDV) A C97(EDMA 2	Nuclear
CUST_P10005943	36301	36360	10.50	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen Nuclear
CUST_P10005961	37425	37477	1963	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen
CUST P10005962	37566	37625	1964	Human herpesvirus 4 (EBV),AG876	EBNA-2	Nuclear antigen
CUS1_F10003902	37300	37023	1065	Titilian herpesvitus 4 (EBV),AG670	EDINA-2	Nuclear
CUST_P10005965	37982	38041	1965	Human herpesvirus 4 (EBV),AG876	EBNA-2	antigen
CUST P10005981	41069	41128	1966	Human herpesvirus 4 (EBV),AG876	BFLF2	Nuclear antigen
<u> </u>	41007	71120	1967	Truman herpesvitus + (EB v);210070	DI LI Z	Nuclear
CUST_P10005994	42062	42114	1907	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CUST P10005995	42170	42229	1968	Human herpesvirus 4 (EBV),AG876	BFLF2	Nuclear antigen
_			1969	•		Nuclear
CUST_P10005996	42338	42397	1707	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CUST P10005997	42368	42427	1970	Human herpesvirus 4 (EBV),AG876	BFLF2	Nuclear antigen
_			1971			Nuclear
CUST_P10005998	42421	42480	17/1	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen Nuclear
CUST P10006001	42542	42594	1972	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CTICE PAGE COOK			1973			Nuclear
CUST_P10006009	43272	43331		Human herpesvirus 4 (EBV),AG876	BFLF2	antigen Nuclear
CUST_P10006010	43296	43355	1974	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CLICT DIOOCOLI	42222	42201	1975	Harmon harmon inter 4 (EDV) AC976	DELEO	Nuclear
CUST_P10006011	43322	43381	1056	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen Nuclear
CUST_P10006026	44210	44266	1976	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CUST P10006062	46628	46687	1977	Human herpesvirus 4 (EBV),AG876	BFLF2	Nuclear antigen
CUS1_F10000002	40028	40067	1079	Titilian herpesvitus 4 (EBV),AG870	DITLITZ	Nuclear
CUST_P10006104	49867	49926	1978	Human herpesvirus 4 (EBV),AG876	BFLF2	antigen
CUST_P10006292	64392	64446	1979	Human herpesvirus 4 (EBV),AG876	BaRF1	Protein
CUST_P10006337	67573	67632	1980	Human herpesvirus 4 (EBV),AG876	BaRF1	Protein
CUST_P10006338	67734	67780	1981	Human herpesvirus 4 (EBV),AG876	BaRF1	Protein
CUST P10006346	68303	68351	1982	Human herpesvirus 4 (EBV),AG876	BaRF1	Protein
CUST P10006354	68922	68968	1983	Human herpesvirus 4 (EBV),AG876	BaRF1	Protein
CUST P10006495	79411	79470	1984	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006496			1985	Human herpesvirus 4 (EBV),AG876		
_	79445	79504	1986	•	EBNA-3C	Protein
CUST_P10006497	79520	79575	1987	Human herpesvirus 4 (EBV), AG876	EBNA-3C	Protein
CUST_P10006499	79742	79801	1988	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006506	80288	80346		Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006513	80822	80881	1989	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006515	80901	80955	1990	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006542	83005	83064	1991	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein

			SEQ			
ProbeID	Start	End	ID NO:	Virus	Genomic Region	Product
CUST P10006547	83394	83446	1992	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006549	83520	83575	1993	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006559	84220	84279	1994	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006560	84245	84304	1995	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006562	84360	84419	1996	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006563	84394	84453	1997	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006619	87106	87160	1998	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006629	87723	87782	1999	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006659	90250	90309	2000	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006735	95481	95540	2001	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST_P10006749	96426	96485	2002	Human herpesvirus 4 (EBV),AG876	EBNA-3C	Protein
CUST P10006975	114037	114096	2003	Human herpesvirus 4 (EBV),AG876	BZLF1	Transcription factor
_			2004	-		Transcription
CUST_P10007058	119518	119568		Human herpesvirus 4 (EBV),AG876	BZLF1	factor Transcription
CUST_P10007154	127252	127301	2005	Human herpesvirus 4 (EBV),AG876	BZLF1	factor
CUST_P10007332	140366	140418	2006	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007342	141133	141189	2007	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007350	141491	141550	2008	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007368	146390	146444	2009	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007370	146461	146520	2010	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007371	146485	146544	2011	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007385	147651	147710	2012	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007389	147919	147978	2013	Human herpesvirus 4 (EBV),AG876	BRRF1	Early Protein
CUST_P10007496	155451	155495	2014	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007497	155595	155639	2015	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007498	155833	155878	2016	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007499	155874	155918	2017	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007511	156741	156785	2018	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007512	156802	156846	2019	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007519	157248	157292	2020	Human herpesvirus 4 (EBV),AG876	BALF5	Pol
CUST_P10007686	169787	169844	2021	Human herpesvirus 4 (EBV),AG876	BALF4	Pol
CUST_P10007687	169910	169964	2022	Human herpesvirus 4 (EBV),AG876	BALF4	Pol
CUST_P10007688	169977	170032	2023	Human herpesvirus 4 (EBV),AG876	BALF4	Pol
CUST_P10007838	8641	8685		Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007845	9121	9173	2025	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007846	9136	9192	2026	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007847	9164	9219	2027	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007848	9291	9338	2028	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007849	9301	9352	2029	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007850	9325	9380	2030	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007859	10189	10234	2031	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007861	10387	10436	2032	Human herpesvirus 8 (HHV-8)	UL27	Core

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CUST_P10007862	10525	10584	2033	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007865	10694	10743	2034	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007870	11141	11191	2035	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007871	11189	11243	2036	Human herpesvirus 8 (HHV-8)	UL27	Core
CUST_P10007875	11324	11370	2037	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007882	11596	11644	2038	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007889	12191	12244	2039	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007890	12231	12276	2040	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007892	12408	12453	2041	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007894	12597	12642	2042	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007895	12731	12786	2043	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007896	12803	12855	2044	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007900	13330	13383	2045	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007902	13405	13449	2046	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007903	13429	13473	2047	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007906	13774	13821	2048	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007907	13815	13859	2049	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007910	14391	14438	2050	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST P10007912	14506	14551	2051	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007915	14605	14655	2052	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007916	14632	14686	2053	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007921	15015	15062	2054	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007922	15051	15095	2055	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007923	15187	15232	2056	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007925	15488	15536	2057	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007929	15833	15879	2058	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007933	16005	16057	2059	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007936	16274	16324	2060	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007937	16293	16350	2061	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007942	16565	16614	2062	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007943	16679	16733	2063	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007944	16760	16804	2064	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007946	16874	16922	2065	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10007947	17007	17064	2066	Human herpesvirus 8 (HHV-8)	UL30	DNA Pol
CUST_P10008350	47027	47078	2067	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008352	47180	47235	2068	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008353	47205	47256	2069	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008354	47279	47328	2070	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008355	47290	47343	2071	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008356	47379	47429	2072	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008357	47404	47448	2073	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008358	47526	47583	2074	Human herpesvirus 8 (HHV-8)	ORF26	Capsid

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CUST_P10008362	47811	47857	2075	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008363	47833	47889	2076	Human herpesvirus 8 (HHV-8)	ORF26	Capsid
CUST_P10008367	48249	48296	2077	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008370	48367	48418	2078	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008371	48393	48441	2079	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008373	48456	48500	2080	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008374	48487	48538	2081	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008376	48548	48592	2082	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008377	48585	48643	2083	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008378	48655	48702	2084	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10008380	48859	48918	2085	Human herpesvirus 8 (HHV-8)	ORF27	PolyA
CUST_P10009322	112342	112396	2086	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009323	112362	112421	2087	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009324	112390	112439	2088	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009462	123077	123124	2089	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009466	123331	123382	2090	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009467	123379	123425	2091	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009468	123391	123441	2092	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009469	123537	123593	2093	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009470	123611	123664	2094	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009471	123635	123692	2095	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009472	123655	123714	2096	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009473	123682	123736	2097	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009474	123710	123769	2098	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009475	123738	123788	2099	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009482	124109	124164	2100	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009484	124384	124437	2101	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009486	124635	124686	2102	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009487	124654	124707	2103	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009488	124679	124723	2104	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009489	126493	126541	2105	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009493	126960	127005	2106	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009503	127324	127368	2107	Human herpesvirus 8 (HHV-8)	ORF73	Poly A
CUST_P10009504	127347	127395	2108	Human herpesvirus 8 (HHV-8)	ORF73	PolyA
CUST_P10009640	3	59	2109	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein
CUST P10009641	34	85	2110	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein
CUST P10009642	57	116	2111	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein
CUST_P10009644	148	207	2112	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein
CUST_P10009645	207	266	2113	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein
CUST_P10009646	347	406	2114	Human papillomavirus type 6b (HPV 6b)	E6	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2115	Human papillomavirus type 6b		Regulatory
CUST_P10009647 CUST_P10009648	527	582	2116	(HPV 6b) Human papillomavirus type 6b (HPV 6b)	E6 E6	Protein Regulatory Protein
CLICT PLOODOCAO	645	702	2117	Human papillomavirus type 6b	F7	Regulatory
CUST_P10009649	645	702	2118	(HPV 6b) Human papillomavirus type 6b	E7	Protein Regulatory
CUST_P10009651	952	1005	2118	(HPV 6b) Human papillomavirus type 6b	E7	Protein
CUST_P10009652	975	1034	2119	(HPV 6b) Human papillomavirus type 6b	E7	Regulatory Protein Regulatory
CUST_P10009654	1048	1099	2120	(HPV 6b)	E1	Protein
CUST_P10009655	1079	1138	2121	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
CUST P10009656	1101	1160	2122	Human papillomavirus type 6b (HPV 6b)	E1	Regulatory Protein
CUST_P10009657	1140	1199	2123	Human papillomavirus type 6b (HPV 6b)	E1	Regulatory Protein
CUST P10009658	1168	1221	2124	Human papillomavirus type 6b (HPV 6b)	E1	Regulatory Protein
_			2125	Human papillomavirus type 6b		Regulatory
CUST_P10009659	1204	1249		(HPV 6b) Human papillomavirus type 6b	E1	Protein Regulatory
CUST_P10009660	1418	1477	2126	(HPV 6b)	E1	Protein
CUST P10009661	1492	1551	2127	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
CUST P10009662	1852	1908	2128	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
CUST P10009663	1899	1958	2129	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
_	2059		2130	Human papillomavirus type 6b	E1	Regulatory
CUST_P10009664	2058	2117	2131	(HPV 6b) Human papillomavirus type 6b	EI	Protein Regulatory
CUST_P10009665	2086	2145		(HPV 6b) Human papillomavirus type 6b	E1	Protein Regulatory
CUST_P10009666	2353	2412	2132	(HPV 6b)	E1	Protein
CUST_P10009667	2463	2522	2133	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
CUST P10009668	2507	2566	2134	Human papillomavirus type 6b (HPV 6b)	El	Regulatory Protein
CUST P10009669	2554	2613	2135	Human papillomavirus type 6b (HPV 6b)	E1	Regulatory Protein
CUST_P10009670	2601	2660	2136	Human papillomavirus type 6b (HPV 6b)	E1	Regulatory Protein
COS1_110007070	2001	2000	2137	Human papillomavirus type 6b	EI	Regulatory
CUST_P10009671	2686	2734		(HPV 6b) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009672	2894	2946	2138	(HPV 6b)	E2	Protein
CUST_P10009673	2916	2975	2139	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009674	2942	3001	2140	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009675	2963	3022	2141	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009676	3002	3061	2142	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009677	3030	3089	2143	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009678	3061	3120	2144	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009679	3091	3148	2145	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009680	3265	3324	2146	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2147	Human papillomavirus type 6b		Regulatory
CUST_P10009681 CUST_P10009686	3305 3592	3364 3651	2148	(HPV 6b) Human papillomavirus type 6b (HPV 6b)	E2 E2	Protein Regulatory Protein
_	2614		2149	Human papillomavirus type 6b	770	Regulatory
CUST_P10009687	3614	3673		(HPV 6b) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009689	3686	3740	2150	(HPV 6b)	E2	Protein
CUST_P10009690	3724	3783	2151	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009691	3751	3810	2152	Human papillomavirus type 6b (HPV 6b)	E2	Regulatory Protein
CUST_P10009692	3937	3996	2153	Human papillomavirus type 6b (HPV 6b)	E5	Regulatory Protein
CUST P10009693	4048	4107	2154	Human papillomavirus type 6b (HPV 6b)	E5	Regulatory Protein
CUST P10009694	4077	4136	2155	Human papillomavirus type 6b (HPV 6b)	E5	Regulatory Protein
_	4116		2156	Human papillomavirus type 6b	F.5	Regulatory
CUST_P10009695	4116	4175		(HPV 6b) Human papillomavirus type 6b	E5	Protein Regulatory
CUST_P10009696	4140	4199	2157	(HPV 6b)	E5	Protein
CUST_P10009697	4281	4340	2158	Human papillomavirus type 6b (HPV 6b)	E5	Regulatory Protein
CUST P10009698	4505	4557	2159	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009702	4718	4773	2160	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009705	4804	4863	2161	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST P10009706	4937	4991	2162	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009707	4970	5029	2163	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009709	5118	5175	2164	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009710	5237	5285	2165	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009711	5508	5567	2166	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009712	5568	5617	2167	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST_P10009713	5581	5640	2168	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST P10009714	5611	5663	2169	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST P10009715	5664	5716	2170	Human papillomavirus type 6b (HPV 6b)	L2	Capsid
CUST P10009716	5699	5758	2171	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009717	5835	5893	2172	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009718	5882	5941	2173	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009719	5917	5971	2174	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009720	5980	6039	2175	Human papillomavirus type 6b (HPV 6b)	L1	PolyA
CUST_P10009721	6023	6077	2176	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009723	6106	6157	2177	Human papillomavirus type 6b (HPV 6b)	L1	PolyA
CUST_P10009724	6131	6190	2178	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST P10009726	6346	6399	2179	Human papillomavirus type 6b (HPV 6b)	L1	PolyA
CUST_P10009727	6387	6446	2180	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST P10009728	6426	6485	2181	Human papillomavirus type 6b (HPV 6b)	L1	PolyA
CUST P10009729	6587	6641	2182	Human papillomavirus type 6b (HPV 6b)	L1	PolyA
CUST_P10009731	6661	6710	2183	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009732	6674	6727	2184	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009733	6713	6771	2185	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009734	6799	6858	2186	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009735	6914	6973	2187	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009736	7025	7070	2188	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009737	7146	7201	2189	Human papillomavirus type 6b (HPV 6b)	Ll	PolyA
CUST_P10009739	7409	7456	2190	Human papillomavirus type 6b (HPV 6b)		PolyA
CUST_P10009740	7560	7619	2191	Human papillomavirus type 6b (HPV 6b)	?	PolyA
CUST_P10009742	7703	7762	2192	Human papillomavirus type 6b (HPV 6b)	?	PolyA
CUST_P10009743	9	65	2193	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST_P10009744	45	104	2194	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009745	97	149	2195	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009746	146	201	2196	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST_P10009747	203	257	2197	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009748	226	284	2198	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009749	267	311	2199	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009750	444	503	2200	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009751	477	531	2201	Human papillomavirus type 6b (HPV 11)	E6	Regulatory Protein
CUST P10009752	642	696	2202	Human papillomavirus type 6b (HPV 11)	E7	Regulatory Protein
CUST P10009753	676	724	2203	Human papillomavirus type 6b (HPV 11)	E7	Regulatory Protein
CUST P10009755	744	796	2204	Human papillomavirus type 6b (HPV 11)	E7	Regulatory Protein
CUST_P10009756	980	1039	2205	Human papillomavirus type 6b (HPV 11)	E7	Regulatory Protein
CUST_P10009758	1159	1212	2206	Human papillomavirus type 6b (HPV 11)	El	Regulatory Protein
CUST_P10009759	1195	1242	2207	Human papillomavirus type 6b (HPV 11)	E1	Regulatory Protein
CUST_P10009760	1393	1452	2208	Human papillomavirus type 6b (HPV 11)	E1	Regulatory Protein
CUST_P10009761	1419	1478	2209	Human papillomavirus type 6b (HPV 11)	E1	Regulatory Protein
CUST_P10009762	1450	1509	2210	Human papillomavirus type 6b (HPV 11)	El	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CHICE PIOCOGGO			2211	Human papillomavirus type 6b		Regulatory
CUST_P10009763 CUST_P10009765	1476 1847	1535 1899	2212	(HPV 11) Human papillomavirus type 6b (HPV 11)	El El	Protein Regulatory Protein
_			2213	Human papillomavirus type 6b		Regulatory
CUST_P10009766	1864	1923		(HPV 11) Human papillomavirus type 6b	E1	Protein Regulatory
CUST_P10009767	1923	1982	2214	(HPV 11)	E1	Protein
CUST_P10009768	1962	2017	2215	Human papillomavirus type 6b (HPV 11) Human papillomavirus type 6b	El	Regulatory Protein
CUST_P10009769	2003	2062	2216	Human papinomavirus type 60 (HPV 11)	El	Regulatory Protein
CUST_P10009770	2127	2186	2217	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009771	2265	2316	2218	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009772	2303	2362	2219	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
	2227	2284	2220	Human papillomavirus type 6b	Ea	Regulatory
CUST_P10009773	2327	2384	2221	(HPV 11) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009774	2370	2420	2221	(HPV 11)	E2	Protein
CUST_P10009775	2422	2481	2222	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009776	2458	2517	2223	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009777	2590	2649	2224	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009778	2625	2684	2225	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
_	2655		2226	Human papillomavirus type 6b	E2	Regulatory
CUST_P10009779	2655	2708	2227	(HPV 11) Human papillomavirus type 6b	EZ	Protein Regulatory
CUST_P10009780	2692	2740		(HPV 11) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009781	2920	2979	2228	(HPV 11)	E2	Protein
CUST_P10009782	2985	3035	2229	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST_P10009783	3047	3106	2230	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009784	3081	3140	2231	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST_P10009785	3120	3176	2232	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST P10009786	3265	3324	2233	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
			2234	Human papillomavirus type 6b		Regulatory
CUST_P10009787	3380	3424	2235	(HPV 11) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009788	3432	3476		(HPV 11) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009789	3505	3560	2236	(HPV 11) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009790	3678	3735	2237	(HPV 11)	E2	Protein
CUST_P10009791	3709	3768	2238	Human papillomavirus type 6b (HPV 11)	E2	Regulatory Protein
CUST_P10009792	3901	3960	2239	Human papillomavirus type 6b (HPV 11)	E5	Regulatory Protein
CUST_P10009793	4136	4195	2240	Human papillomavirus type 6b (HPV 11)	E5	Regulatory Protein
CUST_P10009794	4283	4342	2241	Human papillomavirus type 6b (HPV 11)	E5	Regulatory Protein
CUST_P10009795	4408	4458	2242	Human papillomavirus type 6b (HPV 11)	E5	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST_P10009796	4497	4556	2243	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009798	4792	4851	2244	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST P10009799	4818	4875	2245	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST P10009800	4855	4912	2246	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009802	4936	4993	2247	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009804	5164	5223	2248	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009805	5341	5397	2249	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009806	5423	5480	2250	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009808	5491	5548	2251	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009809	5514	5566	2252	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009810	5539	5586	2253	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009811	5576	5622	2254	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009812	5603	5651	2255	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009813	5618	5670	2256	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009814	5745	5800	2257	Human papillomavirus type 6b (HPV 11)	L2	Capsid
CUST_P10009815	5819	5875	2258	Human papillomavirus type 6b (HPV 11)	L1	PolyA
CUST_P10009816	5978	6034	2259	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009817	6008	6059	2260	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009818	6031	6075	2261	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009819	6069	6113	2262	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009820	6089	6139	2263	Human papillomavirus type 6b (HPV 11)	L1	PolyA
CUST_P10009821	6118	6177	2264	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009822	6338	6390	2265	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009823	6356	6415	2266	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009824	6383	6442	2267	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009825	6408	6467	2268	Human papillomavirus type 6b (HPV 11)	LI	PolyA
CUST_P10009826	6707	6757	2269	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009827	6796	6855	2270	Human papillomavirus type 6b (HPV 11)	Ll	PolyA
CUST_P10009828	7130	7187	2271	Human papillomavirus type 6b (HPV 11)	L1	PolyA
CUST_P10009831	13	69	2272	Human papillomavirus type 6b (HPV 16)	E6	Regulatory Protein
CUST_P10009832	54	113	2273	Human papillomavirus type 6b (HPV 16)	E6	Regulatory Protein
CUST_P10009833	221	280	2274	Human papillomavirus type 6b (HPV 16)	E6	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2275	Human papillomavirus type 6b		Regulatory
CUST_P10009834 CUST_P10009836	355 564	623	2276	(HPV 16) Human papillomavirus type 6b (HPV 16)	E6 E6	Protein Regulatory Protein
2001_110007030	301	023	2277	Human papillomavirus type 6b	20	Regulatory
CUST_P10009837	704	758	2211	(HPV 16)	E7	Protein
CUST_P10009838	816	867	2278	Human papillomavirus type 6b (HPV 16)	E7	Regulatory Protein
CUST_P10009839	969	1028	2279	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST P10009840	994	1053	2280	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST_P10009841	1049	1098	2281	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST P10009842	1131	1190	2282	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
CUST P10009843	1269	1316	2283	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
			2284	Human papillomavirus type 6b		Regulatory
CUST_P10009844	1296	1346	2285	(HPV 16) Human papillomavirus type 6b	E1	Protein Regulatory
CUST_P10009845	1461	1520	2283	(HPV 16)	El	Protein
CUST_P10009846	1734	1793	2286	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
CUST P10009847	1841	1900	2287	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST P10009848	2010	2069	2288	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
CUST P10009849	2153	2212	2289	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST P10009850	2326	2385	2290	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
_			2291	Human papillomavirus type 6b		Regulatory
CUST_P10009851	2372	2431		(HPV 16) Human papillomavirus type 6b	E1	Protein Regulatory
CUST_P10009852	2583	2642	2292	(HPV 16)	E1	Protein
CUST_P10009853	2679	2732	2293	Human papillomavirus type 6b (HPV 16)	El	Regulatory Protein
CUST_P10009854	2745	2803	2294	Human papillomavirus type 6b (HPV 16)	E1	Regulatory Protein
CUST P10009855	2862	2921	2295	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST P10009856	2895	2951	2296	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST P10009857	2022	2991	2297	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
	2932		2298	Human papillomavirus type 6b		Regulatory
CUST_P10009858	2974	3033		(HPV 16) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009859	2995	3054	2299	(HPV 16) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009860	3091	3150	2300	(HPV 16)	E2	Protein
CUST_P10009861	3190	3249	2301	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST_P10009862	3325	3384	2302	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST_P10009864	3437	3481	2303	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST_P10009867	3503	3547	2304	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST_P10009868	3777	3836	2305	Human papillomavirus type 6b (HPV 16)	E2	Regulatory Protein
CUST_P10009869	3949	4008	2306	Human papillomavirus type 6b (HPV 16)	E5	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2307	Human papillomavirus type 6b		Regulatory
CUST_P10009870 CUST_P10009871	4245	4382	2308	(HPV 16) Human papillomavirus type 6b (HPV 16)	E5 L2	Protein Capsid
CUST P10009872	4347	4406	2309	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009873	4510	4566	2310	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009874	4532	4591	2311	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009875	4644	4703	2312	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009876	4680	4739	2313	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009878	4821	4880	2314	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009879	4842	4890	2315	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009880	4898	4951	2316	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009881	4931	4990	2317	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009882	5068	5125	2318	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009883	5237	5296	2319	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009884	5292	5351	2320	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009885	5444	5503	2321	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009886	5527	5586	2322	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST_P10009887	5685	5744	2323	Human papillomavirus type 6b (HPV 16)	L2	Capsid
CUST P10009888	5849	5908	2324	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST_P10009891	6051	6110	2325	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST_P10009892	6078	6137	2326	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST P10009893	6192	6251	2327	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST_P10009894	6527	6586	2328	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST P10009895	6551	6610	2329	Human papillomavirus type 6b (HPV 16)	Ll	Poly A
CUST_P10009896	6735	6794	2330	Human papillomavirus type 6b (HPV 16)	Li	PolyA
CUST_P10009897	6786	6845	2331	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST_P10009898	6868	6923	2332	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST_P10009899	7030	7089	2333	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST_P10009900	7329	7388	2334	Human papillomavirus type 6b (HPV 16)	LI	PolyA
CUST_P10009901	7571	7620	2335	Human papillomavirus type 6b (HPV 16)	LI	PolyA
CUST_P10009902	7677	7736	2336	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST_P10009903	7700	7759	2337	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST_P10009904	7723	7782	2338	Human papillomavirus type 6b (HPV 16)	Ll	PolyA

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST P10009905	7756	7815	2339	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST_P10009906	7789	7848	2340	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST P10009907	7824	7880	2341	Human papillomavirus type 6b (HPV 16)	Ll	PolyA
CUST P10009908	7846	7905	2342	Human papillomavirus type 6b (HPV 16)	L1	PolyA
CUST P10009909	6	65	2343	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009910	60	116	2344	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST_P10009911	182	241	2345	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009912	233	292	2346	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009913	254	313	2347	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST_P10009914	291	350	2348	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009915	339	398	2349	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST_P10009916	369	428	2350	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST_P10009917	422	468	2351	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009918	535	583	2352	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST_P10009919	560	619	2353	Human papillomavirus type 6b (HPV 18)	E6	Regulatory Protein
CUST P10009920	594	651	2354	Human papillomavirus type 6b (HPV 18)	E7	Regulatory Protein
CUST_P10009921	643	694	2355	Human papillomavirus type 6b (HPV 18)	E7	Regulatory Protein
CUST_P10009922	681	740	2356	Human papillomavirus type 6b (HPV 18)	E7	Regulatory Protein
CUST_P10009925	1017	1071	2357	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009926	1134	1187	2358	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009927	1302	1357	2359	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009928	1663	1722	2360	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009929	1691	1750	2361	Human papillomavirus type 6b (HPV 18)	El	Regulatory Protein
CUST_P10009930	1719	1778	2362	Human papillomavirus type 6b (HPV 18)	El	Regulatory Protein
CUST_P10009931	1883	1942	2363	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009932	1937	1996	2364	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009933	2186	2245	2365	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009934	2210	2269	2366	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009935	2392	2451	2367	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009936	2430	2489	2368	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009937	2471	2520	2369	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009938	2512	2571	2370	Human papillomavirus type 6b (HPV 18)	El	Regulatory Protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2371	Human papillomavirus type 6b		Regulatory
CUST_P10009939 CUST_P10009940	2558 2606	2617 2665	2372	(HPV 18) Human papillomavirus type 6b (HPV 18)	E1 E1	Protein Regulatory Protein
COS1_110007740	2000	2003	2373	Human papillomavirus type 6b	LI	Regulatory
CUST_P10009941	2642	2701	23/3	(HPV 18)	E1	Protein
CUST_P10009942	2808	2852	2374	Human papillomavirus type 6b (HPV 18)	E1	Regulatory Protein
CUST_P10009943	2837	2891	2375	Human papillomavirus type 6b (HPV 18)	E2	Regulatory Protein
CUST_P10009944	2858	2917	2376	Human papillomavirus type 6b (HPV 18)	E2	Regulatory Protein
CUST_P10009945	2885	2944	2377	Human papillomavirus type 6b (HPV 18)	E2	Regulatory Protein
CUCT D10000046	2014	2973	2378	Human papillomavirus type 6b (HPV 18)	E2	Regulatory
CUST_P10009946	2914	29/3	2270	Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009947	3085	3133	2379	(HPV 18)	E2	Protein
CUST P10009948	3205	3264	2380	Human papillomavirus type 6b (HPV 18)	E2	Regulatory Protein
CLICTE DIAGONALIA	2260	2212	2381	Human papillomavirus type 6b	F2	Regulatory
CUST_P10009949	3260	3312	2202	(HPV 18) Human papillomavirus type 6b	E2	Protein Regulatory
CUST_P10009952	3727	3781	2382	(HPV 18)	E2	Protein
CUST P10009953	3753	3807	2383	Human papillomavirus type 6b (HPV 18)	E4	Regulatory Protein
_			2384	Human papillomavirus type 6b	7.5	Regulatory
CUST_P10009954	4025	4080	2205	(HPV 18) Human papillomavirus type 6b	E5	Protein
CUST_P10009955	4262	4316	2385	(HPV 18)	L2	Capsid
CUST P10009956	4357	4414	2386	Human papillomavirus type 6b (HPV 18)	L2	Capsid
_	1511		2387	Human papillomavirus type 6b		-
CUST_P10009959	4544	4599	2200	(HPV 18) Human papillomavirus type 6b	L2	Capsid
CUST_P10009960	4678	4735	2388	(HPV 18)	L2	Capsid
CUST_P10009961	4704	4762	2389	Human papillomavirus type 6b (HPV 18)	L2	Capsid
CUST_P10009962	4796	4852	2390	Human papillomavirus type 6b (HPV 18)	L2	Capsid
COST_110007702	7/70		2391	Human papillomavirus type 6b		
CUST_P10009964	4933	4979	2371	(HPV 18) Human papillomavirus type 6b	L2	Capsid
CUST_P10009965	4947	5002	2392	(HPV 18)	L2	Capsid
CUST P10009967	5016	5075	2393	Human papillomavirus type 6b (HPV 18)	L2	Capsid
_	3010		2394	Human papillomavirus type 6b		
CUST_P10009968	5037	5096	2374	(HPV 18) Human papillomavirus type 6b	L2	Capsid
CUST_P10009969	5067	5119	2395	(HPV 18)	L2	Capsid
CUST P10009970	5218	5269	2396	Human papillomavirus type 6b (HPV 18)	L2	Capsid
COS1_110007970	3218	3209	2397	Human papillomavirus type 6b	1.2	-
CUST_P10009971	5412	5462	4371	(HPV 18) Human papillomavirus type 6b	L2	Capsid
CUST_P10009972	5437	5495	2398	(HPV 18)	L2	Capsid
CUST_P10009973	5635	5693	2399	Human papillomavirus type 6b (HPV 18)	L2	Capsid
_			2400	Human papillomavirus type 6b		•
CUST_P10009975	5781	5840		(HPV 18) Human papillomavirus type 6b	L1	PolyA
CUST_P10009976	5823	5882	2401	(HPV 18)	Ll	PolyA
CUST_P10009977	5844	5903	2402	Human papillomavirus type 6b (HPV 18)	Ll	PolyA

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
			2403	Human papillomavirus type 6b		
CUST_P10009978	5873	5927	2404	(HPV 18) Human papillomavirus type 6b	L1	PolyA
CUST_P10009979	6014	6068		(HPV 18) Human papillomavirus type 6b	L1	PolyA
CUST_P10009980	6030	6089	2405	(HPV 18)	Ll	PolyA
CUST_P10009981	6111	6158	2406	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10009982	6122	6167	2407	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST_P10009983	6149	6200	2408	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST_P10009984	6175	6234	2409	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10009985	6284	6343	2410	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST_P10009986	6409	6462	2411	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST P10009987	6516	6575	2412	Human papillomavirus type 6b (HPV 18)	LI	PolyA
CUST P10009988	6547	6606	2413	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST P10009989	6669	6728	2414	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10009990	6765	6824	2415	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10009991	6890	6947	2416	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST_P10009992	6911	6970	2417	Human papillomavirus type 6b (HPV 18)	Ll	PolyA
CUST_P10009993	6954	7013	2418	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10009994	6997	7042	2419	Human papillomavirus type 6b (HPV 18)	L1	PolyA
CUST_P10010004	44	88	2420	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010005	78	126	2421	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010006	158	202	2422	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010008	230	281	2423	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010009	267	311	2424	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010010	328	372	2425	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010011	394	453	2426	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010012	419	475	2427	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010013	441	494	2428	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010015	600	647	2429	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010016	624	668	2430	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010017	840	899	2431	Hepatitis B virus subtype adw	S	surface protein
CUST_P10010018	981	1036	2432	Hepatitis B virus subtype adw	C	Core
CUST_P10010019	1040	1099	2433	Hepatitis B virus subtype adw	С	Core
CUST_P10010020	1085	1144	2434	Hepatitis B virus subtype adw	С	Core
CUST_P10010021	1130	1174	2435	Hepatitis B virus subtype adw	С	Core
CUST_P10010022	1170	1214	2436	Hepatitis B virus subtype adw	С	Core
CUST_P10010023	1216	1260	2437	Hepatitis B virus subtype adw	С	Core
CUST_P10010024	1241	1285	2438	Hepatitis B virus subtype adw	С	Core

			SEQ ID		Genomic	
ProbeID	Start	End	NO: 2439	Virus	Region	Product
CUST_P10010025	1282	1326	2440	Hepatitis B virus subtype adw	C	Core
CUST_P10010026	1453	1497	2441	Hepatitis B virus subtype adw	C	Core
CUST_P10010027	1560	1605	2442	Hepatitis B virus subtype adw	C	Core
CUST_P10010028	1581	1625	2443	Hepatitis B virus subtype adw	С	Core
CUST_P10010029	1623	1667		Hepatitis B virus subtype adw	С	Core
CUST_P10010030	1643	1691	2444	Hepatitis B virus subtype adw	С	Core
CUST_P10010031	1679	1728	2445	Hepatitis B virus subtype adw	C	Core
CUST_P10010032	1696	1743	2446	Hepatitis B virus subtype adw	C	Core
CUST_P10010033	1743	1796	2447	Hepatitis B virus subtype adw	С	Core
CUST_P10010034	1948	1998	2448	Hepatitis B virus subtype adw	С	Core
CUST_P10010035	2054	2099	2449	Hepatitis B virus subtype adw	С	Core
CUST_P10010036	2131	2190	2450	Hepatitis B virus subtype adw	С	Core
CUST_P10010037	2164	2223	2451	Hepatitis B virus subtype adw	C	Core
CUST_P10010038	2208	2267	2452	Hepatitis B virus subtype adw	С	Core
CUST_P10010039	2238	2285	2453	Hepatitis B virus subtype adw	С	Core
CUST_P10010040	2275	2321	2454	Hepatitis B virus subtype adw	С	Core
CUST_P10010041	2293	2349	2455	Hepatitis B virus subtype adw	С	Core
CUST_P10010042	2334	2378	2456	Hepatitis B virus subtype adw	С	Core
CUST P10010044	2416	2463	2457	Hepatitis B virus subtype adw	С	Core
CUST P10010045	2431	2490	2458	Hepatitis B virus subtype adw	С	Core
CUST P10010046	2469	2528	2459	Hepatitis B virus subtype adw	С	Core
CUST P10010047	2510	2569	2460	Hepatitis B virus subtype adw	С	Core
CUST P10010048	2539	2598	2461	Hepatitis B virus subtype adw	С	Core
CUST P10010049	2666	2725	2462	Hepatitis B virus subtype adw	С	Core
CUST P10010050	2690	2749	2463	Hepatitis B virus subtype adw	С	Core
CUST_P10010051	2723	2782	2464	Hepatitis B virus subtype adw	С	Core
CUST P10010052	2868	2912	2465	Hepatitis B virus subtype adw	С	Core
CUST P10010053	2933	2980	2466	Hepatitis B virus subtype adw	P	Pol
CUST P10010054	2961	3007	2467	Hepatitis B virus subtype adw	Р	Pol
CUST P10010055	2976	3020	2468	Hepatitis B virus subtype adw	Р	Pol
CUST P10010056	3014	3058	2469	Hepatitis B virus subtype adw	P	Pol
CUST P10010058	3163	3207	2470	Hepatitis B virus subtype adw	P	Pol
CUST P10010059	1	46	2471	Hepatitis B virus subtype ayw	S	surface protein
CUST P10010060	74	118	2472	Hepatitis B virus subtype ayw	s	surface protein
CUST P10010061	93	138	2473	Hepatitis B virus subtype ayw	s	surface protein
CUST P10010062	114	158	2474	Hepatitis B virus subtype ayw	s	surface protein
CUST P10010063	155	201	2475	Hepatitis B virus subtype ayw	S	surface protein
CUST P10010064	190	240	2476	Hepatitis B virus subtype ayw	S	surface protein
CUST P10010065	234	283	2477	Hepatitis B virus subtype ayw	S	surface protein
CUST P10010066			2478		S	
_	264	313	2479	Hepatitis B virus subtype ayw		surface protein
CUST_P10010067	295	339	2480	Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010068	330	374		Hepatitis B virus subtype ayw	S	surface protein

			SEQ ID		Genomic	
ProbeID	Start	End	NO: 2481	Virus	Region	Product
CUST_P10010069	369	416	2482	Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010070	392	447	2483	Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010071	443	493	2484	Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010072	473	517		Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010073	600	645	2485	Hepatitis B virus subtype ayw	S	surface protein
CUST_P10010076	851	907	2486	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010077	983	1033	2487	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010078	1028	1087	2488	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010079	1091	1147	2489	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010080	1161	1205	2490	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010081	1218	1262	2491	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010082	1265	1309	2492	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010083	1319	1374	2493	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010084	1384	1429	2494	Hepatitis B virus subtype ayw	X	x-protein
CUST_P10010085	1446	1490	2495	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010086	1476	1520	2496	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010087	1528	1572	2497	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010088	1552	1596	2498	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010089	1610	1654	2499	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010090	1636	1685	2500	Hepatitis B virus subtype ayw	X	x-protein
CUST P10010092	1815	1870	2501	Hepatitis B virus subtype ayw	C	Core
CUST P10010093	2042	2088	2502	Hepatitis B virus subtype ayw	С	Core
CUST_P10010094	2133	2192	2503	Hepatitis B virus subtype ayw	C	Core
CUST P10010095	2162	2221	2504	Hepatitis B virus subtype ayw	С	Core
CUST P10010096	2210	2269	2505	Hepatitis B virus subtype ayw	С	Core
CUST P10010097	2343		2506	Hepatitis B virus subtype ayw		
CUST P10010098		2387	2507	Hepatitis B virus subtype ayw	C	Core
_	2390	2434	2508	Hepatitis B virus subtype ayw		Core
CUST_P10010099	2427	2477	2509		C	Core
CUST_P10010100	2535	2594	2510	Hepatitis B virus subtype ayw	C	Core
CUST_P10010101	2577	2636	2511	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010102	2641	2700	2512	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010103	2698	2757	2513	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010104	2756	2815	2514	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010105	2794	2845	2515	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010106	2824	2872	2516	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010107	2856	2900	2517	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010108	2885	2929	2517	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010109	2915	2963		Hepatitis B virus subtype ayw	P	Pol
CUST_P10010110	3046	3090	2519	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010111	3121	3165	2520	Hepatitis B virus subtype ayw	P	Pol
CUST_P10010112	8	55	2521	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010113	79	125	2522	Hepatitis B virus, subtype adr	P	Pol

			SEQ ID		Genomic	
ProbeID	Start	End	NO:	Virus	Region	Product
CUST_P10010114	112	156	2523	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010119	325	370	2524	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010122	451	497	2525	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010123	477	521	2526	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010124	638	682	2527	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010125	667	714	2528	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010126	705	754	2529	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010127	839	894	2530	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010128	971	1022	2531	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010129	1088	1145	2532	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010131	1160	1204	2533	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010132	1203	1247	2534	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010133	1315	1361	2535	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010134	1458	1502	2536	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010136	1556	1600	2537	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010137	1635	1683	2538	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010138	1679	1729	2539	Hepatitis B virus, subtype adr	С	Core
CUST_P10010139	1810	1864	2540	Hepatitis B virus, subtype adr	С	Core
CUST_P10010140	1999	2043	2541	Hepatitis B virus, subtype adr	С	Core
CUST_P10010141	2109	2153	2542	Hepatitis B virus, subtype adr	С	Core
CUST_P10010142	2220	2279	2543	Hepatitis B virus, subtype adr	С	Core
CUST_P10010143	2247	2294	2544	Hepatitis B virus, subtype adr	С	Core
CUST_P10010144	2295	2346	2545	Hepatitis B virus, subtype adr	С	Core
CUST_P10010145	2365	2409	2546	Hepatitis B virus, subtype adr	С	Core
CUST_P10010148	2545	2604	2547	Hepatitis B virus, subtype adr	P	Pol
CUST_P10010149	2575	2634	2548	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010150	2618	2677	2549	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010151	2646	2705	2550	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010152	2672	2731	2551	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010153	2699	2758	2552	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010154	2735	2794	2553	Hepatitis B virus, subtype adr	Р	Pol
CUST_P10010156	2928	2972	2554	Hepatitis B virus, subtype adr	S1	surface protein
CUST_P10010157	2976	3020	2555	Hepatitis B virus, subtype adr	S1	surface protein
CUST_P10010158	3063	3107	2556	Hepatitis B virus, subtype adr	S1	surface protein
CUST P10010159	42	86	2557	Hepatitis B virus, subtype ayr	Р	Pol
CUST_P10010160	79	126	2558	Hepatitis B virus, subtype ayr	Р	Pol
CUST_P10010161	133	177	2559	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010162	158	202	2560	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010163	190	238	2561	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010164	227	280	2562	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010165	272	316	2563	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010166	328	372	2564	Hepatitis B virus, subtype ayr	S	surface protein

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUST P10010167	366	414	2565	Hepatitis B virus, subtype ayr	S	surface protein
CUST P10010168	390	447	2566	Hepatitis B virus, subtype ayr	S	surface protein
CUST P10010169	452	500	2567	Hepatitis B virus, subtype ayr	S	surface protein
CUST P10010170	477	521	2568	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010171	598	642	2569	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010172	659	707	2570	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010173	839	898	2571	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010174	971	1023	2572	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010175	1087	1146	2573	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010176	1116	1163	2574	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010177	1151	1195	2575	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010179	1318	1366	2576	Hepatitis B virus, subtype ayr	P	Pol
CUST_P10010180	1356	1400	2577	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010181	1388	1432	2578	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010182	1419	1463	2579	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010183	1472	1516	2580	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010185	1565	1609	2581	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010187	1643	1690	2582	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010188	1675	1725	2583	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010189	1808	1856	2584	Hepatitis B virus, subtype ayr	X	x-protein
CUST_P10010190	1941	1996	2585	Hepatitis B virus, subtype ayr	C	Core
CUST_P10010191	2001	2045	2586	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010192	2111	2155	2587	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010193	2210	2266	2588	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010194	2290	2335	2589	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010195	2365	2409	2590	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010196	2410	2456	2591	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010197	2430	2484	2592	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010198	2516	2571	2593	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010199	2577	2636	2594	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010200	2629	2688	2595	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010201	2675	2734	2596	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010202	2702	2761	2597	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010203	2742	2801	2598	Hepatitis B virus, subtype ayr	С	Core
CUST_P10010204	2890	2936	2599	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010205	2955	3001	2600	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010206	2978	3022	2601	Hepatitis B virus, subtype ayr	S	surface protein
CUST_P10010207	3012	3056	2602	Hepatitis B virus, subtype ayr	S	surface protein
CUST P10010208	57	104	2603	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010209	227	271	2604	Human parvovirus B19	NS	non-structural protein NS2
CUST_P10010211	637	693	2605	Human parvovirus B19	NS	non-structural protein NS1

ProbeID	Start	End	SEQ ID NO:	Virus	Genomic Region	Product
CUCT D10010212	685	744	2606	II nom.o.im.a D10	NS	non-structural protein NS1
CUST_P10010212 CUST_P10010214	973	1032	2607	Human parvovirus B19 Human parvovirus B19	NS	non-structural protein NS1
_			2608			non-structural
CUST_P10010215	1065	1124		Human parvovirus B19	NS	protein NS1 non-structural
CUST_P10010216	1165	1210	2609	Human parvovirus B19	NS	protein NS1
CUST_P10010217	1220	1279	2610	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010218	1258	1317	2611	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010219	1357	1416	2612	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010220	1408	1467	2613	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010221	1542	1601	2614	Human parvovirus B19	NS	non-structural protein NS1
CUST_P10010222	1628	1687	2615	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010223	1767	1812	2616	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010224	1845	1902	2617	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010225	1911	1970	2618	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010226	2041	2096	2619	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010227	2257	2301	2620	Human parvovirus B19	NS	non-structural protein NS1
CUST P10010228	2351	2399	2621	Human parvovirus B19	NS	non-structural protein NS1
_			2622	•		non-structural
CUST_P10010229	2395	2446	2623	Human parvovirus B19	NS	protein NS1 non-structural
CUST_P10010230	2426	2478	2624	Human parvovirus B19	NS	protein NS1 non-structural
CUST_P10010231	2552	2607		Human parvovirus B19	NS	protein NS1 minor capsid
CUST_P10010232	2787	2846	2625	Human parvovirus B19	VP1	protein minor capsid
CUST_P10010233	2836	2895	2626	Human parvovirus B19	VP1	protein minor capsid
CUST_P10010234	2868	2915	2627	Human parvovirus B19	VP1	protein minor capsid
CUST_P10010235	2914	2973	2628	Human parvovirus B19	VP1	protein
CUST_P10010236	3081	3140	2629	Human parvovirus B19	VPI	minor capsid protein
CUST_P10010237	3252	3297	2630	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010238	3276	3330	2631	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010239	3422	3481	2632	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010240	3524	3583	2633	Human parvovirus B19	VPI	minor capsid protein
CUST P10010241	3652	3711	2634	Human parvovirus B19	VP1	minor capsid protein
CUST P10010242	3801	3856	2635	Human parvovirus B19	VP1	minor capsid protein
CUST P10010243	3826	3885	2636	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010243	3864	3923	2637	Human parvovirus B19	VPI	minor capsid protein
CODI_I 10010244	J J J J J J	3743		Transan parvovilus D17	1 11	l broteni

			SEQ ID		Genomic	
ProbeID	Start	End	NO:	Virus	Region	Product
CUST_P10010245	3996	4042	2638	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010246	4097	4156	2639	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010247	4334	4393	2640	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010248	4463	4522	2641	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010249	4587	4646	2642	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010250	4723	4782	2643	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010251	4820	4864	2644	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010252	4915	4960	2645	Human parvovirus B19	VP1	minor capsid protein
CUST_P10010254	5087	5146	2646	Human parvovirus B19	VP2	major capsid protein
CUST_P10010257	5492	5539	2647	Human parvovirus B19	VP2	major capsid protein

Table 9. Exemplary bacterial and protozoan probes

SEQ ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2648	CUST_P10011833	115100	115153	Treponema pallidum	polA	Polymerase
2649	CUST_P10011835	115167	115219	Treponema pallidum	polA	Polymerase
2650	CUST_P10011836	115187	115237	Treponema pallidum	polA	Polymerase
2651	CUST_P10011838	115259	115314	Treponema pallidum	polA	Polymerase
2652	CUST_P10011840	115554	115613	Treponema pallidum	polA	Polymerase
2653	CUST_P10011841	115579	115638	Treponema pallidum	polA	Polymerase
2654	CUST_P10011842	115605	115664	Treponema pallidum	polA	Polymerase
2655	CUST_P10011843	115667	115716	Treponema pallidum	polA	Polymerase
2656	CUST_P10011844	115696	115740	Treponema pallidum	polA	Polymerase
2657	CUST_P10011845	115755	115807	Treponema pallidum	polA	Polymerase
2658	CUST_P10011847	116076	116126	Treponema pallidum	polA	Polymerase
2659	CUST_P10011848	116171	116223	Treponema pallidum	polA	Polymerase
2660	CUST_P10011849	116242	116294	Treponema pallidum	polA	Polymerase
2661	CUST_P10011850	116332	116384	Treponema pallidum	polA	Polymerase
2662	CUST_P10011851	116352	116396	Treponema pallidum	polA	Polymerase
2663	CUST_P10011852	116408	116459	Treponema pallidum	polA	Polymerase
2664	CUST_P10011853	116430	116488	Treponema pallidum	polA	Polymerase
2665	CUST_P10011854	116601	116649	Treponema pallidum	polA	Polymerase
2666	CUST_P10011855	116623	116674	Treponema pallidum	polA	Polymerase
2667	CUST_P10011856	116654	116713	Treponema pallidum	polA	Polymerase
2668	CUST_P10011857	116677	116736	Treponema pallidum	polA	Polymerase
2669	CUST_P10011858	116707	116760	Treponema pallidum	polA	Polymerase
2670	CUST_P10011860	116852	116906	Treponema pallidum	polA	Polymerase
2671	CUST_P10011862	116903	116962	Treponema pallidum	polA	Polymerase
2672	CUST_P10011863	116925	116978	Treponema pallidum	polA	Polymerase
2673	CUST_P10011864	116987	117032	Treponema pallidum	polA	Polymerase

SEQ						
ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2674	CUST P10011865	117028	117077	Treponema pallidum	polA	Polymerase
2675	CUST_P10011866	117128	117176	Treponema pallidum	polA	Polymerase
2676	CUST_P10011867	117270	117329	Treponema pallidum	polA	Polymerase
2677	CUST_P10011868	117441	117488	Treponema pallidum	polA	Polymerase
2678	CUST_P10011870	117516	117575	Treponema pallidum	polA	Polymerase
2679	CUST_P10011871	117570	117620	Treponema pallidum	polA	Polymerase
2680	CUST_P10011872	117777	117836	Treponema pallidum	polA	Polymerase
2681	CUST_P10011873	117806	117865	Treponema pallidum	polA	Polymerase
2682	CUST_P10011874	117873	117932	Treponema pallidum	polA	Polymerase
2683	CUST_P10011875	118152	118211	Treponema pallidum	polA	Polymerase
2684	CUST_P10011876	118181	118240	Treponema pallidum	polA	Polymerase
2685	CUST_P10011877	118281	118340	Treponema pallidum	polA	Polymerase
2686	CUST_P10011878	118302	118361	Treponema pallidum	polA	Polymerase
2687	CUST_P10011880	118541	118600	Treponema pallidum	polA	Polymerase
2688	CUST_P10011882	118756	118810	Treponema pallidum	polA	Polymerase
2689	CUST_P10018873	622214	622258	Treponema pallidum	TP0576	protein
2690	CUST_P10018877	622589	622637	Treponema pallidum	TP0576	protein
2691	CUST_P10018878	622725	622775	Treponema pallidum	TP0576	protein
2692	CUST_P10018881	622908	622961	Treponema pallidum	TP0576	protein
2693	CUST_P10018882	622953	622997	Treponema pallidum	TP0576	protein
2694	CUST_P10018883	622978	623030	Treponema pallidum	TP0576	protein
2695	CUST_P10018884	623033	623087	Treponema pallidum	TP0576	protein
2696	CUST_P10018887	623258	623302	Treponema pallidum	TP0576	protein
2697	CUST_P10024966	1067780	1067830	Treponema pallidum	aspS	aspartatetRNA ligase
2698	CUST_P10024967	1067910	1067970	Treponema pallidum	aspS	aspartatetRNA ligase
2699	CUST_P10024968	1067940	1067990	Treponema pallidum	aspS	aspartatetRNA ligase
2700	CUST_P10024969	1068070	1068120	Treponema pallidum	aspS	aspartatetRNA ligase
2701	CUST_P10024970	1068180	1068230	Treponema pallidum	aspS	aspartatetRNA ligase
2702	CUST_P10024971	1068330	1068380	Treponema pallidum	aspS	aspartatetRNA ligase
2703	CUST_P10024972 CUST_P10024976	1068410	1068470	Treponema pallidum Treponema pallidum	aspS	aspartatetRNA ligase
2704 2705	CUST_P10024976 CUST_P10024981	1068840 1069090	1068900 1069140	Treponema pallidum	aspS	aspartatetRNA ligase aspartatetRNA ligase
2706	CUST_P10024981	1069090	1069140	Treponema pallidum	aspS aspS	aspartatetRNA ligase
2707	CUST_P10024984	1069200	1069200	Treponema pallidum	aspS aspS	aspartatetRNA ligase
2707	CUST P10024980	1069380	1069790	Treponema pallidum	aspS aspS	aspartatetRNA ligase
2709	CUST_P10024991	1069740	1069790	Treponema pallidum	aspS	aspartatetRNA ligase
2710	CUST P10024994	1070010	1070060	Treponema pallidum	aspS aspS	aspartatetRNA ligase
2711	CUST P10024997	1070010	1070080	Treponema pallidum	aspS	aspartatetRNA ligase
2712	CUST P10024998	1070040	1070130	Treponema pallidum	aspS	aspartatetRNA ligase
2713	CUST P10024999	1070140	1070190	Treponema pallidum	aspS	aspartatetRNA ligase
2714	CUST P10025000	1070250	1070300	Treponema pallidum	aspS	aspartatetRNA ligase
2715	CUST P10025003	1070380	1070430	Treponema pallidum	aspS	aspartatetRNA ligase
2716	CUST P10025005	1070670	1070710	Treponema pallidum	aspS	aspartatetRNA ligase
2717	CUST P10025006	1070800	1070850	Treponema pallidum	TP0986	protein
2718	CUST_P10025009	1071210	1071260	Treponema pallidum	TP0986	protein

SEQ						
ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2719	CUST P10025010	1071230	1071290	Treponema pallidum	TP0986	protein
2720	CUST P10025018	1071990	1072040	Treponema pallidum	TP0986	protein
2721	CUST P10025019	1072210	1072260	Treponema pallidum	TP0989	protein
2722	CUST P10025024	1072490	1072540	Treponema pallidum	TP0989	protein
2723	CUST P10025027	1072660	1072710	Treponema pallidum	TP0989	protein
2724	CUST P10025028	1072870	1072910	Treponema pallidum	TP0989	protein
2725	CUST P10025029	1072990	1073040	Treponema pallidum	TP0989	protein
2726	CUST_P10025030	1073010	1073060	Treponema pallidum	TP0989	protein
2727	CUST P10025044	1074070	1074120	Treponema pallidum	TP0990	protein
2728	CUST P10025045	1074230	1074270	Treponema pallidum	TP0991	protein
2729	CUST P10025047	1074310	1074360	Treponema pallidum	TP0992	protein
2730	CUST P10025050	1074480	1074520	Treponema pallidum	TP0993	protein
2731	CUST P10025051	1074520	1074560	Treponema pallidum	TP0994	protein
2731	CUST_P10025051	1074560	1074500	Treponema pallidum	TP0995	protein
2733	_	1074500	1074670		TP0996	-
2734	CUST_P10025054		1074670	Treponema pallidum Treponema pallidum	TP0996 TP0997	protein
	CUST_P10025055	1074740		• •		protein
2735	CUST_P10025056	1074790	1074830	Treponema pallidum	TP0998	protein
2736	CUST_P10025058	1075040	1075090	Treponema pallidum	TP0999	protein
2737	CUST_P10025059	1075150	1075210	Treponema pallidum	TP1000	protein
2738	CUST_P10025061	1075310	1075360	Treponema pallidum	TP1001	protein
2739	CUST_P10025062	1075380	1075430	Treponema pallidum	TP1002	protein
2740	CUST_P10025063	1075540	1075600	Treponema pallidum	TP1003	protein
2741	CUST_P10025064	1075600	1075640	Treponema pallidum	TP1004	protein
2742	CUST_P10025065	1075670	1075720	Treponema pallidum	TP1005	protein
2743	CUST_P10025067	1075970	1076030	Treponema pallidum	TP1006	protein
2744	CUST_P10025068	1076040	1076100	Treponema pallidum	TP1007	protein
2745	CUST_P10025069	1076170	1076220	Treponema pallidum	TP0990	protein
2746	CUST_P10025073	1076400	1076450	Treponema pallidum	TP0991	protein
2747	CUST_P10025084	1077230	1077280	Treponema pallidum	TP0992	protein
2748	CUST_P10025095	1077820	1077870	Treponema pallidum	TP0992	protein
2749	CUST_P10025097	1077980	1078030	Treponema pallidum	TP0993	protein
2750	CUST_P10025098	1078120	1078170	Treponema pallidum	TP0993	protein
2751	CUST_P10025104	1078320	1078370	Treponema pallidum	TP0993	protein
2752	CUST_P10025934	479	538	Ehrlichia chaffeensis	ECH_RS00020	protein
2753	CUST_P10026529	69254	69313	Ehrlichia chaffeensis	argF	protein
2754	CUST_P10026957	118031	118090	Ehrlichia chaffeensis	ECH_RS00525	protein
2755	CUST_P10027106	133725	133784	Ehrlichia chaffeensis	ECH_RS00595	protein
2756	CUST_P10027296	155652	155711	Ehrlichia chaffeensis	ECH_RS00695	protein
2757	CUST_P10027314	158001	158060	Ehrlichia chaffeensis	ECH_RS00710	protein
2758	CUST_P10027972	235733	235792	Ehrlichia chaffeensis	ECH_RS01035	protein
2759	CUST_P10027973	235768	235827	Ehrlichia chaffeensis	ECH_RS01035	protein
2760	CUST_P10028360	279872	279931	Ehrlichia chaffeensis	ECH_RS01185	protein
2761	CUST_P10028636	313330	313389	Ehrlichia chaffeensis	ECH_RS01325	protein
2762	CUST_P10028976	353675	353734	Ehrlichia chaffeensis	groL	chaperonin GroEL
2763	CUST_P10028977	353852	353911	Ehrlichia chaffeensis	groL	chaperonin GroEL

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ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2764	CUST P10028978	354008	354067	Ehrlichia chaffeensis	groL	chaperonin GroEL
2765	CUST P10028979	354044	354103	Ehrlichia chaffeensis	groL	chaperonin GroEL
2766	CUST P10028980	354207	354266	Ehrlichia chaffeensis	groL	chaperonin GroEL
2767	CUST_P10028981	354405	354464	Ehrlichia chaffeensis	groL	chaperonin GroEL
2768	CUST P10028982	354433	354492	Ehrlichia chaffeensis	groL	chaperonin GroEL
2769	CUST_P10028983	354474	354533	Ehrlichia chaffeensis	groL	chaperonin GroEL
2770	CUST_P10028984	354504	354563	Ehrlichia chaffeensis	groL	chaperonin GroEL
2771	CUST_P10028985	354573	354632	Ehrlichia chaffeensis	groL	chaperonin GroEL
2772	CUST_P10028986	354646	354694	Ehrlichia chaffeensis	groL	chaperonin GroEL
2773	CUST_P10028987	354808	354867	Ehrlichia chaffeensis	groL	chaperonin GroEL
2774	CUST_P10028988	354995	355054	Ehrlichia chaffeensis	groL	chaperonin GroEL
2775	CUST_P10028989	355085	355144	Ehrlichia chaffeensis	groL	chaperonin GroEL
2776	CUST_P10028990	355336	355395	Ehrlichia chaffeensis	groL	chaperonin GroEL
2777	CUST_P10028991	355454	355508	Ehrlichia chaffeensis	groL	chaperonin GroEL
2778	CUST_P10029114	369147	369206	Ehrlichia chaffeensis	groL	chaperonin GroEL
2779	CUST_P10029290	392046	392105	Ehrlichia chaffeensis	sppA	signal peptide
2780	CUST_P10029649	429284	429343	Ehrlichia chaffeensis	ECH_RS01865	Protein
2781	CUST_P10029666	431631	431690	Ehrlichia chaffeensis	ECH_RS01866	Protein
2782	CUST_P10029696	434789	434848	Ehrlichia chaffeensis	ECH_RS01867	Protein
2783	CUST_P10029724	437453	437512	Ehrlichia chaffeensis	ECH_RS01868	Protein
2784	CUST_P10030575	531280	531339	Ehrlichia chaffeensis	ECH_RS01869	Protein
2785	CUST_P10030591	532929	532988	Ehrlichia chaffeensis	ECH_RS01870	Protein
2786	CUST_P10030711	547792	547851	Ehrlichia chaffeensis	ECH_RS01871	Protein
2787	CUST_P10030738	551432	551491	Ehrlichia chaffeensis	ECH_RS01872	Protein
2788	CUST_P10030817	563329	563388	Ehrlichia chaffeensis	ECH_RS01873	Protein
2789	CUST_P10030998	588404	588463	Ehrlichia chaffeensis	ECH_RS02440	Protein
2790	CUST_P10031006	590051	590110	Ehrlichia chaffeensis	ECH_RS02441	Protein
2791	CUST_P10031019	591869	591928	Ehrlichia chaffeensis	ECH_RS02442	Protein
2792	CUST_P10031129	603725	603784	Ehrlichia chaffeensis	ECH_RS02443	Protein
2793	CUST_P10031152	607138	607197	Ehrlichia chaffeensis	ECH_RS02444	Protein
2794	CUST_P10031295	626729	626788	Ehrlichia chaffeensis	ECH_RS02445	Protein
2795	CUST_P10031314	628696	628755	Ehrlichia chaffeensis	ECH_RS02446	Protein
2796	CUST_P10031320	629770	629829	Ehrlichia chaffeensis	ECH_RS02447	Protein
2797	CUST_P10031396	640107	640166	Ehrlichia chaffeensis	ECH_RS02448	Protein
2798	CUST_P10031397	640131	640190	Ehrlichia chaffeensis	ECH_RS02449	Protein
2799	CUST_P10031498	651172	651231	Ehrlichia chaffeensis	ECH_RS02450	Protein
2800	CUST_P10031499	651236	651295	Ehrlichia chaffeensis	ECH_RS02451	Protein
2801	CUST_P10031500	651472	651531	Ehrlichia chaffeensis	ECH_RS02452	Protein
2802	CUST_P10031501	651648	651707	Ehrlichia chaffeensis	ECH_RS02453	Protein
2803	CUST_P10031502	651715	651774	Ehrlichia chaffeensis	ECH_RS02454	Protein
2804	CUST_P10031503	651749	651808	Ehrlichia chaffeensis	ECH_RS02455	Protein
2805	CUST_P10031504	651916	651975	Ehrlichia chaffeensis	ECH_RS02456	Protein
2806	CUST_P10031720	672910	672969	Ehrlichia chaffeensis	ECH_RS02457	Protein
2807	CUST_P10031846	688686	688745	Ehrlichia chaffeensis	ECH_RS02458	Protein
2808	CUST_P10031955	700839	700898	Ehrlichia chaffeensis	ECH_RS02459	Protein

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ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2809	CUST P10032107	718318	718377	Ehrlichia chaffeensis	ECH RS02460	Protein
2810	CUST P10032134	720951	721010	Ehrlichia chaffeensis	ECH RS02461	Protein
2811	CUST P10032155	723928	723987	Ehrlichia chaffeensis	ECH RS02462	Protein
2812	CUST P10032156	724045	724104	Ehrlichia chaffeensis	ECH RS02463	Protein
2813	CUST P10032157	724081	724140	Ehrlichia chaffeensis	ECH RS02464	Protein
2814	CUST P10032207	729136	729195	Ehrlichia chaffeensis	ECH RS02465	Protein
2815	CUST P10032413	753701	753760	Ehrlichia chaffeensis	ECH RS02466	Protein
2816	CUST P10032541	768672	768731	Ehrlichia chaffeensis	ECH RS02467	Protein
2817	CUST P10032560	770310	770369	Ehrlichia chaffeensis	ECH RS02468	Protein
2818	CUST P10032563	770754	770813	Ehrlichia chaffeensis	ECH RS02469	Protein
2819	CUST P10032708	789240	789299	Ehrlichia chaffeensis	ECH RS02470	Protein
2820	CUST P10032835	805456	805515	Ehrlichia chaffeensis	ECH RS02471	Protein
2821	CUST P10032934	816181	816240	Ehrlichia chaffeensis	ECH RS02472	Protein
2822	CUST P10032949	818626	818685	Ehrlichia chaffeensis	ECH RS02473	Protein
2823	CUST P10033029	827167	827226	Ehrlichia chaffeensis	ECH RS02474	Protein
2824	CUST_P10033095	834972	835031	Ehrlichia chaffeensis	ECH RS02475	Protein
2825	CUST P10033283	854588	854647	Ehrlichia chaffeensis	ECH RS02476	Protein
2826	CUST P10033296	856372	856431	Ehrlichia chaffeensis	ECH RS02477	Protein
2827	CUST P10033303	858073	858132	Ehrlichia chaffeensis	ECH RS02478	Protein
2828	CUST_P10033406	871304	871363	Ehrlichia chaffeensis	ECH RS02479	Protein
2829	CUST P10033442	875535	875594	Ehrlichia chaffeensis	ECH RS02480	Protein
2830	CUST_P10033524	883572	883631	Ehrlichia chaffeensis	ECH_RS02481	Protein
2831	CUST_P10033559	887845	887904	Ehrlichia chaffeensis	ECH_RS02482	Protein
2832	CUST_P10033633	897694	897753	Ehrlichia chaffeensis	ECH_RS02483	Protein
2833	CUST_P10033864	922188	922247	Ehrlichia chaffeensis	ECH_RS02484	Protein
2834	CUST_P10033889	925077	925136	Ehrlichia chaffeensis	ECH_RS02485	Protein
2835	CUST_P10034084	946234	946293	Ehrlichia chaffeensis	ECH_RS02486	Protein
2836	CUST_P10034141	950852	950911	Ehrlichia chaffeensis	ECH_RS02487	Protein
2837	CUST_P10034279	966861	966920	Ehrlichia chaffeensis	ECH_RS02488	Protein
2838	CUST_P10034323	971540	971599	Ehrlichia chaffeensis	ECH_RS02489	Protein
2839	CUST_P10034725	1012370	1012430	Ehrlichia chaffeensis	ECH_RS02490	Protein
2840	CUST_P10034780	1018290	1018350	Ehrlichia chaffeensis	ECH_RS02491	Protein
2841	CUST_P10034783	1018550	1018610	Ehrlichia chaffeensis	ECH_RS02492	Protein
2842	CUST_P10034934	1034960	1035020	Ehrlichia chaffeensis	ECH_RS02493	Protein
2843	CUST_P10035002	1039980	1040040	Ehrlichia chaffeensis	ECH_RS02494	Protein
2844	CUST_P10035116	1053370	1053430	Ehrlichia chaffeensis	ECH_RS02495	Protein
2845	CUST_P10035418	1084080	1084130	Ehrlichia chaffeensis	ECH_RS02496	Protein
2846	CUST_P10035470	1089260	1089310	Ehrlichia chaffeensis	ECH_RS02497	Protein
2847	CUST_P10035547	1098110	1098170	Ehrlichia chaffeensis	ECH_RS02498	Protein
2848	CUST_P10035833	1129330	1129390	Ehrlichia chaffeensis	ECH_RS02499	Protein
2849	CUST_P10035846	1131120	1131180	Ehrlichia chaffeensis	ECH_RS02500	Protein
2850	CUST_P10036040	1151290	1151350	Ehrlichia chaffeensis	ECH_RS02501	Protein
2851	CUST_P10036201	1166620	1166680	Ehrlichia chaffeensis	ECH_RS02502	Protein
2852	CUST_P10036255	1172870	1172930	Ehrlichia chaffeensis	ECH_RS02503	Protein
2853	CUST_P10036280	37	96	Ehrlichia ewingii	16S ribosomal	16S ribosomal RNA

SEQ ID					Genomic	
NO:	ProbeID	Start	End	Pathogen	Region	Product
					RNA	
					16S ribosomal	
2854	CUST_P10036282	142	201	Ehrlichia ewingii	RNA	16S ribosomal RNA
2855	CUST P10036288	828	872	Ehrlichia ewingii	16S ribosomal RNA	16S ribosomal RNA
2033	CUS1_F10030288	020	0/2	Emilema ewingii	16S ribosomal	103 Hoosoniai KIVA
2856	CUST_P10036289	859	903	Ehrlichia ewingii	RNA	16S ribosomal RNA
					16S ribosomal	
2857	CUST_P10036290	885	938	Ehrlichia ewingii	RNA 16S ribosomal	16S ribosomal RNA
2858	CUST P10036291	915	969	Ehrlichia ewingii	RNA	16S ribosomal RNA
					16S ribosomal	
2859	CUST_P10036293	1099	1144	Ehrlichia ewingii	RNA	16S ribosomal RNA
2860	CUST_P10036294	1120	1164	Ehrlichia ewingii	16S ribosomal RNA	16S ribosomal RNA
2800	CUS1_F10030294	1120	1104	Emilicina ewingii	16S ribosomal	105 Hoosoiliai KINA
2861	CUST_P10036296	1282	1328	Ehrlichia ewingii	RNA	16S ribosomal RNA
					16S ribosomal	
2862	CUST_P10041026	540829	540888	Ehrlichia muris	RNA 16S ribosomal	16S ribosomal RNA
2863	CUST P10041027	540929	540988	Ehrlichia muris	RNA	16S ribosomal RNA
2003	2001_110011021	0.0020	210700		16S ribosomal	100 110 000111111111
2864	CUST_P10041028	541043	541102	Ehrlichia muris	RNA	16S ribosomal RNA
2965	CUCT D10041030	541102	541050	Eledialeia accesia	16S ribosomal RNA	LCC wile a name of DNIA
2865	CUST_P10041029	541193	541252	Ehrlichia muris	16S ribosomal	16S ribosomal RNA
2866	CUST_P10041030	541329	541388	Ehrlichia muris	RNA	16S ribosomal RNA
					16S ribosomal	
2867	CUST_P10041031	541437	541496	Ehrlichia muris	RNA	16S ribosomal RNA
2868	CUST P10041032	541659	541718	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2000	0051_110011032	311037	311710	Difficult mans	16S ribosomal	105 11005011111 11111
2869	CUST_P10041033	541758	541817	Ehrlichia muris	RNA	16S ribosomal RNA
2070	CLICT DIOCCOSO	222101	222250	Ehrlichia muris	16S ribosomal	LCC wiles we will DNIA
2870	CUST_P10038359	233191	233250	Enricina muns	RNA 16S ribosomal	16S ribosomal RNA
2871	CUST_P10038360	233399	233458	Ehrlichia muris	RNA	16S ribosomal RNA
					16S ribosomal	
2872	CUST_P10038361	233444	233503	Ehrlichia muris	RNA	16S ribosomal RNA
2873	CUST P10041027	540929	540988	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
20,0	0001_1100/1102/	0.0020	2 ,0700		16S ribosomal	100120000
2874	CUST_P10041028	541043	541102	Ehrlichia muris	RNA	16S ribosomal RNA
2875	CUST P10041029	541193	541252	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
20/3	CUS1_F10041029	341193	341232	Emilicina muns	16S ribosomal	105 HOOSOIIIAI KINA
2876	CUST_P10041030	541329	541388	Ehrlichia muris	RNA	16S ribosomal RNA
2055	CITCE PIOCITOR	543465	541404		16S ribosomal	160 1 17311
2877	CUST_P10041031	541437	541496	Ehrlichia muris	RNA 16S ribosomal	16S ribosomal RNA
2878	CUST P10041032	541659	541718	Ehrlichia muris	RNA	16S ribosomal RNA
	_				16S ribosomal	
2879	CUST_P10041771	642662	642721	Ehrlichia muris	RNA	16S ribosomal RNA
2880	CUST P10041772	642918	642977	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2000	COSI_I 10041//2	U72710	UT47//	Limitina munis	16S ribosomal	100 Hotsomal KINA
2881	CUST_P10041773	642945	643004	Ehrlichia muris	RNA	16S ribosomal RNA
2002	GUIGE PICCUIES:	6400E0	(42020		16S ribosomal	160 1 17311
2882	CUST_P10041774	642970	643029	Ehrlichia muris	RNA 16S ribosomal	16S ribosomal RNA
2883	CUST_P10041775	642995	643054	Ehrlichia muris	RNA	16S ribosomal RNA
					16S ribosomal	
2884	CUST_P10041776	643229	643288	Ehrlichia muris	RNA	16S ribosomal RNA

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ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2885	CUST_P10041777	643324	643383	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2886	CUST_P10041778	643453	643512	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2887	CUST_P10041779	643509	643562	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2888	CUST P10041780	643629	643688	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2889	CUST_P10041784	644380	644439	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2890	CUST_P10041785	644514	644573	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2891	CUST_P10041786	644749	644808	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2892	CUST_P10041787	644886	644945	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2893	CUST_P10041788	645057	645116	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2894	CUST P10041789	645158	645217	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2895	CUST P10041790	645281	645340	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2896	CUST_P10041791	645374	645433	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2897	CUST_P10041792	645397	645456	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2898	CUST_P10044860	996657	996716	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2899	CUST_P10044861	996761	996820	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2900	CUST_P10044862	996859	996918	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2901	CUST_P10044863	996901	996960	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2902	CUST_P10044864	996958	997017	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2903	CUST_P10044865	996983	997042	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2904	CUST P10044866	997035	997094	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2905	CUST_P10044867	997148	997207	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2906	CUST_P10044868	997264	997323	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2907	CUST_P10046461	1170365	1170424	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2908	CUST_P10046462	1170579	1170638	Ehrlichia muris	16S ribosomal RNA	16S ribosomal RNA
2909	CUST_P10043391	833268	833320	Ehrlichia muris	groL	chaperonin GroEL
2910	CUST_P10043392	833417	833476	Ehrlichia muris	groL	chaperonin GroEL
2911	CUST_P10043393	833446	833505	Ehrlichia muris	groL	chaperonin GroEL
2912	CUST_P10043394	833575	833634	Ehrlichia muris	groL	chaperonin GroEL
2913	CUST_P10043395	833777	833833	Ehrlichia muris	groL	chaperonin GroEL
2914	CUST_P10043396	833923	833982	Ehrlichia muris	groL	chaperonin GroEL
2915	CUST_P10043397	834065	834124	Ehrlichia muris	groL	chaperonin GroEL
2916	CUST_P10043398	834287	834346	Ehrlichia muris	groL	chaperonin GroEL
2917	CUST_P10043399	834382	834441	Ehrlichia muris	groL	chaperonin GroEL
2918	CUST_P10043400	834405	834464	Ehrlichia muris	groL	chaperonin GroEL
2919	CUST_P10043401	834509	834568	Ehrlichia muris	groL	chaperonin GroEL

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ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2920	CUST P10043402	834678	834737	Ehrlichia muris	groL	chaperonin GroEL
2921	CUST P10043403	834745	834804	Ehrlichia muris	groL	chaperonin GroEL
2922	CUST P10043404	834891	834950	Ehrlichia muris	groL	chaperonin GroEL
2923	CUST P10049214	444536	444595	Borrelia burgdorferi	16s	16S ribosomal RNA
2924	CUST P10049215	444623	444673	Borrelia burgdorferi	16s	16S ribosomal RNA
2925	CUST P10049216	444762	444821	Borrelia burgdorferi	16s	16S ribosomal RNA
2926	CUST P10049217	444920	444964	Borrelia burgdorferi	16s	16S ribosomal RNA
2927	CUST P10049218	444963	445012	Borrelia burgdorferi	16s	16S ribosomal RNA
2928	CUST P10049219	445091	445150	Borrelia burgdorferi	16s	16S ribosomal RNA
2929	CUST P10049220	445133	445179	Borrelia burgdorferi	16s	16S ribosomal RNA
2930	CUST P10049221	445305	445355	Borrelia burgdorferi	16s	16S ribosomal RNA
2931	CUST P10049222	445327	445373	Borrelia burgdorferi	16s	16S ribosomal RNA
2931	CUST_P10049222	445379	445426	Borrelia burgdorferi	16s	16S ribosomal RNA
2932	CUST_P10049223	445405	445464	Borrelia burgdorferi	16s	16S ribosomal RNA
2933	CUST_P10049224	445403	445487	Borrelia burgdorferi	16s	16S ribosomal RNA
	_					
2935	CUST_P10049226	445547	445591	Borrelia burgdorferi	16s	16S ribosomal RNA
2936	CUST_P10049227	445605	445664	Borrelia burgdorferi	16s	16S ribosomal RNA
2937	CUST_P10049228	445696	445740	Borrelia burgdorferi	16s	16S ribosomal RNA
2938	CUST_P10049229	445821	445867	Borrelia burgdorferi	16s	16S ribosomal RNA
2939	CUST_P10049230	445995	446040	Borrelia burgdorferi	16s	16S ribosomal RNA
2940	CUST_P10049231	446027	446077	Borrelia burgdorferi	16s	16S ribosomal RNA
2941	CUST_P10049138	435304	435363	Borrelia burgdorferi	23S	23S ribosomal RNA
2942	CUST_P10049139	435400	435453	Borrelia burgdorferi	23S	23S ribosomal RNA
2943	CUST_P10049140	435509	435553	Borrelia burgdorferi	23S	23S ribosomal RNA
2944	CUST_P10049141	435580	435627	Borrelia burgdorferi	23S	23S ribosomal RNA
2945	CUST_P10049142	435666	435710	Borrelia burgdorferi	23S	23S ribosomal RNA
2946	CUST_P10049143	435821	435872	Borrelia burgdorferi	23S	23S ribosomal RNA
2947	CUST_P10049144	435909	435958	Borrelia burgdorferi	23S	23S ribosomal RNA
2948	CUST_P10049145	435971	436030	Borrelia burgdorferi	23S	23S ribosomal RNA
2949	CUST_P10049146	436150	436201	Borrelia burgdorferi	23S	23S ribosomal RNA
2950	CUST_P10049147	436235	436279	Borrelia burgdorferi	23S	23S ribosomal RNA
2951	CUST_P10049148	436286	436334	Borrelia burgdorferi	23S	23S ribosomal RNA
2952	CUST_P10049149	436313	436371	Borrelia burgdorferi	23S	23S ribosomal RNA
2953	CUST_P10049150	436369	436413	Borrelia burgdorferi	23S	23S ribosomal RNA
2954	CUST_P10049151	436388	436446	Borrelia burgdorferi	23S	23S ribosomal RNA
2955	CUST_P10049152	436410	436469	Borrelia burgdorferi	23S	23S ribosomal RNA
2956	CUST_P10049153	436512	436558	Borrelia burgdorferi	23S	23S ribosomal RNA
2957	CUST_P10049154	436617	436676	Borrelia burgdorferi	23S	23S ribosomal RNA
2958	CUST_P10049155	436713	436766	Borrelia burgdorferi	23S	23S ribosomal RNA
2959	CUST_P10049156	436847	436891	Borrelia burgdorferi	23S	23S ribosomal RNA
2960	CUST_P10049157	436877	436926	Borrelia burgdorferi	23S	23S ribosomal RNA
2961	CUST_P10049158	436896	436952	Borrelia burgdorferi	23S	23S ribosomal RNA
2962	CUST_P10049166	438226	438285	Borrelia burgdorferi	23S	23S ribosomal RNA
2963	CUST_P10049167	438549	438608	Borrelia burgdorferi	23S	23S ribosomal RNA
2964	CUST_P10049168	438645	438697	Borrelia burgdorferi	23S	23S ribosomal RNA

SEQ						
ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
2965	CUST P10049169	438825	438872	Borrelia burgdorferi	238	23S ribosomal RNA
2966	CUST P10049170	438911	438955	Borrelia burgdorferi	23S	23S ribosomal RNA
2967	CUST P10049171	439032	439076	Borrelia burgdorferi	23S	23S ribosomal RNA
2968	CUST P10049172	439154	439203	Borrelia burgdorferi	23S	23S ribosomal RNA
2969	CUST P10049173	439168	439212	Borrelia burgdorferi	23S	23S ribosomal RNA
2970	CUST P10049174	439245	439304	Borrelia burgdorferi	23S	23S ribosomal RNA
2971	CUST P10049175	439395	439446	Borrelia burgdorferi	23S	23S ribosomal RNA
2972	CUST P10049176	439480	439524	Borrelia burgdorferi	23S	23S ribosomal RNA
2973	CUST P10049177	439531	439579	Borrelia burgdorferi	23S	23S ribosomal RNA
2974	CUST_P10049178	439558	439616	Borrelia burgdorferi	238	23S ribosomal RNA
2975	CUST P10049179	439619	439664	Borrelia burgdorferi	23S	23S ribosomal RNA
2976	CUST P10049180	439633	439691	Borrelia burgdorferi	23S	23S ribosomal RNA
2977					23S	23S ribosomal RNA
2977	CUST_P10049181	439655	439714 439803	Borrelia burgdorferi Borrelia burgdorferi	23S 23S	23S ribosomal RNA
	CUST_P10049182	439757		-		
2979	CUST_P10049183	439856	439915	Borrelia burgdorferi	23S	23S ribosomal RNA
2980	CUST_P10049184	439958	440011	Borrelia burgdorferi	23S	23S ribosomal RNA
2981	CUST_P10049185	440092	440136	Borrelia burgdorferi	23S	23S ribosomal RNA
2982	CUST_P10049186	440122	440171	Borrelia burgdorferi	23S	23S ribosomal RNA
2983	CUST_P10049187	440141	440197	Borrelia burgdorferi	23S	23S ribosomal RNA
2984	CUST_P10049188	440177	440233	Borrelia burgdorferi	23S	23S ribosomal RNA
2985	CUST_P10049189	440469	440528	Borrelia burgdorferi	23S	23S ribosomal RNA
2986	CUST_P10049190	440564	440623	Borrelia burgdorferi	23S	23S ribosomal RNA
2987	CUST_P10049191	440760	440811	Borrelia burgdorferi	23S	23S ribosomal RNA
2988	CUST_P10049192	440807	440865	Borrelia burgdorferi	23S	23S ribosomal RNA
2989	CUST_P10049193	440843	440896	Borrelia burgdorferi	23S	23S ribosomal RNA
2990	CUST_P10049194	440888	440945	Borrelia burgdorferi	23S	23S ribosomal RNA
2991	CUST_P10049195	441471	441530	Borrelia burgdorferi	23S	23S ribosomal RNA
2992	CUST_P10047332	126269	126328	Borrelia burgdorferi	recA	recombinase A
2993	CUST_P10047333	126457	126516	Borrelia burgdorferi	recA	recombinase A
2994	CUST_P10047334	126609	126668	Borrelia burgdorferi	recA	recombinase A
2995	CUST_P10047335	126748	126807	Borrelia burgdorferi	recA	recombinase A
2996	CUST_P10047336	126867	126926	Borrelia burgdorferi	recA	recombinase A
2997	CUST_P10047337	126934	126993	Borrelia burgdorferi	recA	recombinase A
2998	CUST_P10047338	127133	127188	Borrelia burgdorferi	recA	recombinase A
2999	CUST_P10047339	127173	127220	Borrelia burgdorferi	recA	recombinase A
3000	CUST_P10047340	127196	127247	Borrelia burgdorferi	recA	recombinase A
3001	CUST_P10047341	127219	127278	Borrelia burgdorferi	recA	recombinase A
3002	CUST D10051040	6651	6701	Coviollo hymatii	IS1111A	IS1111 A transmasses
3002	CUST_P10051940	0031	6701	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3003	CUST_P10051941	6794	6851	Coxiella burnetii	transposase	IS1111A transposase
3004	CUST P10051942	6831	6880	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3004	_	0031			IS1111A	
3005	CUST_P10051943	6911	6955	Coxiella burnetii	transposase	IS1111A transposase
3006	CUST P10051944	6942	6986	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3007	CUST P10051945	6981	7034	Coxiella burnetii	IS1111A	IS1111A transposase
2001	1 0001,1100	0701	,007	Comena cantem	1011111	1 1011111 Hamsposase

SEQ ID					Genomic	
NO:	ProbeID	Start	End	Pathogen	Region	Product
					transposase	
2000	CUCE PIOCEINA	7 000	5120	G ' 11 1 .''	IS1111A	TG1111A
3008	CUST_P10051946	7090	7139	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3009	CUST P10051947	7101	7154	Coxiella burnetii	transposase	IS1111A transposase
					IS1111A	
3010	CUST_P10051948	7164	7210	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3011	CUST P10051949	7287	7337	Coxiella burnetii	transposase	IS1111A transposase
	_		,,,,,		IS1111A	
3012	CUST_P10051950	7318	7367	Coxiella burnetii	transposase	IS1111A transposase
3013	CUST P10051951	7437	7483	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3013	0001_110001701	, 137	7 103	COMENIA OUNICII	IS1111A	15111111 duasposase
3014	CUST_P10051952	7459	7506	Coxiella burnetii	transposase	IS1111A transposase
3015	CUST P10051953	7499	7544	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3013	COS1_110031733	7477	7,544	COMENIA GUINCUI	IS1111A	15111177 ttansposase
3016	CUST_P10051954	7516	7565	Coxiella burnetii	transposase	IS1111A transposase
3017	CUST P10051955	7551	7603	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3017	CUS1_F10031933	7331	7003	Coxiena duniem	IS1111A	151111A transposase
3018	CUST_P10051956	7660	7704	Coxiella burnetii	transposase	IS1111A transposase
3019	CUCT D10051057	7712	77(2	Carrialla larromatii	IS1111A	ICIIII A tuonema sona
3019	CUST_P10051957	7712	7763	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3020	CUST_P10051958	7817	7867	Coxiella burnetii	transposase	IS1111A transposase
2021	CUICE PLOOS	247400	245450	G ' 11 1 .''	IS1111A	TC11114
3021	CUST_P10056626	345409	345458	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3022	CUST_P10056627	345420	345473	Coxiella burnetii	transposase	IS1111A transposase
	GYYGT DIOGECCE	217102	245520	G	IS1111A	701111
3023	CUST_P10056628	345483	345529	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3024	CUST_P10056629	345606	345656	Coxiella burnetii	transposase	IS1111A transposase
2025	CITCH PIOCECCO	245525	215606	G : 11 1	IS1111A	TG1111
3025	CUST_P10056630	345637	345686	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3026	CUST_P10056631	345756	345802	Coxiella burnetii	transposase	IS1111A transposase
2025	GYYGT DIOGECCO	2.1.7.7.0	2.4.502.5	G	IS1111A	701111
3027	CUST_P10056632	345778	345825	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3028	CUST_P10056633	345818	345863	Coxiella burnetii	transposase	IS1111A transposase
					IS1111A	
3029	CUST_P10056634	345835	345884	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3030	CUST P10056635	345870	345922	Coxiella burnetii	transposase	IS1111A transposase
					IS1111A	
3031	CUST_P10056636	345979	346023	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3032	CUST P10056637	346031	346082	Coxiella burnetii	transposase	IS1111A transposase
	_				IS1111A	
3033	CUST_P10056638	346136	346186	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3034	CUST P10058309	465895	465941	Coxiella burnetii	transposase	IS1111A transposase
	_				IS1111A	
3035	CUST_P10058310	465926	465970	Coxiella burnetii	transposase	IS1111A transposase
3036	CUST P10058311	466027	466080	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3037	CUST_P10058312	466064	466113	Coxiella burnetii	transposase	IS1111A transposase
3038	CUST P10058313	466123	466170	Coxiella burnetii	IS1111A transposase	IS1111A transposase
2020		.00123	.55170	Coment ounten	Lamposase	1 -5 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1

SEQ						
ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
3039	CUST D10059214	466146	466192	Coxiella burnetii	IS1111A	IS1111A transposase
3039	CUST_P10058314	400140	400192	Coxiena oumem	transposase IS1111A	151111A transposase
3040	CUST_P10058315	466263	466311	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3041	CUST_P10058316	466301	466354	Coxiella burnetii	transposase	IS1111A transposase
3042	CUST P10058317	466422	466466	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3043	CUST_P10058318	466457	466504	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3044	CUST_P10058319	466479	466530	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3045	CUST_P10058320	466511	466555	Coxiella burnetii	transposase	IS1111A transposase
3046	CUST P10058321	466595	466648	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3047	CUST_P10058322	466644	466688	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3048	CUST_P10058323	466684	466728	Coxiella burnetii	transposase	IS1111A transposase
3049	CUST_P10058324	466749	466798	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3050	CUST P10058325	466778	466835	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3051	CUST_P10058326	466943	466999	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3052	CUST_P10058816	502390	502443	Coxiella burnetii	transposase	IS1111A transposase
3053	CUST_P10058817	502499	502548	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3054	CUST P10058818	502510	502563	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3055	CUST_P10058819	502573	502619	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3056	CUST_P10058820	502696	502746	Coxiella burnetii	transposase	IS1111A transposase
3057	CUST_P10058821	502727	502776	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3058	CUST P10058822	502846	502892	Coxiella burnetii	IS1111A	
3038	_				transposase IS1111A	IS1111A transposase
3059	CUST_P10058823	502868	502915	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3060	CUST_P10058824	502908	502953	Coxiella burnetii	transposase	IS1111A transposase
3061	CUST P10058825	502925	502974	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3062	CUST P10058826	502960	503012	Coxiella burnetii	IS1111A	IS1111A transposase
	_		303012		transposase IS1111A	
3063	CUST_P10058827	503069	503113	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3064	CUST_P10058828	503121	503172	Coxiella burnetii	transposase	IS1111A transposase
3065	CUST P10058829	503226	503276	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3066	CUST_P10058830	503308	503358	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3067	CUST_P10058831	503329	503384	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3068	CUST_P10058832	503374	503433	Coxiella burnetii	transposase	IS1111A transposase
3069	CUST P10058833	503541	503597	Coxiella burnetii	IS1111A transposase	IS1111A transposase
	_				IS1111A	
3070	CUST_P10058834	503609	503658	Coxiella burnetii	transposase	IS1111A transposase

SEQ ID					Genomic	
NO:	ProbeID	Start	End	Pathogen	Region	Product
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3071	CUST_P10058835	503681	503725	Coxiella burnetii	transposase	IS1111A transposase
3072	CUST_P10058836	503718	503765	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3073	CUST P10058837	503745	503791	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3073	COST_110038837	303743	303771	Coxicila ourileur	IS1111A	131111A ttatisposase
3074	CUST_P10058838	503852	503911	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3075	CUST_P10065644	1021442	1021488	Coxiella burnetii	transposase	IS1111A transposase
3076	CUST_P10065645	1021559	1021607	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3077	CUST_P10065646	1021597	1021650	Coxiella burnetii	IS1111A transposase	IS1111A transposase
					IS1111A	
3078	CUST_P10065647	1021718	1021762	Coxiella burnetii	transposase	IS1111A transposase
3079	CUST_P10065648	1021753	1021800	Coxiella burnetii	IS1111A transposase	IS1111A transposase
2000	CLICT D10065640	1021775	1021926	Carrialla larmatii	IS1111A	ICIIII A tuomana anna
3080	CUST_P10065649	1021775	1021826	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3081	CUST_P10065650	1021807	1021851	Coxiella burnetii	transposase	IS1111A transposase
3082	CUST P10065651	1021891	1021944	Coxiella burnetii	IS1111A transposase	IS1111A transposase
3082	COST_110003031	1021671	1021744	Coxicila bullicui	IS1111A	131111A ttalisposase
3083	CUST_P10065652	1021940	1021984	Coxiella burnetii	transposase IS1111A	IS1111A transposase
3084	CUST P10065653	1021980	1022024	Coxiella burnetii	transposase	IS1111A transposase
					IS1111A	
3085	CUST_P10065654	1022045	1022094	Coxiella burnetii	transposase	IS1111A transposase
3086	CUST_P10079271	1019	1078	Trypanosoma brucei	kinetoplast apocy	kinetoplast apocy
	GT.G				kinetoplast	
3087	CUST_P10079269	471	530	Trypanosoma brucei	apocy	kinetoplast apocy
3088	CUST P10079274	1363	1414	Trypanosoma brucei	kinetoplast apocy	kinetoplast apocy
3000	<u> </u>	1303	1111	11ypanosonia oracei	kinetoplast	Miletopiasi apoey
3089	CUST_P10079272	1279	1334	Trypanosoma brucei	apocy	kinetoplast apocy
3090	CUST_P10079270	628	687	Trypanosoma brucei	kinetoplast apocy	kinetoplast apocy
3070	<u> </u>	020	007	11y panosonia oracei	kinetoplast	Kinetopiasi apoey
3091	CUST_P10079273	1329	1373	Trypanosoma brucei	apocy	kinetoplast apocy
2002	CLICE PLOSSOSO	605	7.46	TD 1 '	kinetoplast	1
3092	CUST_P10079280	687	746	Trypanosoma brucei	DNA m kinetoplast	kinetoplast DNA m
3093	CUST P10079276	478	526	Trypanosoma brucei	DNA m	kinetoplast DNA m
					kinetoplast	
3094	CUST_P10079277	547	601	Trypanosoma brucei	DNA m	kinetoplast DNA m
3095	CUST P10079275	1	60	Transposome beread	kinetoplast DNA m	kinetonlast DNA m
3093	CUST_F100/92/3	1	00	Trypanosoma brucei	kinetoplast	kinetoplast DNA m
3096	CUST_P10079279	677	736	Trypanosoma brucei	DNA m kinetoplast	kinetoplast DNA m
3097	CUST_P10079278	554	610	Trypanosoma brucei	DNA m	kinetoplast DNA m
3098	CUST P10079281	23	67	Trypanosoma Cruzi	Mini satellite	Mini satellite
	_				kinetoplast	
3099	CUST_P10079284	267	312	Leishmania major	DNA kinetoplast	kinetoplast DNA
3100	CUST P10079285	319	365	Leishmania major	kinetoplast DNA	kinetoplast DNA
					kinetoplast	
3101	CUST_P10079286	360	404	Leishmania major	DNA kinetoplast	kinetoplast DNA
3102	CUST_P10079283	146	205	Leishmania major	DNA	kinetoplast DNA

SEQ ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
3103	CUST_P10079287	382	426	Leishmania major	kinetoplast DNA	kinetoplast DNA
3104	CUST_P10079282	1	60	Leishmania major	kinetoplast DNA	kinetoplast DNA
3105	CUST P10079294	504	548	Leishmania major	kinetoplast DNA	kinetoplast DNA
3106	CUST_P10079292	333	377	Leishmania major	kinetoplast DNA	kinetoplast DNA
3107	CUST_P10079296	588	632	Leishmania major	kinetoplast DNA	kinetoplast DNA
3108	CUST_P10079291	298	342	Leishmania major	kinetoplast DNA	kinetoplast DNA
3109	CUST_P10079290	257	303	Leishmania major	kinetoplast DNA	kinetoplast DNA
3110	CUST_P10079295	551	595	Leishmania major	kinetoplast DNA	kinetoplast DNA
3111	CUST_P10079289	148	200	Leishmania major	kinetoplast DNA	kinetoplast DNA
3112	CUST_P10079288	116	168	Leishmania major	kinetoplast DNA	kinetoplast DNA
3113	CUST_P10079293	462	507	Leishmania major	kinetoplast DNA	kinetoplast DNA
3114	CUST_P10079326	82	141	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3115	CUST_P10079327	140	189	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3116	CUST_P10079328	168	227	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3117	CUST_P10079329	320	364	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3118	CUST_P10079330	336	380	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3119	CUST_P10079331	368	412	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3120	CUST_P10079332	398	450	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3121	CUST_P10079333	434	493	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3122	CUST_P10079334	699	758	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3123	CUST_P10079335	722	781	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3124	CUST_P10079336	771	825	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3125	CUST_P10079337	801	860	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3126	CUST_P10079338	826	885	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3127	CUST_P10079339	891	947	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3128	CUST_P10079340	933	987	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3129	CUST_P10079341	952	1006	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3130	CUST_P10079342	990	1042	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3131	CUST_P10079343	1016	1060	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3132	CUST_P10079344	1055	1101	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3133	CUST_P10079345	1108	1152	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3134	CUST_P10079346	1239	1298	Babesia microti	18S ribosomal RNA	18S ribosomal RNA

SEQ ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
3135	CUST P10079347	1357	1405	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3136	CUST P10079347	1435	1479	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
2125	CHICE PLOGGOMA	1450	1515	D 1 1 1 1	18S ribosomal	100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3137	CUST_P10079349	1458	1517	Babesia microti	RNA 18S ribosomal	18S ribosomal RNA
3138	CUST_P10079350	1620	1675	Babesia microti	RNA	18S ribosomal RNA
3139	CUST_P10079351	1659	1718	Babesia microti	18S ribosomal RNA 18S ribosomal	18S ribosomal RNA
3140	CUST_P10079352	1736	1786	Babesia microti	RNA	18S ribosomal RNA
3141	CUST_P10079353	1758	1802	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3142	CUST_P10079354	1811	1855	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3143	CUST_P10079355	1845	1889	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3144	CUST P10079356	1894	1938	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
					18S ribosomal	
3145	CUST_P10079357	1914	1962	Babesia microti	RNA 18S ribosomal	18S ribosomal RNA
3146	CUST_P10079358	1947	1997	Babesia microti	RNA	18S ribosomal RNA
3147	CUST P10079359	1975	2019	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
	_				18S ribosomal	
3148	CUST_P10079360	2034	2093	Babesia microti	RNA 18S ribosomal	18S ribosomal RNA
3149	CUST_P10079361	2056	2115	Babesia microti	RNA 18S ribosomal	18S ribosomal RNA
3150	CUST_P10079362	2125	2174	Babesia microti	RNA	18S ribosomal RNA
3151	CUST_P10079363	2266	2322	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3152	CUST P10079364	2342	2392	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
3153	CUST P10079365	2363	2418	Babesia microti	18S ribosomal RNA	18S ribosomal RNA
	_				18S ribosomal	
3154	CUST_P10079366	2389	2446	Babesia microti	RNA 18S ribosomal	18S ribosomal RNA
3155	CUST_P10079478	328	375	Plasmodium falciparum	RNA	18S ribosomal RNA
3156	CUST_P10079479	433	492	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3157	CUST P10079480	517	566	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
	_			•	18S ribosomal	
3158	CUST_P10079481	612	671	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3159	CUST_P10079482	820	879	Plasmodium falciparum	RNA	18S ribosomal RNA
3160	CUST_P10079483	945	1003	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3161	CUST_P10079484	971	1030	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3162	CUST_P10079485	1018	1077	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3163	CUST_P10079486	1211	1257	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3164	CUST_P10079487	1284	1343	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3165	CUST_P10079488	1386	1445	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3166	CUST_P10079489	1673	1727	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA

SEQ ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
					18S ribosomal	
3167	CUST_P10079490	1817	1876	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3168	CUST_P10079491	1852	1911	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3169	CUST_P10079492	70	129	Plasmodium falciparum	RNA	18S ribosomal RNA
3170	CUST_P10079493	321	373	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3171	CUST_P10079494	460	519	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3172	CUST_P10079495	489	548	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3173	CUST_P10079496	519	569	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
2174	CUCT D10070407	500	(50	Dla anna diama falainanana	18S ribosomal	10C .::l 1 DNI A
3174	CUST_P10079497	599	658	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3175	CUST_P10079498	800	859	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3176	CUST_P10079499	826	885	Plasmodium falciparum	RNA	18S ribosomal RNA
2177	CUCT D10070500	990	1046	Dla maa diama falainaman	18S ribosomal	19C wiles a served DNIA
3177	CUST_P10079500	990	1046	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3178	CUST_P10079501	1014	1073	Plasmodium falciparum	RNA 18S ribosomal	18S ribosomal RNA
3179	CUST P10079502	1053	1112	Plasmodium falciparum	RNA	18S ribosomal RNA
3180	CUST_P10079503	1264	1310	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3181	CUST_P10079504	1332	1391	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3182	CUST_P10079505	1450	1509	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3183	CUST_P10079506	1721	1770	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3184	CUST P10079507	1742	1801	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3185	CUST P10079508	1890	1949	Plasmodium falciparum	18S ribosomal RNA	18S ribosomal RNA
3186	CUST_P10079572	2	61	Plasmodium vivax	SSU rRNA	external transcribed spacer
	-					external transcribed
3187	CUST_P10079573	38	89	Plasmodium vivax	SSU rRNA	spacer external transcribed
3188	CUST_P10079574	68	127	Plasmodium vivax	SSU rRNA	spacer external transcribed
3189	CUST_P10079575	112	171	Plasmodium vivax	SSU rRNA	spacer
3190	CUST_P10079576	249	308	Plasmodium vivax	SSU rRNA	external transcribed spacer
3191	CUST_P10079577	279	338	Plasmodium vivax	SSU rRNA	external transcribed spacer
3192	CUST_P10079578	319	372	Plasmodium vivax	SSU rRNA	external transcribed spacer
3193	CUST_P10079579	421	480	Plasmodium vivax	SSU rRNA	external transcribed spacer
3194	CUST_P10079580	590	645	Plasmodium vivax	SSU rRNA	external transcribed spacer
3195	CUST_P10079581	671	719	Plasmodium vivax	SSU rRNA	external transcribed spacer
3196	CUST P10079582	783	842	Plasmodium vivax	SSU rRNA	external transcribed spacer
3197	CUST P10079583	803	862	Plasmodium vivax	SSU rRNA	external transcribed spacer
3198	CUST_P10079584	829	888	Plasmodium vivax	SSU rRNA	external transcribed spacer

SEQ ID NO:	ProbeID	Start	End	Pathogen	Genomic Region	Product
110.	TTOBELD	Start	Enu	Tathogen	Region	external transcribed
3199	CUST_P10079585	849	899	Plasmodium vivax	SSU rRNA	spacer
3200	CUST_P10079586	946	1005	Plasmodium vivax	SSU rRNA	external transcribed spacer
3201	CUST P10079587	1153	1212	Plasmodium vivax	SSU rRNA	external transcribed spacer
3202	CUST_P10079588	1314	1373	Plasmodium vivax	SSU rRNA	external transcribed spacer
3203	CUST_P10079589	1346	1405	Plasmodium vivax	SSU rRNA	external transcribed spacer
3204	CUST_P10079590	1545	1591	Plasmodium vivax	SSU rRNA	external transcribed spacer
3205	CUST_P10079591	1610	1669	Plasmodium vivax	SSU rRNA	external transcribed spacer
3206	CUST_P10079592	1717	1776	Plasmodium vivax	SSU rRNA	external transcribed spacer
3207	CUST_P10079593	1757	1816	Plasmodium vivax	SSU rRNA	external transcribed spacer

Table 10. Exemplary control probes

SEQ ID NO:	ProbeID	Start	End	Туре	Genomic Region
3208	CUST_P10079594	1561	1605	Housekeeping Gene	ACTB
3209	CUST_P10079595	1703	1750	Housekeeping Gene	ACTB
3210	CUST_P10079596	2220	2264	Housekeeping Gene	ACTB
3211	CUST_P10079597	2242	2286	Housekeeping Gene	ACTB
3212	CUST_P10079598	2276	2320	Housekeeping Gene	ACTB
3213	CUST_P10079599	2402	2446	Housekeeping Gene	ACTB
3214	CUST_P10079600	2489	2533	Housekeeping Gene	ACTB
3215	CUST_P10079601	2659	2703	Housekeeping Gene	ACTB
3216	CUST_P10079602	2696	2740	Housekeeping Gene	ACTB
3217	CUST_P10079603	2823	2867	Housekeeping Gene	ACTB
3218	CUST_P10079604	2847	2891	Housekeeping Gene	ACTB
3219	CUST_P10079605	2874	2918	Housekeeping Gene	ACTB
3220	CUST_P10079606	3005	3049	Housekeeping Gene	ACTB
3221	CUST_P10079607	3046	3090	Housekeeping Gene	ACTB
3222	CUST_P10079608	3213	3257	Housekeeping Gene	ACTB
3223	CUST_P10079609	3338	3382	Housekeeping Gene	ACTB
3224	CUST_P10079610	3376	3420	Housekeeping Gene	ACTB
3225	CUST_P10079611	3393	3437	Housekeeping Gene	ACTB
3226	CUST_P10079612	3438	3482	Housekeeping Gene	ACTB
3227	CUST_P10079613	3545	3593	Housekeeping Gene	ACTB
3228	CUST_P10079614	3568	3622	Housekeeping Gene	ACTB
3229	CUST_P10079615	3601	3645	Housekeeping Gene	ACTB
3230	CUST_P10079616	3744	3788	Housekeeping Gene	ACTB
3231	CUST_P10079617	3858	3902	Housekeeping Gene	ACTB
3232	CUST_P10079618	3973	4017	Housekeeping Gene	ACTB
3233	CUST_P10079619	4130	4177	Housekeeping Gene	ACTB
3234	CUST_P10079620	4223	4267	Housekeeping Gene	ACTB

SEQ					Camania
ID NO:	ProbeID	Start	End	Туре	Genomic Region
3235	CUST_P10079621	4280	4324	Housekeeping Gene	ACTB
3236	CUST_P10079622	4304	4348	Housekeeping Gene	ACTB
3237	CUST_P10079623	4315	4359	Housekeeping Gene	ACTB
3238	CUST_P10079624	4459	4503	Housekeeping Gene	ACTB
3239	CUST_P10079625	4592	4636	Housekeeping Gene	ACTB
3240	CUST_P10079626	4906	4950	Housekeeping Gene	ACTB
3241	CUST_P10079627	4932	4978	Housekeeping Gene	ACTB
3242	CUST_P10079628	4972	5016	Housekeeping Gene	ACTB
3243	CUST_P10079629	5024	5068	Housekeeping Gene	ACTB
3244	CUST_P10079630	5040	5084	Housekeeping Gene	ACTB
3245	CUST_P10079631	5076	5120	Housekeeping Gene	ACTB
3246	CUST_P10079632	5110	5154	Housekeeping Gene	ACTB
3247	CUST_P10079633	5200	5244	Housekeeping Gene	ACTB
3248	CUST_P10079634	5357	5401	Housekeeping Gene	ACTB
3249	CUST_P10079635	5390	5434	Housekeeping Gene	ACTB
3250	CUST_P10079636	5415	5459	Housekeeping Gene	ACTB
3251	CUST_P10079637	5453	5497	Housekeeping Gene	ACTB
3252	CUST_P10079638	5474	5518	Housekeeping Gene	ACTB
3253	CUST P10079639	5622	5666	Housekeeping Gene	ACTB
3254	CUST_P10079640	5662	5706	Housekeeping Gene	ACTB
3255	CUST P10079641	5691	5736	Housekeeping Gene	ACTB
3256	CUST P10079642	5712	5756	Housekeeping Gene	ACTB
3257	CUST P10079643	5760	5804	Housekeeping Gene	ACTB
3258	CUST P10079644	5783	5827	Housekeeping Gene	ACTB
3259	CUST P10079645	5817	5861	Housekeeping Gene	ACTB
3260	CUST P10079646	5963	6007	Housekeeping Gene	ACTB
3261	CUST P10079647	6004	6048	Housekeeping Gene	ACTB
3262	CUST P10079648	6106	6150	Housekeeping Gene	ACTB
3263	CUST P10079649	6310	6354	Housekeeping Gene	ACTB
3264	CUST P10079650	6421	6465	Housekeeping Gene	ACTB
3265	CUST P10079651	6507	6553	Housekeeping Gene	ACTB
3266	CUST P10079652	6696	6740	Housekeeping Gene	ACTB
3267	CUST P10079653	6722	6769	Housekeeping Gene	ACTB
3268	CUST P10079654	6745	6789	Housekeeping Gene	ACTB
3269	CUST_P10079655	6772	6816	Housekeeping Gene	ACTB
3270	CUST_P10079656	6793	6837	Housekeeping Gene	ACTB
3271	CUST_P10079657	6844	6888	Housekeeping Gene	ACTB
3272	CUST_P10079658	7000	7044	Housekeeping Gene	ACTB
3273	CUST_P10079659	7321	7365	Housekeeping Gene	ACTB
3274	CUST_P10079660	7418	7462	Housekeeping Gene	ACTB
3275	CUST_P10079661	7554	7598	Housekeeping Gene	ACTB
3276	CUST P10079662	7683	7727	Housekeeping Gene	ACTB
3277	CUST_P10079663	7777	7821	Housekeeping Gene	ACTB
3278	CUST P10079664	7825	7869	Housekeeping Gene	ACTB
3279	CUST_P10079665	7861	7917	Housekeeping Gene	ACTB

SEQ					Camania
ID NO:	ProbeID	Start	End	Туре	Genomic Region
3280	CUST P10079666	8033	8077	Housekeeping Gene	ACTB
3281	CUST P10079667	8138	8182	Housekeeping Gene	ACTB
3282	CUST P10079668	8344	8388	Housekeeping Gene	ACTB
3283	CUST P10079669	8459	8503	Housekeeping Gene	ACTB
3284	CUST P10079670	8519	8563	Housekeeping Gene	ACTB
3285	CUST P10079671	8543	8587	Housekeeping Gene	АСТВ
3286	CUST P10079672	8574	8618	Housekeeping Gene	ACTB
3287	CUST P10079673	8628	8672	Housekeeping Gene	ACTB
3288	CUST_P10079674	8732	8776	Housekeeping Gene	ACTB
3289	CUST_P10079675	8941	8985	Housekeeping Gene	ACTB
3290	CUST_P10079676	8962	9006	Housekeeping Gene	ACTB
3291	CUST P10079677	8987	9031	Housekeeping Gene	АСТВ
3292	CUST P10079678	9103	9147	Housekeeping Gene	ACTB
3293	CUST_P10079679	9155	9199	Housekeeping Gene	ACTB
3294	CUST P10079680	9429	9474	Housekeeping Gene	ACTB
3295	CUST P10079681	9554	9600	Housekeeping Gene	ACTB
3296	CUST P10079682	9739	9785	Housekeeping Gene	ACTB
3297	CUST P10079683	9774	9820	Housekeeping Gene	ACTB
3298	CUST P10079684	9794	9838	Housekeeping Gene	ACTB
3299	CUST P10079685	10015	10062	Housekeeping Gene	ACTB
3300	CUST P10079686	10064	10108	Housekeeping Gene	ACTB
3301	CUST P10079687	10193	10245	Housekeeping Gene	ACTB
3302	CUST P10079715	3325	3369	Housekeeping Gene	ARL1
3303	CUST P10079713	3255	3314	Housekeeping Gene	ARL1
3304	CUST P10079727	5957	6016	Housekeeping Gene	ARL1
3305	CUST P10079741	10779	10838	Housekeeping Gene	ARL1
3306	CUST P10079759	13558	13604	Housekeeping Gene	ARL1
3307	CUST P10079701	934	979	Housekeeping Gene	ARL1
3308	CUST P10079692	526	570	Housekeeping Gene	ARL1
3309	CUST P10079750	11884	11939	Housekeeping Gene	ARL1
3310	CUST P10079730	6728	6787	Housekeeping Gene	ARL1
3311	CUST P10079746	11349	11397	Housekeeping Gene	ARL1
3312	CUST_P10079744	11307	11354	Housekeeping Gene	ARL1
3313	CUST_P10079732	7235	7286	Housekeeping Gene	ARL1
3314	CUST_P10079733	7270	7314	Housekeeping Gene	ARL1
3315	CUST_P10079760	13597	13641	Housekeeping Gene	ARL1
3316	CUST_P10079762	13648	13693	Housekeeping Gene	ARL1
3317	CUST_P10079758	13449	13508	Housekeeping Gene	ARL1
3318	CUST_P10079728	6518	6577	Housekeeping Gene	ARL1
3319	CUST_P10079738	9891	9950	Housekeeping Gene	ARL1
3320	CUST_P10079742	10939	10998	Housekeeping Gene	ARL1
3321	CUST_P10079696	746	796	Housekeeping Gene	ARL1
3322	CUST_P10079703	1025	1079	Housekeeping Gene	ARL1
3323	CUST_P10079688	137	181	Housekeeping Gene	ARL1
3324	CUST P10079755	12703	12762	Housekeeping Gene	ARL1

SEQ					Genomic
ID NO:	ProbeID	Start	End	Type	Region
3325	CUST_P10079748	11728	11787	Housekeeping Gene	ARL1
3326	CUST_P10079722	5055	5114	Housekeeping Gene	ARL1
3327	CUST P10079724	5213	5268	Housekeeping Gene	ARL1
3328	CUST P10079736	8842	8901	Housekeeping Gene	ARL1
3329	CUST P10079714	3291	3350	Housekeeping Gene	ARL1
3330	CUST P10079726	5923	5982	Housekeeping Gene	ARL1
3331	CUST P10079735	8610	8669	Housekeeping Gene	ARL1
3332	CUST P10079739	10525	10584	Housekeeping Gene	ARL1
3333	CUST P10079747	11552	11599	Housekeeping Gene	ARL1
3334	CUST_P10079753	12428	12487	Housekeeping Gene	ARL1
3335	CUST P10079768	14112	14158	Housekeeping Gene	ARL1
3336	CUST P10079690	310	354	Housekeeping Gene	ARL1
3337	CUST P10079691	435	483	Housekeeping Gene	ARL1
3338	CUST_P10079702	977	1028	Housekeeping Gene	ARL1
3339	CUST P10079689	209	253	Housekeeping Gene	ARL1
3340	CUST P10079743	11265	11317	Housekeeping Gene	ARL1
3341	CUST P10079745	11327	11379	Housekeeping Gene	ARL1
3342	CUST P10079712	3205	3264	Housekeeping Gene	ARL1
3343	CUST P10079740	10708	10767	Housekeeping Gene	ARL1
3344	CUST P10079710	2561	2620	Housekeeping Gene	ARL1
3345	CUST P10079717	3630	3689	Housekeeping Gene	ARL1
3346	CUST P10079761	13619	13672	Housekeeping Gene	ARL1
3347	CUST P10079707	1616	1675	Housekeeping Gene	ARL1
3348	CUST P10079767	14091	14135	Housekeeping Gene	ARL1
3349	CUST P10079699	861	910	Housekeeping Gene	ARL1
3350	CUST P10079697	794	838	Housekeeping Gene	ARL1
3351	CUST P10079694	683	742	Housekeeping Gene	ARL1
3352	CUST P10079749	11842	11901	Housekeeping Gene	ARL1
3353	CUST P10079716	3606	3665	Housekeeping Gene	ARL1
3354	CUST P10079708	2224	2283	Housekeeping Gene	ARL1
3355	CUST P10079719	4420	4479	Housekeeping Gene	ARL1
3356	CUST P10079763	13695	13749	Housekeeping Gene	ARL1
3357	CUST P10079752	12271	12330	Housekeeping Gene	ARL1
3358	CUST P10079721	4794	4853	Housekeeping Gene	ARL1
3359	CUST P10079766	14055	14099	Housekeeping Gene	ARL1
3360	CUST P10079764	13860	13919	Housekeeping Gene	ARL1
3361	CUST P10079765	13910	13963	Housekeeping Gene	ARL1
3362	CUST P10079706	1514	1573	Housekeeping Gene	ARL1
3363	CUST P10079705	1462	1509	Housekeeping Gene	ARLI
3364	CUST P10079695	715	774	Housekeeping Gene	ARL1
3365	CUST P10079698	836	884	Housekeeping Gene	ARLI
3366	CUST P10079693	655	710	Housekeeping Gene	ARL1
3367	CUST P10079754	12585	12644	Housekeeping Gene	ARLI
3368	CUST P10079731	7083	7139	Housekeeping Gene	ARL1
3369	CUST P10079731	5093	5152	Housekeeping Gene	ARLI

SEQ ID NO:	ProbeID	Start	End	Туре	Genomic Region
3370	CUST P10079704	1198	1257	Housekeeping Gene	ARL1
3371	CUST P10079756	12839	12888	Housekeeping Gene	ARL1
3372	CUST P10079711	2977	3036	Housekeeping Gene	ARL1
3373	CUST P10079709	2313	2369	Housekeeping Gene	ARL1
3374	CUST P10079770	14253	14312	Housekeeping Gene	ARL1
3375	CUST P10079700	891	939	Housekeeping Gene	ARL1
3376	CUST P10079734	7994	8053	Housekeeping Gene	ARL1
3377	CUST_P10079729	6688	6746	Housekeeping Gene	ARL1
3378	CUST_P10079718	4205	4249	Housekeeping Gene	ARL1
3379	CUST_P10079751	12179	12229	Housekeeping Gene	ARL1
3380	CUST_P10079720	4653	4712	Housekeeping Gene	ARL1
3381	CUST_P10079725	5683	5733	Housekeeping Gene	ARL1
3382	CUST_P10079769	14139	14193	Housekeeping Gene	ARL1
3383	CUST_P10079771	14283	14342	Housekeeping Gene	ARL1
3384	CUST_P10079737	8984	9043	Housekeeping Gene	ARL1
3385	CUST_P10079757	12965	13024	Housekeeping Gene	ARL1
3386	CUST_P10079772	69	113	Housekeeping Gene	CCDN1
3387	CUST_P10079773	104	148	Housekeeping Gene	CCDN1
3388	CUST_P10079774	297	341	Housekeeping Gene	CCDN1
3389	CUST_P10079775	332	376	Housekeeping Gene	CCDN1
3390	CUST_P10079776	395	439	Housekeeping Gene	CCDN1
3391	CUST_P10079777	680	724	Housekeeping Gene	CCDN1
3392	CUST_P10079778	844	903	Housekeeping Gene	CCDN1
3393	CUST_P10079779	1049	1093	Housekeeping Gene	CCDNI
3394	CUST_P10079780	1146	1190	Housekeeping Gene	CCDN1
3395	CUST_P10079781	1368	1412	Housekeeping Gene	CCDN1
3396	CUST_P10079782	1513	1557	Housekeeping Gene	CCDN1
3397	CUST_P10079783	1553	1597	Housekeeping Gene	CCDN1
3398	CUST_P10079784	1811	1855	Housekeeping Gene	CCDN1
3399	CUST_P10079785	1936	1980	Housekeeping Gene	CCDN1
3400	CUST_P10079786	2041	2085	Housekeeping Gene	CCDN1
3401	CUST_P10079787	2206	2250	Housekeeping Gene	CCDN1
3402	CUST_P10079788	2233	2277	Housekeeping Gene	CCDN1
3403	CUST_P10079789	2279	2323	Housekeeping Gene	CCDN1
3404	CUST_P10079790	2321	2365	Housekeeping Gene	CCDN1
3405	CUST_P10079791	2346	2390	Housekeeping Gene	CCDN1
3406	CUST_P10079792	2376	2420	Housekeeping Gene	CCDN1
3407	CUST_P10079793	2385	2429	Housekeeping Gene	CCDN1
3408	CUST_P10079794	2413	2457	Housekeeping Gene	CCDN1
3409	CUST_P10079795	2455	2499	Housekeeping Gene	CCDN1
3410	CUST_P10079796	2584	2628	Housekeeping Gene	CCDN1
3411	CUST_P10079797	2794	2838	Housekeeping Gene	CCDN1
3412	CUST_P10079798	2842	2886	Housekeeping Gene	CCDN1
3413	CUST_P10079799	2899	2943	Housekeeping Gene	CCDN1
3414	CUST_P10079800	2953	2997	Housekeeping Gene	CCDN1

SEQ ID					Genomic
NO:	ProbeID	Start	End	Туре	Region
3415	CUST_P10079801	3037	3081	Housekeeping Gene	CCDN1
3416	CUST_P10079802	3135	3179	Housekeeping Gene	CCDN1
3417	CUST_P10079803	3194	3238	Housekeeping Gene	CCDN1
3418	CUST_P10079804	3365	3409	Housekeeping Gene	CCDN1
3419	CUST_P10079805	3518	3562	Housekeeping Gene	CCDN1
3420	CUST_P10079806	3675	3719	Housekeeping Gene	CCDN1
3421	CUST_P10079807	3753	3797	Housekeeping Gene	CCDN1
3422	CUST_P10079808	3904	3948	Housekeeping Gene	CCDN1
3423	CUST_P10079809	4120	4164	Housekeeping Gene	CCDN1
3424	CUST P10079810	4201	4245	Housekeeping Gene	CCDN1
3425	CUST P10079811	4312	4356	Housekeeping Gene	CCDN1
3426	CUST P10079812	4419	4463	Housekeeping Gene	CCDN1
3427	CUST P10079813	4486	4530	Housekeeping Gene	CCDN1
3428	CUST P10079814	4518	4562	Housekeeping Gene	CCDN1
3429	CUST P10079815	4542	4586	Housekeeping Gene	CCDN1
3430	CUST P10079816	4560	4609	Housekeeping Gene	CCDNI
3431	CUST P10079817	4595	4639	Housekeeping Gene	CCDN1
3432	CUST P10079818	4633	4677	Housekeeping Gene	CCDNI
3433	CUST P10079819	4645	4692	Housekeeping Gene	CCDN1
3434	CUST P10079820	4674	4720	Housekeeping Gene	CCDNI
3435	CUST P10079821	4726	4770	Housekeeping Gene	CCDN1
3436	CUST P10079822	4753	4797	Housekeeping Gene	CCDNI
3437	CUST_P10079822 CUST_P10079823	4910	4956	Housekeeping Gene	CCDN1
		5081	5131	Housekeeping Gene	
3438	CUST_P10079824			-	CCDN1
3439	CUST_P10079825	5281	5325	Housekeeping Gene	CCDN1
3440	CUST_P10079826	5295	5345	Housekeeping Gene	CCDN1
3441	CUST_P10079827	5319	5363	Housekeeping Gene	CCDN1
3442	CUST_P10079828	5472	5516	Housekeeping Gene	CCDN1
3443	CUST_P10079829	5506	5550	Housekeeping Gene	CCDN1
3444	CUST_P10079830	5654	5698	Housekeeping Gene	CCDN1
3445	CUST_P10079831	5680	5724	Housekeeping Gene	CCDN1
3446	CUST_P10079832	5709	5753	Housekeeping Gene	CCDN1
3447	CUST_P10079833	5736	5780	Housekeeping Gene	CCDN1
3448	CUST_P10079834	5775	5819	Housekeeping Gene	CCDN1
3449	CUST_P10079835	5804	5848	Housekeeping Gene	CCDN1
3450	CUST_P10079836	5828	5872	Housekeeping Gene	CCDN1
3451	CUST_P10079837	5876	5920	Housekeeping Gene	CCDN1
3452	CUST_P10079838	6010	6054	Housekeeping Gene	CCDN1
3453	CUST_P10079839	6083	6133	Housekeeping Gene	CCDN1
3454	CUST_P10079840	6163	6207	Housekeeping Gene	CCDN1
3455	CUST_P10079841	6270	6314	Housekeeping Gene	CCDN1
3456	CUST_P10079842	6395	6442	Housekeeping Gene	CCDN1
3457	CUST_P10079843	6557	6604	Housekeeping Gene	CCDN1
3458	CUST_P10079844	6611	6656	Housekeeping Gene	CCDN1
3459	CUST_P10079845	6635	6679	Housekeeping Gene	CCDNI

SEQ					Cara and a
ID NO:	ProbeID	Start	End	Туре	Genomic Region
3460	CUST P10079846	6770	6814	Housekeeping Gene	CCDN1
3461	CUST_P10079847	6895	6939	Housekeeping Gene	CCDN1
3462	CUST P10079848	6976	7020	Housekeeping Gene	CCDN1
3463	CUST_P10079849	7012	7056	Housekeeping Gene	CCDN1
3464	CUST_P10079850	7064	7108	Housekeeping Gene	CCDN1
3465	CUST_P10079851	7224	7268	Housekeeping Gene	CCDN1
3466	CUST_P10079852	7283	7327	Housekeeping Gene	CCDN1
3467	CUST_P10079853	7444	7488	Housekeeping Gene	CCDN1
3468	CUST_P10079854	7649	7693	Housekeeping Gene	CCDN1
3469	CUST_P10079855	7768	7812	Housekeeping Gene	CCDN1
3470	CUST_P10079856	7794	7838	Housekeeping Gene	CCDN1
3471	CUST_P10079857	7858	7902	Housekeeping Gene	CCDN1
3472	CUST_P10079858	7957	8001	Housekeeping Gene	CCDN1
3473	CUST_P10079859	8092	8136	Housekeeping Gene	CCDN1
3474	CUST_P10079860	8120	8168	Housekeeping Gene	CCDN1
3475	CUST_P10079861	8173	8217	Housekeeping Gene	CCDNI
3476	CUST_P10079862	8228	8272	Housekeeping Gene	CCDN1
3477	CUST_P10079863	8422	8473	Housekeeping Gene	CCDNI
3478	CUST_P10079864	8469	8513	Housekeeping Gene	CCDN1
3479	CUST_P10079865	8649	8693	Housekeeping Gene	CCDNI
3480	CUST_P10079866	8842	8887	Housekeeping Gene	CCDN1
3481	CUST_P10079867	8960	9004	Housekeeping Gene	CCDN1
3482	CUST_P10079868	8995	9039	Housekeeping Gene	CCDN1
3483	CUST_P10079869	9060	9104	Housekeeping Gene	CCDN1
3484	CUST_P10079870	9132	9176	Housekeeping Gene	CCDN1
3485	CUST_P10079871	9183	9227	Housekeeping Gene	CCDN1
3486	CUST_P10079872	9196	9240	Housekeeping Gene	CCDN1
3487	CUST_P10079873	9229	9273	Housekeeping Gene	CCDN1
3488	CUST_P10079874	9266	9310	Housekeeping Gene	CCDN1
3489	CUST_P10079875	9309	9353	Housekeeping Gene	CCDN1
3490	CUST_P10079876	9333	9377	Housekeeping Gene	CCDN1
3491	CUST_P10079877	9390	9434	Housekeeping Gene	CCDNI
3492	CUST_P10079878	9430	9474	Housekeeping Gene	CCDN1
3493	CUST_P10079879	9479	9523	Housekeeping Gene	CCDN1
3494	CUST_P10079880	9508	9552	Housekeeping Gene	CCDN1
3495	CUST_P10079881	9519	9563	Housekeeping Gene	CCDN1
3496	CUST_P10079882	9570	9614	Housekeeping Gene	CCDN1
3497	CUST_P10079883	9592	9639	Housekeeping Gene	CCDN1
3498	CUST_P10079884	9705	9749	Housekeeping Gene	CCDN1
3499	CUST_P10079885	9885	9933	Housekeeping Gene	CCDN1
3500	CUST_P10079886	10029	10073	Housekeeping Gene	CCDN1
3501	CUST_P10079887	10165	10209	Housekeeping Gene	CCDN1
3502	CUST_P10079888	10204	10248	Housekeeping Gene	CCDN1
3503	CUST_P10079889	10442	10501	Housekeeping Gene	CCDN1
3504	CUST_P10079890	10526	10574	Housekeeping Gene	CCDNI

SEQ					G .
ID NO:	ProbeID	Start	End	Туре	Genomic Region
3505	CUST P10079891	10760	10819	Housekeeping Gene	CCDN1
3506	CUST P10079892	10833	10877	Housekeeping Gene	CCDN1
3507	CUST_P10079893	10868	10912	Housekeeping Gene	CCDN1
3508	CUST_P10079894	10900	10944	Housekeeping Gene	CCDN1
3509	CUST_P10079895	10931	10975	Housekeeping Gene	CCDN1
3510	CUST_P10079896	11055	11107	Housekeeping Gene	CCDN1
3511	CUST_P10079897	11190	11242	Housekeeping Gene	CCDN1
3512	CUST_P10079898	11364	11410	Housekeeping Gene	CCDN1
3513	CUST_P10079899	11472	11525	Housekeeping Gene	CCDN1
3514	CUST_P10079900	11490	11547	Housekeeping Gene	CCDN1
3515	CUST_P10079901	11807	11852	Housekeeping Gene	CCDN1
3516	CUST_P10079902	11887	11940	Housekeeping Gene	CCDN1
3517	CUST_P10079903	12162	12221	Housekeeping Gene	CCDN1
3518	CUST_P10079904	12355	12412	Housekeeping Gene	CCDN1
3519	CUST_P10079905	12402	12446	Housekeeping Gene	CCDN1
3520	CUST_P10081361	16	63	Negative Control	Aedes albopictus densovirus 2
3521	CUST_P10081362	47	101	Negative Control	Aedes albopictus densovirus 2
3522	CUST_P10081363	79	131	Negative Control	Aedes albopictus densovirus 2
3523	CUST P10081364	204	248	Negative Control	Aedes albopictus densovirus 2
2524	CLICT D10001265	202	261		Aedes albopictus densovirus
3524	CUST_P10081365	302	361	Negative Control	Aedes albopictus densovirus
3525	CUST_P10081366	330	385	Negative Control	Aedes albopictus densovirus
3526	CUST_P10081367	390	435	Negative Control	2 Aedes albopictus densovirus
3527	CUST_P10081368	426	472	Negative Control	2
3528	CUST_P10081369	590	649	Negative Control	Aedes albopictus densovirus 2
3529	CUST_P10081370	617	673	Negative Control	Aedes albopictus densovirus 2
3530	CUST_P10081371	654	707	Negative Control	Aedes albopictus densovirus 2
2521	CLICT D10081272	752	910		Aedes albopictus densovirus
3531	CUST_P10081372	753	810	Negative Control	Aedes albopictus densovirus
3532	CUST_P10081373	791	844	Negative Control	2
3533	CUST_P10081374	824	880	Negative Control	Aedes albopictus densovirus 2
3534	CUST_P10081375	966	1015	Negative Control	Aedes albopictus densovirus 2
3535	CUST_P10081376	1174	1233	Negative Control	Aedes albopictus densovirus 2
3536	CUST_P10081377	1295	1339	Negative Control	Aedes albopictus densovirus 2
3537	CUST_P10081378	1385	1433	Negative Control	Aedes albopictus densovirus 2
3538	CUST_P10081379	1538	1582	Negative Control	Aedes albopictus densovirus
3539	CUST_P10081380	1556	1601	Negative Control	Aedes albopictus densovirus
					Aedes albopictus densovirus
3540	CUST_P10081381	1636	1689	Negative Control	2

SEQ ID	D of the	64-4	To all	T	Genomic
NO:	ProbeID	Start	End	Туре	Region Aedes albopictus densovirus
3541	CUST_P10081382	1752	1811	Negative Control	2
3542	CUST_P10081383	1810	1854	Negative Control	Aedes albopictus densovirus 2
3543	CUST_P10081384	1836	1893	Negative Control	Aedes albopictus densovirus 2
3544	CUST P10081385	1858	1913	Negative Control	Aedes albopictus densovirus
3545	CUST P10081386	1977	2036	Negative Control	Aedes albopictus densovirus 2
3546	CUST_P10081387	2065	2124	Negative Control	Aedes albopictus densovirus 2
3547	CUST_P10081388	2093	2152	Negative Control	Aedes albopictus densovirus 2
3548	CUST_P10081389	2136	2195	Negative Control	Aedes albopictus densovirus 2
3549	CUST_P10081390	2162	2221	Negative Control	Aedes albopictus densovirus 2 Aedes albopictus densovirus
3550	CUST_P10081391	2209	2257	Negative Control	Aedes albopicius densoviius 2
3551	CUST_P10081392	2384	2434	Negative Control	Aedes albopictus densovirus 2
3552	CUST_P10081393	2497	2546	Negative Control	Aedes albopictus densovirus 2
3553	CUST_P10081394	2530	2589	Negative Control	Aedes albopictus densovirus 3
3554	CUST_P10081395	2697	2754	Negative Control	Aedes albopictus densovirus 2 Aedes albopictus densovirus
3555	CUST_P10081396	2766	2825	Negative Control	2
3556	CUST_P10081397	281	340	Negative Control	Aedes albopictus densovirus 2
3557	CUST P10081398	353	404	Negative Control	Aedes albopictus densovirus 2
3558	CUST P10081399	411	457	Negative Control	Maize streak virus
3559	CUST P10081400	572	630	Negative Control	Maize streak virus
3560	CUST P10081401	727	786	Negative Control	Maize streak virus
3561	CUST P10081402	760	819	Negative Control	Maize streak virus
3562	CUST P10081403	799	852	Negative Control	Maize streak virus
3563	CUST P10081404	839	891	Negative Control	Maize streak virus
3564	CUST P10081405	871	919	Negative Control	Maize streak virus
3565	CUST P10081406	937	988	Negative Control	Maize streak virus
3566	CUST P10081407	961	1011	Negative Control	Maize streak virus
3567	CUST P10081408	1177	1233	Negative Control	Maize streak virus
3568	CUST P10081409	1316	1365	Negative Control	Maize streak virus
3569	CUST P10081410	1362	1420	Negative Control	Maize streak virus
3570	CUST_P10081411	1391	1450	Negative Control	Maize streak virus
3571	CUST_P10081411	1447	1506	Negative Control	
					Maize streak virus
3572	CUST_P10081413	1694	1753	Negative Control	Maize streak virus
3573	CUST_P10081414	1837	1896	Negative Control	Maize streak virus
3574	CUST_P10081415	2047	2106	Negative Control	Maize streak virus
3575	CUST_P10081416	2095	2147	Negative Control	Maize streak virus
3576	CUST_P10081417	2362	2421	Negative Control	Maize streak virus
3577	CUST_P10081418	2387	2446	Negative Control	Maize streak virus
3578	CUST_P10081419	2536	2595	Negative Control	Maize streak virus

SEQ					
ID NO:	ProbeID	Start	End	Туре	Genomic Region
3579	CUST P10081420	2666	2713	Negative Control	Maize streak virus
3580	CUST P10081421	2893	2952	Negative Control	Maize streak virus
3581	CUST P10081422	2953	3012	Negative Control	Maize streak virus
3582	CUST P10081423	2987	3045	Negative Control	Maize streak virus
3583	CUST P10081424	3014	3071	Negative Control	Maize streak virus
3584	CUST P10081425	3054	3105	Negative Control	Maize streak virus
3585	CUST P10081426	3093	3142	Negative Control	Maize streak virus
3586	CUST P10081427	3144	3203	Negative Control	Maize streak virus
3587	CUST P10081428	3194	3253	Negative Control	Maize streak virus
3588	CUST P10081429	3330	3389	Negative Control	Maize streak virus
3589	CUST P10081430	3390	3438	Negative Control	Maize streak virus
3590	CUST P10081431	3414	3469	Negative Control	Maize streak virus
3591	CUST P10081432	3441	3494	Negative Control	Maize streak virus
3592	CUST P10081433	3525	3584	Negative Control	Maize streak virus
3593	CUST P10081434	3586	3645	Negative Control	Maize streak virus
3594	CUST P10081435	3727	3786	Negative Control	Maize streak virus
3595	CUST P10081436	3879	3923	Negative Control	Maize streak virus
3596	CUST P10081437	3967	4011	Negative Control	Maize streak virus
3597	CUST P10081438	112	169	Negative Control	Maize streak virus
3598	CUST_P10081439	272	316	Negative Control	Maize streak virus
3599	CUST P10081440	301	345	Negative Control	Tomato pseudo-curly top virus
3600	CUST P10081441	341	387	Negative Control	Tomato pseudo-curly top virus
2601	CUCT D10001442	126	490	No retire Control	Tomato pseudo-curly top
3601	CUST_P10081442	436	480	Negative Control	virus Tomato pseudo-curly top
3602	CUST_P10081443	468	515	Negative Control	virus Tomato pseudo-curly top
3603	CUST_P10081444	490	534	Negative Control	virus
3604	CUST_P10081446	687	731	Negative Control	Tomato pseudo-curly top virus
2605	CUCT D10001447	902	0.47	Na ration Cantus!	Tomato pseudo-curly top
3605	CUST_P10081447	803	847	Negative Control	virus Tomato pseudo-curly top
3606	CUST_P10081448	813	857	Negative Control	virus
3607	CUST_P10081449	842	887	Negative Control	Tomato pseudo-curly top virus
3608	CUST P10081451	1031	1090	Negative Control	Tomato pseudo-curly top virus
	-				Tomato pseudo-curly top
3609	CUST_P10081452	1120	1164	Negative Control	virus Tomato pseudo-curly top
3610	CUST_P10081453	1166	1214	Negative Control	virus
3611	CUST_P10081454	1187	1246	Negative Control	Tomato pseudo-curly top virus
3612	CUST_P10081455	1216	1260	Negative Control	Tomato pseudo-curly top virus
3613	CUST_P10081456	1332	1385	Negative Control	Tomato pseudo-curly top virus
3614	CUST_P10081457	1370	1429	Negative Control	Tomato pseudo-curly top virus
3615	CUST_P10081458	1407	1459	Negative Control	Tomato pseudo-curly top virus
3616	CUST P10081459	1440	1499	Negative Control	Tomato pseudo-curly top

SEQ ID					Genomic
NO:	ProbeID	Start	End	Туре	Region
					virus
3617	CUST_P10081460	1600	1650	Negative Control	Tomato pseudo-curly top virus
3618	CUST_P10081461	1615	1669	Negative Control	Tomato pseudo-curly top virus
3619	CUST_P10081462	1648	1698	Negative Control	Tomato pseudo-curly top virus
3620	CUST_P10081463	1740	1797	Negative Control	Tomato pseudo-curly top virus
3621	CUST_P10081464	2072	2128	Negative Control	Tomato pseudo-curly top virus
3622	CUST_P10081465	2114	2173	Negative Control	Tomato pseudo-curly top virus
3623	CUST_P10081466	2158	2217	Negative Control	Tomato pseudo-curly top virus
3624	CUST_P10081467	2296	2346	Negative Control	Tomato pseudo-curly top virus
3625	CUST_P10081468	2446	2490	Negative Control	Tomato pseudo-curly top virus
3626	CUST_P10081470	2548	2592	Negative Control	Tomato pseudo-curly top virus
3627	CUST_P10081471	2596	2650	Negative Control	Tomato pseudo-curly top virus
3628	CUST_P10081472	2633	2683	Negative Control	Tomato pseudo-curly top virus

In view of the many possible embodiments to which the principles of the disclosure may be applied, it should be recognized that the illustrated embodiments are only examples and should not be taken as

5 limiting the scope of the invention. Rather, the scope of the invention is defined by the following claims.

We therefore claim as our invention all that comes within the scope and spirit of these claims.

We claim:

1. A probe set comprising probes having at least 90% identity with the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769 or a subset thereof.

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- 2. The probe set of claim 1, wherein the probe set comprises probes having at least 95% identity with the nucleic acid sequences of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769 or a subset thereof.
- 3. The probe set of claim 2, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 1-1300, 1391-1570, and 1691-1769 or a subset thereof.
 - 4. The probe set of any one of claims 1 to 3, wherein the probe set comprises at least 30 probes for each of Chikungunya virus, Dengue virus type 1, Dengue virus type 2, Dengue virus type 3, Dengue virus type 4, Hepatitis A virus, Hepatitis C virus type 1, Hepatitis C virus type 2, Hepatitis C virus type 3,
- Hepatitis E virus, Human immunodeficiency virus type 1, Human immunodeficiency virus type 2, Human T-lymphotropic virus type I, Human T-lymphotropic virus type II, West Nile virus, and Zika virus.
 - 5. The probe set of any one of claims 1 to 4, further comprising at least one negative control probe.
- 20 6. The probe set of claim 5, wherein the at least one negative control probe is a probe with at least 90% identity with the nucleic acid sequences of SEO ID NOs: 1571-1690.
 - 7. The probe set of any one of claims 1 to 6, further comprising at least one positive control probe.
- 25 8. The probe set of any one of claims 1 to 7, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 1-1769.
 - 9. A probe set comprising probes having at least 90% identity with the nucleic acid sequences of SEQ ID NOs: 1770-2647 or a subset thereof.

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- 10. The probe set of claim 9, wherein the probe set comprises probes having at least 95% identity with the nucleic acid sequences of SEQ ID NOs: 1770-2647 or a subset thereof.
- 11. The probe set of claim 10, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 1770-2647 or a subset thereof.

12. The probe set of any one of claims 9 to 11, wherein the probe set comprises at least 30 probes for each of cytomegalovirus, Epstein Barr virus subtype B95-8, Epstein Barr virus subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B19, human papillomavirus type 6, human papillomavirus type 11, human papillomavirus type 16, and human papillomavirus type 18.

- 13. The probe set of any one of claims 9 to 12, further comprising at least one negative control probe.
- 14. The probe set of claim 13, wherein the at least one negative control probe is a probe with at least 90% identity with the nucleic acid sequences of SEQ ID NOs: 3520-3628.

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- 15. The probe set of any one of claims 9 to 14, further comprising at least one positive control probe.
- 16. The probe set of any one of claims 9 to 16, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 1770-2647.
 - 17. A probe set comprising probes having at least 90% identity with the nucleic acid sequences of SEQ ID NOs: 2648-3207 or a subset thereof.
- 20 18. The probe set of claim 17, wherein the probe set comprises probes having at least 95% identity with the nucleic acid sequences of SEQ ID NOs: 2648-3207 or a subset thereof.
 - 19. The probe set of claim 18, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 2648-3207 or a subset thereof.
 - 20. The probe set of any one of claims 17 to 19, wherein the probe set comprises at least one probe for each of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi Leishmania major, Babesia microti, Plasmodium falciparum,* and *Plasmodium vivax*.
 - 21. The probe set of any one of claims 17 to 20, further comprising at least one negative control probe.
 - 22. The probe set of any one of claims 17 to 21, further comprising at least one positive control probe.
- The probe set of claim 22, wherein the at least one positive control probe is a probe with at least 90% identity with the nucleic acid sequences of SEQ ID NOs: 3208-3519.

24. The probe set of any one of claims 17 to 22, wherein the probe set comprises probes comprising the nucleic acid sequence of SEQ ID NOs: 2648-3207.

25. A microarray comprising the probe set of any one of claims 1 to 24, or any combination thereof.

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- 26. The microarray of claim 25, comprising a probe set comprising probes comprising the nucleic acid sequence of SEQ ID NOs: 1-1769.
- 27. The microarray of claim 25, comprising a probe set comprising probes comprising the nucleic acid sequence of SEQ ID NOs: 1770-3628.
 - 28. A method of detecting one or more pathogen nucleic acids in a sample, comprising: contacting the sample with the probe set of any one of claims 1 to 24 or the microarray of any one of claims 25 to 27 under conditions sufficient to allow hybridization of pathogen nucleic acids present in the

measuring hybridization of the sample to one or more of the probes, thereby detecting one or more pathogen nucleic acids in the sample.

- 29. The method of claim 28, wherein the sample comprises a blood, serum, or plasma sample or nucleic acids isolated from a blood, serum, or plasma sample.
 - 30. The method of claim 29, further comprising isolating nucleic acids from the sample prior to contacting the sample with the probe set or the microarray.
- 25 31. The method of claim 30, further comprising labeling the isolated nucleic acids from the sample.
 - 32. The method of claim 31, wherein the isolated nucleic acids are isolated DNA, isolated RNA, isolated cDNA, or a combination of two or more thereof.
- 30 33. The method of claim 32, wherein labeling the isolated nucleic acids comprises labeling the nucleic acids with one or more fluorescent labels.
 - 34. The method of claim 33, wherein the fluorescent label is Cy3 or Cy5.

sample to the probes of the probe set or microarray; and

35. The method of any one of claims 30 to 35, wherein the isolated nucleic acids are cDNA.

36. The method of any one of claims 30 to 35, wherein isolating the nucleic acids does not comprise amplifying total RNA from the sample prior to preparing cDNA.

- 37. The method of any one of claims 28 to 36, wherein measuring hybridization comprises detecting
 5 ≥50% of the probes for the virus have a log ratio of >1.5 and/or the log ratio between the signal intensity mean for the probe set and the mean of a control group probe set is ≥1.5.
 - 38. The method of any one of claims 28 to 37, wherein the pathogen nucleic acids comprise nucleic acids from one or more of Chikungunya virus, Dengue virus types 1, 2, 3, or 4, Hepatitis A virus, Hepatitis C virus types 1, 2, or 3, Hepatitis E virus, Human immunodeficiency virus types 1 or 2, Human T-lymphotropic virus types I or II, West Nile virus, and Zika virus.

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- 39. The method of any one of claims 28 to 37, wherein the pathogen nucleic acids comprise nucleic acids from one or more of cytomegalovirus, Epstein Barr virus subtype B95-8, Epstein Barr virus subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayr, human parvovirus B19, human papillomavirus type 6, human papillomavirus type 11, human papillomavirus type 16, and human papillomavirus type 18.
- 40. The method of any one of claims 28 to 37, wherein the pathogen nucleic acids comprise nucleic acids from one or more of *Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi Leishmania major, Babesia microti, Plasmodium falciparum,* and *Plasmodium vivax*.

Retest

Negative

FIG. 1A



FIG. 1C

c Analysis strategy

Select probes generating positive signal

Define threshold value

Log Ratio ≥ 1.0 to ≤ 1.5

Log Ratio < 1

Log ratio ≥1.5 for 50%

specific probes

Bioinformatics analysis

Pathogen Identification

b Workflow

RNA extraction

Retrieve NCBI RefSeq database accessions

a Chip Design

Candidate sequences to target the

entire genomic region

Ribo-SPIA Amplification Reverse transcription,

Cy3 cDNA labeling

Fragmentation and Hybridization

Washing, scanning and data acquisition

Target regions covered by 10 unique probes

(2750 probes, 60-mer)

SKISK Format

Pathogen Chip, RNA Platform

RNA: Agilent eArray

Find unique probes to target regions

cDNA Yields ng/μl

FIG. 2A



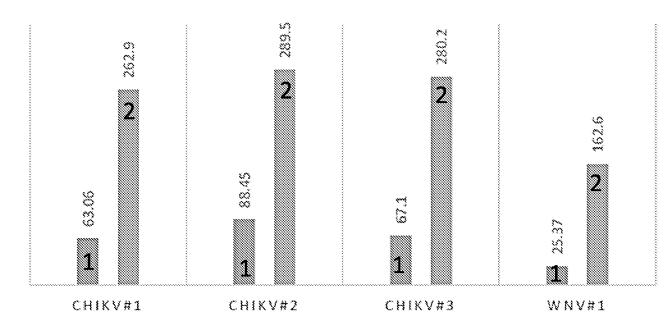


FIG. 2B

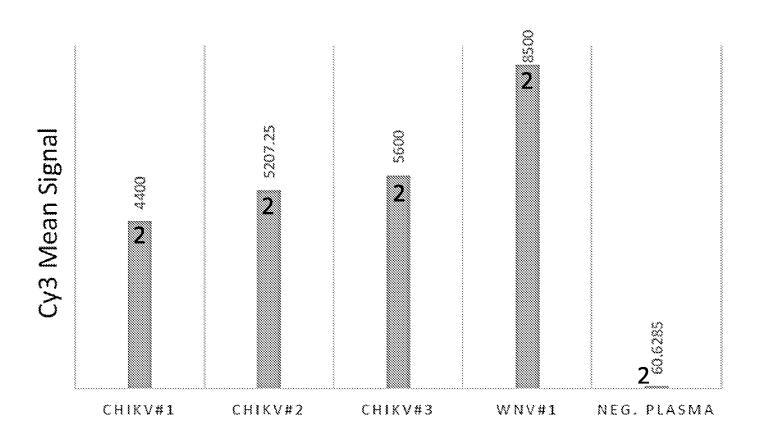
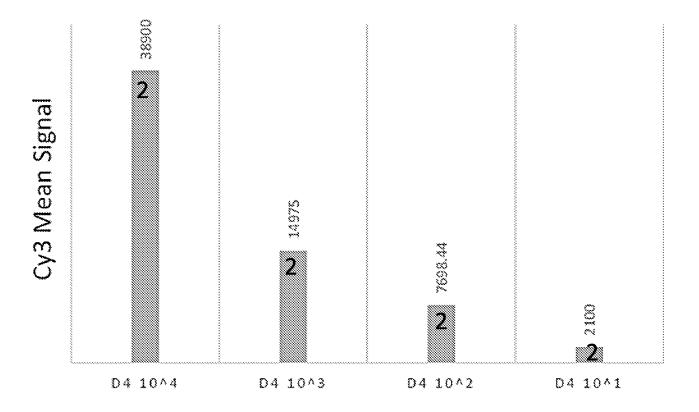


FIG. 2C



INTERNATIONAL SEARCH REPORT

International application No PCT/US2020/016262

a. classification of subject matter INV. C12Q1/70

C. DOCUMENTS CONSIDERED TO BE RELEVANT

ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols) C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data, BIOSIS, Sequence Search, EMBASE

Category*	Citation of document, with indication, where appropriate, of the re	elevant passages	Relevant to claim No.
Α	WO 2012/002594 A1 (BIONEER CORP CHUNG-HYUN [KR] ET AL.) 5 January 2012 (2012-01-05) example 2 table 1 abstract the whole document	[KR]; LEE	1-8,25, 26,28-38
A	US 2013/157258 A1 (BARTELS DOUG ET AL) 20 June 2013 (2013-06-20) paragraphs [0112], [0146] abstract the whole document	_AS J [US] -/	1-8,25, 26,28-38
X Furth	ner documents are listed in the continuation of Box C.	X See patent family annex.	
"A" docume to be o o "E" earlier a filing d. "L" docume cited to specia specia docume means "P" docume	ont which may throw doubts on priority claim(s) or which is o establish the publication date of another citation or other Il reason (as specified) ent referring to an oral disclosure, use, exhibition or other	"T" later document published after the inter date and not in conflict with the applicathe principle or theory underlying the it is document of particular relevance; the considered novel or cannot be considestep when the document is taken alon "Y" document of particular relevance; the considered to involve an inventive stecombined with one or more other such being obvious to a person skilled in the "&" document member of the same patent if	ation but cited to understand invention laimed invention cannot be ered to involve an inventive e laimed invention cannot be p when the document is a documents, such combination e art
Date of the a	actual completion of the international search	Date of mailing of the international sea	rch report
2:	3 April 2020	25/06/2020	
Name and n	nailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Helliot, Bertrand	

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2020/016262

C(Continua	ntion). DOCUMENTS CONSIDERED TO BE RELEVANT	l
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2009/087685 A2 (PREMAS BIOTECH PVT LTD [IN]; SONI RAJEEV [IN] ET AL.) 16 July 2009 (2009-07-16) page 9, lines 16-26 abstract the whole document	1-8,25, 26,28-38
Α	US 2012/088904 A1 (BARTELS DOUGLAS JOHN [US] ET AL) 12 April 2012 (2012-04-12) example 2 abstract the whole document	1-8,25, 26,28-38
Х	CN 106 011 309 A (KAIJIE BIOLOGICAL ENG CO LTD) 12 October 2016 (2016-10-12)	1-3,5-7, 25,28-38
A	table 1 sequence 3 paragraphs [0029] - [0030] abstract the whole document	4,8,26
X,P	VALERIA DE GIORGI ET AL: "A microarray-based pathogen chip for simultaneous molecular detection of transfusion-transmitted infectious agents", JOURNAL OF TRANSLATIONAL MEDICINE, vol. 17, no. 1, 14 May 2019 (2019-05-14), XP055687373, DOI: 10.1186/s12967-019-1905-4 figure 1 abstract the whole document	1-8,25, 26,28-38

International application No. PCT/US2020/016262

INTERNATIONAL SEARCH REPORT

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)
This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-8, 25, 26, 28-38(all partially)
Remark on Protest The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-8, 25, 26, 28-38(all partially)

A probe set comprising probes having at least 90% identity with the nucleic acid sequences of SEQ ID 1-110 or a subset thereof.

A microarray comprising the probe set of claim 1. A method for detecting HCV type 1 with the probe set of claim 1.

2-14. claims: 1-8, 25, 26, 28-38(all partially)

A probe set or a subset thereof.

A microarray.

A method for detecting one pathogen selected within Chikungunya virus, Dengue virus, Dengue virus type 3, Dengue virus type 4, Hepatitis A virus, Hepatitis C virus type 2, Hepatitis C virus type 3, Hepatitis E virus, Human immunodeficiency virus type 1, Human immunodeficiency virus type 2, Human T-lymphotropic virus type I, Human T-lymphotropic virus type I, Human T-lymphotropic virus type II, West Nile virus, and Zika virus.

15. claims: 9-16, 39(completely); 25, 27-37(partially)

A probe set comprising the probes listed as SEQ ID N° 1770-2647, or subset thereof;

An array;

A method for detecting one pathogen selected within cytomegalovirus, Epstein Barr virus subtype B95-8, Epstein Barr virus subtype AG876, human herpes virus 8, Hepatitis B virus subtype adw, Hepatitis B virus subtype ayw, Hepatitis B virus subtype adr, Hepatitis B virus subtype ayr, human parvovirus B 19, human papillomavirus type 6, human papillomavirus type 11, human papillomavirus type 16, and human papillomavirus type 18..

16. claims: 17-24, 40(completely); 25, 27-37(partially)

A probe set comprising the probes listed as SEQ ID N $^\circ$ 2648-3207, or subset thereof;

An array;

A method for detecting one pathogen selected within Treponema pallidum, Ehrlichia chaffeensis, Ehrlichia ewingii, Ehrlichia muris, Borrelia burgdorferi, Coxiella burnetii, Trypanosoma brucei, Trypanosoma cruzi Leishmania major, Babesia microti, Plasmodium falciparum, and Plasmodium vivax.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2020/016262

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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