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(54) Title: METHODS OF MODULATING HEPATITIS C VIRUS INFECTION

(57) Abstract: The present invention relates to the discovery that numerous factors produced by the host cell modulate (i.e., increase or decrease) hepatitis C virus (HCV) infection. Such host factors can be proviral host factors or antiviral host factors. The present invention provides a method to use these host factors to identify compounds that modulate viral infection. Also provided are inhibitory compounds as well as enhancing compounds that modulate viral infection. Such inhibitory or enhancing compounds act on host factors of the present invention, or on biochemical pathways comprising such host factors. Also provided are methods to inhibit or enhance viral infection, using such inhibitory compounds or enhancing compounds, respectively, as well as methods to protect a patient from viral infection by administering such inhibitory compounds to the patient.



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METHODS OF MODULATING HEPATITIS C VIRUS INFECTION

Field of the Invention

5 The present invention relates to methods of identifying inhibitors or enhancers of hepatitis C virus infection, and the use of such inhibitors in protecting patients from hepatitis C virus infection.

Background of the Invention

10 Hepatitis C virus (HCV) is an important cause of liver disease worldwide. The virus causes a chronic infection resulting in progressive liver damage. Hepatitis C virus (HCV) enters hepatocytes via interactions between the viral envelope proteins, E1 and E2, and four known host receptors, CD81, Claudin-1, SBR-I and occludin (Ploss, *Nature* 457, 2009, pp
15 882-886). Subsequent to entry, host ribosomes bind to the internal ribosomal entry site (IRES) of the HCV genome, and translate viral polyproteins on the rough endoplasmic reticulum (ER) (Moradpour (2007) *Nat Rev Microbiol* 5, 453-463). Host and viral proteases process the polyprotein into both structural (core, and envelope proteins, E1 and E2) and non-structural proteins (p7, NS2-3, NS3, NS4A, NS4B, NS5A, and NS5B, (Lindenbach (2005)
20 *Nature* 436, 933-938; Wolk (2008) *J Virol* 82, 10519-10531.). Oligomerization of NS4B distorts the host ER into membranous webs, which house HCV replication complexes (RCs), within which the RNA-dependent RNA polymerase, NS5B, transcribes viral genomic RNAs (Moradpour (2007) *Nat Rev Microbiol* 5, 453-463.). Progeny viral genomes generated in the RCs are translocated to lipid droplet-containing organelles and assemble into virions, which
25 then traffic to the cell surface for release (Miyanari (2007) *Nat Cell Biol* 9, 1089-1097.). However, while progress has been made in the areas of entry and replication, the later stages of the viral lifecycle, e.g., assembly, budding, maturation and secretion, remain less explored.

 The *in vitro* study of HCV replication has benefited from the use of the replicon system, consisting of sub-genomic or whole genome viral RNAs stably expressed in
30 permissive tissue culture cells. Using the replicon system, several recent functional genomic screens, using either partial or genome-wide siRNA libraries, have identified a number of host factors involved in HCV replication (Tai (2009) *Cell Host Microbe* 5, 298-307; Supekova (2008) *J Biol Chem* 283, 29-36; Ng (2007) *Hepatology* 45, 1413-1421.). However, the replicon system is unable to address the role of host factors in the entire HCV lifecycle.

The infection-competent HCV cell culture system (HCVcc) recapitulates the complete HCV lifecycle, thereby permitting a greater range of host-viral interactions to be studied (Wakita (2005) *Nat Med* **11**, 791-796; Zhong (2005) *Proc Natl Acad Sci U S A* **102**, 9294-9299; Lindenbach (2005) *Science* **309**, 623-626; Tellinghuisen (2007) *J Virol* **81**, 8853-8867.)); see
5 also PCT International Publication WO 2007/013882 A2, published Feb 1, 2007. Two efforts have employed the HCVcc system using limited candidate gene siRNA screens of either 65 or 140 curated targets. (Randall (2007) *Proc Natl Acad Sci U S A* **104**, 12884-12889; Berger (2009) *PNAS*).

There remains a need to identify factors involved during the HCV life-cycle, and to
10 obtain compounds to protect individuals from HCV infection.

Summary of the Invention

The present invention identifies, for the first time, numerous host factors that are involved in modulating hepatitis C infection. Because these host factors are involved in
15 modulating viral infection, they represent new targets that can be used to identify compounds capable of inhibiting or enhancing viral infection. Thus the present invention relates to methods of using host factors of the present invention to identify compounds that modulate viruses of the present invention. The invention further relates to compounds that interact with host factors of the present invention, or biological pathways comprising host factors of
20 the present invention, in such a way as to inhibit or enhance viral infection. The present invention also relates to methods to inhibit or enhance viral infection using inhibitory or enhancement compounds, and methods to protect a patient from viral infection using such compounds.

One embodiment of the present invention is a method to identify a compound that
25 modulates viral infection, the method comprising assaying a candidate compound for the ability to interact with a host factor of the present invention in such a manner as to modulate viral infection. In a preferred embodiment, the virus is hepatitis C virus.

One embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising;

(a) contacting a candidate compound with at least one isolated host factor under conditions suitable for formation of a complex between said compound and said host factor; and,

(b) detecting the presence of a complex, if present;

5 wherein the presence of said complex indicates that the test compound modulates viral infection.

Another embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising;

10 (a) contacting a candidate compound with at least one isolated host factor under conditions suitable for allowing an interaction between the compound and the at least one host factor; and

(b) determining if said interaction results in modification of said host factor;

wherein modification of the host factor indicates that the test compound modulates viral infection.

15 Still another embodiment of the present invention is a method to identify a compound that modulates viral infection, which comprises:

(a) combining a candidate compound with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for such candidate compound to interact with such host factor,

20 (b) assaying for the presence of such interaction between such candidate compound and such host factor and;

(c) determining if such an interaction decreases or increases viral infectivity, wherein a decrease or increase in viral infectivity indicates that the compound modulates viral infection.

25 In one embodiment, an inhibitory compound of the present invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby inhibiting viral infection.

In another embodiment, an enhancing compound of the present invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby enhancing viral infection.

Another embodiment of the present invention is an inhibitory compound for inhibiting
5 infection by a virus of the present invention, wherein the inhibitory compound interacts with a host factor of the present invention, thereby inhibiting the viral infection. In one embodiment, an inhibitory compound of the present invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby inhibiting viral infection. In another embodiment, an enhancing compound of the present
10 invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby enhancing viral infection.

One embodiment of the present invention is a method to inhibit viral infection, the method comprising contacting a cell infected with the virus with an inhibitory compound that interacts with a host factor of the present invention in such a manner as to inhibit viral
15 infection. Another embodiment of the present invention is a method to enhance viral infection, the method comprising contacting an infected cell with an enhancing compound that interacts with a host factor in such a manner as to increase the amount of virus produced. In a preferred embodiment, the cell is infected with hepatitis C virus.

Another embodiment is a method to protect a patient from virus infection, comprising
20 administering to a patient an inhibitory compound that modulates a pathway comprising a host factor of the present invention in such a manner as to inhibit viral infection.

The embodiments include a method to inhibit viral infection, wherein such a method comprises contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a
25 nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection. In certain embodiments, such a method comprises contacting a patient with such an inhibitory compound. Such a patient can be infected with such a virus. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

The embodiments include a method to inhibit viral infection, wherein such a method
30 comprises contacting a cell with an inhibitory compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor

encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection. In certain embodiments, such a method comprises contacting a patient with such an inhibitory compound. Such a patient can be infected with such a virus. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

5 The embodiments include a method to protect a patient from hepatitis C virus infection, wherein such a method comprises administering an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1. In certain embodiments, such a method can provide prophylactic protection. In certain embodiments,
10 such a method can provide therapeutic protection.

 The embodiments include a method to protect a patient from hepatitis C virus infection, wherein such a method comprises administering an inhibitory compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in
15 Table 1. In certain embodiments, such a method can provide prophylactic protection. In certain embodiments, such a method can provide therapeutic protection.

 The embodiments include a method to enhance viral infection, wherein such a method comprises contacting a cell with an enhancing compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a
20 nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

 The embodiments include a method to enhance viral infection, wherein such a method comprises contacting a cell with an enhancing compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor
25 encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

 The embodiments include an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a
30 nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection. The embodiments include an inhibitory compound that modulates a pathway

comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

5 The embodiments include an enhancing compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection. The embodiments include an enhancing compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor
10 encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus.

 The embodiments include a method to identify a compound that inhibits viral infection, wherein such a method comprises assaying a candidate compound for the ability to
15 interact with a host factor in such a manner as to inhibit such an infection, wherein such a host factor is encoded by a nucleic acid molecule listed in Table 5 or is encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus. The embodiments include an inhibitory compound identified by such a method.

20 The embodiments include a method to identify a compound that inhibits viral infection, wherein such a method comprises: (a) combining a candidate compound with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for such a candidate compound to interact with such a host factor; (b) assaying for the
25 presence of such an interaction; and (c) determining if such an interaction results in a decrease in the amount of virus obtained upon infection of a cell with such a virus; wherein a decrease in the amount of virus indicates that such a compound inhibits viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus. The embodiments include an inhibitory compound identified by such a method.

30 The embodiments include a method to identify a compound that inhibits viral infection, wherein such a method comprises assaying a candidate compound for the ability to modulate a pathway comprising a host factor encoded by a nucleic acid molecule listed in

Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, wherein the ability to modulate such a pathway identifies a compound that inhibits viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus. The embodiments include an inhibitory compound identified by such a method.

5 The embodiments include a method to identify a compound that enhances viral infection, wherein such a method comprises assaying a candidate compound for the ability to interact with a host factor in such a manner as to enhance such an infection, wherein such a host factor is encoded by a nucleic acid molecule listed in Table 5 or is encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1. In certain embodiments such a virus is
10 a Flavivirus, such as a hepatitis C virus.

 The embodiments include a method to identify a compound that enhances viral infection, wherein such a method comprises: (a) combining a candidate compound with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable
15 for such a candidate compound to interact with such a host factor; (b) assaying for the presence of such an interaction; and (c) determining if such an interaction results in an increase in the amount of virus obtained upon infection of a cell with such a virus; wherein an increase in the amount of virus indicates that such a compound enhances viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus. The
20 embodiments include an inhibitory compound identified by such a method.

 The embodiments include a method to identify a compound that enhances viral infection, wherein such a method comprises assaying a candidate compound for the ability to modulate a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in
25 Table 1, wherein the ability to modulate such a pathway identifies a compound that enhances viral infection. In certain embodiments such a virus is a Flavivirus, such as a hepatitis C virus. The embodiments include an inhibitory compound identified by such a method.

 The embodiments include a host factor encoded by a nucleic acid molecule listed in Table 2. The embodiments include a host factor encoded by a nucleic acid molecule listed in
30 Table 11, Table 12, Table 13 or Table 14. The embodiments include a host factor encoded by a nucleic acid molecule comprising SEQ ID NO:79. The embodiments include a host factor comprising amino acid sequence SEQ ID NO:80.

The embodiments include one or more inhibitory compounds listed in Table 3. The embodiments include one or more of the following inhibitory compounds: colchicine, cytochalasin, EIPA, rottlerin, UO126 or wortmannin. The embodiments include one or more of the following inhibitory compounds: brefeldin A or golgicide A. The embodiments include an inhibitory compound comprising a small interfering RNA (siRNA). Such siRNA can be one or more of the siRNAs listed in Table 4.

Brief Description of the Figures

Fig. 1 Effect of siRNA screen on HCV infected cells

10 Fig. 2 Network of connections between HCV proteins

Fig. 3 Map of interactions between HCV host factors from siRNA screen and host factors that interact with HCV core components

Fig. 4 Common network modules amongst various Flaviviridae

15 Fig. S1 Effect of siRNA treatment on stages of HCV infection and cellular molecular function

Fig. 5 Effect of siRNA silencing of IKK α gene expression on HCV infection

Fig. 6 (A) Effect of siRNA silencing of expression of various NF- κ B pathway-related factors on HCV RNA levels. (B) Relative knock-down efficiency of various host factors by the siRNAs.

20 Fig. 7 (A) Effect of expression of IKK α dominant negative mutant (HA-IKK α KA) on HCV RNA levels. (B) Western blot illustrating levels of HA-IKK α KA.

Fig. 8 Effect of siRNA silencing of IKK α expression on (A) intracellular HCV RNA levels and (B) extracellular HCV RNA levels. (C) Relative silencing efficiency of IKK α expression as measured by quantitative PCR.

25 Fig. 9 (A) Effect of siRNA silencing of IKK α expression on (A) viral entry of an HCV pseudovirus and (B) RNA replication.

Fig 10 Effect of (A) rotterlin, (B) colchicines, (C) EIPA, (D) wortmannin, (E) cytochalasin, or (F) U0126 on HCV entry.

Fig. 11 Effect of (A) rottlerin or (B) EIPA on HCV RNA levels.

Fig. 12 Effect of (A) golgicide or (B) brefeldin on HCV RNA levels.

5

Detailed Description of the Invention

Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing
10 particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. It is further noted that the claims may be drafted to exclude any optional element. As such, this
15 statement is intended to serve as antecedent basis for use of such exclusive terminology as "solely," "only" and the like in connection with the recitation of claim elements, or use of a "negative" limitation.

It should be understood that as used herein, the term "a" entity or "an" entity refers to one or more of that entity. For example, a host factor refers to one or more host factors. As
20 such, the terms "a", "an", "one or more" and "at least one" can be used interchangeably. Similarly the terms "comprising", "including" and "having" can be used interchangeably.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.
25 Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

Unless defined otherwise, 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 invention belongs. Although any methods and materials similar or equivalent to those described herein

can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

5 It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments are specifically embraced by the
10 present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

The present invention generally relates to the discovery that numerous host factors are
15 involved in modulating (e.g., inhibiting or enhancing) hepatitis C virus (HCV) infection. The present invention relates to methods of using host factors of the present invention to identify compounds that modulate viral infection. Also encompassed are compounds that interact with host factors of the present invention, and the use of such compounds to modulate infection by viruses of the present invention. The instant invention is novel since, prior to the
20 inventors' surprising discovery, it was not appreciated that host factors disclosed herein were involved in modulating viral infection. Thus, host factors of the present invention represent new tools for identifying compounds that can modulate viral infection. The present invention also teaches novel methods for protecting (e.g., prophylactically or therapeutically) a patient from viral infection, and in particular hepatitis C virus infection.

25 As defined herein, a host factor of the present invention is a molecule produced by the host cell that modulates HCV infection. Host factors are biological molecules, examples of which include proteins, peptides, lipids, nucleic acid molecules, carbohydrates, lipoproteins, glycoproteins, metabolic products, and the like. As used herein, a host factor modulates HCV infection if, when the host factor-related activity is altered (e.g., reduced or eliminated, or
30 increased) the amount of virus is decreased or increased. Accordingly, host factors can be proviral or antiviral, and the amount of virus produced during an infection is influenced by interactions between viral components, proviral host factors and antiviral host factors. A

proviral host factor is a molecule that positively influences virus production. Consequently when the amount or activity of a proviral host factor is reduced or eliminated, the amount of virus produced is decreased. For example, 3-hydroxy-3-methylglutaryl CoA reductase is known to be required for replication of HCV and thus is a proviral host factor (Ye, PNAS, Dec. 23, 2003, pp15865-15870). An antiviral host factor is a molecule that negatively influences virus production. Consequently when the amount or activity of an antiviral host factor is reduced or eliminated, the amount of virus produced is increased. One example of an antiviral host factor is interleukin 7 receptor β . Host factors of the present invention can be identified by those skilled in the art using the screening methods disclosed herein, e.g., siRNA screening.

Certain host factors of the present invention or the nucleic acid molecules encoding such host factors are listed in one or more of the Tables included in this disclosure. These nucleic acid molecules are characterized in various ways appreciated by those skilled in the art, e.g., Entrez Gene Symbol, Entrez Gene ID, Genbank Accession Number, Gene Name, SEQ ID NO: (or SEQ NO). In certain embodiments, host factors of the present invention are encoded by the nucleic acid molecules listed in Table 1, with their corresponding nucleic acid sequence SEQ ID NO:s. Preferred host factors are those encoded by nucleic acid molecules listed in Table 2. In some embodiments, host factors are described by their amino acid sequences as listed in Table 1. Certain host factors are encoded by nucleic acid molecules listed in Table 5. Certain host factors are encoded by a nucleic acid molecule listed in Table 5 or are encoded by a nucleic acid molecule having a SEQ ID NO listed in Table 1. Certain host factors involved in viral entry are encoded by nucleic acid molecules listed in Table 11. Certain host factors involved in viral IRES-mediated translation are encoded by nucleic acid molecules listed in Table 12. Certain host factors involved in viral replication are encoded by nucleic acid molecules listed in Table 13. Certain host factors involved in viral trafficking, assembly and/or release are encoded by nucleic acid molecules listed in Table 14. In some embodiments, host factors are encoded by nucleic acid molecules listed in Table 11, Table 12, Table 13 or Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule comprising SEQ ID NO:79. In certain embodiments, a host factor comprises amino acid sequence SEQ ID NO:80.

As used herein, the phrases viral infection, viral infectivity, infection by a virus of the present invention, viral propagation, and the like, refers to the ability of a virus to carry out all steps in the viral life cycle, resulting in the production of infectious particles. Such a life

cycle comprises a variety of steps including, for example, attachment, uncoating, transcription, translation, protein processing, replication of nucleic acid molecules, assembly of viral particles, intracellular transport of viral particles, budding, release and the like. Other steps may also be included depending on the virus.

5 One embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising assaying a candidate compound for the ability to interact with a host factor of the present invention in such a manner as to modulate viral infection. In a preferred embodiment, the virus is hepatitis C virus. In a preferred
10 embodiment, the method identifies a compound that inhibits viral infection by assaying a candidate compound for the ability to interact with a host factor of the present invention in such a manner as to inhibit viral infection. In another preferred embodiment, the method identifies a compound that enhances viral infection by assaying a candidate compound for the ability to interact with a host factor of the present invention in such a manner as to enhance viral infection.

15 As used herein, the phrases modulate viral infection, modulate infection by a virus of the present invention, modulate viral infectivity, modulate viral propagation, and the like, refers to increasing or decreasing the amount of virus present in an infected cell or patient relative to the amount of virus present in a cell or patient that has not been treated using the disclosed methods or compounds. Also encompassed is the ability to prevent viral infection.
20 It should be appreciated that the terms amount and concentration can be used interchangeably. An amount of virus can also be referred to as a titer. It is also understood by those of skill in the art that the amount of virus can refer to the total number of viral particles, or it can refer to the number of viral particles that are infectious, i.e. capable of carrying out the viral life cycle, including the ability to effect another cycle of infectious particle
25 formation. For example, in a given population of virus particles, some or all of the particles may be unable to carry out a specific step in its life cycle (e.g., attachment or entry) due to a deficiency in a molecule needed to perform that step. While the number of particles in the population may be large, the number of infectious particles could be small to none. Thus the amount of virus determined by counting virus particles may differ from that determined by
30 measuring functional virus in, for example, a plaque assay. Accordingly methods of the present invention can be used to identify compounds that affect the total number of viral particles produced, as well as the number of infectious viral particles produced. Appropriate methods of determining the amount of virus are understood by those skilled in the art and

include, but are not limited to, directly counting virus particles, titering virus in cell culture (e.g., plaque assay), measuring the amount of viral protein(s), measuring the amount of viral nucleic acids, or measuring the amount of a reporter protein, e.g., luciferase.

Modulation of viral infection can result in a partial reduction in the amount of virus, or it can result in complete elimination of virus from a cell or patient or in prevention of viral infection. In one embodiment of the present invention, the amount of virus is reduced by at least 5%, 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%, or at least 95%. In another embodiment, the amount of virus is reduced by a factor of at least 10, at least 100, at least 1000, or at least 10,000. In one embodiment the viral infection is completely inhibited (i.e., there are no infectious particles). In another embodiment, the amount of virus is increased by at least 5%, 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%, or at least 95%. In a particular embodiment of the present, the amount of virus is increased by a factor of at least 10, at least 100, at least 1000, or at least 10,000.

As used herein, a candidate compound is any compound which may have the ability to modulate viral infection by interacting with a host factor of the present invention, but that has not yet been tested for such activity. Candidate compounds encompassed by the present invention include, but are not limited to, proteins, peptides, antibodies, lipids, nucleic acid molecules, small interfering RNA's (siRNA's), carbohydrates, sugars, lipoproteins, small molecule compounds and combinations thereof. Such compounds can be isolated from nature (e.g., isolated from organisms) or they can be produced in a laboratory (e.g., recombinantly or synthetically). Also encompassed are compounds that are combinations of natural and synthetic molecules. Methods to isolate or produce recombinant or synthetic candidate compounds are known to those skilled in the art.

Candidate compounds that are shown to interact with a host factor, or a pathway comprising a host factor, thereby inhibiting viral infection are referred to as inhibitory compounds. Thus, as used herein, an inhibitory compound of the present invention is any molecule that inhibits (e.g., reduces, eliminates or prevents) a virus of the present invention by interacting with a proviral host factor of the present invention to reduce the host factor's amount or activity, or by interacting with an antiviral host factor of the present invention to increase that host factor's amount or activity. Inhibitory compounds of the present invention also encompass any molecule that inhibits a virus of the present invention by interacting with

a pathway comprising a host factor of the present invention in such a manner as to inhibit viral infection.

Candidate compounds that are shown to interact with a host factor, or a pathway comprising a host factor, to enhance viral infection are referred to as enhancing compounds.

5 Thus, as used herein, an enhancing compound of the present invention is any molecule that enhances infection of a virus of the present invention by interacting with an antiviral host factor of the present invention to reduce that host factor's amount or activity, or by interacting with a proviral host factor of the present invention to increase that host factor's amount or activity. Enhancing compounds of the present invention also encompass any
10 molecule that enhances infection of a virus of the present invention by interacting with a pathway comprising a host factor of the present invention in such a manner as to enhance viral infection.

As defined herein, a virus of the present invention is any virus, the infectivity of which is modulated by a host factor of the present invention (i.e., a host factor that modulates
15 HCV infection), or a pathway comprising a host factor of the present invention. Using the methodology taught herein, one of skill in the art can identify viruses of the present invention. Such viruses include those in a family selected from the group consisting of adenoviridae, herpesviridae, pappillomaviridae, polyomaviridae, poxviridae, parvoviridae, hepadnaviridae, retroviridae, arenaviridae, bornaviridae, bunyaviridae, filoviridae,
20 orthomyxoviridae, paramyxoviridae, rhabdoviridae, arteriviridae, astroviridae, caliciviridae, coronaviridae, flaviviridae, hepatitis-E-like viruses, picornaviridae, and togaviridae that require a host factor of the present invention. A preferred virus is one from the Flaviviridae family of viruses, which includes the genera Flavivirus, Pestivirus, and Hepacivirus. Suitable Flaviviruses for practicing the instant invention include Gadget's Gully virus,
25 Kadam virus, Kyasanur Forrest disease virus, Langat virus, Omsk hemorrhagic fever virus, Tick-borne encephalitis virus, Louping ill virus, Aroa virus, Dengue viruses 1-4, Kedougou virus, Cacipacore virus, Koutango virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus group, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey meningoencephalomyelitis virus,
30 Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, Yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat

virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, hepatitis C virus, e.g., hepatitis C virus genotypes 1-6, and GB virus A and B. A preferred virus is a member of the Hepacivirus genus of viruses, with hepatitis C virus being particularly preferred.

5 As used herein, the term interact indicates that the candidate compound and the host factor come into sufficient physical proximity so that the compound affects the host factor in such a manner as to inhibit or enhance viral infection. Preferred compounds are those that selectively interact with a host factor of the present invention. As used herein, the terms selectively, selective, specifically, and the like, indicate the compound has a greater affinity
10 for the host factor than it does for molecules unrelated to the host factor. One type of interaction is a binding interaction. In such an interaction the compound associates with the host factor to form a complex. An example of complex formation is the association of an antigen with an antibody or a drug with its target. According to the present invention, association of a compound with a host factor can be reversible or non-reversible. One useful
15 measure of the strength of binding between a compound and a host factor is the dissociation constant (Kd). Formation of a complex may or may not result in modification of the host factor. Methods of measuring and analyzing interactions, including binding interactions, between a compound and a host factor are known by those of skill in the art. In some instances, the interaction between a compound and a host factor can result in modification of
20 the host factor. In these instances, the host factor and the compound may or may not form a complex. For example, a compound may have proteolytic activity, and may cleave the host factor thereby reducing the amount of host factor present, or affecting any activity possessed by the host factor. Examples of host factor modifications include, but are not limited to, cleavage, phosphorylation, myristylation, ligation, and the like.

25 Suitable techniques for assaying candidate compounds for their ability to interact with host factors of the present invention are known to those skilled in the art. Such assays can be *in vitro* or *in vivo* assays. Examples of useful assays include, but are not limited to, an enzyme-linked immunoassay, a competitive enzyme-linked immunoassay, a radioimmunoassay, a fluorescence immunoassay, a chemiluminescent assay, a lateral flow
30 assay, a flow-through assay, an agglutination assay, a particulate-based assay (e.g., using particulates such as, but not limited to, magnetic particles or plastic polymers, such as latex or polystyrene beads), an immunoprecipitation assay, an immunoblot assay (e.g., a western blot), a phosphorescence assay, a flow-through assay, a chromatography assay, a

polyacrylamide gel electrophoresis (PAGE)-based assay, a surface plasmon resonance assay, a spectrophotometric assay, a particulate-based assay, and an electronic sensory assay. Such assays are well known to those skilled in the art. In one embodiment, an assay can be performed in cells in culture or it can be performed in a whole animal. Assays can be
5 designed to give qualitative, quantitative or semi-quantitative results, depending on how they are used and the type of result that is desired.

One embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising;

(a) contacting a candidate compound with at least one isolated host factor under
10 conditions suitable for formation of a complex between said compound and said host factor; and,

(b) detecting the presence of a complex, if present;

wherein the presence of said complex indicates that the test compound modulates viral infection.

15 Suitable methods for detecting the formation of a complex between a candidate compound and a host factor have been disclosed herein. For example, utilizing an assay technology disclosed herein, a compound can be immobilized on a substrate and the immobilized compound then brought into contact with a host factor under conditions suitable for formation of a complex. Following a wash step to eliminate non-specific binding, the
20 presence of a complex can be detected using a detectable marker. Examples of detectable markers include, but are not limited to, a radioactive marker, a colorimetric marker, a fluorescent marker, and a chemiluminescent marker. In some instances, the detectable marker is directly linked (e.g., covalently) to the host factor. Alternatively, the complex can be detected by using a detection molecule that binds to the host factor, and that is labeled
25 with a detectable marker. A detection molecule is any molecule that binds to the host factor, and can be used detect its presence. Examples of such molecules include, but are not limited to, antibodies, ligand, and nucleic acid molecules. Alternatively, the host factor can be immobilized on a substrate and a candidate compound introduced under conditions suitable for formation of a complex. Similar methodology to that described above can then be used to
30 detect binding of the candidate compound to the immobilized host factor. In one embodiment, the K_d of a complex formed by a host factor of the present invention and a

compound that selectively interacts with the host factor is at least 10^{-4} , 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} , 10^{-11} or 10^{-12} . In another embodiment of the present invention, binding of a host factor to a compound that selectively interacts with the host factor is irreversible. In one embodiment, a compound forms a covalent bond with the host factor. In one embodiment of the present invention, a host factor is encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1. In another embodiment, a host factor is encoded by a nucleic acid molecule listed in Table 2. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5 or encoded by a nucleic acid molecule having a SEQ ID NO listed in Table 1. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 12. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 13. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule having SEQ ID NO:79. In certain embodiments, a host factor comprises amino acid sequence SEQ ID NO:80.

Another embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising;

- (a) contacting a candidate compound with at least one isolated host factor under conditions suitable for allowing an interaction between the compound and the at least one host factor; and
- (b) determining if said interaction results in modification of said host factor;

wherein modification of the host factor indicates that the test compound modulates viral infection.

As noted elsewhere, modifications to the host factor include changes to physical properties such as, for example, size and charge. In one embodiment, the step of determining includes determining if the host factor has been altered by, for example, enzymatic cleavage, ligation, esterification, polymerization, phosphorylation, myristylation, acetylation, deacetylation, alkylation, glutamylation, hydroxylation, sulfation, or combinations thereof. Other types of modifications known by those skilled in the art are also encompassed. In one

embodiment, a host factor is encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1. In another embodiment, the host factor is encoded by a nucleic acid molecule listed in Table 2. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5 or encoded by a nucleic acid molecule having a SEQ ID NO listed in Table 1. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 12. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 13. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule having SEQ ID NO:79. In certain embodiments, a host factor comprises amino acid sequence SEQ ID NO:80.

In some instances a host factor can possess activity, such as enzymatic activity. For example, one host factor identified using the methods disclosed herein is encoded by the AGPAT3 gene, which encodes a protein having O-acetyltransferase activity. In instances where the host factor has enzymatic activity, interaction with a compound can increase, decrease, or completely eliminate, the enzymatic activity of the host factor. Thus in one embodiment, compounds that modulate viral infection are identified by contacting a host factor with a compound, and measuring the level of host factor-related activity. In such a method, the level of host factor-related activity is compared to the level of host factor-related activity measured in the absence of the compound. Suitable assays for measuring host factor-related activity can be determined by those skilled in the art, and depend on the type of activity being measured.

In another embodiment, candidate compounds that form a complex with a host factor, or that modify a host factor can be further assayed for their ability to modulate viral infection. Such assays can be conducted in cells in culture or they can be conducted using whole animals. For example, the amount of virus produced by cells in culture in the presence and absence of a compound that interacts with a host factor can be compared. Similarly, a candidate compound that interacts with a host factor can be administered to an animal infected with a virus, and the amount of virus produced determined.

One embodiment of the present invention is a method to identify a compound that modulates viral infection, which comprises (a) combining a candidate compound with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for such candidate compound to interact with such host factor, (b)

5 assaying for the presence of such interaction between such candidate compound and such host factor and (c) determining if such an interaction decreases or increases viral infectivity, wherein a decrease or increase in viral infectivity indicates that the compound modulates viral infection. One embodiment is a method to identify a compound that modulates viral infection, which comprises (a) combining a candidate compound with a host factor encoded
10 by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for such candidate compound to interact with such host factor, (b) assaying for the presence of such interaction between such candidate compound and such host factor and (c) determining if such an interaction decreases or increases viral infectivity, wherein a decrease or increase in viral
15 infectivity indicates that the compound modulates viral infection. One embodiment is a method to identify a compound that modulates viral infection, which comprises (a) combining a candidate compound with a host factor encoded by a nucleic acid molecule listed in Table 5 under conditions suitable for such candidate compound to interact with such host factor, (b) assaying for the presence of such interaction between such candidate
20 compound and such host factor and (c) determining if such an interaction decreases or increases viral infectivity, wherein a decrease or increase in viral infectivity indicates that the compound modulates viral infection. In one embodiment, viral infectivity is decreased, indicating that the compound inhibits viral infection. In another embodiment, viral infectivity is increased, indicating that the compound enhances viral infection. Viral infectivity can be
25 measured by determining the amount of virus, as described herein. The interaction can be a binding interaction in which a complex is formed between the candidate compound and host factor or it can be an interaction in which the host factor is modified.

In some instances, a host factor of the present invention is known to interact with existing compounds (e.g., drugs) used to treat non-HCV related disease. Some of these
30 compounds have already been shown to modulate HCV infection. For example, the cholesterol-lowering drug simvastatin, which is known to reduce the activity of the host factor diacylglycerol-2-acetyltransferase (Waterman, Diabetes (2002);51:1708-13), has been shown to inhibit HCV propagation. However, the potential of many existing compounds to

modulate HCV infection was not appreciated since, prior to the present invention, it was not known that the targets of these compounds (i.e., host factors that interact with these compounds) were involved in modulating HCV infection. For example, FLT4 targeted by the drugs sunitinib and sorafenib, as well as TOP1, targeted by the drugs topotecan, camptothecin and related drugs, were not previously known to modulate HCV infection. In view of the inventor's discovery, these drugs are promising candidates for compounds capable of modulating infection by HCV and related viruses. Thus, one embodiment of the present invention is a method to inhibit viral infection by contacting a cell infected with the virus or susceptible to the virus with a compound selected from Table 3. Table 3 provides examples of host factors of the present invention, and pathways comprising such host factors, that appear to have some association with existing drugs used to treat non-HCV related disease. To the inventors' knowledge, host factors and pathways listed in Table 3 were previously unknown to be involved in modulating HCV infection. Thus drugs listed in Table 3 have previously unappreciated potential to modulate viral infection by interacting with host factors or pathways comprising one or more of such host factors.

It will be appreciated by one of skill in the art that one or more host factors can interact with each other as part of (or as an entire) pathway, and thus assays of the present invention can comprise more than one host factor. Therefore, the present invention also discloses pathways that modulate viral infectivity. Thus one embodiment of the present invention is a method to identify a compound that modulates viral infection, the method comprising assaying a candidate compound for the ability to modulate a pathway comprising a host factor of the present invention in such a manner as to modulate viral infection. In a preferred embodiment, the virus is a hepatitis C virus. In a preferred embodiment, the method identifies a compound that inhibits viral infection by assaying a candidate compound for the ability to modulate a pathway comprising a host factor of the present invention in such a manner as to inhibit viral infection. In another preferred embodiment, the method identifies a compound that enhances viral infection by assaying a candidate compound for the ability to modulate a pathway comprising a host factor of the present invention in such a manner as to enhance viral infection.

As used herein, the term pathway refers to a sequence of biochemical molecules and/or related activities (e.g., reactions) that result in the production of an end product. The end product can be a biological molecule, such as a protein, or it can be an activity, such as an enzymatic activity (e.g., a phosphorylation event). As an example, the glycolytic pathway

consists of several enzymatic proteins, the end product of which is pyruvate. As a further example, the tumor growth factor beta (TGF-beta) signaling pathway comprises several proteins that interact in a sequential manner, resulting in regulation of gene expression. Examples of other biological pathways are known by those of skill in the art.

5 A pathway of the present invention comprises at least one host factor of the present invention. It is appreciated by those of skill in the art that the end result of one pathway can be an activity that effects, or modulates, another pathway. The interaction of biological pathways is referred to in the art as a network. Examples of pathways and networks of the present invention are shown in Figures 2, 3 and 4. Because of the inter-related nature of
10 biological pathways, it will be appreciated by those of skill in the art that modulation of one pathway frequently results in modulation of one or more other pathways. Thus methods and compounds of the present invention can modulate viral infection by modulating a pathway that directly affects viral infection, or a pathway that indirectly affects viral infection. As used herein, a pathway that directly modulates viral infection is one in which the host factors
15 that comprise the pathway directly interact with components of the virus. In contrast, a pathway that indirectly modulates viral infection is one in which the end result of the pathway does not directly interact with components of the virus, but affects another pathway that directly modulates viral infection.

 As used herein, to modulate a pathway refers to changing, varying, or altering the
20 activity of that pathway by altering the amount of a host factor associated with the pathway, or the level of activity (e.g., enzymatic activity) resulting from a host factor or a pathway. As used herein, modulation can refer to an increase (e.g., up-regulation) or a decrease (e.g., down-regulation) in the amount of a host factor or activity. Regardless, the end result of modulating a host factor or pathway of the present invention is modulation of viral infection.
25 In one embodiment, such viral infection is preferably inhibited. Table S3 lists pathways of the present invention.

 The present invention also includes inhibitory compounds and enhancing compounds identified by the methods disclosed herein. Thus one embodiment of the present invention is an inhibitory compound for inhibiting infection by a virus of the present invention, wherein
30 the inhibitory compound interacts with a host factor of the present invention, thereby inhibiting the viral infection. For example, an inhibitory compound can inhibit infection either by decreasing the amount or activity of a proviral host factor or by increasing the

amount or activity of an antiviral host factor. A further embodiment of the present invention is an inhibitory compound for inhibiting infection by a virus of the present invention, wherein the inhibitory compound modulates a pathway comprising a host factor of the present invention, thereby inhibiting viral infection. For example, an inhibitory compound can

5 inhibit infection either by decreasing the activity of a pathway required for viral infection, or by increasing the activity of a pathway that inhibits viral infection. Another embodiment of the present invention is an enhancing compound for enhancing infection by a virus of the present invention, wherein the enhancing compound interacts with a host factor of the present invention, thereby enhancing the viral infection. For example, an enhancing compound can

10 enhance infection either by increasing the amount or activity of a proviral host factor or by decreasing the amount or activity of an antiviral host factor. A further embodiment of the present invention is an enhancing compound for enhancing infection by a virus of the present invention, wherein the enhancing compound modulates a pathway comprising a host factor of the present invention, thereby enhancing viral infection. For example, an enhancing

15 compound can enhance infection either by increasing the activity of a pathway required for viral infection, or by decreasing the activity of a pathway that inhibits viral infection. As has been discussed herein, useful compounds can be isolated from a natural source or they can be synthetic. Examples of useful inhibitory and enhancing compounds include, but are not limited to, proteins, peptides, antibodies, lipids, lipoproteins, nucleic acid molecules (e.g.,

20 microRNA and small interfering RNAs), an organic molecule, a synthetic molecule, small molecule compounds, and combinations thereof.

One example of an inhibitory compound is an antibody that binds a host factor encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1 in such a manner as to inhibit viral infection. One example of an enhancing compound is an antibody that

25 binds a host factor encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1 in such a manner as to enhance viral infection. One example of an inhibitory compound is an antibody that binds a host factor encoded by a nucleic acid molecule listed in Table 5 in such a manner as to inhibit viral infection. One example of an enhancing compound is an antibody that binds a host factor encoded by a nucleic acid molecule listed in Table 5 in such

30 a manner as to enhance viral infection.

One example of a compound of the present invention is a small interfering RNA (siRNA). These molecules are short (approximately 20-30 nucleotides) double stranded RNA molecules that, in association with the RNA-induced silencing complex (RISC), pair

with complementary messenger RNA resulting in the cleavage of the messenger RNA molecule, thereby reducing expression of the target gene. siRNAs useful for practicing the instant invention are listed in Table 4. siRNAs can be proviral or antiviral, depending on the host factor they target. In one embodiment, a siRNA interacts with the same host factor as that targeted by a siRNA listed in Table 4 in such a manner as to inhibit viral infection. The siRNA's can interact with the host factor at the same site, at overlapping sites, or at completely different sites.

In one embodiment, an inhibitory compound of the present invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby inhibiting viral infection. In another embodiment, an enhancing compound of the present invention modulates a pathway comprising a host factor of the present invention by interacting with said host factor, thereby enhancing viral infection. Preferred host factors with which inhibitory compounds or enhancing compounds can interact are those encoded by a nucleic acid molecule listed in Table 1. In certain embodiments, host factors with which inhibitory compounds or enhancing compounds can interact are those encoded by a nucleic acid molecule listed in Table 5. In certain embodiments, host factors with which inhibitory compounds or enhancing compounds can interact are those encoded by a nucleic acid molecule listed in Table 1 or in Table 5. Types of interactions have been discussed previously. In one embodiment, the compound binds to the host factor with a K_d of at least 10^{-4} , 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} , 10^{-11} or 10^{-12} . In another embodiment, the binding is irreversible. In another embodiment the compound modifies the host factor thereby modulating its activity. In one embodiment of the present invention, a compound that interacts with a host factor of the present invention reduces the amount of virus produced by at least 5%, 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% or at least 95%. In another embodiment, the amount of virus is reduced by a factor of at least 10, at least 100, at least 1000, or at least 10,000. In one embodiment the viral infection is completely inhibited.

Also contemplated is the use of methods and compounds of the present invention to modulate infection by viruses of the present invention. Modulation of viral infection can be effected in a patient infected with HCV, or it can be effected in cells in culture (e.g., tissue culture). Thus one embodiment of the present invention is a method to inhibit viral infection, the method comprising contacting a cell infected with the virus with an inhibitory compound that interacts with a host factor of the present invention in such a manner as to inhibit viral

infection. In a preferred embodiment, the cell is infected with hepatitis C virus. In some circumstances it may be desirable to increase the amount of virus produced during an infection. For example, during the production of a vaccine, it would be useful to be able to increase the yield of virus obtained from a culture or animal. Thus one embodiment of the present invention is a method to enhance viral infection, the method comprising contacting an infected cell with an enhancing compound that interacts with a host factor in such a manner as to increase the amount of virus produced. In a preferred embodiment, the cell is infected with hepatitis C virus.

As used herein, the term contacting refers to bringing the compound and the cell into proximity so that the compound is capable of interacting with a host factor of the present invention. Such contacting can be achieved by introducing the compound to the cell when the cell is in a tissue culture environment, or it can be achieved when the cell is present in a whole body. Consequently contacting the compound with the infected cell can be achieved through introducing the compound into a patient, for example, through an oral medication, an injection or other route of administration. The compound can interact with and remain on outside of the cell, or it can enter the cell and interact with a host factor within the cell. Regardless, the end result of such contact is modulation of a pathway comprising a host factor of the present invention.

One embodiment of the present invention is a method to inhibit viral infection, the method comprising contacting a cell with an inhibitory compound that modulates a pathway comprising a host factor of the present invention in such a manner as to inhibit viral infection. Another embodiment of the present invention is a method to enhance viral infection, the method comprising contacting a cell with an enhancing compound that modulates a pathway comprising a host factor of the present invention in such a manner as to enhance viral infection. Suitable host factors are those encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1. Preferred host factors are those encoded by nucleic acid molecules listed in Table 2. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5 or encoded by a nucleic acid molecule having a SEQ ID NO listed in Table 1. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 12. In certain embodiments, a host factor is encoded

by a nucleic acid molecule listed in Table 13. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule having SEQ ID NO:79. In certain embodiments, a host factor comprises amino acid sequence SEQ ID NO:80.

5 As discussed previously, an inhibitory compound of the present invention is useful for inhibiting infection by a virus of the present invention. Consequently such a compound can be used to protect a patient from viral infection, such as hepatitis C infection. As used herein, the term protect refers to prophylactic as well as therapeutic use. Thus, one embodiment of the present invention is a method to prevent viral infection in a patient capable of being
10 infected by a virus of the present invention by administering a pharmaceutical composition comprising an inhibitory compound that interacts with a host factor of the present invention in such a manner as to inhibit viral infection.

 Another embodiment is a method to reduce the amount of virus in a patient infected with a virus, said method comprising administering a pharmaceutical composition comprising
15 an inhibitory compound that interacts with a host factor of the present invention. In one embodiment, the patient is infected with Flavivirus. In a preferred embodiment, the patient is infected with hepatitis C virus.

 Another embodiment is a method to protect a patient from virus infection, comprising administering to a patient an inhibitory compound that modulates a pathway comprising a
20 host factor of the present invention in such a manner as to inhibit viral infection. Suitable host factors are those encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1. A preferred host factor is one encoded by a nucleic acid molecule listed in Table 2. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 5 or
25 encoded by a nucleic acid molecule having a SEQ ID NO listed in Table 1. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 11. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 12. In certain embodiments, a host factor is encoded by a
30 nucleic acid molecule listed in Table 13. In certain embodiments, a host factor is encoded by a nucleic acid molecule listed in Table 14. In certain embodiments, a host factor is encoded by a nucleic acid molecule having SEQ ID NO:79. In certain embodiments, a host factor

comprises amino acid sequence SEQ ID NO:80. In a preferred embodiment, the patient is infected with hepatitis C virus.

Examples of inhibitory compounds include, but are not limited to, inhibitory compounds that inhibit viral entry, viral translation, viral replication or viral trafficking, assembly or release. In certain embodiments, an inhibitory compound inhibits viral entry. In certain embodiments, an inhibitory compound inhibits viral translation. In certain embodiments, an inhibitory compound inhibits viral replication. In certain embodiments, an inhibitory compound inhibits viral trafficking, assembly or release. Examples of preferred inhibitory compounds are listed in Table 3.

Table 3. Drugs and Small Molecule Inhibitors that Affect Pathways and Host Factors of the Present Invention

A. Drugs

Host Factor/Pathway	Related drugs*
ALAD	Aminolevulinic acid (T)
CHKA	Choline (T)
DGAT1	Atorvastatin
	Ezetimibe
	Fluvastatin
	Lovastatin
	Pravastatin
	Rosuvastatin
	Simvastatin
FLT4	Sunitinib (T)
	Sorafenib (T)
GCAT	Glycine (T)
	Pyridoxal phosphate (T)
KCNJ3	Antiarrhythmics class
	Halothane (T)
LTC4S	Glucocorticoids
	Methacholine chloride
	Montelukast
	Glutathione (T)

NMT1	Mercaptopurine
	Methotrexate
NOL1	Warfarin
NOS1AP	Isradipine
	Verapamil
PECR	Adenine (T)
PTHR1	Teriparatide (T)
RAC1	Azathioprine
	Pravastatin
	Simvastatin
	Mercaptopurine
SLC6A8	Creatine (T)
	Cisplatin
SRI	Clomipramine
TOP1	Irinotecan (T)
	Topotecan (T)
	Lucanthone (T)
	Camptothecin (T)
	Sodium stibogluconate (T)
TWIST1	Cisplatin
VAMP1	BTX-B (T)
WIF1	Mercaptopurine
	Methotrexate
CACNA1F	Verapamil
CSF3R	Pegfilgrastim (T)
	Filgrastim (T)
	Granulocyte CSF
	Etoposide
IMPDH1	Ribavirin (T)
	Mycophenolate mofetil (T)
	Tibavirin (T)
	Azathioprine (T)
	Thioguanine (T)

	Nadh (T)
	Mercaptopurine (T)
KCNA1	Desflurane (T)
	Isoflurane (T)
	Seroflurane (T)
	Methoxyflurane (T)
	Enflurane (T)
CCL26/CX3CL1	Aplaviroc
	Maraviroc
	Vicriviroc

* - data obtained on July 22, 2009, from the PharmacoGenomics Knowledge Base maintained by Stanford University at <http://www.pharmgkb.org/>

(T) = the product of the gene is the direct drug target

5 B. Small Molecule Inhibitors

Host Factors	Small Molecule Inhibitors*	References
ADAMTS 4	Epigallocatechin Gallate	http://www.genecards.org/cgi-bin/carddisp.pl?gene=ADAMTS4&search=adamts4
APLP2	DAPT	Vincent et al., 2009, J Neurosci 29:6752-60
ATP10D	Bufalin	http://www.genecards.org/cgi-bin/carddisp.pl?gene=ATP10D&search=atp10d
CCNB2	Butyrolactone I	http://www.genecards.org/cgi-bin/carddisp.pl?gene=CCNB2&search=ccnb2
	Olomoucine	http://www.genecards.org/cgi-bin/carddisp.pl?gene=CCNB2&search=ccnb2
	Roscovitine	Whittaker et al., 2007, Cell Cycle 6:3114-31
DGAT1	Fungal Beauveriolide III	Tomoda H et al, Pharmacol Ther 2007;115:375-89
	Biaryl Keto acids (Compound 4a)	Zhao G et al, I Med Chem 2008;51:380-3
	A-922500	King AJ et al, J Pharmacol Exp Ther 2009; 330:526-31
GNG8	Gallein	http://www.genecards.org/cgi-bin/carddisp.pl?gene=GNG8&search=gng8
GUCY1A2	NS-2028	http://www.genecards.org/cgi-bin/carddisp.pl?gene=GUCY1A2&search=gucy1a2
LTC4S	BAY-u9773	http://www.genecards.org/cgi-bin/carddisp.pl?gene=LTC4S&search=ltc4s
NMT1	Tris DBA	http://www.genecards.org/cgi-bin/carddisp.pl?gene=NMT1&search=nmt1
PARP11	3-Aminobenzamide	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PARP11&search=parp11
	4-Amino-1,8-naphthalimide	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PARP11&search=parp11

	4-HQN	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PARP11&search=parp11
	1,5-Isoquinolinediol	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PARP11&search=parp11
	6(5H)-Phenanthridinone	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PARP11&search=parp11
PPP2R1A	Calyculin A	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PPP2R1A&search=ppp2r1a
	Cantharidic Acid	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PPP2R1A&search=ppp2r1a
	Cantharidin	http://www.genecards.org/cgi-bin/carddisp.pl?gene=PPP2R1A&search=ppp2r1a
	Okadaic acid	Li et al., 2007, J Biol Chem 282:7287-98
RAC1	NSC 23766	Ferri et al., 2009, J Med Chem 52:4087-90
TOP1	CPT-11	Pommier et al., 2006, Nat Rev Cancer 6:789-802
	SN-38	Pommier et al., 2006, Nat Rev Cancer 6:789-802
	Camptothecin	Cinelli et al., 2008, J Med Chem 51:4609-19
	10-Hydroxycamptothecin	Cinelli et al., 2008, J Med Chem 51:4609-19
	beta-Lapachone	http://www.genecards.org/cgi-bin/carddisp.pl?gene=TOP1&search=Top1
IGFBP6	Picropodophyllin	http://www.genecards.org/cgi-bin/carddisp.pl?gene=IGFBP6&search=igfbp6
IMPDH1	Mycophenolic acid	Chen et al., 2007, J Med Chem, 50:5743-51
	Ribavirin	http://www.genecards.org/cgi-bin/carddisp.pl?gene=IMPDH1&search=impdh1

* - all data obtained July 22, 2009

5 In one embodiment, a preferred inhibitory compound is a siRNA, such as those listed in Table 4.

Table 4. Small Interfering RNA's that Interact with Host Factors of the Present Invention

SEQ ID NO	Sequence	Vendor Id	Gene Name
Part One, Decreased Infection			
790	CAAACCAGAGGCUC CAUUG	D-003807-04	ADAM metalloproteinase with thrombospondin type 1 motif, 4
791	GGACACACGCCUCC GAUAC	D-003807-03	ADAM metalloproteinase with thrombospondin type 1 motif, 4
792	GAGAUCGUGUUUCC AGAGA	D-003807-01	ADAM metalloproteinase with thrombospondin type 1 motif, 4
793	UGUUAGGCGUGUUA CAAUA	D-003807-02	ADAM metalloproteinase with thrombospondin type 1 motif, 4
794	GAUGACAUACAGCC UAUCA	D-008458-04	aminolevulinate, delta-, dehydratase

795	GGCCUACGCGUGU CUUGA	D-008458-03	aminolevulinate, delta-, dehydratase
796	GGACUUGGCAACAG GGUAU	D-008458-02	aminolevulinate, delta-, dehydratase
797	GAGCUACAGUGCCA AAUUU	D-008458-01	aminolevulinate, delta-, dehydratase
798	GAGGAGAUCUUAAG CAUGU	D-012375-01	AP1 gamma subunit binding protein 1
799	CCAAUACUCUGAAU GAGAA	D-012375-04	AP1 gamma subunit binding protein 1
800	GGACAUCGAUAAAG UAUGG	D-012375-02	AP1 gamma subunit binding protein 1
801	CAAAUAUGAUGCCC UAAAA	D-012375-03	AP1 gamma subunit binding protein 1
802	CAUCAGAGACCGUA CAAGA	D-017533-04	adaptor-related protein complex 3, beta 1 subunit
803	AGUAUUAGAGUGCC AAUUA	D-017533-03	adaptor-related protein complex 3, beta 1 subunit
804	GCAAUAGGGAGGUG CAGUA	D-017533-02	adaptor-related protein complex 3, beta 1 subunit
805	GUGAUAAAGAUGGUC UCUAU	D-017533-01	adaptor-related protein complex 3, beta 1 subunit
806	GAAGAGCGUCACCU GAACA	D-004179-05	amyloid beta (A4) precursor-like protein 2
807	GAACAAAGAUCGCU UACAU	D-004179-01	amyloid beta (A4) precursor-like protein 2
808	GGAAUGACCUUAUA UAGCU	D-004179-04	amyloid beta (A4) precursor-like protein 2
809	CAAAGGAGAUGACU ACAAU	D-004179-03	amyloid beta (A4) precursor-like protein 2
810	GGGAUCAGCUUUUC UACUA	D-019080-02	Rho GTPase activating protein 22
811	AUUACAACCUGCUC AGAU	D-019080-03	Rho GTPase activating protein 22
812	CUAGGAAGCUUGAC UGUUG	D-019080-01	Rho GTPase activating protein 22
813	GGGAUUUAUUUCUC UACAA	D-019080-04	Rho GTPase activating protein 22
814	CCAAGUAUGUGGUG AAGUG	D-017096-01	Rho guanine nucleotide exchange factor (GEF) 10-like
815	GACGAGAGCCCGAC AGUUG	D-017096-02	Rho guanine nucleotide exchange factor (GEF) 10-like
816	CCAUGGUGCUAGAU GUGUA	D-017096-03	Rho guanine nucleotide exchange factor (GEF) 10-like
817	GGAUGGCCGUGAUG CGCAA	D-017096-04	Rho guanine nucleotide exchange factor (GEF) 10-like
818	GCCCGAUCCUGGUA CUGUA	D-013874-02	arrestin domain containing 2
819	UGACAUCUUCGAG GGCAA	D-013874-04	arrestin domain containing 2
820	ACGCAGAGCUACAG UGAAC	D-013874-03	arrestin domain containing 2
821	GACAACGGCUCCAC ACGUC	D-013874-01	arrestin domain containing 2
822	GCCGACAGCUUUA GGAUU	D-018890-01	B melanoma antigen family, member 2
823	AGUCACAUCUCCU GCUUU	D-018890-02	B melanoma antigen family, member 2
824	GAUCGAAGGAAGAU	D-018890-04	B melanoma antigen family, member 2

	GCAAA		
825	AGAAAUGUACCCAG AUGUA	D-018890-03	B melanoma antigen family, member 2
826	GGACAACACGGACC UGGUG	D-012563-03	branched chain keto acid dehydrogenase E1, alpha polypeptide
827	CAACUUCGCGCCA CACUU	D-012563-01	branched chain keto acid dehydrogenase E1, alpha polypeptide
828	UCGGCGGAGUUUAU AGAUA	D-012563-04	branched chain keto acid dehydrogenase E1, alpha polypeptide
829	GAACGCCACUUCGU CACUA	D-012563-02	branched chain keto acid dehydrogenase E1, alpha polypeptide
830	GGAGGACUGUGAAG GAGGU	D-017422-02	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
831	GGAUGAAGCGGGAC UGGAU	D-017422-03	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
832	GGAAGAGGCUCACG GAAUU	D-017422-01	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
833	GGUCAAAAGUGUGUG AGUCC	D-017422-04	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
834	CCGACACGCUCUAC AAUAA	D-015854-01	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
835	CGGAACUCAUACAG ACAUU	D-015854-04	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
836	CCACUACGCAGCAG CCUAU	D-015854-03	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
837	GCUCACCGGCCUCC ACAAA	D-015854-02	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
838	GAGAAGAACUGUCA CUGUU	D-026465-04	chromosome 10 open reading frame 112
839	GAAGAGAGCAGAAG UGUUU	D-026465-02	chromosome 10 open reading frame 112
840	AAACGAAGGUUCUA CUUAA	D-026465-03	chromosome 10 open reading frame 112
841	GAAAGCAGAUGUGU UAAUA	D-026465-01	chromosome 10 open reading frame 112
842	GCGGAACCAGCAUC UCUUG	D-022006-03	chromosome 14 open reading frame 73
843	CAUCAGGCGGGACC ACAUA	D-022006-01	chromosome 14 open reading frame 73
844	GCUGAUCACCUGCG UCUAG	D-022006-02	chromosome 14 open reading frame 73
845	CCGGUCAUCUCCAG CGUGU	D-022006-04	chromosome 14 open reading frame 73
846	CAGCUUAUUCGGAG GAUUU	D-014802-04	chromosome 19 open reading frame 44
847	GAAAGAACCUGCUA GAACA	D-014802-01	chromosome 19 open reading frame 44
848	ACAGAACACUGGAC GCUUU	D-014802-03	chromosome 19 open reading frame 44
849	GCACAGAACGCGAA GGUCA	D-014802-02	chromosome 19 open reading frame 44
850	GAACCGACACUCC ACAUG	D-006381-03	chromosome 20 open reading frame 20
851	ACAAAGUCCUGACC GCAAA	D-006381-04	chromosome 20 open reading frame 20
852	GAACUUCGUCCUUC	D-006381-02	chromosome 20 open reading frame 20

	CAGAA		
853	GAAGAACUCCUCAG ACUUG	D-006381-01	chromosome 20 open reading frame 20
854	GCAAGCUGGUCAUC GACGU	D-015458-04	chromosome 21 open reading frame 56
855	GGAGCUACUACCUC AAUGA	D-015458-01	chromosome 21 open reading frame 56
856	CAUCAACACCUACG GAAUC	D-015458-02	chromosome 21 open reading frame 56
857	CCGAGAAGAUCGAG CAGAC	D-015458-03	chromosome 21 open reading frame 56
858	GAGAGGCUACGGUG GAAUA	D-019047-01	calmodulin binding transcription activator 2
859	GAUCCUAGGCCUUC CAUGA	D-019047-02	calmodulin binding transcription activator 2
860	GGUGAAAUAUCGGA AGGAU	D-019047-03	calmodulin binding transcription activator 2
861	CCACCGAGGUUGCU GAAAA	D-019047-04	calmodulin binding transcription activator 2
862	GGACUAUAGUGUAG AUGUA	D-004404-01	caspase 4, apoptosis-related cysteine peptidase
863	GGGCAAAGAUUCC UCACU	D-004404-03	caspase 4, apoptosis-related cysteine peptidase
864	GAGGGAAUCUGCGG AACUG	D-004404-04	caspase 4, apoptosis-related cysteine peptidase
865	GAGACUAUGUAAAG AAAGA	D-004404-02	caspase 4, apoptosis-related cysteine peptidase
866	GGGAGAGGCUGCAG AUAGU	D-014775-04	coiled-coil domain containing 8
867	GGGAGGACGUCGAC UAUUU	D-014775-02	coiled-coil domain containing 8
868	GAAGCGACCUGGAG AGUGA	D-014775-01	coiled-coil domain containing 8
869	GGGAAGAGGCCGUA CAUGA	D-014775-03	coiled-coil domain containing 8
870	GUGACUACGUUAAG GAUUA	D-003207-08	cyclin B2
871	CAACAAAUGUCAAC AAACA	D-003207-05	cyclin B2
872	GCAGCAAACUCCUG AAGAU	D-003207-06	cyclin B2
873	CCAGUGAUUUGGAG AAUAU	D-003207-07	cyclin B2
874	GAUUGUAUGUUGAG GCAAA	D-013998-03	cell cycle progression 1
875	AAACGAACCUUGCU ACAGA	D-013998-01	cell cycle progression 1
876	GUUAAGUGGUAGUC AGUUA	D-013998-02	cell cycle progression 1
877	CCGAAGACAGUAUC UAUAU	D-013998-04	cell cycle progression 1
878	ACAAUUAAGUCUCC UAGCA	D-003233-09	cell division cycle 6 homolog (S. cerevisiae)
879	GGAAAUUAUCUUAGC UACUG	D-003233-07	cell division cycle 6 homolog (S. cerevisiae)
880	GAGCAGAGAUGUCC ACUGA	D-003233-06	cell division cycle 6 homolog (S. cerevisiae)
881	GGACGAAGAUUGGU AUUUG	D-003233-08	cell division cycle 6 homolog (S. cerevisiae)

882	ACCAGAACCUCGAA CUAUA	D-003877-05	cadherin 1, type 1, E-cadherin (epithelial)
883	GAGAACGCAUUGCC ACAUA	D-003877-06	cadherin 1, type 1, E-cadherin (epithelial)
884	GGAGAGCGGUGGUC AAAGA	D-003877-02	cadherin 1, type 1, E-cadherin (epithelial)
885	GCAGUACAUUCUAC ACGUA	D-003877-07	cadherin 1, type 1, E-cadherin (epithelial)
886	GCUAUUCACUGGUG CCAUA	D-004799-04	cyclin-dependent kinase-like 5
887	GAUGGAAGCUUGAG CAUAG	D-004799-02	cyclin-dependent kinase-like 5
888	GGACUCACGUCGAA CCACA	D-004799-06	cyclin-dependent kinase-like 5
889	GAUAGACGCUUCAU GUUAA	D-004799-01	cyclin-dependent kinase-like 5
890	GAAUACAGCAGUUA CAAUU	D-006704-04	choline kinase alpha
891	CAGAUGAGGUCCUG UAAUA	D-006704-02	choline kinase alpha
892	GAGCAAACAUCGGG AAGUA	D-006704-03	choline kinase alpha
893	GAAUUAAGUUUGCC AGAUA	D-006704-01	choline kinase alpha
894	CAAAGAAGCUGACA AUACU	D-003473-03	conserved helix-loop-helix ubiquitous kinase
895	GAAGUUCGGUUUAG UAGCC	D-003473-05	conserved helix-loop-helix ubiquitous kinase
896	AAAUUAUGGCAUCUC CUUAA	D-003473-06	conserved helix-loop-helix ubiquitous kinase
897	CCAGAUACUUUCUU UACUA	D-003473-04	conserved helix-loop-helix ubiquitous kinase
898	GACAACACCUGCAG AAGAU	D-017381-01	cytokine inducible SH2-containing protein
899	CCGACUACCUCGGA CAGUA	D-017381-04	cytokine inducible SH2-containing protein
900	GAAGGCACGUUCUU AGUAC	D-017381-02	cytokine inducible SH2-containing protein
901	CCACUGCUGUACAC CUAAA	D-017381-03	cytokine inducible SH2-containing protein
902	CACCAAGGCCCUAU CCAAA	D-017369-04	claudin 1
903	GGUGCGAUUUUCU UCUUG	D-017369-01	claudin 1
904	CAAUAGAAUCGUUC AAGAA	D-017369-02	claudin 1
905	UGAAGUGUAUGAAG UGC UU	D-017369-03	claudin 1
906	GCGAUUUGCAGGUG AGAUU	D-020393-04	calsyntenin 1
907	CCGGGAAACUCGCG GAUAA	D-020393-01	calsyntenin 1
908	GGAGACAUGUGACG AGCCA	D-020393-03	calsyntenin 1
909	GACGUGCCCUUAC UGUUG	D-020393-02	calsyntenin 1
910	GCAAUAUAAUCGUG CAGUU	D-015369-04	CCR4-NOT transcription complex, subunit 1
911	GAGUGUGCGUUGCU	D-015369-03	CCR4-NOT transcription complex, subunit 1

	GAUUA		
912	CAAGUUAGCACUAU GGUAA	D-015369-02	CCR4-NOT transcription complex, subunit 1
913	AUAAGUGGCUCACA GAUAA	D-015369-01	CCR4-NOT transcription complex, subunit 1
914	GAAGAACGAGUAUG GAUUA	D-020313-01	CCR4-NOT transcription complex, subunit 2
915	UAACGAACAUCAC AUUAG	D-020313-02	CCR4-NOT transcription complex, subunit 2
916	UUACCAGGCUCCAG CUAUA	D-020313-03	CCR4-NOT transcription complex, subunit 2
917	AAUCGCAGCUUAUC ACAAG	D-020313-04	CCR4-NOT transcription complex, subunit 2
918	GCACUAAGGCACAG UAUCU	D-020319-02	CCR4-NOT transcription complex, subunit 3
919	AGACAUGGGUAGCG UCCAA	D-020319-04	CCR4-NOT transcription complex, subunit 3
920	GGACGACGUUGAGU ACUAU	D-020319-01	CCR4-NOT transcription complex, subunit 3
921	GGACAAGAGGCAGC UUAUA	D-020319-03	CCR4-NOT transcription complex, subunit 3
922	UACAAUGAGUGUCU UAUGA	D-016411-03	CCR4-NOT transcription complex, subunit 6-like
923	UGACAGCGCUGCAC CUAAA	D-016411-01	CCR4-NOT transcription complex, subunit 6-like
924	GGUAUUAGAGGUCC ACAAA	D-016411-04	CCR4-NOT transcription complex, subunit 6-like
925	GAGCAGGUAUGAAG CCUAU	D-016411-02	CCR4-NOT transcription complex, subunit 6-like
926	CAUUGGCACUGUCC GAUUA	D-004681-04	casein kinase 1, alpha 1-like
927	GCACUGGUAUGGUC AGGAA	D-004681-05	casein kinase 1, alpha 1-like
928	GUACUGGGCGUCAC UGUAA	D-004681-02	casein kinase 1, alpha 1-like
929	AAACAACAGCGGCU CCAAA	D-004681-01	casein kinase 1, alpha 1-like
930	UAACUUAGAUGAUC CUCUG	D-018312-02	CTAGE family, member 6
931	GAGAAAGAAACCAC AUUAU	D-018312-04	CTAGE family, member 6
932	GGAGGAAAAUUACC GAUAU	D-018312-01	CTAGE family, member 6
933	GAACGACGGGCUAU AGCAA	D-018312-03	CTAGE family, member 6
934	GAAGACAUACCGAG CUAAA	D-012633-05	connective tissue growth factor
935	GCACAAGGGCCUCU UCUGU	D-012633-03	connective tissue growth factor
936	ACAAUGACAUCUUU GAAUC	D-012633-04	connective tissue growth factor
937	UAAAUUCUGUGGAG UAUGU	D-012633-02	connective tissue growth factor
938	GCUCAGUCAUUCC CUGUU	D-005837-04	cathepsin F
939	UGAGAAGGGUUACU ACUAC	D-005837-05	cathepsin F
940	GCAACAAGAUGAAG CAAGC	D-005837-06	cathepsin F

941	GAGGAGGAGUCCG CACUA	D-005837-03	cathepsin F
942	GCUGUGGUAGUAAU UCAUA	D-007870-05	chemokine (C-X3-C motif) ligand 1
943	UAGCUUUGCUCAUC CACUA	D-007870-04	chemokine (C-X3-C motif) ligand 1
944	GAGCUGUGGUAGUA AUUCA	D-007870-01	chemokine (C-X3-C motif) ligand 1
945	CAAACGCGCAAUCA UCUUG	D-007870-03	chemokine (C-X3-C motif) ligand 1
946	UACCAGGAAUUACU AUGUU	D-011020-02	cytochrome b-245, alpha polypeptide
947	GGACAGAAGCACAU GACCG	D-011020-03	cytochrome b-245, alpha polypeptide
948	GAAGAAGGGCUCCA CCAUG	D-011020-01	cytochrome b-245, alpha polypeptide
949	CCAUGUGGGCCAAC GAGCA	D-011020-04	cytochrome b-245, alpha polypeptide
950	GGAACUGCAUCGGG AAACA	D-021791-02	cytochrome P450, family 4, subfamily A, polypeptide 22
951	GUGCUGAGGUGGAC ACGUU	D-021791-01	cytochrome P450, family 4, subfamily A, polypeptide 22
952	GGACAAAUGGGAAG AGCUC	D-021791-03	cytochrome P450, family 4, subfamily A, polypeptide 22
953	UGGCACGACUUGUG UUGAA	D-021791-04	cytochrome P450, family 4, subfamily A, polypeptide 22
954	GAGAAUCGCCUGCC UUCAG	D-015690-01	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
955	CGGGUUCUCUCAAG GUCAU	D-015690-04	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
956	AAUCAAAAGCUUCCC ACGCG	D-015690-02	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
957	GAGAGCGAAUCGAG CGCCA	D-015690-03	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
958	GGACACGUUUCUCA CUGUG	D-014275-02	dysbindin (dystrobrevin binding protein 1) domain containing 1
959	GACAAUGGCCACAC GCCUG	D-014275-04	dysbindin (dystrobrevin binding protein 1) domain containing 1
960	ACGAGAACCUCAAC ACCGA	D-014275-03	dysbindin (dystrobrevin binding protein 1) domain containing 1
961	GGAGCUGGCCGAGG UCUUU	D-014275-01	dysbindin (dystrobrevin binding protein 1) domain containing 1
962	CUAUAUCCUCCUC AUUUA	D-006874-04	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
963	GAAAUACGAUGACA UUCCA	D-006874-03	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
964	ACAUUGAGCUUACU CGUUA	D-006874-02	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
965	GCAAAUACUUGGUG UUAGA	D-006874-01	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
966	GAAGACAACCAGGA CCUUG	D-013143-02	defensin, alpha 5, Paneth cell-specific
967	CCUCAGGUUCUCAG GCAAG	D-013143-04	defensin, alpha 5, Paneth cell-specific
968	GCUACAACCCAGAA GCAGU	D-013143-03	defensin, alpha 5, Paneth cell-specific

969	GAAAUGGACUCUCU GCUCU	D-013143-01	defensin, alpha 5, Paneth cell-specific
970	CCUGAAGAGAUGCA UGUAA	D-019046-04	defensin, beta 126
971	UCAGGUAAUUGGUA UGUGA	D-019046-01	defensin, beta 126
972	GCUGACAGACGUGC UAAUU	D-019046-02	defensin, beta 126
973	GGCAAUGUGCGGCA AACAA	D-019046-03	defensin, beta 126
974	UGACCUACCGCGAU CUCUA	D-003922-02	diacylglycerol O-acyltransferase homolog 1 (mouse)
975	CUACCGCGAUCUCU ACUAC	D-003922-04	diacylglycerol O-acyltransferase homolog 1 (mouse)
976	UCAUGUACGUCCAC GACUA	D-003922-01	diacylglycerol O-acyltransferase homolog 1 (mouse)
977	GUGCUACGAGCUCA ACUUU	D-003922-03	diacylglycerol O-acyltransferase homolog 1 (mouse)
978	AAACAGCGGCAUUG GCAAA	D-014418-04	dehydrogenase/reductase (SDR family) member 12
979	GAACUAUGGUCUAU GCACA	D-014418-01	dehydrogenase/reductase (SDR family) member 12
980	GAUCUCCAGUCCGA AAGAA	D-014418-03	dehydrogenase/reductase (SDR family) member 12
981	GCAGGUUGCAUGGU CAAUA	D-014418-02	dehydrogenase/reductase (SDR family) member 12
982	AAGUGGAGCUCAAC AGUGA	D-011251-02	deiodinase, iodothyronine, type III
983	GCACUUGGUUGGAA CGCUA	D-011251-01	deiodinase, iodothyronine, type III
984	GCCCGCUGGUUCUC AAUUU	D-011251-03	deiodinase, iodothyronine, type III
985	GCGCCUACUUCGAG CGUCU	D-011251-04	deiodinase, iodothyronine, type III
986	GCAGACAGCAUCGA GAUUU	D-009452-04	discs, large (Drosophila) homolog-associated protein 4
987	CAAAGAAGCCAGCC AAAUC	D-009452-03	discs, large (Drosophila) homolog-associated protein 4
988	GCCAAUGACUCAAG CUGUA	D-009452-02	discs, large (Drosophila) homolog-associated protein 4
989	GAACAACCUCUCUG AAGAA	D-009452-01	discs, large (Drosophila) homolog-associated protein 4
990	GAAAGAGCAUUCGA AACGA	D-012735-01	DnaJ (Hsp40) homolog, subfamily B, member 1
991	CAACAACAUUCCAG CUGAU	D-012735-03	DnaJ (Hsp40) homolog, subfamily B, member 1
992	GCUCUGAUGUCAUU UAUCC	D-012735-04	DnaJ (Hsp40) homolog, subfamily B, member 1
993	GAGCAGGUUCUUC AAUAU	D-012735-02	DnaJ (Hsp40) homolog, subfamily B, member 1
994	GAAGAUAGGCUGCA CUGUU	D-012695-01	dedicator of cytokinesis 3
995	CGAGAUCACUGGCG AGUAU	D-012695-02	dedicator of cytokinesis 3
996	GACCUGUGAUGGAC ACGUA	D-012695-04	dedicator of cytokinesis 3
997	UGACGCCCAUUCCA GAUUA	D-012695-03	dedicator of cytokinesis 3
998	CCUUGGACCAGGAC	D-003260-09	E2F transcription factor 2

	GACUA		
999	UGAAGGAGCUGAUG AACAC	D-003260-07	E2F transcription factor 2
1000	GGGAGAAGACUCGG UAUGA	D-003260-05	E2F transcription factor 2
1001	GAGGACAACCUGCA GAUUA	D-003260-06	E2F transcription factor 2
1002	CGAGAUGAGUCAAU UAAAA	D-013008-04	ELKS/RAB6-interacting/CAST family member 2
1003	GGAAUUGUCUGCCU CCAAA	D-013008-02	ELKS/RAB6-interacting/CAST family member 2
1004	GAAAAGGGAUUCCA AAUUA	D-013008-01	ELKS/RAB6-interacting/CAST family member 2
1005	UAAUUGAGCGCUUG AAAGA	D-013008-03	ELKS/RAB6-interacting/CAST family member 2
1006	GAACGCACCUGCUG CUGUA	D-006626-02	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
1007	GAAAGAAGAUGCUA AACGU	D-006626-03	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
1008	GAACGAACUUUGCC CAUAU	D-006626-04	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
1009	CAUGAAAUCUUGAC UGAUA	D-006626-01	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
1010	AAUGUUAGCGGAUG AGUUU	D-019840-04	eukaryotic translation termination factor 1
1011	UAACUAUGUUCGGA AAGUA	D-019840-02	eukaryotic translation termination factor 1
1012	GAAACACGGUAGAG GAGGU	D-019840-03	eukaryotic translation termination factor 1
1013	GAUCAGAGGUUACA AUCAA	D-019840-01	eukaryotic translation termination factor 1
1014	GAGUAGCUAUGGUC AACAA	D-005119-09	Ewing sarcoma breakpoint region 1
1015	CUACACAGCCGACU AGUUA	D-005119-10	Ewing sarcoma breakpoint region 1
1016	GGAACAGAUGGGAG GAAGA	D-005119-05	Ewing sarcoma breakpoint region 1
1017	AGGAAAGCCCAAAG GCGAU	D-005119-06	Ewing sarcoma breakpoint region 1
1018	CCGCAUGCUUGGAG GUAAA	D-013149-02	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
1019	GAAACGGUCGCCCA GAUCA	D-013149-01	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
1020	AAGAAGACAGGUCG GGCUA	D-013149-04	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30

1021	GGUCAGACUCCUAA GGUGG	D-013149-03	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
1022	UAACCAAAAUGGCG GGUAU	D-017621-04	fibulin 5
1023	GGACGAGUGUGCAA CAGAU	D-017621-02	fibulin 5
1024	GCAGACGUGCUACA AUUUA	D-017621-01	fibulin 5
1025	GUGCAAACCUGCGU CAACA	D-017621-03	fibulin 5
1026	CAAUUACUGUUCAU GAUUC	D-018163-03	F-box protein 38
1027	GCCGAGAGUGGAAA UAAUA	D-018163-04	F-box protein 38
1028	GGACUCGAUUGGUU GAUUA	D-018163-02	F-box protein 38
1029	GCAGAUAAAUCCAC UAGUA	D-018163-01	F-box protein 38
1030	GCGAUGAGCACCAC UACUG	D-017906-04	Fc fragment of IgG, receptor, transporter, alpha
1031	GGCGAGGAGUUCAU GAAUU	D-017906-03	Fc fragment of IgG, receptor, transporter, alpha
1032	GGAGCUCUGUUGUG GAGAA	D-017906-02	Fc fragment of IgG, receptor, transporter, alpha
1033	CGUCAUCGGUGUCU UGCUA	D-017906-01	Fc fragment of IgG, receptor, transporter, alpha
1034	CCACAGGAAUGCAC GGUUA	D-013584-01	fer-1-like 3, myoferlin (C. elegans)
1035	GAACGGCUGCAAAC AAAUA	D-013584-02	fer-1-like 3, myoferlin (C. elegans)
1036	GAAGAUGGGAGUAG AAUCA	D-013584-03	fer-1-like 3, myoferlin (C. elegans)
1037	CGUCUUUGCUGAAA UGUAU	D-013584-04	fer-1-like 3, myoferlin (C. elegans)
1038	GGUUGGAGGUUCCC GGAGU	D-014521-02	hypothetical protein FLJ22659
1039	AAAUGGAAGUGCUU GGUGA	D-014521-01	hypothetical protein FLJ22659
1040	GAGCCGAAGAGCAG CCAAU	D-014521-03	hypothetical protein FLJ22659
1041	AUGUCGAAGUGGAG GCUCA	D-014521-04	hypothetical protein FLJ22659
1042	GCAAGAACGUGCAU CUGUU	D-003138-05	fms-related tyrosine kinase 4
1043	GAGCAGCCAUUCAU CAACA	D-003138-08	fms-related tyrosine kinase 4
1044	GCGAAUACCUGUCC UACGA	D-003138-06	fms-related tyrosine kinase 4
1045	GAAGACAUUUGAGG AAUUC	D-003138-07	fms-related tyrosine kinase 4
1046	GAACACCACUACGC CUUCA	D-010089-02	forkhead box A2
1047	ACGAACAGGUGAUG CACUA	D-010089-03	forkhead box A2
1048	CAACGACUGUUUCC UGAAG	D-010089-01	forkhead box A2
1049	CCGCAGAUACCUCU UACUA	D-010089-04	forkhead box A2

1050	GAACUUAUCAGGAG CGCUA	D-024802-01	FERM and PDZ domain containing 3
1051	CCACAGCCCGUAAC CUUAA	D-024802-03	FERM and PDZ domain containing 3
1052	GCAAAGCUCCAGUA UCUAC	D-024802-02	FERM and PDZ domain containing 3
1053	GCGCAAAUGAU AUG GAAUG	D-024802-04	FERM and PDZ domain containing 3
1054	CCAAGGAUGUGCUG AGUGU	D-006876-03	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
1055	GAUAAGACCAUCAU CAUGU	D-006876-02	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
1056	CAAUACACUGUCC AGGAU	D-006876-01	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
1057	GAGAU AAGACCAUC AUCAU	D-006876-04	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
1058	AGGUGAACAU CGAC CGCAU	D-031976-04	guanine nucleotide binding protein (G protein), gamma 8
1059	CCAACAACAUGGCC AAGAU	D-031976-01	guanine nucleotide binding protein (G protein), gamma 8
1060	GCGAGACGCAUGCC AAAGA	D-031976-02	guanine nucleotide binding protein (G protein), gamma 8
1061	GAAGGUGUCG CAGG CAGCA	D-031976-03	guanine nucleotide binding protein (G protein), gamma 8
1062	AUUACGAGGUGGAG AUUCU	D-009537-02	glycoprotein, synaptic 2
1063	UGGAGAUUCUGGAC GCAAA	D-009537-01	glycoprotein, synaptic 2
1064	GAUUCUGGACGCAA AGACA	D-009537-04	glycoprotein, synaptic 2
1065	GAGCUCAGCAGGUG AAACU	D-009537-03	glycoprotein, synaptic 2
1066	GCAAUGAAACAAAG UCUCA	D-012635-03	general transcription factor IIIA
1067	GAAACAAGGGCAAG GCUUA	D-012635-01	general transcription factor IIIA
1068	CCAUAAAGAGGAAA UACUA	D-012635-02	general transcription factor IIIA
1069	GACCAUUUGUUUGU GACUA	D-012635-04	general transcription factor IIIA
1070	CCAGAAAGUUUGAU GAGU	D-006730-03	guanylate cyclase 1, soluble, alpha 2
1071	GACAGUGGAUCUUC UAUAU	D-006730-02	guanylate cyclase 1, soluble, alpha 2
1072	GAACAUCAAGUUAU UGGUU	D-006730-04	guanylate cyclase 1, soluble, alpha 2
1073	AGAGGACACUGCAG UAUUA	D-006730-01	guanylate cyclase 1, soluble, alpha 2
1074	GGACAGAAAGUUAGA UAUGU	D-009226-02	holocytochrome c synthase (cytochrome c heme-lyase)
1075	GGAAGGAGAUUUUG AAGUG	D-009226-04	holocytochrome c synthase (cytochrome c heme-lyase)
1076	GAAAGGCUGUCCAG UGAAU	D-009226-03	holocytochrome c synthase (cytochrome c heme-lyase)
1077	GGAAUGCAAUGUUA AAGAA	D-009226-01	holocytochrome c synthase (cytochrome c heme-lyase)
1078	UGGGUUAAGUUGCU UGAUA	D-015939-04	HEAT repeat containing 1

1079	UAAAGAAGCUUGAA AGUGU	D-015939-01	HEAT repeat containing 1
1080	CCGCUGACAUUUA AUUAA	D-015939-03	HEAT repeat containing 1
1081	GCUCAGAAGUCCUC AGAUA	D-015939-02	HEAT repeat containing 1
1082	GAUUGAAGCGCAAG AGUGA	D-004810-04	homeodomain interacting protein kinase 3
1083	GAAGUGAGCAUAU AGCAA	D-004810-01	homeodomain interacting protein kinase 3
1084	GGAAAUCCAGUGAC AGUUG	D-004810-03	homeodomain interacting protein kinase 3
1085	GAAGGUGACUAUCA GUUAG	D-004810-02	homeodomain interacting protein kinase 3
1086	CCACAGCCCUAGAG ACCAU	D-011697-03	histidine rich calcium binding protein
1087	ACACAGUGGUCAAG GAUAG	D-011697-02	histidine rich calcium binding protein
1088	GGAGUGAAGACACG GAAGA	D-011697-04	histidine rich calcium binding protein
1089	CAAGGAAUAUGGGC ACCUA	D-011697-01	histidine rich calcium binding protein
1090	UAACAAUCGUGGUG AAUAA	D-018524-02	hydroxysteroid (17-beta) dehydrogenase 13
1091	GAACGCGCCUCAGC GAUUU	D-018524-03	hydroxysteroid (17-beta) dehydrogenase 13
1092	GGAGACAGAUGAAG UCGUA	D-018524-01	hydroxysteroid (17-beta) dehydrogenase 13
1093	GAUGGAAUACUUAC CAAUA	D-018524-04	hydroxysteroid (17-beta) dehydrogenase 13
1094	GCUCCGACCUGUUC CGAAG	D-005168-05	heat shock 70kDa protein 1A
1095	GAGAUCGACUCCCU GUUUG	D-005168-01	heat shock 70kDa protein 1A
1096	GAUCAACGACGGAG ACAAG	D-005168-03	heat shock 70kDa protein 1A
1097	GCGCUGAACCCGCA GAACA	D-005168-04	heat shock 70kDa protein 1A
1098	GCAUUCGCCUACUC CGUGA	D-014116-04	interferon induced transmembrane protein 3 (1-8U)
1099	UCAACACCCUCUUC AUGAA	D-014116-03	interferon induced transmembrane protein 3 (1-8U)
1100	CAAACCUUCUUCUC UCCUG	D-014116-02	interferon induced transmembrane protein 3 (1-8U)
1101	GGAAGAUGGUUGGC GACGU	D-014116-01	interferon induced transmembrane protein 3 (1-8U)
1102	CAACAUACCAUCCA UUUAU	D-010688-01	immunoglobulin superfamily, member 11
1103	CAGGAACAUGGAC UAAUA	D-010688-04	immunoglobulin superfamily, member 11
1104	GAACAUCAGUGCCC UGUCU	D-010688-03	immunoglobulin superfamily, member 11
1105	GGAACGAAUUGGUG CAGUA	D-010688-02	immunoglobulin superfamily, member 11
1106	GCUGGUGGCCUGUG AGAAA	D-009658-02	ilvB (bacterial acetolactate synthase)-like
1107	UGACUGCGGUGAAG AAUGC	D-009658-03	ilvB (bacterial acetolactate synthase)-like
1108	GUUGAUCAGCUGUC	D-009658-04	ilvB (bacterial acetolactate synthase)-like

	CCUUU		
1109	GGUGUGCGGUUCAU CUUCA	D-009658-01	ilvB (bacterial acetolactate synthase)-like
1110	GCAAUGUGGUCAUG CGGCA	D-015116-04	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
1111	AAACCAGGACGACU ACAUA	D-015116-03	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
1112	UCUCUGACAUCCUC CGAUA	D-015116-02	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
1113	GAACCGAGGUCGAC AUGAA	D-015116-01	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
1114	AUGCACAGCAGGAG GAUUU	D-006875-03	interferon regulatory factor 3
1115	GGGAAGAGUGGGAG UUCGA	D-006875-04	interferon regulatory factor 3
1116	CCAAGAGGCUCGUG AUGGU	D-006875-05	interferon regulatory factor 3
1117	GCAAAGAAGGGUUG CGUUU	D-006875-01	interferon regulatory factor 3
1118	GAGGAGUACUCAGC UGUGA	D-008004-04	integrin, alpha 7
1119	CCAGGGAGCUGAUA UGCAA	D-008004-02	integrin, alpha 7
1120	CCACGGAACUGGAG GUAGA	D-008004-03	integrin, alpha 7
1121	GAGAAUGCCUCCCA UGUUG	D-008004-01	integrin, alpha 7
1122	GAACCUUCCAGCCA AAUUA	D-006248-01	potassium inwardly-rectifying channel, subfamily J, member 3
1123	GAAAAUUACUGGAA GAGAA	D-006248-02	potassium inwardly-rectifying channel, subfamily J, member 3
1124	CCAGUUCCAUGCAA CAUUU	D-006248-04	potassium inwardly-rectifying channel, subfamily J, member 3
1125	GAGGGAUUCUUUAA AGUUG	D-006248-03	potassium inwardly-rectifying channel, subfamily J, member 3
1126	GUACAAGAGCCGCG AGAAG	D-006262-01	potassium channel, subfamily K, member 3
1127	UCAACACCUUGGUG AGGUA	D-006262-03	potassium channel, subfamily K, member 3
1128	ACGCGGAGGUGCUG CACUU	D-006262-04	potassium channel, subfamily K, member 3
1129	ACGAGGAGCUGGAG CGCGU	D-006262-02	potassium channel, subfamily K, member 3
1130	AAAGGCACCUGAAG GAAUA	D-007025-02	KIAA1166
1131	CAAGAAAUCAUGUG CAAAU	D-007025-04	KIAA1166
1132	GCACCUAUAUGCCC UCUUU	D-007025-01	KIAA1166
1133	GAACAAGACCCUGC AGAUG	D-007025-03	KIAA1166
1134	GUGAGAAUGCCCUU AAAGA	D-011711-02	keratin 4
1135	CGGAAGAGCGCGAA CAGAU	D-011711-04	keratin 4
1136	AGGCAUCAGCGGAG	D-011711-03	keratin 4

	GAUUA		
1137	CAAGAGAGGUGCCU UCAGC	D-011711-01	keratin 4
1138	GGACAUAGCUCCGG UAUUA	D-017976-01	LINE-1 type transposase domain containing 1
1139	AGACAACACUAACG AAUAC	D-017976-03	LINE-1 type transposase domain containing 1
1140	GCAAGGACGUAUCA GCAAU	D-017976-02	LINE-1 type transposase domain containing 1
1141	CUACUAGUGUACAA UCAA	D-017976-04	LINE-1 type transposase domain containing 1
1142	CAACUUUCCUGGAC UUAAA	D-028236-01	hypothetical protein LOC285556
1143	CCAAGUUGCUCACG CCCAA	D-028236-03	hypothetical protein LOC285556
1144	GAACGUCUGCAGCG GAGAA	D-028236-04	hypothetical protein LOC285556
1145	UCUACUCGUUCGUG GAUUA	D-028236-02	hypothetical protein LOC285556
1146	GGAAUUGGCUUGGA AAUGA	D-004965-01	KIF4B
1147	GGUAACAGCCACAC UCUUA	D-004965-03	KIF4B
1148	GCAAGAUCUGAAA GAGAU	D-004965-04	KIF4B
1149	AGAAACAUCUCCU AAUGA	D-004965-02	KIF4B
1150	GAUGAGGACUCCAC AGUAU	D-032129-01	hypothetical gene supported by AK075564; BC060873
1151	GAAAUUGGCGCCACU AAAUG	D-032129-02	hypothetical gene supported by AK075564; BC060873
1152	AAAGAAGACACGCA AGUAU	D-032129-04	hypothetical gene supported by AK075564; BC060873
1153	CGACAUCAAAUACA GGUAA	D-032129-03	hypothetical gene supported by AK075564; BC060873
1154	AGGACGAGGUAGCU CUACU	D-008637-04	leukotriene C4 synthase
1155	CGAGGUAGCUCUAC UGGCU	D-008637-02	leukotriene C4 synthase
1156	CACCCGAGUUCGAG CGCGU	D-008637-03	leukotriene C4 synthase
1157	GAAGGACGAGGUAG CUCUA	D-008637-01	leukotriene C4 synthase
1158	CGAGGAGGAUUCUG UGUUA	D-011724-04	microtubule-associated protein 4
1159	GGACAUGUCUCCAC UAUCA	D-011724-01	microtubule-associated protein 4
1160	CAACACCAGUCCA AUUAA	D-011724-03	microtubule-associated protein 4
1161	GGAAUCACCCACCA AAUUA	D-011724-02	microtubule-associated protein 4
1162	AAACAGAUCUUUAC AAGCU	D-003555-03	mitogen-activated protein kinase 1
1163	CAAGAGGAUUGAAG UAGAA	D-003555-04	mitogen-activated protein kinase 1
1164	CAAAGCUCUGGAC UUAAU	D-003555-01	mitogen-activated protein kinase 1
1165	GUACAGGGCUCCAG AAAUU	D-003555-09	mitogen-activated protein kinase 1

1166	GAAGUUACCUCUCG UACCA	D-003517-04	MAP/microtubule affinity-regulating kinase 3
1167	GGAAUGACACGACG AAAUA	D-003517-03	MAP/microtubule affinity-regulating kinase 3
1168	GAAAUACGAUGAAA UCACA	D-003517-02	MAP/microtubule affinity-regulating kinase 3
1169	GGAAUGCAAGUAAU CCUAA	D-003517-10	MAP/microtubule affinity-regulating kinase 3
1170	CGAAGGUCAUCAAA UUUAA	D-005548-03	melanin-concentrating hormone receptor 2
1171	GAACAAGGUACAAG ACCAU	D-005548-05	melanin-concentrating hormone receptor 2
1172	GGAGAUGUAUCAAC AGAAU	D-005548-02	melanin-concentrating hormone receptor 2
1173	GCAGCAGCAUUAAC CCUUU	D-005548-04	melanin-concentrating hormone receptor 2
1174	CAGAGCAGGUGACA UAUCA	D-003273-07	minichromosome maintenance complex component 2
1175	GCCGUGGGCUCCUG UAUGA	D-003273-08	minichromosome maintenance complex component 2
1176	GGAUAAAGGCUCGUC AGAUC	D-003273-06	minichromosome maintenance complex component 2
1177	GAAGAUCUUUGCCA GCAUU	D-003273-05	minichromosome maintenance complex component 2
1178	CAACAACAGCUCUC UAAUA	D-009092-03	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
1179	GCAGAGAAAUUACG UUGUA	D-009092-01	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
1180	UUAGAACCCUCCUC UUAUA	D-009092-04	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
1181	UCACUCAUCUCAUG UUAUA	D-009092-02	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
1182	GAAGAGAGAUGUCU ACCUA	D-014854-01	hypothetical protein MGC13057
1183	GAACCUCCAGGGAC CAAUA	D-014854-02	hypothetical protein MGC13057
1184	UAUCUUGUGUGAUG CCUUG	D-014854-04	hypothetical protein MGC13057
1185	CAAUGGGCAUGCAA UAACA	D-014854-03	hypothetical protein MGC13057
1186	GAGACUGGCCACUU CAAUG	D-016352-04	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
1187	CCUACGACCUGUUC CUGAA	D-016352-03	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
1188	GACAAGGCCUACAC GGAUG	D-016352-02	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
1189	GCAAAGACUCCGAG AGCAA	D-016352-01	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
1190	GCCCAUGCCUUCAA ACUUC	D-009253-04	MLX interacting protein-like
1191	GACACUCUCUUCAC CAUGA	D-009253-01	MLX interacting protein-like
1192	ACAAGUGGCGCAUC UACUA	D-009253-02	MLX interacting protein-like
1193	GGGCACAUCUACCA GUAUC	D-009253-03	MLX interacting protein-like

1194	GCCAGGAAGUAUGG UUAUA	D-013052-03	mitochondrial ribosomal protein L15
1195	GGCGGAUCCUGCCA AAUUU	D-013052-01	mitochondrial ribosomal protein L15
1196	GAUCCUAGUCAACC UAUUG	D-013052-02	mitochondrial ribosomal protein L15
1197	UGGUGAAUAUGGCC GAUAA	D-013052-04	mitochondrial ribosomal protein L15
1198	GGACCUACCGAGAG UAUUU	D-013573-02	mitochondrial ribosomal protein L38
1199	UAACCAACAUCCCG GGUAA	D-013573-04	mitochondrial ribosomal protein L38
1200	CCAAAGAGAAGAUU GAUAU	D-013573-01	mitochondrial ribosomal protein L38
1201	GCAAUGAGGUGACU CCAAC	D-013573-03	mitochondrial ribosomal protein L38
1202	CCAUAGAAGUGUUG CAGUU	D-017512-02	mitochondrial ribosomal protein L48
1203	GGGGACAGAUUAUG AAUAU	D-017512-04	mitochondrial ribosomal protein L48
1204	CGAGGAAAGUUAUG CAAUG	D-017512-01	mitochondrial ribosomal protein L48
1205	AUUCAAAGCUCGAC CAGAA	D-017512-03	mitochondrial ribosomal protein L48
1206	CCAGAGUCCUCGUG GAUUU	D-013745-02	methenyltetrahydrofolate synthetase domain containing
1207	CGGGAUUGUUUAAU AAGAU	D-013745-03	methenyltetrahydrofolate synthetase domain containing
1208	GCUACGCCGAUCUG GAAUA	D-013745-04	methenyltetrahydrofolate synthetase domain containing
1209	GGACAUACGUGAAC AAAUU	D-013745-01	methenyltetrahydrofolate synthetase domain containing
1210	CGGAAUACUUAUACU GAACU	D-010591-05	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
1211	GAACCCAGCCCUCA GCUUU	D-010591-01	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
1212	CAAGGCCACGGAU ACUUA	D-010591-03	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
1213	GAUAACGUUCGCG GUUCU	D-010591-04	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
1214	GAACAGCAAUUGGA UACCA	D-004862-03	myosin IIIA
1215	GAAGAGGGGUGAAA GAAUG	D-004862-04	myosin IIIA
1216	GCAAUUGGAUACCA CUUAU	D-004862-02	myosin IIIA
1217	GAAAGGCAAUAACA UUCUA	D-004862-01	myosin IIIA
1218	GCACCGAGCUUAUU UACCG	D-022928-03	myosin VIIB
1219	GAGCAUCCUUCUAG CCUAU	D-022928-02	myosin VIIB
1220	GCGAGUACAGCUUC GAGAA	D-022928-04	myosin VIIB
1221	CAACAUAUCCUCCAG GGAAG	D-022928-01	myosin VIIB
1222	UUAAGGAGCUACAG ACUCA	D-005975-03	N-acetylated alpha-linked acidic dipeptidase-like 1
1223	GGACAUUGCCUAUA	D-005975-02	N-acetylated alpha-linked acidic dipeptidase-like 1

	CCUAU		
1224	GGACACAGCUUCUG GAUCU	D-005975-01	N-acetylated alpha-linked acidic dipeptidase-like 1
1225	GCAGAUCAAUCGUG UUUGC	D-005975-04	N-acetylated alpha-linked acidic dipeptidase-like 1
1226	GCAGAAAUAUGACC AUGCA	D-004316-03	N-myristoyltransferase 1
1227	GAAAUUGGUUGGGU UCAUU	D-004316-01	N-myristoyltransferase 1
1228	CAGCAAACAUCCAU AUCUA	D-004316-02	N-myristoyltransferase 1
1229	ACGGCAACCGCAG UAUUA	D-004316-04	N-myristoyltransferase 1
1230	GGAAGUACAAGGUG UGGAU	D-014293-03	nucleolar complex associated 4 homolog (S. cerevisiae)
1231	GCGCACUCCUGAAG UUUGU	D-014293-04	nucleolar complex associated 4 homolog (S. cerevisiae)
1232	GCACUUCACGCUCA GCUGA	D-014293-02	nucleolar complex associated 4 homolog (S. cerevisiae)
1233	GAACAAUGCCUUCA CGCUG	D-014293-01	nucleolar complex associated 4 homolog (S. cerevisiae)
1234	AGACAGAACUCGUC AGAUU	D-020084-02	nucleolar protein 1, 120kDa
1235	GCAACGAUCACCUA AAUUA	D-020084-01	nucleolar protein 1, 120kDa
1236	GCAUACCCAUGAAA UUUAA	D-020084-03	nucleolar protein 1, 120kDa
1237	AAGCGUUGCUGCCC AUUGA	D-020084-05	nucleolar protein 1, 120kDa
1238	GGAGAGAUACCACG AAAGA	D-019143-02	nucleolar protein 5A (56kDa with KKE/D repeat)
1239	GAGCGACUGUCCUU CUAUG	D-019143-04	nucleolar protein 5A (56kDa with KKE/D repeat)
1240	CAACGACAAUGCCA CAUAC	D-019143-03	nucleolar protein 5A (56kDa with KKE/D repeat)
1241	GGACAUAUCUGCCA UUGAC	D-019143-01	nucleolar protein 5A (56kDa with KKE/D repeat)
1242	UGAGAAGUGUCUUG CAGUU	D-017285-03	nucleolar protein family 6 (RNA-associated)
1243	CUUAAUCGCCUUCG GGAGA	D-017285-04	nucleolar protein family 6 (RNA-associated)
1244	GGACGGAGCCAUUC GGGAA	D-017285-01	nucleolar protein family 6 (RNA-associated)
1245	GGGAUCAGUUUAUG UCUCA	D-017285-02	nucleolar protein family 6 (RNA-associated)
1246	GGAAUUAGUUGGAG CACGG	D-017973-01	nucleolar protein NOP5/NOP58
1247	CCUCAAAUCUAGAC GGGAU	D-017973-04	nucleolar protein NOP5/NOP58
1248	ACAACUACAUAUG CGAUG	D-017973-03	nucleolar protein NOP5/NOP58
1249	GAUUGAAGUUUAGC GCUGA	D-017973-02	nucleolar protein NOP5/NOP58
1250	GCGACGGCCUGGAU GAUGA	D-013446-03	nitric oxide synthase 1 (neuronal) adaptor protein
1251	GGACGUGGAUGAG AGCAA	D-013446-04	nitric oxide synthase 1 (neuronal) adaptor protein
1252	GGUAUGAGUUUAAA GCCAA	D-013446-02	nitric oxide synthase 1 (neuronal) adaptor protein

1253	GGUGUAACGUCUUU AAAUC	D-013446-01	nitric oxide synthase 1 (neuronal) adaptor protein
1254	GGUGUCAGCCUCUG CAGAA	D-005374-05	NUAK family, SNF1-like kinase, 2
1255	GCAGGCGACGUGUU UGUGA	D-005374-07	NUAK family, SNF1-like kinase, 2
1256	GCAGAAGCCUCCGC AAGCU	D-005374-06	NUAK family, SNF1-like kinase, 2
1257	GGACGCAGGCGACG UGUUU	D-005374-01	NUAK family, SNF1-like kinase, 2
1258	GAAGAAGGCAGUAG UUUGG	D-010374-03	oral cancer overexpressed 1
1259	GAAAUUCCCUAUG AUGAC	D-010374-01	oral cancer overexpressed 1
1260	GGUCUGAGAUCGGG UGCUA	D-010374-04	oral cancer overexpressed 1
1261	GCAGAAGGUUCCGG ACUUU	D-010374-02	oral cancer overexpressed 1
1262	GAUUAGAGGAGAAU GGGUA	D-009747-05	oxysterol binding protein
1263	GAACGAGCCACACU CUUUA	D-009747-04	oxysterol binding protein
1264	GCAUUGACUUGAUA GCUAA	D-009747-02	oxysterol binding protein
1265	GGAGACAAGUGUAA UCUUA	D-009747-01	oxysterol binding protein
1266	CAUGCAGCCUCCUU CCAAA	D-016115-04	poly (ADP-ribose) polymerase family, member 11
1267	GACGGGAGCUAUGU GAAUU	D-016115-03	poly (ADP-ribose) polymerase family, member 11
1268	GAGAUUACAUA AAC GGAGA	D-016115-02	poly (ADP-ribose) polymerase family, member 11
1269	UCACAAAGCAGAAG AAUUA	D-016115-01	poly (ADP-ribose) polymerase family, member 11
1270	GAGGAUCUAUCGUC AAUAU	D-009855-01	peroxisomal trans-2-enoyl-CoA reductase
1271	GAAUGGGCCUGCAG UGGAA	D-009855-04	peroxisomal trans-2-enoyl-CoA reductase
1272	GGACCUUUCUGUUG UCAAA	D-009855-02	peroxisomal trans-2-enoyl-CoA reductase
1273	AGGAGGAGGUGAAU AAUUU	D-009855-03	peroxisomal trans-2-enoyl-CoA reductase
1274	CUCAAGGAGGCGAG AGUGA	D-010392-02	phosphatidylethanolamine N-methyltransferase
1275	CCGCUGAGAUCUAC CGGCA	D-010392-04	phosphatidylethanolamine N-methyltransferase
1276	GAACUUUCCUAGGU GAUUA	D-010392-01	phosphatidylethanolamine N-methyltransferase
1277	ACAUAGUGGCUCUC CUAUA	D-010392-03	phosphatidylethanolamine N-methyltransferase
1278	GGAGACCACUGUCC AGGAU	D-008671-04	peptidoglycan recognition protein 4
1279	CGAAGUAUGGCAUC AUUAU	D-008671-03	peptidoglycan recognition protein 4
1280	CGACAUUGGUUAUA ACUUC	D-008671-02	peptidoglycan recognition protein 4
1281	GCUGUUGGCUGCAG UAUUC	D-008671-01	peptidoglycan recognition protein 4
1282	CCACAGGCCUCUCC	D-006776-03	phosphatidylinositol 4-kinase, catalytic, alpha

	UACUU		
1283	GUGAAGCGAUGUGG AGUUA	D-006776-02	phosphatidylinositol 4-kinase, catalytic, alpha
1284	GCAGAAAUUUGGCC UGUUU	D-006776-09	phosphatidylinositol 4-kinase, catalytic, alpha
1285	GAGCAUCUCUCCCU ACCUA	D-006776-01	phosphatidylinositol 4-kinase, catalytic, alpha
1286	GAAAUCAAGGAAUG UAGAA	D-018033-02	partner of NOB1 homolog (S. cerevisiae)
1287	CGAAGAAACGACAG GCUGA	D-018033-04	partner of NOB1 homolog (S. cerevisiae)
1288	GCUAACAGAUACAC ACCAU	D-018033-03	partner of NOB1 homolog (S. cerevisiae)
1289	GGACUUCAGAUACG CUUUA	D-018033-01	partner of NOB1 homolog (S. cerevisiae)
1290	CAACAAAGAAGACC ACACA	D-013602-02	DNA directed RNA polymerase II polypeptide J-related
1291	GGUACCCAAUGCCU GUUUA	D-013602-03	DNA directed RNA polymerase II polypeptide J-related
1292	GCGAGAAGAUACCC AUUAA	D-013602-01	DNA directed RNA polymerase II polypeptide J-related
1293	GGAAACAUCAUUAA AUCAC	D-013602-04	DNA directed RNA polymerase II polypeptide J-related
1294	GCAGACAAGGUCCC AAAGA	D-004979-04	peptidylprolyl isomerase A (cyclophilin A)
1295	AGACAAGGUCCCAA AGACA	D-004979-01	peptidylprolyl isomerase A (cyclophilin A)
1296	AGAAUUAUUCAGG GUUUA	D-004979-03	peptidylprolyl isomerase A (cyclophilin A)
1297	GGAAUGGCAAGACC AGCAA	D-004979-02	peptidylprolyl isomerase A (cyclophilin A)
1298	UAGACGAACUCCGC AAUGA	D-010259-05	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform
1299	GAACAUCAUCUCUA ACCUG	D-010259-07	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform
1300	UCUCUAACCUGGAC UGUGU	D-010259-04	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform
1301	AGGCGGAACUUCGA CAGUA	D-010259-06	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform
1302	GGCAACAGAUGGAC UCUUU	D-017008-03	PTC7 protein phosphatase homolog (S. cerevisiae)
1303	GAAGGACGGUUCGU ACCUA	D-017008-04	PTC7 protein phosphatase homolog (S. cerevisiae)
1304	GACAUUAUCCUGAC GGCAA	D-017008-05	PTC7 protein phosphatase homolog (S. cerevisiae)
1305	CAACAUGCCUGAUU AUAUG	D-017008-01	PTC7 protein phosphatase homolog (S. cerevisiae)
1306	GAAUUUGUCCGAGA UGUCA	D-014399-03	PRKR interacting protein 1 (IL11 inducible)
1307	GACAAAGCAGUUCC AAUUC	D-014399-02	PRKR interacting protein 1 (IL11 inducible)
1308	CGACAGGACUACAU GGAUG	D-014399-01	PRKR interacting protein 1 (IL11 inducible)
1309	AAGAAGCGCCAGAA GUUAA	D-014399-04	PRKR interacting protein 1 (IL11 inducible)
1310	GCAAAGAUGUUGAU CCUUC	D-016913-01	prospero-related homeobox 1

1311	GACGUAAAGUUCAA CAGAU	D-016913-02	prospero-related homeobox 1
1312	GGAGAAGUACGCAC GUCAA	D-016913-04	prospero-related homeobox 1
1313	GGGCCAAACUCCUU ACAAC	D-016913-03	prospero-related homeobox 1
1314	GAUGCUGUCUGGGA AGAUA	D-027984-04	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>)
1315	GGAAAGCCUUAUA UUAUA	D-027984-03	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>)
1316	GGACAUAAACUCUAG AAUCU	D-027984-01	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>)
1317	GGAAUGAUGUCGUC AGUAA	D-027984-02	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>)
1318	CCAAUACAAUCCA CAUGA	D-006795-02	phosphoribosyl pyrophosphate synthetase- associated protein 2
1319	GAAAGAGGUGCAUA UAAGA	D-006795-04	phosphoribosyl pyrophosphate synthetase- associated protein 2
1320	GAAGAGAUGCCAGA UUACA	D-006795-01	phosphoribosyl pyrophosphate synthetase- associated protein 2
1321	GAUGGCAACUCAUG GCUUG	D-006795-05	phosphoribosyl pyrophosphate synthetase- associated protein 2
1322	GAAGACCUCUGUAC CAAGA	D-012254-01	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
1323	GUGGUGAUGCAGUG ACUAA	D-012254-04	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
1324	GCAGAUACCUCGGA UUGAG	D-012254-03	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
1325	GAAGCCAACUUGAG CAAUC	D-012254-02	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
1326	GACCCUCUCUGACA AAUAC	D-021366-04	pentatricopeptide repeat domain 1
1327	AACCAGAGGUGGAU ACUAA	D-021366-01	pentatricopeptide repeat domain 1
1328	GGAUGUGCCUCGAU GUGUU	D-021366-03	pentatricopeptide repeat domain 1
1329	GAACUACACCUAUC UCAUC	D-021366-02	pentatricopeptide repeat domain 1
1330	CGUCAUGACUAAAG AGGAA	D-005717-04	parathyroid hormone receptor 1
1331	GGGAAGCCCAGGAA AGAUA	D-005717-03	parathyroid hormone receptor 1
1332	GCAAUCAUAUACUG UUUCU	D-005717-02	parathyroid hormone receptor 1
1333	CAGCGAGUGUGUCA AAUUU	D-005717-01	parathyroid hormone receptor 1
1334	GCAAGGGAGCAUGG UAUUA	D-010823-04	RAB10, member RAS oncogene family
1335	GGAAUAGACUUCAA GAUCA	D-010823-02	RAB10, member RAS oncogene family
1336	CAAUGAAGAUGUGG AAAGA	D-010823-03	RAB10, member RAS oncogene family
1337	GAAAGAAGAUCAAG CUACA	D-010823-01	RAB10, member RAS oncogene family
1338	GGAGUAGAGUUUGC AACAA	D-004726-06	RAB11A, member RAS oncogene family

1339	GCAACAAUGUGGUU CCUAU	D-004726-02	RAB11A, member RAS oncogene family
1340	CAAGAGCGAUUUCG AGCUA	D-004726-03	RAB11A, member RAS oncogene family
1341	GUAGGUGCCUUAUU GGUUU	D-004726-01	RAB11A, member RAS oncogene family
1342	GGAAAUCGAAAUUG UCUAC	D-019457-04	Rab9 effector protein with kelch motifs
1343	GGAUUCAGCUGACA AAGUA	D-019457-02	Rab9 effector protein with kelch motifs
1344	CCACAGCUGUUCAU AUUUA	D-019457-01	Rab9 effector protein with kelch motifs
1345	GAAACCAGCUAUAU GUCUU	D-019457-03	Rab9 effector protein with kelch motifs
1346	AGACGGAGCUGUAG GUAAA	D-003560-05	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
1347	UAAAGACACGAUCG AGAAA	D-003560-08	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
1348	UAAGGAGAUUGGUG CUGUA	D-003560-07	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
1349	CGGCACCACUGUCC CAACA	D-003560-09	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
1350	UGCCAAACCUGCAG UAAAU	D-021186-03	RNA binding motif protein 22
1351	CAACAAAGAGUACU AUACA	D-021186-02	RNA binding motif protein 22
1352	CCAUUAUCCGAAU GACCA	D-021186-04	RNA binding motif protein 22
1353	GUAAAUGGCCGCAG ACUGA	D-021186-01	RNA binding motif protein 22
1354	AUAUGCAAUUGGUU GGAAA	D-020616-04	RNA binding motif protein 9
1355	CCGCUUACAGUGAC GGUUA	D-020616-02	RNA binding motif protein 9
1356	GACAGUAUAUGGUG CAGUC	D-020616-01	RNA binding motif protein 9
1357	CGAGAAUAGUGCUG AUGCA	D-020616-03	RNA binding motif protein 9
1358	GGACAGCACUGAUG GCUUA	D-008607-01	Ral-GDS related protein Rgr
1359	GGAUAAAGCUGGCC UUCAG	D-008607-03	Ral-GDS related protein Rgr
1360	ACACUUCAGUUUAC UAUCA	D-008607-04	Ral-GDS related protein Rgr
1361	GCACAUGGCACCCA CAGUU	D-008607-02	Ral-GDS related protein Rgr
1362	GGAAUUAUCUCUGA ACAUA	D-003602-01	receptor-interacting serine-threonine kinase 2
1363	GCACGUAUGAUCUC UCUAA	D-003602-04	receptor-interacting serine-threonine kinase 2
1364	GAAAGGAUGUCUUA AGAGA	D-003602-02	receptor-interacting serine-threonine kinase 2
1365	GGACAUCGACCUGU UAUUA	D-003602-03	receptor-interacting serine-threonine kinase 2
1366	UGGCAUAGAAGCAG CUACA	D-032070-04	ring finger protein 207
1367	CGUGUCUUCUGGAC UGUUU	D-032070-03	ring finger protein 207

1368	CAGCAUGUCUUCAG AGGAC	D-032070-02	ring finger protein 207
1369	GAGCAGAGGGUACC CGGUU	D-032070-01	ring finger protein 207
1370	GCGAUUAUAUGGCU ACACA	D-021419-02	ring finger protein 31
1371	GGCGUGGUGUCAAG UUUAA	D-021419-04	ring finger protein 31
1372	AGUCAAGUCUGGUA CUGUA	D-021419-03	ring finger protein 31
1373	GCAGAAUACUCAUC CAAGA	D-021419-01	ring finger protein 31
1374	GCAACUGGCUCGUU CAAUU	D-004610-03	Rho-associated, coiled-coil containing protein kinase 2
1375	GAGGAAAGCUGAUC AUGAA	D-004610-01	Rho-associated, coiled-coil containing protein kinase 2
1376	GUAGAAACCUUCCC AAUUC	D-004610-02	Rho-associated, coiled-coil containing protein kinase 2
1377	GCAAAUCUGUAAU ACUCG	D-004610-05	Rho-associated, coiled-coil containing protein kinase 2
1378	GGACUUCUCCGAAC CUUCU	D-005372-04	ribosomal protein S6 kinase-like 1
1379	GCUGUGAAGCUGAA AAUUA	D-005372-03	ribosomal protein S6 kinase-like 1
1380	GAGCGAGGACUCCA UCUUC	D-005372-02	ribosomal protein S6 kinase-like 1
1381	GGGAGUGCCUGACA UGACA	D-005372-01	ribosomal protein S6 kinase-like 1
1382	GGAUCGUGGUGACG UUUAA	D-016937-01	SH3 domain and tetratricopeptide repeats 1
1383	CAGGGAAGAUCUAU UACAU	D-016937-02	SH3 domain and tetratricopeptide repeats 1
1384	GAACGUGGCCUGU ACACA	D-016937-03	SH3 domain and tetratricopeptide repeats 1
1385	GCUCUCAGACUGCU ACCUA	D-016937-04	SH3 domain and tetratricopeptide repeats 1
1386	GGAAACAUCGAGUC AGAUC	D-007380-08	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
1387	UCAAUGAUCUGCUC AACGU	D-007380-07	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
1388	GCAAGCACCUCCCA GAGAG	D-007380-06	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
1389	GCACGGCCAUGCA UUCAA	D-007380-05	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
1390	GAAGAAGAGCGCCG AGAAC	D-007608-06	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1391	GGAAAGAUCGUGUA CUUCA	D-007608-01	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1392	GCGGAGGUGUGUUC CUUAU	D-007608-05	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1393	CAACACCUACUACA UCAUG	D-007608-02	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1394	GAUCAGAUGGGUCA AGAUA	D-015791-03	SMAD family member 5
1395	AGUCUUACCUCCAG UAUUA	D-015791-02	SMAD family member 5

1396	UCACAGAUCCUUC AAUAA	D-015791-01	SMAD family member 5
1397	GAGUAAAUGUGUC CUAUU	D-015791-04	SMAD family member 5
1398	GCUACCAACUCCCU CAUCA	D-015362-01	SMAD family member 6
1399	GACCAGGCCGUCAG CAUCU	D-015362-03	SMAD family member 6
1400	GUGCGGCGACUUUG GCGAA	D-015362-04	SMAD family member 6
1401	CCACAUUGUCUAC ACUGA	D-015362-02	SMAD family member 6
1402	UCAGUGCUCUGGAC AGUAA	D-009459-01	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
1403	UGACAAGGAAUACA UCAAU	D-009459-03	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
1404	GAAGAAGACGGCGU GCUAU	D-009459-05	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
1405	UAAACCAGCUCAAG AUCCA	D-009459-02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
1406	GGACUGCAGAGGAC UGUUA	D-007191-04	SMAD specific E3 ubiquitin protein ligase 1
1407	GGAAGAAGGUUUGG AUUAC	D-007191-03	SMAD specific E3 ubiquitin protein ligase 1
1408	GCACUAUGAUCUAU AUGUU	D-007191-01	SMAD specific E3 ubiquitin protein ligase 1
1409	AAAGAGAUCUAGUC CAGAA	D-007191-02	SMAD specific E3 ubiquitin protein ligase 1
1410	GACCAUACCUUCUG UGUUG	D-007194-02	SMAD specific E3 ubiquitin protein ligase 2
1411	GAACAACACAAUUU ACAGA	D-007194-04	SMAD specific E3 ubiquitin protein ligase 2
1412	GAUGAGAACACUCC AAUUA	D-007194-01	SMAD specific E3 ubiquitin protein ligase 2
1413	CAAAGUGGAAUCAG CAUUA	D-007194-03	SMAD specific E3 ubiquitin protein ligase 2
1414	UUAGGUGGCUCAAC AAGGA	D-020199-02	SAM pointed domain containing ets transcription factor
1415	GCUCCAUCCGCCAG UAUUA	D-020199-04	SAM pointed domain containing ets transcription factor
1416	GAGGAGAGCUGGAC CGACA	D-020199-01	SAM pointed domain containing ets transcription factor
1417	GCGAAGUGCUCUAG GACAU	D-020199-03	SAM pointed domain containing ets transcription factor
1418	GGAAUUGAAACCUG ACAUA	D-015445-03	serum response factor binding protein 1
1419	GCGAAGAAACCAAU ACAUA	D-015445-02	serum response factor binding protein 1
1420	GAAGAGAAUUCGAG UUUUA	D-015445-01	serum response factor binding protein 1
1421	CUAAAGCAGUGACU AUUGC	D-015445-04	serum response factor binding protein 1
1422	GAAGAGGGAACACG AGCGA	D-019342-03	stathmin-like 2
1423	CAACAAACGUGCCU	D-019342-04	stathmin-like 2

	CUGGC		
1424	GAGCUGAUCUUGAA GCCAC	D-019342-02	stathmin-like 2
1425	CAACAUCUAUACUU ACGAU	D-019342-01	stathmin-like 2
1426	GAGGAGAUUAGAAA CAGUA	D-021379-03	syntaxin 2
1427	GUUAAAGGCUAUUG AACAA	D-021379-01	syntaxin 2
1428	CACCAAACCCGGAA GGAAA	D-021379-04	syntaxin 2
1429	GAAAU CGAGUCACG UCACA	D-021379-02	syntaxin 2
1430	GCGCAGAGCCCAUC UUCAU	D-011786-06	surfeit 1
1431	GAACCUGAUUGCAG AGUUG	D-011786-05	surfeit 1
1432	GAAGCUAUGGCCAG AAUCA	D-011786-04	surfeit 1
1433	CAUCCUACCUGUGG UUUAA	D-011786-02	surfeit 1
1434	GAGGAGAACAUGCU ACUUA	D-013366-01	suppressor of variegation 4-20 homolog 1 (Drosophila)
1435	UAGCAAUAUGGAC UCAGA	D-013366-04	suppressor of variegation 4-20 homolog 1 (Drosophila)
1436	GAGGCAAGUUGUCU AAUGA	D-013366-02	suppressor of variegation 4-20 homolog 1 (Drosophila)
1437	GAGAGGAGGUCGAA CAGAU	D-013366-03	suppressor of variegation 4-20 homolog 1 (Drosophila)
1438	GAACACCUAUCACA CAUUA	D-006957-01	suppressor of zeste 12 homolog (Drosophila)
1439	GAAUUUAUGUCGAA ACUUC	D-006957-04	suppressor of zeste 12 homolog (Drosophila)
1440	GCAACAAACUGAAG CAAGA	D-006957-02	suppressor of zeste 12 homolog (Drosophila)
1441	GAACAGCAAAGAAC AUUAU	D-006957-03	suppressor of zeste 12 homolog (Drosophila)
1442	AACCAAAGAUUCUG AGUCA	D-012550-02	Treacher Collins-Franceschetti syndrome 1
1443	GCAGAGGAUUCUUC AAGCA	D-012550-03	Treacher Collins-Franceschetti syndrome 1
1444	GAGGAGGACUCAAG AAGCA	D-012550-01	Treacher Collins-Franceschetti syndrome 1
1445	CAAGGAGUCCAGUC GGAUA	D-012550-04	Treacher Collins-Franceschetti syndrome 1
1446	UAGAAGACCCGGGU AUUAA	D-006348-05	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
1447	CCAAAGCAGUAGCU GAAUU	D-006348-03	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
1448	GGAAAUUGACGGAU AAUAU	D-006348-01	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
1449	GUAGAAGACCCGGG UAUUA	D-006348-02	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
1450	GAUGAGCGCCCUAA UCCUG	D-032313-03	transmembrane 6 superfamily member 2
1451	GGAUGGCACUGUUC ACUAC	D-032313-02	transmembrane 6 superfamily member 2

1452	GCACAGUUCUCGCA CAUGG	D-032313-01	transmembrane 6 superfamily member 2
1453	GGAAGAGAUACCGG AAUUU	D-032313-04	transmembrane 6 superfamily member 2
1454	GCACCUGUUUGCGC UCAUG	D-014998-04	transmembrane protein 142A
1455	GGCCUGAUCUUUAU CGUCU	D-014998-02	transmembrane protein 142A
1456	UGAGCAACGUGCAC AAUCU	D-014998-03	transmembrane protein 142A
1457	GCUCACUGGUAGC CAUAA	D-014998-01	transmembrane protein 142A
1458	GAAGAAGGCUGUUC AGAGA	D-005278-02	topoisomerase (DNA) I
1459	ACAUAAAGGUCCAG UAUUU	D-005278-04	topoisomerase (DNA) I
1460	GAAAGGAAAUGACU AAUGA	D-005278-01	topoisomerase (DNA) I
1461	GGAAGUAGCUACGU UCUUU	D-005278-03	topoisomerase (DNA) I
1462	GGAUCAGACACUAA ACGAA	D-019753-04	tropomyosin 4
1463	GAACGUGGGCUUAC AUCAG	D-019753-03	tropomyosin 4
1464	GCGGAGGUGUCUGA ACUAA	D-019753-02	tropomyosin 4
1465	CCAAGCACAUUGCG GAAGA	D-019753-01	tropomyosin 4
1466	GCGCGUUGCUCUUC GUCAA	D-024079-04	trafficking protein particle complex 5
1467	GAACAGCACGCUCA ACUGC	D-024079-03	trafficking protein particle complex 5
1468	GCACCACGCUCAUG AUCAA	D-024079-01	trafficking protein particle complex 5
1469	GCGCGCACCUUCUA CAUCA	D-024079-02	trafficking protein particle complex 5
1470	CAGAAUACGUGUUU AAAGU	D-007173-04	tripartite motif-containing 42
1471	CCAAUGAUCCCAAC UGUAA	D-007173-02	tripartite motif-containing 42
1472	GCAAUACCAUCAUC ACUUU	D-007173-01	tripartite motif-containing 42
1473	CAAGUUCUCUUUCC ACAAU	D-007173-03	tripartite motif-containing 42
1474	UCGGACGACUGCAC CAUUG	D-007010-03	tripartite motif-containing 62
1475	GAUCAACACCGUCC UCAUC	D-007010-02	tripartite motif-containing 62
1476	CUACAAUGCUGAUG ACAUG	D-007010-01	tripartite motif-containing 62
1477	CGCCAAAGCGCUUC GAUGU	D-007010-04	tripartite motif-containing 62
1478	GAACAGGCGUGGUA UGCAA	D-005394-05	transformation/transcription domain-associated protein
1479	CAAUGUAGCUCUGG AUAUA	D-005394-03	transformation/transcription domain-associated protein
1480	GGACUUAACUGGAG AGGUU	D-005394-01	transformation/transcription domain-associated protein
1481	GAAAGGAGCUUCUG	D-005394-02	transformation/transcription domain-associated

	AUUGC		protein
1482	CUACGUGGCUUAGU GGUAA	D-014755-02	testis-specific transcript, Y-linked 5
1483	GGGUGUCACUGGCC UGUUA	D-014755-01	testis-specific transcript, Y-linked 5
1484	GCACCUGCAGCACU GGAAU	D-014755-04	testis-specific transcript, Y-linked 5
1485	GGACCCACAUGCUG UCGUC	D-014755-03	testis-specific transcript, Y-linked 5
1486	GAGCAAGAUUCAGA CCCUC	D-006434-06	twist homolog 1 (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)
1487	GCGACGAGCUGGAC UCCAA	D-006434-01	twist homolog 1 (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)
1488	CUGCAGACGCAGCG GGUCA	D-006434-02	twist homolog 1 (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)
1489	GGAGUCCGCAGUCU UACGA	D-006434-05	twist homolog 1 (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)
1490	GCUGUCAACUGCCG CAAGA	D-011794-01	ubiquitin A-52 residue ribosomal protein fusion product 1
1491	CAAGUGCUAUGCUC GCCUU	D-011794-04	ubiquitin A-52 residue ribosomal protein fusion product 1
1492	GACCAGCAGCGUCU GAUUA	D-011794-03	ubiquitin A-52 residue ribosomal protein fusion product 1
1493	CCUGCGAGGUGGCA UUAUU	D-011794-02	ubiquitin A-52 residue ribosomal protein fusion product 1
1494	GGGCAAUUCUCACA CUGUU	D-006063-01	ubiquitin specific peptidase 11
1495	GAACAAGGUUGGCC AUUUU	D-006063-02	ubiquitin specific peptidase 11
1496	GAUGAUUUCUUCGU CUAUG	D-006063-03	ubiquitin specific peptidase 11
1497	GAGAAGCACUGGUA UAAGC	D-006063-04	ubiquitin specific peptidase 11
1498	GUUAAUAGGUCCUC AGUGA	D-006089-03	ubiquitin specific peptidase 42
1499	UGACAAAGCUUCUG AAUCU	D-006089-01	ubiquitin specific peptidase 42
1500	UUAGAGACCUUCAG GCUUA	D-006089-02	ubiquitin specific peptidase 42
1501	CAACCUAACCUUCA UAGUA	D-006089-04	ubiquitin specific peptidase 42
1502	AAACAAAGCAGCAC CAUUU	D-032247-02	ubiquitin specific peptidase 51
1503	GAGCAGGGAUGACC ACAUA	D-032247-01	ubiquitin specific peptidase 51
1504	GGCGAAAGAUUAAU ACCUU	D-032247-03	ubiquitin specific peptidase 51
1505	GCUUUAAGUAGGU AAGAA	D-032247-04	ubiquitin specific peptidase 51
1506	CUCCUAAACUAGACC AGUAA	D-012497-01	vesicle-associated membrane protein 1 (synaptobrevin 1)
1507	CAUCACAAUUUGAG AGCAG	D-012497-02	vesicle-associated membrane protein 1 (synaptobrevin 1)
1508	AGGCACAAGUGGAG GAGGU	D-012497-04	vesicle-associated membrane protein 1 (synaptobrevin 1)
1509	CCAUCAUCGUGGUA GUUAU	D-012497-03	vesicle-associated membrane protein 1 (synaptobrevin 1)

1510	GCACGGACUCUGCC AUUAA	D-020390-02	WD repeat domain 37
1511	GAAAUUCGACACUCU UAAUG	D-020390-01	WD repeat domain 37
1512	GAGAUUCAGACUGCU CAUUAU	D-020390-03	WD repeat domain 37
1513	GCGCAAUCCCAUA GCCUU	D-020390-04	WD repeat domain 37
1514	CGAUGAACCGUCU AUUUU	D-022651-03	WD repeat domain 43
1515	ACGAAUAGCUUCC AGUUC	D-022651-04	WD repeat domain 43
1516	CCUCAUAUGUGUUU AGUAA	D-022651-02	WD repeat domain 43
1517	GUACAUGACCGGUU ACUUA	D-022651-01	WD repeat domain 43
1518	UGAAGAAGAUUCC UGAUU	D-012386-04	WNT inhibitory factor 1
1519	GUACGAAGCCAGCC UCAUA	D-012386-03	WNT inhibitory factor 1
1520	GCACACGCCUUCAC UAAAA	D-012386-02	WNT inhibitory factor 1
1521	GGAGGUAAAUGCAU UGGUA	D-012386-01	WNT inhibitory factor 1
1522	GGACAAACACCCA GAACA	D-016083-02	WW domain containing transcription regulator 1
1523	AGGAACAAACGUUG ACUUA	D-016083-03	WW domain containing transcription regulator 1
1524	AAGCCUAGCUCGUG GCGGA	D-016083-04	WW domain containing transcription regulator 1
1525	GACAUGAGAUCCA CACUA	D-016083-01	WW domain containing transcription regulator 1
1526	GGUAUUGACUCUUC AGAUU	D-009552-01	X-box binding protein 1
1527	CAACUUGGACCCAG UCAUG	D-009552-03	X-box binding protein 1
1528	GCAAGUGGUAGAUU UAGAA	D-009552-06	X-box binding protein 1
1529	CGAAAGAAGGCUCG AAUGA	D-009552-02	X-box binding protein 1
1530	GUGAGUAUAUUGCU CCAUG	D-006101-06	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
1531	GGAGCACAAUCCAG UAUUU	D-006101-04	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
1532	CUUCAGAGCUGCUU CGGCA	D-006101-07	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
1533	CCAAAGCUGUGAAG AAUUC	D-006101-05	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
1534	AAACUGAACCGUG GAUUA	D-006564-04	zinc finger E-box binding homeobox 1
1535	GAUAGCACUUGUCU UCUGU	D-006564-05	zinc finger E-box binding homeobox 1
1536	GAAGCAGGAUGUAC AGUAA	D-006564-03	zinc finger E-box binding homeobox 1
1537	GAACCACCCUUGAA AGUGA	D-006564-02	zinc finger E-box binding homeobox 1
1538	GCACUGCAAUGCUG CCUUU	D-012658-03	zinc finger protein 148
1539	UGGAAUAGCUACUC	D-012658-02	zinc finger protein 148

	AAUUU		
1540	GGACUACAGUAUGC ACUUA	D-012658-04	zinc finger protein 148
1541	GAACAGAUCGUGUA UUGAA	D-012658-01	zinc finger protein 148
1542	CGAAGAAGCUAGAC UCAGA	D-012450-01	zinc finger protein 346
1543	GAAGAGAUACCUAG CAAUC	D-012450-02	zinc finger protein 346
1544	GCGCCUUGCUUAUU UCUGA	D-012450-03	zinc finger protein 346
1545	AGACCAAGCUCAAA CUAAU	D-012450-04	zinc finger protein 346
1546	CAGCAUCUAUCGUU ACUUC	D-025367-02	zinc finger protein 467
1547	CACCUGGGCUCGCA CCAAA	D-025367-03	zinc finger protein 467
1548	GGAGGAAGGUGCCC ACACA	D-025367-01	zinc finger protein 467
1549	CAGAAGAGGAGGUC GAAUG	D-025367-04	zinc finger protein 467
1550	UGAGUAAUGUGGCA CUUGA	D-024395-03	zinc finger protein 608
1551	GCUAAUCCCGGGUC AAUAU	D-024395-04	zinc finger protein 608
1552	GGGAAACUCUAUGU UGGUA	D-024395-02	zinc finger protein 608
1553	GGCCAUCAGUGCCU AAUAA	D-024395-01	zinc finger protein 608
1554	AAACCGGGAUGGCC GAGAA	D-014511-01	zinc finger family member 767
1555	GAUUC CAGAUGUUC CUGUG	D-014511-03	zinc finger family member 767
1556	GCUCACCUGCUUUC CCUAG	D-014511-04	zinc finger family member 767
1557	GAAGGAGCCCUGCA ACUGG	D-014511-02	zinc finger family member 767
1558	CAUAAAGGCUGCAU AGAUG	D-007165-03	zinc and ring finger 2
1559	GCACAUGUUUGGAG GAUUU	D-007165-01	zinc and ring finger 2
1560	UGAGCACCCUUCAG AUUAA	D-007165-04	zinc and ring finger 2
1561	CAUAUGCCUUGAA GAAUU	D-007165-02	zinc and ring finger 2
Part Two Decreased Infection			
1561	GAAGGGCCGUAUUG AGUUU	D-007304-02	ATP-binding cassette, sub-family B (MDR/TAP), member 6
1562	UCGAGACGGUGAAG UAUUA	D-007304-03	ATP-binding cassette, sub-family B (MDR/TAP), member 6
1563	GAGAGGCCAUCAUC AAUUA	D-007304-01	ATP-binding cassette, sub-family B (MDR/TAP), member 6
1564	GCGCAUACUUUGUC ACUGA	D-007304-04	ATP-binding cassette, sub-family B (MDR/TAP), member 6
1565	CAGGAAACCUUCAU GCAAU	D-008331-02	abhydrolase domain containing 2
1566	GAGGAAGUUUCACG GCUAU	D-008331-05	abhydrolase domain containing 2

1567	CACCGGAAGUUCAU CACUA	D-008331-04	abhydrolase domain containing 2
1568	GAAACGAGAGAACG UCAUG	D-008331-03	abhydrolase domain containing 2
1569	UCCAGGAGAUUAU AAUCA	D-008620-03	1-acylglycerol-3-phosphate O-acyltransferase 3
1570	GCUCCAAGGUCCUC GCUAA	D-008620-01	1-acylglycerol-3-phosphate O-acyltransferase 3
1571	GGGAGCAGCUUCCU UUGGA	D-008620-02	1-acylglycerol-3-phosphate O-acyltransferase 3
1572	GCAGCUGUCUAUGA UGUAA	D-008620-04	1-acylglycerol-3-phosphate O-acyltransferase 3
1573	GCACUUAAGGACAG CCGAU	D-014729-04	AMME chromosomal region gene 1-like
1574	CCAUGGGAUUCGAA UUGAA	D-014729-03	AMME chromosomal region gene 1-like
1575	GGAAUACACGUUAA CCAGU	D-014729-02	AMME chromosomal region gene 1-like
1576	GGUCAAGAAGCCCA AAUUA	D-014729-01	AMME chromosomal region gene 1-like
1577	GAAAUGCGUGGCU UGUAC	D-014816-03	ankyrin repeat domain 20 family, member A1
1578	GAAAUACUCCAAAU CGGGA	D-014816-02	ankyrin repeat domain 20 family, member A1
1579	GAAAACAGGAGGAG UAGUA	D-014816-01	ankyrin repeat domain 20 family, member A1
1580	CAUGCUGCUGUAU ACUAU	D-014816-04	ankyrin repeat domain 20 family, member A1
1581	GGACAUCACCAGCC UGUAC	D-009847-03	adenomatosis polyposis coli 2
1582	UUAUGAAGCUGUCC UUUGA	D-009847-01	adenomatosis polyposis coli 2
1583	AGGAGAAGCUCUGG UACUA	D-009847-02	adenomatosis polyposis coli 2
1584	GCUCCGGGAUCACA ACUGU	D-009847-04	adenomatosis polyposis coli 2
1585	GUUACGAGCUGGAC UCAUU	D-018004-02	ATPase, Class V, type 10D
1586	GUGGUGGUCCUAC AAUUA	D-018004-03	ATPase, Class V, type 10D
1587	UCACAGAGCUGCCA AUUUA	D-018004-01	ATPase, Class V, type 10D
1588	GGUAUAAGCGCAGC AAAUU	D-018004-04	ATPase, Class V, type 10D
1589	GCAGCUAGCACAGG AUUAC	D-016789-04	chromosome 7 open reading frame 41
1590	GCAAGAAGACGCUC CACGA	D-016789-02	chromosome 7 open reading frame 41
1591	GAGCACGUGUGGAG UGAGA	D-016789-01	chromosome 7 open reading frame 41
1592	ACGAUGCGUUUGAA GAGUA	D-016789-03	chromosome 7 open reading frame 41
1593	UUACUAACCUGGAU AUACA	D-014865-02	chromosome 9 open reading frame 125
1594	GGGUUUAGCUGGCC UGUAA	D-014865-01	chromosome 9 open reading frame 125
1595	GCAGGACUAUGUCU AUUGC	D-014865-03	chromosome 9 open reading frame 125
1596	GAGCGUAGUGUGAG	D-014865-04	chromosome 9 open reading frame 125

	CCAUU		
1597	UGGCAUGAAUUGAG UAUUA	D-016035-01	cell adhesion molecule 2
1598	GGCAUAAAGGAACG UAUUU	D-016035-04	cell adhesion molecule 2
1599	GGAUUCUCAUCACC AGUUA	D-016035-03	cell adhesion molecule 2
1600	GAAAUACACUAUAC ACCAU	D-016035-02	cell adhesion molecule 2
1601	GAUAUUCACUACCA AAAGA	D-007838-02	chemokine (C-C motif) ligand 26
1602	GAAAGUCUGUACCC AUCCA	D-007838-03	chemokine (C-C motif) ligand 26
1603	GGAGUGACAUAUCC AAGAC	D-007838-04	chemokine (C-C motif) ligand 26
1604	GCUAUGAAUUCACC AGUAA	D-007838-01	chemokine (C-C motif) ligand 26
1605	CGCAAUAGAUGGAA ACCAA	D-016149-02	cell division cycle associated 3
1606	GCAAGACAGCCAC AGAAA	D-016149-01	cell division cycle associated 3
1607	UGACACUACGACAG GGUAA	D-016149-04	cell division cycle associated 3
1608	GGUAUUGCACGGAC ACCUA	D-016149-03	cell division cycle associated 3
1609	GGGAGCGCAUGUAU UCAUA	D-016940-01	chromosome X open reading frame 22
1610	UGACCGAGCUGCAA CUAUC	D-016940-03	chromosome X open reading frame 22
1611	GAUAUUGGACCUUC AUACA	D-016940-04	chromosome X open reading frame 22
1612	GCGAAUCGAUUGUU AACCA	D-016940-02	chromosome X open reading frame 22
1613	GGAAUUCCUCUAUG ACAAU	D-015786-03	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
1614	CGACGUGUAUGGUG UAUUC	D-015786-02	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
1615	GACCAUCAGUGCCU UUAUU	D-015786-01	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
1616	GACAGGCAACUAUG AACUA	D-015786-04	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
1617	CAAAGACGCCAACU UGUAC	D-003773-05	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
1618	UCAAGACGCCAAC UUGUA	D-003773-04	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
1619	GAUCAAGACGCCA ACUUG	D-003773-01	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
1620	GCAAUUACCAGUUU CAAUG	D-003773-02	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
1621	GAAAUUCCUAAGCA GGUUA	D-016505-02	family with sequence similarity 116, member A
1622	GUAAGAAGGUACG GAUUC	D-016505-03	family with sequence similarity 116, member A
1623	UGACAAAGAUUUAC CAGUU	D-016505-01	family with sequence similarity 116, member A
1624	GGCCACACAUUAUU CGAAU	D-016505-04	family with sequence similarity 116, member A
1625	UGGUGAACCUGCAG CCGGA	D-009139-03	forkhead box E3

1626	CUUCAUCACCGAAC GCUUU	D-009139-04	forkhead box E3
1627	CGUCGGGGCUGGAG CGCUA	D-009139-01	forkhead box E3
1628	CCGCGCAAGUGGCA GAACA	D-009139-02	forkhead box E3
1629	GGCCAUACCUCUUC UCCAA	D-009547-01	glycine C-acetyltransferase (2-amino-3- ketobutyrate coenzyme A ligase)
1630	UAACUUCUGUGCCA ACAAC	D-009547-04	glycine C-acetyltransferase (2-amino-3- ketobutyrate coenzyme A ligase)
1631	GCUGCUGGCUUCAC UAUCU	D-009547-03	glycine C-acetyltransferase (2-amino-3- ketobutyrate coenzyme A ligase)
1632	GAACCAUGCCUCCA UCAUC	D-009547-02	glycine C-acetyltransferase (2-amino-3- ketobutyrate coenzyme A ligase)
1633	CGAAGAAAGCCGUG ACUAA	D-013323-01	histone cluster 1, H2bk
1634	CCUCUAAGGCCAUG GGAAU	D-013323-02	histone cluster 1, H2bk
1635	UCGAAGAAAGCCGU GACUA	D-013323-04	histone cluster 1, H2bk
1636	UCGAACGCAUCGCG GGUGA	D-013323-03	histone cluster 1, H2bk
1637	GAACAGCGCUACCC CUUAA	D-012226-01	homeobox B13
1638	GAACCCACCAGGUC CCUUU	D-012226-03	homeobox B13
1639	CCACUGAGUUUGCC UUCUA	D-012226-02	homeobox B13
1640	GUAUGCGGCUAACA AGUUC	D-012226-04	homeobox B13
1641	ACCCAAGGAUCUUA UCUAU	D-021206-02	IQ motif containing B1
1642	CCAAAUAGGAUCUG CAGUC	D-021206-04	IQ motif containing B1
1643	GAGGCCAUGUUGAA CUUAU	D-021206-03	IQ motif containing B1
1644	GAGCAGAAUGUCCC UGUUA	D-021206-01	IQ motif containing B1
1645	GGAAGGCGGUCCUA GACAA	D-014252-01	potassium channel tetramerisation domain containing 14
1646	GGUACAAGGUAUUC UCCAA	D-014252-04	potassium channel tetramerisation domain containing 14
1647	GUUCAAGUCUGUUG UCAAG	D-014252-03	potassium channel tetramerisation domain containing 14
1648	GAAAUCAAGCCUUU GGUCA	D-014252-02	potassium channel tetramerisation domain containing 14
1649	CUACACAGCUUGUC UCGAU	D-022286-02	KIAA1024 protein
1650	GGAUACGAUUCAUU ACUAA	D-022286-01	KIAA1024 protein
1651	GCACCGUCAUCCUC GUUAU	D-022286-04	KIAA1024 protein
1652	GCGCCCAACUUACC UUGUG	D-022286-03	KIAA1024 protein
1653	UAAUAAAGAGCCCA UAGUG	D-030126-04	organic anion transporter LST-3b
1654	GGACUUACCUCUAU UCCCG	D-030126-03	organic anion transporter LST-3b
1655	GAAGGUAGCCCUAA	D-030126-01	organic anion transporter LST-3b

	UAUUU		
1656	GGGAAUGACUGGUC UAGUU	D-030126-02	organic anion transporter LST-3b
1657	ACAAGGAUCUGCCA UAAUA	D-019599-01	nuclear protein, ataxia-telangiectasia locus
1658	CCAAAUAAGUACCA GCAUA	D-019599-02	nuclear protein, ataxia-telangiectasia locus
1659	UGAAAUGGCUAUAG GGAUU	D-019599-03	nuclear protein, ataxia-telangiectasia locus
1660	GAGCGAAACUCUCG UCCUU	D-019599-04	nuclear protein, ataxia-telangiectasia locus
1661	UCAGUUGGCUGGUG AACAA	D-013814-02	pellino homolog 1 (Drosophila)
1662	AAAUAUCGGUGUGU GGAAA	D-013814-04	pellino homolog 1 (Drosophila)
1663	AAUCAUAUGUGAAC GGAAU	D-013814-03	pellino homolog 1 (Drosophila)
1664	UCAAGGACCUCUAG ACUAA	D-013814-01	pellino homolog 1 (Drosophila)
1665	CAGGAAGACUGGAA GAUAA	D-008684-02	phospholipase B1
1666	GAACUUCACAGACA ACAUU	D-008684-03	phospholipase B1
1667	GAUGAUAACUCAAC AGAAC	D-008684-04	phospholipase B1
1668	GCAAUGACCUCUGU GAUUU	D-008684-01	phospholipase B1
1669	GACAUGAAAUCCAA CAAUA	D-003601-03	v-raf-1 murine leukemia viral oncogene homolog 1
1670	CAAAGAACAUCAUC CAUAG	D-003601-04	v-raf-1 murine leukemia viral oncogene homolog 1
1671	GCAAAGAACAUCAU CCAUA	D-003601-02	v-raf-1 murine leukemia viral oncogene homolog 1
1672	GCACGGAGAUGUUG CAGUA	D-003601-01	v-raf-1 murine leukemia viral oncogene homolog 1
1673	GCAAAGCUGUAUUA UGAAG	D-012007-01	RANBP2-like and GRIP domain containing 5
1674	UUACAGGCGUUCAG UGGAA	D-012007-04	RANBP2-like and GRIP domain containing 5
1675	GUUCCAAGACCAAA GAUUA	D-012007-02	RANBP2-like and GRIP domain containing 5
1676	GAAGUCCUGCAAUU UAUAA	D-012007-03	RANBP2-like and GRIP domain containing 5
1677	GAAUUGUCCAGAAG ACUUG	D-014848-04	RPA interacting protein
1678	GGAAUGCUUUGCAG UCAGU	D-014848-03	RPA interacting protein
1679	GUACAAAUCUUCUG AGUUG	D-014848-01	RPA interacting protein
1680	CCACUACUCGUCC UGUAU	D-014848-02	RPA interacting protein
1681	GACCGGGUAUCUUC UAAUA	D-007332-01	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
1682	UACAUGAAGUGGAG AAGGA	D-007332-03	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
1683	GGACAUCGUUUUCU ACAUG	D-007332-04	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
1684	UGACUACGGUGAUG AGUAC	D-007332-02	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6

1685	GGACCGACUCUCC AAUUU	D-004778-10	SNF1-like kinase 2
1686	GAAGAUUGCGAGCA CCUUA	D-004778-03	SNF1-like kinase 2
1687	GGUAUGUCCUGGUG AAUUA	D-004778-05	SNF1-like kinase 2
1688	CAAGAGCUAUAACC ACUUU	D-004778-09	SNF1-like kinase 2
1689	CGACAAGAAACCAG GGGAA	D-020577-04	signal peptidase complex subunit 1 homolog (S. cerevisiae)
1690	GCCAGAAGCUAGCU GAACA	D-020577-03	signal peptidase complex subunit 1 homolog (S. cerevisiae)
1691	CGGGUGGACUGUCU AUAUA	D-020577-02	signal peptidase complex subunit 1 homolog (S. cerevisiae)
1692	GUGGUUACCUGUUC AAGAA	D-020577-01	signal peptidase complex subunit 1 homolog (S. cerevisiae)
1693	GAUGACAAAUACAC CUUGA	D-020897-04	signal peptidase complex subunit 2 homolog (S. cerevisiae)
1694	CAAAGUCCAUUGCU AAGUU	D-020897-01	signal peptidase complex subunit 2 homolog (S. cerevisiae)
1695	CAGCUGUCCUCCAG UCUUA	D-020897-03	signal peptidase complex subunit 2 homolog (S. cerevisiae)
1696	GAAUGGAUCCUGAU GAUUA	D-020897-02	signal peptidase complex subunit 2 homolog (S. cerevisiae)
1697	GAACCAAGUUGUCC UAUGG	D-010124-04	signal peptidase complex subunit 3 homolog (S. cerevisiae)
1698	GAUAUGGUCUCAAG GGAAA	D-010124-01	signal peptidase complex subunit 3 homolog (S. cerevisiae)
1699	ACACGUAUCUGUCC CAUUU	D-010124-03	signal peptidase complex subunit 3 homolog (S. cerevisiae)
1700	GAAGUGAUCUGGGA UUUAU	D-010124-02	signal peptidase complex subunit 3 homolog (S. cerevisiae)
1701	GAAGACGGGAUACU GCUCA	D-019727-04	sorcin
1702	CAAUGUGUCAUGAG UGUUU	D-019727-03	sorcin
1703	GAUAGAUGCUGAUG AAUUG	D-019727-01	sorcin
1704	ACAAUGGGAUUUAG GUUGA	D-019727-02	sorcin
1705	GGAAUGAAAGAUAU ACCUA	D-015368-05	serine/arginine repetitive matrix 2
1706	GAGCAAUUCUCAA CAUCA	D-015368-01	serine/arginine repetitive matrix 2
1707	AAAGAAUGUCCAC AAGUA	D-015368-03	serine/arginine repetitive matrix 2
1708	GACAGCAAUUCUCG ACUAU	D-015368-06	serine/arginine repetitive matrix 2
1709	CCACUUUGGUGUUU CAUAA	D-003544-03	signal transducer and activator of transcription 3 (acute-phase response factor)
1710	CCAACGACCGUCAG CAAUA	D-003544-01	signal transducer and activator of transcription 3 (acute-phase response factor)
1711	UCAGGUUGCUGGUC AAAUU	D-003544-04	signal transducer and activator of transcription 3 (acute-phase response factor)
1712	GGAGAAGCAUCGUG AGUGA	D-003544-02	signal transducer and activator of transcription 3 (acute-phase response factor)
1713	GCUUUCAGAUAGCC CAUAA	D-013166-02	stromal interaction molecule 2
1714	AGACACAGCUUCAG	D-013166-01	stromal interaction molecule 2

	AAUGU		
1715	CUUUAAGCCUCGAG AUAUA	D-013166-03	stromal interaction molecule 2
1716	AGAAGCAGUUGGUC UGUUC	D-013166-04	stromal interaction molecule 2
1717	GUACACGCAGCCAA UGAUA	D-013416-01	tubulin folding cofactor D
1718	CAAGCACGAAUGUC CAUAA	D-013416-02	tubulin folding cofactor D
1719	GGUGUUUGACCGAG ACAUA	D-013416-04	tubulin folding cofactor D
1720	GUCCAGAUCUUCAC AUGAG	D-013416-03	tubulin folding cofactor D
1721	UGGUAGAGACAAUG UAUUU	D-018130-04	transmembrane protein 135
1722	GCAAGUCCAUCCCU CAUAA	D-018130-01	transmembrane protein 135
1723	GGGCUGCUCACAAU UUAUA	D-018130-02	transmembrane protein 135
1724	GCGCUGGAUCAGAA ACUUA	D-018130-03	transmembrane protein 135
1725	GAAGUGGUAUCAUG AGAGA	D-015350-02	tetratricopeptide repeat domain 14
1726	GGAGAAGUGUUGAG CUAAA	D-015350-03	tetratricopeptide repeat domain 14
1727	GAGCAAAGAUACCG UUUAA	D-015350-01	tetratricopeptide repeat domain 14
1728	UAUUGAGCGUGGUG AUAUA	D-015350-04	tetratricopeptide repeat domain 14
1729	CAUGCUGGCGAGCG CGAUA	D-009707-04	ubiquitin-conjugating enzyme E2S
1730	AUAAGAAGCUGGCG GCCAA	D-009707-01	ubiquitin-conjugating enzyme E2S
1731	GCCAAGAAAAAGAC GGACA	D-009707-03	ubiquitin-conjugating enzyme E2S
1732	ACAAGGAGGUGACG ACACU	D-009707-02	ubiquitin-conjugating enzyme E2S
1733	CAACGUGAUCCGCU GGUUU	D-021403-04	zinc finger, DHHC-type containing 16
1734	GGAAGGCACUGGCU UACUC	D-021403-02	zinc finger, DHHC-type containing 16
1735	GAGAAAGGAUGACU CACAA	D-021403-01	zinc finger, DHHC-type containing 16
1736	GGAGAGACGUCGGC UACAG	D-021403-03	zinc finger, DHHC-type containing 16
1737	GAGCGAAGCUUUAG CCAAA	D-006970-02	zinc finger protein 337
1738	GGACGAGGCUUUAU CCAAA	D-006970-03	zinc finger protein 337
1739	GGACGAGGCUAUAC CAGUA	D-006970-04	zinc finger protein 337
1740	GGACGAAAGUUUAG CAAUA	D-006970-01	zinc finger protein 337
Part One Increased Infection			
1741	UCAAAGAGCUCGAG AGACA	D-009616-03	Rho guanine nucleotide exchange factor (GEF) 7
1742	GGAAGAAGAUGCUC AGAUU	D-009616-01	Rho guanine nucleotide exchange factor (GEF) 7

1743	GGAGGGCGAUGACA UUAAA	D-009616-04	Rho guanine nucleotide exchange factor (GEF) 7
1744	GAAGAGCCCUCCCA AAGGA	D-009616-02	Rho guanine nucleotide exchange factor (GEF) 7
1745	GAGCACGUGUCCUU ACCAU	D-014588-02	chromosome 16 open reading frame 59
1746	CCAAGACCAUGUCC UGUGG	D-014588-01	chromosome 16 open reading frame 59
1747	GACCAGUGAUUCCA CGGAU	D-014588-03	chromosome 16 open reading frame 59
1748	UGGACUGGAUGCAG GAGUA	D-014588-04	chromosome 16 open reading frame 59
1749	UGAAGGAGGUCGUA CAGAA	D-013104-01	coactosin-like 1 (Dictyostelium)
1750	GAGCGGAGUACCAG CACUU	D-013104-04	coactosin-like 1 (Dictyostelium)
1751	GCACAGAUGACGUC CGGUU	D-013104-02	coactosin-like 1 (Dictyostelium)
1752	AGCAAGAGGUCCAA GUUUG	D-013104-03	coactosin-like 1 (Dictyostelium)
1753	GAGCAACUGUGAUG AGGAA	D-015349-02	EMI domain containing 2
1754	GCGCCAACCUCGUA AGUUA	D-015349-01	EMI domain containing 2
1755	CGACCUGGAAUGAG GACUU	D-015349-04	EMI domain containing 2
1756	CAAAGACAAUGGAG ACUCA	D-015349-03	EMI domain containing 2
1757	ACAAAUACGUGGUG GUCUA	D-007944-04	interleukin 17 receptor B
1758	GAAGUGAGGUCAUC CUUGA	D-007944-01	interleukin 17 receptor B
1759	GAAAGGAUCAAGAA GACUU	D-007944-03	interleukin 17 receptor B
1760	GAACAUCACUGCUU GUAAG	D-007944-02	interleukin 17 receptor B
1761	GACGGCAACUGUUU CUAUC	D-021061-03	OTU domain, ubiquitin aldehyde binding 1
1762	CCGACUACCUUGUG GUCUA	D-021061-02	OTU domain, ubiquitin aldehyde binding 1
1763	GACGGACUGUCAAG GAGUU	D-021061-04	OTU domain, ubiquitin aldehyde binding 1
1764	GACAACAUCUAUCA ACAGA	D-021061-01	OTU domain, ubiquitin aldehyde binding 1
1765	CCAAUGAGGUCACA GAUCU	D-009448-03	protein tyrosine phosphatase, receptor type, H
1766	GAACCCGGGUGUUU GUAUG	D-009448-04	protein tyrosine phosphatase, receptor type, H
1767	GGAAUGACGUAGCC AGUUC	D-009448-02	protein tyrosine phosphatase, receptor type, H
1768	GAAUGAAGGUCGUG UCUCA	D-009448-01	protein tyrosine phosphatase, receptor type, H
1769	GAACAUCAUCCAGG UGUAU	D-004050-06	testis-specific serine kinase 3
1770	GAAGGGACCUACUC AAAAG	D-004050-07	testis-specific serine kinase 3
1771	CAAAGAAAAGUGGC AAUUA	D-004050-08	testis-specific serine kinase 3
1772	GCAUGGGUGUGGUC	D-004050-05	testis-specific serine kinase 3

	CUGUA		
1773	GAUCAAAGCUUACC GAGAU	D-012359-01	U11/U12 snRNP 35K
1774	GGGUGUGGCCCGAC AAUGA	D-012359-04	U11/U12 snRNP 35K
1775	GGAGGACAAAUUA AGGAA	D-012359-03	U11/U12 snRNP 35K
1776	GGGACUUGGUCACA GGUUU	D-012359-02	U11/U12 snRNP 35K
1777	GGGCUUAUAUCCUG UUCUA	D-023019-01	ubiquitin specific peptidase 43
1778	GUGAAAGGCAGAAG CAUUA	D-023019-02	ubiquitin specific peptidase 43
1779	GAAGAGGACCUGAA UACCA	D-023019-03	ubiquitin specific peptidase 43
1780	GUGCUAAUCCUCUU CUGUA	D-023019-04	ubiquitin specific peptidase 43
Part Two , Increased Infection			
1781	GGAGUGAUCUGGCC GUUCC	D-021769-07	ATPase, Class VI, type 11A
1782	GCUGUUCUACGUUG UCUUU	D-021769-05	ATPase, Class VI, type 11A
1783	GAGGAUGUACUACG UGUUC	D-021769-06	ATPase, Class VI, type 11A
1784	GCAGUCCAUCCCA AGUCA	D-021769-08	ATPase, Class VI, type 11A
1785	GCACAUUGCUCUGG ACAUU	D-006126-03	calcium channel, voltage-dependent, L type, alpha 1F subunit
1786	GGAAACAUAUGAU UGUCA	D-006126-04	calcium channel, voltage-dependent, L type, alpha 1F subunit
1787	GAUCAUAAAUCUCU UUGUG	D-006126-02	calcium channel, voltage-dependent, L type, alpha 1F subunit
1788	GAGGACAGCUCCCG CAUUU	D-006126-01	calcium channel, voltage-dependent, L type, alpha 1F subunit
1789	UGGAGGCCCUUCAG UAUGA	D-007867-04	colony stimulating factor 3 receptor (granulocyte)
1790	CAACCACACUCAGG CCUUU	D-007867-03	colony stimulating factor 3 receptor (granulocyte)
1791	GAUCCAAGGUUAUG UGGUU	D-007867-01	colony stimulating factor 3 receptor (granulocyte)
1792	CAUCGUGACUCCCU UGUAC	D-007867-02	colony stimulating factor 3 receptor (granulocyte)
1793	ACACCUGGGUCAAG UACAA	D-018916-04	gastrokine 2
1794	CAGUGACAAUUGAU AAUGA	D-018916-03	gastrokine 2
1795	UGAACAAUCUCCAA UGGUA	D-018916-01	gastrokine 2
1796	UCAAGACGUGGAU UGGUU	D-018916-02	gastrokine 2
1797	GUCGGGAGCUUCGA UCAAA	D-011692-04	heterogeneous nuclear ribonucleoprotein K
1798	GAUCUUGGUGGACC UAUUA	D-011692-02	heterogeneous nuclear ribonucleoprotein K
1799	GGUCAGCGGAUUAA ACAAA	D-011692-03	heterogeneous nuclear ribonucleoprotein K
1800	GAGCGCAUAUUGAG UAUCA	D-011692-01	heterogeneous nuclear ribonucleoprotein K

1801	GGAGAAUCCUAAGG AGAGU	D-006625-04	insulin-like growth factor binding protein 6
1802	GCGCGGAAGCUGAG GGCUG	D-006625-02	insulin-like growth factor binding protein 6
1803	GCAGAGACCAACAG AGGAA	D-006625-01	insulin-like growth factor binding protein 6
1804	UUGCAGAGGAGAAU CCUAA	D-006625-03	insulin-like growth factor binding protein 6
1805	GCGAGUACUUCUUC UCAGA	D-009687-02	IMP (inosine monophosphate) dehydrogenase 1
1806	CAACACGGCUGCCA GGAUA	D-009687-01	IMP (inosine monophosphate) dehydrogenase 1
1807	GUGAUGACGCCAAG GAUUG	D-009687-04	IMP (inosine monophosphate) dehydrogenase 1
1808	GGGCUAGCAUGGCG GACUA	D-009687-03	IMP (inosine monophosphate) dehydrogenase 1
1809	UGCCAUCGCUGGUG UGCUA	D-006210-04	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
1810	GCUACUGACCGAUG UUUAA	D-006210-05	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
1811	UAGCAUAGCCCAUU AUAGA	D-006210-01	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
1812	CCGAGGAGAUCAAG UUUUA	D-006210-03	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
1813	ACGCGGAGGUGGUG GAUGA	D-006274-03	potassium voltage-gated channel, KQT-like subfamily, member 4
1814	AGGAAGUAGCAGAG GAGAA	D-006274-01	potassium voltage-gated channel, KQT-like subfamily, member 4
1815	UAGCAGAGGAGAA AGCUA	D-006274-02	potassium voltage-gated channel, KQT-like subfamily, member 4
1816	CAAAAGAGCUGGAG CUUCA	D-006274-04	potassium voltage-gated channel, KQT-like subfamily, member 4
1817	GGAUUAUCAGUUUCU AGACA	D-020758-03	myotubularin related protein 10
1818	GACUUGAGCUGUUG UGUAG	D-020758-02	myotubularin related protein 10
1819	GAACACGAUGUCCC UUUAA	D-020758-04	myotubularin related protein 10
1820	GCAGUGCUCUUGUG CGAAU	D-020758-01	myotubularin related protein 10
1821	GAAGCAGAGCGUCG UAUUAU	D-020525-03	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
1822	GGAAGCAGGCCAAC CGUAU	D-020525-02	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
1823	GCUCUUAGCUGAUC UCGAA	D-020525-01	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
1824	CGGGAUAAGUACUC AAAGA	D-020525-04	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
1825	GGUAAAUCCACCUU AAUCA	D-006373-06	septin 9
1826	GGAGAUCACCAUCG UCAAA	D-006373-03	septin 9
1827	GAGAAAGGCGUCCG GAUGA	D-006373-02	septin 9
1828	CCAACGGCAUCGAC	D-006373-05	septin 9

	GUGUA		
1829	GAACAGCACCGCUU AAGGA	D-005948-04	transmembrane protease, serine 12
1830	GGACAUGGCUGUGG UCGAA	D-005948-03	transmembrane protease, serine 12
1831	GCAAGGGUCUCGGA UUAUA	D-005948-02	transmembrane protease, serine 12
1832	GAAGGUAACGCUAC AAUA	D-005948-01	transmembrane protease, serine 12
1833	AGCGAUCGGCAGAG GAGAA	D-006449-07	tumor necrosis factor receptor superfamily, member 18
1834	GGGUACAGUCCCAG GGGAA	D-006449-06	tumor necrosis factor receptor superfamily, member 18
1835	CCACGAAGGCCACU GCAAA	D-006449-05	tumor necrosis factor receptor superfamily, member 18
1836	CUGAGGAGUCAGUG CAUGU	D-006449-08	tumor necrosis factor receptor superfamily, member 18
1837	GGACUACCUUCGCA UUAAG	D-008614-03	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
1838	GCACAAGACGAACU CAGUA	D-008614-02	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
1839	GAAGGUGGCUAUUA UCAUG	D-008614-01	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
1840	GUAUAGAGACGUCG GACUU	D-008614-04	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)

In certain embodiments, an inhibitory compound can be colchicine, cytochalasin, EIPA, rottlerin, UO126, wortmannin or a mixture of two or more of such compounds. In certain embodiments, an inhibitory compound can be brefeldin A, golgicide A or a mixture thereof. In certain embodiments, an inhibitory compound can be colchicine. In certain embodiments, an inhibitory compound can be, cytochalasin. In certain embodiments, an inhibitory compound can be EIPA. In certain embodiments, an inhibitory compound can be rottlerin. In certain embodiments, an inhibitory compound can be UO126. In certain embodiments, an inhibitory compound can be wortmannin. In certain embodiments, an inhibitory compound can be brefeldin A. In certain embodiments, an inhibitory compound can be golgicide A.

Another embodiment of the present invention is a pharmaceutical composition. As used herein, a pharmaceutical composition comprises an inhibitory compound that interacts with a host factor of the present invention and a pharmaceutically acceptable vehicle, such as a diluent, carrier, excipient, adjuvant or a combination thereof. Selection of such a vehicle is known to those skilled in the art.

As used herein the term "patient" refers to an animal infected with a virus of the present invention. The animal can be a human or a non-human animal. A preferred animal to treat is a mammal.

A compound of the present invention, or a pharmaceutical composition thereof can be administered to a patient by a variety of routes, including, but limited to, by injection (e.g., intravenous, intramuscular, subcutaneous, intrathecal, intraperitoneal), by inhalation, by oral (e.g., in a pill, tablet, capsule, powder, syrup, solution, suspension, thin film, dispersion or emulsion.), transdermal, transmucosal, pulmonary, buccal, intranasal, sublingual, intracerebral, intravaginal rectal or topical administration or by any other convenient method known to those of skill in the art.

The amount of a compound of the present invention and/or a pharmaceutical composition thereof that will be effective can be determined by standard clinical techniques known in the art. Such an amount is dependent on, among other factors, the patient being treated, including, but not limited to the weight, age, and condition of the patient, the intended effect of the compound, the manner of administration and the judgment of the prescribing physician.

A compound of the present invention, or a pharmaceutical composition thereof, can be administered alone or in combination with one or more other pharmaceutical agents, including other compounds of the present invention. A compound can be administered or applied *per se* or as pharmaceutical compositions. The specific pharmaceutical composition depends on the desired mode of administration, as is well known to the skilled artisan.

In a preferred embodiment, a patient is protected using a composition comprising an inhibitory compound that inhibits viral infection by at least 5%, 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% or at least 95%. In another embodiment, the amount of virus is reduced by a factor of at least 10, 100, 1000, or 10,000. In one embodiment the viral infection is completely inhibited.

The present invention also includes kits to identify a compound that modulates viral infection. One embodiment is a kit to identify an inhibitory compound, the kit comprising a means for determining if a candidate compound is capable of inhibiting viral infection by interacting with a host factor of the present invention. Another embodiment is a kit to identify an enhancing compound, the kit comprising a means for determining if a candidate

compound is capable of enhancing viral infection by interacting with a host factor of the present invention. Kits can also comprise means for identifying both inhibitory compounds and enhancing compounds. Suitable and preferred means are disclosed herein. As such, a kit can also comprise host factors of the present invention. The kit can also contain
5 associated reagents and components, such as, but not limited to, buffers, labels, containers, inserts, tubings, vials, syringes and the like.

The following Examples are provided for the purpose of illustration and are not intended to limit the scope of the invention.

Examples

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the embodiments, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Standard abbreviations may be used. For example, amino acids can be denoted by either the standard 3-letter or 1-letter code.

Example 1.

This Example illustrates the identification of host factors required for completion of the HCV life-cycle.

siRNA screen: To identify host factors required for HCV infection, a high-throughput RNAi-based screen was undertaken on an arrayed library targeting 19,470 genes (Dharmacon siARRAY siRNA Library (Human Genome, G-005000-05, Thermo Fisher Scientific, Lafayette, CO, the remaining 1,651 pools of the original 21,121 gene library were not screened because the vast majority have been retired due to revised refseq annotation). Part one of the screen: siRNAs were transiently transfected into the Huh 7.5.1 cells at a 50 nM final concentration, using a reverse transfection protocol employing 0.44% Oligofectamine (Invitrogen, Carlsbad, CA) in a 384-well format (384 well, black plastic, clear bottomed assay plate, Corning 3712). The Oligofectamine was diluted in Opti-MEM (Invitrogen) and allowed to incubate ten minutes. The lipid solution was then aliquoted into the wells (9 ul/well) using a Wellmate liquid handling robot (Thermo Fisher Matrix). The plates were spun down at 1,000 RPM and the arrayed siRNAs were added robotically, 1.5 µL of a 1 µM stock solution per well. After a twenty minute incubation, 800 Huh 7.5.1 cells were added per well, in 20 µL of Dulbecco's modified minimal essential media (DMEM, Invitrogen), supplemented with 15% fetal bovine serum (FBS, Invitrogen). The plates were next spun at 1000 RPM and then placed in a tissue culture incubator at 37°C and 5% CO₂. The subsequent day, 5 µL of fresh complete media (10% FBS) was added to the outer two wells at the plate

margins to decrease edge effects. After 72 h of siRNA-mediated gene knockdown the medium was removed and the cells were infected with the JFH-1 genotype 2a virus, at an MOI of approximately 0.2-0.4 in 40 μ L DMEM with 10% FBS (which translated to 12-20% infected cells at 48 h post infection as determined by HCV core staining and Hoechst 33342 DNA staining of nuclei). After an additional 48 h incubation (when silencing is still operative), 30 μ L of media was removed and replica plated onto a new 384 well plate, which had received 2500 Huh 7.5.1 cells per well 24 h prior to viral supernatant addition (beginning of part two of screen). The "part one" cells were then fixed with 4% Formalin, permeabilized with 0.3% Triton-X100 (Sigma) in Dulbecco's Phosphate Buffered Saline (D-PBS, Invitrogen) containing 3% FBS and 3% bovine serum albumin Fraction V (BSA, Sigma Aldrich), then stained for HCV core, using purified anti-HCV core monoclonal antibody (produced from the anti-HCV core 6G7 hybridoma cells generously provided by Drs. Harry Greenberg and Xiaosong He, Stanford University) diluted in D-PBS with 1% BSA. The cells were then incubated with an Alexa 488 goat anti-mouse secondary at 1:1,000 in D-PBS with 1% BSA (A11001, Invitrogen), and stained for DNA with Hoechst 33342 at 1:5,000-10,000 (Invitrogen). Each step was followed by two washes with 30 μ L D-PBS. The cells were then imaged on an automated Image Express Micro (IXM) microscope (Molecular Devices) at 4X magnification, using two wavelengths, 488 nm to detect HCV infected cells expressing core, and 350 nm for nuclear DNA bound by Hoechst 33342. Images were then analyzed using the Metamorph Cell Scoring software program (Molecular Devices Inc.) to determine the total cells per well, and the percentage of core positive cells in each well (percent infected). A negative control (NT, siCONTROL Non-Targeting siRNA #2, Dharmacon D-001210-02), and positive control siRNA SMARTpools against CD81 (Dharmacon SMARTpool M-017257-02) and ApoE (Dharmacon SMARTpool M-006470-00) were present on each plate. In addition wells containing either buffer alone, or an siRNA pool directed against Polo like kinase one (PLK1, Dharmacon) were present on all plates transfected. The screen was performed in triplicate.

TaqMan Real-Time PCR Analysis: To determine the amount of HCV RNA, total RNA was extracted with QIAamp Viral RNA Mini Kit (Qiagen, Valencia, CA) from 140 μ L of culture medium, or with RNeasy Mini Kit (Qiagen) from whole cell lysate. Copy numbers of HCV RNA were determined by quantitative PCR with the probe and primers listed below, using the TaqMan EZ RT-PCR CORE REAGENTS (Applied Biosystems) on an ABI 7500 Real

Time PCR System (Applied Biosystem). PCR parameters consisted of 1 cycle of 50°C X 2 min, then 60 °C X 30 min, and 95°C X 3:30 min, followed by 50 cycles of PCR at 95 °C X 20 s, and 62 °C X 1 min. The relative amount of HCV RNA was normalized to the internal control Human 18S rRNA (Applied Biosystems). HCV TaqMan probe used was 6-FAM
5 CTGCGGAACCGGTGAGTACACTAMRA (IDT, Coralville, IA). HCV primer sequences were 5' CGGGAGAGCCATAGTGG, and 3' AGTACCACAAGGCCTTTCG. To quantify the expression levels of CD81 and ApoE, total RNA was prepared from whole cell lysate with RNeasy Mini Kit according to manufacturer's instructions. Complementary DNA (cDNA) was synthesized from total RNA with First Strand cDNA Synthesis Kit (Roche,
10 Indianapolis, IN). The mRNA expression levels of CD81 and ApoE were quantified by quantitative PCR using a TaqMan Gene Express Master Mix (Applied Biosystems) on an ABI 7500 Real Time PCR System. PCR parameters were 1 cycle of 50°C X 2 min, then 95°C X 10 min, followed by 50 cycles of PCR at 95 °C X 15 s, and 60 °C X 1 min. Each reaction was performed in duplicate, and the relative amount of target gene mRNA was normalized to
15 the internal control Human 18S rRNA. The primers and probes used were TaqMan Gene Expression Assays (Applied Biosystems, Foster City, CA). Accession Numbers: CD81 Hs00174717-m1, and ApoE Hs00171168-m1.

siRNA screen: Part one: siRNAs were transiently transfected into the Huh 7.5.1 cells at a 50
20 nM final concentration, using 0.44% Oligofectamine (Invitrogen, Carlsbad, CA) in a 384-well format (384 well, black plastic, clear bottomed assay plate, Corning 3712). The next day, 5 µL of fresh complete media (10% FBS) was added to the outer two wells at the plate margins to decrease edge effects. After 72 h of siRNA-mediated gene knockdown, the medium was removed and the cells were infected with the JFH-1 genotype 2a virus, at an
25 MOI of approximately 0.2-0.4 in 40 µL DMEM with 10% FBS. After 48h, 30 µl of media was removed and replica plated onto a new 384-well plate with 2500 Huh 7.5.1 cells per well plated 24 h earlier for part 2. The "part one" cells were then fixed with 4% Formalin and stained with anti-HCV core 6G7 monoclonal antibody provided by Drs. Harry Greenberg and Xiaosong He, (Stanford University) using an Alexa 488 goat anti-mouse secondary antibody
30 at 1:1,000 (A11001, Invitrogen) and cells were imaged on an automated Image Express Micro (IXM) microscope (Molecular Devices) Images were then analyzed using the Metamorph Cell Scoring software program (Molecular Devices Inc.) Part two: As noted, to search for host factors whose depletion leads to defects in producing HCV infectious

particles, 30 μ L of conditioned media containing JFH-1 HCV virus from each well in the first round screen was removed prior to fixation and transferred to a new well containing uninfected Huh 7.5.1 cells. 48 h later these cells were stained for HCV core expression and imaged identically to samples in part one described above.

- 5 siRNA pools were classified as hits (decreased infection) if the average of the triplicate plates showed that the percentage of core positive cells was less than 50% of the plate mean, and cell number was not less than 50% of the mean of the plate. Pools which increased infection by greater than 150% of the plate mean were also selected as hits (increased infection).

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Table 1. Host Factors Identified by siRNA Screening

SEQ NO	Entrez Gene Symbol	Genbank Acc. No.	Gene Name
1	ADAMTS4	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4
2			<i>Translation</i>
3			Complement
4	ALAD	NM_000031	aminolevulinate, delta-, dehydratase
5			<i>Translation</i>
6			Complement
7	AP1GBP1	NM_007247	AP1 gamma subunit binding protein 1
8			<i>Translation</i>
9			Complement
10	AP3B1	NM_003664	adaptor-related protein complex 3, beta 1 subunit
11			<i>Translation</i>
12			Complement
13	APLP2	NM_001642	amyloid beta (A4) precursor-like protein 2
14			<i>Translation</i>
15			Complement
16	ARHGAP22	NM_021226	Rho GTPase activating protein 22
17			<i>Translation</i>
18			Complement
19	ARHGEF10L	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like
20			<i>Translation</i>
21			Complement
22	ARRDC2	NM_015683	arrestin domain containing 2
23			<i>Translation</i>
24			Complement
25	BAGE2	NM_182482	B melanoma antigen family, member 2
26			<i>Translation</i>
27			Complement
28	BCKDHA	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide

29			<i>Translation</i>
30			Complement
31	BRF1	NM_001519	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
32			<i>Translation</i>
33			Complement
34	BRUNOL6	NM_052840	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
35			<i>Translation</i>
36			Complement
37	C10orf112	XM_295865	chromosome 10 open reading frame 112
38			<i>Translation</i>
39			Complement
40	C14orf73	XM_040910	chromosome 14 open reading frame 73
41			<i>Translation</i>
42			Complement
43	C19orf44	NM_032207	chromosome 19 open reading frame 44
44			<i>Translation</i>
45			Complement
46	C20orf20	NM_018270	chromosome 20 open reading frame 20
47			<i>Translation</i>
48			Complement
49	C21orf56	NM_032261	chromosome 21 open reading frame 56
50			<i>Translation</i>
51			Complement
52	CAMTA2	NM_015099	calmodulin binding transcription activator 2
53			<i>Translation</i>
54			Complement
55	CASP4	NM_001225	caspase 4, apoptosis-related cysteine peptidase
56			<i>Translation</i>
57			Complement
58	CCDC8	NM_032040	coiled-coil domain containing 8
59			<i>Translation</i>
60			Complement
61	CCNB2	NM_004701	cyclin B2
62			<i>Translation</i>
63			Complement
64	CCPG1	NM_004748	cell cycle progression 1
65			<i>Translation</i>
66			Complement
67	CDC6	NM_001254	cell division cycle 6 homolog (<i>S. cerevisiae</i>)
68			<i>Translation</i>
69			Complement
70	CDH1	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)
71			<i>Translation</i>
72			Complement
73	CDKL5	NM_003159	cyclin-dependent kinase-like 5
74			<i>Translation</i>
75			Complement
76	CHKA	NM_001277	choline kinase alpha
77			<i>Translation</i>
78			Complement
79	CHUK	NM_001278	conserved helix-loop-helix ubiquitous kinase

80			<i>Translation</i>
81			Complement
82	CISH	NM_013324	cytokine inducible SH2-containing protein
83			<i>Translation</i>
84			Complement
85	CLDN1	NM_021101	claudin 1
86			<i>Translation</i>
87			Complement
88	CLSTN1	NM_014944	calsyntenin 1
89			<i>Translation</i>
90			Complement
91	CNOT1	NM_016284	CCR4-NOT transcription complex, subunit 1
92			<i>Translation</i>
93			Complement
94	CNOT2	NM_014515	CCR4-NOT transcription complex, subunit 2
95			<i>Translation</i>
96			Complement
97	CNOT3	NM_014516	CCR4-NOT transcription complex, subunit 3
98			<i>Translation</i>
99			Complement
100	CNOT6L	NM_144571	CCR4-NOT transcription complex, subunit 6-like
101			<i>Translation</i>
102			Complement
103	CSNK1A1L	NM_145203	casein kinase 1, alpha 1-like
104			<i>Translation</i>
105			Complement
106	CTAGE6	NM_178561	CTAGE family, member 6
107			<i>Translation</i>
108			Complement
109	CTGF	NM_001901	connective tissue growth factor
110			<i>Translation</i>
111			Complement
112	CTSF	NM_003793	cathepsin F
113			<i>Translation</i>
114			Complement
115	CX3CL1	NM_002996	chemokine (C-X3-C motif) ligand 1
116			<i>Translation</i>
117			Complement
118	CYBA	NM_000101	cytochrome b-245, alpha polypeptide
119			<i>Translation</i>
120			Complement
121	CYP4A22	NM_001010969	cytochrome P450, family 4, subfamily A, polypeptide 22
122			<i>Translation</i>
123			Complement
124	DACT3	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)
125			<i>Translation</i>
126			Complement
127	DBNDD1	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1
128			<i>Translation</i>

129			Complement
130	DDX3X	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
131			<i>Translation</i>
132			Complement
133	DEFA5	NM_021010	defensin, alpha 5, Paneth cell-specific
134			<i>Translation</i>
135			Complement
136	DEFB126	NM_030931	defensin, beta 126
137			<i>Translation</i>
138			Complement
139	DGAT1	NM_012079	diacylglycerol O-acyltransferase homolog 1 (mouse)
140			<i>Translation</i>
141			Complement
142	DHRS12	NM_024705	dehydrogenase/reductase (SDR family) member 12
143			<i>Translation</i>
144			Complement
145	DIO3	NM_001362	deiodinase, iodothyronine, type III
146			<i>Translation</i>
147			Complement
148	DLGAP4	NM_014902	discs, large (Drosophila) homolog-associated protein 4
149			<i>Translation</i>
150			Complement
151	DNAJB1	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1
152			<i>Translation</i>
153			Complement
154	DOCK3	NM_004947	dedicator of cytokinesis 3
155			<i>Translation</i>
156			Complement
157	E2F2	NM_004091	E2F transcription factor 2
158			<i>Translation</i>
159			Complement
160	ERC2	NM_015576	ELKS/RAB6-interacting/CAST family member 2
161			<i>Translation</i>
162			Complement
163	ERCC5	NM_000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
164			<i>Translation</i>
165			Complement
166	ETF1	NM_004730	<i>eukaryotic Translation termination factor 1</i>
167			<i>Translation</i>
168			Complement
169	EWSR1	NM_005243	Ewing sarcoma breakpoint region 1
170			<i>Translation</i>
171			Complement
172	FAU	NM_001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30

173			<i>Translation</i>
174			Complement
175	FBLN5	NM_006329	fibulin 5
176			<i>Translation</i>
177			Complement
178	FBXO38	NM_030793	F-box protein 38
179			<i>Translation</i>
180			Complement
181	FCGRT	NM_004107	Fc fragment of IgG, receptor, transporter, alpha
182			<i>Translation</i>
183			Complement
184	FER1L3	NM_013451	fer-1-like 3, myoferlin (C. elegans)
185			<i>Translation</i>
186			Complement
187	FLJ22659	XM_378723	hypothetical protein FLJ22659
188			<i>Translation</i>
189			Complement
190	FLT4	NM_002020	fms-related tyrosine kinase 4
191			<i>Translation</i>
192			Complement
193	FOXA2	NM_021784	forkhead box A2
194			<i>Translation</i>
195			Complement
196	FRMPD3	XM_042978	FERM and PDZ domain containing 3
197			<i>Translation</i>
198			Complement
199	GNB2L1	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
200			<i>Translation</i>
201			Complement
202	GNG8	NM_033258	guanine nucleotide binding protein (G protein), gamma 8
203			<i>Translation</i>
204			Complement
205	GPSN2	NM_004868	glycoprotein, synaptic 2
206			<i>Translation</i>
207			Complement
208	GTF3A	NM_002097	general transcription factor IIIA
209			<i>Translation</i>
210			Complement
211	GUCY1A2	NM_000855	guanylate cyclase 1, soluble, alpha 2
212			<i>Translation</i>
213			Complement
214	HCCS	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)
215			<i>Translation</i>
216			Complement
217	HEATR1	XM_375853	HEAT repeat containing 1
218			<i>Translation</i>
219			Complement
220	HIPK3	NM_005734	homeodomain interacting protein kinase 3
221			<i>Translation</i>
222			Complement

223	HRC	NM_002152	histidine rich calcium binding protein
224			<i>Translation</i>
225			Complement
226	HSD17B13	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13
227			<i>Translation</i>
228			Complement
229	HSPA1A	NM_005345	heat shock 70kDa protein 1A
230			<i>Translation</i>
231			Complement
232	IFITM3	NM_021034	interferon induced transmembrane protein 3 (1-8U)
233			<i>Translation</i>
234			Complement
235	IGSF11	NM_152538	immunoglobulin superfamily, member 11
236			<i>Translation</i>
237			Complement
238	ILVBL	NM_006844	ilvB (bacterial acetolactate synthase)-like
239			<i>Translation</i>
240			Complement
241	IMP4	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
242			<i>Translation</i>
243			Complement
244	IRF3	NM_001571	interferon regulatory factor 3
245			<i>Translation</i>
246			Complement
247	ITGA7	NM_002206	integrin, alpha 7
248			<i>Translation</i>
249			Complement
250	KCNJ3	NM_002239	potassium inwardly-rectifying channel, subfamily J, member 3
251			<i>Translation</i>
252			Complement
253	KCNK3	NM_002246	potassium channel, subfamily K, member 3
254			<i>Translation</i>
255			Complement
256	KIAA1166	NM_018684	KIAA1166
257			<i>Translation</i>
258			Complement
259	KRT4	NM_002272	keratin 4
260			<i>Translation</i>
261			Complement
262	L1TD1	NM_019079	LINE-1 type transposase domain containing 1
263			<i>Translation</i>
264			Complement
265	LOC285556	XM_373030	hypothetical protein LOC285556
266			<i>Translation</i>
267			Complement
268	LOC285643	XM_209695	KIF4B
269			<i>Translation</i>
270			Complement
271	LOC400451	NM_207446	hypothetical gene supported by AK075564; BC060873

272			<i>Translation</i>
273			Complement
274	LTC4S	NM_000897	leukotriene C4 synthase
275			<i>Translation</i>
276			Complement
277	MAP4	NM_002375	microtubule-associated protein 4
278			<i>Translation</i>
279			Complement
280	MAPK1	NM_138957	mitogen-activated protein kinase 1
281			<i>Translation</i>
282			Complement
283	MARK3	NM_002376	MAP/microtubule affinity-regulating kinase 3
284			<i>Translation</i>
285			Complement
286	MCHR2	NM_032503	melanin-concentrating hormone receptor 2
287			<i>Translation</i>
288			Complement
289	MCM2	NM_004526	minichromosome maintenance complex component 2
290			<i>Translation</i>
291			Complement
292	MED12	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
293			<i>Translation</i>
294			Complement
295	MGC13057	NM_032321	hypothetical protein MGC13057
296			<i>Translation</i>
297			Complement
298	MLLT1	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
299			<i>Translation</i>
300			Complement
301	MLXIPL	NM_032951	MLX interacting protein-like
302			<i>Translation</i>
303			Complement
304	MRPL15	NM_014175	mitochondrial ribosomal protein L15
305			<i>Translation</i>
306			Complement
307	MRPL38	NM_032478	mitochondrial ribosomal protein L38
308			<i>Translation</i>
309			Complement
310	MRPL48	NM_016055	mitochondrial ribosomal protein L48
311			<i>Translation</i>
312			Complement
313	MTHFSD	NM_022764	methenyltetrahydrofolate synthetase domain containing
314			<i>Translation</i>
315			Complement
316	MYCL2	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
317			<i>Translation</i>
318			Complement

319	MYO3A	NM_017433	myosin IIIA
320			<i>Translation</i>
321			Complement
322	MYO7B	XM_291001	myosin VIIB
323			<i>Translation</i>
324			Complement
325	NAALADL1	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1
326			<i>Translation</i>
327			Complement
328	NMT1	NM_021079	N-myristoyltransferase 1
329			<i>Translation</i>
330			Complement
331	NOC4L	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)
332			<i>Translation</i>
333			Complement
334	NOL1	NM_006170	nucleolar protein 1, 120kDa
335			<i>Translation</i>
336			Complement
337	NOL5A	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)
338			<i>Translation</i>
339			Complement
340	NOL6	NM_022917	nucleolar protein family 6 (RNA-associated)
341			<i>Translation</i>
342			Complement
343	NOP5/NOP58	NM_015934	nucleolar protein NOP5/NOP58
344			<i>Translation</i>
345			Complement
346	NOS1AP	NM_014697	nitric oxide synthase 1 (neuronal) adaptor protein
347			<i>Translation</i>
348			Complement
349	NUAK2	NM_030952	NUAK family, SNF1-like kinase, 2
350			<i>Translation</i>
351			Complement
352	ORAOV1	NM_153451	oral cancer overexpressed 1
353			<i>Translation</i>
354			Complement
355	OSBP	NM_002556	oxysterol binding protein
356			<i>Translation</i>
357			Complement
358	PARP11	NM_020367	poly (ADP-ribose) polymerase family, member 11
359			<i>Translation</i>
360			Complement
361	PECR	NM_018441	peroxisomal trans-2-enoyl-CoA reductase
362			<i>Translation</i>
363			Complement
364	PEMT	NM_007169	phosphatidylethanolamine N-methyltransferase
365			<i>Translation</i>
366			Complement
367	PGLYRP4	NM_020393	peptidoglycan recognition protein 4

368			<i>Translation</i>
369			Complement
370	PI4KA	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha
371			<i>Translation</i>
372			Complement
373	PNO1	NM_020143	partner of NOB1 homolog (S. cerevisiae)
374			<i>Translation</i>
375			Complement
376	POLR2J2	NM_032958	DNA directed RNA polymerase II polypeptide J-related
377			<i>Translation</i>
378			Complement
379	PPIA	NM_021130	peptidylprolyl isomerase A (cyclophilin A)
380			<i>Translation</i>
381			Complement
382	PPP2R1A	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform
383			<i>Translation</i>
384			Complement
385	PPTC7	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)
386			<i>Translation</i>
387			Complement
388	PRKRIP1	NM_024653	PRKR interacting protein 1 (IL11 inducible)
389			<i>Translation</i>
390			Complement
391	PROX1	NM_002763	prospero-related homeobox 1
392			<i>Translation</i>
393			Complement
394	PRPF40A	XM_371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
395			<i>Translation</i>
396			Complement
397	PRPSAP2	NM_002767	phosphoribosyl pyrophosphate synthetase-associated protein 2
398			<i>Translation</i>
399			Complement
400	PSME1	NM_176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
401			<i>Translation</i>
402			Complement
403	PTCD1	NM_015545	pentatricopeptide repeat domain 1
404			<i>Translation</i>
405			Complement
406	PTHR1	NM_000316	parathyroid hormone receptor 1
407			<i>Translation</i>
408			Complement
409	RAB10	NM_016131	RAB10, member RAS oncogene family
410			<i>Translation</i>
411			Complement
412	RAB11A	NM_004663	RAB11A, member RAS oncogene family
413			<i>Translation</i>
414			Complement

415	RABEPK	NM_005833	Rab9 effector protein with kelch motifs
416			<i>Translation</i>
417			Complement
418	RAC1	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
419			<i>Translation</i>
420			Complement
421	RBM22	NM_018047	RNA binding motif protein 22
422			<i>Translation</i>
423			Complement
424	RBM9	NM_014309	RNA binding motif protein 9
425			<i>Translation</i>
426			Complement
427	Rgr	NM_153615	Ral-GDS related protein Rgr
428			<i>Translation</i>
429			Complement
430	RIPK2	NM_003821	receptor-interacting serine-threonine kinase 2
431			<i>Translation</i>
432			Complement
433	RNF207	NM_207396	ring finger protein 207
434			<i>Translation</i>
435			Complement
436	RNF31	NM_017999	ring finger protein 31
437			<i>Translation</i>
438			Complement
439	ROCK2	NM_004850	Rho-associated, coiled-coil containing protein kinase 2
440			<i>Translation</i>
441			Complement
442	RPS6KL1	NM_031464	ribosomal protein S6 kinase-like 1
443			<i>Translation</i>
444			Complement
445	SH3TC1	NM_018986	SH3 domain and tetratricopeptide repeats 1
446			<i>Translation</i>
447			Complement
448	SLC11A1	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
449			<i>Translation</i>
450			Complement
451	SLC6A8	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
452			<i>Translation</i>
453			Complement
454	SMAD5	NM_005903	SMAD family member 5
455			<i>Translation</i>
456			Complement
457	SMAD6	NM_005585	SMAD family member 6
458			<i>Translation</i>
459			Complement
460	SMARCD3	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
461			<i>Translation</i>

462			Complement
463	SMURF1	NM_020429	SMAD specific E3 ubiquitin protein ligase 1
464			<i>Translation</i>
465			Complement
466	SMURF2	NM_022739	SMAD specific E3 ubiquitin protein ligase 2
467			<i>Translation</i>
468			Complement
469	SPDEF	NM_012391	SAM pointed domain containing ets transcription factor
470			<i>Translation</i>
471			Complement
472	SRFBP1	NM_152546	serum response factor binding protein 1
473			<i>Translation</i>
474			Complement
475	STMN2	NM_007029	stathmin-like 2
476			<i>Translation</i>
477			Complement
478	STX2	NM_001980	syntaxin 2
479			<i>Translation</i>
480			Complement
481	SURF1	NM_003172	surfeit 1
482			<i>Translation</i>
483			Complement
484	SUV420H1	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)
485			<i>Translation</i>
486			Complement
487	SUZ12	NM_015355	suppressor of zeste 12 homolog (Drosophila)
488			<i>Translation</i>
489			Complement
490	TCOF1	NM_000356	Treacher Collins-Franceschetti syndrome 1
491			<i>Translation</i>
492			Complement
493	TFAP2A	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
494			<i>Translation</i>
495			Complement
496	TM6SF2	NM_001001524	transmembrane 6 superfamily member 2
497			<i>Translation</i>
498			Complement
499	TMEM142A	NM_032790	transmembrane protein 142A
500			<i>Translation</i>
501			Complement
502	TOP1	NM_003286	topoisomerase (DNA) I
503			<i>Translation</i>
504			Complement
505	TPM4	NM_003290	tropomyosin 4
506			<i>Translation</i>
507			Complement
508	TRAPPC5	XM_058961	trafficking protein particle complex 5
509			<i>Translation</i>
510			Complement
511	TRIM42	NM_152616	tripartite motif-containing 42

512			<i>Translation</i>
513			Complement
514	TRIM62	NM_018207	tripartite motif-containing 62
515			<i>Translation</i>
516			Complement
517	TRRAP	NM_003496	transformation/transcription domain-associated protein
518			<i>Translation</i>
519			Complement
520	TTY5	NM_031926	testis-specific transcript, Y-linked 5
521			<i>Translation</i>
522			Complement
523	TWIST1	NM_000474	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)
524			<i>Translation</i>
525			Complement
526	UBA52	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1
527			<i>Translation</i>
528			Complement
529	USP11	NM_004651	ubiquitin specific peptidase 11
530			<i>Translation</i>
531			Complement
532	USP42	XM_166526	ubiquitin specific peptidase 42
533			<i>Translation</i>
534			Complement
535	USP51	NM_201286	ubiquitin specific peptidase 51
536			<i>Translation</i>
537			Complement
538	VAMP1	NM_014231	vesicle-associated membrane protein 1 (synaptobrevin 1)
539			<i>Translation</i>
540			Complement
541	WDR37	NM_014023	WD repeat domain 37
542			<i>Translation</i>
543			Complement
544	WDR43	XM_087089	WD repeat domain 43
545			<i>Translation</i>
546			Complement
547	WIF1	NM_007191	WNT inhibitory factor 1
548			<i>Translation</i>
549			Complement
550	WWTR1	NM_015472	WW domain containing transcription regulator 1
551			<i>Translation</i>
552			Complement
553	XBP1	NM_005080	X-box binding protein 1
554			<i>Translation</i>
555			Complement
556	XPNPEP1	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
557			<i>Translation</i>
558			Complement
559	ZEB1	NM_030751	zinc finger E-box binding homeobox 1

560			Translation
561			Complement
562	ZNF148	NM_021964	zinc finger protein 148
563			Translation
564			Complement
565	ZNF346	NM_012279	zinc finger protein 346
566			Translation
567			Complement
568	ZNF467	XM_095168	zinc finger protein 467
569			Translation
570			Complement
571	ZNF608	XM_114432	zinc finger protein 608
572			Translation
573			Complement
574	ZNF767	NM_024910	zinc finger family member 767
575			Translation
576			Complement
577	ZNRF2	NM_147128	zinc and ring finger 2
578			Translation
579			Complement

SEQ ID NO	ENTREZ GENE SYMBOL	GENBANK ACC.NO.	GENE NAME
580	ABCB6	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6
581			Translation
582			Complement
583	ABHD2	NM_007011	abhydrolase domain containing 2
584			Translation
585			Complement
586	AGPAT3	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3
587			Translation
588			Complement
589	AMMECR1L	NM_031445	AMME chromosomal region gene 1-like
590			Translation
591			Complement
592	ANKRD20A1	NM_032250	ankyrin repeat domain 20 family, member A1
593			Translation
594			Complement
595	APC2	NM_005883	adenomatosis polyposis coli 2
596			Translation
597			Complement
598	ATP10D	NM_020453	ATPase, Class V, type 10D
599			Translation
600			Complement
601	C7orf41	NM_152793	chromosome 7 open reading frame 41
602			Translation
603			Complement
604	C9orf125	NM_032342	chromosome 9 open reading frame 125
605			Translation

606			Complement
607	CADM2	NM_153184	cell adhesion molecule 2
608			Translation
609			Complement
610	CCL26	NM_006072	chemokine (C-C motif) ligand 26
611			Translation
612			Complement
613	CDCA3	NM_031299	cell division cycle associated 3
614			Translation
615			Complement
616	CXorf22	NM_152632	chromosome X open reading frame 22
617			Translation
618			Complement
619	DDOST	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
620			Translation
621			Complement
622	ELAVL1	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
623			Translation
624			Complement
625	FAM116A	NM_152678	family with sequence similarity 116, member A
626			Translation
627			Complement
628	FOXE3	NM_012186	forkhead box E3
629			Translation
630			Complement
631	GCAT	NM_014291	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
632			Translation
633			Complement
634	HIST1H2BK	NM_080593	histone cluster 1, H2bk
635			Translation
636			Complement
637	HOXB13	NM_006361	homeobox B13
638			Translation
639			Complement
640	IQCB1	NM_014642	IQ motif containing B1
641			Translation
642			Complement
643	KCTD14	NM_023930	potassium channel tetramerisation domain containing 14
644			Translation
645			Complement
646	KIAA1024	XM_044580	KIAA1024 protein
647			Translation
648			Complement
649	LST-3TM12	XM_292093	organic anion transporter LST-3b
650			Translation
651			Complement
652	NPAT	NM_002519	nuclear protein, ataxia-telangiectasia locus
653			Translation
654			Complement

655	PELI1	NM_020651	pellino homolog 1 (Drosophila)
656			Translation
657			Complement
658	PLB1	NM_153021	phospholipase B1
659			Translation
660			Complement
661	RAF1	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1
662			Translation
663			Complement
664	RGPD5	NM_005054	RANBP2-like and GRIP domain containing 5
665			Translation
666			Complement
667	RPAIN	NM_032308	RPA interacting protein
668			Translation
669			Complement
670	SLC24A6	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
671			Translation
672			Complement
673	SNF1LK2	NM_015191	SNF1-like kinase 2
674			Translation
675			Complement
676	SPCS1	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)
677			Translation
678			Complement
679	SPCS2	NM_014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)
680			Translation
681			Complement
682	SPCS3	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)
683			Translation
684			Complement
685	SRI	NM_003130	sorcin
686			Translation
687			Complement
688	SRRM2	NM_016333	serine/arginine repetitive matrix 2
689			Translation
690			Complement
691	STAT3	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)
692			Translation
693			Complement
694	STIM2	NM_020860	stromal interaction molecule 2
695			Translation
696			Complement
697	TBCD	NM_005993	tubulin folding cofactor D
698			Translation
699			Complement
700	TMEM135	NM_022918	transmembrane protein 135

701			Translation
702			Complement
703	TTC14	NM_133462	tetratricopeptide repeat domain 14
704			Translation
705			Complement
706	UBE2S	NM_014501	ubiquitin-conjugating enzyme E2S
707			Translation
708			Complement
709	ZDHHC16	NM_032327	zinc finger, DHHC-type containing 16
710			Translation
711			Complement
712	ZNF337	NM_015655	zinc finger protein 337
713			Translation
714			Complement
715	ARHGEF7	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7
716			Translation
717			Complement
718	C16orf59	NM_025108	chromosome 16 open reading frame 59
719			Translation
720			Complement
721	COTL1	NM_021149	coactosin-like 1 (Dictyostelium)
722			Translation
723			Complement
724	EMID2	NM_133457	EMI domain containing 2
725			Translation
726			Complement
727	IL17RB	NM_018725	interleukin 17 receptor B
728			Translation
729			Complement
730	OTUB1	NM_017670	OTU domain, ubiquitin aldehyde binding 1
731			Translation
732			Complement
733	PTPRH	NM_002842	protein tyrosine phosphatase, receptor type, H
734			Translation
735			Complement
736	TSSK3	NM_052841	testis-specific serine kinase 3
737			Translation
738			Complement
739	U1SNRNPBP	NM_007020	U11/U12 snRNP 35K
740			Translation
741			Complement
742	USP43	XM_371015	ubiquitin specific peptidase 43
743			Translation
744			Complement
745	ATP11A	NM_015205	ATPase, Class VI, type 11A
746			Translation
747			Complement
748	CACNA1F	NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit
749			Translation
750			Complement

751	CSF3R	NM_000760	colony stimulating factor 3 receptor (granulocyte)
752			Translation
753			Complement
754	GKN2	NM_182536	gastrokin 2
755			Translation
756			Complement
757	HNRPK	NM_002140	heterogeneous nuclear ribonucleoprotein K
758			Translation
759			Complement
760	IGFBP6	NM_002178	insulin-like growth factor binding protein 6
761			Translation
762			Complement
763	IMPDH1	NM_000883	IMP (inosine monophosphate) dehydrogenase 1
764			Translation
765			Complement
766	KCNA1	NM_000217	potassium voltage-gated channel, shaker- related subfamily, member 1 (episodic ataxia with myokymia)
767			Translation
768			Complement
769	KCNQ4	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4
770			Translation
771			Complement
772	MTMR10	NM_017762	myotubularin related protein 10
773			Translation
774			Complement
775	PRPF31	NM_015629	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
776			Translation
777			Complement
778	SEPT9	NM_006640	septin 9
779			Translation
780			Complement
781	TMPRSS12	NM_182559	transmembrane protease, serine 12
782			Translation
783			Complement
784	TNFRSF18	NM_004195	tumor necrosis factor receptor superfamily, member 18
785			Translation
786			Complement
787	UBE2J2	NM_058167	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
788			Translation
789			Complement

Preferred host factors identified by the disclosed screens are listed in Table 2.

Table 2. Preferred Host Factors

Entrez Gene Symbol	Genbank Acc. No.	Gene Name
ABCB6	NM_005689	<i>ATP-binding cassette, sub-family B (MDR/TAP), member 6</i>
ABHD2	NM_007011	<i>abhydrolase domain containing 2</i>
ADAMTS4	NM_005099	<i>ADAM metalloproteinase with thrombospondin type 1 motif, 4</i>
AGPAT3	NM_020132	<i>1-acylglycerol-3-phosphate O-acyltransferase 3</i>
ALAD	NM_000031	<i>aminolevulinate, delta-, dehydratase</i>
AMMECR1L	NM_031445	<i>AMME chromosomal region gene 1-like</i>
ANKRD20A1	NM_032250	<i>ankyrin repeat domain 20 family, member A1</i>
AP1GBP1	NM_007247	<i>AP1 gamma subunit binding protein 1</i>
AP3B1	NM_003664	<i>adaptor-related protein complex 3, beta 1 subunit</i>
APC2	NM_005883	<i>adenomatosis polyposis coli 2</i>
APLP2	NM_001642	<i>amyloid beta (A4) precursor-like protein 2</i>
ARHGAP22	NM_021226	<i>Rho GTPase activating protein 22</i>
ARHGEF10L	NM_018125	<i>Rho guanine nucleotide exchange factor (GEF) 10-like</i>
ARRDC2	NM_015683	<i>arrestin domain containing 2</i>
ATP10D	NM_020453	<i>ATPase, Class V, type 10D</i>
BAGE2	NM_182482	<i>B melanoma antigen family, member 2</i>
BCKDHA	NM_000709	<i>branched chain keto acid dehydrogenase E1, alpha polypeptide</i>
BRF1	NM_001519	<i>BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)</i>
BRUNOL6	NM_052840	<i>bruno-like 6, RNA binding protein (Drosophila)</i>
C10orf112	XM_295865	<i>chromosome 10 open reading frame 112</i>
C14orf73	XM_040910	<i>chromosome 14 open reading frame 73</i>
C19orf44	NM_032207	<i>chromosome 19 open reading frame 44</i>
C20orf20	NM_018270	<i>chromosome 20 open reading frame 20</i>
C21orf56	NM_032261	<i>chromosome 21 open reading frame 56</i>
C7orf41	NM_152793	<i>chromosome 7 open reading frame 41</i>
C9orf125	NM_032342	<i>chromosome 9 open reading frame 125</i>
CADM2	NM_153184	<i>cell adhesion molecule 2</i>
CAMTA2	NM_015099	<i>calmodulin binding transcription activator 2</i>
CASP4	NM_001225	<i>caspase 4, apoptosis-related cysteine peptidase</i>
CCDC8	NM_032040	<i>coiled-coil domain containing 8</i>
CCL26	NM_006072	<i>chemokine (C-C motif) ligand 26</i>
CCNB2	NM_004701	<i>cyclin B2</i>
CCPG1	NM_004748	<i>cell cycle progression 1</i>
CDC6	NM_001254	<i>cell division cycle 6 homolog (S. cerevisiae)</i>
CDCA3	NM_031299	<i>cell division cycle associated 3</i>
CDH1	NM_004360	<i>cadherin 1, type 1, E-cadherin (epithelial)</i>
CDKL5	NM_003159	<i>cyclin-dependent kinase-like 5</i>
CHKA	NM_001277	<i>choline kinase alpha</i>
CISH	NM_013324	<i>cytokine inducible SH2-containing protein</i>
CLSTN1	NM_014944	<i>calsyntenin 1</i>

CNOT1	NM_016284	<i>CCR4-NOT transcription complex, subunit 1</i>
CNOT2	NM_014515	<i>CCR4-NOT transcription complex, subunit 2</i>
CNOT3	NM_014516	<i>CCR4-NOT transcription complex, subunit 3</i>
CNOT6L	NM_144571	<i>CCR4-NOT transcription complex, subunit 6-like</i>
CSNK1A1L	NM_145203	<i>casein kinase 1, alpha 1-like</i>
CTAGE6	NM_178561	<i>CTAGE family, member 6</i>
CXorf22	NM_152632	<i>chromosome X open reading frame 22</i>
CYBA	NM_000101	<i>cytochrome b-245, alpha polypeptide</i>
CYP4A22	XM_208213, NM_001010969	<i>cytochrome P450, family 4, subfamily A, polypeptide 22</i>
DACT3	NM_145056	<i>dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)</i>
DBNDD1	NM_024043	<i>dysbindin (dystrobrein binding protein 1) domain containing 1</i>
DDOST	NM_005216	<i>dolichyl-diphosphooligosaccharide-protein glycosyltransferase</i>
DEFA5	NM_021010	<i>defensin, alpha 5, Paneth cell-specific</i>
DEFB126	NM_030931	<i>defensin, beta 126</i>
DGAT1	NM_012079	<i>diacylglycerol O-acyltransferase homolog 1 (mouse)</i>
DHRS12	NM_024705	<i>dehydrogenase/reductase (SDR family) member 12</i>
DIO3	NM_001362	<i>deiodinase, iodothyronine, type III</i>
DLGAP4	NM_014902	<i>discs, large (Drosophila) homolog-associated protein 4</i>
DNAJB1	NM_006145	<i>DnaJ (Hsp40) homolog, subfamily B, member 1</i>
DOCK3	NM_004947	<i>dedicator of cytokinesis 3</i>
E2F2	NM_004091	<i>E2F transcription factor 2</i>
ERC2	NM_015576	<i>ELKS/RAB6-interacting/CAST family member 2</i>
ERCC5	NM_000123	<i>excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))</i>
ETF1	NM_004730	<i>eukaryotic translation termination factor 1</i>
FAM116A	NM_152678	<i>family with sequence similarity 116, member A</i>
FAU	NM_001997	<i>Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30</i>
FBXO38	NM_030793	<i>F-box protein 38</i>
FCGRT	NM_004107	<i>Fc fragment of IgG, receptor, transporter, alpha</i>
FER1L3	NM_013451	<i>fer-1-like 3, myoferlin (C. elegans)</i>
FLJ22659	XM_378723	<i>hypothetical protein FLJ22659</i>
FLT4	NM_002020	<i>fms-related tyrosine kinase 4</i>
FOXA2	NM_021784	<i>forkhead box A2</i>
FOXE3	NM_012186	<i>forkhead box E3</i>
FRMPD3	XM_042978	<i>FERM and PDZ domain containing 3</i>
GCAT	NM_014291	<i>glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)</i>
GNB2L1	NM_006098	<i>guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1</i>
GNG8	NM_033258	<i>guanine nucleotide binding protein (G protein), gamma 8</i>
GPSN2	NM_004868	<i>glycoprotein, synaptic 2</i>
GTF3A	NM_002097	<i>general transcription factor IIIA</i>
GUCY1A2	NM_000855	<i>guanylate cyclase 1, soluble, alpha 2</i>

HCCS	NM_005333	<i>holocytochrome c synthase (cytochrome c heme-lyase)</i>
HEATR1	XM_375853	<i>HEAT repeat containing 1</i>
HIPK3	NM_005734	<i>homeodomain interacting protein kinase 3</i>
HIST1H2BK	NM_080593	<i>histone cluster 1, H2bk</i>
HOXB13	NM_006361	<i>homeobox B13</i>
HRC	NM_002152	<i>histidine rich calcium binding protein</i>
HSD17B13	NM_178135	<i>hydroxysteroid (17-beta) dehydrogenase 13</i>
IFITM3	NM_021034	<i>interferon induced transmembrane protein 3 (1-8U)</i>
IGSF11	NM_152538	<i>immunoglobulin superfamily, member 11</i>
ILVBL	NM_006844	<i>ilvB (bacterial acetolactate synthase)-like</i>
IMP4	NM_033416	<i>IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)</i>
IQCB1	NM_014642	<i>IQ motif containing B1</i>
KCNJ3	NM_002239	<i>potassium inwardly-rectifying channel, subfamily J, member 3</i>
KCNK3	NM_002246	<i>potassium channel, subfamily K, member 3</i>
KCTD14	NM_023930	<i>potassium channel tetramerisation domain containing 14</i>
KIAA1024	XM_044580	<i>KIAA1024 protein</i>
KIAA1166	NM_018684	<i>KIAA1166</i>
KRT4	NM_002272	<i>keratin 4</i>
L1TD1	NM_019079	<i>LINE-1 type transposase domain containing 1</i>
LOC285556	XM_373030	<i>hypothetical protein LOC285556</i>
LOC285643	XM_209695	<i>KIF4B</i>
LOC400451	NM_207446	<i>hypothetical gene supported by AK075564; BC060873</i>
LST-3TM12	XM_292093	<i>organic anion transporter LST-3b</i>
LTC4S	NM_000897	<i>leukotriene C4 synthase</i>
MAP4	NM_002375	<i>microtubule-associated protein 4</i>
MARK3	NM_002376	<i>MAP/microtubule affinity-regulating kinase 3</i>
MCHR2	NM_032503	<i>melanin-concentrating hormone receptor 2</i>
MED12	NM_005120	<i>mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)</i>
MGC13057	NM_032321	<i>hypothetical protein MGC13057</i>
MLLT1	NM_005934	<i>myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1</i>
MLXIPL	NM_032951	<i>MLX interacting protein-like</i>
MRPL15	NM_014175	<i>mitochondrial ribosomal protein L15</i>
MRPL38	NM_032478	<i>mitochondrial ribosomal protein L38</i>
MRPL48	NM_016055	<i>mitochondrial ribosomal protein L48</i>
MTHFSD	NM_022764	<i>methenyltetrahydrofolate synthetase domain containing</i>
MYCL2	NM_005377	<i>v-myc myelocytomatosis viral oncogene homolog 2 (avian)</i>
MYO3A	NM_017433	<i>myosin IIIA</i>
MYO7B	XM_291001	<i>myosin VIIB</i>
NAALADL1	NM_005468	<i>N-acetylated alpha-linked acidic dipeptidase-like 1</i>
NMT1	NM_021079	<i>N-myristoyltransferase 1</i>
NOC4L	NM_024078	<i>nucleolar complex associated 4 homolog (S. cerevisiae)</i>
NOL1	NM_006170	<i>nucleolar protein 1, 120kDa</i>
NOL5A	NM_006392	<i>nucleolar protein 5A (56kDa with KKE/D repeat)</i>

NOL6	NM_022917	<i>nucleolar protein family 6 (RNA-associated)</i>
NOS1AP	NM_014697	<i>nitric oxide synthase 1 (neuronal) adaptor protein</i>
NPAT	NM_002519	<i>nuclear protein, ataxia-telangiectasia locus</i>
ORAOV1	NM_153451	<i>oral cancer overexpressed 1</i>
OSBP	NM_002556	<i>oxysterol binding protein</i>
PARP11	NM_020367	<i>poly (ADP-ribose) polymerase family, member 11</i>
PECR	NM_018441	<i>peroxisomal trans-2-enoyl-CoA reductase</i>
PELI1	NM_020651	<i>pellino homolog 1 (Drosophila)</i>
PEMT	NM_007169	<i>phosphatidylethanolamine N-methyltransferase</i>
PGLYRP4	NM_020393	<i>peptidoglycan recognition protein 4</i>
PLB1	NM_153021	<i>phospholipase B1</i>
PNO1	NM_020143	<i>partner of NOB1 homolog (S. cerevisiae)</i>
POLR2J2	NM_032958	<i>DNA directed RNA polymerase II polypeptide J-related</i>
PPP2R1A	NM_014225	<i>protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform</i>
PPTC7	NM_139283	<i>PTC7 protein phosphatase homolog (S. cerevisiae)</i>
PRKRIP1	NM_024653	<i>PRKR interacting protein 1 (IL11 inducible)</i>
PROX1	NM_002763	<i>prospero-related homeobox 1</i>
PRPF40A	XM_371575	<i>PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)</i>
PRPSAP2	NM_002767	<i>phosphoribosyl pyrophosphate synthetase-associated protein 2</i>
PTCD1	NM_015545	<i>pentatricopeptide repeat domain 1</i>
PTHRI	NM_000316	<i>parathyroid hormone receptor 1</i>
RAB10	NM_016131	<i>RAB10, member RAS oncogene family</i>
RAB11A	NM_004663	<i>RAB11A, member RAS oncogene family</i>
RAC1	NM_018890	<i>ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)</i>
RBM22	NM_018047	<i>RNA binding motif protein 22</i>
RBM9	NM_014309	<i>RNA binding motif protein 9</i>
RGPD5	NM_005054	<i>RANBP2-like and GRIP domain containing 5</i>
Rgr	NM_153615	<i>Ral-GDS related protein Rgr</i>
RIPK2	NM_003821	<i>receptor-interacting serine-threonine kinase 2</i>
RNF207	NM_207396	<i>ring finger protein 207</i>
RPAIN	NM_032308	<i>RPA interacting protein</i>
RPS6KL1	NM_031464	<i>ribosomal protein S6 kinase-like 1</i>
SH3TC1	NM_018986	<i>SH3 domain and tetratricopeptide repeats 1</i>
SLC11A1	NM_000578	<i>solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1</i>
SLC24A6	NM_024959	<i>solute carrier family 24 (sodium/potassium/calcium exchanger), member 6</i>
SLC6A8	NM_005629	<i>solute carrier family 6 (neurotransmitter transporter, creatine), member 8</i>
SMAD5	NM_005903	<i>SMAD family member 5</i>
SMAD6	NM_005585	<i>SMAD family member 6</i>
SMARCD3	NM_003078	<i>SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3</i>
SMURF1	NM_020429	<i>SMAD specific E3 ubiquitin protein ligase 1</i>

SNF1LK2	NM_015191	<i>SNF1-like kinase 2</i>
SPCS1	NM_014041	<i>signal peptidase complex subunit 1 homolog (S. cerevisiae)</i>
SPCS2	NM_014752	<i>signal peptidase complex subunit 2 homolog (S. cerevisiae)</i>
SPCS3	NM_021928	<i>signal peptidase complex subunit 3 homolog (S. cerevisiae)</i>
SPDEF	NM_012391	<i>SAM pointed domain containing ets transcription factor</i>
SRFBP1	NM_152546	<i>serum response factor binding protein 1</i>
SRI	NM_003130	<i>sorcin</i>
SRRM2	NM_016333	<i>serine/arginine repetitive matrix 2</i>
STIM2	NM_020860	<i>stromal interaction molecule 2</i>
STX2	NM_001980	<i>syntaxin 2</i>
SURF1	NM_003172	<i>surfeit 1</i>
SUV420H1	NM_016028	<i>suppressor of variegation 4-20 homolog 1 (Drosophila)</i>
SUZ12	NM_015355	<i>suppressor of zeste 12 homolog (Drosophila)</i>
TBCD	NM_005993	<i>tubulin folding cofactor D</i>
TCOF1	NM_000356	<i>Treacher Collins-Franceschetti syndrome 1</i>
TM6SF2	NM_001001524	<i>transmembrane 6 superfamily member 2</i>
TMEM135	NM_022918	<i>transmembrane protein 135</i>
TMEM142A	NM_032790	<i>transmembrane protein 142A</i>
TOP1	NM_003286	<i>topoisomerase (DNA) I</i>
TPM4	NM_003290	<i>tropomyosin 4</i>
TRAPPC5	XM_058961	<i>trafficking protein particle complex 5</i>
TRIM42	NM_152616	<i>tripartite motif-containing 42</i>
TRRAP	NM_003496	<i>transformation/transcription domain-associated protein</i>
TTC14	NM_133462	<i>tetratricopeptide repeat domain 14</i>
TTY5	NM_031926	<i>testis-specific transcript, Y-linked 5</i>
TWIST1	NM_000474	<i>twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)</i>
UBA52	NM_003333	<i>ubiquitin A-52 residue ribosomal protein fusion product 1</i>
UBE2S	NM_014501	<i>ubiquitin-conjugating enzyme E2S</i>
USP11	NM_004651	<i>ubiquitin specific peptidase 11</i>
USP42	XM_166526	<i>ubiquitin specific peptidase 42</i>
USP51	NM_201286	<i>ubiquitin specific peptidase 51</i>
VAMP1	NM_014231	<i>vesicle-associated membrane protein 1 (synaptobrevin 1)</i>
WDR37	NM_014023	<i>WD repeat domain 37</i>
WDR43	XM_087089	<i>WD repeat domain 43</i>
WIF1	NM_007191	<i>WNT inhibitory factor 1</i>
WWTR1	NM_015472	<i>WW domain containing transcription regulator 1</i>
XPNPEP1	NM_020383	<i>X-prolyl aminopeptidase (aminopeptidase P) 1, soluble</i>
ZDHHC16	NM_032327	<i>zinc finger, DHHC-type containing 16</i>
ZEB1	NM_030751	<i>zinc finger E-box binding homeobox 1</i>
ZNF148	NM_021964	<i>zinc finger protein 148</i>
ZNF337	NM_015655	<i>zinc finger protein 337</i>
ZNF346	NM_012279	<i>zinc finger protein 346</i>
ZNF467	XM_095168	<i>zinc finger protein 467</i>
ZNF608	XM_114432	<i>zinc finger protein 608</i>

ZNF767	NM_024910	<i>zinc finger family member 767</i>
ZNRF2	NM_147128	<i>zinc and ring finger 2</i>
Antiviral factors (24)		
ARHGEF7	NM_003899	<i>Rho guanine nucleotide exchange factor (GEF) 7</i>
ATP11A	XM_085028, XM_495964	<i>ATPase, Class VI, type 11A</i>
C16orf59	NM_025108	<i>chromosome 16 open reading frame 59</i>
CACNA1F	NM_005183	<i>calcium channel, voltage-dependent, L type, alpha 1F subunit</i>
COTL1	NM_021149	<i>coactosin-like 1 (Dictyostelium)</i>
CSF3R	NM_000760	<i>colony stimulating factor 3 receptor (granulocyte)</i>
EMID2	NM_133457	<i>EMI domain containing 2</i>
GKN2	NM_182536	<i>gastrokine 2</i>
IGFBP6	NM_002178	<i>insulin-like growth factor binding protein 6</i>
IL17RB	NM_018725	<i>interleukin 17 receptor B</i>
IMPDH1	NM_000883	<i>IMP (inosine monophosphate) dehydrogenase 1</i>
KCNA1	NM_000217	<i>potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)</i>
KCNQ4	NM_004700	<i>potassium voltage-gated channel, KQT-like subfamily, member 4</i>
MTMR10	NM_017762	<i>myotubularin related protein 10</i>
OTUB1	NM_017670	<i>OTU domain, ubiquitin aldehyde binding 1</i>
PRPF31	NM_015629	<i>PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)</i>
PTPRH	NM_002842	<i>protein tyrosine phosphatase, receptor type, H</i>
SEPT9	NM_006640	<i>septin 9</i>
TMPRSS12	NM_182559	<i>transmembrane protease, serine 12</i>
TNFRSF18	NM_004195	<i>tumor necrosis factor receptor superfamily, member 18</i>
TSSK3	NM_052841	<i>testis-specific serine kinase 3</i>
U1SNRNPBP	NM_007020	<i>U11/U12 snRNP 35K</i>
UBE2J2	NM_058167	<i>ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)</i>
USP43	XM_371015	<i>ubiquitin specific peptidase 43</i>

The validation round screen in which the four individual oligos comprising each pool were placed into separate wells, and screened again using identical methods as above. siRNA pools were considered validated if two or more of the individual oligos scored (50% or less infected cells (decreased infection) or 150% or greater infected cells (increased infection)) as compared to the negative control wells on the plate, in either both part one and two or part two alone, and the cell number was not less than 40% of the average of the negative control wells on the plate. The percent of infected cells relative to controls, as well as the normalized cell numbers for each of the individual genes that confirmed with two or more siRNAs is provided in Table S1. Visual spot inspections of control images were done throughout the screen to confirm the accuracy of the automated imaging and cell scoring systems.

Table S1A Part One: Decreased Infection											
Entrez Gene Symbol	Entrez Gene ID	Genbank Accession Number	Gene Name	Sequence	Vendor ID	Average Normalized Cell Number Part One	SD	Average Normalized Percent Infected Cells Part One	SD	Average Normalized Percent Infected Cells Part two	SD
ADAMTS4	9507	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4	CAAACCAGAGGCUCCA UUG	D-003807-04	0.80	0.04	0.34	0.04	0.04	0.01
ADAMTS4	9507	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4	GGACACACGCCUCCGA UAC	D-003807-03	0.53	0.25	0.27	0.00	0.06	0.06
ADAMTS4	9507	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4	GAGAUCGUGUUUCCA GAGA	D-003807-01	1.22	0.26	0.51	0.16	0.15	0.14
ADAMTS4	9507	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4	UGUUAGGCGUGUUAC AAUA	D-003807-02	1.25	0.26	0.78	0.43	0.89	0.15
ALAD	210	NM_000031	aminolevulinatase, delta-	GAUGACAUAACAGCCU AUCA	D-008458-04	0.96	0.13	0.51	0.04	0.47	0.18
ALAD	210	NM_000031	aminolevulinatase, delta-	GGCCUACGCUGUGUCU UGA	D-008458-03	0.86	0.08	0.56	0.29	0.57	0.01
ALAD	210	NM_000031	aminolevulinatase, delta-	GGACUUGGCAACAGG GUAU	D-008458-02	0.78	0.03	0.10	0.02	0.17	0.04
ALAD	210	NM_000031	aminolevulinatase, delta-	GAGCUACAGUGCCAA AUUU	D-008458-01	0.66	0.10	0.22	0.01	0.21	0.03
APIGBP1	11276	NM_007247	API gamma subunit binding protein 1	GAGGAGAUUUUAAGC AUGU	D-012375-01	0.78	0.12	0.27	0.14	0.05	0.02
APIGBP1	11276	NM_007247	API gamma subunit binding protein 1	CCAAUACUCUGAAUG AGAA	D-012375-04	1.46	0.43	1.30	0.12	0.60	0.32
APIGBP1	11276	NM_007247	API gamma subunit binding protein 1	GGACAUCGAUAAAGU AUGG	D-012375-02	0.60	0.14	0.35	0.13	0.11	0.02
APIGBP1	11276	NM_007247	API gamma subunit binding protein 1	CAAAUAUGAUGCCCU UAAA	D-012375-03	0.77	0.20	0.27	0.32	0.07	0.04
AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit	CAUCAGAGACCGUACA AGA	D-017533-04	1.20	0.16	0.68	0.18	0.54	0.18

AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit	AGUAUUAGAGUGCCA AUUA	D-017533-03	0.34	0.25	0.13	0.15	0.06	0.08
AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit	GCAAUAGGGAGGUGC AGUA	D-017533-02	0.48	0.01	0.20	0.21	0.05	0.06
AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit	GUGAUAAAGAUGGUCU CUAU	D-017533-01	1.05	0.32	0.27	0.12	0.14	0.01
APLP2	334	NM_001642	amyloid beta (A4) precursor-like protein 2	GAAGAGCGUCACCUG AACA	D-004179-05	1.51	0.32	0.33	0.01	0.11	0.02
APLP2	334	NM_001642	amyloid beta (A4) precursor-like protein 2	GAACAAAAGAUCCGUU ACAU	D-004179-01	0.63	0.43	0.47	0.20	0.39	0.30
APLP2	334	NM_001642	amyloid beta (A4) precursor-like protein 2	GGAAUAGACCUUAUAU AGCU	D-004179-04	0.93	0.21	0.28	0.01	0.09	0.07
APLP2	334	NM_001642	amyloid beta (A4) precursor-like protein 2	CAAAAGGAGUAGACUA CAAU	D-004179-03	1.10	0.41	0.56	0.13	0.15	0.05
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22	GGGAUCAGCUUUUCU ACUA	D-019080-02	1.18	0.37	0.41	0.14	0.36	0.06
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22	AUUACAAACCUUCUCAG AUA	D-019080-03	0.60	0.09	0.41	0.13	0.29	0.14
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22	CUAGGAAGCUUGACU GUUG	D-019080-01	0.74	0.10	0.14	0.04	0.24	0.03
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22	GGGAUUUAUUUCUCU ACAA	D-019080-04	0.36	0.09	0.35	0.08	0.22	0.14
ARHGEF10L	55160	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like	CCAAAGUAUGUGGUGA AGUG	D-017096-01	0.49	0.19	0.14	0.05	0.10	0.11
ARHGEF10L	55160	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like	GACGAGAGCCCGACAG UUG	D-017096-02	1.59	0.13	0.64	0.10	0.45	0.13
ARHGEF10L	55160	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like	CCAUGGUGCUAGAUG UGUA	D-017096-03	0.83	0.31	0.54	0.11	0.76	0.36
ARHGEF10L	55160	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like	GGAUGGCCGUGAUGC GCAA	D-017096-04	0.76	0.22	0.32	0.20	0.30	0.13
ARRDC2	27106	NM_015683	arrestin domain containing 2	GCCCGAUCCUGGUACU GUA	D-013874-02	1.09	0.09	0.22	0.04	0.35	0.26

ARRDC2	27106	NM_015683	arrestin domain containing 2	UGACAUCUUCGAGG GCAA	D-013874-04	0.72	0.23	0.40	0.17	0.22	0.08
ARRDC2	27106	NM_015683	arrestin domain containing 2	ACGCAGAGCUACAGU GAAC	D-013874-03	1.18	0.17	0.73	0.33	0.45	0.17
ARRDC2	27106	NM_015683	arrestin domain containing 2	GACAAACGGCUCCACAC GUC	D-013874-01	1.03	0.37	0.20	0.11	0.37	0.04
BAGE2	85319	NM_182482	B melanoma antigen family, member 2	GCCGACAGCUUUCAGG AUU	D-018890-01	0.96	0.08	0.85	0.10	0.81	0.04
BAGE2	85319	NM_182482	B melanoma antigen family, member 2	AGUCACAUCUUCUCC UUU	D-018890-02	1.36	0.27	0.65	0.29	0.47	0.01
BAGE2	85319	NM_182482	B melanoma antigen family, member 2	GAUCGAAAGGAAGAUG CAAA	D-018890-04	1.53	0.08	0.31	0.09	0.19	0.02
BAGE2	85319	NM_182482	B melanoma antigen family, member 2	AGAAAUGUACCCAGA UGUA	D-018890-03	0.50	0.04	0.43	0.06	0.32	0.17
BCKDHA	593	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide	GGACAACACGGACCUG GUG	D-012563-03	0.49	0.07	0.13	0.06	0.31	0.00
BCKDHA	593	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide	CAACUUCGUGGCCACA CUU	D-012563-01	0.21	0.02	0.54	0.01	0.25	0.01
BCKDHA	593	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide	UCGGCGGAGUUUAUA GAUA	D-012563-04	0.88	0.22	0.31	0.06	0.21	0.16
BCKDHA	593	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide	GAACGCCACUUCGUCA CUA	D-012563-02	0.50	0.14	0.26	0.09	0.03	0.01
BRF1	2972	NM_001519	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	GGAGGACUGUGAAGG AGGU	D-017422-02	0.59	0.11	0.17	0.09	0.25	0.00
BRF1	2972	NM_001519	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	GGAUGAAGCGGGACU GGAU	D-017422-03	1.43	0.51	0.72	0.14	0.61	0.01
BRF1	2972	NM_001519	BRF1 homolog, subunit of RNA polymerase III transcription initiation	GGAAGAGGCUCACGG AAUU	D-017422-01	0.60	0.13	0.24	0.09	0.39	0.18

[illegible]

C19orf44	84167	NM_032207	chromosome 19 open reading frame 44	GAAAGAACCUGCUAG ACA	D-014802-01	1.56	0.01	0.93	0.17	0.52	0.34
C19orf44	84167	NM_032207	chromosome 19 open reading frame 44	ACAGAACACUGGACGC UUU	D-014802-03	0.49	0.18	0.27	0.25	0.22	0.22
C19orf44	84167	NM_032207	chromosome 19 open reading frame 44	GCACAGAACGCGAAG GUCA	D-014802-02	0.47	0.32	0.06	0.01	0.12	0.04
C20orf20	55257	NM_018270	chromosome 20 open reading frame 20	GAACCGACACUUCAC AUG	D-006381-03	0.88	0.35	0.28	0.11	0.63	0.28
C20orf20	55257	NM_018270	chromosome 20 open reading frame 20	ACAAAGUCCUGACCGC AAA	D-006381-04	0.61	0.04	0.16	0.08	0.07	0.00
C20orf20	55257	NM_018270	chromosome 20 open reading frame 20	GAACUUCGUCCUCCA GAA	D-006381-02	1.71	0.34	0.80	0.40	0.44	0.15
C20orf20	55257	NM_018270	chromosome 20 open reading frame 20	GAAAGAACUCCUCAGAC UUG	D-006381-01	1.21	0.03	0.46	0.13	0.26	0.19
C21orf56	84221	NM_032261	chromosome 21 open reading frame 56	GCAAGCUGGUCUAUCG ACGU	D-015458-04	1.05	0.14	0.40	0.16	0.37	0.06
C21orf56	84221	NM_032261	chromosome 21 open reading frame 56	GGAGCUACUACCUCAA UGA	D-015458-01	0.53	0.12	0.23	0.15	0.21	0.17
C21orf56	84221	NM_032261	chromosome 21 open reading frame 56	CAUCAACACCUACGGA AUC	D-015458-02	0.88	0.44	0.36	0.01	0.31	0.15
C21orf56	84221	NM_032261	chromosome 21 open reading frame 56	CCGAGAAUAUCGAGC AGAC	D-015458-03	0.26	0.02	0.13	0.01	0.04	0.01
CAMTA2	23125	NM_015099	calmodulin binding transcription activator 2	GAGAGGCUACGGUGG AAUA	D-019047-01	1.64	0.23	0.36	0.02	0.14	0.04
CAMTA2	23125	NM_015099	calmodulin binding transcription activator 2	GAUCCUAGGCCUCCA UGA	D-019047-02	1.51	0.01	0.71	0.11	0.47	0.01
CAMTA2	23125	NM_015099	calmodulin binding transcription activator 2	GGUGAAAUACGGAA GGAU	D-019047-03	0.20	0.09	0.08	0.07	0.23	0.06
CAMTA2	23125	NM_015099	calmodulin binding transcription activator 2	CCACCGAGGUUGCUGA AAA	D-019047-04	0.45	0.15	0.26	0.14	0.32	0.03
CASP4	837	NM_001225	caspase 4, apoptosis-related cysteine peptidase	GGACUUAUGUGUAGA UGUA	D-004404-01	0.51	0.02	0.43	0.08	0.16	0.11

CASP4	837	NM_001225	caspase 4, apoptosis-related cysteine peptidase	GGGCAAAAGAUUUCCU CACU	D-004404-03	0.86	0.32	0.39	0.23	0.10	0.07
CASP4	837	NM_001225	caspase 4, apoptosis-related cysteine peptidase	GAGGGAUUCUGCGA ACUG	D-004404-04	0.66	0.32	0.52	0.30	0.59	0.52
CASP4	837	NM_001225	caspase 4, apoptosis-related cysteine peptidase	GAGACUAUGUAAAGA AAGA	D-004404-02	0.74	0.20	0.65	0.26	0.44	0.04
CCDC8	83987	NM_032040	coiled-coil domain containing 8	GGGAGAGGCGUCAGA UAGU	D-014775-04	1.09	0.17	0.66	0.17	0.71	0.52
CCDC8	83987	NM_032040	coiled-coil domain containing 8	GGGAGGACGUCGACU AUUU	D-014775-02	0.99	0.41	0.47	0.01	0.15	0.07
CCDC8	83987	NM_032040	coiled-coil domain containing 8	GAAGCGACCGGAGA GUGA	D-014775-01	0.36	0.07	0.24	0.05	0.16	0.09
CCDC8	83987	NM_032040	coiled-coil domain containing 8	GGGAAGAGGCCGUAC AUGA	D-014775-03	0.90	0.44	0.10	0.02	0.16	0.06
CCNB2	9133	NM_004701	cyclin B2	GUGACUACGUUAAGG AUUU	D-003207-08	0.30	0.11	0.35	0.11	0.21	0.17
CCNB2	9133	NM_004701	cyclin B2	CAACAAAUGUCAACA AACA	D-003207-05	0.77	0.04	0.06	0.03	0.05	0.02
CCNB2	9133	NM_004701	cyclin B2	GCAGCAACUCCUGAA GAU	D-003207-06	0.43	0.28	0.24	0.08	0.06	0.02
CCNB2	9133	NM_004701	cyclin B2	CCAGUGAUUUUGGAGA AUUU	D-003207-07	0.60	0.08	0.27	0.15	0.25	0.04
CCPG1	9236	NM_004748	cell cycle progression 1	GAUUGUAUGUUGAGG CAAA	D-013998-03	0.68	0.33	0.34	0.14	0.17	0.00
CCPG1	9236	NM_004748	cell cycle progression 1	AAACGAAACCUUGCUAC AGA	D-013998-01	0.27	0.09	0.19	0.06	0.19	0.12
CCPG1	9236	NM_004748	cell cycle progression 1	GUUAAUGUGUAGUCA GUUA	D-013998-02	0.90	0.20	0.45	0.09	0.29	0.09
CCPG1	9236	NM_004748	cell cycle progression 1	CCGAAGACAGUAUCU AUUU	D-013998-04	0.39	0.25	0.45	0.05	0.27	0.13
CDC6	990	NM_001254	cell division cycle 6 homolog (S. cerevisiae)	ACAAUUAAGUCUCCU AGCA	D-003233-09	1.10	0.03	0.34	0.14	0.13	0.04
CDC6	990	NM_001254	cell division cycle 6 homolog (S. cerevisiae)	GGAAUUAUCUUAAGCU ACUG	D-003233-07	0.86	0.26	0.36	0.27	0.24	0.30
CDC6	990	NM_001254	cell division cycle 6 homolog (S. cerevisiae)	GAGCAGAGAUGUCCA CUGA	D-003233-06	0.66	0.12	0.16	0.03	0.07	0.05

CDC6	990	NM_001254	cell division cycle 6 homolog (S. cerevisiae)	GGACGAAAUUGGUAUUUG	D-003233-08	0.52	0.10	0.51	0.07	0.44	0.02
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)	ACCAGAACCUUGAUAUA	D-003877-05	0.86	0.29	0.48	0.05	0.39	0.06
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)	GAGAACGCAUUGCCACAUA	D-003877-06	0.58	0.02	0.32	0.11	0.17	0.02
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)	GGAGAGCGGUGGUCAAGA	D-003877-02	0.93	0.23	0.90	0.02	0.72	0.20
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)	GCAGUACAUAUCUACACGUA	D-003877-07	1.19	0.18	0.29	0.03	0.34	0.17
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5	GCUAUUCACUGGUGCCAUUA	D-004799-04	1.43	0.02	1.40	0.42	0.69	0.35
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5	GAUGGAAGCUUGAGCAUAG	D-004799-02	1.15	0.34	0.36	0.03	0.23	0.06
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5	GGACUCACGUCGAAACACA	D-004799-06	0.65	0.09	0.21	0.01	0.04	0.02
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5	GAUAGACGCUUCAUGUUA	D-004799-01	1.05	0.27	0.97	0.02	0.62	0.46
CHKA	1119	NM_001277	choline kinase alpha	GAUAACAGCAGUUAUUAU	D-006704-04	1.70	0.45	0.33	0.09	0.23	0.08
CHKA	1119	NM_001277	choline kinase alpha	CAGAUGAGGUCCUGUAUA	D-006704-02	0.62	0.15	0.59	0.30	0.48	0.24
CHKA	1119	NM_001277	choline kinase alpha	GAGCAACAUCUCCGGAAGUA	D-006704-03	0.53	0.13	0.11	0.01	0.11	0.02
CHKA	1119	NM_001277	choline kinase alpha	GAUUUAAAGUUUGCCAUAUA	D-006704-01	0.89	0.03	0.53	0.22	0.56	0.10
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase	CAAAGAAAGCUGACAAUACU	D-003473-03	1.58	0.14	0.78	0.04	0.60	0.09
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase	GAAGUUCGGUUUAUAGUAGCC	D-003473-05	1.32	0.28	0.79	0.13	0.58	0.05
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase	AAAUUGGCAUUCUUAUA	D-003473-06	0.57	0.07	0.05	0.06	0.02	0.03
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase	CCAGAUACUUUCUUUAACUA	D-003473-04	0.78	0.18	0.47	0.08	0.30	0.02
CISH	1154	NM_013324	cytokine inducible SH2-containing protein	GACAACACCUGCAGAAUAU	D-017381-01	0.78	0.27	0.53	0.01	0.67	0.13

CISH	1154	NM_013324	cytokine inducible SH2-containing protein	CCGACUACCUCCGACA GUA	D-017381-04	0.51	0.31	0.20	0.10	0.14	0.11
CISH	1154	NM_013324	cytokine inducible SH2-containing protein	GAAAGCACGUUCUUA GUAC	D-017381-02	0.66	0.06	0.42	0.10	0.32	0.05
CISH	1154	NM_013324	cytokine inducible SH2-containing protein	CCACUGCUGUACACCU AAA	D-017381-03	0.44	0.21	0.21	0.10	0.21	0.20
CLDN1	9076	NM_021101	claudin 1	CACCAAGGCCCUAUCC AAA	D-017369-04	1.73	0.12	0.44	0.13	0.25	0.26
CLDN1	9076	NM_021101	claudin 1	GGUGCGAUUUUCUU CUUG	D-017369-01	1.71	0.07	0.88	0.22	0.43	0.24
CLDN1	9076	NM_021101	claudin 1	CAAUAGAAUCGUUCA AGAA	D-017369-02	0.76	0.26	0.39	0.15	0.16	0.07
CLDN1	9076	NM_021101	claudin 1	UGAAGUGUAUGAAGU GCUU	D-017369-03	0.37	0.06	0.07	0.03	0.04	0.02
CLSTN1	22883	NM_014944	calsyntenin 1	GCGAUUUGCAGGUGA GAUU	D-020393-04	0.40	0.04	0.20	0.03	0.12	0.09
CLSTN1	22883	NM_014944	calsyntenin 1	CCGGGAAACUCGCGGA UAA	D-020393-01	0.92	0.02	0.47	0.01	0.32	0.01
CLSTN1	22883	NM_014944	calsyntenin 1	GGAGACAUGUGACGGA GCCA	D-020393-03	0.49	0.05	0.21	0.05	0.14	0.15
CLSTN1	22883	NM_014944	calsyntenin 1	GACGUGCCCUUUAACUG UUG	D-020393-02	1.36	0.42	0.28	0.19	0.94	0.82
CNOT1	23019	NM_016284	CCR4-NOT transcription complex, subunit 1	GCAAUAUAAUCGUGC AGUU	D-015369-04	0.18	0.06	0.17	0.07	0.07	0.03
CNOT1	23019	NM_016284	CCR4-NOT transcription complex, subunit 1	GAGUGUGCGUUGCUG AUUA	D-015369-03	1.18	0.22	0.19	0.02	0.13	0.01
CNOT1	23019	NM_016284	CCR4-NOT transcription complex, subunit 1	CAAGUUAGCACUAUG GUAA	D-015369-02	1.14	0.08	0.30	0.01	0.23	0.09
CNOT1	23019	NM_016284	CCR4-NOT transcription complex, subunit 1	AUAAGUGGCUCACAG AUAA	D-015369-01	0.68	0.30	0.13	0.02	0.04	0.02
CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2	GAAGAACGAGUAUGG AUUA	D-020313-01	1.13	0.33	0.47	0.03	0.17	0.03
CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2	UAACGAACAUCACACA UUAG	D-020313-02	1.20	0.38	0.87	0.38	0.78	0.21

CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2	UUACCAAGGCCUCCAGCU AUA	D-020313-03	0.58	0.10	0.14	0.05	0.06	0.00
CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2	AAUCCGACGCUUAUCAC AAG	D-020313-04	0.56	0.16	0.19	0.03	0.09	0.04
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3	GCACUAAAGGCACAGU AUCU	D-020319-02	0.75	0.01	0.27	0.13	0.17	0.04
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3	AGACAUGGGUAGCGU CCAA	D-020319-04	0.69	0.24	0.08	0.04	0.09	0.02
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3	GGACGACGUUGAGUA CUAU	D-020319-01	0.96	0.28	0.09	0.11	0.15	0.07
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3	GGACAAGAGGCAGCU UAUA	D-020319-03	1.22	0.24	0.35	0.03	0.32	0.16
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like	UACAAUGAGUGUCUU AUGA	D-016411-03	1.13	0.02	0.65	0.06	0.72	0.42
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like	UGACAGCGCUGCACC UAAA	D-016411-01	0.95	0.47	0.30	0.21	0.23	0.22
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like	GGUAUUAGAGGUCCA CAAA	D-016411-04	0.97	0.49	0.27	0.08	0.20	0.03
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like	GAGCAGGUUAUGAAGC CUAU	D-016411-02	0.88	0.04	0.10	0.00	0.09	0.03
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like	CAUUGGCACUGUCCGA UAU	D-004681-04	1.02	0.26	0.41	0.25	0.06	0.04
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like	GCACUGGUUAGGUCA GGAA	D-004681-05	0.57	0.04	0.44	0.06	0.26	0.06
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like	GUACUGGGGUGUCACU GUAA	D-004681-02	1.07	0.13	0.20	0.04	0.02	0.00
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like	AAACAACAGCGGCUCC AAA	D-004681-01	0.73	0.18	0.40	0.00	0.11	0.13
CTAGE6	340307	NM_178561	CTAGE family, member 6	UAAACUUAGAUGAUCC UCUG	D-018312-02	0.87	0.13	0.94	0.30	0.76	0.01
CTAGE6	340307	NM_178561	CTAGE family, member 6	GAGAAAAGAAACCACA UUAU	D-018312-04	0.62	0.09	0.44	0.04	0.24	0.11
CTAGE6	340307	NM_178561	CTAGE family, member 6	GGAGGAAAAUUACCG AAUA	D-018312-01	1.53	0.13	0.96	0.04	0.32	0.03

CTAGE6	340307	NM_178561	CTAGE family, member 6	GAACGACGGGCUAUA GCAA	D-018312-03	1.61	0.12	0.36	0.00	0.16	0.08
CTGF	1490	NM_001901	connective tissue growth factor	GAAGACAUACCGAGC UAAA	D-012633-05	1.27	0.34	0.38	0.03	0.04	0.00
CTGF	1490	NM_001901	connective tissue growth factor	GCACAAAGGGCCUUC UGU	D-012633-03	1.42	0.22	0.58	0.06	0.32	0.13
CTGF	1490	NM_001901	connective tissue growth factor	ACAAUGACAUCUUUG AAUC	D-012633-04	1.28	0.06	0.71	0.15	0.35	0.10
CTGF	1490	NM_001901	connective tissue growth factor	UAAAUCUGUGGAGU AUGU	D-012633-02	0.56	0.06	0.37	0.07	0.07	0.06
CTSF	8722	NM_003793	cathepsin F	GCUCAGUCAUUUCCCU GUU	D-005837-04	0.54	0.34	0.33	0.15	0.08	0.01
CTSF	8722	NM_003793	cathepsin F	UGAGAAAGGUUAACUA CUAC	D-005837-05	0.99	0.28	0.59	0.12	0.60	0.19
CTSF	8722	NM_003793	cathepsin F	GCAACAAGAUAAAGC AAGC	D-005837-06	1.23	0.20	0.32	0.08	0.22	0.16
CTSF	8722	NM_003793	cathepsin F	GAGGAGGAGUUCGCG ACUA	D-005837-03	0.59	0.07	0.15	0.02	0.23	0.18
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1	GCUGUGGUAGUAAU CAUA	D-007870-05	1.30	0.05	0.93	0.00	0.50	0.31
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1	UAGCUUUGCUCUAUCCA CUA	D-007870-04	0.71	0.11	0.54	0.15	0.65	0.19
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1	GAGCUGUGGUAGUAA UUA	D-007870-01	1.00	0.07	0.38	0.09	0.18	0.03
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1	CAAAACGCGCAAUCAUC UUUG	D-007870-03	1.03	0.06	0.49	0.02	0.32	0.10
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide	UACCAGGAUUUAACUA UGUU	D-011020-02	0.72	0.15	0.30	0.17	0.17	0.14
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide	GGACAGAAAGCACAUG ACCG	D-011020-03	0.30	0.05	0.45	0.16	0.20	0.03
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide	GAAGAAAGGGCUCCACC AUG	D-011020-01	0.79	0.45	0.29	0.11	0.29	0.22
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide	CCAUGUGGGCCAAACGA GCA	D-011020-04	1.61	0.09	0.44	0.06	0.38	0.03
CYP4A22	284541	XM_208213, NM_0010109	cytochrome P450, family 4, subfamily A, polypeptide 22	GGAACUGCAUCGGGA AACA	D-021791-02	1.00	0.00	0.50	0.12	0.14	0.01
CYP4A22	284541	XM_208213, NM_0010109	cytochrome P450, family 4, subfamily A, polypeptide 22	GUGCUGAGGUGGACA CGUU	D-021791-01	1.36	0.10	0.98	0.07	0.94	0.21
CYP4A22	284541	XM_208213, NM_0010109	cytochrome P450, family 4, subfamily A, polypeptide 22	GGACAAAUGGGAAGA GCUC	D-021791-03	0.49	0.03	0.44	0.00	0.34	0.02

CYP4A22	284541	XM_208213, NM_0010109 69	cytochrome P450, family 4, subfamily A, polypeptide 22	UGGCACGACUUGUGU UGAA	D-021791- 04	1.36	0.10	0.94	0.05	0.53	0.01
DACT3	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	GAGAAUCGCCUGCCUU CAG	D-015690- 01	0.75	0.08	0.10	0.02	0.05	0.00
DACT3	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	CGGGUUCUCUCAAGG UCAU	D-015690- 04	0.25	0.15	0.20	0.08	0.21	0.06
DACT3	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	AAUCAAAGCUUCCAC GCG	D-015690- 02	1.84	0.14	1.41	0.12	0.99	0.30
DACT3	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	GAGAGCGAAUCGAGC GCCA	D-015690- 03	0.69	0.11	0.49	0.17	0.28	0.10
DBNDD1	79007	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1	GGACACGUUUCACU GUG	D-014275- 02	1.63	0.28	0.22	0.13	0.31	0.31
DBNDD1	79007	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1	GACAAUGGCCACACGC CUG	D-014275- 04	1.15	0.09	0.77	0.09	0.57	0.21
DBNDD1	79007	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1	ACGAGAAACCUCAACAC CGA	D-014275- 03	0.93	0.18	0.48	0.25	0.37	0.22
DBNDD1	79007	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1	GGAGCUGGCCGAGGU CUUU	D-014275- 01	0.82	0.06	1.20	0.19	0.52	0.25
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala- Asp) box polypeptide 3, X-linked	CUAUUUUCCUCCUCAU UUA	D-006874- 04	0.65	0.10	0.26	0.07	0.11	0.05
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala- Asp) box polypeptide 3, X-linked	GAAUACGAUGACAU UCCA	D-006874- 03	0.78	0.33	0.67	0.34	0.66	0.24
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala- Asp) box polypeptide 3, X-linked	ACAUUGAGCUUACUC GUUA	D-006874- 02	0.81	0.29	0.31	0.14	0.09	0.07
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala- Asp) box polypeptide 3, X-linked	GCAAAUACUUGGUGU UAGA	D-006874- 01	0.96	0.10	0.80	0.10	0.20	0.03

DEFA5	1670	NM_021010	defensin, alpha 5, Paneth cell-specific	GAAAGACAAACGAGGACC UUG	D-013143- 02	0.73	0.17	0.32	0.04	0.22	0.04
DEFA5	1670	NM_021010	defensin, alpha 5, Paneth cell-specific	CCUCAGGUUCUCAGGC AAG	D-013143- 04	0.22	0.06	0.13	0.05	0.16	0.09
DEFA5	1670	NM_021010	defensin, alpha 5, Paneth cell-specific	GCUACAAACCCAGAAAGC AGU	D-013143- 03	1.47	0.33	0.63	0.17	0.52	0.12
DEFA5	1670	NM_021010	defensin, alpha 5, Paneth cell-specific	GAAAUGGACUCUCUG CUCU	D-013143- 01	0.42	0.11	0.29	0.25	0.11	0.05
DEFB126	81623	NM_030931	defensin, beta 126	CCUGAAGAGAUUGCAU GUA	D-019046- 04	0.48	0.06	0.45	0.03	0.30	0.14
DEFB126	81623	NM_030931	defensin, beta 126	UCAGGUAAUUGGUU GUGA	D-019046- 01	1.40	0.30	0.97	0.38	0.85	0.43
DEFB126	81623	NM_030931	defensin, beta 126	GCUGACAGACGUGCU AAU	D-019046- 02	1.22	0.07	0.45	0.04	0.29	0.12
DEFB126	81623	NM_030931	defensin, beta 126	GGCAAUUGCGGCAA ACAA	D-019046- 03	0.21	0.08	0.12	0.04	0.07	0.01
DGAT1	8694	NM_012079	diacylglycerol O- acyltransferase homolog 1 (mouse)	UGACCUACCGCGAUUCU CUA	D-003922- 02	0.43	0.25	0.30	0.04	0.37	0.01
DGAT1	8694	NM_012079	diacylglycerol O- acyltransferase homolog 1 (mouse)	CUACCGGAUCUCUAC UAC	D-003922- 04	0.55	0.12	0.28	0.14	0.13	0.08
DGAT1	8694	NM_012079	diacylglycerol O- acyltransferase homolog 1 (mouse)	UCAUGUACGUCACGA CUA	D-003922- 01	1.54	0.27	0.52	0.08	0.63	0.19
DGAT1	8694	NM_012079	diacylglycerol O- acyltransferase homolog 1 (mouse)	GUGCUACGAGCUCUAC UUU	D-003922- 03	0.96	0.51	0.54	0.06	0.43	0.18
DHRS12	79758	NM_024705	dehydrogenase/reducta se (SDR family) member 12	AAACAGCGGCAUUGG CAAA	D-014418- 04	0.55	0.19	0.61	0.04	0.64	0.13
DHRS12	79758	NM_024705	dehydrogenase/reducta se (SDR family) member 12	GAACUAUGGUCUAUG CACA	D-014418- 01	0.45	0.10	0.28	0.15	0.31	0.23
DHRS12	79758	NM_024705	dehydrogenase/reducta se (SDR family) member 12	GAUCUCCAGUCCGAAA GAA	D-014418- 03	0.99	0.40	0.31	0.10	0.28	0.28
DHRS12	79758	NM_024705	dehydrogenase/reducta se (SDR family) member 12	GCAGGUUGCAUGGUC AAUA	D-014418- 02	0.88	0.48	0.39	0.08	0.19	0.02
DIO3	1735	NM_001362	deiodinase, iodothyronine, type III	AAGUGGAGCUCUACA GUGA	D-011251- 02	0.45	0.03	0.18	0.04	0.24	0.23

DIO3	1735	NM_001362	deiodinase, iodothyronine, type III	GCACUUGGUUGGAAC GCUA	D-011251-01	1.59	0.11	1.03	0.08	0.65	0.00
DIO3	1735	NM_001362	deiodinase, iodothyronine, type III	GCCCGCUGGUUCUCAA UUU	D-011251-03	0.20	0.04	0.09	0.06	0.06	0.05
DIO3	1735	NM_001362	deiodinase, iodothyronine, type III	GCGCCUACUUCGAGCG UCU	D-011251-04	0.92	0.09	0.21	0.01	0.19	0.12
DLGAP4	22839	NM_014902	discs, large (Drosophila) homolog-associated protein 4	GCAGACAGCAUCGAG AUUU	D-009452-04	0.91	0.38	0.82	0.17	0.51	0.46
DLGAP4	22839	NM_014902	discs, large (Drosophila) homolog-associated protein 4	CAAAGAAGCCAGCCAA AUC	D-009452-03	0.80	0.16	0.36	0.10	0.26	0.01
DLGAP4	22839	NM_014902	discs, large (Drosophila) homolog-associated protein 4	GCCAAUGACUCAAGCU GUA	D-009452-02	0.68	0.11	0.30	0.09	0.11	0.07
DLGAP4	22839	NM_014902	discs, large (Drosophila) homolog-associated protein 4	GAACAACCCUCUCUGAA GAA	D-009452-01	0.63	0.09	0.57	0.17	0.42	0.01
DNAJB1	3337	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	GAAAGAGCAUUCGAA ACGA	D-012735-01	1.25	0.33	0.59	0.09	0.90	0.35
DNAJB1	3337	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	CAACAACAUCUCCAGCU GAU	D-012735-03	1.21	0.01	0.24	0.08	0.39	0.05
DNAJB1	3337	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	GCUCUGAUGUCAUUU AUCC	D-012735-04	1.15	0.19	0.68	0.07	0.33	0.32
DNAJB1	3337	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	GAGCAGGUUCUUCUCCA AUUU	D-012735-02	0.59	0.05	0.22	0.08	0.13	0.03
DOCK3	1795	NM_004947	dedicator of cytokinesis 3	GAAGAUAGGCUGCAC UGUU	D-012695-01	0.65	0.09	0.08	0.00	0.08	0.00
DOCK3	1795	NM_004947	dedicator of cytokinesis 3	CGAGAUCACUGGCGA GUUU	D-012695-02	0.33	0.08	0.45	0.12	0.39	0.13
DOCK3	1795	NM_004947	dedicator of cytokinesis 3	GACCUGAUGGAGCA CGUA	D-012695-04	0.71	0.02	0.26	0.12	0.34	0.03
DOCK3	1795	NM_004947	dedicator of cytokinesis 3	UGACGCCCAUUCUCCAGA UUA	D-012695-03	0.66	0.09	0.35	0.02	0.20	0.04
E2F2	1870	NM_004091	E2F transcription factor 2	CCUUGGACCAGGACGA CUA	D-003260-09	1.29	0.05	0.64	0.04	1.09	0.29

E2F2	1870	NM 004091	E2F transcription factor 2	UGAAGGAGCUGAUGA ACAC	D-003260-07	0.66	0.32	0.17	0.09	0.09	0.07
E2F2	1870	NM 004091	E2F transcription factor 2	GGGAGAAAGACUCGGU AUGA	D-003260-05	1.86	0.25	0.54	0.09	0.54	0.45
E2F2	1870	NM 004091	E2F transcription factor 2	GAGGACAAACCUGCAG AUUAU	D-003260-06	0.78	0.03	0.15	0.02	0.14	0.08
ERC2	26059	NM 015576	ELKS/RAB6-interacting/CST family member 2	CGAGAUGAGUCAAUU AAAA	D-013008-04	1.57	0.49	0.74	0.17	0.56	0.36
ERC2	26059	NM 015576	ELKS/RAB6-interacting/CST family member 2	GGAAUUGUCUGCCUCC AAA	D-013008-02	1.24	0.26	0.40	0.07	0.22	0.17
ERC2	26059	NM 015576	ELKS/RAB6-interacting/CST family member 2	GAAAAGGGAUUCCAA AUUA	D-013008-01	1.39	0.55	0.57	0.34	0.53	0.14
ERC2	26059	NM 015576	ELKS/RAB6-interacting/CST family member 2	UAAUUGAGCGCUUGA AAGA	D-013008-03	0.92	0.28	0.31	0.01	0.37	0.33
ERCC5	2073	NM 000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	GAACGCACCUGCUGCU GUA	D-006626-02	0.48	0.01	0.33	0.03	0.19	0.05
ERCC5	2073	NM 000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	GAAAGAAGAUUCUAA ACGU	D-006626-03	1.36	0.13	0.43	0.03	0.24	0.13

ERCC5	2073	NM_000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	GAAACGAACUUUGCCCAUUAU	D-006626-04	0.55	0.09	0.22	0.02	0.08	0.05
ERCC5	2073	NM_000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	CAUGAAAUCUUGACUGAUA	D-006626-01	0.69	0.19	0.46	0.10	0.70	0.16
ETF1	2107	NM_004730	eukaryotic translation termination factor 1	AAUGUUAGCGGAUGAGUUU	D-019840-04	0.18	0.15	0.15	0.21	0.18	0.07
ETF1	2107	NM_004730	eukaryotic translation termination factor 1	UAAUCUAUUGUUCGGAAAGUA	D-019840-02	0.19	0.06	0.08	0.07	0.11	0.10
ETF1	2107	NM_004730	eukaryotic translation termination factor 1	GAAACACGGUAGAGAGAGGU	D-019840-03	0.59	0.42	0.11	0.06	0.39	0.01
ETF1	2107	NM_004730	eukaryotic translation termination factor 1	GAUCAGAGGUUACAAUCAA	D-019840-01	0.50	0.16	0.04	0.03	0.06	0.02
EWSR1	2130	NM_005243	Ewing sarcoma breakpoint region 1	GAGUAGCUAUGGUCAACAA	D-005119-09	0.18	0.11	0.14	0.14	0.07	0.03
EWSR1	2130	NM_005243	Ewing sarcoma breakpoint region 1	CUACACAGCCGACUAGUUA	D-005119-10	1.18	0.65	0.45	0.21	0.35	0.01
EWSR1	2130	NM_005243	Ewing sarcoma breakpoint region 1	GGAACAGAUUGGGAGGAGA	D-005119-05	0.89	0.45	0.20	0.13	0.35	0.08
EWSR1	2130	NM_005243	Ewing sarcoma breakpoint region 1	AGGAAAGCCCAAAAGGCGAU	D-005119-06	0.38	0.20	0.31	0.07	0.07	0.04
FAU	2197	NM_001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	CCGCAUGCUUGGAGGUAAAA	D-013149-02	0.21	0.02	0.07	0.09	0.05	0.00

FAU	2197	NM 001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	GAAACGGUGGCCAGAG UCA	D-013149-01	0.46	0.02	0.04	0.03	0.06	0.06
FAU	2197	NM 001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	AAGAAAGACAGGUCGG GCUA	D-013149-04	0.53	0.02	0.26	0.12	0.29	0.14
FAU	2197	NM 001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	GGUCAGACUCCUAG GUGG	D-013149-03	0.20	0.11	0.14	0.20	0.08	0.03
FBLN5	10516	NM 006329	Fibulin 5	UAAACCAAAUUGGCGG GUAAU	D-017621-04	0.78	0.41	0.62	0.15	0.59	0.37
FBLN5	10516	NM 006329	Fibulin 5	GGACGAGUGGCAAC AGAU	D-017621-02	0.46	0.08	0.34	0.05	0.14	0.00
FBLN5	10516	NM 006329	Fibulin 5	GCAGACGUGCUACAA UUAU	D-017621-01	1.21	0.02	0.74	0.06	0.91	0.02
FBLN5	10516	NM 006329	Fibulin 5	GUGCAAAACUUGGCUA ACA	D-017621-03	0.59	0.04	0.22	0.15	0.20	0.06
FBXO38	81545	NM 030793	F-box protein 38	CAAUUACUGUUAUG AUUC	D-018163-03	0.86	0.19	0.90	0.27	0.43	0.11
FBXO38	81545	NM 030793	F-box protein 38	GCCGAGAGUGGAAAU AAUA	D-018163-04	1.33	0.13	0.67	0.19	0.22	0.02
FBXO38	81545	NM 030793	F-box protein 38	GGACUCGAUUGGUUG AUUAU	D-018163-02	0.88	0.08	0.31	0.02	0.16	0.05
FBXO38	81545	NM 030793	F-box protein 38	GCAGAUAAAUCCACU AGUA	D-018163-01	0.57	0.04	0.33	0.11	0.21	0.08
FCGRT	2217	NM 004107	Fc fragment of IgG, receptor, transporter, alpha	GCGAUGAGCACCACUA CUG	D-017906-04	1.01	0.27	0.24	0.09	0.33	0.29
FCGRT	2217	NM 004107	Fc fragment of IgG, receptor, transporter, alpha	GCGGAGGAGUUAUG AAUU	D-017906-03	0.89	0.18	0.57	0.08	0.61	0.20
FCGRT	2217	NM 004107	Fc fragment of IgG, receptor, transporter, alpha	GGAGCUCUGUUGUGG AGAA	D-017906-02	0.65	0.27	0.38	0.10	0.31	0.28

FCGRT	2217	NM 004107	Fc fragment of IgG, receptor, transporter, alpha	CGUCAUCGGUGUCUU GCUA	D-017906-01	0.43	0.35	0.42	0.02	0.21	0.11
FERIL3	26509	NM 013451	fer-1-like 3, myoferlin (C. elegans)	CCACAGGAUUGCACGG UUA	D-013584-01	1.18	0.22	0.64	0.01	0.29	0.03
FERIL3	26509	NM 013451	fer-1-like 3, myoferlin (C. elegans)	GAACGGCUGCAAACA AAUA	D-013584-02	0.67	0.03	0.43	0.00	0.20	0.03
FERIL3	26509	NM 013451	fer-1-like 3, myoferlin (C. elegans)	GAAGAUGGGAGUAGA AUA	D-013584-03	0.43	0.05	0.39	0.16	0.40	0.05
FERIL3	26509	NM 013451	fer-1-like 3, myoferlin (C. elegans)	CGUCUUUGCUGAAAU GUUA	D-013584-04	1.57	0.05	0.99	0.03	0.62	0.10
FLJ22659	79999	XM 378723	hypothetical protein FLJ22659	GUUUGGAGGUUCCCG GAGU	D-014521-02	0.70	0.02	0.41	0.16	0.22	0.12
FLJ22659	79999	XM 378723	hypothetical protein FLJ22659	AAAUGGAAUGUCUUG GUGA	D-014521-01	1.06	0.05	1.03	0.14	1.07	0.05
FLJ22659	79999	XM 378723	hypothetical protein FLJ22659	GAGCCGAAAGCAGCC AAU	D-014521-03	0.50	0.20	0.27	0.17	0.06	0.01
FLJ22659	79999	XM 378723	hypothetical protein FLJ22659	AUGUCGAAUGUGGAGG CUCA	D-014521-04	1.01	0.30	0.69	0.02	0.55	0.24
FLT4	2324	NM 002020	fms-related tyrosine kinase 4	GCAAGAACGUGCAUC UGUU	D-003138-05	0.96	0.07	1.02	0.16	0.57	0.20
FLT4	2324	NM 002020	fms-related tyrosine kinase 4	GAGCAGCCAUUCAUCA ACA	D-003138-08	0.75	0.34	0.29	0.02	0.15	0.05
FLT4	2324	NM 002020	fms-related tyrosine kinase 4	GCGAAUACCUUGUCCUA CGA	D-003138-06	1.24	0.13	0.35	0.00	0.17	0.05
FLT4	2324	NM 002020	fms-related tyrosine kinase 4	GAAACAUUUUGAGGA AUUC	D-003138-07	0.76	0.27	0.22	0.07	0.09	0.02
FOXA2	3170	NM 021784	forkhead box A2	GAACACCAUACGCCU UCA	D-010089-02	0.74	0.06	0.14	0.05	0.05	0.01
FOXA2	3170	NM 021784	forkhead box A2	ACGAACAGGUGAUGC ACUA	D-010089-03	1.87	0.01	0.48	0.03	0.19	0.02
FOXA2	3170	NM 021784	forkhead box A2	CAACGACUGUUUCCUG AAG	D-010089-01	1.25	0.27	0.30	0.06	0.12	0.05
FOXA2	3170	NM 021784	forkhead box A2	CCGCAGAUACCUCCUA CUA	D-010089-04	2.05	0.36	1.67	0.25	1.54	0.45
FRMPD3	84443	XM 042978	FERM and PDZ domain containing 3	GAACUUUAUCAGGAGC GCUA	D-024802-01	1.58	0.33	0.90	0.25	0.83	0.62
FRMPD3	84443	XM 042978	FERM and PDZ domain containing 3	CCACAGCCGUAACCU UAA	D-024802-03	0.72	0.15	0.13	0.04	0.13	0.11
FRMPD3	84443	XM 042978	FERM and PDZ domain containing 3	GCAAGCUCAGUAUC UAC	D-024802-02	1.53	0.08	0.69	0.01	0.57	0.03
FRMPD3	84443	XM 042978	FERM and PDZ domain containing 3	GCGAAAUGAUAUGG AAUG	D-024802-04	1.40	0.22	0.39	0.07	0.09	0.09

GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	CCAAGGAUGUGCUA GUGU	D-006876-03	1.15	0.12	0.15	0.01	0.20	0.21
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAUAAGACCAUCAU AUGU	D-006876-02	1.28	0.13	0.31	0.14	0.33	0.15
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	CAAAUACACUGUCCAG GAU	D-006876-01	0.93	0.27	0.97	0.09	1.14	0.58
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAGAUAAAGACCAUCA UCAU	D-006876-04	0.56	0.14	0.12	0.04	0.21	0.07
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	AGGUGAACAUCGACC GAU	D-031976-04	0.67	0.17	0.25	0.04	0.15	0.04
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	CCAACAACAUGGCCAA GAU	D-031976-01	0.72	0.15	0.36	0.03	0.35	0.01
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GCGAGACGCAUGCCAA AGA	D-031976-02	1.60	0.37	0.82	0.08	0.45	0.00
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAAGGUGUCGACGGC AGCA	D-031976-03	0.73	0.15	0.57	0.05	1.02	0.06
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	AUUACGAGGUGGAGA UUCU	D-009537-02	0.75	0.11	0.16	0.01	0.13	0.02
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	UGGAGAUUCUGGACG CAAA	D-009537-01	0.79	0.02	0.14	0.06	0.13	0.09
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAUUCUGGACGCAAA GACA	D-009537-04	1.08	0.05	0.21	0.13	0.08	0.06
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAGCUCAGCAGGUGA AACU	D-009537-03	0.33	0.01	0.17	0.05	0.18	0.08
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GCAAUGAAAACAAAAGU CUCA	D-012635-03	0.76	0.09	1.36	0.01	0.31	0.03
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GAAACAAGGGCAAGG CUUA	D-012635-01	0.69	0.42	0.59	0.18	0.47	0.00
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	CCAUAAAAGAGGAAAACU	D-012635-02	0.97	0.17	0.13	0.04	0.22	0.12
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GACCAUUUGUUUGUG ACUA	D-012635-04	1.19	0.22	0.44	0.06	0.05	0.03

GUCY1A2	2977	NM_000855	guanylate cyclase 1, soluble, alpha 2	CCAGAAAAGUUUGAUG AUGU	D-006730-03	0.71	0.16	0.25	0.07	0.13	0.10
GUCY1A2	2977	NM_000855	guanylate cyclase 1, soluble, alpha 2	GACAGUGGAUCUUCU AUUU	D-006730-02	1.85	0.08	0.94	0.20	0.66	0.13
GUCY1A2	2977	NM_000855	guanylate cyclase 1, soluble, alpha 2	GAACAUAAGUUUUU GUGU	D-006730-04	1.25	0.71	0.47	0.33	0.39	0.13
GUCY1A2	2977	NM_000855	guanylate cyclase 1, soluble, alpha 2	AGAGGACACUGCAGU AUUA	D-006730-01	1.61	0.13	0.07	0.01	0.12	0.02
HCCS	3052	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)	GGACAGAAUUAUAGU AUGU	D-009226-02	0.81	0.14	0.49	0.01	0.24	0.04
HCCS	3052	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)	GGAAGGAGAUUUUGA AGUG	D-009226-04	0.98	0.07	0.47	0.06	0.34	0.10
HCCS	3052	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)	GAAAAGGCUUCCAGU GAUU	D-009226-03	1.02	0.42	0.47	0.14	0.17	0.07
HCCS	3052	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)	GGAUUGCAAUUGUAA AGAA	D-009226-01	1.59	0.39	1.25	0.04	1.12	0.10
HEATR1	55127	XM_375853	HEAT repeat containing 1	UGGGUUAAUUGUUCU GAUA	D-015939-04	1.26	0.10	0.19	0.07	0.35	0.12
HEATR1	55127	XM_375853	HEAT repeat containing 1	UAAAAGAAAGCUUGAAA GUGU	D-015939-01	1.58	0.29	0.94	0.07	0.61	0.09
HEATR1	55127	XM_375853	HEAT repeat containing 1	CCGUGACAUUUUAA UUAA	D-015939-03	1.25	0.07	0.55	0.02	0.43	0.02
HEATR1	55127	XM_375853	HEAT repeat containing 1	GCUCAGAAAGUCCUCAG AUA	D-015939-02	0.53	0.04	0.13	0.05	0.25	0.10
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3	GAUUGAAAGCGCAAGA GUGA	D-004810-04	1.18	0.06	0.52	0.07	0.66	0.22
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3	GAAUGAGCAUUAUUA GCAA	D-004810-01	1.10	0.14	0.44	0.04	0.09	0.03
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3	GGAAAUCCAGUGACA GUUG	D-004810-03	0.63	0.20	0.48	0.27	0.20	0.18
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3	GAAGGUGACUAUCAG UUAG	D-004810-02	0.63	0.27	0.53	0.01	0.52	0.23
HRC	3270	NM_002152	histidine rich calcium binding protein	CCACAGCCCUAGAGAC CAU	D-011697-03	0.94	0.26	0.35	0.25	0.16	0.01
HRC	3270	NM_002152	histidine rich calcium binding protein	ACACAGUGGUCAAGG AUAG	D-011697-02	1.07	0.34	0.62	0.10	0.63	0.16

HRC	3270	NM_002152	histidine rich calcium binding protein	GGAGUGAAGACACGG AAGA	D-011697-04	0.97	0.08	0.58	0.08	0.61	0.06
HRC	3270	NM_002152	histidine rich calcium binding protein	CAAGGAAUAGGGCA CUA	D-011697-01	0.73	0.07	0.21	0.01	0.15	0.05
HSD17B13	345275	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13	UAACAAUCGUGGUGA AUAA	D-018524-02	1.48	0.13	0.47	0.08	0.19	0.06
HSD17B13	345275	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13	GAACGCGCCUCAGCGA UUU	D-018524-03	0.56	0.10	0.62	0.10	0.09	0.11
HSD17B13	345275	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13	GGAGACAGAUAGAAGU CGUA	D-018524-01	1.30	0.06	0.71	0.04	0.50	0.20
HSD17B13	345275	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13	GAUGGAAUACUUAACC AAUA	D-018524-04	1.00	0.17	0.23	0.04	0.17	0.17
HSPA1A	3303	NM_005345	heat shock 70kDa protein 1A	GCUCCGACCUGUUCGG AAG	D-005168-05	1.95	0.62	0.79	0.22	0.92	0.16
HSPA1A	3303	NM_005345	heat shock 70kDa protein 1A	GAGAUCCGACUCCUUGU UUG	D-005168-01	1.66	0.25	0.90	0.15	0.81	0.08
HSPA1A	3303	NM_005345	heat shock 70kDa protein 1A	GAUCAACGACGGAGA CAAG	D-005168-03	0.53	0.15	0.20	0.05	0.14	0.01
HSPA1A	3303	NM_005345	heat shock 70kDa protein 1A	GCGCUGAACCCGCGACA ACA	D-005168-04	0.49	0.01	0.10	0.04	0.09	0.05
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)	GCAUUCCGCUACUCCG UGA	D-014116-04	2.14	0.03	1.37	0.04	1.61	0.66
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)	UCAACACCCUUCUUCAU GAA	D-014116-03	1.64	0.16	0.33	0.04	0.39	0.01
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)	CAAAACUUUCUUCUUC CUG	D-014116-02	0.83	0.19	0.22	0.02	0.05	0.00
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)	GGAAGAUGGUUGGCG ACGU	D-014116-01	1.33	0.08	0.19	0.07	0.35	0.10
IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11	CAACAUACCAUCCAUAU UAU	D-010688-01	1.10	0.13	0.59	0.11	0.41	0.05
IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11	CAGGAACAUGGACU AAUA	D-010688-04	1.09	0.16	0.53	0.01	0.49	0.18

IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11	GAAACAUCAGUGCCUUG UCU	D-010688-03	0.81	0.10	0.25	0.13	0.06	0.08
IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11	GGAAACGAUUGGUGC AGUA	D-010688-02	0.46	0.08	0.15	0.10	0.13	0.06
ILVBL	10994	NM_006844	ilvB (bacterial acetolactate synthase)-like	GCUGGUGGCCUGUGA GAAA	D-009658-02	1.64	0.05	1.02	0.28	1.50	0.60
ILVBL	10994	NM_006844	ilvB (bacterial acetolactate synthase)-like	UGACUGCGGUGAAGA AUGC	D-009658-03	0.54	0.10	0.32	0.07	0.11	0.04
ILVBL	10994	NM_006844	ilvB (bacterial acetolactate synthase)-like	GUUGAUCAGCUGUCCC UUU	D-009658-04	0.54	0.13	0.27	0.01	0.21	0.03
ILVBL	10994	NM_006844	ilvB (bacterial acetolactate synthase)-like	GGUGGCGGUUCAUC UUCA	D-009658-01	0.66	0.13	0.46	0.13	0.10	0.03
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	GCAAUGUGGUCAUGC GGCA	D-015116-04	0.71	0.07	0.14	0.06	0.35	0.11
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	AAACCAGGACGACUAC AUA	D-015116-03	0.59	0.10	0.39	0.06	0.39	0.06
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	UCUCUGACAUCUCCUG AUA	D-015116-02	1.38	0.21	0.52	0.05	0.52	0.14
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	GAAACCGAGGUGGACA UGAA	D-015116-01	0.32	0.01	0.18	0.17	0.21	0.13
IRF3	3661	NM_001571	interferon regulatory factor 3	AUGCACAGCAGGAGG AUUU	D-006875-03	0.56	0.21	0.20	0.06	0.04	0.02
IRF3	3661	NM_001571	interferon regulatory factor 3	GGGAAGAGUGGGAGU UCGA	D-006875-04	1.73	0.15	0.84	0.12	0.59	0.20
IRF3	3661	NM_001571	interferon regulatory factor 3	CCAAGAGGCUCUGA UGGU	D-006875-05	1.40	0.17	0.48	0.13	0.40	0.08
IRF3	3661	NM_001571	interferon regulatory factor 3	GCAAAGAAGGUUGC GUUU	D-006875-01	0.55	0.00	0.52	0.08	0.41	0.26
ITGA7	3679	NM_002206	integrin, alpha 7	GAGGAGUACUCAGCU GUGA	D-008004-04	0.66	0.42	0.39	0.04	0.20	0.12

ITGA7	3679	NM 002206	integrin, alpha 7	CCAGGGAGCUGAUU GCAA	D-008004- 02	1.66	0.40	0.42	0.08	0.15	0.06
ITGA7	3679	NM 002206	integrin, alpha 7	CCACGGAAACUGGAGG UAGA	D-008004- 03	1.23	0.61	0.57	0.39	0.71	0.72
ITGA7	3679	NM 002206	integrin, alpha 7	GAGAAUGCCUCCCAUG UUU	D-008004- 01	1.58	0.05	0.77	0.13	0.41	0.01
KCNJ3	3760	NM 002239	potassium inwardly- rectifying channel, subfamily J, member 3	GAACCUUCCAGCCAAA UUA	D-006248- 01	0.81	0.92	0.08	0.11	0.13	0.16
KCNJ3	3760	NM 002239	potassium inwardly- rectifying channel, subfamily J, member 3	GAAAAUUACUGGAAG AGAA	D-006248- 02	1.48	0.53	0.69	0.22	0.47	0.25
KCNJ3	3760	NM 002239	potassium inwardly- rectifying channel, subfamily J, member 3	CCAGUUCCAUGCAACA UUU	D-006248- 04	0.94	0.53	0.29	0.03	0.26	0.10
KCNJ3	3760	NM 002239	potassium inwardly- rectifying channel, subfamily J, member 3	GAGGAUUUUUUAAA GUUG	D-006248- 03	1.60	0.28	0.67	0.02	0.51	0.09
KCNK3	3777	NM 002246	potassium channel, subfamily K, member 3	GUACAAGAGCCGCGA GAAG	D-006262- 01	0.53	0.25	0.23	0.18	0.12	0.03
KCNK3	3777	NM 002246	potassium channel, subfamily K, member 3	UCAACACCUUGGUGA GGUA	D-006262- 03	0.78	0.12	0.82	0.02	1.03	0.43
KCNK3	3777	NM 002246	potassium channel, subfamily K, member 3	ACGCGGAGGUGCUGC ACUU	D-006262- 04	0.93	0.10	0.12	0.03	0.08	0.02
KCNK3	3777	NM 002246	potassium channel, subfamily K, member 3	ACGAGGAGCUGGAGC GCGU	D-006262- 02	2.00	0.03	1.03	0.23	0.74	0.23
KIAA1166	55906	NM 018684	KIAA1166	AAAGGCACCCUGAAG AAUA	D-007025- 02	0.29	0.05	0.26	0.08	0.13	0.04
KIAA1166	55906	NM 018684	KIAA1166	CAAGAAAUCAUGUGC AAAU	D-007025- 04	1.51	0.03	0.74	0.10	0.56	0.00
KIAA1166	55906	NM 018684	KIAA1166	GCACCUAAUAGCCUC UUU	D-007025- 01	0.44	0.01	0.22	0.08	0.21	0.07
KIAA1166	55906	NM 018684	KIAA1166	GAACAAGACCCUGCAG AUG	D-007025- 03	1.32	0.34	0.35	0.01	0.37	0.11
KRT4	3851	NM 002272	keratin 4	GUGAGAAUGCCCUUA AAGA	D-011711- 02	1.62	0.14	1.15	0.05	0.93	0.62
KRT4	3851	NM 002272	keratin 4	CGGAAGAGCGCGAAC AGAU	D-011711- 04	0.70	0.31	0.28	0.09	0.10	0.12
KRT4	3851	NM 002272	keratin 4	AGGCAUCAGCGGAGG AUUA	D-011711- 03	0.96	0.68	0.56	0.06	0.43	0.37

KRT4	3851	NM_002272	keratin 4	CAAGAGAGGUGCCUU CAGC	D-011711-01	0.90	0.15	0.45	0.11	0.49	0.25
L1TD1	54596	NM_019079	LINE-1 type transposase domain containing 1	GGACAUAGCUCCGGU AUUA	D-017976-01	1.74	0.19	0.29	0.04	0.15	0.02
L1TD1	54596	NM_019079	LINE-1 type transposase domain containing 1	AGACAAACUAAACGA AUAC	D-017976-03	0.99	0.14	0.98	0.07	0.44	0.31
L1TD1	54596	NM_019079	LINE-1 type transposase domain containing 1	GCAAGGACGUACAG CAAU	D-017976-02	0.71	0.32	0.47	0.10	0.13	0.01
L1TD1	54596	NM_019079	LINE-1 type transposase domain containing 1	CUACUAGUGUACAAU CAAA	D-017976-04	1.37	0.18	1.16	0.05	0.86	0.30
LOC285556	285556	XM_373030	hypothetical protein LOC285556	CAACUUUCCUGGACUU AAA	D-028236-01	1.24	0.15	0.31	0.04	0.22	0.08
LOC285556	285556	XM_373030	hypothetical protein LOC285556	CCAAAGUUGCUCACGCC CAA	D-028236-03	0.66	0.13	0.38	0.06	0.16	0.06
LOC285556	285556	XM_373030	hypothetical protein LOC285556	GAACGUCUGCAGCGG AGAA	D-028236-04	1.15	0.29	1.12	0.45	0.97	0.58
LOC285556	285556	XM_373030	hypothetical protein LOC285556	UCUACUCGUUCUGUGG AUUA	D-028236-02	0.90	0.18	0.59	0.02	0.38	0.14
LOC285643	285643	XM_209695	KIF4B	GGAAUUGGCUUGGAA AUGA	D-004965-01	0.79	0.01	0.10	0.04	0.07	0.04
LOC285643	285643	XM_209695	KIF4B	GGUAAACAGCCACACUC UUUA	D-004965-03	0.45	0.05	0.48	0.42	0.76	0.35
LOC285643	285643	XM_209695	KIF4B	GCAAGAUCUUGAAAG AGAU	D-004965-04	0.49	0.31	1.09	0.21	0.56	0.37
LOC285643	285643	XM_209695	KIF4B	AGAAACAUCUUCUUA AUGA	D-004965-02	0.44	0.02	0.25	0.02	0.20	0.10
LOC400451	400451	NM_207446	hypothetical gene supported by AK075564; BC060873	GAUGAGGACUCCACA GUUAU	D-032129-01	1.31	0.16	0.49	0.12	0.12	0.09
LOC400451	400451	NM_207446	hypothetical gene supported by AK075564; BC060873	GAAAUUGGCGCCACUA AAUG	D-032129-02	0.61	0.31	0.45	0.19	0.16	0.03
LOC400451	400451	NM_207446	hypothetical gene supported by AK075564; BC060873	AAAGAAAGACACGCAA GUUAU	D-032129-04	1.52	0.22	0.87	0.21	0.15	0.15

LOC400451	400451	NM_207446	hypothetical gene supported by AK075564; BC060873	CGACAUCAAAUACAG GUAA	D-032129-03	0.69	0.32	0.63	0.26	0.24	0.04
LTC4S	4056	NM_000897	leukotriene C4 synthase	AGGACGAGGUAGCUC UACU	D-008637-04	0.56	0.09	0.56	0.07	0.65	0.03
LTC4S	4056	NM_000897	leukotriene C4 synthase	CGAGGUAGCUCUACU GGCU	D-008637-02	1.35	0.26	0.55	0.03	0.79	0.26
LTC4S	4056	NM_000897	leukotriene C4 synthase	CACCCGAGUUCGAGCG CGU	D-008637-03	0.76	0.34	0.32	0.00	0.41	0.11
LTC4S	4056	NM_000897	leukotriene C4 synthase	GAAGGACGAGGUAGC UCUA	D-008637-01	0.57	0.30	0.23	0.03	0.42	0.05
MAP4	4134	NM_002375	microtubule-associated protein 4	CGAGGAGGAUUCUGU GUUA	D-011724-04	1.44	0.17	0.61	0.01	1.00	0.42
MAP4	4134	NM_002375	microtubule-associated protein 4	GGACAUGUCUCCACUA UCA	D-011724-01	1.38	0.34	0.08	0.00	0.14	0.10
MAP4	4134	NM_002375	microtubule-associated protein 4	CAACACCAGUUCCAAU UAA	D-011724-03	1.90	0.04	0.51	0.02	0.44	0.13
MAP4	4134	NM_002375	microtubule-associated protein 4	GGAAUACCCACCAA UUA	D-011724-02	1.34	0.16	0.33	0.08	0.34	0.07
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1	AAACAGAUUUUACA AGCU	D-003555-03	0.88	0.11	0.41	0.14	0.25	0.22
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1	CAAGAGGAUUGAAGU AGAA	D-003555-04	0.79	0.15	0.54	0.00	0.23	0.16
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1	CCAAAGCUCUGGACUU AUU	D-003555-01	0.55	0.29	0.32	0.21	0.26	0.18
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1	GUACAGGGCUCACAGA AAUU	D-003555-09	0.65	0.08	0.55	0.01	0.22	0.01
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3	GAAGUUACCUUCUCGU ACCA	D-003517-04	0.79	0.17	0.22	0.05	0.11	0.03
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3	GGAAUGACACGACGA AAUA	D-003517-03	1.25	0.66	0.59	0.35	0.41	0.25
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3	GAAAUACGAUGAAAU CACA	D-003517-02	1.53	0.10	0.64	0.11	0.45	0.17
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3	GGAAUGCAAGUAAUC CUAA	D-003517-10	0.73	0.07	0.29	0.04	0.42	0.15
MCHR2	84539	NM_032503	melanin-concentrating hormone receptor 2	CGAAGGUCAUCAAU UUAU	D-005548-03	2.04	0.99	0.84	0.11	0.17	0.09

MCHR2	84539	NM_032503	melanin-concentrating hormone receptor 2	GAACAAGGUACAAGA CCAU	D-005548-05	0.88	0.17	0.37	0.23	0.19	0.09
MCHR2	84539	NM_032503	melanin-concentrating hormone receptor 2	GGAGAUGUAUCAACA GAU	D-005548-02	1.96	0.45	0.96	0.06	0.33	0.11
MCHR2	84539	NM_032503	melanin-concentrating hormone receptor 2	GCAGCAGCAUUAACCC UUU	D-005548-04	0.71	0.40	0.48	0.31	0.24	0.28
MCM2	4171	NM_004526	minichromosome maintenance complex component 2	CAGAGCAGGUGACAU AUA	D-003273-07	1.02	0.14	0.56	0.30	0.26	0.07
MCM2	4171	NM_004526	minichromosome maintenance complex component 2	GCCGUGGGCUCUUGUA	D-003273-08	1.16	0.08	0.38	0.02	0.33	0.01
MCM2	4171	NM_004526	minichromosome maintenance complex component 2	GGAUAAAGGCUCGUCA GAUC	D-003273-06	1.28	0.17	0.48	0.17	0.14	0.10
MCM2	4171	NM_004526	minichromosome maintenance complex component 2	GAAGAUCUUUGCCAG CAU	D-003273-05	0.24	0.18	0.50	0.39	0.18	0.14
MED12	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)	CAACAACAGCUCUCUA AUA	D-009092-03	1.39	0.20	0.41	0.10	0.27	0.09
MED12	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)	GCAGAGAAAUUACGU UGUA	D-009092-01	1.76	0.61	0.31	0.16	0.33	0.25
MED12	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)	UUAGAACCCUCCUUCUU AUA	D-009092-04	1.92	0.63	0.38	0.05	0.38	0.12
MED12	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)	UCACUCAUCUCAUGUU AUA	D-009092-02	0.62	0.29	0.26	0.11	0.12	0.05
MGC13057	84281	NM_032321	hypothetical protein MGC13057	GAAAGAGAGUUGUCUA CCUA	D-014854-01	0.89	0.04	0.48	0.08	0.21	0.04
MGC13057	84281	NM_032321	hypothetical protein MGC13057	GAACCUCCAGGGACCA AUA	D-014854-02	1.09	0.28	0.20	0.01	0.28	0.21

MGC13057	84281	NM_032321	hypothetical protein MGC13057	UAUCUUUGUGUGAUGC CUUG	D-014854-04	1.19	0.00	0.88	0.05	0.52	0.23
MGC13057	84281	NM_032321	hypothetical protein MGC13057	CAUUGGGCAUGCAAU AACA	D-014854-03	0.94	0.34	0.75	0.11	0.60	0.08
MLLT1	4298	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	GAGACUGGCCACUUCA AUG	D-016352-04	2.15	0.19	0.35	0.19	0.23	0.16
MLLT1	4298	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	CCUACGACCUGUUCU GAA	D-016352-03	1.75	0.08	0.46	0.01	0.28	0.25
MLLT1	4298	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	GACAAAGGCCUACACGG AUG	D-016352-02	1.23	0.25	0.47	0.01	0.39	0.13
MLLT1	4298	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	GCAAAGACUCCGAGA GCAA	D-016352-01	0.87	0.14	0.22	0.17	0.35	0.05
MLX1PL	51085	NM_032951	MLX interacting protein-like	GCCCAUGCCUUAAC UUC	D-009253-04	0.82	0.36	0.10	0.04	0.10	0.01
MLX1PL	51085	NM_032951	MLX interacting protein-like	GACACUCUUAACCA UGA	D-009253-01	0.34	0.17	0.14	0.01	0.02	0.00
MLX1PL	51085	NM_032951	MLX interacting protein-like	ACAAGUGGCGCAUCU ACUA	D-009253-02	1.20	0.17	0.24	0.11	0.20	0.08
MLX1PL	51085	NM_032951	MLX interacting protein-like	GGGCACAUCAACCAU AUC	D-009253-03	0.73	0.20	0.47	0.19	0.38	0.14
MRPL15	29088	NM_014175	mitochondrial ribosomal protein L15	GCCAGGAAGUAUGGU UAUA	D-013052-03	1.00	0.27	0.85	0.06	0.29	0.05
MRPL15	29088	NM_014175	mitochondrial ribosomal protein L15	GGCGGAUCCUGCCAAA UUU	D-013052-01	0.60	0.02	0.27	0.08	0.14	0.01
MRPL15	29088	NM_014175	mitochondrial ribosomal protein L15	GAUCCUAGUCAACCUA UUG	D-013052-02	0.94	0.31	0.47	0.18	0.38	0.04
MRPL15	29088	NM_014175	mitochondrial ribosomal protein L15	UGGUGAAUAUGGCCG AUAA	D-013052-04	1.50	0.33	0.38	0.01	0.23	0.00
MRPL38	64978	NM_032478	mitochondrial ribosomal protein L38	GGACCUACCGAGAGU AUUU	D-013573-02	0.43	0.12	0.05	0.01	0.08	0.04
MRPL38	64978	NM_032478	mitochondrial ribosomal protein L38	UAAACCAACAUCGCGG UAA	D-013573-04	0.90	0.12	0.66	0.17	0.57	0.17

MRPL38	64978	NM_032478	mitochondrial ribosomal protein L38	CCAAAGAGAAUAUUG	D-013573-01	1.65	0.17	0.79	0.23	0.50	0.24
MRPL38	64978	NM_032478	mitochondrial ribosomal protein L38	GCAAUGAGGUGACUC	D-013573-03	1.41	0.09	0.45	0.04	0.28	0.12
MRPL48	51642	NM_016055	mitochondrial ribosomal protein L48	CCAUAGAAAGUGUUGC	D-017512-02	1.15	0.02	0.32	0.07	0.12	0.05
MRPL48	51642	NM_016055	mitochondrial ribosomal protein L48	GGGACAGAUUAUGA	D-017512-04	0.74	0.04	0.42	0.12	0.25	0.03
MRPL48	51642	NM_016055	mitochondrial ribosomal protein L48	CGAGGAAAGUUAUGC	D-017512-01	1.44	0.23	0.41	0.13	0.17	0.08
MRPL48	51642	NM_016055	mitochondrial ribosomal protein L48	AUUCAAAAGCUCGACCA	D-017512-03	0.59	0.09	0.32	0.09	0.27	0.09
MTHFSD	64779	NM_022764	methenyltetrahydrofolate synthetase domain containing	CCAGAGUCCUCGUGGA	D-013745-02	0.46	0.10	0.40	0.05	0.13	0.04
MTHFSD	64779	NM_022764	methenyltetrahydrofolate synthetase domain containing	CGGGAUUGUUUAAUA	D-013745-03	1.46	0.07	1.05	0.04	0.47	0.04
MTHFSD	64779	NM_022764	methenyltetrahydrofolate synthetase domain containing	GCUACGCCGUAUCUGGA	D-013745-04	1.03	0.47	0.35	0.17	0.17	0.20
MTHFSD	64779	NM_022764	methenyltetrahydrofolate synthetase domain containing	GGACAUACGUGAACA	D-013745-01	1.08	0.07	0.48	0.16	0.23	0.17
MYCL2	4611	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	CGGAAUACUUACAUG	D-010591-05	2.21	0.18	0.52	0.15	0.16	0.06
MYCL2	4611	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	GAAACCCAGCCUCAGC	D-010591-01	0.45	0.26	0.70	0.14	0.60	0.09
MYCL2	4611	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	CAAGGCCACGGAAUAC	D-010591-03	0.74	0.23	0.38	0.01	0.09	0.08
MYCL2	4611	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	GAUCAACGUUCGCGG	D-010591-04	0.87	0.37	0.46	0.21	0.15	0.10
MYO3A	53904	NM_017433	myosin IIIA	GAACAGCAAUUGGAU	D-004862-03	0.52	0.02	0.22	0.01	0.07	0.03
MYO3A	53904	NM_017433	myosin IIIA	GAAAGGGGUGAAAAG	D-004862-04	0.47	0.02	0.21	0.05	0.22	0.08

MYO3A	53904	NM_017433	myosin IIIA	GCAAUUGGAUACAC	D-004862-02	1.16	0.45	0.29	0.15	0.07	0.02
MYO3A	53904	NM_017433	myosin IIIA	GAAAGGCAUAACAU	D-004862-01	0.71	0.30	0.65	0.03	0.41	0.09
MYO7B	4648	XM_291001	myosin VIIIB	GCACGAGCUUAUUU	D-022928-03	1.24	0.17	0.38	0.05	0.34	0.03
MYO7B	4648	XM_291001	myosin VIIIB	ACCG	D-022928-02	0.57	0.06	0.11	0.03	0.16	0.07
MYO7B	4648	XM_291001	myosin VIIIB	GAGCAUCCUUCUAGCC	D-022928-04	0.89	0.11	1.00	0.37	0.56	0.09
MYO7B	4648	XM_291001	myosin VIIIB	UAU	D-022928-01	1.22	0.24	0.98	0.35	0.48	0.05
NAALADL1	10004	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1	CGAGUACAGCUUCG	D-005975-03	1.13	0.16	0.13	0.11	0.38	0.40
NAALADL1	10004	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1	AGAA	D-005975-02	1.25	0.21	0.46	0.25	0.28	0.03
NAALADL1	10004	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1	CAACAUUCCUCCAGG	D-005975-01	0.39	0.03	0.25	0.03	0.15	0.08
NAALADL1	10004	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1	UAU	D-005975-04	1.34	0.23	1.33	0.21	0.91	0.30
NMT1	4836	NM_021079	N-myristoyltransferase 1	GGACACAGCUUCUGG	D-004316-03	1.14	0.50	0.47	0.08	0.31	0.04
NMT1	4836	NM_021079	N-myristoyltransferase 1	GCAGAUCAAUCGUGU	D-004316-01	0.56	0.05	0.45	0.00	0.25	0.03
NMT1	4836	NM_021079	N-myristoyltransferase 1	UUGC	D-004316-02	1.10	0.11	1.27	0.10	0.53	0.17
NMT1	4836	NM_021079	N-myristoyltransferase 1	GCAGAAUAUGACCA	D-004316-04	1.88	0.08	0.55	0.18	0.33	0.02
NOC4L	79050	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)	UUA	D-014293-03	0.86	0.10	0.36	0.09	0.38	0.06
NOC4L	79050	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)	GGAAGUACAAGGUGU	D-014293-04	1.19	0.46	0.40	0.17	0.16	0.00
NOC4L	79050	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)	GCGCACUCCUGAAGUU	D-014293-02	1.06	0.18	0.21	0.07	0.28	0.16
NOC4L	79050	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)	UGU	D-014293-01	0.73	0.26	0.12	0.03	0.21	0.08

NOL1	4839	NM_006170	nucleolar protein 1, 120kDa	AGACAGAAACUCGUCA GAUU	D-020084- 02	0.42	0.12	0.30	0.13	0.14	0.07
NOL1	4839	NM_006170	nucleolar protein 1, 120kDa	GCAACGAUCACCUAAA UUA	D-020084- 01	1.18	0.23	0.65	0.37	0.49	0.06
NOL1	4839	NM_006170	nucleolar protein 1, 120kDa	GCAUACCCCAUGAAAU UUA	D-020084- 03	1.56	0.49	0.84	0.01	0.28	0.04
NOL1	4839	NM_006170	nucleolar protein 1, 120kDa	AAGGUUGCUGCCCCAU UGA	D-020084- 05	0.54	0.22	0.29	0.04	0.24	0.23
NOL5A	10528	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)	GGAGAGAUACCCACGA AAGA	D-019143- 02	1.32	0.22	0.66	0.10	0.82	0.14
NOL5A	10528	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)	GAGCGACUGUCCUUCU AUG	D-019143- 04	0.63	0.03	0.14	0.03	0.11	0.05
NOL5A	10528	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)	CAACGACAAUGCCACA UAC	D-019143- 03	0.67	0.21	0.34	0.02	0.38	0.18
NOL5A	10528	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)	GGACAUUUCUGCCAU UGAC	D-019143- 01	0.50	0.25	0.43	0.11	0.18	0.11
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA- associated)	UGAGAAUGUGUCUUGC AGUU	D-017285- 03	1.07	0.21	0.11	0.06	0.05	0.02
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA- associated)	CUUAAUCGCCUUCGGG AGA	D-017285- 04	1.33	0.11	1.02	0.21	0.75	0.00
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA- associated)	GGACGGAGCCAUUCG GGAA	D-017285- 01	1.19	0.01	0.30	0.02	0.21	0.18
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA- associated)	GGGAUCAGUUUAUGU CUCA	D-017285- 02	0.78	0.22	0.41	0.25	0.39	0.16
NOP5/NOP58	51602	NM_015934	nucleolar protein NOP5/NOP58	GGAAUUAGUUGGAGC ACGG	D-017973- 01	0.53	0.08	0.09	0.00	0.04	0.02
NOP5/NOP58	51602	NM_015934	nucleolar protein NOP5/NOP58	CCUCAAUUCUAGACGG GAU	D-017973- 04	1.37	0.21	0.74	0.04	0.45	0.11
NOP5/NOP58	51602	NM_015934	nucleolar protein NOP5/NOP58	ACAAUUAUUAUUGC GAUG	D-017973- 03	1.66	0.14	1.16	0.18	0.82	0.07
NOP5/NOP58	51602	NM_015934	nucleolar protein NOP5/NOP58	GAUUGAAGUUUAGCG CUGA	D-017973- 02	0.69	0.11	0.10	0.08	0.22	0.09
NOS1AP	9722	NM_014697	nitric oxide synthase 1 (neuronal) adaptor protein	GCGACGGCCUGGAUG AUGA	D-013446- 03	0.29	0.00	0.06	0.01	0.12	0.09

NOS1AP	9722	NM 014697	nitric oxide synthase 1 (neuronal) adaptor protein	GGACGUGGAUGAGA GCAA	D-013446-04	0.63	0.08	0.17	0.03	0.20	0.05
NOS1AP	9722	NM 014697	nitric oxide synthase 1 (neuronal) adaptor protein	GGUAUGAGUUUAAAAG CCAA	D-013446-02	0.42	0.04	0.40	0.07	0.17	0.10
NOS1AP	9722	NM 014697	nitric oxide synthase 1 (neuronal) adaptor protein	GGUGUAACGUCUUUA AAUC	D-013446-01	1.57	0.51	0.61	0.13	0.41	0.11
NUAK2	81788	NM 030952	NUAK family, SNF1-like kinase, 2	GGUGUCAGCCUCUGCA GAA	D-005374-05	0.76	0.39	0.22	0.21	0.19	0.11
NUAK2	81788	NM 030952	NUAK family, SNF1-like kinase, 2	GCAGGCGACGUGUUU GUGA	D-005374-07	1.38	0.16	0.71	0.16	0.72	0.43
NUAK2	81788	NM 030952	NUAK family, SNF1-like kinase, 2	GCAGAAAGCCUCCGCAA GCU	D-005374-06	0.54	0.07	0.20	0.01	0.14	0.10
NUAK2	81788	NM 030952	NUAK family, SNF1-like kinase, 2	GGACGCGAGCGGACGU GUUU	D-005374-01	1.27	0.73	0.64	0.23	0.53	0.03
ORAOV1	220064	NM 153451	oral cancer overexpressed 1	GAAGAAAGGCGAGUAGU UUGG	D-010374-03	1.74	0.06	1.24	0.06	0.96	0.03
ORAOV1	220064	NM 153451	oral cancer overexpressed 1	GAUUUCCCUUAUGA UGAC	D-010374-01	1.38	0.10	0.36	0.08	0.16	0.08
ORAOV1	220064	NM 153451	oral cancer overexpressed 1	GGUCUGAGAUCCGGGU GCUA	D-010374-04	0.98	0.42	0.09	0.10	0.24	0.26
ORAOV1	220064	NM 153451	oral cancer overexpressed 1	GCAGAAAGGUUCCGGA CUUU	D-010374-02	0.69	0.15	0.70	0.02	0.94	0.24
OSBP	5007	NM 002556	oxysterol binding protein	GAUUAGAGGAGAAUG GGUA	D-009747-05	0.51	0.06	0.57	0.04	0.45	0.02
OSBP	5007	NM 002556	oxysterol binding protein	GAACGAGCCACACUCU UUA	D-009747-04	1.24	0.08	0.16	0.05	0.09	0.09
OSBP	5007	NM 002556	oxysterol binding protein	GCAAUGACUUUAUAG CUA	D-009747-02	1.03	0.31	0.32	0.03	0.17	0.05
OSBP	5007	NM 002556	oxysterol binding protein	GGAGACAAGUGUAAU CUUA	D-009747-01	1.00	0.02	0.58	0.17	0.17	0.09
PARP11	57097	NM 020367	poly (ADP-ribose) polymerase family, member 11	CAUGCGACCUCUCC AAA	D-016115-04	1.05	0.12	0.40	0.04	0.23	0.20
PARP11	57097	NM 020367	poly (ADP-ribose) polymerase family, member 11	GACGGGAGCUAUGUG AAUU	D-016115-03	0.93	0.42	0.15	0.12	0.37	0.09
PARP11	57097	NM 020367	poly (ADP-ribose) polymerase family, member 11	GAGAUUACAUAACG GAGA	D-016115-02	1.33	0.13	0.99	0.19	0.64	0.03

PARP11	57097	NM_020367	poly (ADP-ribose) polymerase family, member 11	UCACAAAAGCAGAAAGA AUUA	D-016115-01	1.68	0.06	1.34	0.06	0.49	0.31
PECR	55825	NM_018441	peroxisomal trans-2-enoyl-CoA reductase	GAGGAUCUAUCGUCA AUUA	D-009855-01	0.48	0.06	0.18	0.20	0.14	0.08
PECR	55825	NM_018441	peroxisomal trans-2-enoyl-CoA reductase	GAAUGGGCCUGCAGU GGAA	D-009855-04	1.53	0.00	0.99	0.22	0.37	0.11
PECR	55825	NM_018441	peroxisomal trans-2-enoyl-CoA reductase	GGACCUUUCUGUUGU CAAA	D-009855-02	1.90	0.24	0.98	0.24	0.64	0.41
PECR	55825	NM_018441	peroxisomal trans-2-enoyl-CoA reductase	AGGAGGAGGUGAAUA AUUU	D-009855-03	0.90	0.04	0.46	0.16	0.10	0.06
PEMT	10400	NM_007169	phosphatidylethanolamine N-methyltransferase	CUCAAGGAGGCGAGA GUGA	D-010392-02	0.85	0.02	0.49	0.04	0.12	0.02
PEMT	10400	NM_007169	phosphatidylethanolamine N-methyltransferase	CCGUGAGAUUCUACCG GCA	D-010392-04	1.02	0.28	0.30	0.15	0.13	0.04
PEMT	10400	NM_007169	phosphatidylethanolamine N-methyltransferase	GAACUUUCCUAGGUG AUUA	D-010392-01	1.62	0.02	0.78	0.05	0.21	0.01
PEMT	10400	NM_007169	phosphatidylethanolamine N-methyltransferase	ACAUAGUGGUCUCUCCU AUA	D-010392-03	1.42	0.18	0.96	0.08	0.22	0.02
PGLYRP4	57115	NM_020393	peptidoglycan recognition protein 4	GGAGACCACUGUCCAG GAU	D-008671-04	0.44	0.05	0.64	0.15	0.55	0.02
PGLYRP4	57115	NM_020393	peptidoglycan recognition protein 4	CGAAGUAUGGCAUCA UUUA	D-008671-03	0.61	0.12	0.34	0.15	0.38	0.11
PGLYRP4	57115	NM_020393	peptidoglycan recognition protein 4	CGACAUUGGUUAUAA CUUC	D-008671-02	0.92	0.27	1.03	0.04	0.60	0.26
PGLYRP4	57115	NM_020393	peptidoglycan recognition protein 4	GCUGUUGGCGUCCAGU AUUC	D-008671-01	1.45	0.18	0.09	0.09	0.04	0.03
PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha	CCACAGGCCUCUCCUA CUU	D-006776-03	0.17	0.04	0.01	0.02	0.03	0.01
PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha	GUGAAGCGAUUGUGGA GUUA	D-006776-02	1.15	0.38	0.19	0.12	0.07	0.01
PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha	GCAGAAAUUUGGCCU GUUU	D-006776-09	1.39	0.17	0.58	0.10	0.40	0.11

P14KA	5297	NM 002650	phosphatidylinositol 4-kinase, catalytic, alpha	GAGCAUCUCUCCCUAC CUA	D-006776-01	0.61	0.19	0.05	0.02	0.04	0.02
PNO1	56902	NM 020143	partner of NOB1 homolog (S. cerevisiae)	GAAAUCAAAGGAAUGU AGAA	D-018033-02	0.95	0.22	0.88	0.09	0.56	0.03
PNO1	56902	NM 020143	partner of NOB1 homolog (S. cerevisiae)	CGAAGAAACGACAGG CUGA	D-018033-04	1.13	0.10	0.31	0.05	0.33	0.13
PNO1	56902	NM 020143	partner of NOB1 homolog (S. cerevisiae)	GCUAACAGAUACACAC CAU	D-018033-03	0.68	0.09	0.31	0.19	0.23	0.19
PNO1	56902	NM 020143	partner of NOB1 homolog (S. cerevisiae)	GGACUUCAGAUACGC UUUU	D-018033-01	0.61	0.07	0.11	0.06	0.31	0.10
POLR2J2	246721	NM 032958	DNA directed RNA polymerase II polypeptide J-related	CAACAAAGAAAGACCAC ACA	D-013602-02	0.50	0.23	0.22	0.26	0.14	0.01
POLR2J2	246721	NM 032958	DNA directed RNA polymerase II polypeptide J-related	GGUACCCAAUGCCUGU UUA	D-013602-03	0.89	0.17	0.62	0.08	0.21	0.16
POLR2J2	246721	NM 032958	DNA directed RNA polymerase II polypeptide J-related	GCGAGAAAGAUACACCA UUA	D-013602-01	0.60	0.28	0.24	0.24	0.17	0.06
POLR2J2	246721	NM 032958	DNA directed RNA polymerase II polypeptide J-related	GGAAACAUCAUUAAA UCAC	D-013602-04	1.17	0.15	1.19	0.14	0.74	0.05
PPIA	5478	NM 021130	peptidylprolyl isomerase A (cyclophilin A)	GCAGACAAAGGUCCCAA AGA	D-004979-04	0.96	0.34	1.23	0.09	0.40	0.05
PPIA	5478	NM 021130	peptidylprolyl isomerase A (cyclophilin A)	AGACAAAGGUCCCAA GACA	D-004979-01	1.15	0.12	0.47	0.01	0.10	0.01
PPIA	5478	NM 021130	peptidylprolyl isomerase A (cyclophilin A)	AGAAUUUAUCCAGGG UUUU	D-004979-03	1.21	0.35	0.51	0.07	0.84	0.32
PPIA	5478	NM 021130	peptidylprolyl isomerase A (cyclophilin A)	GGAAUGGCAAGACCA GCAA	D-004979-02	0.34	0.04	0.37	0.00	0.16	0.11
PPP2R1A	5518	NM 014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	UAGACGAAACUCCGCAA UGA	D-010259-05	1.31	0.45	0.39	0.19	0.22	0.02

PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	GAACAUCUUCUUAAC CUG	D-010259-07	0.84	0.31	0.41	0.07	0.14	0.04
PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	UCUCUAAACCUGGACUG UGU	D-010259-04	2.01	0.07	0.86	0.03	0.95	0.00
PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	AGGCGGAACUUCGAC AGUA	D-010259-06	0.85	0.15	0.22	0.02	0.13	0.04
PPTC7	160760	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)	GGCAACAGAUUGGACU CUUU	D-017008-03	0.85	0.13	0.39	0.13	0.37	0.14
PPTC7	160760	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)	GAAGGACGGUUCGUA CCUA	D-017008-04	0.16	0.01	0.06	0.05	0.09	0.04
PPTC7	160760	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)	GACAUUAUCCUGACG GCAA	D-017008-05	0.67	0.08	0.27	0.05	0.13	0.01
PPTC7	160760	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)	CAACAUGCCUGAUUA UAUG	D-017008-01	0.76	0.14	0.69	0.09	0.58	0.28
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)	GAAUUUGUCCGAGAU GUCA	D-014399-03	0.47	0.17	0.39	0.00	0.24	0.16
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)	GACAAAAGCAGUUCUA AUUC	D-014399-02	0.86	0.06	0.13	0.06	0.14	0.08
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)	CGACAGGACUACAUG GAUG	D-014399-01	0.77	0.30	0.56	0.07	0.46	0.20
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)	AAGAAAGCGCCAGAAG UTUAA	D-014399-04	0.55	0.01	0.41	0.11	0.13	0.09
PROX1	5629	NM_002763	prospero-related homeobox 1	GCAAAAGAUUGUUGAUC CUUC	D-016913-01	0.91	0.34	0.16	0.08	0.08	0.03
PROX1	5629	NM_002763	prospero-related homeobox 1	GACGUAAAAGUUCACAC AGAU	D-016913-02	1.08	0.01	0.21	0.13	0.05	0.00
PROX1	5629	NM_002763	prospero-related homeobox 1	GGAGAAGUACGCACG UCAA	D-016913-04	0.97	0.11	0.16	0.06	0.08	0.06
PROX1	5629	NM_002763	prospero-related homeobox 1	GGCCAAACUCCUUAAC AAC	D-016913-03	1.08	0.07	0.17	0.00	0.14	0.09

PRPF40A	55660	XM 371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	GAUGCUGUCUGGAA GAUA	D-027984-04	0.48	0.07	0.13	0.02	0.16	0.02
PRPF40A	55660	XM 371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	GGAAAGCCUUAUAU	D-027984-03	0.74	0.13	0.44	0.09	0.36	0.07
PRPF40A	55660	XM 371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	GGACAUAAACUCUAGA AUCU	D-027984-01	0.27	0.08	0.12	0.10	0.24	0.07
PRPF40A	55660	XM 371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	GGAAUGAUGUCGUCA GUAA	D-027984-02	0.57	0.25	0.19	0.00	0.18	0.07
PRPSAP2	5636	NM 002767	phosphoribosyl pyrophosphate synthetase-associated protein 2	CCAAUACAAUCCACA UGA	D-006795-02	0.50	0.04	0.20	0.01	0.27	0.10
PRPSAP2	5636	NM 002767	phosphoribosyl pyrophosphate synthetase-associated protein 2	GAAAGAGGUGCAUAU AAGA	D-006795-04	1.46	0.05	1.06	0.04	0.61	0.22
PRPSAP2	5636	NM 002767	phosphoribosyl pyrophosphate synthetase-associated protein 2	GAAAGAUCCAGAU UACA	D-006795-01	0.46	0.18	0.49	0.02	0.36	0.12
PRPSAP2	5636	NM 002767	phosphoribosyl pyrophosphate synthetase-associated protein 2	GAUGGCAACUCAUGG CUUG	D-006795-05	1.04	0.15	0.61	0.03	0.50	0.09
PSME1	5720	NM 176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	GAAAGACCUCUGUACCA AGA	D-012254-01	0.69	0.20	0.39	0.18	0.44	0.01
PSME1	5720	NM 176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	GUGGUGAUGCAGUGA CUA	D-012254-04	0.68	0.03	0.26	0.04	0.04	0.02
PSME1	5720	NM 176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	GCAGAUACCUCGGAU UGAG	D-012254-03	0.87	0.03	0.95	0.06	0.40	0.16

PSME1	5720	NM_176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	GAAGCCAAACUUGAGC AAUC	D-012254-02	1.44	0.21	0.45	0.05	0.37	0.06
PTCD1	26024	NM_015545	pentatricopeptide repeat domain 1	GACCCUCUCUGACAAA UAC	D-021366-04	1.38	0.14	0.64	0.10	0.57	0.09
PTCD1	26024	NM_015545	pentatricopeptide repeat domain 1	AACCAGAGGUGGAUA CUAA	D-021366-01	0.75	0.03	0.08	0.10	0.07	0.05
PTCD1	26024	NM_015545	pentatricopeptide repeat domain 1	GGAUGUGCCUCGGAUG UGUU	D-021366-03	0.74	0.09	0.61	0.29	0.98	0.23
PTCD1	26024	NM_015545	pentatricopeptide repeat domain 1	GAACUACACCUAUCUC AUC	D-021366-02	0.76	0.17	0.49	0.05	0.35	0.18
PTHR1	5745	NM_000316	parathyroid hormone receptor 1	CGUCAUGACUAAAAGA GGAA	D-005717-04	0.78	0.33	0.72	0.58	0.55	0.46
PTHR1	5745	NM_000316	parathyroid hormone receptor 1	GGGAAGCCCGAGGAAA GAUA	D-005717-03	0.64	0.16	0.16	0.10	0.02	0.01
PTHR1	5745	NM_000316	parathyroid hormone receptor 1	GCAAUCAUAUACUGU UUCU	D-005717-02	0.82	0.12	0.43	0.00	0.23	0.03
PTHR1	5745	NM_000316	parathyroid hormone receptor 1	CAGCGAGUGUGUCAA AUUU	D-005717-01	1.07	0.55	0.48	0.09	0.15	0.07
RAB10	10890	NM_016131	RAB10, member RAS oncogene family	GCAAGGGAGCAUGGU AUUA	D-010823-04	0.98	0.73	0.11	0.02	0.16	0.15
RAB10	10890	NM_016131	RAB10, member RAS oncogene family	GGAAUAGACUUAAG AUCA	D-010823-02	0.49	0.09	0.31	0.06	0.39	0.14
RAB10	10890	NM_016131	RAB10, member RAS oncogene family	CAAUGAAGAUUGGGA AAGA	D-010823-03	0.32	0.03	0.31	0.25	0.12	0.03
RAB10	10890	NM_016131	RAB10, member RAS oncogene family	GAAAGAAAGAUCAAAG UACA	D-010823-01	0.13	0.02	0.13	0.07	0.12	0.05
RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family	GGAGUAGAGUUUGCA ACAA	D-004726-06	0.78	0.13	0.37	0.28	0.19	0.12
RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family	GCAACAAUGUGGUUC CUUU	D-004726-02	1.11	0.25	0.36	0.12	0.19	0.11
RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family	CAAGAGCGAUUAUCGA GCUA	D-004726-03	1.14	0.17	0.68	0.03	0.86	0.04
RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family	GUAGGUGCCUUAUUG GUUU	D-004726-01	1.53	0.29	0.78	0.29	0.98	0.39
RABEPK	10244	NM_005833	Rab9 effector protein with kelch motifs	GGAAAUCGAAAUAUUG CUAC	D-019457-04	0.61	0.03	0.55	0.05	0.47	0.01

RABPK	10244	NM_005833	Rab9 effector protein with kelch motifs	GGAUUCAGCUGACAAAGUA	D-019457-02	0.55	0.13	0.18	0.02	0.24	0.05
RABPK	10244	NM_005833	Rab9 effector protein with kelch motifs	CCACAGCUGUUCUAUUA	D-019457-01	1.26	0.37	0.97	0.15	0.54	0.18
RABPK	10244	NM_005833	Rab9 effector protein with kelch motifs	GAAACACGCUAUUAUGUCUU	D-019457-03	0.51	0.11	0.47	0.10	0.13	0.07
RAC1	5879	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	AGACGGAGCUGUAGGUAAA	D-003560-05	0.56	0.20	0.22	0.20	0.31	0.29
			ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	UAAAGACACGAUCGAGAAA	D-003560-08	0.96	0.12	0.71	0.30	0.68	0.46
RAC1	5879	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	UAAAGGAGAUUGGUGUGUA	D-003560-07	0.81	0.35	0.33	0.14	0.30	0.03
			ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	CGGCACCACUGUCCCCACA	D-003560-09	1.90	0.40	0.56	0.00	0.24	0.01
RBM22	55696	NM_018047	RNA binding motif protein 22	UGCCAAAACCCUGCAGUA	D-021186-03	1.56	0.15	1.52	0.37	0.69	0.68
RBM22	55696	NM_018047	RNA binding motif protein 22	CAACAAAGAGUACUAUACA	D-021186-02	0.97	0.01	0.51	0.10	0.36	0.15
RBM22	55696	NM_018047	RNA binding motif protein 22	CCAUUAUACCGAAUUGACCA	D-021186-04	0.57	0.01	0.42	0.04	0.15	0.01
RBM22	55696	NM_018047	RNA binding motif protein 22	GUAAUUGGCCGCAGACUGA	D-021186-01	0.80	0.05	0.21	0.12	0.24	0.01
RBM9	23543	NM_014309	RNA binding motif protein 9	AUAUGCAAAUUGGUUGGAAA	D-020616-04	1.03	0.39	0.37	0.14	0.31	0.02
RBM9	23543	NM_014309	RNA binding motif protein 9	CCGCUUACAGUGACGGUUA	D-020616-02	1.82	0.11	0.94	0.24	0.51	0.17
RBM9	23543	NM_014309	RNA binding motif protein 9	GACAGUAUAUUGGUGCAGUC	D-020616-01	0.61	0.01	0.19	0.01	0.12	0.03
RBM9	23543	NM_014309	RNA binding motif protein 9	CGAGAAUAGUGCUGAUGCA	D-020616-03	1.13	0.01	0.77	0.17	0.41	0.15

Rgr	266747	NM_153615	Ral-GDS related protein Rgr	GGACAGCACUGAUGG CUUA	D-008607-01	1.33	0.11	0.45	0.26	0.38	0.03
Rgr	266747	NM_153615	Ral-GDS related protein Rgr	GGAUAAAGCUGGCCU UCAG	D-008607-03	0.79	0.06	0.10	0.04	0.27	0.03
Rgr	266747	NM_153615	Ral-GDS related protein Rgr	ACACUUCAGUUUACU AUC	D-008607-04	0.51	0.10	0.09	0.08	0.13	0.09
Rgr	266747	NM_153615	Ral-GDS related protein Rgr	GCACAUAGGCACCCACA GUU	D-008607-02	0.50	0.55	0.62	0.66	0.66	0.87
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2	GGAAUUUAUCUCUGAA CAUA	D-003602-01	1.26	0.09	0.38	0.15	0.08	0.04
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2	GCACGUUAUGAUCUCUC UAA	D-003602-04	0.67	0.17	0.21	0.06	0.11	0.03
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2	GAAAGGAUGUCUUAA GAGA	D-003602-02	1.95	0.34	1.36	0.06	1.06	0.37
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2	GGACAUAGCACCUGUU AUUA	D-003602-03	1.17	0.20	0.70	0.03	0.43	0.03
RNF207	388591	NM_207396	ring finger protein 207	UGGCAUAGAAAGCAGC UACA	D-032070-04	0.37	0.15	0.11	0.06	0.12	0.03
RNF207	388591	NM_207396	ring finger protein 207	CGUGUCUUCUGGACU GUUU	D-032070-03	1.09	0.05	0.23	0.04	0.32	0.01
RNF207	388591	NM_207396	ring finger protein 207	CAGCAUGUCUUCAGAGGAC	D-032070-02	0.83	0.20	0.99	0.25	1.59	0.74
RNF207	388591	NM_207396	ring finger protein 207	GAGCAGAGGGUACCC GGUU	D-032070-01	0.69	0.08	0.08	0.04	0.06	0.03
RNF31	55072	NM_017999	ring finger protein 31	GCGAUUAUUAUGGCUA CACA	D-021419-02	0.71	0.11	0.23	0.13	0.41	0.31
RNF31	55072	NM_017999	ring finger protein 31	GGCGUGGUGUCAAGU UUA	D-021419-04	1.08	0.01	0.37	0.08	0.10	0.03
RNF31	55072	NM_017999	ring finger protein 31	AGUCAAGUCUGGUAC UGUA	D-021419-03	1.52	0.01	0.40	0.01	0.41	0.04
RNF31	55072	NM_017999	ring finger protein 31	GCAGAAUACUCAUCCA AGA	D-021419-01	1.09	0.37	0.51	0.07	0.25	0.04
ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2	GCAACUGGCUCGUUCA AUU	D-004610-03	1.34	0.48	0.42	0.19	0.14	0.07
ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2	GAGGAAAGCUGAUAU UGAA	D-004610-01	1.41	0.01	0.45	0.01	0.32	0.15

ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2	GUAGAAACCUUCCCAAUUC	D-004610-02	1.42	0.15	0.20	0.10	0.15	0.06
ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2	GCAAAUCUGUUAUAUCUG	D-004610-05	0.81	0.13	0.17	0.01	0.20	0.13
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1	GGACUUUCCGAAACCUUCU	D-005372-04	0.82	0.32	0.17	0.01	0.21	0.11
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1	GCUGUGAAGCUGAAAAUUA	D-005372-03	1.24	0.03	0.40	0.14	0.19	0.19
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1	GAGCGAGGACUCCAUUCUUC	D-005372-02	0.57	0.22	0.33	0.04	0.37	0.01
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1	GGGAGUGCCUGACAU GACA	D-005372-01	0.62	0.06	0.10	0.07	0.07	0.04
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1	GGAUUCGUGGUGACGUUUA	D-016937-01	1.05	0.04	0.71	0.06	0.64	0.03
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1	CAGGGAAGAUCUAUUAACAU	D-016937-02	1.35	0.09	0.20	0.04	0.39	0.04
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1	GAACGUGGCCUUGUACACA	D-016937-03	1.23	0.23	0.56	0.17	1.03	0.24
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1	GCUCUCAGACUGCUACCUA	D-016937-04	1.18	0.36	0.48	0.07	0.04	0.01
SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	GGAAACAUCGAGUCA GAUC	D-007380-08	1.10	0.26	0.52	0.14	0.12	0.03
SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	UCAAUGAUCUGCUACACGU	D-007380-07	2.13	0.03	0.86	0.34	0.71	0.16
SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	GCAAGCACCUCUCCAGAGAG	D-007380-06	0.43	0.08	0.21	0.06	0.28	0.13

SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	GCACGGCCAUGCAUCAA	D-007380-05	0.57	0.04	0.35	0.05	0.05	0.00
SLC6A8	6535	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	GAAGAAAGAGCGCCGA GAAC	D-007608-06	0.49	0.36	0.25	0.17	0.39	0.29
SLC6A8	6535	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	GGAAGAAGUCGUGUAC UUCA	D-007608-01	1.11	0.06	0.78	0.07	0.40	0.08
SLC6A8	6535	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	GCGGAGGUGUGUCC UUAU	D-007608-05	0.96	0.14	0.19	0.04	0.07	0.04
SLC6A8	6535	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	CAACACCUACUACAUC AUG	D-007608-02	0.99	0.04	1.00	0.06	0.50	0.12
SMAD5	4090	NM_005903	SMAD family member 5	GAUCAGAUGGGUCAA GAUA	D-015791-03	1.06	0.18	0.60	0.10	0.46	0.15
SMAD5	4090	NM_005903	SMAD family member 5	AGUCUUACCUCCAGUA UUA	D-015791-02	1.10	0.15	0.06	0.01	0.06	0.04
SMAD5	4090	NM_005903	SMAD family member 5	UCACAGAUCCUUCAAA UAA	D-015791-01	1.30	0.09	0.82	0.08	0.54	0.07
SMAD5	4090	NM_005903	SMAD family member 5	GAGUAAAUGUGUCAC UAUU	D-015791-04	0.97	0.04	0.49	0.20	0.39	0.13
SMAD6	4091	NM_005585	SMAD family member 6	GCUACCAACUCCCUCA UCA	D-015362-01	1.09	0.45	0.17	0.10	0.29	0.14
SMAD6	4091	NM_005585	SMAD family member 6	GACCAGGCCGUCAGCA UCU	D-015362-03	0.68	0.30	0.54	0.26	0.52	0.17
SMAD6	4091	NM_005585	SMAD family member 6	GUGCGGCGACUUUGG CGAA	D-015362-04	1.67	0.28	0.75	0.16	0.88	0.17
SMAD6	4091	NM_005585	SMAD family member 6	CCACAUUGUCUUACAC UGA	D-015362-02	1.73	0.23	0.47	0.08	0.37	0.11
SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	UCAGUGCUCUGGACA GUAA	D-009459-01	1.32	0.07	0.37	0.20	0.09	0.01

SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	UGACAAAGGAAUACAU CAAU	D-009459-03	0.64	0.07	0.15	0.05	0.07	0.04
SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	GAAGAAAGACGGCGUG CUAU	D-009459-05	1.66	0.31	0.65	0.22	0.25	0.00
SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	UAAACACGACUCAA UCCA	D-009459-02	1.22	0.38	0.59	0.16	0.32	0.12
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1	GGACUGCAGAGGACU GUUA	D-007191-04	1.19	0.01	0.24	0.08	0.39	0.06
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1	GGAAGAAAGGUUUGGA UUAC	D-007191-03	0.49	0.17	0.24	0.08	0.26	0.11
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1	GCACUAUGAUCUAUA UGUU	D-007191-01	0.64	0.03	0.49	0.02	0.24	0.16
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1	AAAGAGAUCUAGUCC AGAA	D-007191-02	0.25	0.10	0.28	0.02	0.14	0.04
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2	GACCAUACCUUCUGUG UUG	D-007194-02	1.29	0.11	0.84	0.22	0.89	0.58
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2	GAACAACACAAUUUA CAGA	D-007194-04	1.62	0.28	0.77	0.12	0.86	0.49
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2	GAUGAGAACACUCCA AUUA	D-007194-01	0.94	0.04	0.40	0.08	0.10	0.10
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2	CAAGUGGAAUCAGC AUUA	D-007194-03	0.83	0.21	0.38	0.18	0.18	0.09

SPDEF	25803	NM_012391	SAM pointed domain containing ets transcription factor	UUAGGUGGCUCAACA AGGA	D-020199- 02	1.52	0.03	1.08	0.12	0.66	0.14
SPDEF	25803	NM_012391	SAM pointed domain containing ets transcription factor	GCUCCAUCCGCCAGUA UUA	D-020199- 04	1.04	0.10	0.59	0.19	0.78	0.06
SPDEF	25803	NM_012391	SAM pointed domain containing ets transcription factor	GAGGAGAGCUGGACC GACA	D-020199- 01	1.28	0.01	0.43	0.18	0.40	0.03
SPDEF	25803	NM_012391	SAM pointed domain containing ets transcription factor	GCGAAGUGCUCAAAG ACAU	D-020199- 03	1.68	0.54	0.10	0.04	0.11	0.03
SRFBP1	153443	NM_152546	serum response factor binding protein 1	GGAAUUGAAACCUGA CAUA	D-015445- 03	0.54	0.28	0.13	0.05	0.32	0.37
SRFBP1	153443	NM_152546	serum response factor binding protein 1	GCGAAGAAACCAUA CAUA	D-015445- 02	1.01	0.06	0.82	0.05	0.50	0.11
SRFBP1	153443	NM_152546	serum response factor binding protein 1	GAAAGAGAAUUCGAGU UUUA	D-015445- 01	1.55	0.43	0.43	0.19	0.30	0.20
SRFBP1	153443	NM_152546	serum response factor binding protein 1	CUAAAAGCAGUGACUA UUGC	D-015445- 04	0.69	0.00	0.32	0.10	0.38	0.07
STMN2	11075	NM_007029	stathmin-like 2	GAGAGGGAAACACGA GCGA	D-019342- 03	0.94	0.01	0.22	0.06	0.42	0.04
STMN2	11075	NM_007029	stathmin-like 2	CAACAAACGUGCCUCU GGC	D-019342- 04	1.37	0.26	0.60	0.02	1.01	0.00
STMN2	11075	NM_007029	stathmin-like 2	GAGCUGAUCUUGAAG CCAC	D-019342- 02	0.42	0.19	0.34	0.08	0.16	0.01
STMN2	11075	NM_007029	stathmin-like 2	CAACAUCUAUACUAC GAU	D-019342- 01	1.42	0.48	0.86	0.29	0.75	0.18
STX2	2054	NM_001980	syntaxin 2	GAGGAGAUUAGAAAC AGUA	D-021379- 03	0.96	0.02	0.36	0.01	0.15	0.13
STX2	2054	NM_001980	syntaxin 2	GUUAAAAGGCUAUUGA ACAA	D-021379- 01	2.19	0.54	0.74	0.22	0.45	0.05
STX2	2054	NM_001980	syntaxin 2	CACCAAAACCCGGAAGG AAA	D-021379- 04	1.18	0.00	0.41	0.05	0.35	0.13
STX2	2054	NM_001980	syntaxin 2	GAAAUCGAGUCACGU CACA	D-021379- 02	0.89	0.12	0.53	0.27	0.58	0.05
SURF1	6834	NM_003172	surfeit 1	GCGCAGAGCCCAUCUU CAU	D-011786- 06	1.20	0.16	0.54	0.03	0.55	0.02
SURF1	6834	NM_003172	surfeit 1	GAACCUGAUUGCAGA GUUG	D-011786- 05	0.49	0.10	0.30	0.13	0.13	0.02
SURF1	6834	NM_003172	surfeit 1	GAGCUAUGGCCAGA AUA	D-011786- 04	0.60	0.06	0.32	0.00	0.33	0.20

SURF1	6834	NM_003172	surfeit 1	CAUCCUACCUGUGGUU UAA	D-011786- 02	0.85	0.02	0.58	0.11	0.58	0.25
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)	GAGGAGAAUUGCUA CUUA	D-013366- 01	1.22	0.11	0.29	0.08	0.10	0.02
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)	UAGCAAAUUAUGGACU CAGA	D-013366- 04	1.18	0.06	0.80	0.03	0.83	0.12
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)	GAGGCAAGUUGUCUA AUGA	D-013366- 02	1.45	0.02	0.53	0.07	0.24	0.01
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)	GAGAGGAGGUCGAAC AGAU	D-013366- 03	1.12	0.23	0.36	0.27	0.22	0.13
SUZ12	23512	NM_015355	suppressor of zeste 12 homolog (Drosophila)	GAACACCUAUCACACA UAU	D-006957- 01	1.07	0.48	0.41	0.14	0.36	0.21
SUZ12	23512	NM_015355	suppressor of zeste 12 homolog (Drosophila)	GAUUUAUUGUCGAAA CUUC	D-006957- 04	1.53	0.16	0.49	0.01	0.19	0.04
SUZ12	23512	NM_015355	suppressor of zeste 12 homolog (Drosophila)	GCAACAAACUGAAAGC AAGA	D-006957- 02	1.09	0.28	0.22	0.02	0.08	0.06
SUZ12	23512	NM_015355	suppressor of zeste 12 homolog (Drosophila)	GAACAGCAAAAGAAACA UAUA	D-006957- 03	1.81	0.29	0.49	0.18	0.27	0.05
TCOF1	6949	NM_000356	Treacher Collins- Franceschetti syndrome 1	AACCAAAAGAUUCUGA GUCA	D-012550- 02	0.53	0.06	0.35	0.09	0.33	0.03
TCOF1	6949	NM_000356	Treacher Collins- Franceschetti syndrome 1	GCAGAGGAUUCUUA AGCA	D-012550- 03	0.68	0.20	0.18	0.02	0.16	0.15
TCOF1	6949	NM_000356	Treacher Collins- Franceschetti syndrome 1	GAGGAGGACUCAAGA AGCA	D-012550- 01	0.40	0.12	0.12	0.09	0.04	0.01
TCOF1	6949	NM_000356	Treacher Collins- Franceschetti syndrome 1	CAAGGAGUCCAGUCG GAUA	D-012550- 04	1.13	0.44	0.35	0.07	0.28	0.16
TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	UAGAAAGACCCGGGUA UUAA	D-006348- 05	1.59	0.17	0.19	0.02	0.15	0.16

TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	CCAAAGCAGUAGCUG AAUU	D-006348- 03	0.57	0.06	0.59	0.12	0.43	0.17
TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	GGAAAUUGACGGUA AUUU	D-006348- 01	1.16	0.13	0.57	0.09	0.87	0.04
TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	GUAGAAAGACCCGGU AUUA	D-006348- 02	1.64	0.29	0.15	0.02	0.32	0.00
TM6SF2	53345	NM_0010015 24	transmembrane 6 superfamily member 2	GAUGAGCGCCCUAAUC CUG	D-032313- 03	1.36	0.13	0.66	0.40	0.68	0.23
TM6SF2	53345	NM_0010015 24	transmembrane 6 superfamily member 2	GGAUGGCACUGUUA CUAC	D-032313- 02	0.63	0.30	0.42	0.16	0.25	0.03
TM6SF2	53345	NM_0010015 24	transmembrane 6 superfamily member 2	GCACAGUUCUCGCACA UGG	D-032313- 01	0.57	0.12	0.14	0.04	0.29	0.01
TM6SF2	53345	NM_0010015 24	transmembrane 6 superfamily member 2	GGAAGAGAUACCGGA AUUU	D-032313- 04	0.26	0.01	0.05	0.04	0.11	0.09
TMEM142A	84876	NM_032790	transmembrane protein 142A	GCACCUUUUUGCGCUC AUG	D-014998- 04	0.59	0.14	0.19	0.09	0.39	0.06
TMEM142A	84876	NM_032790	transmembrane protein 142A	GGCCUGAUCUUUAUC GUCU	D-014998- 02	0.98	0.42	0.72	0.31	0.35	0.06
TMEM142A	84876	NM_032790	transmembrane protein 142A	UGAGCAACGUGCACA AUCU	D-014998- 03	0.53	0.27	0.04	0.05	0.27	0.33
TMEM142A	84876	NM_032790	transmembrane protein 142A	GCUCACUGGUUAGCCA UAA	D-014998- 01	0.91	0.05	0.56	0.08	0.85	0.52
TOP1	7150	NM_003286	topoisomerase (DNA) I	GAAGAAAGGCUUUA GAGA	D-005278- 02	1.10	0.27	0.50	0.11	0.30	0.15
TOP1	7150	NM_003286	topoisomerase (DNA) I	ACAUAAAAGGUCCAGU AUUU	D-005278- 04	0.58	0.16	0.04	0.01	0.04	0.01
TOP1	7150	NM_003286	topoisomerase (DNA) I	GAAAGGAAAUAGACUA AUGA	D-005278- 01	1.27	0.05	0.52	0.29	0.47	0.06
TOP1	7150	NM_003286	topoisomerase (DNA) I	GGAAAGUAGCUACGUU CUUU	D-005278- 03	0.31	0.05	0.34	0.07	0.24	0.02
TPM4	7171	NM_003290	tropomyosin 4	GGAUCAGACACUAAA CGAA	D-019753- 04	1.20	0.05	0.43	0.11	0.30	0.18
TPM4	7171	NM_003290	tropomyosin 4	GAAACGUGGCUUACA UCAG	D-019753- 03	0.71	0.03	0.27	0.08	0.17	0.02
TPM4	7171	NM_003290	tropomyosin 4	GCGGAGGUGUCUGAA CUAA	D-019753- 02	0.87	0.21	0.48	0.04	0.04	0.05

TPM4	7171	NM_003290	tropomyosin 4	CCAAGCACAUUGCGGA AGA	D-019753- 01	1.69	0.08	0.73	0.07	1.04	0.23
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5	GCGGUUGUCUUCUGU CAA	D-024079- 04	1.36	0.15	0.80	0.04	0.83	0.22
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5	GAACAGCACGCUAAC UGC	D-024079- 03	0.91	0.04	0.27	0.01	0.34	0.04
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5	GCACCAGCUCUAGAU CAA	D-024079- 01	0.75	0.29	0.23	0.09	0.38	0.17
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5	GCGGCACCUUCUACA UCA	D-024079- 02	0.80	0.16	0.32	0.08	0.35	0.02
TRIM42	287015	NM_152616	tripartite motif- containing 42	CAGAAUACGUGUUUA AAGU	D-007173- 04	1.85	0.05	1.18	0.02	0.76	0.27
TRIM42	287015	NM_152616	tripartite motif- containing 42	CCAAUGAUCCCAACUG UAA	D-007173- 02	0.48	0.15	0.22	0.00	0.04	0.01
TRIM42	287015	NM_152616	tripartite motif- containing 42	GCAAUACCAUCAUCAC UUU	D-007173- 01	0.67	0.11	0.65	0.23	0.55	0.04
TRIM42	287015	NM_152616	tripartite motif- containing 42	CAAGUUCUCUUUCCAC AAU	D-007173- 03	0.78	0.22	0.26	0.06	0.19	0.10
TRIM62	55223	NM_018207	tripartite motif- containing 62	UCGGACGACUGCACCA UUG	D-007010- 03	1.01	0.18	0.03	0.00	0.07	0.07
TRIM62	55223	NM_018207	tripartite motif- containing 62	GAUCAACACCGUCCUC AUC	D-007010- 02	1.33	0.15	0.44	0.11	0.19	0.01
TRIM62	55223	NM_018207	tripartite motif- containing 62	CUACAAUGCUGAUGA CAUG	D-007010- 01	1.08	0.09	0.56	0.07	0.95	0.18
TRIM62	55223	NM_018207	tripartite motif- containing 62	CGCCAAAAGCGCUUCGA UGU	D-007010- 04	1.38	0.24	1.14	0.07	1.27	0.06
TRRAP	8295	NM_003496	transformation/transcri ption domain- associated protein	GAACAGGCGUGGUUAU GCAA	D-005394- 05	0.55	0.39	0.31	0.18	0.10	0.09
TRRAP	8295	NM_003496	transformation/transcri ption domain- associated protein	CAAUGUAGCUCUGGA UAUA	D-005394- 03	0.59	0.06	0.62	0.13	0.27	0.02
TRRAP	8295	NM_003496	transformation/transcri ption domain- associated protein	GGACUUAAACUGGAGA GGUU	D-005394- 01	0.71	0.27	0.46	0.01	0.12	0.03
TRRAP	8295	NM_003496	transformation/transcri ption domain- associated protein	GAAAGGAGCUUCUGA UUGC	D-005394- 02	0.42	0.11	0.09	0.06	0.27	0.15
TTTY5	83863	NM_031926	testis-specific transcript, Y-linked 5	CUACGUGGCUUAGUG GUAA	D-014755- 02	0.98	0.25	0.94	0.27	1.77	0.56
TTTY5	83863	NM_031926	testis-specific transcript, Y-linked 5	GGUGUCACUGGCCU GUUA	D-014755- 01	0.67	0.17	0.48	0.12	0.26	0.04
TTTY5	83863	NM_031926	testis-specific transcript, Y-linked 5	GCACCUAGCAGCACUGG AAU	D-014755- 04	1.06	0.08	0.50	0.04	0.23	0.14

TTTTY5	83863	NM_031926	testis-specific transcript, Y-linked 5	GGACCCACAUGCUGUC GUC	D-014755-03	1.74	0.08	0.85	0.04	0.59	0.05
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyl y 3; Saethre-Chotzen syndrome) (Drosophila)	GAGCAAGAUUCAGAC CCUC	D-006434-06	0.60	0.31	0.43		0.32	0.32
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyl y 3; Saethre-Chotzen syndrome) (Drosophila)	GCGACGAGCUGGACUC CAA	D-006434-01	0.45	0.01	0.11	0.05	0.08	0.09
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyl y 3; Saethre-Chotzen syndrome) (Drosophila)	CUGCAGACGCAGCGGG UCA	D-006434-02	0.72	0.01	0.22	0.14	0.14	0.13
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyl y 3; Saethre-Chotzen syndrome) (Drosophila)	GGAGUCCGCAGUCUU ACGA	D-006434-05	0.68	0.04	0.33	0.08	0.27	0.03
UBA52	7311	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1	GCUGUCAACUGCCGCA AGA	D-011794-01	0.64	0.05	0.16	0.08	0.17	0.01
UBA52	7311	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1	CAAGUGCUAUGCUCGC CUU	D-011794-04	0.29	0.06	0.09	0.04	0.03	0.01
UBA52	7311	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1	GACCAGCAGCGUCUGA UAU	D-011794-03	0.52	0.02	0.16	0.16	0.15	0.19
UBA52	7311	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1	CCUGCGAGGUGGCAU UAUU	D-011794-02	2.55	0.32	1.32	0.14	1.39	0.72
USP11	8237	NM_004651	ubiquitin specific peptidase 11	GGCAAAUUCACACU GUU	D-006063-01	0.5	0.03	0.25	0.05	No Data	
USP11	8237	NM_004651	ubiquitin specific peptidase 11	GAACAAGGUUGGCCA UUUU	D-006063-02	0.5	0.06	0.46	0.13	No Data	
USP11	8237	NM_004651	ubiquitin specific peptidase 11	GAUGAUUUCUUCGUC UAUG	D-006063-03	0.7	0.04	0.67	0.19	No Data	
USP11	8237	NM_004651	ubiquitin specific peptidase 11	GAGAAACACUGGUUAU AAGC	D-006063-04	1.3	0.01	1.27	0.03	No Data	
USP42	84132	XM_166526	ubiquitin specific peptidase 42	GUUAAUAGGUCCUCA GUGA	D-006089-03	0.50	0.14	0.13	0.09	0.17	0.00

USP42	84132	XM 166526	ubiquitin specific peptidase 42	UGACAAAAGCUUCUGA AUCU	D-006089- 01	1.83	0.15	0.82	0.25	0.82	0.19
USP42	84132	XM 166526	ubiquitin specific peptidase 42	UUAGAGACCUUCAGG CUUA	D-006089- 02	1.10	0.05	0.47	0.17	0.30	0.10
USP42	84132	XM 166526	ubiquitin specific peptidase 42	CAACCUAACCUUCAUA GUA	D-006089- 04	0.73	0.32	0.67	0.10	0.27	0.19
USP51	158880	NM 201286	ubiquitin specific peptidase 51	AAACAAAAGCAGCACCA UUU	D-032247- 02	1.24	0.36	0.47	0.02	0.11	0.01
USP51	158880	NM 201286	ubiquitin specific peptidase 51	GAGCAGGGAUGACCA CAUA	D-032247- 01	1.16	0.43	0.52	0.36	0.57	0.04
USP51	158880	NM 201286	ubiquitin specific peptidase 51	GGGAAAAGAUUAUA CCUU	D-032247- 03	0.41	0.17	0.11	0.03	0.12	0.14
USP51	158880	NM 201286	ubiquitin specific peptidase 51	GCUUUAAGGUAAGGUA AGAA	D-032247- 04	1.17	0.01	0.43	0.01	0.36	0.03
VAMP1	6843	NM 014231	vesicle-associated membrane protein 1 (synaptobrevin 1)	CUCCUAAACAUGACCAG UAA	D-012497- 01	1.35	0.23	1.12	0.02	0.12	0.04
VAMP1	6843	NM 014231	vesicle-associated membrane protein 1 (synaptobrevin 1)	CAUCACAAUUUUGAGA GCAG	D-012497- 02	0.80	0.28	0.43	0.09	0.23	0.22
VAMP1	6843	NM 014231	vesicle-associated membrane protein 1 (synaptobrevin 1)	AGGCACAAAGUGGAGG AGGU	D-012497- 04	0.79	0.21	0.44	0.13	0.33	0.06
VAMP1	6843	NM 014231	vesicle-associated membrane protein 1 (synaptobrevin 1)	CCAUCUAGUGUGGUAG UUUU	D-012497- 03	1.50	0.06	1.33	0.01	0.55	0.14
WDR37	22884	NM 014023	WD repeat domain 37	GCACGGACUCUGCCAU UAA	D-020390- 02	1.07	0.17	0.29	0.02	0.30	0.06
WDR37	22884	NM 014023	WD repeat domain 37	GAAUUGGACACUCUU AAUG	D-020390- 01	1.08	0.56	1.05	0.23	0.61	0.01
WDR37	22884	NM 014023	WD repeat domain 37	GAGAUACAGACUGCUC AUUU	D-020390- 03	0.53	0.05	0.20	0.05	0.32	0.33
WDR37	22884	NM 014023	WD repeat domain 37	GCGCAAAUCCCAUAGC CUU	D-020390- 04	0.43	0.27	0.13	0.16	0.22	0.11
WDR43	23160	XM 087089	WD repeat domain 43	CGAUGAACCCUGUCUA UAUU	D-022651- 03	0.89	0.28	0.13	0.10	0.09	0.01
WDR43	23160	XM 087089	WD repeat domain 43	ACGAAUAGCUUUCCA GUUC	D-022651- 04	1.03	0.17	0.63	0.02	0.49	0.01
WDR43	23160	XM 087089	WD repeat domain 43	CCUCAUAUGUGUUUA GUAA	D-022651- 02	0.25	0.02	0.05	0.02	0.04	0.01
WDR43	23160	XM 087089	WD repeat domain 43	GUACAUGACCGGUUA CUUA	D-022651- 01	0.67	0.18	0.14	0.04	0.10	0.04
WIF1	11197	NM 007191	WNT inhibitory factor 1	UGAAGAAGAUAUCCU GAUU	D-012386- 04	0.74	0.12	0.31	0.09	0.19	0.11

WIF1	11197	NM_007191	WNT inhibitory factor 1	GUACGAAGCCAGCCUC AUA	D-012386-03	1.11	0.10	0.24	0.07	0.09	0.00
WIF1	11197	NM_007191	WNT inhibitory factor 1	GCACAGCCUUCACUU AAA	D-012386-02	0.65	0.11	0.35	0.19	0.10	0.02
WIF1	11197	NM_007191	WNT inhibitory factor 1	GGAGGUAAAUGCAUU GGUA	D-012386-01	1.22	0.06	0.43	0.07	0.36	0.09
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1	GGACAAAACCCCAUGA ACA	D-016083-02	1.06	0.07	0.38	0.08	0.22	0.06
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1	AGGAACAAAACGUUGA CUUA	D-016083-03	0.85	0.29	0.54	0.04	0.43	0.20
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1	AAGCCUAGCUCGUGGC GGA	D-016083-04	0.98	0.06	0.83	0.00	0.45	0.01
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1	GACAUGAGAUCCAUCA	D-016083-01	1.00	0.10	0.35	0.23	0.30	0.14
XBPI	7494	NM_005080	X-box binding protein 1	GGUAUUGACUCUUA GAUU	D-009552-01	0.93	0.15	0.35	0.08	0.11	0.01
XBPI	7494	NM_005080	X-box binding protein 1	CAACUUGGACCCAGUC AUG	D-009552-03	1.35	0.31	0.46	0.12	0.36	0.01
XBPI	7494	NM_005080	X-box binding protein 1	GCAAGUGGUAGAUUU AGAA	D-009552-06	1.39	0.05	0.74	0.13	0.23	0.07
XBPI	7494	NM_005080	X-box binding protein 1	CGAAAGAAAGGCUCGA AUGA	D-009552-02	1.21	0.17	0.70	0.07	0.66	0.22
XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	GUGAGUAUAUUGCUC CAUG	D-006101-06	1.14	0.00	1.03	0.26	0.60	0.01
XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	GGAGCACAAUCCAGU AUUU	D-006101-04	1.36	0.28	0.09	0.03	0.06	0.02
XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	CUUCAGAGCUGCUUCG GCA	D-006101-07	1.16	0.39	0.26	0.10	0.28	0.06

XPNEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	CCAAAGCUGUGAAGA AUUC	D-006101- 05	0.18	0.19	0.16	0.22	0.14	0.11
ZEB1	6935	NM_030751	zinc finger E-box binding homeobox 1	AAACUGAACCCUGUGG AUUA	D-006564- 04	0.43	0.17	0.59	0.04	0.53	0.12
ZEB1	6935	NM_030751	zinc finger E-box binding homeobox 1	GAUAGCACUUGUCUU CUGU	D-006564- 05	1.35	0.33	0.53	0.04	0.61	0.25
ZEB1	6935	NM_030751	zinc finger E-box binding homeobox 1	GAAGCAGGAUGUACA GUAA	D-006564- 03	1.22	0.03	0.39	0.09	0.50	0.12
ZEB1	6935	NM_030751	zinc finger E-box binding homeobox 1	GAACACCCUUGAAAG UGA	D-006564- 02	1.51	0.35	0.32	0.04	0.32	0.03
ZNF148	7707	NM_021964	zinc finger protein 148	GCACUGCAAUUGCUGCC UUU	D-012658- 03	0.18	0.11	0.28	0.11	0.28	0.28
ZNF148	7707	NM_021964	zinc finger protein 148	UGGAAUAGCUACUCA AUUU	D-012658- 02	0.86	0.12	0.26	0.07	0.05	0.04
ZNF148	7707	NM_021964	zinc finger protein 148	GGACUACAGUAUGCA CUUA	D-012658- 04	0.70	0.26	0.15	0.09	0.07	0.02
ZNF148	7707	NM_021964	zinc finger protein 148	GAACAGAUCCUGUAU UGAA	D-012658- 01	1.00	0.00	0.35	0.14	0.17	0.07
ZNF346	23567	NM_012279	zinc finger protein 346	CGAAGAAAGCUAGACU CAGA	D-012450- 01	1.61	0.01	0.96	0.20	0.79	0.13
ZNF346	23567	NM_012279	zinc finger protein 346	GAAGAGAUACCUAGC AAUC	D-012450- 02	0.62	0.01	0.21	0.08	0.12	0.09
ZNF346	23567	NM_012279	zinc finger protein 346	GGCCUUGCUUAUUUC UGA	D-012450- 03	1.30	0.22	0.93	0.27	1.00	0.03
ZNF346	23567	NM_012279	zinc finger protein 346	AGACCAAGCUCAAACU AAU	D-012450- 04	1.43	0.04	0.04	0.02	0.07	0.06
ZNF467	168544	XM_095168	zinc finger protein 467	CAGCAUCUAUCGUUAC UUC	D-025367- 02	1.88	0.05	1.02	0.26	0.91	0.12
ZNF467	168544	XM_095168	zinc finger protein 467	CACCUGGGCUCGCACC AAA	D-025367- 03	0.85	0.11	0.47	0.14	0.19	0.04
ZNF467	168544	XM_095168	zinc finger protein 467	GGAGGAAGGUGCCCA CACA	D-025367- 01	0.63	0.19	0.49	0.07	0.17	0.01
ZNF467	168544	XM_095168	zinc finger protein 467	CAGAAGAGGAGGUCG AAUG	D-025367- 04	0.57	0.00	0.59	0.13	0.69	0.10
ZNF608	57507	XM_114432	zinc finger protein 608	UGAGUAAUUGGGCAC UUGA	D-024395- 03	1.27	0.21	0.91	0.27	0.71	0.09
ZNF608	57507	XM_114432	zinc finger protein 608	GUAAUCCCCGGGUCAA UAU	D-024395- 04	0.51	0.04	0.23	0.10	0.10	0.03
ZNF608	57507	XM_114432	zinc finger protein 608	GGGAAACUCUAUGUU GGUA	D-024395- 02	1.21	0.20	0.52	0.03	0.48	0.13
ZNF608	57507	XM_114432	zinc finger protein 608	GGCCAUCAGUGCCUAA UAA	D-024395- 01	0.88	0.12	0.15	0.03	0.29	0.03

ZNF767	79970	NM_024910	zinc finger family member 767	AAACCCGGGAUGGCCG AGAA	D-014511-01	0.79	0.09	0.65	0.19	1.13	0.37
ZNF767	79970	NM_024910	zinc finger family member 767	GAUCCAGAUUUCC UGUG	D-014511-03	0.91	0.11	0.57	0.08	0.45	0.04
ZNF767	79970	NM_024910	zinc finger family member 767	GCUCACCUGCUUUCCC UAG	D-014511-04	0.44	0.07	0.29	0.14	0.15	0.02
ZNF767	79970	NM_024910	zinc finger family member 767	GAAAGAGCCCUUGCAAC UGG	D-014511-02	0.80	0.03	0.29	0.22	0.19	0.05
ZNRF2	223082	NM_147128	zinc and ring finger 2	CAUAAAGGCGUGCAUA GAUG	D-007165-03	0.75	0.08	0.55	0.13	0.47	0.21
ZNRF2	223082	NM_147128	zinc and ring finger 2	GCACAUUUUUGGAGG AUUU	D-007165-01	0.60	0.09	0.50	0.23	0.20	0.01
ZNRF2	223082	NM_147128	zinc and ring finger 2	UGAGCACCCUUCAGAU UAA	D-007165-04	0.91	0.00	0.30	0.05	0.26	0.02
ZNRF2	223082	NM_147128	zinc and ring finger 2	CAUAUAGCCCUUGAAG AAUU	D-007165-02	0.35	0.19	0.47	0.06	0.22	0.18

Table S1B

TABLE S1B - Part Two: Decreased Infection											
Entrez Gene Symbol	Entrez Gene ID	Genbank Accession Number	Gene Name	Sequence	Vendor ID	Average Normalized Cell Number Part One	SD	Average Normalized Percent Infected Cells Part One	SD	Average Normalized Percent Infected Cells Part two	SD
ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6	GAAGGGCCGUAUUG AGUUU	D-007304-02	1.38	0.14	0.85	0.13	0.31	0.02
ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6	UCGAGACGGUGAAG UAUUA	D-007304-03	1.48	0.33	0.99	0.18	0.34	0.08
ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6	GAGAGGCCCAUCAUC AAAUA	D-007304-01	1.01	0.16	0.50	0.09	0.30	0.21

ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6	GCGCAUACUUUGUCACUGA	D-007304-04	0.85	0.16	0.39	0.16	0.35	0.07
ABHD2	11057	NM_007011	abhydrolase domain containing 2	CAGGAAACCUUCAUGCAAU	D-008331-02	1.38	0.23	0.59	0.25	0.49	0.11
ABHD2	11057	NM_007011	abhydrolase domain containing 2	GAGGAAGUUUUCACGGCUAU	D-008331-05	0.98	0.12	0.56	0.17	0.64	0.33
ABHD2	11057	NM_007011	abhydrolase domain containing 2	CACCGGAAGUUCAUCACUA	D-008331-04	1.27	0.52	0.36	0.06	0.21	0.15
ABHD2	11057	NM_007011	abhydrolase domain containing 2	GAAACGAGAGAAACGUAUG	D-008331-03	1.36	0.01	0.73	0.14	0.56	0.10
AGPAT3	56894	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3	UCCAGGAGAUUAUAUAAUCA	D-008620-03	1.36	0.22	1.11	0.13	0.55	0.02
AGPAT3	56894	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3	GCUCCAAGGUCCUCGCUAA	D-008620-01	1.51	0.07	0.53	0.21	0.15	0.16
AGPAT3	56894	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3	GGGAGCAGCUUCCUUGGA	D-008620-02	0.65	0.11	0.44	0.02	0.25	0.03
AGPAT3	56894	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3	GCAGCUGUCUAUGAUGUAA	D-008620-04	0.99	0.14	0.58	0.22	0.74	0.36
AMMECR1L	83607	NM_031445	AMME chromosomal region gene 1-like	GCACUUAAGGACAGCCGAU	D-014729-04	0.70	0.14	0.64	0.22	0.21	0.07
AMMECR1L	83607	NM_031445	AMME chromosomal region gene 1-like	CCAUUGGAUUCGAAUUGAA	D-014729-03	1.25	0.05	0.59	0.23	0.19	0.15
AMMECR1L	83607	NM_031445	AMME chromosomal region gene 1-like	GGAUACACGUUAACAGU	D-014729-02	1.96	0.07	1.56	0.14	0.45	0.26
AMMECR1L	83607	NM_031445	AMME chromosomal region gene 1-like	GGUCAAGAAGCCCAAUUA	D-014729-01	1.37	0.23	0.61	0.09	0.75	0.54
ANKRD20A1	84210	NM_032250	ankyrin repeat domain 20 family, member A1	GAAAUGCGUGGCUUGUAC	D-014816-03	0.75	0.11	0.60	0.07	0.09	0.06
ANKRD20A1	84210	NM_032250	ankyrin repeat domain 20 family, member A1	GAAUACUCCAAAUCCGGA	D-014816-02	1.42	0.06	1.34	0.16	0.75	0.82
ANKRD20A1	84210	NM_032250	ankyrin repeat domain 20 family, member A1	GAAAACAGGAGGAGUAGUA	D-014816-01	1.15	0.10	0.51	0.13	0.18	0.19

ANKRD20A1	84210	NM_032250	ankyrin repeat domain 20 family, member A1	CAUGCUGCUGUAU ACUAAU	D-014816-04	1.14	0.06	0.61	0.27	0.20	0.00
APC2	10297	NM_005883	adenomatosis polyposis coli 2	GGACAUCACACGCC UGUAC	D-009847-03	0.62	0.16	0.39	0.07	0.10	0.07
APC2	10297	NM_005883	adenomatosis polyposis coli 2	UUUGA	D-009847-01	1.00	0.07	0.78	0.15	0.23	0.11
APC2	10297	NM_005883	adenomatosis polyposis coli 2	AGGAGAAGCUCUGG UACUA	D-009847-02	1.34	0.07	0.65	0.38	0.30	0.16
APC2	10297	NM_005883	adenomatosis polyposis coli 2	GUCCGGGAUCACA ACUGU	D-009847-04	1.77	0.53	0.81	0.21	0.29	0.07
ATP10D	57205	NM_020453	ATPase, Class V, type 10D	GUUACGAGCUGGAC UCAUU	D-018004-02	1.49	0.35	0.68	0.24	0.51	0.30
ATP10D	57205	NM_020453	ATPase, Class V, type 10D	GUGGUGGUCCUUAU AAUUA	D-018004-03	1.41	0.34	0.54	0.04	0.62	0.50
ATP10D	57205	NM_020453	ATPase, Class V, type 10D	UCACAGAGCUGCCA AUUUA	D-018004-01	1.52	0.00	0.69	0.25	0.25	0.05
ATP10D	57205	NM_020453	ATPase, Class V, type 10D	GGUAUAAAGCGCAGC AAAUU	D-018004-04	0.64	0.22	0.55	0.02	0.26	0.04
C7orf41	22216	NM_152793	chromosome 7 open reading frame 41	GCAGCUAGCACAGG AUUAC	D-016789-04	1.14	0.26	1.14	0.06	0.44	0.08
C7orf41	22216	NM_152793	chromosome 7 open reading frame 41	GCAAGAAGACGCUC CACGA	D-016789-02	1.49	0.05	0.65	0.07	0.19	0.12
C7orf41	22216	NM_152793	chromosome 7 open reading frame 41	GAGCACGUGUGGAG UGAGA	D-016789-01	0.78	0.13	0.69	0.33	0.21	0.05
C7orf41	22216	NM_152793	chromosome 7 open reading frame 41	ACGAUGCGUUUGAA GAGUA	D-016789-03	1.19	0.09	0.47	0.03	0.09	0.04
C9orf125	84302	NM_032342	chromosome 9 open reading frame 125	UUACUAAACUUGAU AUACA	D-014865-02	0.66	0.07	0.96	0.65	0.24	0.03
C9orf125	84302	NM_032342	chromosome 9 open reading frame 125	GGUUUAGCUGGCC UGUAA	D-014865-01	0.80	0.17	0.33	0.08	0.06	0.06
C9orf125	84302	NM_032342	chromosome 9 open reading frame 125	GCAGGACUAUGUCU AUUGC	D-014865-03	1.40	0.24	1.04	0.28	1.27	0.38
C9orf125	84302	NM_032342	chromosome 9 open reading frame 125	GAGCGUAGUGUGAG CCAUU	D-014865-04	0.37	0.14	0.67	0.10	0.25	0.15
CADM2	25355	NM_153184	cell adhesion molecule 2	UGGCAUGAAUUGAG UAUUA	D-016035-01	1.73	0.27	0.65	0.25	0.33	0.08
CADM2	25355	NM_153184	cell adhesion molecule 2	GGCAUAAAGGAACG UAUUU	D-016035-04	1.45	0.40	0.87	0.20	0.20	0.01
CADM2	25355	NM_153184	cell adhesion molecule 2	GGAUUCUCAUCACC AGUUA	D-016035-03	0.82	0.01	0.74	0.04	0.40	0.05

CADM2	2535	9	NM_153184	cell adhesion molecule 2	GAAUACACUUAUACACCAU	D-016035-02	0.58	0.11	0.44	0.05	0.25	0.09
CCL26	10344		NM_006072	chemokine (C-C motif) ligand 26	GAUUAUCACUACCAAAAGA	D-007838-02	0.91	0.20	0.88	0.11	0.36	0.12
CCL26	10344		NM_006072	chemokine (C-C motif) ligand 26	GAAAGUCUGUACCCAUCCA	D-007838-03	0.32	0.08	0.63	0.26	0.86	0.02
CCL26	10344		NM_006072	chemokine (C-C motif) ligand 26	GGAGUGACAUUAUCCAAAGAC	D-007838-04	0.56	0.07	0.71	0.19	0.75	0.03
CCL26	10344		NM_006072	chemokine (C-C motif) ligand 26	GCUAUGAAUUAUACCAAGUAA	D-007838-01	0.70	0.17	0.96	0.31	0.10	0.08
CDCA3	83461		NM_031299	cell division cycle associated 3	CGCAAUAGAUGGAAACCAA	D-016149-02	1.26	0.17	0.50	0.05	0.10	0.05
CDCA3	83461		NM_031299	cell division cycle associated 3	GCAAGACAGCCACAGAAA	D-016149-01	1.30	0.12	0.53	0.11	0.36	0.09
CDCA3	83461		NM_031299	cell division cycle associated 3	UGACACUACGACAGGGUAA	D-016149-04	1.14	0.01	0.48	0.10	0.37	0.07
CDCA3	83461		NM_031299	cell division cycle associated 3	GGUUAUUGCACGGACACCUA	D-016149-03	0.95	0.15	0.54	0.01	0.40	0.03
CXorf22	17006	3	NM_152632	chromosome X open reading frame 22	GGGAGCGCAUGUAUUCUAUA	D-016940-01	1.72	0.03	0.80	0.05	0.48	0.19
CXorf22	17006	3	NM_152632	chromosome X open reading frame 22	UGACCGAGCUGCAAUAUC	D-016940-03	0.85	0.37	0.25	0.08	0.17	0.06
CXorf22	17006	3	NM_152632	chromosome X open reading frame 22	GAUUAUGGACCUUCUAACA	D-016940-04	0.27	0.05	0.49	0.24	0.20	0.18
CXorf22	17006	3	NM_152632	chromosome X open reading frame 22	GCGAAUCGAUUGUUAAACA	D-016940-02	1.24	0.14	0.51	0.04	0.08	0.07
DDOST	1650		NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	GGAAUUCUUAUGACAAU	D-015786-03	0.65	0.02	0.70	0.06	0.39	0.10
DDOST	1650		NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	CGACGUGUAUGGUGUAUUC	D-015786-02	1.67	0.02	1.09	0.02	0.70	0.51
DDOST	1650		NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	GACCAUCAGUGCCUUUAUU	D-015786-01	1.71	0.18	1.02	0.25	0.38	0.00

DDOST	1650	NM_005216	dolichyl- diphosphooligosacchar ide-protein glycosyltransferase	GACAGGCAACUAUG AACUA	D-015786- 04	1.26	0.28	1.12	0.02	0.38	0.22
ELAVL1	1994	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)- like 1 (Hu antigen R)	CAAAGACGCCAACU UGUAC	D-003773- 05	2.15	0.25	1.17	0.26	0.40	0.16
ELAVL1	1994	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)- like 1 (Hu antigen R)	UCAAAGACGCCAAC UUGUA	D-003773- 04	1.03	0.12	0.30	0.09	0.12	0.03
ELAVL1	1994	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)- like 1 (Hu antigen R)	GAUCAAAGACGCCA ACUUG	D-003773- 01	0.68	0.14	0.59	0.01	0.33	0.07
ELAVL1	1994	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)- like 1 (Hu antigen R)	GCAAUUACCAUUU CAAUG	D-003773- 02	1.58	0.19	0.93	0.07	0.68	0.24
FAM116A	20162	7	family with sequence similarity 116, member A	GAAAUUCCUAAAGCA GGUUA	D-016505- 02	0.83	0.24	0.92	0.14	0.28	0.11
FAM116A	20162	7	family with sequence similarity 116, member A	GUAAUGAAGGUACG GAUUC	D-016505- 03	1.06	0.05	1.54	0.09	0.83	0.02
FAM116A	20162	7	family with sequence similarity 116, member A	UGACAAAGAUUUAC CAGUU	D-016505- 01	0.92	0.17	0.73	0.03	0.12	0.03
FAM116A	20162	7	family with sequence similarity 116, member A	GGCCACACAUUAUU CGAAU	D-016505- 04	1.63	0.10	1.11	0.08	0.78	0.04
FOXE3	2301	NM_012186	forkhead box E3	UGGUGAACCTUGCAG CCGGA	D-009139- 03	0.95	0.05	0.77	0.23	0.48	0.01
FOXE3	2301	NM_012186	forkhead box E3	CUUCAUCACCCGAAC GCUUU	D-009139- 04	1.11	0.18	0.71	0.28	0.59	0.12
FOXE3	2301	NM_012186	forkhead box E3	CGUCGGGGCUGGAG CGCUA	D-009139- 01	1.75	0.29	1.09	0.20	0.92	0.05
FOXE3	2301	NM_012186	forkhead box E3	CCGCGCAAGUGGCA GAACA	D-009139- 02	0.75	0.11	0.19	0.00	0.21	0.04
GCAT	23464	NM_014291	glycine C- acetyltransferase (2- amino-3-ketobutyrate coenzyme A ligase)	GGCCAUACCUCUC UCCAA	D-009547- 01	1.06	0.21	0.15	0.01	0.10	0.01

GCAT	23464	NM 014291	glycine C- acetyltransferase (2- amino-3-ketobutyrate coenzyme A ligase)	UACUUCUGUGCCA ACAAC	D-009547- 04	1.10	0.43	1.26	0.38	0.86	0.20
GCAT	23464	NM 014291	glycine C- acetyltransferase (2- amino-3-ketobutyrate coenzyme A ligase)	GCUGCUGGCUUCAC UAUCU	D-009547- 03	1.12	0.04	0.63	0.22	0.17	0.11
GCAT	23464	NM 014291	glycine C- acetyltransferase (2- amino-3-ketobutyrate coenzyme A ligase)	GAACCAUGCCUCCA UCAUC	D-009547- 02	1.03	0.07	0.93	0.22	0.49	0.05
HIST1H2BK	85236	NM 080593	histone cluster 1, H2bk	CGAAGAAAGCCGUG ACUAA	D-013323- 01	1.46	0.14	0.56	0.11	0.14	0.13
HIST1H2BK	85236	NM 080593	histone cluster 1, H2bk	CCUCUAAAGGCCAUG GGAU	D-013323- 02	1.79	0.08	1.00	0.22	1.02	0.21
HIST1H2BK	85236	NM 080593	histone cluster 1, H2bk	UCGAAGAAAGCCGU GACUA	D-013323- 04	1.70	0.04	0.70	0.17	0.11	0.11
HIST1H2BK	85236	NM 080593	histone cluster 1, H2bk	UCGAACGCAUCGCG GGUGA	D-013323- 03	0.64	0.05	0.36	0.08	0.28	0.06
HOXB13	10481	NM 006361	homeobox B13	GAACAGGCUACCC CUUAA	D-012226- 01	0.55	0.02	0.08	0.07	0.24	0.08
HOXB13	10481	NM 006361	homeobox B13	GAACCCACCAAGGUC CUUUU	D-012226- 03	1.35	0.31	0.60	0.25	0.49	0.05
HOXB13	10481	NM 006361	homeobox B13	CCACUGAGUUUGCC UUCUA	D-012226- 02	0.98	0.28	0.71	0.42	0.63	0.16
HOXB13	10481	NM 006361	homeobox B13	GUAGCGGCUAACA AGUUC	D-012226- 04	1.41	0.08	1.06	0.07	0.88	0.33
IQCB1	9657	NM 014642	IQ motif containing B1	ACCCAAGGAUCUUA UCUUA	D-021206- 02	1.49	0.06	1.44	0.23	0.85	0.10
IQCB1	9657	NM 014642	IQ motif containing B1	CCAAUAGGAUCUG CAGUC	D-021206- 04	1.67	0.12	0.71	0.18	0.51	0.01
IQCB1	9657	NM 014642	IQ motif containing B1	GAGGCCAUGUUGAA CUUUA	D-021206- 03	1.00	0.13	0.82	0.24	0.37	0.01
IQCB1	9657	NM 014642	IQ motif containing B1	GAGCAGAAUGUCC UGUUA	D-021206- 01	0.61	0.08	0.66	0.17	0.27	0.07
KCTD14	65987	NM 023930	potassium channel tetramerisation domain containing 14	GGAAGCGGCUCCA GACAA	D-014252- 01	1.05	0.15	0.63	0.03	0.10	0.09
KCTD14	65987	NM 023930	potassium channel tetramerisation domain containing 14	GGUACAAGGUUUC UCCAA	D-014252- 04	1.82	0.10	0.42	0.03	0.10	0.01

KCTD14	65987	NM_023930	potassium channel tetramerisation domain containing 14	GUUCAAGUCUGUUG UCAAG	D-014252-03	1.77	0.05	1.39	0.10	0.78	0.01
KCTD14	65987	NM_023930	potassium channel tetramerisation domain containing 14	GAAAUCAAGCCUUU GGUA	D-014252-02	1.51	0.11	0.86	0.28	1.05	0.09
KIAA1024	23251	XM_044580	KIAA1024 protein	CUACACAGCUUGUC UCGAU	D-022286-02	1.20	0.21	2.25	0.01	1.73	0.24
KIAA1024	23251	XM_044580	KIAA1024 protein	GGUACGAUUCUUAU ACUAA	D-022286-01	1.54	0.19	1.34	0.10	0.72	0.13
KIAA1024	23251	XM_044580	KIAA1024 protein	GCACCGUCAUCCUC GUUAU	D-022286-04	1.57	0.10	0.68	0.16	0.09	0.05
KIAA1024	23251	XM_044580	KIAA1024 protein	GGCCCAACUUAACC UUGUG	D-022286-03	0.11	0.03	0.49	0.46	0.01	0.01
LST-3TMI2	33882	1 XM_292093	organic anion transporter LST-3b	UAAUAAAGAGCCCA UAGUG	D-030126-04	2.05	0.17	1.41	0.01	1.12	0.12
LST-3TMI2	33882	1 XM_292093	organic anion transporter LST-3b	GGACUUAACCUCAUA UUCCG	D-030126-03	0.66	0.19	0.24	0.06	0.20	0.12
LST-3TMI2	33882	1 XM_292093	organic anion transporter LST-3b	GAAGGUAGCCCUAA UAUUU	D-030126-01	1.29	0.33	0.76	0.08	0.17	0.00
LST-3TMI2	33882	1 XM_292093	organic anion transporter LST-3b	GGGAAUGACUGGUC UAGUU	D-030126-02	0.45	0.04	0.55	0.09	0.18	0.13
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus	ACAAGGAUCUGCCA UAAUA	D-019599-01	1.21	0.42	0.61	0.01	0.15	0.11
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus	CCAAUUAAGUACCA GCAUA	D-019599-02	1.50	0.06	0.89	0.09	0.18	0.02
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus	UGAAUUGGCUAUAG GGAUU	D-019599-03	1.14	0.13	0.62	0.05	0.29	0.04
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus	GAGCGAAACUCUCG UCCUU	D-019599-04	0.69	0.16	0.78	0.22	0.72	0.02
PELI1	57162	NM_020651	pellino homolog 1 (Drosophila)	UCAGUUGGCUUGGUG AACAA	D-013814-02	1.05	0.01	0.32	0.01	0.25	0.09
PELI1	57162	NM_020651	pellino homolog 1 (Drosophila)	AAAUUUCGGUGUGU GGAAA	D-013814-04	1.09	0.12	0.53	0.04	0.68	0.14
PELI1	57162	NM_020651	pellino homolog 1 (Drosophila)	AAUCAUUGUGAAC GGAUU	D-013814-03	0.58	0.43	0.50	0.33	0.16	0.10

PELI	57162	NM_020651	pellino homolog 1 (Drosophila)	UCAAGGACCUCUAG ACUAA	D-013814-01	0.22	0.01	0.18	0.06	0.04	0.01
PLB1	15105	NM_153021	phospholipase B1	CAGGAAGACUGGAA GAUAA	D-008684-02	0.80	0.21	0.40	0.03	0.30	0.10
PLB1	15105	NM_153021	phospholipase B1	GAACUUCACAGACA ACAUU	D-008684-03	0.40	0.27	0.42	0.12	0.10	0.05
PLB1	15105	NM_153021	phospholipase B1	GAUGAUAAACUCAAC AGAAC	D-008684-04	0.90	0.58	0.53	0.10	0.18	0.17
PLB1	15105	NM_153021	phospholipase B1	GCAUUGACCUCUCUGU GAUUU	D-008684-01	0.66	0.24	0.69	0.04	0.25	0.07
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1	GACAUGAAAUCUCAA CAUUA	D-003601-03	1.18	0.21	0.82	0.09	0.62	0.23
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1	CAAAGAACAUCUAC CAUAG	D-003601-04	1.21	0.03	0.84	0.01	0.58	0.29
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1	GCAAAGAACAUCAU CCAUAA	D-003601-02	1.72	0.20	0.66	0.22	0.37	0.23
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1	GCACGGAGAUUGUUG CAGUA	D-003601-01	1.20	0.44	0.41	0.27	0.16	0.02
RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5	GCAAAGCUGUAUUA UGAAG	D-012007-01	1.11	0.33	0.60	0.06	0.26	0.12
RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5	UUACAGGCGUUCAG UGGAA	D-012007-04	0.70	0.05	0.44	0.02	0.22	0.02
RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5	GUUCCAAGACCACAA GAUUA	D-012007-02	1.51	0.32	0.94	0.06	0.53	0.03
RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5	GAAGUCCUGCAAUU UAUAA	D-012007-03	0.62	0.01	0.58	0.23	0.33	0.02
RPAIN	84268	NM_032308	RPA interacting protein	GAAUUGUCCAGAAG ACUUG	D-014848-04	0.80	0.14	0.43	0.16	0.33	0.00
RPAIN	84268	NM_032308	RPA interacting protein	GGAUUGCUUUGCAG UCAGU	D-014848-03	1.55	0.07	1.19	0.11	0.30	0.15
RPAIN	84268	NM_032308	RPA interacting protein	GUACAAAUUCUUCUG AGUUG	D-014848-01	0.90	0.50	0.93	0.19	0.63	0.01
RPAIN	84268	NM_032308	RPA interacting protein	CCACUACUCUGUCC UGUAU	D-014848-02	0.63	0.09	0.56	0.17	0.14	0.00

SLC24A6	80024	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	GACCGGGUAUCUUCUAAUA	D-007332-01	1.59	0.35	0.94	0.16	0.41	0.21
SLC24A6	80024	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	UACAUGAAGUGGAGAAAGGA	D-007332-03	0.99	0.01	1.14	0.13	0.40	0.04
SLC24A6	80024	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	GGACAUCGUUUUCUACAUG	D-007332-04	0.80	0.10	0.65	0.06	0.55	0.30
SLC24A6	80024	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	UGACUACGGUGAUGAGUAC	D-007332-02	0.92	0.04	1.00	0.19	0.18	0.02
SNF1LK2	23235	NM_015191	SNF1-like kinase 2	GGACCGACUCUCCAAUUU	D-004778-10	0.68	0.44	0.26	0.05	0.07	0.04
SNF1LK2	23235	NM_015191	SNF1-like kinase 2	GAAGAUGCGAGCAUUUA	D-004778-03	1.33	0.01	0.56	0.15	0.58	0.04
SNF1LK2	23235	NM_015191	SNF1-like kinase 2	GGUAUGUCCUGGUGAAUUA	D-004778-05	1.23	0.22	0.59	0.19	0.05	0.02
SNF1LK2	23235	NM_015191	SNF1-like kinase 2	CAAGAGCUAUAACCAUUU	D-004778-09	1.31	0.31	0.53	0.14	0.52	0.22
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)	CGACAAGAAACCAGGGGAA	D-020577-04	1.13	0.03	0.54	0.06	0.08	0.02
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)	GCCAGAAGCUAGCUAAACA	D-020577-03	1.29	0.11	0.54	0.01	0.02	0.02
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)	CGGGUGGACUGUCUAAUAUA	D-020577-02	1.08	0.24	0.41	0.07	0.05	0.01
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)	GUGGUUACCUGUUCAAAGAA	D-020577-01	0.81	0.09	0.98	0.04	0.04	0.01

SPCS2	9789	NM 014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)	GAUGACAAAUACAC CUUGA	D-020897- 04	1.09	0.04	0.88	0.06	0.21	0.11
SPCS2	9789	NM 014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)	CAAAGUCCAUUGCU AAGUU	D-020897- 01	1.10	0.13	0.96	0.09	0.71	0.34
SPCS2	9789	NM 014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)	CAGCUGUCCUCCAG UCUUA	D-020897- 03	1.75	0.09	0.52	0.01	0.07	0.07
SPCS2	9789	NM 014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)	GAAUGGAUCCUGAU GAUUA	D-020897- 02	0.28	0.02	0.72	0.04	0.05	0.02
SPCS3	60559	NM 021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	GAACCAAGUUGUCC UAUGG	D-010124- 04	0.99	0.09	1.05	0.33	0.97	0.61
SPCS3	60559	NM 021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	GAAUUGGUCUCAAG GGAAA	D-010124- 01	0.94	0.25	0.56	0.07	0.07	0.08
SPCS3	60559	NM 021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	ACACGUAUCUGUCC CAUUU	D-010124- 03	0.67	0.08	0.52	0.06	0.03	0.04
SPCS3	60559	NM 021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	GAAGUGAUCUGGGA UUUUA	D-010124- 02	1.24	0.19	0.46	0.13	0.10	0.11
SRI	6717	NM 003130	sorcin	GAAGACGGGAUACU GCUCA	D-019727- 04	1.43	0.18	0.53	0.24	0.18	0.10
SRI	6717	NM 003130	sorcin	CAAUGUGUCAUGAG UGUUU	D-019727- 03	0.35	0.25	0.12	0.09	0.06	0.06
SRI	6717	NM 003130	sorcin	GAUAGAUGCUGAUG AAUUG	D-019727- 01	1.59	0.29	0.92	0.10	0.74	0.17
SRI	6717	NM 003130	sorcin	ACAAUGGGAUUUAG GUUGA	D-019727- 02	0.56	0.17	0.17	0.13	0.30	0.03
SRRM2	23524	NM 016333	serine/arginine repetitive matrix 2	GGAAUGAAAGAUUAU ACCUA	D-015368- 05	1.50	0.10	0.75	0.09	0.55	0.26

SRRM2	23524	NM 016333	serine/arginine repetitive matrix 2	GAGCAAAUUCUCAA CAUCA	D-015368- 01	1.88	0.36	0.71	0.20	0.34	0.18
SRRM2	23524	NM 016333	serine/arginine repetitive matrix 2	AAAGAAAUGUCCAC AAGUA	D-015368- 03	1.09	0.05	0.95	0.12	0.05	0.03
SRRM2	23524	NM 016333	serine/arginine repetitive matrix 2	GACAGCAAAUUCUG ACUAU	D-015368- 06	1.83	0.45	0.88	0.33	0.19	0.06
STAT3	6774	NM 003150	activator of transcription 3 (acute- phase response factor)	CCACUUUGGUGUUU CAUAA	D-003544- 03	1.57	0.14	0.81	0.04	0.37	0.23
STAT3	6774	NM 003150	signal transducer and activator of transcription 3 (acute- phase response factor)	CCAACGACCUCGAG CAUAU	D-003544- 01	0.95	0.16	0.60	0.09	0.18	0.01
STAT3	6774	NM 003150	signal transducer and activator of transcription 3 (acute- phase response factor)	UCAGGUUGCUGGUC AAAUU	D-003544- 04	0.40	0.00	0.22	0.09	0.17	0.03
STAT3	6774	NM 003150	signal transducer and activator of transcription 3 (acute- phase response factor)	GGAGAAAGCAUCGUG AGUGA	D-003544- 02	0.65	0.15	0.45	0.14	0.31	0.12
STM2	57620	NM 020860	stromal interaction molecule 2	GCUUCAGAUAGCC CAUAA	D-013166- 02	1.05	0.03	0.61	0.01	0.22	0.04
STM2	57620	NM 020860	stromal interaction molecule 2	AGACACAGCUUCAG AAUGU	D-013166- 01	1.68	0.03	0.76	0.20	0.70	0.09
STM2	57620	NM 020860	stromal interaction molecule 2	CUUUAAGCCUCGAG AUAAU	D-013166- 03	1.02	0.14	0.76	0.29	0.43	0.33
STM2	57620	NM 020860	stromal interaction molecule 2	AGAAGCAGUUGGUC UGUUC	D-013166- 04	0.71	0.03	0.22	0.19	0.38	0.23
TBCD	6904	NM 005993	tubulin folding cofactor D	GUACACGCAGCCAA UGAUA	D-013416- 01	1.41	0.20	1.04	0.27	0.75	0.22
TBCD	6904	NM 005993	tubulin folding cofactor D	CAAGCACGAAUUGUC CAUAA	D-013416- 02	0.64	0.23	0.95	0.03	0.39	0.06
TBCD	6904	NM 005993	tubulin folding cofactor D	GGUUGUUGACCGAG ACAUA	D-013416- 04	1.02	0.35	0.43	0.07	0.23	0.10
TBCD	6904	NM 005993	tubulin folding cofactor D	GUCCAGAUUCUUCAC AUGAG	D-013416- 03	0.22	0.06	0.14	0.16	0.10	0.07
TMEM135	65084	NM 022918	transmembrane protein 135	UGGUAGAGACAAUG UAUUU	D-018130- 04	0.80	0.10	0.20	0.06	0.07	0.05
TMEM135	65084	NM 022918	transmembrane protein 135	GCAAGUCCAUCCCU CAUAA	D-018130- 01	1.15	0.23	0.52	0.02	0.14	0.00

TMEM135	65084	NM 022918	transmembrane protein 135	GGGUGGUCACAAU UUUA	D-018130-02	1.41	0.18	0.83	0.12	0.85	0.25
TMEM135	65084	NM 022918	transmembrane protein 135	GGGUGGUAUCAGAA ACUUA	D-018130-03	1.15	0.11	0.71	0.13	0.60	0.38
TTC14	15161	3 NM 133462	tetratricopeptide repeat domain 14	GAAGUGUAUCAUG AGAGA	D-015350-02	1.67	0.26	0.93	0.01	0.51	0.15
TTC14	15161	3 NM 133462	tetratricopeptide repeat domain 14	GGAGAAAGUUGAG CUAAA	D-015350-03	1.35	0.23	0.55	0.11	0.33	0.18
TTC14	15161	3 NM 133462	tetratricopeptide repeat domain 14	GAGCAAGAUACCG UUUAA	D-015350-01	1.75	0.05	0.89	0.09	0.63	0.43
TTC14	15161	3 NM 133462	tetratricopeptide repeat domain 14	UAUUGAGCGUGGUG AUUA	D-015350-04	1.18	0.09	0.42	0.01	0.11	0.10
UBE2S	27338	NM 014501	ubiquitin-conjugating enzyme E2S	CAUGCUGGCGAGCG CGAUA	D-009707-04	1.66	0.34	0.65	0.01	0.21	0.02
UBE2S	27338	NM 014501	ubiquitin-conjugating enzyme E2S	AUAAGAAGCUGGCG GCCAA	D-009707-01	1.05	0.16	0.30	0.01	0.37	0.03
UBE2S	27338	NM 014501	ubiquitin-conjugating enzyme E2S	GCCAAAGAAAAGAC GGACA	D-009707-03	0.91	0.02	0.80	0.09	0.72	0.27
UBE2S	27338	NM 014501	ubiquitin-conjugating enzyme E2S	ACAAGGAGGUGACG ACACU	D-009707-02	1.24	0.15	0.83	0.37	0.50	0.30
ZDHHC16	84287	NM 032327	zinc finger, DHHC-type containing 16	CAACGUGAUCCGCU GGUUU	D-021403-04	0.86	0.39	0.60	0.29	0.31	0.16
ZDHHC16	84287	NM 032327	zinc finger, DHHC-type containing 16	GGAAGGCACUGGCU UACUC	D-021403-02	1.56	0.29	0.54	0.04	0.37	0.28
ZDHHC16	84287	NM 032327	zinc finger, DHHC-type containing 16	GAGAAAGGAUGACU CACAA	D-021403-01	1.10	0.07	0.57	0.25	0.22	0.19
ZDHHC16	84287	NM 032327	zinc finger, DHHC-type containing 16	GGAGAGACGUCGGC UACAG	D-021403-03	0.97	0.08	0.18	0.05	0.22	0.14
ZNF337	26152	NM 015655	zinc finger protein 337	GAGCGAAGCUUAG CCAAA	D-006970-02	0.93	0.07	0.28	0.04	0.13	0.02
ZNF337	26152	NM 015655	zinc finger protein 337	GGACGAGGCUUUAU CCAAA	D-006970-03	0.83	0.03	0.56	0.08	0.13	0.08
ZNF337	26152	NM 015655	zinc finger protein 337	GGACGAGGCUUUAU CAGUA	D-006970-04	0.81	0.01	0.60	0.01	0.07	0.01
ZNF337	26152	NM 015655	zinc finger protein 337	GGACGAAAGUUUAG CAUA	D-006970-01	0.90	0.16	0.56	0.23	0.17	0.03

Table S1C

TABLE S1C - Part One: Increased Infection											
Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name	Sequence	Vendor ID	Average Normalized Cell Number Part One	SD	Average Normalized Percent Infected Cells Part One	SD	Average Normalized Percent Infected Cells Part two	SD
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7	UCAAAGAGCUCGAGAGACA	D-009616-03	1.17	0.20	1.50	0.22	1.51	0.08
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7	GGAAGAAAGAUGCUCAGAUU	D-009616-01	1.13	0.02	0.87	0.00	0.82	0.07
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7	GGAGGGCGAUGACAUAUAAA	D-009616-04	1.01	0.08	1.15	0.08	1.15	0.28
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7	GAAGAGCCCUCGCCAAAGGA	D-009616-02	0.62	0.16	1.53	0.02	1.57	0.12
C16orf59	80178	NM_025108	chromosome 16 open reading frame 59	GAGCACGUGUCCUUACCAU	D-014588-02	1.04	0.26	0.59	0.05	0.51	0.16
C16orf59	80178	NM_025108	chromosome 16 open reading frame 59	CCAAGACCAUGUCCUGUGG	D-014588-01	1.26	0.16	1.29	0.10	0.85	0.12

C16orf59	80178	NM_025108	chromosome 16 open reading frame 59	GACCAGUGAUUCCACGGAU	D-014588- 03	1.16	0.06	1.55	0.29	1.55	0.16
C16orf59	80178	NM_025108	chromosome 16 open reading frame 59	UGGACUGGAUGCAGGAGUA	D-014588- 04	0.78	0.17	2.52	0.24	2.30	0.48
COTL1	23406	NM_021149	coactosin-like 1 (Dictyostelium)	UGAAGGAGGUCGUACAGAA	D-013104- 01	0.92	0.24	1.55	0.30	1.97	0.17
COTL1	23406	NM_021149	coactosin-like 1 (Dictyostelium)	GAGCGGAGUACCCAGCACUU	D-013104- 04	1.36	0.30	0.93	0.22	0.52	0.10
COTL1	23406	NM_021149	coactosin-like 1 (Dictyostelium)	GCACAGAUGACGUCGCGGUU	D-013104- 02	1.23	0.34	1.18	0.23	1.38	0.19
COTL1	23406	NM_021149	coactosin-like 1 (Dictyostelium)	AGCAAGAGGUCCAAGUUUG	D-013104- 03	1.11	0.05	1.86	0.29	1.97	0.12
EMID2	136227	NM_133457	EMI domain containing 2	GAGCAACUGUGAUGAGGAA	D-015349- 02	1.27	0.35	1.10	0.22	1.19	0.51
EMID2	136227	NM_133457	EMI domain containing 2	GCGCCAACUCUGAAAGUUA	D-015349- 01	1.31	0.28	2.00	0.07	1.64	0.18
EMID2	136227	NM_133457	EMI domain containing 2	CGACCCUGGAUUGAGGACUU	D-015349- 04	0.48	0.33	1.98	0.49	2.28	0.63
EMID2	136227	NM_133457	EMI domain containing 2	CAAAGACAAUGGAGACUCA	D-015349- 03	0.36	0.24	0.80	0.61	0.20	0.10
IL17RB	55540	NM_018725	interleukin 17 receptor B	ACAAAUACGUGGUGGUCUA	D-007944- 04	1.10	0.29	1.75	0.17	1.55	0.09
IL17RB	55540	NM_018725	interleukin 17 receptor B	GAAGUGAGGUCAUCCUUGA	D-007944- 01	1.02	0.22	1.54	0.19	2.13	0.38
IL17RB	55540	NM_018725	interleukin 17 receptor B	GAAAGGAUCAAGAAGACUU	D-007944- 03	1.05	0.18	0.70	0.03	1.09	0.22
IL17RB	55540	NM_018725	interleukin 17 receptor B	GAACAUCACUGCUUGUAAG	D-007944- 02	1.34	0.04	0.96	0.13	1.13	0.10
OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1	GACGGCAACUGUUUUAUC	D-021061- 03	1.17	0.20	1.12	0.39	1.07	0.24

OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1	CCGACUACCUUGUGGUCUA	D-021061- 02	1.00	0.12	1.64	0.19	1.58	0.10
OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1	GACGGACUGUCAAGGAGUU	D-021061- 04	0.54	0.03	1.58	0.19	1.89	0.36
OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1	GACAACAUCUAUCAACAGA	D-021061- 01	0.90	0.06	1.12	0.08	1.16	0.08
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H	CCAAUGAGGUCACAGAUCU	D-009448- 03	1.09	0.28	1.27	0.29	1.43	0.03
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H	GAACCCGGGUGUUUGUAUG	D-009448- 04	1.05	0.26	1.02	0.02	1.09	0.07
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H	GGAAUGACGUAGCCAGUUC	D-009448- 02	0.92	0.25	1.73	0.18	1.45	0.01
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H	GAAUGAAGGUCGUGUCUCA	D-009448- 01	0.58	0.33	1.59	0.05	1.52	1.19
TSSK3	81629	NM_052841	testis-specific serine kinase 3	GAACAUCAUCCAGGUGUAU	D-004050- 06	0.96	0.21	2.09	0.26	1.64	0.24
TSSK3	81629	NM_052841	testis-specific serine kinase 3	GAAGGGACCUACUCAAAAAG	D-004050- 07	1.16	0.12	0.89	0.12	0.87	0.13
TSSK3	81629	NM_052841	testis-specific serine kinase 3	CAAAGAAAAGUGGGCAAUUA	D-004050- 08	1.04	0.01	0.76	0.06	0.66	0.03
TSSK3	81629	NM_052841	testis-specific serine kinase 3	GCAUGGGUGUGGUCCUGUA	D-004050- 05	0.99	0.24	1.54	0.08	1.54	0.17
UISNRNP BP	11066	NM_007020	U11/U12 snRNP 35K	GAUCAAAGCUUACCGAGAU	D-012359- 01	1.52	0.31	2.01	0.30	1.58	0.45

U1SNRNP BP	11066	NM_007020	U11/U12 snRNP 35K	GGGUGUGGCCCGACAAUGA	D-012359-04	1.50	0.32	1.33	0.22	0.67	0.14
U1SNRNP BP	11066	NM_007020	U11/U12 snRNP 35K	GGAGGACAAAUUAAAGGAA	D-012359-03	1.06	0.05	1.65	0.30	1.84	0.36
U1SNRNP BP	11066	NM_007020	U11/U12 snRNP 35K	GGGACUUGGUCACAGGUUU	D-012359-02	0.46	0.07	0.80	0.27	0.55	0.13
USP43	124739	XM_371015	ubiquitin specific peptidase 43	GGGCUUAUAUCCUGUUCUA	D-023019-01	0.75	0.67	0.78	0.36	0.37	0.27
USP43	124739	XM_371015	ubiquitin specific peptidase 43	GUGAAAGGCAGAAAGCAUUA	D-023019-02	1.43	0.26	0.90	0.12	0.90	0.43
USP43	124739	XM_371015	ubiquitin specific peptidase 43	GAAGAGGACCUGAAUACCA	D-023019-03	0.67	0.13	1.53	0.05	1.74	0.42
USP43	124739	XM_371015	ubiquitin specific peptidase 43	GUGCUAAUCCUUCUUCUGUA	D-023019-04	1.05	0.29	1.51	0.16	1.76	0.16

TABLE SID - Part Two: Increased Infection

Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name	Sequence	Vendor ID	Average Normalized Cell Number Part One	SD	Average Normalized Percent Infected Cells Part One	SD	Average Normalized Percent Infected Cells Part two	SD
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A	GGAGUGAUCUGGCCGUGU CC	D-021769-07	1.50	0.34	1.81	0.12	2.46	0.01
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A	GCUGUUCUACGUUGUCU UU	D-021769-05	1.49	0.29	1.21	0.23	1.12	0.19
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A	GAGGAUGUACUACGUGU UC	D-021769-06	1.39	0.23	1.30	0.05	1.52	0.06
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A	GCAGUUCUCCAUCCCAAGU CA	D-021769-08	1.06	0.05	1.28	0.10	0.59	0.26
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A	GGAGUGAUCUGGCCGUGU	D-021769-09	1.50	0.34	1.81	0.12	2.46	0.01

			XM_495964	VI, type 11A	CC	07							
ATP11A	23250		XM_085028,	ATPase, Class	GCUGUUCUACGUUGUCU	D-021769-05	1.49	0.29	1.21	0.23	1.12	0.19	
			XM_495964	VI, type 11A	UU								
			XM_085028,	ATPase, Class	GAGGAUGUACUACGUGU	D-021769-06							
ATP11A	23250		XM_495964	VI, type 11A	UC	D-021769-08	1.39	0.23	1.30	0.05	1.52	0.06	
ATP11A	23250		XM_085028,	ATPase, Class	GCAGUUCCAUCCECAAGU	D-021769-08	1.06	0.05	1.28	0.10	0.59	0.26	
			XM_495964	VI, type 11A	CA								
				calcium channel, voltage-dependent, L type, alpha 1F subunit									
CACNA1F	778		NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit	GCACAUUGCUCUGGACA	D-006126-03	1.00	0.12	0.95	0.06	1.84	0.15	
CACNA1F	778		NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit	GGAAACAUCAUCAUGAUUGU	D-006126-04	1.14	0.05	1.15	0.20	0.75	0.28	
					CA								
CACNA1F	778		NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit	GAUCAUAAAUCUCUUUG	D-006126-02							1.18
CACNA1F	778		NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit	GAGGACAGCUCUCCGCAU	D-006126-01	1.02	0.27	1.77	0.09	2.05	0.23	
					UU								
				colony stimulating factor 3 receptor (granulocyte)	UGGAGGCCCUUCAGUAU	D-007867-04							1.00
CSF3R	1441		NM_000760	colony stimulating factor 3 receptor (granulocyte)	CAACCACACUCAGGCCU	D-007867-03	1.27	0.01	1.16	0.10	1.63	0.12	
					UU								
CSF3R	1441		NM_000760	colony stimulating factor 3 receptor (granulocyte)	GAUCCAAGGUUAUGUGG	D-007867-01							1.16

CSF3R	1441	NM_000760	colony stimulating factor 3 receptor (granulocyte)	CAUCGUGACUCCCUUGU AC	D-007867-02	0.82	0.33	0.71	0.26	1.03	0.10
GKN2	200504	NM_182536	gastrokine 2	ACACCUUGGUCAAGUAC AA	D-018916-04	0.74	0.57	0.61	0.33	1.52	0.27
GKN2	200504	NM_182536	gastrokine 2	CAGUGACAAUUGAUAAU GA	D-018916-03	0.97	0.25	1.00	0.32	0.58	0.21
GKN2	200504	NM_182536	gastrokine 2	UGAACAAUCUCCAAUGG UA	D-018916-01	0.88	0.50	1.24	0.18	1.70	0.35
GKN2	200504	NM_182536	gastrokine 2	UCAAAGACGUGGAUUGG UU	D-018916-02	0.73	0.14	0.65	0.01	0.90	0.51
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K	GUCGGGAGCUUCGAUCA AA	D-011692-04	0.94	0.15	0.33	0.08	2.47	0.67
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K	GAUCUUGGUGGACCUAU UA	D-011692-02	0.64	0.05	0.67	0.17	1.92	0.01
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K	GGUCAGCGGAUUAACA AA	D-011692-03	1.40	0.36	0.87	0.02	0.94	0.31
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K	GAGCGCAUUAUGAGUAU CA	D-011692-01	1.26	0.11	0.90	0.07	1.87	1.34
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6	GGAGAAUCCUAAGGAGA GU	D-006625-04	1.09	0.12	1.28	0.07	0.88	0.18
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6	GCGCGGAAGCUGAGGGC UG	D-006625-02	1.18	0.09	1.08	0.32	1.10	0.25
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6	GCAGAGACCAACAGAGG AA	D-006625-01	1.08	0.14	1.77	0.03	1.70	0.70
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6	UUGCAGAGGAGAAUCCU AA	D-006625-03	1.15	0.04	0.70	0.04	1.73	0.07

IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1	GCGAGUACUUCUUCUCA GA	D-009687-02	1.52	0.31	1.19	0.00	0.97	0.20
IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1	CAACACGGCUGCCAGGA UA	D-009687-01	0.82	0.36	1.56	0.20	1.51	0.13
IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1	GUGAUGACGCCAAGGAU UG	D-009687-04	0.59	0.36	1.18	0.17	0.78	0.44
IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1	GGGCUAGCAUGGGCGGAC UA	D-009687-03	0.83	0.07	1.01	0.73	1.61	0.90
KCNA1	3736	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	UGCCAUCGCUGGUGUGC UA	D-006210-04	1.20	0.02	1.31	0.06	2.59	0.52
KCNA1	3736	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	GCUACUGACCGAUGUUU AA	D-006210-05	1.16	0.04	0.73	0.30	0.54	0.28

KCNA1	3736	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	UAGCAUAGCCCAUUAUA GA	D-006210-01	1.15	0.20	1.50	0.07	1.95	0.26
KCNA1	3736	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	CCGAGGAGAUCAAAGUUU UA	D-006210-03	0.58	0.36	0.66	0.09	0.60	0.14
KCNQ4	9132	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4	ACGCGGAGGUGGUGGAU GA	D-006274-03	1.28	0.00	1.02	0.08	1.11	0.13
KCNQ4	9132	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4	AGGAAGUAGCAGAGGAG AA	D-006274-01	1.32	0.01	1.64	0.15	1.52	0.29
KCNQ4	9132	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4	UAGCAGAGGAGAAAGAGC UA	D-006274-02	1.02	0.11	0.43	0.16	0.45	0.19
KCNQ4	9132	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4	CAAAGAGCUGGAGCUU CA	D-006274-04	0.54	0.08	1.49	0.27	1.74	0.10
MTMR10	54893	NM_017762	myotubularin related protein 10	GGAUAUCAGUUUCUAGA CA	D-020758-03	1.47	0.24	1.00	0.00	0.78	0.09
MTMR10	54893	NM_017762	myotubularin related protein 10	GACUUGAGCUGUUGUGU AG	D-020758-02	1.19	0.28	1.58	0.26	1.72	0.17

MTMR10	54893	NM_017762	myotubularin related protein 10	GAACACGAUGUCCCUUU AA	D-020758- 04	1.24	0.22	0.73	0.04	1.80	0.48
MTMR10	54893	NM_017762	myotubularin related protein 10	GCAGUGCUCUUGUGCGA AU	D-020758- 01	1.45	0.24	1.46	0.04	0.92	0.49
PRPF31	26121	NM_015629	PRP31 pre- mRNA processing factor 31 homolog (S. cerevisiae)	GAAGCAGAGCGUCGUU AU	D-020525- 03	0.41	0.32	0.89	0.16	0.41	0.26
PRPF31	26121	NM_015629	PRP31 pre- mRNA processing factor 31 homolog (S. cerevisiae)	GGAAGCAGGCCAACCGU AU	D-020525- 02	0.66	0.23	1.39	0.03	1.79	0.23
PRPF31	26121	NM_015629	PRP31 pre- mRNA processing factor 31 homolog (S. cerevisiae)	GCUCUUAGCUGAUCUCG AA	D-020525- 01	0.59	0.15	1.08	0.13	2.46	0.15
PRPF31	26121	NM_015629	PRP31 pre- mRNA processing factor 31 homolog (S. cerevisiae)	CGGGAUAAAGUACUCAA GA	D-020525- 04	0.49	0.48	1.04	0.38	1.68	0.46
SEPT9	10801	NM_006640	septin 9	GGUAAAUCCACCUUAAU CA	D-006373- 06	1.17	0.18	0.93	0.26	0.83	0.09
SEPT9	10801	NM_006640	septin 9	GGAGAUCAACCAUCGUCA AA	D-006373- 03	1.32	0.00	1.30	0.09	0.81	0.24
SEPT9	10801	NM_006640	septin 9	GAGAAAGGCGUCCGGAU GA	D-006373- 02	1.24	0.10	1.03	0.04	1.85	0.09
SEPT9	10801	NM_006640	septin 9	CCAACGGCAUCGACGUG UA	D-006373- 05	0.68	0.20	1.46	0.01	2.60	0.36
TMPRSS12	283471	NM_182559	transmembrane protease, serine 12	GAACAGCACCGCUUAAAG GA	D-005948- 04	1.29	0.00	1.30	0.00	1.78	0.03
TMPRSS12	283471	NM_182559	transmembrane protease, serine 12	GGACAUGGCGUGGGUCG AA	D-005948- 03	1.18	0.18	0.97	0.30	1.64	0.17

TMPRSS12	283471	NM_182559	transmembrane protease, serine 12	GCAAGGGUCUCGGAUUA UA	D-005948- 02	1.26	0.03	1.03	0.28	0.95	0.23
TMPRSS12	283471	NM_182559	transmembrane protease, serine 12	GAAGGUAAACGCUACAAA UA	D-005948- 01	1.38	0.28	1.41	0.05	0.86	0.27
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	AGCGAUCGGCAGAGGAG AA	D-006449- 07	0.98	0.19	1.36	0.32	1.57	0.01
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	GGGUACAGUCCCAGGGG AA	D-006449- 06	1.08	0.24	0.88	0.02	2.25	0.35
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	CCACGAAGGCCACUGCA AA	D-006449- 05	1.02	0.28	0.94	0.02	1.09	0.05
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	CUGAGGAGUCAGUGCAU GU	D-006449- 08	0.68	0.21	0.68	0.27	1.94	0.10
UBE2J2	118424	NM_058167	ubiquitin- conjugating enzyme E2, J2 (UBC6 homolog, yeast)	GGACUACCUUCGCAUUA AG	D-008614- 03	0.93	0.22	1.08	0.44	1.24	0.33
UBE2J2	118424	NM_058167	ubiquitin- conjugating enzyme E2, J2 (UBC6 homolog, yeast)	GCACAAGACGAACUCAG UA	D-008614- 02	1.09	0.19	0.93	0.42	1.38	0.20
UBE2J2	118424	NM_058167	ubiquitin- conjugating enzyme E2, J2 (UBC6 homolog, yeast)	GAAGGUGGCUAUUAUCA UG	D-008614- 01	1.02	0.05	0.95	0.10	1.65	0.06

UBE2J2	118424	NM_058167	ubiquitin- conjugating enzyme E2, J2 (UBC6 homolog, yeast)	GUAUAAGAGACGUCCGGAC UU	D-008614- 04	1.30	0.12	1.15	0.11	1.86	0.24
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Cell lines and culture conditions: Huh 7.5.1 cells were grown in DMEM supplemented with 10% FBS.

Viral propagation and titration: JFH-1 was propagated and viral infectivity was titrated as previously described (Wakita (2005) *Nat Med* **11**, 791-796; Kato (2007) *J Virol* **81**, 4405-4411.).

5

Bioinformatic Meta-analysis:

Enrichment analyses: siRNA screen hits were classified into molecular function and biological process categories according to the Panther classification system, and statistical enrichment of these categories were assessed for the set of hit genes relative to their representation in the global set of genes examined in the siRNA screen. P-values were computed using the hypergeometric distribution, implemented in the R statistical computing language.

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Network analyses: Networks were generated with data extracted from interactome screens and curated literature entries in HPRD (Keshava (2009) *Nucleic Acids Res* **37**, D767-772.) and proteome-wide mapping efforts from the I-MAP project examining HCV-host protein interactions (de Chassey (2008) *Mol Syst Biol* **4**, 230.). Network constructions were implemented in the Perl programming language and incorporate graph theoretical representations by abstracting gene products as nodes and interactions as edges.

15

A two-part screen was used to identify host proteins required for virus infection. This screen utilizes the HCVcc system, which consists of the infectious JFH-1 genotype 2a virus and the Huh 7.5.1 human hepatocellular cell line (Brass (2008) *Science* **319**, 921-926.).

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In the first part of the screen, Huh 7.5.1 cells were transfected with small siRNAs for 72 hours, and then challenged with JFH-1 virus. After 48 h the cells were stained and imaged for expression of the HCV core protein as a marker for productive viral infection (Fig 1A). To find host factors involved in later stages of viral infection, we undertook part two of the screen, by exposing fresh Huh 7.5.1 cells to culture supernatant from part one for 48 h, then detecting core protein expression. This approach detects proteins needed for the complete viral lifecycle, from viral-host receptor binding to the successful completion of a second round of viral infection. In addition, genes functioning in either anti-viral responses or safeguarding the cells against the stress of infection, may be detected in this screen.

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The screen was optimized using siRNAs against the host proteins, CD81 (part one) and ApoE (part two). ApoE, a host protein involved in lipoprotein biosynthesis, has been shown to be required for infectious particle formation (Hao (2008) *Nature* **454**, 890-893; Huang (2007) *Proc Natl Acad Sci U S A* **104**, 5848-5853; Chang (2007) *J Virol* **81**, 13783-13793.). siRNAs against CD81 resulted in inhibition of part one infection (5-6 fold, Fig 1A, S1A, B). siRNAs targeting ApoE, however, did not affect infection in part one, but did inhibit HCV infection in part two by 2-3 fold, in keeping with its previously assigned role in infectious particle formation (Fig 1A, S1A, B). The levels of infection were verified using quantitative RT-PCR and found to be directly proportional to the levels determined microscopically (Fig S1 C, D). The image-based platform was then used for a genetic screen with a commercially available siRNA whole-genome library (Dharmacon siGenome, 19,470 pools of four siRNAs per gene). Pools were classified as hits (decreased infection) if the percentage of infected cells was less than 50% of the plate mean in either part one and two, or in part two alone, and did not decrease cell numbers to less than 50% of the plate mean in part one. Using these criteria we selected 407 pools for further validation (2% of the total genes screened, Fig 1B & Table S2). siRNA pools whose transfection increased core protein expression by greater than 150% of the plate mean in either part one or two, were also selected (increased infection) for validation (114 pools, 0.6%, Fig 1C & Table S2). In the validation round, we tested the four non-overlapping siRNAs from each pool separately, and found that 263 out of the 521 total pools selected (50%) were confirmed with at least two siRNAs, decreasing the likelihood of off-target effects (Table S1, Materials and Methods, the list of all genes scoring in the primary round is shown in Table S2 (Echeverri (2006) *Nat Methods* **3**, 777-779.). Forty-five genes decreased viral infection with multiple siRNAs predominantly in part two, implicating them primarily in late-stage viral infection (Table S1).

Table S2A: Replicon, JFH1, WNV									
HCV Replicon, all and JFH1 (Tai et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7
Comments	Comments	Comments	Comments	Comments	Comments	Comments	Comments	Comments	Comments
COPB2									
COPA	COPA								
CHMP2A									
COP21									
ARCN1	ARCN1								
PI4KA	PI4KA								
CKAP5									
CDC42									
TGM1									
SLC34A2									
COPB1	COPB1								
DLX6	DLX6								
FANCE									
NAPA									
TRIM62	TRIM62								
COPG									
BCKDHB									
SPATA13									
CHST12									
HAMP									
OR6K3									
IL4I1	IL4I1								
NAB1									
TUBA1C									
FXYD2									
SERBP1									
NOX1									
ERCC1									
RNF152									
OR8K1									
TSHZ1									
YEATS4									
TBK1									
WDR46									
BPII2									
HSF1									

Table S2A: Replicon, JFH1, WNV											
HCV Replicon: (Tai et al) multi-siRNA Candidate Genes	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV replicon (Tai et al) and JFH1 (Li et al) primary screen, data 12	Comments	Overlap HCV Replicon (Tai et al) and WNV (Krishnan et al) multi-siRNA Candidate Genes 1	Overlap WNV (Krishnan et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 6	Overlap WNV (Krishnan et al) and JFH1 (Li et al) primary screen, data 14	Comment	Randall et al. JFH1 Host Factor Candidate Genes > 3-fold inhibition	Overlap JFH1 (Randall et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 6	Berger et al. JFH1 Host Factor Candidate Genes	Overlap JFH1 (Berger et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 2
INOM1					BCKDHA	BCKDHA					
ARL1					BEAN						
KRT31					BICC1						
NUAK2	NUAK2	NUAK2			BPESC1						
			Two siRNAs inhibited infection less than 50% of negative controls but with low cell numbers								
HAS1		HAS1			BRUNOL5						
CACNG1					C10orf119						
			One out of four (1/4) siRNAs inhibited infection less than 50% of negative controls, one additional siRNA was toxic in validation round								
CEBPD		CEBPD			C10orf79						
SERPINE2					C18orf22						
HRASLS2					CACNA1A						
TAS2R1					CALCB						
JMJD2A					CBLL1						
CTSF	CTSF	CTSF			CD164L1						
TPS1					CEACAM6						
ZNF550					CFHL5						
PSMD3					CHML						
NUF2					CITED2						
RABEPK	RABEPK	RABEPK			CLEC4C						
RAN					CLEC7A						
SNX4					CLEC5F6						
POU3F2					CLIC1						
SIVA1					CLK1						
IDS		IDS	low cell number (less than 50% of mean cell number)		CNP						
MAGEA9					CNTN3						
WFDC13					COIL						
UPK3A					CORO1B						
GGB8					CSNK2A1						
LOC54103					CST1						
TBL3					CST3						
C11orf35					CST5						
SSPO					CTEN						
LTBR2					CTSE						
THAP11					DDX42						
HNRPA8					DDX28						
HPS4					DEFB118						
MLNR					DEFB129						
HYAL4					DERL2						
PSMD1					DHX15						
COASY					DHX40						

Table S2A: Replicon, JFH1, WNV

Table S2A: Replicon, JFH1, WNV												
	Overlap HCV Replicon (Tal et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tal et al) and JFH1 (Li et al) multi-siRNA primary screen data) 12		Overlap HCV Replicon (Tal et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 1	WNV screen (Krishnan et al) multi-siRNA Candidate Genes 6	Overlap WNV (Krishnan et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 6	Overlap WNV (Krishnan et al) and JFH1 (Li et al) primary screen data) 14	Comment	Randall et al JFH1 Host Factor Candidate Genes > 3-fold inhibition	Overlap JFH1 (Randall et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 6	Berger et al JFH1 Host Factor Candidate Genes	Overlap JFH1 (Berger et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 2
		Comments										
DLK1		DLK1		DMRTC2								
HIFX				DOX1								
NCOA6				EBF2								
DTX3L				EGFL4								
HHOM				ELMOD1								
KCNK4				ESPN								
MAP3K14				EXOSC9								
IFITM1				FBF1								
BCAT1				FBN3								
LXN2				FIBCD1								
ACOT8				FKSG44								
ITGA7	ITGA7			FLJ13305								
CCDC99				FLJ22684								
OPTC				FOXP4								
GTAG1A				FUT4								
CCDC12				GAB1								
NOP5/NOP58	NOP5/NOP58	NOP5/NOP58		GAB3								
RAB7A				GAL3ST2								
BAAT				GCL				1/4 siRNAs validated, Required by both WNV and Dengue (Krishnan et al)				
LNP1												
CBX1				GFER			GFER					
LOC390205				GLCO11								
				GRK6								
				GRM2								
				GSC								
				HAPLN2								
				HERC1								
				HMG4L								
				HOXC12								
				HOXC5								
				HRBL								
				HRD1								
				IBRDC2								
				IER2								
				IL411								
				ITFG3								
				KAL1								
				KCNH3								
				KCNK6								
				KENAE								
				KIAA1394								
				KIAA1539								
				KIF17								
				KIF1A								
				KLHL1								
				LACRT								
				LAS1L								

Table S2A: Replicon, JFH1, WNV

HCV Replicon (Tai et al) multi- siRNA Candidate Genes	Overlap HCV Replicon (Tai et al) and JFH1 multi-siRNA Candidate Genes 7	Overlap HCV replicon (Tai et al) and JFH1 (Li et al) primary screen data) 12		Overlap HCV Replicon (Tai et al) and WNV multi-siRNA Candidate Genes) 1	WNV screen (Krishnan et al) multi-siRNA Candidate Genes	Overlap WNV and JFH1 (Li et al) both multi-siRNA Candidate Genes) 6	Overlap WNV and JFH1 (Li et al) primary screen data) 14	Comment	Randall et al JFH1 Host Factor Candidate Genes > 3-fold inhibition	Overlap JFH1 (Randall et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 6	Berger et.al JFH1 Host Factor Candidate Genes	Overlap JFH1 (Berger et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 2
					PLK4							
					PIVAP							
					PNU11							
					PNU12							
					PP1Z01							
					PR1							
					PRG-3							
					PSCA							
					PSMF1							
					PSORS1C2							
					PTGES2							
								1/4 siRNAs validated, Required by WNV not Dengue (Krishnan et al)				
					PTK2B			PTK2B				
					PTPNS1							
					PXN							
					RAB33B							
					RAB34							
					RAB3D							
					RARGE1							
					RAD51							
								1/4 siRNAs validated, Required by both WNV and Dengue (Krishnan et al)				
					RASSF1			RASSF1				
					RBM20							
								Required by both WNV and Dengue (Krishnan et al)				
					RBM22			RBM22				
					RBM5							
					RBPMS							
					RFWD2							
					RIMS4							
					RLBP1							
					RNF123							
					RNF28							
					RNF44							
					RNPEPL1							
								Required by both WNV and Dengue (Krishnan et al)				
					RPS6K1 1			RPS6K1 1				
					RPS6K1 1			RPS6K1 1				
					RPS6K1 1			RPS6K1 1				

Table S2A: Replicon, JFH1, WNV											
HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 7	Overlap HCV Replicon (Tai et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 12	Overlap HCV Replicon (Tai et al) and WNV (Krishnan et al) multi-siRNA Candidate Genes 1	Overlap WNV (Krishnan et al) and JFH1 (Li et al) both multi-siRNA Candidate Genes 9	Overlap WNV (Krishnan et al) and JFH1 (Li et al) primary screen data 14	Comment	Randall et al JFH1 Host Factor Candidate Genes > 3-fold inhibition	Overlap JFH1 (Randall et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 6	Berger et al JFH1 Host Factor Candidate Genes	Overlap JFH1 (Berger et al) and JFH1 (Li et al) multi-siRNA Candidate Genes 2		

Table S2B: Replicon, JFH1 primary data						
HCV Replicon screen (Tai et al) multi-siRNA Candidate Genes	Gene ID	Accession number	JFH1 Primary screen data normalized cell number	JFH1 Primary screen data normalized percent infected cells	JFH1 screen data level	Comment
COPB2	9276	NM_004766	0.39	0.64		Low cell number
COPA	1314	NM_004371	0.08	0.24		Low cell number
CHMP2A	27243	NM_014453	0.53	0.82		
COPZ1	22818	NM_016057	0.21	1.06		Low cell number
ARCN1	372	NM_001655	0.31	0.41		Low cell number
PI4KA	5297	NM_002650	Validation round data provided Table S1		Validation Round	
CKAP5	9793	NM_014756	0.31	0.79		Low cell number
CDC42	998	NM_001791	1.01	0.93		
TGM1	7051	NM_000359	0.57	0.76		
SLC34A2	10568	NM_006424	1.09	0.84		
COPB1	1315	NM_016451	0.37	0.46		Low cell number
DLX6	0	NM_005222	1.00	0.50	Smartpool (SP)	
FANCE	2178	NM_021922	1.06	0.73		
NAPA	8775	NM_003827	0.41	1.15		
TRIM62	55223	NM_018207	Validation round data provided Table S1		Validation Round	
COPG	22820	NM_016128	0.63	1.13		
BCKDHB	594	NM_000056	0.72	1.27		
SPATA13	221178	NM_153023	0.54	1.11		
CHST12	55501	NM_018641	1.18	0.92		
HAMP	57817	NM_021175	1.03	0.76		
OR6K3	391114	NM_001005327	1.11	1.47		
IL4I1	259307	NM_152899	1.11	1.32		
NAB1	4664	NM_005966	0.79	1.08		
TUBA1C	84790	NM_032704	0.42	0.81		
FXD2	486	NM_001680	0.73	0.80		
SERBP1	26135	NM_015640	0.75	1.23		
NOX1	27035	NM_007052	1.20	0.58		
ERCC1	2067	NM_001983	0.89	0.78		
RNF152	220441	NM_173557	1.56	1.08		
OR8K1	390157	NM_001002907	1.18	0.93		

TSHZ1	10194	NM_005786	1.16	1.12		
YEATS4	8089	NM_006530	0.61	1.02		
TBK1	29110	NM_013254	0.47	0.70		
WDR46	9277	NM_005452	0.65	0.68		
BPIL2	254240	NM_174932	0.65	0.90		
HSF1	3297	NM_005526	0.45	1.21		
NOM1	64434	NM_138400	1.20	0.79		
ARL1	400	NM_001177	0.98	1.21		
KRT31	3881	NM_002277	0.86	0.72		
NUAK2/SNARK	81788	NM_030952	Validation round data provided Table S1		Validation Round	
HAS1	3036	NM_001523	0.90	0.49	Validation Round	Two siRNAs inhibited infection less than 50% of negative controls but with low cell numbers
CACNG1	786	NM_000727	1.09	1.55		
CEBPD	1052	NM_005195	0.75	0.51	Validation Round	One out four siRNAs inhibited infection less than 50% of negative controls, one additional siRNA was toxic in validation round
SERPINB2	5055	NM_002575	1.25	0.94		
HRASLS2	54979	NM_017878	1.14	1.06		
TAS2R1	50834	NM_019599	0.67	0.90		
JMJD2A	9682	NM_014663	1.08	1.15		
CTSF	8722	NM_003793	Validation round data provided Table S1		Validation Round	
TPS1	7176	NM_003293	0.91	0.78		
ZNF550	162972	NM_153231	1.15	1.02		
PSMD3	5709	NM_002809	0.53	1.23		
NUF2	83540	NM_031423	0.54	0.88		
RABEPK	10244	NM_005833	Validation round data provided Table S1		Validation Round	
RAN	5901	NM_006325	0.22	0.95		
SNX4	8723	NM_003794	1.11	0.91		
POU3F2	5454	NM_005604	0.66	0.53		

SIVA1	10572	NM_006427	0.68	0.94		
IDS	3423	NM_000202	0.46	0.41	SP	Low cell number
MAGEA9	4108	NM_005365	0.91	0.82		
WFDC13	164237	NM_172005	1.02	0.78		
UPK3A	7380	NM_006953	1.07	1.12		
CGB8	94115	NM_033183	1.39	0.85		
LOC54103	0	NM_017439	1.03	1.09		
TBL3	10607	NM_006453	0.82	0.79		
C11orf35	256329	NM_173573	0.77	1.04		
SSPO	23145	NM_198455	ND	ND		
LTB4R2	56413	NM_019839	0.16	0.91		
THAP11	57215	NM_020457	0.92	0.83		
HNRPAB	3182	NM_004499	1.14	0.87		
HPS4	89781	NM_022081	1.10	0.83		
MLNR	2862	NM_001507	1.14	0.62		
HYAL4	23553	NM_012269	0.53	1.19		
PSMD1	5707	NM_002807	0.50	1.17		
COASY	80347	NM_025233	0.39	0.94		
DLK1	8788	NM_003836	0.66	0.44	SP	
H1FX	8971	NM_006026	1.17	0.83		
NCOA6	23054	NM_014071	1.15	0.63		
DTX3L	151636	NM_138287	0.71	0.83		
HHCM	10639	NM_001001731	1.46	1.05		
KCNK4	50801	NM_016611	1.19	0.90		
MAP3K14	9020	NM_003954	1.04	1.07		
IFITM1	8519	NM_003641	1.06	1.11		
BCAT1	586	NM_005504	0.62	0.84		
LHX2	9355	NM_004789	1.27	1.09		
ACOT8	10005	NM_005469	1.24	1.04		
ITGA7	3679	NM_002206	Validation round data provided Table S1		Validation Round	
CCDC99	54908	NM_017785	1.01	0.89		
OPTC	26254	NM_014359	0.98	0.72		
CTAG1A	246100	NM_139250	1.29	0.86		
CCDC12	151903	NM_144716	0.69	0.99		
NOP5/NOP58	51602	NM_015934	Validation round data provided Table S1		Validation Round	
RAB7A	7879	NM_004637	0.61	0.89		
BAAT	570	NM_001701	0.73	0.88		
LNP1	348801	NM_001085451	0.92	0.83		
CBX1	10951	NM_006807	1.04	0.97		
LOC390205	0	XM_372416	ND	ND		

TABLE S2C: Randall, et al., JFH1 primary data						
Randall et. al. siRNA screen Candidate Genes	Accession number	Gene ID	JFH1 Primary screen data normalized cell number	JFH1 Primary screen data normalized percent infected cells	Comment	Viral interacting protein (Randall et al)
ADI1	NM_018269	55256	0.89	1.39		
AHSA1	NM_012111	9863	0.68	1.49		NS5A
AKT1	NM001014431	207	1.10	1.22		
ATF6	NM_007348	22926	0.52	1.20		
CALR	NM_004343	811	0.44	0.98		
CANX	NM_001024649	821	1.84	1.49		
CDC2	NM_001786	983	1.08	1.11		
CDK2	NM_001798	1017	0.86	0.62		
CDK6	NM_001259	1021	0.97	1.09		NS5A
CD81	NM_004356	975	Validation round data provided Table S1			
CSNK2A1	NM_001895	1457	0.91	0.69		
DDX3X	NM_001356	1654	Validation round data provided Table S1			
DGCR8	NM_022720	54487	1.01	0.53		
DICER1	NM_030621	23405	0.92	0.51		
DNAJC14	NM_032364	85406	1.08	0.90		
EIF2AK2	NM_002759	5610	1.14	1.33		
EIF2AK3	NM_004836	9451	1.34	1.19		
EIF2B3	NM_020365	8891	0.82	0.71		
EIF2C1	NM_012199	26523	0.75	0.79		
EIF2C2	NM_012154	27161	1.38	0.99		
EIF2C3	NM_024852	168544	1.25	1.10		
EIF2C4	NM_017629	192670	0.75	0.79		
EIF2S3	NM_001415	1968	0.30	0.18	Low cell number	
ELAVL1	NM_001419	1994	Validation round data provided Table S1			
G1P2	NM_005101	9636	1.33	1.04		
GAPDH	NM_002046	2597	1.22	1.02		
GRB2	NM_002086	2885	0.96	1.02		
HM13	NM_030789	81502	0.91	1.95	Increased Infection, one out of 4 siRNA validated	
HNRPC	NM_004500	3183	0.40	1.11		
HRMT1L2	NM_001536	3276	1.22	0.98		

HSPA1A (no data provided in Randall et al.)	NM_005345	3303	Validation round data provided Table S1			
HSPCA	NM_005348	3320	0.94	0.72		
IPO4	NM_024658	79711	0.86	0.67		NS5A
ISGF3G	NM_006084	10379	1.30	1.43		
LSM1	NM_014462	27257	1.09	1.19		
MAPK1	NM_002745	5594	Validation round data provided Table S1			
MAPK12	NM_002969	6300	0.71	0.73		
NCL	NM_005381	4691	0.92	0.94		
PCBP1	NM_006196	5093	1.25	1.35		
PCBP2	NM_005016	5094	0.68	0.91		
PDPK1	NM_002613	5170	0.76	1.06		
PRKACA	NM_002730	5566	1.05	0.99		
PSMA7	NM_002792	5688	0.64	0.93		
PTBP1	NM_002819	5725	0.88	0.96		
RAF1	NM_002880	5894	Validation round data provided Table S1			
RANBP5	NM_002271	3843	1.02	1.05		
RELA	NM_021975	5970	2.05	1.48		
RNASEN	NM_013235	29102	0.72	0.79		
RPL22	NM_000983	6146	1.31	1.11		
RPL3	NM_007208	11222	1.05	1.30		
SCARB1	NM_002966	6281	0.87	0.77		
SCD	NM_005063	6319	1.05	0.69		
SEC11L1	NM_014300	23478	1.41	1.07		
SKB1	NM_006109	10419	0.87	1.21		
SNX1	NM_003099	6642	0.88	1.49		
SRCAP	NM_006662	10847	0.53	0.64		
SSB	NM_003142	6741	1.21	1.01		
STAT3	NM_003150	6774	Validation round data provided Table S1			
TP53	NM_000546	7157	0.88	0.79		
USP18	NM_017414	11274	0.89	0.82		
VAPA	NM_003574	9218	1.09	0.87		
VAPB	NM_004738	9217	1.05	0.94		
VPS35	NM_018206	55737	0.70	0.93		NS5A
VPS4A	NM_013245	27183	0.58	0.73		
XBP1	NM_005080	7494	0.68	1.38		

TABLE S2D: Ng et al., JFH1 primary data					
Ng et al siRNA screen Candidate Genes	Accession number	Gene ID	JFH1 Primary screen data normalized cell number	JFH1 Primary screen data normalized percent infected cells	
TBXA2R	NM_001060.4	6915	1.03	0.79	
RelA	NM_021975.3	5970	2.05	1.48	
NFKB2	NM_001077493.1	4791	0.47	0.75	Low cell number
LTB	NM_002341.1	4050	0.52	1.25	
MKK7	NM_145185.2	5609	0.88	0.83	
TRAF2	NM_021138.3	7186	0.72	1.26	
NUAK2/SNARK	NM_030952.1	81788	Validation round data provided Table S1		
SLC12A4	NM.005072.4	6560	1.22	0.80	
SLC12A5	NM_001134771.1	57468	0.89	1.17	

TABLE S2E: Berger et al., primary data				
Berger et al. JFH-1 Screen Candidat Genes	Accession number	Gene ID	JFH1 Primary screen data normalized cell number	JFH1 Primary screen data normalized percent infected cells
CDC42	NM_001791	998	0.92	1.26
ROCK2	NM_004850	9475	Validation round data provided Table S1	
Rab7L1	NM_003929	8934	0.71	0.69
EEA1	NM_003566	8411	1.16	1.00
Rab5A	NM_004162	5868	0.72	0.70
PIK3C2G	NM_004570	5288	1.12	1.03
PIK4A	NM_030952.1	81788	Validation round data provided Table S1	

TABLE S2F: JFH (Li et al.) Increased Infection			
Primary Screen Candidates Increased Infection			
Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
ACBD3	64746	NM_022735	acyl-Coenzyme A binding domain containing 3
ACSS2	55902	NM_018677	acyl-CoA synthetase short-chain family member 2
ACTR10	55860	NM_018477	actin-related protein 10 homolog (S. cerevisiae)
ANKH	56172	NM_054027	ankylosis, progressive homolog (mouse)
ANXA13	312	NM_004306	annexin A13
APC2	10297	NM_005883	adenomatosis polyposis coli 2
ARAF	369	NM_001654	v-raf murine sarcoma 3611 viral oncogene homolog
ARHGEF15	22899	NM_173728	Rho guanine nucleotide exchange factor (GEF) 15
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7
ARL10	285598	NM_173664	ADP-ribosylation factor-like 10
ART5	116969	NM_053017	ADP-ribosyltransferase 5
ATIC	471	NM_004044	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ATP11A	23250	XM_085028, XM_495964	ATPase, Class VI, type 11A
ATXN8OS	6315	AF126749	ataxin 8 opposite strand
C16orf59	80178	NM_025108	chromosome 16 open reading frame 59
CABP1	9478	NM_004276	calcium binding protein 1
CACNA1F	778	NM_005183	calcium channel, voltage-dependent, L type, alpha 1F subunit
CCDC18	343099	NM_206886	coiled-coil domain containing 18
CCL26	10344	NM_006072	chemokine (C-C motif) ligand 26
CCRK	23552	NM_012119	cell cycle related kinase
CDC23	8697	NM_004661	cell division cycle 23 homolog (S. cerevisiae)
CEACAM3	1084	NM_001815	carcinoembryonic antigen-related cell adhesion molecule 3
CETN2	1069	NM_004344	centrin, EF-hand protein, 2
CHM	1121	NM_000390	choroideremia (Rab escort protein 1)
COTL1	23406	NM_021149	coactosin-like 1 (Dictyostelium)
CPD	1362	NM_001304	carboxypeptidase D

CRADD	8738	NM_003805	CASP2 and RIPK1 domain containing adaptor with death domain
CRLF3	51379	NM_015986	cytokine receptor-like factor 3
CSF3R	1441	NM_000760	colony stimulating factor 3 receptor (granulocyte)
CSTF3	1479	NM_001326	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
CTBP2	1488	NM_001329	C-terminal binding protein 2
CTNNAL1	8727	NM_003798	catenin (cadherin-associated protein), alpha-like 1
CXCL12	6387	NM_000609	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
CYP2C19	1557	NM_000769	cytochrome P450, family 2, subfamily C, polypeptide 19
DMXL2	23312	NM_015263	Dmx-like 2
DNM3	26052	NM_015569	dynamamin 3
DOCK11	139818	NM_144658	dedicator of cytokinesis 11
ECT2	1894	NM_018098	epithelial cell transforming sequence 2 oncogene
EMID2	136227	NM_133457	EMI domain containing 2
EPB41L2	2037	NM_001431	erythrocyte membrane protein band 4.1-like 2
ERBB2	2064	NM_004448	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
ERN1	2081	NM_001433	endoplasmic reticulum to nucleus signaling 1
EZR	7430	NM_003379	ezrin
FARP1	10160	NM_005766	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
GATM	2628	NM_001482	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GKN2	200504	NM_182536	gastrokine 2
GNAZ	2781	NM_002073	guanine nucleotide binding protein (G protein), alpha z polypeptide
HM13	81502	NM_030789	histocompatibility (minor) 13
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K
IFIH1	64135	NM_022168	interferon induced with helicase C domain 1
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6
IL17RB	55540	NM_018725	interleukin 17 receptor B
IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1
INSM1	3642	NM_002196	insulinoma-associated 1

IRF7	3665	NM_001572	interferon regulatory factor 7
ISGF3G	10379	NM_006084	interferon-stimulated transcription factor 3, gamma 48kDa
ISLR2	57611	NM_020851	immunoglobulin superfamily containing leucine-rich repeat 2
KCNA1	3736	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
KCNQ4	9132	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4
KIAA1219	57148	NM_020336	KIAA1219
KRT33A	3883	NM_004138	keratin 33A
LCK	3932	NM_005356, NM_001042771	lymphocyte-specific protein tyrosine kinase
MMP11	4320	NM_005940	matrix metalloproteinase 11 (stromelysin 3)
MMP9	4318	NM_004994	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
MPG	4350	NM_002434	N-methylpurine-DNA glycosylase
MTMR10	54893	NM_017762	myotubularin related protein 10
NDRG1	10397	NM_006096	N-myc downstream regulated gene 1
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus
OSTbeta	123264	NM_178859	organic solute transporter beta
OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1
PDE8B	8622	NM_003719	phosphodiesterase 8B
PET112L	5188	NM_004564	PET112-like (yeast)
PKD1L3	342372	NM_181536	polycystic kidney disease 1-like 3
PLA2R1	22925	NM_007366	phospholipase A2 receptor 1, 180kDa
PPP2R2A	5520	NM_002717	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
PRG2	5553	NM_002728	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)
PRPF31	26121	NM_015629	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
PRSS3	5646	NM_002771	protease, serine, 3 (mesotrypsin)
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H
PYHIN1	149628	NM_152501	pyrin and HIN domain family, member 1
RFWD3	55159	NM_018124	ring finger and WD repeat domain 3

RIN3	79890	NM_024832	Ras and Rab interactor 3
SAP130	79595	NM_024545	Sin3A-associated protein, 130kDa
SEPT9	10801	NM_006640	septin 9
SCNM1	79005	NM_024041	sodium channel modifier 1
SDK1	221935	NM_152744	sidekick homolog 1, cell adhesion molecule (chicken)
SETD7	80854	NM_030648	SET domain containing (lysine methyltransferase) 7
SGSH	6448	NM_000199	N-sulfoglucosamine sulfohydrolase (sulfamidase)
SH3PX3	257364	NM_153271	SH3 and PX domain containing 3
SLC25A36	55186	NM_018155	solute carrier family 25, member 36
SLC47A2	146802	NM_152908	solute carrier family 47, member 2
SNRPD1	6632	NM_006938	small nuclear ribonucleoprotein D1 polypeptide 16kDa
SUPT4H1	6827	NM_003168	suppressor of Ty 4 homolog 1 (S. cerevisiae)
TGFR1	7046	NM_004612	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
TMEM45A	55076	NM_018004	transmembrane protein 45A
TMEM54	113452	NM_033504	transmembrane protein 54
TMEM57	55219	NM_018202	transmembrane protein 57
TMPRSS12	283471	NM_182559	transmembrane protease, serine 12
TNFRSF10C	8794	NM_003841	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
TNFRSF10D	8793	NM_003840	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18
TNS1	7145	NM_022648	tensin 1
TP53I3	9540	NM_004881	tumor protein p53 inducible protein 3
TSSK3	81629	NM_052841	testis-specific serine kinase 3
TUBB3	10381	NM_006086	tubulin, beta 3
U1SNRNPBP	11066	NM_007020	U11/U12 snRNP 35K
UBE2J2	118424	NM_058167	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
USP43	124739	XM_371015	ubiquitin specific peptidase 43
WSB1	26118	NM_134264	WD repeat and SOCS box-containing 1
YIPF4	84272	NM_032312	Yip1 domain family, member 4
ZCCHC3	85364	NM_033089	zinc finger, CCHC domain containing 3
ZNF160	90338	NM_033288	zinc finger protein 160
ZNF200	7752	NM_003454	zinc finger protein 200
ZNF74	7625	NM_003426	zinc finger protein 74

TABLE S2G: JFH1 (Li et al.) Decreased Infection

Primary Screen Candidates Decreased Infection			
Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
A2ML1	144568	NM_144670	alpha-2-macroglobulin-like 1
AASDHPPT	60496	NM_015423	aminoadipate-semialdehyde dehydrogenase- phosphopantetheinyl transferase
ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6
ABCE1	6059	NM_002940	ATP-binding cassette, sub-family E (OABP), member 1
ABHD2	11057	NM_007011	abhydrolase domain containing 2
ADAMTS4	9507	NM_005099	ADAM metalloproteinase with thrombospondin type 1 motif, 4
ADFP	123	NM_001122	adipose differentiation-related protein
AGPAT3	56894	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3
AIF1	199	NM_001623	allograft inflammatory factor 1
ALAD	210	NM_000031	aminolevulinate, delta-, dehydratase
ALDH1L2	160428	XM_090294	aldehyde dehydrogenase 1 family, member L2
AMMECR1L	83607	NM_031445	AMME chromosomal region gene 1-like
ANKRD20A1	84210	NM_032250	ankyrin repeat domain 20 family, member A1
AP1GBP1	11276	NM_007247	AP1 gamma subunit binding protein 1
AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit
APC2	10297	NM_005883	adenomatosis polyposis coli 2
APLP2	334	NM_001642	amyloid beta (A4) precursor-like protein 2
APOBEC2	10930	NM_006789	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2
APOC1	341	NM_001645	apolipoprotein C-I
APOE	348	NM_000041	apolipoprotein E
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22
ARHGEF10L	55160	NM_018125	Rho guanine nucleotide exchange factor (GEF) 10-like
ARRDC2	27106	NM_015683	arrestin domain containing 2
ATP10D	57205	NM_020453	ATPase, Class V, type 10D
ATP6V0B	533	NM_004047	ATPase, H ⁺ transporting, lysosomal 21kDa, V0 subunit b
BAGE2	85319	NM_182482	B melanoma antigen family, member 2
BAIAP2	10458	NM_006340	BAI1-associated protein 2
BCKDHA	593	NM_000709	branched chain keto acid dehydrogenase E1, alpha polypeptide
BCL7A	605	NM_020993	B-cell CLL/lymphoma 7A
BCL9L	283149	NM_182557	B-cell CLL/lymphoma 9-like
BLOC1S3	388552	NM_212550	biogenesis of lysosome-related organelles complex-1, subunit 3

BRF1	2972	NM_001519	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (<i>S. cerevisiae</i>)
BRUNOL6	60677	NM_052840	bruno-like 6, RNA binding protein (<i>Drosophila</i>)
BRWD1	54014	NM_018963	bromodomain and WD repeat domain containing 1
C10orf112	340895	XM_295865	chromosome 10 open reading frame 112
C14orf73	91828	XM_040910	chromosome 14 open reading frame 73
C16orf80	29105	NM_013242	chromosome 16 open reading frame 80
C19orf44	84167	NM_032207	chromosome 19 open reading frame 44
C1orf49	84066	NM_032126	chromosome 1 open reading frame 49
C1orf53	388722	XM_371331	chromosome 1 open reading frame 53
C1QA	712	NM_015991	complement component 1, q subcomponent, A chain
C1QB	713	NM_000491	complement component 1, q subcomponent, B chain
C20orf20	55257	NM_018270	chromosome 20 open reading frame 20
C20orf29	55317	NM_018347	chromosome 20 open reading frame 29
C20orf66	343629	XM_293121	chromosome 20 open reading frame 66
C21orf56	84221	NM_032261	chromosome 21 open reading frame 56
C7orf41	222166	NM_152793	chromosome 7 open reading frame 41
C8orf34	116328	NM_052958	chromosome 8 open reading frame 34
C9orf121	158046	NM_145283	chromosome 9 open reading frame 121
C9orf125	84302	NM_032342	chromosome 9 open reading frame 125
CA5A	763	NM_001739	carbonic anhydrase VA, mitochondrial
CADM2	253559	NM_153184	cell adhesion molecule 2
CAMTA2	23125	NM_015099	calmodulin binding transcription activator 2
CASP4	837	NM_001225	caspase 4, apoptosis-related cysteine peptidase
CCDC8	83987	NM_032040	coiled-coil domain containing 8
CCL26	10344	NM_006072	chemokine (C-C motif) ligand 26
CCL3L1	6349	NM_021006	chemokine (C-C motif) ligand 3-like 1
CCNB2	9133	NM_004701	cyclin B2
CCPG1	9236	NM_004748	cell cycle progression 1
CD3E	916	NM_000733	CD3e molecule, epsilon
CD55	1604	NM_000574	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
CD81	975	NM_004356	CD81 molecule
CDC42EP3	10602	NM_006449	CDC42 effector protein (Rho GTPase binding) 3
CDC6	990	NM_001254	cell division cycle 6 homolog (<i>S. cerevisiae</i>)
CDCA3	83461	NM_031299	cell division cycle associated 3
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5
CDX1	1044	NM_001804	caudal type homeobox transcription factor 1
CEBPD	1052	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta
CENPQ	55166	NM_018132	centromere protein Q
CHKA	1119	NM_001277	choline kinase alpha
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase
CIRH1A	84916	NM_032830	cirrhosis, autosomal recessive 1A (cirhin)
CISH	1154	NM_013324	cytokine inducible SH2-containing protein
CITED2	10370	NM_006079	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
CLDN1	9076	NM_021101	claudin 1
CLDN12	9069	NM_012129	claudin 12

CLDN14	23562	NM_012130	claudin 14
CLSTN1	22883	NM_014944	calsyntenin 1
CNOT1	23019	NM_016284	CCR4-NOT transcription complex, subunit 1
CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like
CRLF2	64109	NM_022148	cytokine receptor-like factor 2
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like
CTAGE6	340307	NM_178561	CTAGE family, member 6
CTGF	1490	NM_001901	connective tissue growth factor
CTSF	8722	NM_003793	cathepsin F
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1
CXorf22	170063	NM_152632	chromosome X open reading frame 22
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide
CYP4A22	284541	XM_208213, NM_001010969	cytochrome P450, family 4, subfamily A, polypeptide 22
DACT1	51339	NM_016651	dapper, antagonist of beta-catenin, homolog 1 (<i>Xenopus laevis</i>)
DACT3	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
DBNDD1	79007	NM_024043	dysbindin (dystrobrevin binding protein 1) domain containing 1
DCTN3	11258	NM_007234	dynactin 3 (p22)
DDIT3	1649	NM_004083	DNA-damage-inducible transcript 3
DDOST	1650	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
DDX21	9188	NM_004728	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
DDX6	1656	NM_004397	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
DEFA5	1670	NM_021010	defensin, alpha 5, Paneth cell-specific
DEFB123	245936	NM_153324	defensin, beta 123
DEFB126	81623	NM_030931	defensin, beta 126
DGAT1	8694	NM_012079	diacylglycerol O-acyltransferase homolog 1 (mouse)
DHRS12	79758	NM_024705	dehydrogenase/reductase (SDR family) member 12
DIO3	1735	NM_001362	deiodinase, iodothyronine, type III
DLGAP4	22839	NM_014902	discs, large (<i>Drosophila</i>) homolog-associated protein 4
DNAJB1	3337	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1
DNMT1	1786	NM_001379	DNA (cytosine-5-)-methyltransferase 1
DOCK3	1795	NM_004947	dedicator of cytokinesis 3
DTNB	1838	NM_021907	dystrobrevin, beta
DYRK1B	9149	NM_004714	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
DYSF	8291	NM_003494	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
E2F1	1869	NM_005225	E2F transcription factor 1
E2F2	1870	NM_004091	E2F transcription factor 2
EGLN2	112398	NM_053046	egl nine homolog 2 (<i>C. elegans</i>)
EIF3S6	3646	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa
ELAVL1	1994	NM_001419	ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 1 (Hu antigen R)

ENDOG	2021	NM_004435	endonuclease G
ERC2	26059	NM_015576	ELKS/RAB6-interacting/CAST family member 2
ERCC5	2073	NM_000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
ETF1	2107	NM_004730	eukaryotic translation termination factor 1
EWSR1	2130	NM_005243	Ewing sarcoma breakpoint region 1
FAIM3	9214	NM_005449	Fas apoptotic inhibitory molecule 3
FAM100B	283991	NM_182565	family with sequence similarity 100, member B
FAM116A	201627	NM_152678	family with sequence similarity 116, member A
FAM73A	374986	NM_198549	family with sequence similarity 73, member A
FAU	2197	NM_001997	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
FBLN5	10516	NM_006329	fibulin 5
FBXO38	81545	NM_030793	F-box protein 38
FBXO40	51725	NM_016298	F-box protein 40
FCGRT	2217	NM_004107	Fc fragment of IgG, receptor, transporter, alpha
FER1L3	26509	NM_013451	fer-1-like 3, myoferlin (C. elegans)
FIGN	55137	NM_018086	fidgetin
FKBPL	63943	NM_022110	FK506 binding protein like
FLJ22659	79999	XM_378723	hypothetical protein FLJ22659
FLJ36874	219988	NM_152716	FLJ36874 protein
FLJ39639	283876	XM_370932	hypothetical protein FLJ39639
FLT4	2324	NM_002020	fms-related tyrosine kinase 4
FOXA2	3170	NM_021784	forkhead box A2
FOXE3	2301	NM_012186	forkhead box E3
FOXN1	8456	NM_003593	forkhead box N1
FOXP3	50943	NM_014009	forkhead box P3
FRMPD3	84443	XM_042978	FERM and PDZ domain containing 3
FSCN3	29999	NM_020369	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)
FUNDC1	139341	NM_173794	FUN14 domain containing 1
FXVD6	53826	NM_022003	FXVD domain containing ion transport regulator 6
GCAT	23464	NM_014291	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
GCM1	8521	NM_003643	glial cells missing homolog 1 (Drosophila)
GFER	2671	NM_005262	growth factor, augmentor of liver regeneration (ERV1 homolog, S. cerevisiae)
GLI4	2738	NM_138465	GLI-Kruppel family member GLI4
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
GNG8	94235	NM_033258	guanine nucleotide binding protein (G protein), gamma 8
GPC1	2817	NM_002081	glypican 1
GPR153	387509	XM_291419	G protein-coupled receptor 153
GPR62	118442	NM_080865	G protein-coupled receptor 62
GPSN2	9524	NM_004868	glycoprotein, synaptic 2
GPT	2875	NM_005309	glutamic-pyruvate transaminase (alanine aminotransferase)

GRIK3	2899	NM_000831	glutamate receptor, ionotropic, kainate 3
GSPT1	2935	NM_002094	G1 to S phase transition 1
GTF3A	2971	NM_002097	general transcription factor IIIA
GUCY1A2	2977	NM_000855	guanylate cyclase 1, soluble, alpha 2
HAS1	3036	NM_001523	hyaluronan synthase 1
HCCS	3052	NM_005333	holocytochrome c synthase (cytochrome c heme-lyase)
HEATR1	55127	XM_375853	HEAT repeat containing 1
HEG1	57493	XM_087386	HEG homolog 1 (zebrafish)
HEXA	3073	NM_000520	hexosaminidase A (alpha polypeptide)
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3
HIST1H2BK	85236	NM_080593	histone cluster 1, H2bk
HIST1H2BN	8341	NM_003520	histone cluster 1, H2bn
HMGB4	127540	NM_145205	high-mobility group box 4
HOXB13	10481	NM_006361	homeobox B13
HPX	3263	NM_000613	hemopexin
HRC	3270	NM_002152	histidine rich calcium binding protein
HSD17B13	345275	NM_178135	hydroxysteroid (17-beta) dehydrogenase 13
HSPA1A	3303	NM_005345	heat shock 70kDa protein 1A
IDE	3416	NM_004969	insulin-degrading enzyme
IFITM2	10581	NM_006435	interferon induced transmembrane protein 2 (1-8D)
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)
IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11
ILVBL	10994	NM_006844	ilvB (bacterial acetolactate synthase)-like
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
INTS6	26512	NM_012141	integrator complex subunit 6
IQCB1	9657	NM_014642	IQ motif containing B1
IREB2	3658	NM_004136	iron-responsive element binding protein 2
IRF3	3661	NM_001571	interferon regulatory factor 3
ITGA7	3679	NM_002206	integrin, alpha 7
ITGB1BP2	26548	NM_012278	integrin beta 1 binding protein (melusin) 2
KCNJ3	3760	NM_002239	potassium inwardly-rectifying channel, subfamily J, member 3
KCNK3	3777	NM_002246	potassium channel, subfamily K, member 3
KCNRG	283518	NM_173605	potassium channel regulator
KCTD14	65987	NM_023930	potassium channel tetramerisation domain containing 14
KIAA0776	23376	NM_015323	KIAA0776
KIAA1024	23251	XM_044580	KIAA1024 protein
KIAA1166	55906	NM_018684	KIAA1166
KRT4	3851	NM_002272	keratin 4
L1TD1	54596	NM_019079	LINE-1 type transposase domain containing 1
LHX5	64211	NM_022363	LIM homeobox 5
LOC283523	283523	XM_208097	similar to telomeric repeat binding factor 1 isoform 2
LOC285556	285556	XM_373030	hypothetical protein LOC285556
LOC285643	285643	XM_209695	KIF4B
LOC400451	400451	NM_207446	hypothetical gene supported by AK075564; BC060873
LOC90826	90826	NM_138364	hypothetical protein BC004337
LRRC62	114794	XM_056282	leucine rich repeat containing 62
LST-3TM12	338821	XM_292093	organic anion transporter LST-3b

LTC4S	4056	NM_000897	leukotriene C4 synthase
MAFK	7975	NM_002360	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)
MAGEB2	4113	NM_002364	melanoma antigen family B, 2
MAP3K6	9064	NM_004672	mitogen-activated protein kinase kinase kinase 6
MAP4	4134	NM_002375	microtubule-associated protein 4
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3
MATN2	4147	NM_002380	matrilin 2
MCHR2	84539	NM_032503	melanin-concentrating hormone receptor 2
MCM2	4171	NM_004526	minichromosome maintenance complex component 2
MCM3	4172	NM_002388	minichromosome maintenance complex component 3
MED12	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
MGAT4B	11282	NM_014275	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B
MGC13057	84281	NM_032321	hypothetical protein MGC13057
MLLT1	4298	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
MLXIPL	51085	NM_032951	MLX interacting protein-like
MRPL15	29088	NM_014175	mitochondrial ribosomal protein L15
MRPL38	64978	NM_032478	mitochondrial ribosomal protein L38
MRPL48	51642	NM_016055	mitochondrial ribosomal protein L48
MTHFSD	64779	NM_022764	methenyltetrahydrofolate synthetase domain containing
MTX1	4580	NM_002455	metaxin 1
MUS81	80198	NM_025128	MUS81 endonuclease homolog (S. cerevisiae)
MVD	4597	NM_002461	mevalonate (diphospho) decarboxylase
MYCL2	4611	NM_005377	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
MYL5	4636	NM_002477	myosin, light chain 5, regulatory
MYO3A	53904	NM_017433	myosin IIIA
MYO7B	4648	XM_291001	myosin VIIB
NAALADL1	10004	NM_005468	N-acetylated alpha-linked acidic dipeptidase-like 1
NDUFB4	4710	NM_004547	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
NEK4	6787	NM_003157	NIMA (never in mitosis gene a)-related kinase 4
NIPA1	123606	NM_144599	non imprinted in Prader-Willi/Angelman syndrome 1
NMT1	4836	NM_021079	N-myristoyltransferase 1
NOC4L	79050	NM_024078	nucleolar complex associated 4 homolog (S. cerevisiae)
NOL1	4839	NM_006170	nucleolar protein 1, 120kDa
NOL5A	10528	NM_006392	nucleolar protein 5A (56kDa with KKE/D repeat)
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA-associated)
NOP5/NOP58	51602	NM_015934	nucleolar protein NOP5/NOP58
NOS1AP	9722	NM_014697	nitric oxide synthase 1 (neuronal) adaptor protein
NPAT	4863	NM_002519	nuclear protein, ataxia-telangiectasia locus
NTN1	9423	NM_004822	netrin 1
NUAK2	81788	NM_030952	NUAK family, SNF1-like kinase, 2
ORAOV1	220064	NM_153451	oral cancer overexpressed 1

OSBP	5007	NM_002556	oxysterol binding protein
PARN	5073	NM_002582	poly(A)-specific ribonuclease (deadenylation nuclease)
PARP11	57097	NM_020367	poly (ADP-ribose) polymerase family, member 11
PDAP1	11333	NM_014891	PDGFA associated protein 1
PDZD7	79955	NM_024895	PDZ domain containing 7
PECR	55825	NM_018441	peroxisomal trans-2-enoyl-CoA reductase
PELI1	57162	NM_020651	pellino homolog 1 (Drosophila)
PEMT	10400	NM_007169	phosphatidylethanolamine N-methyltransferase
PEPD	5184	NM_000285	peptidase D
PFDN2	5202	NM_012394	prefoldin subunit 2
PGLYRP4	57115	NM_020393	peptidoglycan recognition protein 4
PHF3	23469	NM_015153	PHD finger protein 3
PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha
PLB1	151056	NM_153021	phospholipase B1
PLEK2	26499	NM_016445	pleckstrin 2
PMS2L5	5383	NM_174930	postmeiotic segregation increased 2-like 5
PNKD	25953	NM_015488	paroxysmal nonkinesigenic dyskinesia
PNO1	56902	NM_020143	partner of NOB1 homolog (S. cerevisiae)
POLR2J2	246721	NM_032958	DNA directed RNA polymerase II polypeptide J-related
PON3	5446	NM_000940	paraoxonase 3
PPIA	5478	NM_021130	peptidylprolyl isomerase A (cyclophilin A)
PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform
PPTC7	160760	NM_139283	PTC7 protein phosphatase homolog (S. cerevisiae)
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)
PROC	5624	NM_000312	protein C (inactivator of coagulation factors Va and VIIIa)
PROX1	5629	NM_002763	prospero-related homeobox 1
PRPF40A	55660	XM_371575	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
PRPSAP2	5636	NM_002767	phosphoribosyl pyrophosphate synthetase-associated protein 2
PRSS36	146547	NM_173502	protease, serine, 36
PSME1	5720	NM_176783	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
PTCD1	26024	NM_015545	pentatricopeptide repeat domain 1
PTHR1	5745	NM_000316	parathyroid hormone receptor 1
PTK2B	2185	NM_004103	PTK2B protein tyrosine kinase 2 beta
PTPN22	26191	NM_012411	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
QTRT1	81890	NM_031209	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)
QTRTD1	79691	NM_024638	queuine tRNA-ribosyltransferase domain containing 1
RAB10	10890	NM_016131	RAB10, member RAS oncogene family
RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family
RABEPK	10244	NM_005833	Rab9 effector protein with kelch motifs
RABIF	5877	NM_002871	RAB interacting factor
RAC1	5879	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1

RASSF1	11186	NM_007182	Ras association (RalGDS/AF-6) domain family 1
RBM22	55696	NM_018047	RNA binding motif protein 22
RBM25	58517	XM_027330	RNA binding motif protein 25
RBM9	23543	NM_014309	RNA binding motif protein 9
RBP4	5950	NM_006744	retinol binding protein 4, plasma
RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5
Rgr	266747	NM_153615	Ral-GDS related protein Rgr
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2
RIT1	6016	NM_006912	Ras-like without CAAX 1
RNF169	254225	XM_495886	ring finger protein 169
RNF207	388591	NM_207396	ring finger protein 207
RNF31	55072	NM_017999	ring finger protein 31
ROBO1	6091	NM_002941	roundabout, axon guidance receptor, homolog 1 (Drosophila)
ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2
RPAIN	84268	NM_032308	RPA interacting protein
RPS13	6207	NM_001017	ribosomal protein S13
RPS25	6230	NM_001028	ribosomal protein S25
RPS26	6231	NM_001029	ribosomal protein S26
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1
RYK	6259	NM_002958	RYK receptor-like tyrosine kinase
SCN11A	11280	NM_014139	sodium channel, voltage-gated, type XI, alpha subunit
SCO2	9997	NM_005138	SCO cytochrome oxidase deficient homolog 2 (yeast)
SCYL3	57147	NM_020423	SCY1-like 3 (S. cerevisiae)
SERINC1	57515	NM_020755	serine incorporator 1
SESN2	83667	NM_031459	sestrin 2
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1
SKI	6497	NM_003036	v-ski sarcoma viral oncogene homolog (avian)
SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
SLC24A6	80024	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
SLC25A20	788	NM_000387	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
SLC25A22	79751	NM_024698	solute carrier family 25 (mitochondrial carrier: glutamate), member 22
SLC6A8	6535	NM_005629	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
SMAD5	4090	NM_005903	SMAD family member 5
SMAD6	4091	NM_005585	SMAD family member 6
SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2
SNF1LK2	23235	NM_015191	SNF1-like kinase 2
SNX27	81609	NM_030918	sorting nexin family member 27
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)
SPCS2	9789	NM_014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)

SPCS3	60559	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)
SPDEF	25803	NM_012391	SAM pointed domain containing ets transcription factor
SRFBP1	153443	NM_152546	serum response factor binding protein 1
SRI	6717	NM_003130	sorcin
SRRM2	23524	NM_016333	serine/arginine repetitive matrix 2
SSTR2	6752	NM_001050	somatostatin receptor 2
STAT3	6774	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)
STIM2	57620	NM_020860	stromal interaction molecule 2
STMN2	11075	NM_007029	stathmin-like 2
STX2	2054	NM_001980	syntaxin 2
SURF1	6834	NM_003172	surfeit 1
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)
SUZ12	23512	NM_015355	suppressor of zeste 12 homolog (Drosophila)
SYMPK	8189	NM_004819	symplekin
SYT3	84258	NM_032298	synaptotagmin III
SYVN1	84447	NM_032431	synovial apoptosis inhibitor 1, synoviolin
TAP2	6891	NM_000544	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
TBCD	6904	NM_005993	tubulin folding cofactor D
TCEB2	6923	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
TCOF1	6949	NM_000356	Treacher Collins-Franceschetti syndrome 1
TDRD10	126668	NM_182499	tudor domain containing 10
TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
THSD4	79875	NM_024817	thrombospondin, type I, domain containing 4
TM6SF2	53345	NM_001001524	transmembrane 6 superfamily member 2
TMEM135	65084	NM_022918	transmembrane protein 135
TMEM142A	84876	NM_032790	transmembrane protein 142A
TOP1	7150	NM_003286	topoisomerase (DNA) I
TPM4	7171	NM_003290	tropomyosin 4
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5
TRIM42	287015	NM_152616	tripartite motif-containing 42
TRIM43	129868	NM_138800	tripartite motif-containing 43
TRIM46	80128	NM_025058	tripartite motif-containing 46
TRIM62	55223	NM_018207	tripartite motif-containing 62
TRRAP	8295	NM_003496	transformation/transcription domain-associated protein
TTC14	151613	NM_133462	tetratricopeptide repeat domain 14
TTY5	83863	NM_031926	testis-specific transcript, Y-linked 5
TUBGCP6	85378	NM_020461	tubulin, gamma complex associated protein 6
TWF1	5756	NM_002822	twinfilin, actin-binding protein, homolog 1 (Drosophila)
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)
UBA52	7311	NM_003333	ubiquitin A-52 residue ribosomal protein fusion product 1
UBE1L	7318	NM_003335	ubiquitin-activating enzyme E1-like
UBE2E3	10477	NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
UBE2J1	51465	NM_016021	ubiquitin-conjugating enzyme E2, J1

UBE2M	9040	NM_003969	ubiquitin-conjugating enzyme E2M
UBE2S	27338	NM_014501	ubiquitin-conjugating enzyme E2S
UBTD2	92181	NM_152277	ubiquitin domain containing 2
UBXD7	26043	XM_087353	UBX domain containing 7
USP10	9100	NM_005153	ubiquitin specific peptidase 10
USP11	8237	NM_004651	ubiquitin specific peptidase 11
USP16	10600	NM_006447	ubiquitin specific peptidase 16
USP42	84132	XM_166526	ubiquitin specific peptidase 42
USP51	158880	NM_201286	ubiquitin specific peptidase 51
UTP14A	10813	NM_006649	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
UTP6	55813	NM_018428	UTP6, small subunit (SSU) processome component, homolog (yeast)
VAMP1	6843	NM_014231	vesicle-associated membrane protein 1 (synaptobrevin 1)
VTN	7448	NM_000638	vitronectin
WBSR23	80112	NM_025042	Williams-Beuren syndrome chromosome region 23
WDR37	22884	NM_014023	WD repeat domain 37
WDR43	23160	XM_087089	WD repeat domain 43
WIF1	11197	NM_007191	WNT inhibitory factor 1
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1
XBP1	7494	NM_005080	X-box binding protein 1
XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
YBX1	4904	NM_004559	Y box binding protein 1
ZBED3	84327	NM_032367	zinc finger, BED-type containing 3
ZDHHC16	84287	NM_032327	zinc finger, DHHC-type containing 16
ZEB1	6935	NM_030751	zinc finger E-box binding homeobox 1
ZNF148	7707	NM_021964	zinc finger protein 148
ZNF197	10168	NM_006991	zinc finger protein 197
ZNF337	26152	NM_015655	zinc finger protein 337
ZNF346	23567	NM_012279	zinc finger protein 346
ZNF467	168544	XM_095168	zinc finger protein 467
ZNF608	57507	XM_114432	zinc finger protein 608
ZNF767	79970	NM_024910	zinc finger family member 767
ZNRF2	223082	NM_147128	zinc and ring finger 2
ZNRF3	84133	XM_290972	zinc and ring finger 3

siRNA screen bioinformatics and meta-analysis.

Among the host factors whose knockdown decreased HCV infection in the primary screen, we recovered both positive controls, CD81 and ApoE, and over thirty proteins previously implicated by functional genetic studies to be needed for the replication of HCV or West Nile virus (WNV), a related Flavivirus (Table S1 and S2, (Yang (2008) *J Virol* **82**, 5269-5278. Flisiak (2008) *Hepatology* **47**, 817-826.). The screen recovered 6 of the 26 HCV-associated host proteins determined by Randall et. al. to decrease JFH-1 levels by greater than 3-fold after intensive siRNA targeting (Table S2, (Randall (2007) *Proc Natl Acad Sci U S A* **104**, 12884-

12889.)). Among these shared candidates are the kinases MAPK1 and Raf1/MAPK3, the RNA-binding protein, ELAVL1 and the RNA-helicase, DDX3X. Proteomic studies, including the HCV infection mapping project (I-MAP) and experiments by Randall et al., have reported a direct physical interaction between Raf1/MAPK3, Stat3 and DDX3X and one or more of the HCV-encoded proteins (Randall (2007) *Proc Natl Acad Sci U S A* **104**, 12884-12889; de Chassey (2008) *Mol Syst Biol* **4**, 230.). This screen detected 15 of 96 factors recently reported by Tai et. al. in a whole-genome siRNA screen using an HCV sub-genomic replicon platform (Table S2, (Tai (2009) *Cell Host Microbe* **5**, 298-307.)); the common genes include the kinases PI4KA and NUA1/SNARK, and the enzymes HAS1, CTSF, and IDS. NUA1/SNARK, an AMPK-related kinase functioning in the cellular stress response, was one of nine host factors found by Ng et. al. to be necessary for HCV replicon function in a siRNA screen targeting ~4,000 genes (Ng (2007) *Hepatology* **45**, 1413-1421; Kuga (2008) *Biochem Biophys Res Commun* **377**, 1062-1066.). A critical role for PI4KA was also apparent in an HCVcc-based screen using a pre-selected library of genes implicated in endocytic trafficking (Berger (2009) *PNAS*.). In that study, 7 of the 140 genes tested were needed by HCV, including the actin-regulating kinase, ROCK2, which we also recovered in our screen (Berger (2009) *PNAS*; Riento K (2003) *Nat Rev Mol Cell Biol* **4**, 446-456.). Consistent with Tai et al., we observed that multiple sub-units (ARCN1, COPA, and COPB1) of the Golgi-associated retrograde transport complex, coatamer 1 (COP1), were needed for JFH-1 infection, albeit with cell numbers sufficiently decreased to preclude these genes from further validation (Table S2 (Tai (2009) *Cell Host Microbe* **5**, 298-307.)). The essentialness of two of the COP1 subunits (COPA and COPB2) for cell viability, as well as for HCV replication, was similarly observed in the trafficking-focused screen (Berger (2009) *PNAS*.).

Interestingly, the study detected 14 genes in common with those previously found in an RNAi screen for human proteins required for WNV infection, among them the enzymes BCKDHA, RPS6KL1, and USP11 (Table S2 (Krishnan (2008) *Nature* **455**, 242-245.)). The WNV siRNA screen was designed to detect host factors involved in viral entry through genome replication, and thus would not find genes detected in part two of our study. However, the small degree of overlap (4.9%), between the host genes needed by these related viruses could arise in part from viral-specific host factor requirements, as well as differences in experimental methodologies. For example, none of the HCV siRNA screening efforts have identified the ER-

associated-degradation pathway (ERAD) as important for viral replication, even though multiple components of this pathway were required for WNV replication (Krishnan (2008) *Nature* **455**, 242-245.), indicating differential dependencies.

Analysis for functionally enriched gene categories demonstrates a significant number of HCV host factors reside in the nucleus (82, $p=0.002$). This includes ribonucleoprotein complex components (e.g. RBM22, SRRM2, UBA52), and transcription factors (e.g. BRF1, E2F2, ERCC5, FOXE3, MLXIPL, SMAD5, SMAD6, TRRAP, WWTR1). Classification of the host genes into higher level molecular function and biological process categories showed significant enrichment for kinases (14 in total, $p=0.01$), factors involved in protein metabolism and modification ($p=0.03$), oncogenesis ($p=0.006$), nucleic acid binding ($p=0.01$) and nucleic acid metabolism ($p=0.03$, Figure S1E and F, and Table S3).

TABLE S3

Row Sort	Enriched Overarching Category	KeySub Categorization	Description	Gene Symbol	Molecular Function	Biological Process	Pathway
1	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	BRF1	Basal transcription factor	mRNA transcription initiation;mRNA transcription regulation	General transcription regulation->TFIIB;;Transcription regulation by bZIP transcription factor->TFIIB;;
2	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	calmodulin binding transcription activator 2	CAMTA 2	Other transcription factor	Other mRNA transcription; Calcium mediated signaling	
3	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	CCR4-NOT transcription complex, subunit 1	CNOT1	Transcription factor	mRNA transcription	
4	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	CCR4-NOT transcription complex, subunit 2	CNOT2	Other transcription factor	mRNA transcription regulation	
5	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	CCR4-NOT transcription complex, subunit 3	CNOT3	Other transcription factor	mRNA transcription regulation	
6	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	CCR4-NOT transcription complex, subunit 6-like	CNOT6L	Exoribonuclease	mRNA transcription regulation	

7	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	E2F transcription factor 2	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; Signal transduction; Developmental processes; Cell cycle control; Cell proliferation and differentiation	
8	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	forkhead box A2	Other transcription factor; Nucleic acid binding	Carbohydrate metabolism; mRNA transcription regulation; Other receptor mediated signaling pathway; Cell communication; Vision; Embryogenesis; Anterior/posterior patterning; Segment specification; Neurogenesis; Mesoderm development; Cell cycle control; Cell proliferation and differentiation; Cell structure	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;
9	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	forkhead box E3	Other transcription factor; Nucleic acid binding	Carbohydrate metabolism; mRNA transcription regulation; Other receptor mediated signaling pathway; Cell communication; Vision; Embryogenesis; Anterior/posterior patterning; Segment specification; Neurogenesis; Mesoderm development; Cell	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;

							cycle control; Cell proliferation and differentiation; Cell structure	
10	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	homeobox B13	HOXB13	Homeobox transcription factor; Other DNA-binding protein	mRNA transcription regulation		
11	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	interferon regulatory factor 3	IRF3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; Interferon-mediated immunity; Oncogenesis	Toll receptor signaling pathway-> Interferon (INF) regulatory factor 3;;	
12	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)	MED12	Transcription cofactor; Nucleic acid binding	mRNA transcription regulation		
13	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila), translocated to, 1	MLLT1	Transcription factor	mRNA transcription; Developmental processes; Oncogene		
14	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	MLX interacting protein-like	MLXIP1	Basic helix-loop-helix transcription factor; Nucleic acid binding	mRNA transcription regulation		

15	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	DNA directed RNA polymerase II polypeptide J-related gene	POLR2J2	DNA-directed RNA polymerase; Nucleic acid binding	General mRNA transcription activities	
16	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	prospero-related homeobox 1	PROX1	Homeobox transcription factor; Nucleic acid binding	mRNA transcription regulation; Other developmental processes; Neurogenesis; Gut mesoderm development; Cell proliferation and differentiation; Oncogenesis	
17	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	SMAD family member 5	SMAD5	Other transcription factor	mRNA transcription regulation; Receptor protein serine/threonine kinase signaling pathway; Other intracellular signaling cascade; Ligand-mediated signaling; Developmental processes; Oncogenesis	Wnt signaling pathway- > Mothers against decapentaplegic homolog 4;; TGF-beta signaling pathway- > RSmads;;

18	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	SMAD family member 6	SMAD6	Other transcription factor	mRNA transcription regulation; Receptor protein serine/threonine kinase signaling pathway; Other intracellular signaling cascade; Ligand-mediated signaling; Stress response; Developmental processes; Oncogenesis	TGF-beta signaling pathway->Inhibitory Smads;; TGF-beta signaling pathway->RSmads;; TGF-beta signaling pathway->I-SMAD;;;
19	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	SAM pointed domain containing ets transcription factor	SPDEF	Other transcription factor; Nucleic acid binding	mRNA transcription regulation	PDGF signaling pathway->Ets;;
20	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	serum response factor binding protein 1	SRFBP1	Other transcription factor	mRNA transcription regulation	

21	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	Other transcription factor;Nucleic acid binding	mRNA transcription regulation;JAK-STAT cascade;Stress response;Inhibition of apoptosis;Hematopoiesis;Other oncogenesis;Cell motility	Angiogenesis->Signal Transducer and Activator of Transcription 3;;EGF receptor signaling pathway->signal transducer and activator of transcription;;PDGF signaling pathway->STAT;;Interleukin signaling pathway->Signal transducers and activators of transcription;;Ras Pathway->Signal transducer and activator of transcription;;JAK/STAT signaling pathway->Signal transducers and activators of transcription;;Inflammation mediated by chemokine and cytokine signaling pathway->Signal transducers and activators of transcription;;;
22	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	suppressor of zeste 12 homolog (Drosophila)	SUZ12	Nucleic acid binding	mRNA transcription;Chromatin packaging and remodeling	
23	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	TFAP2A	Other transcription factor	mRNA transcription regulation;Ectoderm development;Oncogenesis	

24	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	topoisomerase (DNA) I	TOP1	DNA topoisomerase	DNA replication, General mRNA transcription activities; DNA replication	DNA replication->DNA Topoisomerase;;DNA replication->Topoisomerase;;;
25	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	twist homolog 1 (acrocephalosyndactyly 3, Saethre-Chotzen syndrome) (Drosophila)	TWIST1	Basic helix-loop-helix transcription factor; Nucleic acid binding	mRNA transcription regulation; Developmental processes; Cell proliferation and differentiation	
26	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	WW domain containing transcription regulator 1	WWTR1	Transcription cofactor; Kinase modulator	mRNA transcription regulation; Other signal transduction	
27	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	X-box binding protein 1	XBP1	Transcription factor	mRNA transcription regulation; Immunity and defense; Other metabolism	
28	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	zinc finger protein 148	ZNF148	Zinc finger transcription factor; Other DNA-binding protein	mRNA transcription regulation	
29	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	zinc finger protein 337	ZNF337	KRAB box transcription factor	mRNA transcription regulation; Cell proliferation and differentiation	
30	Nucleoside, nucleotide & nucleic acid metabolism	mRNA transcription	zinc and ring finger 2	ZNRF2	Zinc finger transcription factor	mRNA transcription	
31							
32	Nucleoside, nucleotide & nucleic acid metabolism	DNA replication	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	MCM2	DNA helicase; Hydrolase	DNA replication; DNA replication; Cell proliferation and differentiation	

33	Nucleoside, nucleotide & nucleic acid metabolism	DNA repair	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	ERCC5	Endonuclease; Single-stranded DNA-binding protein	DNA repair	
34	Nucleoside, nucleotide & nucleic acid metabolism	DNA repair	casein kinase 1, alpha 1-like	CSNK1A1L	Non-receptor serine/threonine protein kinase	DNA repair; Protein phosphorylation; Intracellular signaling cascade; Endocytosis; Meiosis; Cytokinesis; Chromosome segregation; Cell proliferation and differentiation; Cell structure	Wnt signaling pathway->Casein Kinase 1;; Circadian clock system->Casein kinase 1;; Hedgehog signaling pathway->Casein kinase 1;; Parkinson disease->Casein kinase 1;;;
35	Nucleoside, nucleotide & nucleic acid metabolism	DNA replication	topoisomerase (DNA) I	TOP1	DNA topoisomerase	DNA replication; General mRNA transcription activities; DNA replication	DNA replication->DNA Topoisomerase;; DNA replication->Topoisomerase;;
36	Nucleoside, nucleotide & nucleic acid metabolism	DNA replication	cell division cycle 6 homolog (S. cerevisiae)	CDC6	Replication origin binding protein	DNA replication; DNA replication; Cell cycle control	
37							
38	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	nucleolar complex associated 4 homolog (S. cerevisiae)	NOC4L	Other RNA-binding protein	rRNA metabolism; Developmental processes	
39	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	nucleolar protein 1, 120kDa	NOL1	Nucleic acid binding; Methyltransferase	rRNA metabolism	

40	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	IMP4	Ribonucleoprotein	rRNA metabolism	
41	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	nucleolar protein NOP5/NOP58	unassigned	Ribonucleoprotein	rRNA metabolism	
42	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	HEAT repeat containing 1	HEATR1	Ribonucleoprotein	rRNA metabolism	
43	Nucleoside, nucleotide & nucleic acid metabolism	RNA metabolism	nucleolar protein 5A (56kDa with KKE/D repeat)	NOL5A	Ribonucleoprotein	rRNA metabolism	
44							
45	Nucleoside, nucleotide & nucleic acid metabolism	Pre-mRNA processing	bruno-like 6, RNA binding protein (Drosophila)	BRUNO L6	Other RNA-binding protein	mRNA splicing	
46	Nucleoside, nucleotide & nucleic acid metabolism	Pre-mRNA processing	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	ELAVL1	Ribonucleoprotein	mRNA end-processing and stability; Neurogenesis; Cell proliferation and differentiation	
47							
48	Protein metabolism & modification	Protein phosphorylation	homeodomain interacting protein kinase 3	HIPK3	Non-receptor serine/threonine protein kinase	Protein phosphorylation	
49	Protein metabolism & modification	Protein phosphorylation	cyclin-dependent kinase-like 5	CDKL5	Non-receptor serine/threonine protein kinase	Protein phosphorylation; Cell cycle control; Mitosis	

50	Protein metabolism & modification	Protein phosphorylation	ribosomal protein S6 kinase-like 1	RPS6KL1	Non-receptor serine/threonine protein kinase	Protein biosynthesis;Protein phosphorylation;Other intracellular signaling cascade;Cell proliferation and differentiation	PDGF signaling pathway->p90RSK;;
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51	Protein metabolism & modification	Protein phosphorylation	mitogen-activated protein kinase 1	MAPK1	Non-receptor serine/threonine protein kinase	Protein phosphorylation;MAPK cascade	<p>Angiotensin II-stimulated signaling through G proteins and beta-arrestin->mitogen-activated protein kinase;;Interleukin signaling pathway->Extracellular signal-regulated kinase family;;Ras Pathway->Extracellular signal-regulated kinase;;B cell activation->ERK;;Alzheimer disease-amyloid secretase pathway->Mitogen activated protein kinase;;Apoptosis signaling pathway->Mitogen activated protein kinase;;Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade->Mitogen-activated protein kinase;;T cell activation->ERK;;Angiogenesis->Mitogen Activated Protein Kinase Kinase;;Toll receptor signaling pathway->extracellular signal-regulated kinase 1;;FGF signaling pathway->Extracellular signal-regulated kinase;;Parkinson</p>
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disease->ERK;;VEGF signaling pathway- >Extracellular Signal- Regulated Kinase;;VEGF signaling pathway->MAPK/ERK Kinase;;Inflammation mediated by chemokine and cytokine signaling pathway->Mitogen activated protein kinase;;PDGF signaling pathway->Extracellular signal-regulated kinase family;;Toll receptor signaling pathway- >extracellular signal- regulated kinase 2;;Interferon-gamma signaling pathway- >Serine kinase;;Endothelin signaling pathway- >extracellular signal- regulated kinase;EGF receptor signaling pathway->Extracellular signal-regulated kinase;;TGF-beta signaling pathway- >p42/p44MAPKs;;Integr in signalling pathway- >Extracellular signal- regulated kinase;;Angiogenesis- >Extracellular regulated kinase;.....							
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52	Protein metabolism & modification	Protein phosphorylation	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation; Other intracellular signaling cascade; Cell adhesion; Other developmental process; Embryogenesis; Mitosis; Other oncogenesis; Cell motility	Inflammation mediated by chemokine and cytokine signaling pathway->Rho-associated coiled-coil Ser/Thr specific kinase;; Cytoskeletal regulation by Rho GTPase->Rho-associated coiled-coil containing protein kinase;;
53	Protein metabolism & modification	Protein phosphorylation	casein kinase 1, alpha 1-like	CSNK1A1L	Non-receptor serine/threonine protein kinase	DNA repair; Protein phosphorylation; Intracellular signaling cascade; Endocytosis; Meiosis; Cytokinesis; Chromosome segregation; Cell proliferation and differentiation; Cell structure	Wnt signaling pathway->Casein Kinase 1;; Circadian clock system->Casein kinase 1;; Hedgehog signaling pathway->Casein kinase I;; Parkinson disease->Casein kinase I;;
54	Protein metabolism & modification	Protein phosphorylation	NUAK family, SNF1-like kinase, 2	NUAK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation	
55	Protein metabolism & modification	Protein phosphorylation	conserved helix-loop-helix ubiquitous kinase	CHUK	Non-receptor serine/threonine protein kinase	Protein phosphorylation; NF-kappaB cascade; Cytokine/chemokine mediated immunity	Interleukin signaling pathway->Inhibitor of kappa-B kinase;; T cell activation->IKK;; Apoptosis signaling pathway->I-kappa B kinase;; Toll receptor signaling pathway->IkappaB_alpha Kinase;; B cell activation->IKK;;

56	Protein metabolism & modification	Protein phosphorylation	fms-related tyrosine kinase 4	FLT4	Tyrosine protein kinase receptor;Protein kinase	Protein phosphorylation;Receptor protein tyrosine kinase signaling pathway;Angiogenesis;Cell proliferation and differentiation	
57	Protein metabolism & modification	Protein phosphorylation	MAP/microtubule affinity-regulating kinase 3	MARK3	Non-motor microtubule binding protein;Non-receptor serine/threonine protein kinase	Protein phosphorylation;Cell structure	
58	Protein metabolism & modification	Protein phosphorylation	SNF1-like kinase 2	SNF1LK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation;Cell cycle control	
59	Protein metabolism & modification	Protein phosphorylation	PTC7 protein phosphatase homolog (S. cerevisiae)	PPTC7	Protein phosphatase	Protein phosphorylation	
60	Protein metabolism & modification	Protein phosphorylation	receptor-interacting serine-threonine kinase 2	RIPK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation;NF-kappaB cascade;Induction of apoptosis	Apoptosis signaling pathway->Receptor interacting protein;;
61							
62	Protein metabolism & modification	Protein glycosylation	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	DDOST	Glycosyltransferase	Protein glycosylation	
63							
64	Protein metabolism & modification	Protein-lipid modification	N-myristoyltransferase 1	NMT1	Other transferase	Protein-lipid modification	
65							

66	Protein metabolism & modification	Proteolysis	ubiquitin specific peptidase 51	USP51	Cysteine protease	Proteolysis	
67	Protein metabolism & modification	Proteolysis	tripartite motif-containing 42	TRIM42	Ubiquitin-protein ligase	Proteolysis	
68	Protein metabolism & modification	Proteolysis	ubiquitin specific peptidase 42	USP42	Cysteine protease	Proteolysis	
69	Protein metabolism & modification	Proteolysis	tripartite motif-containing 62	TRIM62	Ubiquitin-protein ligase	Proteolysis	
70	Protein metabolism & modification	Proteolysis	ubiquitin specific peptidase 11	USP11	Cysteine protease	Proteolysis	
71	Protein metabolism & modification	Proteolysis	Rho guanine nucleotide exchange factor (GEF) 10-like	ARHGEF10L	Cysteine protease	Proteolysis	
72	Protein metabolism & modification	Proteolysis	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	XPINPEP1	Metalloprotease	Proteolysis	
73	Protein metabolism & modification	Proteolysis	SMAD specific E3 ubiquitin protein ligase 2	SMURF2	Ubiquitin-protein ligase	Proteolysis; Neurogenesis; Skeletal development	TGF-beta signaling pathway->Smad ubiquitination regulatory factors; Ubiquitin proteasome pathway->Ubiquitin protein ligase E3:::

74	Protein metabolism & modification	Proteolysis	SMAD specific E3 ubiquitin protein ligase 1	SMURF 1	Ubiquitin-protein ligase	Proteolysis; Neurogenesis; Skeletal development	TGF-beta signaling pathway->Smad ubiquitination regulatory factors;; Ubiquitin proteasome pathway->Ubiquitin protein ligase E3;;
75	Protein metabolism & modification	Proteolysis	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	PSME1	Other miscellaneous function protein	Proteolysis	
76	Protein metabolism & modification	Proteolysis	caspase 4, apoptosis-related cysteine peptidase	CASP4	Protease inhibitor; Cysteine protease	Proteolysis; Apoptosis	
77	Protein metabolism & modification	Proteolysis	ADAM metalloproteinase with thrombospondin type 1 motif, 4	ADAMTS4	Metalloproteinase	Proteolysis; Cell adhesion-mediated signaling	
78	Protein metabolism & modification	Proteolysis	cathepsin F	CTSF	Cysteine protease	Proteolysis	
79	Protein metabolism & modification	Proteolysis	N-acetylated alpha-linked acidic dipeptidase-like 1	NAALADL1	Other proteases	Proteolysis	
80	Protein metabolism & modification	Proteolysis	signal peptidase complex subunit 3 homolog (S. cerevisiae)	SPCS3	Protease	Proteolysis	Vasopressin synthetase->Signal Peptidase;;
81	Protein metabolism & modification	Proteolysis	ubiquitin A-52 residue ribosomal protein fusion product 1	UBA52	Ribosomal protein	Proteolysis	
82	Protein metabolism & modification	Proteolysis	signal peptidase complex subunit 2 homolog (S. cerevisiae)	SPCS2	Select regulatory molecule	Proteolysis	Vasopressin synthetase->Signal Peptidase;;

83			Protein folding	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJBI	Other chaperones		Protein folding	
84	Protein metabolism & modification	Protein folding	Protein metabolism & modification	peptidyl/prolyl isomerase A (cyclophilin A)	PPIA	Other isomerase		Protein folding;Nuclear transport;Immunity and defense	
85	Protein metabolism & modification	Protein folding	Protein metabolism & modification	heat shock 70kDa protein 1A	HSPA1A	Hsp 70 family chaperone		Protein folding;Protein complex assembly;Stress response	Parkinson disease->Heat shock protein 70;;Apoptosis signaling pathway->Heat shock protein 70;;;
86	Protein metabolism & modification	Protein folding	Protein metabolism & modification	heat shock 70kDa protein 1A	HSPA1A	Hsp 70 family chaperone		Protein folding;Protein complex assembly;Stress response	Parkinson disease->Heat shock protein 70;;Apoptosis signaling pathway->Heat shock protein 70;;;
87									
88	Protein metabolism & modification	Protein complex assembly	Protein metabolism & modification	heat shock 70kDa protein 1A	HSPA1A	Hsp 70 family chaperone		Protein folding;Protein complex assembly;Stress response	Parkinson disease->Heat shock protein 70;;Apoptosis signaling pathway->Heat shock protein 70;;;
89	Protein metabolism & modification	Protein complex assembly	Protein metabolism & modification	surfeit 1	SURF1	Oxidase		Protein complex assembly	
90									
91	Protein metabolism & modification	Protein biosynthesis	Protein metabolism & modification	ribosomal protein S6 kinase-like 1	RPS6KL1	Non-receptor serine/threonine protein kinase		Protein biosynthesis;Protein phosphorylation;Other intracellular signaling cascade;Cell proliferation and differentiation	PDGF signaling pathway->p90RSK;;
92	Protein metabolism & modification	Protein biosynthesis	Protein metabolism & modification	eukaryotic translation termination factor 1	ETF1	Translation release factor		Protein biosynthesis	
93	Protein metabolism &	Protein biosynthesis	Protein metabolism &	mitochondrial ribosomal protein L15	MRPL15	Ribosomal protein		Protein biosynthesis;Other metabolism	

	modification								
94	Protein metabolism & modification	Protein biosynthesis	mitochondrial ribosomal protein L48	MRPL48	Ribosomal protein	Protein biosynthesis			
95									
96		Ion transport	potassium inwardly-rectifying channel, subfamily J, member 3	KCNJ3	Voltage-gated potassium channel	Cation transport			Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway->G-protein receptor kinase;;Muscarinic acetylcholine receptor 2 and 4 signaling pathway->G protein-coupled inwardly rectifying potassium channel;;GABA-B_receptor_II_signaling->Inwardly rectifying potassium channel Kir3.1;;Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway->G protein-activated inward rectifying potassium channel;;;
97		Ion transport	organic anion transporter LST-3b	unassigned	Other transporter	Anion transport			
98		Ion transport	potassium channel tetramerisation domain containing 14	KCTD14	Select regulatory molecule	Cation transport			

99		Ion transport	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	SLC11A1	Other transporter	Cation transport; Stress response	
100		Ion transport	potassium channel, subfamily K, member 3	KCNK3	Voltage-gated potassium channel	Cation transport; Other neuronal activity	Opioid proenkephalin pathway->K+ channel;; 5HT3 type receptor mediated signaling pathway->K+ channel;; 5HT1 type receptor mediated signaling pathway->K+ channel;; Opioid proopiomelanocortin pathway->K+ channel;; Dopamine receptor mediated signaling pathway->K+ channel;; 5HT2 type receptor mediated signaling pathway->K+ channel;; 5HT4 type receptor mediated signaling pathway->K+ channel;;
101		Ion transport	ATPase, Class V, type 10D	ATP10D	Other transporter; Other hydrolase	Lipid and fatty acid transport; Cation transport	
102		Ion transport	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	SLC24A6	Cation transporter	Cation transport	
103							
104		Lipid and fatty acid transport	ATPase, Class V, type 10D	ATP10D	Other transporter; Other hydrolase	Lipid and fatty acid transport; Cation transport	

105		Lipid and fatty acid transport	oxysterol binding protein	OSBP	Transfer/carrier protein	Lipid and fatty acid transport;Cholesterol metabolism;Transport	
106							
107		Electron transport	cytochrome P450, family 4, subfamily A, polypeptide 22	CYP4A22	Oxygenase	Fatty acid metabolism;Electron transport	
108		Electron transport	zinc finger protein 346	ZNF346	Zinc finger transcription factor;Nuclease	Electron transport;Apoptosis;Other metabolism	
109		Electron transport	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	NDUFB4	Reductase	Oxidative phosphorylation	
110							
111		Cell cycle control	cyclin-dependent kinase-like 5	CDKL5	Non-receptor serine/threonine protein kinase	Protein phosphorylation;Cell cycle control;Mitosis	
112		Cell cycle control	adenomatosis polyposis coli 2	APC2	Non-motor microtubule binding protein	Other receptor mediated signaling pathway;Other intracellular signaling cascade;Cell adhesion;Apoptosis;Cell cycle control;Tumor suppressor	Angiogenesis->Adenomatous Polyposis of the Colon;; Wnt signaling pathway->Adenomatous Polyposis Coli;;;
113		Cell cycle control	E2F transcription factor 2	E2F2	Other transcription factor;Nucleic acid binding	mRNA transcription regulation;Signal transduction;Developmental processes;Cell cycle control;Cell proliferation and differentiation	

114	Cell cycle control	cyclin B2	CCNB2	Kinase activator	Cell cycle control	Cell cycle->Cyclin B;;p53 pathway->Cyclin B;;
115	Cell cycle control	cell division cycle 6 homolog (S. cerevisiae)	CDC6	Replication origin binding protein	DNA replication;DNA replication;Cell cycle control	
116	Cell cycle control	SNF1-like kinase 2	SNF1LK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation;Cell cycle control	
117	Cell cycle control	forkhead box A2	FOXA2	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Vision;Embryogenesis;Anterior/posterior patterning;Segment specification;Neurogenesis;Mesoderm development;Cell cycle control;Cell proliferation and differentiation;Cell structure	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;
118	Cell cycle control	forkhead box E3	FOXE3	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Vision;Embryogenesis;Anterior/posterior patterning;Segment specification;Neuro	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators

							genesis; Mesoderm development; Cell cycle control; Cell proliferation and differentiation; Cell structure	or corepressors; ; ; ; ;
119								
120		Immunity & defense	SMAD family member 6	SMAD6	Other transcription factor	mRNA transcription regulation; Receptor protein serine/threonine kinase signaling pathway; Other intracellular signaling cascade; Ligand-mediated signaling; Stress response; Developmental processes; Oncogenesis	TGF-beta signaling pathway->Inhibitory Smads;; TGF-beta signaling pathway->RSmads;; TGF-beta signaling pathway->I-SMAD;;;	
121		Immunity & defense	Fc fragment of IgG, receptor, transporter, alpha	FCGRT	Immunoglobulin receptor family member; Defense /immunity protein	B-cell- and antibody-mediated immunity		

122		Immunity & defense	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; JAK-STAT cascade; Stress response; Inhibition of apoptosis; Hematopoiesis; Other oncogenesis; Cell motility	Angiogenesis->Signal Transducer and Activator of Transcription 3;; EGF receptor signaling pathway->signal transducer and activator of transcription;; PDGF signaling pathway->STAT;; Interleukin signaling pathway->Signal transducers and activators of transcription;; Ras Pathway->Signal transducer and activator of transcription;; JAK/STAT signaling pathway->Signal transducers and activators of transcription;; Inflammation mediated by chemokine and cytokine signaling pathway->Signal transducers and activators of transcription;;
123		Immunity & defense	X-box binding protein 1	XBP1	Transcription factor	mRNA transcription regulation; Immunity and defense; Other metabolism	
124		Immunity & defense	interferon regulatory factor 3	IRF3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; Interferon-mediated immunity; Oncogenesis	Toll receptor signaling pathway->Interferon (INF) regulatory factor 3;;

125		Immunity & defense	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	SLC11A1	Other transporter	Cation transport; Stress response	
126		Immunity & defense	cytokine inducible SH2-containing protein	CISH	Other miscellaneous function protein	JAK-STAT cascade; Macrophage-mediated immunity; Cytokine/chemokine mediated immunity; Inhibition of apoptosis; Developmental processes	Inflammation mediated by chemokine and cytokine signaling pathway->Suppressor of cytokine signaling; Interferon-gamma signaling pathway->Suppressor of cytokine signaling; ;
127		Immunity & defense	conserved helix-loop-helix ubiquitous kinase	CHUK	Non-receptor serine/threonine protein kinase	Protein phosphorylation; NF-kappaB cascade; Cytokine/chemokine mediated immunity	Interleukin signaling pathway->Inhibitor of kappa-B kinase; T cell activation->IKK; Apoptosis signaling pathway->I-kappaB kinase; Toll receptor signaling pathway->I-kappaB kinase; B cell activation->IKK; ; ; ; ; ; ; ; ; ;
128		Immunity & defense	peptidylprolyl isomerase A (cyclophilin A)	PPIA	Other isomerase	Protein folding; Nuclear transport; Immunity and defense	
129		Immunity & defense	heat shock 70kDa protein 1A	HSPA1A	Hsp 70 family chaperone	Protein folding; Protein complex assembly; Stress response	Parkinson disease->Heat shock protein 70; Apoptosis signaling pathway->Heat shock protein 70; ; ;

130		Immunity & defense	leukotriene C4 synthase	LTC4S	Other transferase	Other lipid, fatty acid and steroid metabolism; T-cell mediated immunity; B-cell- and antibody-mediated immunity; Macrophage-mediated immunity; Granulocyte-mediated immunity	Inflammation mediated by chemokine and cytokine signaling pathway->Lipoxygenase;;
131		Immunity & defense	peptidoglycan recognition protein 4	PGLYRP4	Receptor; Signaling molecule; Defense/immunity protein	Carbohydrate metabolism; Immunity and defense; Apoptosis	
132		Immunity & defense	interferon induced transmembrane protein 3 (1-8U)	IFITM3	Other miscellaneous function protein	Immunity and defense; Cell proliferation and differentiation	
133		Immunity & defense	chemokine (C-C motif) ligand 26	CCL26	Chemokine	Cytokine and chemokine mediated signaling pathway; Ligand-mediated signaling; Cytokine/c hemokine mediated immunity	Inflammation mediated by chemokine and cytokine signaling pathway->Chemokine;;
134							
135		Cell adhesion	adenomatous polyposis coli 2	APC2	Non-motor microtubule binding protein	Other receptor mediated signaling pathway; Other intracellular signaling cascade; Cell adhesion; Apoptosis; Cell cycle control; Tumor suppressor	Angiogenesis->Adenomatous Polyposis of the Colon;; Wnt signaling pathway->Adenomatous Polyposis Coli;;

136		Cell adhesion	immunoglobulin superfamily, member 11	IGSF11	Other cell adhesion molecule	Cell adhesion	
137		Cell adhesion	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation; Other intracellular signaling cascade; Cell adhesion; Other developmental process; Embryogenesis; Mitosis; Other oncogenesis; Cell motility	Inflammation mediated by chemokine and cytokine signaling pathway->Rho-associated coiled-coil Ser/Thr specific kinase;; Cytoskeletal regulation by Rho GTPase->Rho-associated coiled-coil-containing protein kinase;;;
138		Cell adhesion	calyntenin 1	CLSTN1	Cell adhesion molecule; Select calcium binding protein	Cell adhesion-mediated signaling; Cell adhesion	
139		Cell adhesion	integrin, alpha 7	ITGA7	Other cell adhesion molecule	Cell adhesion	Integrin signalling pathway->Integrin alpha;;

140		Cell adhesion	cadherin 1, type 1, E-cadherin (epithelial)	CDH1	Cadherin	Cell adhesion-mediated signaling; Cell adhesion	Alzheimer disease-presenilin pathway->E-cadherin transmembrane fragment;; Alzheimer disease-presenilin pathway->E-cadherin C-terminal fragment;; Wnt signaling pathway->Cadherin;; Alzheimer disease-presenilin pathway->E-cadherin N-terminal fragment;; Alzheimer disease-presenilin pathway->E-cadherin signaling pathway->Cadherin;; Alzheimer disease-presenilin pathway->E-cadherin intracellular fragment.....
141							

142	Cell motility	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; JAK-STAT cascade; Stress response; Inhibition of apoptosis; Hematopoiesis; Other oncogenesis; Cell motility	Angiogenesis->Signal Transducer and Activator of Transcription 3;; EGF receptor signaling pathway->signal transducer and activator of transcription;; PDGF signaling pathway->STAT;; Interleukin signaling pathway->Signal transducers and activators of transcription;; Ras Pathway->Signal transducer and activator of transcription;; JAK/STAT signaling pathway->Signal transducers and activators of transcription;; Inflammation mediated by chemokine and cytokine signaling pathway->Signal transducers and activators of transcription;;
143	Cell motility	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation; Other intracellular signaling cascade; Cell adhesion; Other developmental process; Embryogenesis; Mitosis; Other oncogenesis; Cell motility	Inflammation mediated by chemokine and cytokine signaling pathway->Rho-associated coiled-coil Ser/Thr specific kinase;; Cytoskeletal regulation by Rho GTPase->Rho-associated coiled-coil containing protein kinase;;

144		Cell motility	dedicator of cytokinesis 3	DOCK3	Guanylnucleotide exchange factor	Other intracellular signaling cascade; Phagocytosis; Cell motility	
145		Cell motility	tropomyosin 4	TPM4	Actin binding motor protein	Muscle contraction; Muscle development; Cell structure; Cell motility	
146							
147		Cell structure	keratin 4	KRT4	Intermediate filament; Structural protein	Ectoderm development; Cell structure	
148		Cell structure	claudin 1	CLDN1	Tight junction	Cell structure	
149		Cell structure	microtubule-associated protein 4	MAP4	Non-motor microtubule binding protein	Apoptosis; Cell structure	
150		Cell structure	casein kinase 1, alpha 1-like	CSNK1A1L	Non-receptor serine/threonine protein kinase	DNA repair; Protein phosphorylation; Intracellular signaling cascade; Endocytosis; Meiosis; Cytokinesis; Chromosome segregation; Cell proliferation and differentiation; Cell structure	Wnt signaling pathway->Casein Kinase 1;; Circadian clock system->Casein kinase 1;; Hedgehog signaling pathway->Casein kinase 1;; Parkinson disease->Casein kinase 1;;;
151		Cell structure	KIF4B	unassigned	Microtubule binding motor protein	Mitosis; Cell structure	
152		Cell structure	tubulin folding cofactor D	TBCD	Other chaperones; Non-motor microtubule binding protein	Mitosis; Cell structure	

153		Cell structure	MAP/microtubule affinity-regulating kinase 3	MARK3	Non-motor microtubule binding protein;Non- receptor serine/threonine protein kinase	Protein phosphorylation;Cell structure	
154		Cell structure	tropomyosin 4	TPM4	Actin binding motor protein	Muscle contraction;Muscle development;Cell structure;Cell motility	
155		Cell structure	forkhead box A2	FOXA2	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Visi on;Embryogenesis; Anterior/posterior patterning;Segment specification;Neuro genesis;Mesoderm development;Cell cycle control;Cell proliferation and differentiation;Cell structure	Insulin/IGF pathway- protein kinase B signaling cascade- >Forkhead transcription factor;;PI3 kinase pathway- >FOXO;;Interleukin signaling pathway- >Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;

156		Cell structure	forkhead box E3	FOXE3	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Vision;Embryogenesis;Anterior/posterior patterning;Segment specification;Neurogenesis;Mesoderm development;Cell cycle control;Cell proliferation and differentiation;Cell structure	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;;;
157							
158		Cell structure and motility	keratin 4	KRT4	Intermediate filament;Structural protein	Ectoderm development;Cell structure	

159	Cell structure and motility	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; JAK-STAT cascade; Stress response; Inhibition of apoptosis; Hematopoiesis; Other oncogenesis; Cell motility	Angiogenesis->Signal Transducer and Activator of Transcription 3;; EGF receptor signaling pathway->signal transducer and activator of transcription;; PDGF signaling pathway->STAT;; Interleukin signaling pathway->Signal transducers and activators of transcription;; Ras Pathway->Signal transducer and activator of transcription;; JAK/STAT signaling pathway->Signal transducers and activators of transcription;; Inflammation mediated by chemokine and cytokine signaling pathway->Signal transducers and activators of transcription;;
160	Cell structure and motility	Rho-associated, coiled-coil containing protein kinase 2	ROCK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation; Other intracellular signaling cascade; Cell adhesion; Other developmental process; Embryogenesis; Mitosis; Other oncogenesis; Cell motility	Inflammation mediated by chemokine and cytokine signaling pathway->Rho-associated coiled-coil Ser/Thr specific kinase;; Cytoskeletal regulation by Rho GTPase->Rho-associated coiled-coil containing protein kinase;;

161		Cell structure and motility	claudin 1	CLDN1	Tight junction	Cell structure		
162		Cell structure and motility	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	RAC1	Small GTPase	G-protein mediated signaling;Cell structure and motility	Integrin signalling pathway->Rac;;Inflammation mediated by chemokine and cytokine signaling pathway->Ras related C3 botulinum substrate 1;;p38 MAPK pathway->Rac GTPase;;Huntington disease->Rac;;FGF signaling pathway->Rac;;Axon guidance mediated by Slit/Robo->Ras-related C3 botulinum toxin substrate;;T cell activation->rac;;EGF receptor signaling pathway->Rac;;Axon guidance mediated by netrin->Ced-10;;Cytoskeletal regulation by Rho GTPase->Ras-related C3 Botulinum toxin substrate 1;;Ras Pathway->Rac;;B cell activation->Rac;;Axon guidance mediated by semaphorins->Ras-related C3 botulinum toxin substrate;;.....	
163		Cell structure and motility	microtubule-associated protein 4	MAP4	Non-motor microtubule binding protein	Apoptosis;Cell structure		

164		Cell structure and motility	casein kinase 1, alpha 1-like	CSNK1 AIL	Non-receptor serine/threonine protein kinase	DNA repair;Protein phosphorylation;Intracellular signaling cascade;Endocytosis;Meiosis;Cytokinesis;Chromosome segregation;Cell proliferation and differentiation;Cell structure	Wnt signaling pathway->Casein Kinase I;;Circadian clock system->Casein kinase I;;Hedgehog signaling pathway->Casein kinase I;;Parkinson disease->Casein kinase I;;;
165		Cell structure and motility	KIF4B	unassigned	Microtubule binding motor protein	Mitosis;Cell structure	
166		Cell structure and motility	dedicator of cytokinesis 3	DOCK3	Guanylnucleotide exchange factor	Other intracellular signaling cascade;Phagocytosis;Cell motility	
167		Cell structure and motility	tubulin folding cofactor D	TBCD	Other chaperones;Non-motor microtubule binding protein	Mitosis;Cell structure	
168		Cell structure and motility	MAP/microtubule affinity-regulating kinase 3	MARK3	Non-motor microtubule binding protein;Non-receptor serine/threonine protein kinase	Protein phosphorylation;Cell structure	
169		Cell structure and motility	tropomyosin 4	TPM4	Actin binding motor protein	Muscle contraction;Muscle development;Cell structure;Cell motility	

170		Cell structure and motility	forkhead box A2	FOXA2	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Vision;Embryogenesis;Anterior/posterior patterning;Segment specification;Neurogenesis;Mesoderm development;Cell cycle control;Cell proliferation and differentiation;Cell structure	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;
171		Cell structure and motility	forkhead box E3	FOXE3	Other transcription factor;Nucleic acid binding	Carbohydrate metabolism;mRNA transcription regulation;Other receptor mediated signaling pathway;Cell communication;Vision;Embryogenesis;Anterior/posterior patterning;Segment specification;Neurogenesis;Mesoderm development;Cell cycle control;Cell proliferation and differentiation;Cell structure	Insulin/IGF pathway-protein kinase B signaling cascade->Forkhead transcription factor;;PI3 kinase pathway->FOXO;;Interleukin signaling pathway->Forkhead in Rhabdomyosarcoma-like 1;;TGF-beta signaling pathway->Co-activators or corepressors;;;
172							

173		Endocytosis	casein kinase 1, alpha 1-like	CSNK1A1L	Non-receptor serine/threonine protein kinase	DNA repair;Protein phosphorylation;Intracellular signaling cascade;Endocytosis;Meiosis;Cytokinesis;Chromosome segregation;Cell proliferation and differentiation;Cell structure	Wnt signaling pathway->Casein Kinase 1;;Circadian clock system->Casein kinase I;;Hedgehog signaling pathway->Casein kinase I;;Parkinson disease->Casein kinase I;;;
174		Endocytosis	dedicator of cytokinesis 3	DOCK3	Guanylnucleotide exchange factor	Other intracellular signaling cascade;Phagocytosis;Cell motility	
175		Endocytosis	RAB11A, member RAS oncogene family	RAB11A	Small GTPase	Intracellular signaling cascade;Receptor mediated endocytosis;General vesicle transport	Huntington disease->Rab8;;PDGF signaling pathway->Ras;;
176							
177		Exocytosis	syntaxin 2	STX2	SNARE protein	Regulated exocytosis;Protein targeting;Small molecule transport;Synaptic transmission	Synaptic vesicle trafficking->Syntaxin 1/2;;

178	Exocytosis	vesicle-associated membrane protein 1 (synaptobrevin 1)	VAMP1	SNARE protein	Exocytosis;Muscle development	Thyrotropin-releasing hormone receptor signaling pathway->SNARE COMPLEX;;Metabotropic glutamate receptor group II pathway->N-ethylmaleimide-sensitive factor attachment protein receptor;;Opioid proopiomelanocortin pathway->SNARE COMPLEX;;Dopamine receptor mediated signaling pathway->SNARE Complex;;Nicotinic acetylcholine receptor signaling pathway->N-ethylmaleimide-sensitive factor attachment protein receptor;;Muscarinic acetylcholine receptor 2 and 4 signaling pathway->N-ethylmaleimide-sensitive factor attachment protein receptor;;Corticotropin releasing factor receptor signaling pathway->SNARE COMPLEX;;Metabotropic glutamate receptor group III pathway->N-ethylmaleimide-sensitive factor attachment protein receptor;;Muscarinic acetylcholine receptor 1 and 3 signaling pathway->N-ethylmaleimide-
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<p>sensitive factor attachment protein receptor;;5HT2 type receptor mediated signaling pathway- >SNARE Complex;;Alpha adrenergic receptor signaling pathway->N- ethylmaleimide-sensitive factor attachment protein receptor;;Adrenaline and noradrenaline biosynthesis->N- ethylmaleimide-sensitive factor attachment protein receptor;;Opioid prodynorphin pathway- >SNARE COMPLEX;;Beta3 adrenergic receptor signaling pathway- >SNARE COMPLEX;;5HT1 type receptor mediated signaling pathway- >SNARE Complex;;Opioid proenkephalin pathway- >SNARE COMPLEX;;Oxytocin receptor mediated signaling pathway- >SNARE COMPLEX;;Beta2 adrenergic receptor signaling pathway- >SNARE COMPLEX;;5HT4 type receptor mediated</p>						
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							signaling pathway- >SNARE Complex;;Ionotropic glutamate receptor pathway->N- ethylmaleimide-sensitive factor attachment protein receptor;;Synaptic_vesicle trafficking- >Synaptobrevin;;Beta1 adrenergic receptor signaling pathway- >SNARE COMPLEX;;5HT3 type receptor mediated signaling pathway- >SNARE Complex;; ;
179							
180	Nuclear transport	peptidylprolyl isomerase A (cyclophilin A)	PPIA	Other isomerase	Protein folding;Nuclear transport;Immunity		

181									and defense		
182									General vesicle transport		
183									General vesicle transport		
184									General vesicle transport		
185									General vesicle transport		TGF-beta signaling pathway->Ras-GTP;;TGF-beta signaling pathway->Ras-GDP;;
186									Intracellular signaling cascade;Receptor mediated endocytosis;General vesicle transport		Huntington disease->Rab8;;PDGF signaling pathway->Ras;;
187											
188									Phospholipid metabolism;Lipid metabolism;Intracellular signaling cascade		Angiogenesis->Phosphatidylinositol 3-Kinase;;
189									Phospholipid metabolism		
190									Phospholipid metabolism		

191	Lipid, fatty acid & steroid metabolism	diacylglycerol O-acyltransferase homolog 1 (mouse)	DGAT1	Acyltransferase	Cholesterol metabolism	Androgen/estrogen/progesterone biosynthesis->Cholesterol acyltransferase;;
192	Lipid, fatty acid & steroid metabolism	cytochrome P450, family 4, subfamily A, polypeptide 22	CYP4A22	Oxygenase	Fatty acid metabolism;Electron transport	
193	Lipid, fatty acid & steroid metabolism	ATPase, Class V, type 10D	ATP10D	Other transporter;Other hydrolase	Lipid and fatty acid transport;Cation transport	
194	Lipid, fatty acid & steroid metabolism	peroxisomal trans-2-enoyl-CoA reductase	PECR	Dehydrogenase;Reductase	Fatty acid beta-oxidation	
195	Lipid, fatty acid & steroid metabolism	oxysterol binding protein	OSBP	Transfer/carrier protein	Lipid and fatty acid transport;Cholesterol metabolism;Transport	
196	Lipid, fatty acid & steroid metabolism	leukotriene C4 synthase	LTC4S	Other transferase	Other lipid, fatty acid and steroid metabolism;T-cell mediated immunity;B-cell-mediated immunity;Macrophage-mediated immunity;Granulocyte-mediated immunity	Inflammation mediated by chemokine and cytokine signaling pathway->Lipoxygenase;;
197						
198	Induction of apoptosis	receptor-interacting serine-threonine kinase 2	RIPK2	Non-receptor serine/threonine protein kinase	Protein phosphorylation;NF-kappaB cascade;Induction of apoptosis	Apoptosis signaling pathway->Receptor interacting protein;;
199	Induction of apoptosis	caspase 4, apoptosis-related cysteine peptidase	CASP4	Protease inhibitor;Cysteine protease	Proteolysis;Apoptosis	
200						

201	Inhibition of apoptosis	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	Other transcription factor; Nucleic acid binding	mRNA transcription regulation; JAK-STAT cascade; Stress response; Inhibition of apoptosis; Hematopoiesis; Other oncogenesis; Cell motility	Angiogenesis->Signal Transducer and Activator of Transcription 3;; EGF receptor signaling pathway->signal transducer and activator of transcription;; PDGF signaling pathway->STAT;; Interleukin signaling pathway->Signal transducers and activators of transcription;; Ras Pathway->Signal transducer and activator of transcription;; JAK/STAT signaling pathway->Signal transducers and activators of transcription;; Inflammation mediated by chemokine and cytokine signaling pathway->Signal transducers and activators of transcription;;
202	Inhibition of apoptosis	cytokine inducible SH2-containing protein	CISH	Other miscellaneous function protein	JAK-STAT cascade; Macrophage-mediated immunity; Cytokine/chemokine mediated immunity; Inhibition of apoptosis; Developmental processes	Inflammation mediated by chemokine and cytokine signaling pathway->Suppressor of cytokine signaling;; Interferon-gamma signaling pathway->Suppressor of cytokine signaling;;

We encountered several pathways and macromolecular complexes consistent with known phases of the viral lifecycle. As noted, HCV entry depends on the presence of four specific host cell receptors, and our screen recovered two of the four, CD81 and claudin 1 (Evans (2007) *Nature* **446**, 801-805.). Our results confirm recent experiments which
5 identified cyclophilin A (CypA) as the specific host cell peptidyl-prolyl *cis-trans* isomerase required for HCV infection (Yang (2008) *J Virol* **82**, 5269-5278.). Therefore, CypA is the likely target of the anti-HCV non-immunosuppressive cyclosporin analogue, Debio-025, thus demonstrating that functional genomics can identify high-yield leads for host-directed anti-viral therapies (HDAVs) (Flisiak (2008) *Hepatology* **47**, 817-826.).
10 Depletion of three of five components of the signal peptidase complex (SPCS1, 2 and 3), which is believed to process the HCV envelope proteins E1 and E2 in the rER (Lindenbach (2005) *Nature* **436**, 933-938.), inhibited infection specifically in part two, validating both the role of this complex in HCV pathogenesis ($p=6.14e10^{-4}$) and the design of this portion of the screen. Studies have shown the importance of the specific
15 glycosylation of the E1 and E2 viral envelope proteins for HCV entry (Goffard (2003) *Biochimie* **85**, 295-301.), suggesting an explanation for the role of OST48/DDOST, a component of the rER oligosaccharyltransferase complex, which we detected as a late-acting HCV host factor. Previous efforts to find HIV-dependency factors (HDFs) similarly identified OST48 as being required for late-stage viral replication, consistent
20 with its playing an important role in glycosylation of the viral envelope spike (Brass (2008) *Science* **319**, 921-926.).

Previously unappreciated HCV dependencies were also detected. Components of the nucleolus were well represented in the nuclear-associated factors enriched for by the screen (TOP1, TCOF1, PNO1, NOP2, NOL6, NOP5/NOP58, NOC4L, HEATR1 and
25 IMP4). TCOF1 physically associates with nucleolar proteins, and is the gene responsible for Treacher Collins Syndrome, a severe congenital craniofacial developmental disease (Sakai D (2009) *Int J Biochem Cell Biol* **41**, 1229-1232.). Knockout mice deficient in TCOF1 display ribosome biogenesis deficiencies suggesting that cells depleted in TCOF1 may be unable to meet the increased demand for protein production required by HCV
30 (Sakai (2009) *Int J Biochem Cell Biol* **41**, 1229-1232.). In addition, Cherry et al. demonstrated that the IRES-mediated transcription of the picornavirus, Drosophila C, was dependent on the levels of specific ribosomal sub-units (Cherry (2005) *Genes Dev* **19**, 445-452.). Decreased levels of nucleolar factors may adversely impact HCV IRES function by altering ribosomal subunit levels or modifications.

Four of nine components of the Ccr4-Not complex (CNOT1, CNOT2, CNOT3, and CNOT6L) were required for HCV infection. The Ccr4-Not complex is a global regulator of gene expression that functions in transcription and polyadenylation (Collart (2004) *Prog Nucleic Acid Res Mol Biol* **77**, 289-322.). Mutation of each of the components of the orthologous yeast Ccr4-Not complex has shown that each subunit regulates the expression of a largely unique set of genes (Azzouz (2009) *RNA* **15**, 377-383; Cui (2008) *Mol Genet Genomics* **279**, 323-337.). Therefore, the components identified in this screen may control distinct sets of HCV host factors. Interestingly, three mitochondrial ribosomal subunits (MRPL15, 38 and 48) and several mitochondrial-associated proteins (BCKDHA, CYBA, HCCS, PECR, PEMT, PPTC7, PTCD1, SURF1 (Pagliarini (2008) *Cell* **134**, 112-123.)) were found to be required for viral infection.

Integration of HCV-host factor Interactions

To provide a more comprehensive view of HCV-host interactions, we integrated the functional genomic results of our study with the proteome-wide mapping and literature mining data of the HCV infection mapping project (I-MAP), undertaken by Chassey et. al. (Fig 2, (de Chassey B (2008) *Mol Syst Biol* **4**, 230.)). The I-MAP utilized parallel yeast two-hybrid protein interaction screens employing HCV proteins as prey and two human cDNA libraries as bait. The resulting protein-protein interaction (PPI) network was then augmented and extended using expertly curated literature mining and a large human PPI database (de Chassey (2008) *Mol Syst Biol* **4**, 230.). In addition to providing functional evidence for the importance of nine host factors found by the I-MAP (CHUK, CTGF, DDX3X, PI4KA, RAF1, STAT3, FBLN5, RNF31, SMURF2), this network extension analysis revealed numerous first-order (direct) interactions between 63 HCV host factors found in this screen and those factors found in the I-MAP (enrichment $p=0.0001$, Fig 2). This places the candidates detected using functional genomics into the interaction neighborhood of the HCV proteome (core, E, F, p7 and NS components, Fig 3).

HCV, WNV and dengue virus belong to the Flaviviridae family, whose members include the human pathogens Japanese encephalitis virus and yellow fever virus (Murray (2008) *Nat Rev Microbiol* **6**, 699-708; Lindenbach (2003) *Adv Virus Res* **59**, 23-61.). We explored the possibility of uncovering common features presented by host-Flaviviridae interactions. Among the overlapping hits and first-order interactions between host factors

required for HCV, WNV and dengue virus siRNA screens (Krishnan (2008) *Nature* **455**, 242-245.), a striking enrichment of key pathway components and shared common network modules involved in TGF- β signaling ($p=0.0002$), ErbB signaling ($p=0.002$), MAPK signaling ($p=0.004$), focal adhesion ($p=0.006$) and ubiquitin-mediated proteolysis (5 $p=0.04$) was observed (Fig 4A). These could represent potentially important common functional modules utilized by Flaviviridae. An intriguing observation that may delineate the portion of the viral lifecycle that is dependent on TGF- β , is the recurrence of common network modules associated with TGF- β signaling ($p<0.0005$) when we examined overlapping siRNA hits and interactions from this screen and those reported using the 10 HCV replicon system (Fig 4B, C (Tai (2009) *Cell Host Microbe* **5**, 298-307.)).

An estimated 25%–30% of HIV-infected individuals are chronically co-infected with HCV (Andersson (2006) *Clin Liver Dis* **10**, 303-320, viii.). Defining host factors and pathways that both HIV and HCV depend on could suggest a common treatment strategy. 15 Comparing the host factors recovered from the HCVcc and HIV siRNA screens reveals ten genes, DDX3X, DNAJB1, ETF1, HEATR1, MAP4, NMT1, OST48, SPCS3, SUV420H1 and Rap9p40/RABEPK that are needed for replication of both viruses (Brass (2008) *Science* **319**, 921-926.). Rab9p40 functions in the movement of late endosomes to the trans Golgi network (TGN), and along with its interaction partners, Rab9 and 20 PIKfyve, is required for the particle assembly of multiple enveloped viruses (HIV, Marburg, Ebola and measles viruses), though the mechanism remains poorly understood (Murray (2008) *Nat Rev Microbiol* **6**, 699-708; Murray (2005) *J Virol* **79**, 11742-11751; Shisheva (2008) *Cell Biol Int* **32**, 591-604.). This study, and that of Tai et al., now add HCV to the list of Rab9p40-dependent viruses.

25

Example 2

This Example demonstrates the identification points in the HCV life-cycle affected by knock-down of particular host-factor genes.

30 **siRNA Library and Functional Genomic Screens:** Genes identified by the genome-wide siRNA screen in Example 1 served as a starting point for defining the comprehensive interactions between HCV and host. The life cycle of HCV infection broadly encompasses viral entry, intracellular trafficking, viral RNA translation and

replication, and virion assembly and release. Each of these steps engages in a complex set of host cell machineries. To functionally validate the HCV host dependencies discovered from the siRNA screen, and to study how these host factors are relevant for the various steps of HCV life cycle, 199 of the most significant primary screen hits and 33 other cellular genes designated as putative false-negative hits by hypothesis-driven follow-up studies were selected for further analysis. These genes are listed in Table 5.

Table 5. List of Host Factor and Summary of Effect on HCV Life-Cycle

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase				Proviral	
ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6				Proviral	
ABCE1	6059	NM_002940	ATP-binding cassette, sub-family E (OABP), member 1					X
ACBD3	64746	NM_022735	acyl-Coenzyme A binding domain containing 3					X
ADFP	123	NM_001122	adipose differentiation-related protein				Proviral	
AKT2	208	NM_001626	v-akt murine thymoma viral oncogene homolog 2					X
AP1GBP1	11276	NM_007247	AP1 gamma subunit binding protein 1				Proviral	
AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit				Proviral	
APC2	10297	NM_005883	adenomatosis polyposis coli 2					X
APOBEC2	10930	NM_006789	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2			Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
APOBEC3B	9582	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B					X
APOE	348	NM_000041	apolipoprotein E				Proviral	
ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22				Proviral	
ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7	Proviral (HCV & VSV)				
ARL10	285598	NM_173664	ADP-ribosylation factor-like 10					X
ARRDC2	27106	NM_015683	arrestin domain containing 2	Proviral (HCV & VSV)				
ART5	116969	NM_053017	ADP-ribosyltransferase 5					X
BAIAP2	10458	NM_006340	BAI1-associated protein 2					X
BCL7A	605	NM_020993	B-cell CLL/lymphoma 7A					X
BCL9L	283149	NM_182557	B-cell CLL/lymphoma 9-like			Proviral		
C1QA	712	NM_015991	complement component 1, q subcomponent, A chain				Proviral	
C1QB	713	NM_000491	complement component 1, q subcomponent, B chain				Proviral	
CABP1	9478	NM_004276	calcium binding protein 1					X

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
CCDC8	83987	NM_032040	coiled-coil domain containing 8				Proviral	
CCL26	10344	NM_006072	chemokine (C-C motif) ligand 26				Proviral	
CCL3L1	6349	NM_021006	chemokine (C-C motif) ligand 3-like 1					X
CCND1	595	NM_053056	cyclin D1					X
CD3E	916	NM_000733	CD3e molecule, epsilon			Proviral		
CD81	975	NM_004356	CD81 molecule	Proviral (HCV-Specific)				
CDC42EP3	10602	NM_006449	CDC42 effector protein (Rho GTPase binding) 3	Proviral (HCV-Specific)				
CDCA3	83461	NM_031299	cell division cycle associated 3				Proviral	
CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)	Proviral (HCV-Specific)				
CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5					X
CEBPD	1052	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta			Proviral		
CHKA	1119	NM_001277	choline kinase alpha	Proviral (HCV-Specific)		Proviral		
CLSTN1	22883	NM_014944	calsyntenin 1			Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
CNOT1 (KIAA1007)	23019	NM_016284	CCR4-NOT transcription complex, subunit 1	Proviral (HCV & VSV)		Proviral		
CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2	Proviral (HCV & VSV)				
CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3	Proviral (HCV & VSV)				
CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like					X
CPD	1362	NM_001304	carboxypeptidase D				Proviral	
CRLF2	64109	NM_022148	cytokine receptor-like factor 2					X
CRLF3	51379	NM_015986	cytokine receptor-like factor 3		Proviral			X
CSF3R	1441	NM_000760	colony stimulating factor 3 receptor (granulocyte)					X
CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like				Proviral	
CTGF	1490	NM_001901	connective tissue growth factor				Proviral	
CTNNA1	8727	NM_003798	catenin (cadherin-associated protein), alpha-like 1				Proviral	
CTNNB1	1499	NM_001904	catenin (cadherin-associated protein), beta 1, 88kDa					X

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
CTSF	8722	NM_003793	cathepsin F			Proviral		
CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1				Proviral	
CXCL12	6387	NM_000609	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)			Antiviral		
CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide	Proviral (HCV & VSV)				
CYLD	1540	NM_015247	cylindromatosis (turban tumor syndrome)			Proviral		
CD55 (DAF)	1604	NM_000574	CD55 molecule, decay accelerating factor for complement (Cromer blood group)				Proviral	
DDOST	1650	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase					X
DDX21	9188	NM_004728	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21			Proviral		
DDX26	26512	NM_001039938	integrator complex subunit 6			Proviral		
DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	Proviral (HCV & VSV)	Proviral	Proviral		
DDX6	1656	NM_004397	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6			Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
DEFB126	81623	NM_030931	defensin, beta 126				Proviral	
DGAT1	8694	NM_012079	diacylglycerol O-acyltransferase homolog 1 (mouse)			Proviral		
DICER1	23405	NM_030621, NM_177438	dicer 1, ribonuclease type III			Antiviral		
DNMT1	1786	NM_001379	DNA (cytosine-5)-methyltransferase 1			Proviral		
DOCK3	1795	NM_004947	dedicator of cytokinesis 3					X
E2F1	1869	NM_005225	E2F transcription factor 1					X
ECT2	1894	NM_018098	epithelial cell transforming sequence 2 oncogene				Antiviral	
EIF3S6	3646	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa			Proviral		
ERBB2	2064	NM_004448	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)			Antiviral		
FBLN5	10516	NM_006329	fibulin 5		Proviral	Proviral		
FBXO38	81545	NM_030793	F-box protein 38					X
FKBP1	63943	NM_022110	FK506 binding protein like		Proviral	Proviral		
FLT4	2324	NM_002020	fms-related tyrosine		Proviral	Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			kinase 4					
FOXA2	3170	NM_021784	forkhead box A2				Proviral	
FOXP3	50943	NM_014009	forkhead box P3					X
FXVD6	53826	NM_022003	FXVD domain containing ion transport regulator 6		Antiviral	Antiviral		
GCAT	23464	NM_014291	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)				Proviral	
GLG1	2734	NM_012201	golgi glycoprotein 1				Proviral	
GNAZ	2781	NM_002073	guanine nucleotide binding protein (G protein), alpha z polypeptide			Antiviral		
GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1			Proviral		
GNG8	94235	NM_033258	guanine nucleotide binding protein (G protein), gamma 8				Proviral	
GPR145 (MCHR2)	84539	NM_032503	melanin-concentrating hormone receptor 2	Proviral (HCV-Specific)				
GPR153	387509	XM_291419	G protein-coupled receptor 153		Antiviral	Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
GPR62	118442	NM_080865	G protein-coupled receptor 62	Proviral (HCV & VSV)				
GPSN2	9524	NM_004868	glycoprotein, synaptic 2			Proviral		
GSPT1	2935	NM_002094	G1 to S phase transition 1			Proviral		
GTF3A	2971	NM_002097	general transcription factor IIIA			Proviral		
HAS1	3036	NM_001523	hyaluronan synthase 1			Proviral		
HEXA	3073	NM_000520	hexosaminidase A (alpha polypeptide)			Proviral		
HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3				Proviral	
HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K				Antiviral	
HPX	3263	NM_000613	hemopexin					X
HSPCA	3320	NM_005348, NM_001017963	heat shock protein 90kDa alpha (cytosolic), class A member 1					X
IDE	3416	NM_004969	insulin-degrading enzyme				Proviral	
IFITM2	10581	NM_006435	interferon induced transmembrane protein 2 (1-8D)		Antiviral	Antiviral		
IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)		Antiviral	Antiviral		
IFIX (PYHIN1)	149628	NM_152501	pyrin and HIN domain family, member 1					X

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6		Proviral	Proviral		
IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11					X
IGSF4D (CADM2)	253559	NM_153184	cell adhesion molecule 2					X
IKKB	3551	NM_001556	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	Antiviral (HCV & VSV)				
IKBKE	9641	NM_014002	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon				Proviral	
IL10RB	3588	NM_000628	interleukin 10 receptor, beta				Antiviral	
IL17RB	5540	NM_018725	interleukin 17 receptor B				Proviral	
IL1B	3553	NM_000576	interleukin 1, beta					X
IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)			Proviral		
IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1				Antiviral	
IREB2	3658	NM_004136	iron-responsive element binding protein 2					X
IRF3	3661	NM_001571	interferon regulatory factor 3				Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
ITGA7	3679	NM_002206	integrin, alpha 7			Proviral		
ITGB1BP2	26548	NM_012278	integrin beta 1 binding protein (melusin) 2					X
LRR62 (KIAA1904)	114794	XM_056282	leucine rich repeat containing 62			Proviral		
LCK	3932	NM_005356, NM_001042771	lymphocyte-specific protein tyrosine kinase			Proviral		
PN01 (LOC56902)	56902	NM_020143	partner of NOB1 homolog (S. cerevisiae)				Proviral	
LTB	4050	NM_002341, NM_009588	lymphotoxin beta (TNF superfamily, member 3)				Proviral	
MAP3K6	9064	NM_004672	mitogen-activated protein kinase kinase 6			Proviral		
MAP4	4134	NM_002375	microtubule-associated protein 4	Proviral (HCV & VSV)				
MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1		Proviral	Proviral		
MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3		Proviral	Proviral		
MAVS	57506	NM_020746	mitochondrial antiviral signaling protein				Proviral	
YIPF4 (MGC11061)	84272	NM_032312	Yip1 domain family, member 4					X
DACT3 (MGC15476)	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)					X

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
MMP11	4320	NM_005940	matrix metalloproteinase 11 (stromelysin 3)					X
MMP9	4318	NM_004994	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)					X
MVD	4597	NM_002461	mevalonate (diphospho) decarboxylase			Proviral		
MYO3A	53904	NM_017433	myosin IIIA				Proviral	
NCOR2	9612	NM_006312	nuclear receptor co-repressor 2					X
NDRG1	10397	NM_006096	N-myc downstream regulated gene 1				Antiviral	
NDUFB4	4710	NM_004547	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa					X
NEK4	6787	NM_003157	NIMA (never in mitosis gene a)-related kinase 4			Proviral		
NEMO	8517	NM_003639	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma			Antiviral		
NFKB1	4790	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1			Antiviral		
NFKB2	4791	NM_002502	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2	Antiviral (HCV & VSV)				

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			(p49/p100)					
NIK	9020	NM_003954	mitogen-activated protein kinase kinase 14				Proviral	
NOL6	65083	NM_022917	nucleolar protein family 6 (RNA-associated)		Proviral	Proviral		
OSBP	5007	NM_002556	oxysterol binding protein			Proviral		
OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1		Antiviral	Antiviral		
SCYL3 (PACE-1)	57147	NM_020423	SCY1-like 3 (<i>S. cerevisiae</i>)				Proviral	
PARP11	57097	NM_020367	poly (ADP-ribose) polymerase family, member 11				Proviral	
PDAP1	11333	NM_014891	PDGFA associated protein 1					X
PIAS1	8554	NM_016166	protein inhibitor of activated STAT, 1		Proviral	Proviral		
PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha	Proviral (HCV & VSV)		Proviral		
PLB1	151056	NM_153021	phospholipase B1				Proviral	
PLEK2	26499	NM_016445	pleckstrin 2		Antiviral	Antiviral	Proviral	
PPIA	5478	NM_021130	peptidylprolyl isomerase A (cyclophilin A)				Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform				Proviral	
PPP2R2A	5520	NM_002717	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform				Proviral	
PRG2	5553	NM_002728	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)				Proviral	
PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)			Proviral		
PROX1	5629	NM_002763	prospero-related homeobox 1				Proviral	
PTHR1	5745	NM_000316	parathyroid hormone receptor 1				Proviral	
PTK2B	2185	NM_004103	PTK2B protein tyrosine kinase 2 beta			Proviral		
TWF1 (PTK9)	5756	NM_002822	twinfilin, actin-binding protein, homolog 1 (Drosophila)					X
PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H				Antiviral	
RAB10	10890	NM_016131	RAB10, member RAS oncogene family				Proviral	
RAB11A	8766	NM_004663	RAB11A, member RAS					X

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			oncogene family					
RAB34	83871	NM_031934	RAB34, member RAS oncogene family	Proviral (HCV & VSV)				
RAB5A	5868	NM_004162	RAB5A, member RAS oncogene family	Proviral (HCV & VSV)				
RAB9P40 (RABEPK)	10244	NM_005833	Rab9 effector protein with kelch motifs				Proviral	
RAC1	5879	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	Proviral (HCV & VSV)				
RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1				Proviral	
RBM9	23543	NM_014309	RNA binding motif protein 9				Proviral	
RBP4	5950	NM_006744	retinol binding protein 4, plasma	Proviral (HCV & VSV)		Proviral		
RELA	5970	NM_021975	v-rel reticuloendotheliosis viral oncogene homolog A (avian)			Antiviral		
RELB	5971	NM_006509	v-rel reticuloendotheliosis viral oncogene homolog B			Antiviral		
RFWD3	55159	NM_018124	ring finger and WD repeat domain 3					X
RGPD5	84220	NM_005054	RANBP2-like and GRIP		Proviral	Proviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			domain containing 5					
Rgr	266747	NM_153615	Ral-GDS related protein Rgr				Proviral	
RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2		Antiviral	Antiviral	Proviral	
RIT1	6016	NM_006912	Ras-like without CAAX 1					X
RNF207	388591	NM_207396	ring finger protein 207				Proviral	
RNF31	55072	NM_017999	ring finger protein 31					X
ROBO1	6091	NM_002941	roundabout, axon guidance receptor, homolog 1 (Drosophila)					X
ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2				Proviral	
RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1				Proviral	
RSAD2	91543	NM_080657	radical S-adenosyl methionine domain containing 2				Antiviral	
RYK	6259	NM_002958	RYK receptor-like tyrosine kinase				Proviral	
SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1				Proviral	
SIK2 (SNF1LK2)	23235	NM_015191	SNF1-like kinase 2				Proviral	
SMAD5	4090	NM_005903	SMAD family member 5				Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
SMAD6	4091	NM_005585	SMAD family member 6	Proviral (HCV-Specific)	Proviral	Proviral		
SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3				Proviral	
SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1				Proviral	
SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2					X
SNARK (NUAK2)	81788	NM_030952	NUAK family, SNF1-like kinase, 2				Proviral	
SNRPD1	6632	NM_006938	small nuclear ribonucleoprotein D1 polypeptide 16kDa					X
SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)				Proviral	
SPCS2	9789	NM_014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)				Proviral	
SPCS3	60559	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)				Proviral	
SREBP1	6720	NM_004176	sterol regulatory element binding transcription				Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			factor 1					
SRI	6717	NM_003130	sorcin				Proviral	
SRRM2	23524	NM_016333	serine/arginine repetitive matrix 2				Proviral	
STAT1	6772	NM_007315, NM_139266	signal transducer and activator of transcription 1, 91kDa		Antiviral	Antiviral		
STAT3	6774	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)				Proviral	
STK22C (TSSK3)	81629	NM_052841	testis-specific serine kinase 3					X
SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)	Proviral (HCV & VSV)				
TANK (TRAF2)	10010	NM_004180, NM_133484	TRAF family member-associated NFKB activator					X
WWTR1	25937	NM_015472	WW domain containing transcription regulator 1					X
TBK1	29110	NM_013254	TANK-binding kinase 1					X
TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)			Proviral		
TGFBR1	7046	NM_004612	transforming growth factor, beta receptor I			Antiviral		

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
			(activin A receptor type II-like kinase, 53kDa)					
TLK2	11011	NM_006852	tousled-like kinase 2					X
TM6SF2	53345	NM_001001524	transmembrane 6 superfamily member 2				Proviral	
TNFRSF10C	8794	NM_003841	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain					X
TNFRSF10D	8793	NM_003840	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain					X
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18					X
TNRC11 (MED12)	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)		Antiviral	Proviral		
TNS1	7145	NM_022648	tensin 1				Antiviral	
TP53	7157	NM_000546	tumor protein p53			Antiviral		
TRAPPC5	126003	XM_058961	trafficking protein particle complex 5				Proviral	
TRIM42	287015	NM_152616	tripartite motif-containing 42				Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
TRIM46	80128	NM_025058	tripartite motif-containing 46				Proviral	
TRIM62	55223	NM_018207	tripartite motif-containing 62	Proviral (HCV-Specific)				
TRRAP	8295	NM_003496	transformation/transcript ion domain-associated protein				Proviral	
TUBB4 (TUBB3)	10381	NM_006086	tubulin, beta 3					X
TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)			Proviral		
UBE1L	7318	NM_003335	ubiquitin-activating enzyme E1-like				Proviral	
UBE2E3	10477	NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)					X
UBE2J1	51465	NM_016021	ubiquitin-conjugating enzyme E2, J1			Proviral		
UBE2J2	118424	NM_058167	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)					X
UBE2M	9040	NM_003969	ubiquitin-conjugating enzyme E2M				Proviral	
UBE2S	27338	NM_014501	ubiquitin-conjugating enzyme E2S			Proviral	Proviral	

Entrez gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release	No Effect on HCV Life-Cycle
USP11	8237	NM_004651	ubiquitin specific peptidase 11				Proviral	
USP16	10600	NM_006447	ubiquitin specific peptidase 16					X
USP51	158880	NM_201286	ubiquitin specific peptidase 51				Proviral	
UTP14A	10813	NM_006649	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)			Proviral		
VAMP1	6843	NM_014231	vesicle-associated membrane protein 1 (synaptobrevin 1)					X
VTN	7448	NM_000638	vitronectin					X
WIF1	11197	NM_007191	WNT inhibitory factor 1			Proviral		
WNT10B	7480	NM_003394	wingless-type MMTV integration site family, member 10B					X
XBP1	7494	NM_005080	X-box binding protein 1	Proviral (HCV-Specific)				
XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble				Proviral	
ZNF337	26152	NM_015655	zinc finger protein 337					X

High-throughput screens with various *in vitro* HCV model systems (HCVcc, HCVpp, and subgenomic replicons) were undertaken using a custom-designed arrayed library targeting these 232 genes (Dharmacon ON-TARGETplus SMARTpool siRNA library). ON-TARGETplus pools were used to significantly reduce off-target effects while maintaining
5 siRNA potency, and hence provide a highly effective tool for validation and functional stratification following primary screen with the siGENOME SMARTpools.

A. Identification of host factors that affect the early stages of the HCV life-cycle

Core Staining: siRNAs were transiently transfected into the Huh7.5.1 cells at a final concentration of 50 nM, using a transfection protocol employing 0.44% Oligofectamine
10 (Invitrogen) in a 96-well format. Briefly, this protocol is as follows: Oligofectamine was diluted in Opti-MEM (Invitrogen) and incubated for 10 min before being distributed into wells using a Wellmate liquid handling robot (Thermo Fisher Matrix). Following distribution, the plates were spun down at 1,000 RPM and the arrayed siRNAs added. The plates were incubated for 20 minutes, after which 4,500 Huh 7.5.1 cells, in 60 μ L
15 Dulbecco's modified minimal essential media (DMEM, Invitrogen) supplemented with 15% FBS (FBS, Invitrogen), were added to each well. The plates were spun at 1,000 RPM and then placed in a humidified tissue culture incubator at 37°C and 5% CO₂. After 72 h of incubation, to allow for siRNA-mediated gene knockdown, the medium was removed and the cells were infected with the JFH-1 genotype 2a virus, at an MOI of 0.5
20 in 100 mL DMEM with 10% FBS. At 48 h post-infection (when silencing is still operative), 80 mL media was removed and used in "late-stage" experiments, described below. The cells were then fixed with 4% formalin, permeabilized with 0.3% Triton-X100 (Sigma) in Dulbecco's phosphate buffered saline (D-PBS, Invitrogen) containing 3% FBS and 3% BSA Fraction V (BSA, Sigma Aldrich), then stained for HCV core,
25 using purified anti-HCV core monoclonal antibody (produced from the anti-HCV core 6G7 hybridoma cells) diluted in D-PBS with 1% BSA. The cells were then incubated with an Alexa Fluor 488 goat anti-mouse secondary (A-11001, Invitrogen) at 1:1,000 in D-PBS with 1% BSA, and stained for DNA with Hoechst 33342 at 1:5,000–10,000 (Invitrogen). Each step was followed by two washes with D-PBS. The cells were then
30 imaged on an automated Image Express Micro (IXM) microscope (Molecular Devices) at 4x magnification, using two wavelengths: 488 nm to detect HCV infected cells expressing core, and 350 nm for nuclear DNA bound by Hoechst 33342. Images were then analyzed using the Metamorph Cell Scoring software program (Molecular Devices

Inc.) to determine the total cells per well, and the percentage of core positive cells in each well (percent infected).

B. Identification of host factors affecting late-stages of the HCV life-cycle

The 80 ml of medium removed from the infected cells in part A were replica plated onto a new 96-well plate, which contained 10,000 Huh 7.5.1 cells per well plated out 24 h before viral supernatant addition. At 48 h post-infection, the cells were fixed, stained, and imaged using the staining and imaging protocol described in part A.

The experiment described in parts A and B above was performed in triplicate. siRNA pools were classified as hits if the average of the triplicate plates showed that the percentages of core positive cells were decreased (proviral) or increased (antiviral) for more than 1.5-fold comparing with that of non-targeting control siRNA. The results of these experiments are shown in Table 6.

Table 6. Identification of Host Factors Affecting Early and Late Stages of the HCV Life-Cycle

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
ABCB6	1.10	0.05	0.68	0.13		
ABCE1	1.21	0.26	0.72	0.06		
ACBD3	1.19	0.08	0.64	0.13		Proviral
ADFP	1.19	0.38	0.38	0.09		
AKT2	1.07	0.15	0.92	0.14		
AP1GBP1	0.91	0.20	0.51	0.06		Proviral
AP3B1	1.25	0.14	0.74	0.16		
APC2	1.02	0.17	0.71	0.16		
APOBEC2	0.90	0.19	0.68	0.04		
APOBEC3B	1.23	0.19	0.28	0.04		Proviral
APOE	1.14	0.16	0.31	0.02		Proviral
ARHGAP22	1.08	0.17	0.66	0.11		Proviral
ARHGEF7	0.42	0.14	0.41	0.15	Proviral	Proviral
ARL10A	1.16	0.11	1.25	0.21		
ARRDC2	0.34	0.17	0.49	0.12	Proviral	Proviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
ART5	1.21	0.18	0.77	0.07		
BAIAP2	1.17	0.39	0.79	0.07		
BCL7A	1.16	0.13	1.34	0.12		
BCL9L	0.95	0.16	1.09	0.16		
C1QA	0.97	0.10	0.25	0.03		Proviral
C1QB	0.73	0.16	0.37	0.02		Proviral
CABP1	1.10	0.15	0.72	0.22		
CCDC8	1.20	0.18	0.26	0.02		Proviral
CCL26	1.18	0.09	0.47	0.08		Proviral
CCL3L1	0.76	0.04	0.54	0.13		Proviral
CCND1	1.03	0.12	0.89	0.09		
CD3E	0.49	0.13	0.45	0.21	Proviral	Proviral
CD81	0.36	0.07	0.48	0.08	Proviral	Proviral
CDC42EP3	0.98	0.04	0.86	0.11		
CDCA3	1.35	0.11	0.30	0.10		Proviral
CDH1	0.87	0.08	0.57	0.10		Proviral
CDKL5	1.18	0.19	0.94	0.15		
CEBPD	0.39	0.14	0.45	0.17	Proviral	Proviral
CHKA	0.38	0.06	0.27	0.10	Proviral	Proviral
CHUK	0.51	0.08	0.48	0.13	Proviral	Proviral
CLSTN1	0.25	0.13	0.47	0.09	Proviral	Proviral
CNOT1 (KIAA1007)	0.32	0.07	0.05	0.00	Proviral	Proviral
CNOT2	0.39	0.09	0.07	0.03	Proviral	Proviral
CNOT3	0.30	0.05	0.34	0.12	Proviral	Proviral
CNOT6L	0.90	0.11	0.69	0.10		
CPD	1.12	0.16	0.57	0.13		Proviral
CRLF2	0.07	0.02	0.28	0.08	Proviral	Proviral
CRLF3	1.09	0.19	1.53	0.26		Antiviral
CSF3R	0.92	0.14	0.78	0.18		
CSNK1A1L	1.09	0.02	0.36	0.07		Proviral
CTGF	0.91	0.06	0.80	0.19		
CTNNA1	1.13	0.12	0.48	0.09		Proviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
CTNNB1	0.75	0.11	0.84	0.12		
CTSF	0.29	0.13	0.25	0.17	Proviral	Proviral
CX3CL1	0.95	0.11	0.58	0.10		Proviral
CXCL12	1.20	0.12	0.66	0.09		Proviral
CYBA	0.26	0.04	0.38	0.06	Proviral	Proviral
CYLD	1.02	0.13	0.68	0.16		
DAF (CD55)	1.35	0.17	0.38	0.10		Proviral
DDOST	1.27	0.01	0.91	0.20		
DDX21	0.38	0.10	0.37	0.03	Proviral	Proviral
DDX26	0.48	0.05	0.43	0.13	Proviral	Proviral
DDX3X	1.34	0.45	0.17	0.03		Proviral
DDX6	0.29	0.17	0.48	0.11	Proviral	Proviral
DEFB126	0.97	0.02	0.23	0.03		Proviral
DGAT1	0.83	0.16	0.89	0.02		
DICER1	1.08	0.13	1.37	0.20		
DNMT1	0.92	0.26	0.30	0.06		Proviral
DOCK3	1.55	0.17	0.51	0.17	Antiviral	Proviral
E2F1	1.29	0.18	1.07	0.16		
ECT2	1.54	0.07	0.74	0.09	Antiviral	
EIF3S6	1.55	0.27	0.32	0.14	Antiviral	Proviral
ERBB2	0.90	0.12	0.57	0.14		Proviral
FBLN5	0.76	0.14	0.83	0.06		
FBXO38	0.90	0.14	1.03	0.05		
FKBP1	0.31	0.13	0.45	0.14	Proviral	Proviral
FLT4	0.83	0.06	0.45	0.14		Proviral
FOXA2	0.62	0.07	0.46	0.22	Proviral	Proviral
FOXP3	1.06	0.20	0.98	0.11		
FXYD6	1.20	0.08	0.52	0.13		Proviral
GCAT	1.46	0.23	0.95	0.12		
GLG1	1.07	0.02	0.41	0.15		Proviral
GNAZ	0.95	0.05	0.60	0.06		Proviral
GNB2L1	0.51	0.02	0.21	0.05	Proviral	Proviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
GNG8	0.65	0.06	0.17	0.04	Proviral	Proviral
GPR145 (MCHR2)	0.76	0.01	0.10	0.02		Proviral
GPR153	1.02	0.07	0.43	0.06		Proviral
GPR62	0.95	0.04	0.59	0.12		Proviral
GPSN2	0.26	0.03	0.38	0.10	Proviral	Proviral
GSPT1	0.45	0.11	0.47	0.12	Proviral	Proviral
GTF3A	0.74	0.09	1.00	0.15		
HAS1	0.46	0.09	0.18	0.12	Proviral	Proviral
HEXA	0.78	0.04	0.20	0.02		Proviral
HIPK3	1.00	0.03	0.43	0.04		Proviral
HNRPK	0.37	0.05	1.73	0.08	Proviral	Antiviral
HPX	1.36	0.16	0.90	0.03		
HSPCA	1.05	0.22	0.91	0.14		
IDE	1.08	0.19	0.58	0.11		Proviral
IFITM2	0.82	0.13	0.63	0.11		Proviral
IFITM3	0.81	0.11	0.65	0.24		Proviral
IFIX (PYHIN1)	0.92	0.09	0.55	0.10		Proviral
IGFBP6	0.63	0.19	0.98	0.39	Proviral	
IGSF11	1.10	0.11	0.99	0.06		
IGSF4D (CADM2)	1.57	0.31	0.89	0.17	Antiviral	
IKBKB	1.04	0.13	0.58	0.11		Proviral
IKBKE	0.94	0.11	0.70	0.12		
IL10RB	1.26	0.09	0.91	0.08		
IL17RB	0.96	0.03	0.30	0.02		Proviral
IL1B	0.95	0.20	0.99	0.13		
IMP4	0.16	0.09	0.48	0.08	Proviral	Proviral
IMPDH1	0.98	0.17	1.07	0.21		
IREB2	0.81	0.11	0.78	0.16		
IRF3	1.03	0.13	0.62	0.18		Proviral
ITGA7	0.78	0.02	0.40	0.07		Proviral
ITGB1BP2	1.02	0.08	0.97	0.12		
KIAA1904 (LRRC62)	0.92	0.08	0.37	0.03		Proviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
LCK	0.79	0.11	0.53	0.18		Proviral
LOC56902 (PNO1)	0.43	0.31	0.40	0.10	Proviral	Proviral
LTB	0.87	0.15	0.42	0.10		Proviral
MAP3K6	1.08	0.04	0.70	0.22		
MAP4	0.94	0.10	0.69	0.16		
MAPK1	1.12	0.25	0.45	0.15		Proviral
MARK3	1.12	0.09	0.49	0.14		Proviral
MAVS	1.10	0.14	0.58	0.14		Proviral
MGC11061 (YIPF4)	0.93	0.30	0.42	0.18		Proviral
MGC15476 (DACT3)	1.26	0.10	1.00	0.13		
MMP11	1.00	0.13	0.66	0.08		Proviral
MMP9	0.94	0.12	0.49	0.10		Proviral
MVD	0.74	0.05	0.31	0.03		Proviral
MYO3A	1.25	0.13	0.42	0.14		Proviral
NCOR2	1.06	0.15	1.07	0.14		
NDRG1	0.94	0.04	1.00	0.10		
NDUFB4	0.97	0.24	0.97	0.09		
NEK4	1.15	0.10	0.17	0.03		Proviral
NEMO	1.05	0.12	0.97	0.21		
NFKB1	0.92	0.15	0.54	0.23		Proviral
NFKB2	1.17	0.05	0.95	0.23		
NIK	1.03	0.12	0.36	0.09		Proviral
NOL6	0.63	0.19	1.06	0.18	Proviral	
OSBP	0.50	0.06	0.32	0.05	Proviral	Proviral
OTUB1	0.96	0.11	0.67	0.12		Proviral
PACE-1 (SCYL3)	1.25	0.09	0.38	0.08		Proviral
PARP11	1.13	0.10	0.30	0.06		Proviral
PDAP1	0.46	0.07	0.70	0.15	Proviral	
PIAS1	0.29	0.07	0.28	0.15	Proviral	Proviral
PIK4CA	0.02	0.00	0.07	0.01	Proviral	Proviral
PLB1	0.40	0.08	0.40	0.14	Proviral	Proviral
PLEK2	0.85	0.13	0.27	0.04		Proviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
PPIA	0.88	0.24	0.97	0.11		
PPP2R1A	1.00	0.17	0.87	0.08		
PPP2R2A	1.00	0.10	0.34	0.10		Proviral
PRG2	1.10	0.09	0.64	0.18		Proviral
PRKRIP1	1.20	0.27	1.03	0.11		
PROX1	0.78	0.10	0.09	0.05		Proviral
PTHR1	0.45	0.08	0.49	0.12	Proviral	Proviral
PTK2B	0.80	0.07	0.26	0.07		Proviral
PTK9 (TWF1)	0.94	0.11	0.71	0.14		
PTPRH	1.39	0.18	0.76	0.19		
RAB10	1.02	0.12	0.51	0.10		Proviral
RAB11A	1.11	0.12	0.80	0.10		
RAB34	0.35	0.06	0.34	0.14	Proviral	Proviral
RAB5A	0.42	0.14	0.40	0.13	Proviral	Proviral
RAB9P40 (RABEPK)	0.67	0.13	0.35	0.03	Proviral	Proviral
RAC1	0.97	0.07	0.89	0.19		
RAF1	1.14	0.09	0.42	0.05		Proviral
RBM9	1.20	0.18	0.34	0.11		Proviral
RBP4	0.78	0.10	0.12	0.04		Proviral
RELA	1.10	0.18	0.53	0.16		Proviral
RELB	1.04	0.16	0.75	0.20		
RFWD3	0.92	0.05	1.36	0.22		
RGPD5	1.16	0.30	0.30	0.01		Proviral
RGR	0.41	0.05	0.50	0.14	Proviral	Proviral
RIPK2	1.41	0.20	0.62	0.14		Proviral
RIT1	0.78	0.07	0.86	0.06		
RNF207	0.76	0.05	0.46	0.13		Proviral
RNF31	1.23	0.22	0.99	0.15		
ROBO1	1.02	0.05	0.96	0.12		
ROCK2	0.89	0.05	0.27	0.14		Proviral
RPS6KL1	0.45	0.12	0.37	0.02	Proviral	Proviral
RSAD2	1.06	0.24	1.81	0.19		Antiviral

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
RYK	1.19	0.10	0.44	0.08		Proviral
SH3TC1	0.97	0.10	0.50	0.13		Proviral
SIK2 (SNF1LK2)	1.54	0.10	0.86	0.06	Antiviral	
SMAD5	1.09	0.16	0.54	0.04		Proviral
SMAD6	0.67	0.05	0.65	0.12	Proviral	Proviral
SMARCD3	1.04	0.19	0.24	0.04		Proviral
SMURF1	0.76	0.02	0.44	0.09		Proviral
SMURF2	0.97	0.14	0.71	0.18		
SNARK (NUAK2)	0.91	0.06	0.50	0.06		Proviral
SNRPD1	0.61	0.04	1.05	0.07	Proviral	
SPCS1	1.05	0.07	0.07	0.04		Proviral
SPCS2	0.90	0.10	0.11	0.02		Proviral
SPCS3	0.93	0.06	0.11	0.04		Proviral
SREBP1	0.85	0.14	0.36	0.15		Proviral
SRI	0.65	0.13	0.32	0.09		Proviral
SRRM2	1.10	0.11	0.36	0.01		Proviral
STAT1	1.23	0.08	0.84	0.23		
STAT3	1.81	0.34	0.59	0.19	Antiviral	Proviral
STK22C	1.12	0.13	0.71	0.13		
SUV420H1	1.07	0.24	0.39	0.01		Proviral
TANK (TRAF2)	0.79	0.05	0.82	0.07		
TAZ	1.09	0.09	0.76	0.03		
TBK1	0.90	0.16	0.62	0.12		Proviral
TFAP2A	0.92	0.10	0.98	0.09		
TGFBR1	1.05	0.16	0.51	0.11		Proviral
TLK2	1.08	0.12	0.91	0.01		
TM6SF2	0.28	0.10	0.31	0.15	Proviral	Proviral
TNFRSF10C	0.91	0.09	0.67	0.03		Proviral
TNFRSF10D	0.90	0.10	0.42	0.07		Proviral
TNFRSF18	1.09	0.07	0.88	0.17		
TNRC11 (MED12)	1.13	0.14	0.95	0.20		
TNS	1.02	0.14	0.83	0.08		

Entrez Gene Symbol	Early Stage		Late Stage		Early Stage Core Staining Hits	Late Stage Core Staining Hits
	Average Normalized Percent Infected Cells	SD	Average Normalized Percent Infected Cells	SD		
TP53	0.99	0.07	1.09	0.16		
TRAPPC5	1.04	0.15	0.93	0.17		
TRIM42	1.08	0.13	0.86	0.08		
TRIM46	0.85	0.06	0.81	0.19		
TRIM62	0.74	0.10	0.29	0.13		Proviral
TRRAP	0.87	0.12	0.21	0.11		Proviral
TUBB4 (TUBB3)	1.24	0.18	0.99	0.13		
TWIST1	1.00	0.14	0.98	0.15		
UBE1L	0.95	0.09	0.54	0.06		Proviral
UBE2E3	1.29	0.05	0.80	0.06		
UBE2J1	0.43	0.13	0.93	0.09	Proviral	
UBE2J2	0.75	0.12	0.89	0.08		
UBE2M	0.51	0.16	0.76	0.11	Proviral	
UBE2S	1.55	0.05	0.49	0.10	Antiviral	Proviral
USP11	0.43	0.07	0.49	0.19	Proviral	Proviral
USP16	0.84	0.11	0.61	0.15		Proviral
USP51	0.83	0.09	0.39	0.07		Proviral
UTP14A	0.16	0.05	0.73	0.11	Proviral	
VAMP1	1.24	0.09	0.91	0.30		
VTN	0.87	0.13	0.98	0.09		
WIF1	0.83	0.05	0.21	0.03		Proviral
WNT10B	0.88	0.10	0.78	0.13		
XBP1	1.01	0.13	0.28	0.07		Proviral
XPNPEP1	1.18	0.06	0.38	0.01		Proviral
ZNF337	1.15	0.11	0.44	0.09		Proviral

C. Identification of host factors affecting HCV RNA levels

HCV RNA Quantification: Infected cells were prepared as described above in parts A and B. The level of extracellular and intracellular HCV RNA was determined as follows:

- 5 Total RNA was extracted with QIAamp Viral RNA Mini Kit (Qiagen) from 140 mL culture medium, or with RNeasy Mini Kit (Qiagen) from whole-cell lysate. Copy

numbers of HCV RNA were determined by quantitative PCR with the probe and primers listed below, using the TaqMan EZ RT-PCR CORE REAGENTS (Applied Biosystems) on an ABI 7500 Real Time PCR System (Applied Biosystems). PCR parameters consisted of 1 cycle of 50°C for 2 min, then 60°C for 30 min, and 95°C for 3:30 min, followed by 50 cycles of PCR at 95°C for 20 s, and 62°C for 1 min. The relative amount of HCV RNA was normalized to the internal control Human 18S rRNA (Applied Biosystems). HCV TaqMan probe used was 6-FAM CTGCGGAACCGGTGAGTACACTAMRA (IDT). HCV primer sequences were 5' CGGGAGAGCCATAGTGG, and 3' AGTACCACAAGGCCTTTCG. siRNA pools were classified as proviral or antiviral hits if the average normalized HCV RNA levels decreased or increased by more than 1.5-fold comparing with non-targeting control siRNA and the P value was less than 0.05. The results of these experiments are shown in Table 7.

Table 7. HCV RNA Quantification

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
ABCB6	2.04	0.37	0.004	0.58	0.25	0.033	Antiviral	Proviral
ABCE1	0.75	0.18	0.078	0.68	0.17	0.101		Proviral
ACBD3	2.12	1.06	0.072	0.68	0.15	0.174	Antiviral	Proviral
ADFP	0.68	0.37	0.053	0.98	0.30	0.450	Proviral	
AKT2	1.44	0.25	0.020	0.75	0.07	0.035		
AP1GBP1	0.67	0.13	0.032	0.37	0.10	0.001	Proviral	Proviral
AP3B1	1.33	0.19	0.035	0.36	0.07	0.004	Antiviral	Proviral
APC2	1.22	0.40	0.208	1.39	0.61	0.202		
APOBEC2	2.01	0.34	0.004	0.63	0.28	0.053	Antiviral	Proviral
APOBEC3B	0.63	0.13	0.020	0.76	0.17	0.166	Proviral	
APOE	3.22	0.55	0.003	0.27	0.10	0.006	Antiviral	Proviral
ARHGAP22	0.49	0.09	0.029	0.31	0.15	0.171	Proviral	Proviral
ARHGEF7	0.74	0.14	0.024	0.20	0.08	0.000	Proviral	Proviral
ARL10A	4.43	2.30	0.031	1.61	0.80	0.147	Antiviral	Antiviral
ARRDC2	0.49	0.14	0.003	0.21	0.10	0.000	Proviral	Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
ART5	2.08	1.34	0.122	0.72	0.41	0.172	Antiviral	
BAIAP2	0.85	0.18	0.184	0.43	0.23	0.020		Proviral
BCL7A	0.73	0.19	0.063	1.32	0.23	0.123	Proviral	
BCL9L	0.57	0.09	0.009	1.01	0.46	0.497	Proviral	
C1QA	3.14	2.48	0.106	0.30	0.31	0.012	Antiviral	Proviral
C1QB	1.56	0.41	0.042	0.40	0.22	0.009	Antiviral	Proviral
CABP1	2.34	0.45	0.003	0.60	0.06	0.011	Antiviral	Proviral
CCDC8	1.18	0.05	0.049	0.46	0.18	0.016		Proviral
CCL26	1.25	0.20	0.057	0.45	0.21	0.012		Proviral
CCL3L1	1.19	0.33	0.206	0.33	0.16	0.004		Proviral
CCND1	0.90	0.02	0.059	0.78	0.10	0.025		
CD3E	0.34	0.12	0.000	0.29	0.20	0.005	Proviral	Proviral
CD81	0.30	0.09	0.000	0.38	0.17	0.002	Proviral	Proviral
CDC42EP3	0.80	0.18	0.126	1.09	0.66	0.398		
CDCA3	1.40	0.74	0.062	0.40	0.34	0.018		Proviral
CDH1	0.46	0.30	0.045	0.81	0.37	0.196	Proviral	
CDKL5	0.92	0.29	0.337	2.73	0.81	0.000		Antiviral
CEBPD	0.43	0.07	0.003	0.34	0.08	0.003	Proviral	Proviral
CHKA	0.26	0.16	0.000	0.21	0.19	0.004	Proviral	Proviral
CHUK	0.31	0.08	0.005	0.17	0.08	0.001	Proviral	Proviral
CLSTN1	0.86	0.15	0.106	0.27	0.06	0.000		Proviral
CNOT1 (KIAA1007)	0.19	0.16	0.000	0.02	0.03	0.001	Proviral	Proviral
CNOT2	0.21	0.14	0.000	0.13	0.13	0.001	Proviral	Proviral
CNOT3	0.20	0.02	0.000	0.20	0.03	0.001	Proviral	Proviral
CNOT6L	0.94	0.39	0.382	0.82	0.55	0.274		
CPD	1.70	0.40	0.021	0.35	0.22	0.013	Antiviral	Proviral
CRLF2	0.61	0.13	0.005	0.38	0.02	0.000	Proviral	Proviral
CRLF3	1.06	0.16	0.286	2.04	0.77	0.040		Antiviral
CSF3R	0.99	0.06	0.437	0.24	0.07	0.000		Proviral
CSNK1A1L	0.99	0.25	0.474	0.67	0.20	0.097		Proviral
CTGF	1.43	0.29	0.037	0.68	0.26	0.065	Antiviral	Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
CTNNAL1	2.46	1.23	0.057	0.53	0.31	0.038	Antiviral	Proviral
CTNNB1	1.15	0.20	0.145	2.89	1.35	0.036		Antiviral
CTSF	0.46	0.20	0.006	0.15	0.04	0.000	Proviral	Proviral
CX3CL1	1.13	0.65	0.384	0.81	0.58	0.278		
CXCL12	1.90	1.12	0.122	1.23	0.67	0.328	Antiviral	
CYBA	0.68	0.22	0.038	0.13	0.05	0.000	Proviral	Proviral
CYLD	2.41	0.60	0.008	0.70	0.36	0.117	Antiviral	
DAF (CD55)	0.44	0.04	0.002	0.37	0.22	0.014	Proviral	Proviral
DDOST	1.06	0.22	0.369	0.69	0.25	0.113		
DDX21	0.63	0.15	0.020	0.57	0.12	0.048	Proviral	Proviral
DDX26	0.45	0.18	0.008	0.52	0.17	0.024	Proviral	Proviral
DDX3X	0.49	0.02	0.013	0.23	0.20	0.004	Proviral	Proviral
DDX6	0.21	0.04	0.000	0.24	0.02	0.000	Proviral	Proviral
DEFB126	2.00	0.57	0.020	0.39	0.14	0.005	Antiviral	Proviral
DGAT1	0.41	0.08	0.001	0.73	0.57	0.169	Proviral	
DICER1	2.25	0.09	0.000	0.88	0.22	0.242	Antiviral	
DNMT1	0.93	0.41	0.356	0.45	0.71	0.044		Proviral
DOCK3	1.34	0.11	0.014	0.67	0.15	0.049		
E2F1	1.14	0.43	0.307	1.45	0.19	0.028		
ECT2	2.79	0.55	0.003	5.02	3.60	0.063	Antiviral	Antiviral
EIF3S6	1.08	0.25	0.332	0.45	0.19	0.021		Proviral
ERBB2	2.35	0.66	0.012	0.86	0.26	0.198	Antiviral	
FBLN5	0.62	0.28	0.023	0.67	0.43	0.114	Proviral	Proviral
FBXO38	1.76	0.25	0.005	2.02	0.64	0.030	Antiviral	Antiviral
FKBP1	0.59	0.02	0.065	0.16	0.05	0.000	Proviral	Proviral
FLT4	0.76	0.29	0.092	0.42	0.36	0.021		Proviral
FOXA2	0.58	0.13	0.011	0.41	0.03	0.015	Proviral	Proviral
FOXP3	0.53	0.10	0.006	0.74	0.20	0.145	Proviral	Proviral
FXYD6	2.20	0.32	0.002	1.49	0.62	0.127	Antiviral	Antiviral
GCAT	0.83	0.17	0.155	0.70	0.44	0.135		
GLG1	0.74	0.27	0.081	0.45	0.53	0.034		Proviral
GNAZ	1.33	0.46	0.148	0.84	0.66	0.321		

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
GNB2L1	0.26	0.03	0.000	0.41	0.28	0.017	Proviral	Proviral
GNG8	1.18	0.63	0.340	0.15	0.17	0.002		Proviral
GPR145 (MCHR2)	0.47	0.08	0.003	0.19	0.04	0.003	Proviral	Proviral
GPR153	0.61	0.26	0.106	0.04	0.01	0.000	Proviral	Proviral
GPR62	0.42	0.11	0.000	0.45	0.15	0.007	Proviral	Proviral
GPSN2	0.20	0.10	0.000	0.58	0.41	0.063	Proviral	Proviral
GSPT1	0.47	0.09	0.003	0.78	0.45	0.203	Proviral	Proviral
GTF3A	0.50	0.13	0.005	1.15	0.56	0.316	Proviral	
HAS1	0.46	0.13	0.007	0.50	0.16	0.017	Proviral	Proviral
HEXA	0.65	0.14	0.025	0.34	0.14	0.009	Proviral	Proviral
HIPK3	0.68	0.33	0.051	1.36	0.67	0.135	Proviral	
HNRPK	0.69	0.15	0.039	2.96	2.07	0.003	Proviral	Antiviral
HPX	1.22	0.24	0.106	1.52	0.23	0.035		Antiviral
HSPCA	1.33	0.30	0.073	1.07	0.15	0.265		
IDE	1.33	0.64	0.221	0.33	0.05	0.008		Proviral
IFITM2	1.28	0.26	0.076	0.63	0.23	0.038		
IFITM3	1.03	0.31	0.462	0.87	0.95	0.389		
IFIX (PYHIN1)	1.76	0.59	0.046	0.73	0.48	0.176	Antiviral	Proviral
IGFBP6	0.05	0.01	0.006	0.24	0.10	0.000	Proviral	Proviral
IGSF11	1.19	0.45	0.273	2.16	1.53	0.137		Antiviral
IGSF4D (CADM2)	0.76	0.20	0.083	1.07	0.37	0.421		
IKBKB	3.30	1.09	0.011	0.66	0.26	0.056	Antiviral	Proviral
IKBKE	6.08	3.17	0.025	0.39	0.12	0.004	Antiviral	Proviral
IL10RB	1.65	0.10	0.000	5.18	1.56	0.005	Antiviral	Antiviral
IL17RB	0.88	0.18	0.104	0.33	0.19	0.006		Proviral
IL1B	1.80	0.58	0.040	0.94	0.16	0.270	Antiviral	
IMP4	0.55	0.03	0.007	0.65	0.27	0.087	Proviral	Proviral
IMPDH1	4.97	1.31	0.003	1.81	0.29	0.010	Antiviral	Antiviral
IREB2	1.39	0.78	0.229	0.57	0.54	0.117		Proviral
IRF3	2.68	1.19	0.036	0.00	0.00	0.000	Antiviral	Proviral
ITGA7	0.94	0.18	0.285	0.26	0.05	0.000		Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
ITGB1BP2	1.14	0.25	0.206	1.31	0.49	0.150		
KIAA1904 (LRR62)	0.60	0.52	0.124	1.36	1.00	0.307	Proviral	
LCK	0.52	0.33	0.009	0.25	0.38	0.006	Proviral	Proviral
LOC56902 (PNO1)	0.63	0.13	0.020	0.45	0.29	0.024	Proviral	Proviral
LTB	1.55	0.56	0.087	0.11	0.09	0.001	Antiviral	Proviral
MAP3K6	0.52	0.25	0.008	0.77	0.23	0.173	Proviral	
MAP4	0.48	0.18	0.000	0.41	0.16	0.012	Proviral	Proviral
MAPK1	0.70	0.03	0.002	0.56	0.13	0.005	Proviral	Proviral
MARK3	0.86	0.27	0.210	0.92	0.47	0.370		
MAVS	3.91	1.11	0.005	0.52	0.13	0.010	Antiviral	Proviral
MGC11061 (YIPF4)	3.59	0.33	0.000	0.64	0.44	0.115	Antiviral	Proviral
MGC15476 (DACT3)	1.37	0.19	0.015	1.48	0.79	0.179		
MMP11	1.69	1.07	0.167	1.05	1.24	0.496	Antiviral	
MMP9	1.04	0.62	0.472	1.60	1.33	0.253		
MVD	0.51	0.24	0.007	0.53	0.16	0.037	Proviral	Proviral
MYO3A	0.70	0.21	0.049	0.86	0.14	0.278	Proviral	
NCOR2	1.19	0.34	0.203	1.08	0.18	0.280		
NDRG1	0.91	0.29	0.312	2.15	0.58	0.001		Antiviral
NDUFB4	0.93	0.17	0.347	0.88	0.15	0.296		
NEK4	0.59	0.29	0.018	0.15	0.18	0.002	Proviral	Proviral
NEMO	3.38	1.64	0.033	0.98	0.37	0.416	Antiviral	
NFKB1	3.15	1.30	0.023	1.06	0.36	0.461	Antiviral	
NFKB2	3.84	0.70	0.001	1.48	0.80	0.204	Antiviral	
NIK	4.43	2.30	0.031	0.32	0.17	0.004	Antiviral	Proviral
NOL6	1.04	0.26	0.416	1.04	0.62	0.461		
OSBP	0.25	0.13	0.000	0.41	0.26	0.014	Proviral	Proviral
OTUB1	1.57	0.72	0.127	1.33	0.53	0.212	Antiviral	
PACE-1 (SCYL3)	0.89	0.45	0.296	0.55	0.79	0.085		Proviral
PARP11	0.97	0.56	0.449	0.50	0.17	0.030		Proviral
PDAP1	1.13	0.39	0.319	0.64	0.47	0.126		Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
PIAS1	0.43	0.02	0.000	0.11	0.03	0.000	Proviral	Proviral
PIK4CA	0.03	0.01	0.000	0.11	0.04	0.001	Proviral	Proviral
PLB1	0.63	0.04	0.078	0.77	0.31	0.141	Proviral	
PLEK2	1.77	0.51	0.031	0.34	0.19	0.006	Antiviral	Proviral
PPIA	1.03	0.27	0.431	0.72	0.48	0.153		
PPP2R1A	0.69	0.03	0.035	0.67	0.32	0.106	Proviral	Proviral
PPP2R2A	1.54	0.33	0.025	0.51	0.06	0.002	Antiviral	Proviral
PRG2	2.46	0.32	0.001	0.56	0.21	0.034	Antiviral	Proviral
PRKRIP1	1.03	0.32	0.431	1.51	1.40	0.135		Antiviral
PROX1	2.16	0.67	0.021	0.07	0.04	0.001	Antiviral	Proviral
PTHR1	0.60	0.10	0.071	0.41	0.07	0.000	Proviral	Proviral
PTK2B	0.54	0.10	0.007	0.78	0.42	0.200	Proviral	
PTK9 (TWF1)	1.05	0.47	0.447	0.84	0.07	0.088		
PTPRH	2.86	0.58	0.003	2.71	2.71	0.173	Antiviral	Antiviral
RAB10	0.79	0.23	0.088	0.33	0.13	0.003		Proviral
RAB11A	0.92	0.29	0.388	1.33	0.20	0.024		
RAB34	0.35	0.04	0.001	0.31	0.03	0.000	Proviral	Proviral
RAB5A	0.40	0.13	0.010	0.42	0.05	0.003	Proviral	Proviral
RAB9P40 (RABEPK)	1.36	0.57	0.176	0.31	0.38	0.021		Proviral
RAC1	0.97	0.04	0.428	1.09	0.75	0.408		
RAF1	0.86	0.27	0.213	0.90	0.39	0.334		
RBM9	0.88	0.35	0.264	0.46	0.17	0.023		Proviral
RBP4	1.00	0.27	0.461	0.08	0.03	0.001		Proviral
RELA	2.18	0.57	0.012	1.00	0.03	0.381	Antiviral	
RELB	3.12	1.62	0.044	0.89	0.10	0.152	Antiviral	
RFWD3	2.95	1.20	0.025	2.60	2.69	0.186	Antiviral	Antiviral
RGPD5	0.67	0.04	0.001	0.20	0.08	0.000	Proviral	Proviral
RGR	0.47	0.17	0.044	0.47	0.18	0.004	Proviral	Proviral
RIPK2	5.90	1.18	0.001	0.63	0.45	0.111	Antiviral	Proviral
RIT1	0.98	0.39	0.470	1.32	0.21	0.031		
RNF207	0.90	0.44	0.341	0.36	0.23	0.009		Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
RNF31	1.19	0.17	0.068	0.80	0.18	0.071		
ROBO1	1.30	0.14	0.014	0.69	0.60	0.198		
ROCK2	0.70	0.25	0.049	0.41	0.05	0.001	Proviral	Proviral
RPS6KL1	0.31	0.13	0.000	0.36	0.02	0.010	Proviral	Proviral
RSAD2	0.95	0.07	0.241	2.10	0.27	0.001		Antiviral
RYK	0.72	0.33	0.072	0.75	0.81	0.211	Proviral	Proviral
SH3TC1	1.71	0.87	0.120	0.46	0.45	0.054	Antiviral	Proviral
SIK2 (SNF1LK2)	0.94	0.53	0.396	0.38	0.39	0.017		Proviral
SMAD5	1.39	0.49	0.125	0.36	0.16	0.029		Proviral
SMAD6	0.32	0.09	0.000	0.25	0.06	0.000	Proviral	Proviral
SMARCD3	0.83	0.33	0.185	0.49	0.28	0.032		Proviral
SMURF1	1.52	0.38	0.043	0.39	0.32	0.020	Antiviral	Proviral
SMURF2	0.96	0.56	0.439	0.84	0.39	0.240		
SNARK (NUAK2)	1.20	0.09	0.017	0.57	0.16	0.017		Proviral
SNRPD1	0.09	0.01	0.000	0.26	0.13	0.001	Proviral	Proviral
SPCS1	0.80	0.30	0.143	0.08	0.03	0.001		Proviral
SPCS2	0.53	0.09	0.006	0.09	0.03	0.001	Proviral	Proviral
SPCS3	0.40	0.14	0.001	0.08	0.02	0.001	Proviral	Proviral
SREBP1	0.97	0.03	0.090	0.62	0.21	0.022		Proviral
SRI	1.03	0.14	0.370	0.52	0.08	0.001		Proviral
SRRM2	1.07	0.14	0.223	0.66	0.20	0.037		Proviral
STAT1	1.44	0.47	0.093	2.26	0.32	0.002	Antiviral	Antiviral
STAT3	1.74	0.03	0.000	0.63	0.29	0.058	Antiviral	Proviral
STK22C	0.79	0.35	0.139	1.04	0.06	0.456	Proviral	
SUV420H1	0.79	0.48	0.162	1.29	1.04	0.229	Proviral	
TANK (TRAF2)	0.62	0.25	0.022	1.58	0.85	0.053	Proviral	Antiviral
TAZ	0.79	0.23	0.120	0.97	0.36	0.433		
TBK1	3.61	1.85	0.036	0.87	0.15	0.148	Antiviral	
TFAP2A	0.61	0.30	0.024	0.07	0.04	0.000	Proviral	Proviral
TGFBR1	1.67	0.14	0.001	0.63	0.41	0.095	Antiviral	Proviral
TLK2	0.77	0.29	0.109	0.72	0.99	0.212	Proviral	Proviral
TM6SF2	0.81	0.19	0.080	0.70	0.12	0.009		Proviral

Entrez Gene Symbol	Intracellular HCV RNA Quantification			Extracellular HCV RNA Quantification			Intracellular HCV RNA Hits	Extracellular HCV RNA Hits
	Average Normalized HCV RNA	SD	P Values	Average Normalized HCV RNA	SD	P Values		
TNFRSF10C	1.11	0.42	0.355	1.11	0.70	0.436		
TNFRSF10D	0.76	0.42	0.172	0.37	0.08	0.010		Proviral
TNFRSF18	0.93	0.57	0.411	1.85	1.70	0.229		
TNRC11 (MED12)	0.54	0.06	0.002	0.50	0.07	0.001	Proviral	Proviral
TNS	1.63	0.51	0.054	2.38	1.53	0.103	Antiviral	Antiviral
TP53	1.65	0.12	0.001	1.06	0.67	0.479	Antiviral	
TRAPPC5	0.67	0.19	0.033	1.15	0.48	0.315	Proviral	
TRIM42	0.49	0.03	0.001	0.65	0.10	0.004	Proviral	Proviral
TRIM46	1.46	0.62	0.143	0.84	1.00	0.376		Proviral
TRIM62	0.54	0.08	0.000	0.28	0.27	0.009	Proviral	Proviral
TRRAP	2.36	0.47	0.004	0.37	0.15	0.005	Antiviral	Proviral
TUBB4 (TUBB3)	4.42	0.32	0.000	1.30	0.13	0.063	Antiviral	
TWIST1	0.44	0.16	0.003	1.32	1.53	0.385	Proviral	Proviral
UBE1L	1.04	0.31	0.413	0.43	0.10	0.001		Proviral
UBE2E3	0.71	0.15	0.051	0.62	0.19	0.070	Proviral	Proviral
UBE2J1	0.47	0.14	0.001	0.33	0.10	0.002	Proviral	Proviral
UBE2J2	1.55	0.25	0.011	1.36	1.26	0.344	Antiviral	
UBE2M	0.66	0.16	0.010	0.36	0.07	0.002	Proviral	Proviral
UBE2S	1.52	1.00	0.052	0.64	0.57	0.108	Antiviral	Proviral
USP11	1.23	0.19	0.058	0.23	0.05	0.001		Proviral
USP16	0.88	0.43	0.309	1.28	0.98	0.345		
USP51	0.88	0.40	0.264	0.75	0.14	0.156		
UTP14A	0.25	0.06	0.000	0.10	0.01	0.000	Proviral	Proviral
VAMP1	1.43	0.42	0.079	0.99	0.68	0.452		
VTN	0.94	0.31	0.375	1.12	0.52	0.355		
WIF1	0.24	0.19	0.000	0.21	0.13	0.003	Proviral	Proviral
WNT10B	0.71	0.49	0.088	1.45	0.05	0.052		
XBP1	0.42	0.20	0.006	0.41	0.07	0.000	Proviral	Proviral
XPNPEP1	0.67	0.20	0.033	0.24	0.09	0.000	Proviral	Proviral
ZNF337	0.90	0.36	0.295	1.20	0.12	0.237		

D. Identification of host factors affecting viral entry

The effect of various host factors on entry of virus into cells was determined using a virus entry assay. Briefly, HCV pseudoparticles (HCVpp), defective lentiviral or retroviral particles that display the HCV glycoproteins, were used to study HCV entry. The vesicular stomatitis virus pseudoparticles (VSVpp), which enters cells likely via a different mechanism, was employed as a control. Transfected and infected cells were prepared as described above in part A. Virus entry was assessed two days after infection by measuring the firefly luciferase reporter activities in cell lysate using the Bright Glo Luciferase assay system (Promega). This screen identified eight HCV-specific entry factors and 15 common factors for the entry of HCV and VSV. The results of these experiments are shown in Table 8 & 11.

Table 8. Identification of Host Factors Involved in Entry

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
ABCB6	1.36	0.45	0.092	0.96	0.11	0.214	1.41	0.061	
ABCE1	0.44	0.03	0.000	0.61	0.06	0.007	0.73	0.005	
ACBD3	0.82	0.07	0.007	0.75	0.01	0.005	1.09	0.041	
ADFP	1.27	0.31	0.051	1.01	0.14	0.460	1.26	0.060	
AP1GBP1	0.63	0.11	0.036	0.79	0.06	0.010	0.80	0.015	
AP3B1	0.85	0.15	0.107	1.01	0.08	0.393	0.83	0.035	
APC2	0.91	0.10	0.154	0.88	0.13	0.152	1.03	0.394	
APOBEC2	0.93	0.16	0.294	0.63	0.09	0.004	1.48	0.008	
APOBEC3B	0.72	0.14	0.011	0.87	0.13	0.149	0.82	0.020	
APOE	0.78	0.22	0.054	0.69	0.15	0.005	1.13	0.237	
ARHGAP22	1.04	0.27	0.437	1.05	0.20	0.317	0.99	0.469	
ARHGEF7	0.30	0.17	0.010	0.29	0.11	0.000	1.04	0.454	Proviral (HCV & VSV)
ARL10A	0.73	0.09	0.002	0.60	0.07	0.002	1.22	0.059	
ARRDC2	0.29	0.04	0.007	0.39	0.03	0.000	0.74	0.001	Proviral (HCV & VSV)
ART5	0.71	0.09	0.008	0.81	0.09	0.056	0.88	0.032	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
BAIAP2	0.83	0.19	0.124	0.79	0.08	0.000	1.05	0.373	
BCL7A	1.10	0.14	0.136	1.19	0.11	0.060	0.93	0.161	
BCL9L	0.81	0.06	0.006	1.30	0.24	0.012	0.62	0.012	
C1QA	0.74	0.08	0.007	0.95	0.09	0.307	0.78	0.004	
C1QB	0.69	0.21	0.021	0.83	0.09	0.049	0.83	0.178	
CABP1	0.93	0.15	0.233	0.78	0.13	0.082	1.18	0.087	
CCDC8	0.82	0.10	0.069	0.88	0.05	0.127	0.93	0.170	
CCL26	0.63	0.12	0.001	0.54	0.04	0.001	1.17	0.092	
CCL3L1	0.40	0.06	0.000	0.57	0.05	0.003	0.71	0.002	
CD3E	0.84	0.17	0.068	0.81	0.05	0.021	1.04	0.378	
CD81	0.21	0.05	0.000	0.93	0.18	0.264	0.23	0.000	Proviral (HCV-Specific)
CDC42EP3	0.17	0.06	0.000	1.07	0.03	0.085	0.16	0.000	Proviral (HCV-Specific)
CDCA3	1.24	0.18	0.019	1.01	0.18	0.450	1.23	0.039	
CDH1	0.19	0.06	0.000	0.77	0.06	0.001	0.24	0.000	Proviral (HCV-Specific)
CDKL5	0.94	0.11	0.212	1.06	0.16	0.334	0.89	0.045	
CHKA	0.30	0.13	0.000	0.74	0.12	0.002	0.41	0.002	Proviral (HCV-Specific)
CHUK	0.72	0.18	0.018	0.61	0.07	0.000	1.18	0.120	
CLSTN1	1.16	0.18	0.107	1.13	0.13	0.099	1.03	0.370	
CNOT1 (KIAA1007)	0.41	0.09	0.000	0.48	0.06	0.000	0.85	0.166	Proviral (HCV & VSV)
CNOT2	0.23	0.06	0.000	0.38	0.08	0.000	0.60	0.021	Proviral (HCV & VSV)
CNOT3	0.22	0.06	0.000	0.25	0.02	0.000	0.88	0.348	Proviral (HCV & VSV)
CNOT6L	0.94	0.18	0.328	1.07	0.12	0.226	0.87	0.198	
CPD	0.73	0.10	0.002	0.79	0.09	0.020	0.93	0.178	
CRLF2	0.77	0.14	0.035	1.32	0.09	0.013	0.58	0.000	
CRLF3	0.77	0.22	0.058	0.87	0.07	0.058	0.89	0.185	
CSF3R	0.79	0.10	0.006	0.86	0.09	0.104	0.91	0.146	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
CSNK1A1L	0.81	0.15	0.028	0.80	0.09	0.042	1.02	0.423	
CTGF	0.71	0.06	0.002	0.63	0.08	0.002	1.13	0.113	
CTNNAL1	0.69	0.19	0.019	0.66	0.09	0.002	1.03	0.435	
CTSF	0.83	0.04	0.046	0.78	0.09	0.013	1.06	0.149	
CX3CL1	0.59	0.05	0.001	0.85	0.16	0.147	0.70	0.025	
CXCL12	1.06	0.14	0.273	0.86	0.19	0.229	1.23	0.120	
CYBA	0.36	0.21	0.003	0.52	0.20	0.001	0.69	0.004	Proviral (HCV &VSV)
CYLD	1.54	0.16	0.002	1.24	0.06	0.007	1.25	0.008	
DAF (CD55)	0.72	0.06	0.005	0.73	0.14	0.001	0.99	0.435	
DDOST	1.15	0.13	0.039	1.05	0.08	0.172	1.09	0.160	
DDX21	0.72	0.07	0.002	0.81	0.07	0.013	0.89	0.093	
DDX3X	0.24	0.04	0.000	0.47	0.08	0.001	0.51	0.003	Proviral (HCV &VSV)
DEFB126	0.81	0.11	0.075	0.85	0.09	0.066	0.96	0.311	
DGAT1	0.63	0.13	0.007	0.64	0.10	0.012	0.98	0.362	
DICER1	1.13	0.17	0.128	1.04	0.12	0.398	1.09	0.133	
DNMT1	0.84	0.14	0.093	0.72	0.12	0.008	1.17	0.064	
DOCK3	0.81	0.08	0.007	0.92	0.13	0.250	0.88	0.133	
E2F1	0.75	0.12	0.005	1.00	0.09	0.498	0.75	0.015	
ECT2	1.08	0.14	0.245	0.77	0.12	0.029	1.41	0.007	
EIF3S6	0.83	0.07	0.052	1.88	0.23	0.000	0.44	0.001	
ERBB2	0.91	0.12	0.233	0.82	0.16	0.018	1.11	0.215	
FBLN5	0.89	0.09	0.099	0.75	0.12	0.054	1.18	0.035	
FBXO38	1.22	0.09	0.096	1.61	0.06	0.000	0.76	0.000	
FKBP1	0.71	0.19	0.022	0.70	0.14	0.006	1.03	0.435	
FLT4	1.00	0.13	0.484	0.65	0.07	0.001	1.54	0.001	
FOXA2	0.56	0.12	0.037	0.76	0.11	0.030	0.74	0.020	
FOXP3	0.95	0.09	0.135	1.01	0.07	0.447	0.94	0.143	
FXYD6	0.85	0.07	0.000	1.01	0.10	0.434	0.84	0.026	
GCAT	0.92	0.05	0.109	1.07	0.07	0.242	0.86	0.012	
GLG1	0.72	0.09	0.009	0.68	0.11	0.006	1.05	0.372	
GNAZ	1.15	0.26	0.171	0.95	0.07	0.330	1.21	0.141	
GNB2L1	0.76	0.08	0.002	1.08	0.12	0.044	0.70	0.003	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
GNG8	0.52	0.06	0.000	0.70	0.06	0.000	0.75	0.014	
GPR145 (MCHR2)	0.12	0.02	0.000	0.48	0.05	0.000	0.25	0.000	Proviral (HCV-Specific)
GPR153	0.92	0.16	0.286	0.64	0.05	0.000	1.45	0.021	
GPR62	0.14	0.09	0.000	0.32	0.08	0.000	0.44	0.006	Proviral (HCV & VSV)
GPSN2	1.04	0.05	0.200	1.22	0.10	0.026	0.85	0.027	
GSPT1	1.11	0.14	0.118	0.90	0.09	0.087	1.23	0.014	
GTF3A	0.73	0.05	0.001	1.03	0.18	0.409	0.70	0.016	
HEXA	0.92	0.26	0.278	0.53	0.11	0.000	1.75	0.007	
HIPK3	0.99	0.17	0.471	1.17	0.17	0.067	0.85	0.095	
HNRPK	0.35	0.07	0.000	0.33	0.04	0.000	1.06	0.338	
HPX	0.66	0.09	0.022	0.78	0.05	0.044	0.85	0.029	
IDE	0.97	0.05	0.384	0.85	0.13	0.064	1.14	0.033	
IFITM2	1.04	0.15	0.356	0.94	0.07	0.330	1.10	0.177	
IFITM3	0.93	0.06	0.169	0.97	0.18	0.237	0.96	0.382	
IFIX (PYHIN1)	0.50	0.07	0.000	0.53	0.05	0.001	0.94	0.251	
IGFBP6	0.56	0.19	0.001	0.75	0.10	0.011	0.74	0.074	
IGSF11	1.18	0.16	0.077	0.97	0.10	0.379	1.22	0.048	
IGSF4D (CADM2)	0.69	0.09	0.000	0.59	0.04	0.003	1.17	0.065	
IKBKB	1.66	0.08	0.000	1.97	0.32	0.004	0.85	0.051	Antiviral (HCV & VSV)
IKBKE	1.33	0.41	0.079	1.17	0.09	0.091	1.14	0.187	
IL10RB	0.97	0.17	0.424	0.95	0.15	0.295	1.02	0.443	
IL17RB	0.52	0.08	0.000	0.60	0.10	0.006	0.86	0.094	
IL1B	0.89	0.15	0.174	0.83	0.09	0.042	1.08	0.286	
IMP4	0.85	0.10	0.229	1.04	0.15	0.382	0.82	0.062	
IMPDH1	0.69	0.09	0.004	0.62	0.05	0.004	1.11	0.082	
IREB2	0.56	0.09	0.000	0.49	0.09	0.001	1.15	0.194	
IRF3	1.02	0.19	0.437	0.97	0.12	0.368	1.06	0.316	
ITGA7	0.72	0.08	0.000	1.05	0.17	0.335	0.69	0.009	
ITGB1BP2	0.81	0.14	0.026	0.81	0.16	0.063	1.00	0.488	
KIAA1904 (LRRC62)	0.68	0.10	0.005	0.57	0.06	0.002	1.19	0.088	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
LCK	0.88	0.19	0.142	1.29	0.21	0.054	0.69	0.023	
LOC56902 (PNO1)	0.78	0.15	0.074	1.09	0.05	0.160	0.71	0.017	
LTB	0.62	0.17	0.004	0.59	0.11	0.009	1.05	0.385	
MAP3K6	1.02	0.19	0.421	1.01	0.12	0.470	1.02	0.420	
MAP4	0.31	0.08	0.000	0.54	0.10	0.000	0.57	0.002	Proviral (HCV & VSV)
MAPK1	0.75	0.07	0.004	0.81	0.08	0.039	0.92	0.070	
MARK3	1.07	0.08	0.197	0.84	0.17	0.103	1.28	0.055	
MAVS	0.83	0.12	0.040	0.70	0.15	0.021	1.18	0.171	
MGC11061 (YIPF4)	0.68	0.11	0.007	0.79	0.08	0.014	0.86	0.010	
MGC15476 (DACT3)	0.89	0.09	0.246	1.13	0.18	0.148	0.79	0.058	
MMP11	0.75	0.09	0.002	0.66	0.07	0.005	1.14	0.006	
MMP9	0.71	0.20	0.015	0.66	0.03	0.001	1.08	0.330	
MVD	0.64	0.11	0.004	0.70	0.16	0.002	0.92	0.263	
MYO3A	0.89	0.17	0.170	0.82	0.14	0.046	1.09	0.263	
NDRG1	1.09	0.05	0.226	1.14	0.17	0.113	0.95	0.268	
NDUFB4	0.63	0.02	0.001	0.66	0.13	0.008	0.97	0.373	
NEK4	0.74	0.15	0.015	0.68	0.11	0.008	1.10	0.249	
NEMO	0.69	0.13	0.017	0.76	0.14	0.058	0.91	0.316	
NFKB1	0.93	0.14	0.225	0.89	0.14	0.174	1.04	0.380	
NFKB2	1.91	0.38	0.001	1.73	0.09	0.001	1.11	0.211	Antiviral (HCV & VSV)
NIK	1.12	0.21	0.184	1.18	0.18	0.039	0.95	0.364	
NOL6	0.83	0.07	0.038	0.99	0.09	0.466	0.83	0.031	
OSBP	0.82	0.15	0.074	0.68	0.04	0.001	1.21	0.059	
OTUB1	0.59	0.12	0.001	0.82	0.11	0.003	0.72	0.022	
PACE-1 (SCYL3)	0.71	0.15	0.011	0.79	0.12	0.022	0.90	0.231	
PARP11	1.04	0.13	0.371	0.96	0.08	0.189	1.07	0.162	
PDAP1	0.87	0.12	0.160	1.08	0.17	0.233	0.81	0.088	
PIK4CA	0.28	0.16	0.000	0.45	0.10	0.003	0.62	0.063	Proviral (HCV & VSV)
PLB1	0.98	0.10	0.434	0.86	0.10	0.062	1.15	0.045	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
PLEK2	1.01	0.26	0.464	0.78	0.09	0.030	1.29	0.034	
PPIA	1.09	0.10	0.289	1.09	0.12	0.259	1.00	0.499	
PPP2R1A	0.94	0.13	0.197	1.02	0.16	0.413	0.92	0.265	
PPP2R2A	0.36	0.03	0.000	0.42	0.02	0.001	0.85	0.003	
PRG2	0.69	0.14	0.003	0.61	0.04	0.002	1.13	0.150	
PRKRIP1	1.00	0.04	0.414	1.06	0.15	0.243	0.94	0.235	
PROX1	0.43	0.11	0.000	0.55	0.10	0.004	0.78	0.037	
PTHR1	0.98	0.06	0.408	0.75	0.11	0.010	1.30	0.002	
PTK2B	0.58	0.03	0.000	0.80	0.14	0.010	0.73	0.019	
PTK9 (TWF1)	1.09	0.17	0.220	0.91	0.14	0.284	1.20	0.127	
PTPRH	0.60	0.08	0.000	0.69	0.08	0.007	0.87	0.024	
RAB10	0.68	0.17	0.005	0.72	0.09	0.000	0.95	0.358	
RAB11A	0.76	0.16	0.015	0.84	0.09	0.050	0.90	0.151	
RAB34	0.37	0.17	0.002	0.27	0.14	0.000	1.36	0.178	Proviral (HCV & VSV)
RAB5A	0.46	0.10	0.003	0.48	0.19	0.000	0.96	0.428	Proviral (HCV & VSV)
RAB9P40 (RABEPK)	0.54	0.17	0.001	0.43	0.04	0.000	1.26	0.160	
RAC1	0.38	0.15	0.002	0.60	0.11	0.015	0.63	0.012	Proviral (HCV & VSV)
RAF1	1.01	0.09	0.433	1.06	0.08	0.291	0.96	0.089	
RBM9	0.66	0.07	0.007	0.73	0.07	0.016	0.91	0.025	
RBP4	0.27	0.06	0.000	0.32	0.09	0.001	0.85	0.103	Proviral (HCV & VSV)
RELA	0.73	0.11	0.022	0.57	0.09	0.001	1.27	0.087	
RELB	1.09	0.28	0.300	0.76	0.09	0.007	1.44	0.051	
RFWD3	0.44	0.17	0.000	0.32	0.07	0.000	1.38	0.084	
RGPD5	0.60	0.16	0.002	0.63	0.10	0.003	0.95	0.270	
RGR	1.37	0.23	0.013	1.26	0.12	0.009	1.08	0.194	
RIPK2	0.97	0.21	0.413	0.88	0.09	0.103	1.10	0.285	
RIT1	1.01	0.14	0.471	1.33	0.07	0.001	0.76	0.001	
RNF207	0.94	0.17	0.291	1.00	0.11	0.486	0.94	0.213	
RNF31	0.77	0.13	0.010	0.86	0.08	0.082	0.90	0.157	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
ROBO1	1.10	0.12	0.135	1.00	0.06	0.497	1.10	0.132	
ROCK2	0.60	0.05	0.000	0.64	0.07	0.004	0.93	0.085	
RPS6KL1	0.61	0.06	0.000	0.68	0.08	0.007	0.90	0.181	
RYK	1.04	0.14	0.390	0.93	0.10	0.175	1.11	0.169	
SH3TC1	0.97	0.10	0.041	0.84	0.12	0.061	1.16	0.040	
SIK2 (SNF1LK2)	1.05	0.20	0.331	0.75	0.26	0.085	1.41	0.019	
SMAD5	0.95	0.23	0.364	0.79	0.06	0.015	1.19	0.127	
SMAD6	0.13	0.07	0.000	0.74	0.14	0.007	0.18	0.000	Proviral (HCV-Specific)
SMARCD3	0.65	0.10	0.001	0.52	0.08	0.001	1.27	0.022	
SMURF1	0.67	0.14	0.027	1.07	0.14	0.188	0.62	0.016	
SMURF2	0.60	0.20	0.003	0.73	0.08	0.002	0.83	0.164	
SNARK (NUAK2)	0.81	0.19	0.092	0.91	0.12	0.187	0.90	0.115	
SNRPD1	0.38	0.11	0.000	0.25	0.05	0.000	1.51	0.041	
SPCS1	0.89	0.18	0.180	0.79	0.03	0.007	1.13	0.184	
SPCS2	0.94	0.12	0.260	1.18	0.20	0.150	0.80	0.027	
SPCS3	0.63	0.04	0.000	0.69	0.08	0.026	0.92	0.151	
SRI	0.79	0.21	0.054	0.89	0.10	0.106	0.89	0.181	
SRRM2	0.31	0.03	0.000	0.46	0.09	0.002	0.69	0.009	
STAT3	0.55	0.13	0.003	0.45	0.06	0.000	1.22	0.148	
STK22C	0.83	0.14	0.032	0.72	0.09	0.028	1.15	0.051	
SUV420H1	0.39	0.05	0.000	0.47	0.05	0.000	0.83	0.087	Proviral (HCV & VSV)
TANK (TRAF2)	0.78	0.13	0.022	0.77	0.09	0.020	1.01	0.413	
TAZ	0.85	0.12	0.090	0.80	0.05	0.004	1.07	0.164	
TBK1	1.07	0.23	0.334	0.81	0.11	0.074	1.32	0.045	
TFAP2A	0.92	0.07	0.204	1.21	0.15	0.068	0.76	0.018	
TGFBR1	0.74	0.18	0.051	0.73	0.09	0.012	1.02	0.449	
TLK2	0.73	0.16	0.022	0.66	0.13	0.000	1.11	0.235	
TM6SF2	0.97	0.19	0.377	0.84	0.11	0.043	1.15	0.120	
TNFRSF10C	0.63	0.12	0.003	0.73	0.05	0.012	0.86	0.127	
TNFRSF10D	0.42	0.08	0.000	0.46	0.07	0.002	0.91	0.034	

Entrez Gene Symbol	HCV Pseudoparticle (HCVpp) Entry			VSV Pseudoparticle (VSVpp) Entry			HCVpp/VSVpp		Viral Entry Factors
	Average	SD	P values	Average	SD	P values	Ratio	P values	
TNFRSF18	0.49	0.12	0.000	0.48	0.02	0.000	1.02	0.440	
TNRC11 (MED12)	1.06	0.06	0.206	1.00	0.15	0.482	1.05	0.304	
TNS	0.72	0.05	0.007	0.79	0.13	0.035	0.92	0.116	
TP53	0.78	0.16	0.030	0.99	0.07	0.414	0.79	0.052	
TRAPPC5	0.89	0.09	0.092	0.81	0.06	0.005	1.09	0.121	
TRIM42	0.90	0.17	0.108	0.79	0.14	0.013	1.13	0.208	
TRIM46	0.85	0.15	0.140	0.70	0.05	0.001	1.23	0.068	
TRIM62	0.22	0.08	0.000	0.90	0.16	0.140	0.25	0.000	Proviral (HCV-Specific)
TRRAP	1.08	0.24	0.271	2.08	0.10	0.000	0.52	0.001	
TUBB4 (TUBB3)	1.01	0.25	0.482	0.91	0.10	0.109	1.11	0.263	
TWIST1	0.97	0.08	0.376	0.89	0.15	0.141	1.09	0.118	
UBE1L	1.08	0.12	0.233	1.14	0.03	0.000	0.94	0.138	
UBE2E3	0.81	0.15	0.093	0.66	0.07	0.001	1.24	0.015	
UBE2J1	0.55	0.12	0.000	0.69	0.16	0.019	0.80	0.124	
UBE2J2	0.57	0.13	0.002	0.56	0.05	0.002	1.02	0.422	
UBE2M	0.68	0.20	0.020	1.11	0.14	0.206	0.61	0.002	
UBE2S	0.85	0.12	0.090	0.63	0.12	0.006	1.34	0.001	
USP11	0.97	0.16	0.390	0.90	0.08	0.170	1.08	0.226	
USP16	1.21	0.18	0.046	1.01	0.13	0.485	1.20	0.117	
USP51	1.05	0.16	0.360	0.81	0.06	0.003	1.30	0.035	
UTP14A	1.25	0.12	0.011	0.99	0.11	0.447	1.26	0.003	
VAMP1	0.57	0.08	0.001	0.51	0.08	0.000	1.10	0.160	
VTN	0.83	0.11	0.040	0.86	0.15	0.140	0.96	0.267	
WIF1	0.71	0.11	0.001	0.64	0.07	0.012	1.11	0.167	
WNT10B	0.62	0.12	0.001	0.66	0.05	0.006	0.93	0.228	
XBP1	0.47	0.07	0.000	0.72	0.09	0.028	0.66	0.005	Proviral (HCV-Specific)
XPNPEP1	0.74	0.14	0.037	0.80	0.08	0.021	0.92	0.302	
ZNF337	0.65	0.13	0.012	0.61	0.10	0.003	1.07	0.290	

Table 11. Host Factors Modulating HCV Entry

Entry Factors	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral (HCV-Specific)	CD81	975	NM_004356	CD81 molecule
Proviral (HCV-Specific)	CDC42EP3	10602	NM_006449	CDC42 effector protein (Rho GTPase binding) 3
Proviral (HCV-Specific)	CDH1	999	NM_004360	cadherin 1, type 1, E-cadherin (epithelial)
Proviral (HCV-Specific)	CHKA	1119	NM_001277	choline kinase alpha
Proviral (HCV-Specific)	GPR145 (MCHR2)	84539	NM_032503	melanin-concentrating hormone receptor 2
Proviral (HCV-Specific)	SMAD6	4091	NM_005585	SMAD family member 6
Proviral (HCV-Specific)	TRIM62	55223	NM_018207	tripartite motif-containing 62
Proviral (HCV-Specific)	XBP1	7494	NM_005080	X-box binding protein 1
Proviral (HCV & VSV)	ARHGEF7	8874	NM_003899	Rho guanine nucleotide exchange factor (GEF) 7
Proviral (HCV & VSV)	ARRDC2	27106	NM_015683	arrestin domain containing 2
Proviral (HCV & VSV)	CNOT1 (KIAA1007)	23019	NM_016284	CCR4-NOT transcription complex, subunit 1
Proviral (HCV & VSV)	CNOT2	4848	NM_014515	CCR4-NOT transcription complex, subunit 2
Proviral (HCV & VSV)	CNOT3	4849	NM_014516	CCR4-NOT transcription complex, subunit 3
Proviral (HCV & VSV)	CYBA	1535	NM_000101	cytochrome b-245, alpha polypeptide
Proviral (HCV & VSV)	DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
Proviral (HCV & VSV)	GPR62	118442	NM_080865	G protein-coupled receptor 62
Proviral (HCV & VSV)	MAP4	4134	NM_002375	microtubule-associated protein 4
Proviral (HCV & VSV)	PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha
Proviral (HCV & VSV)	RAB34	83871	NM_031934	RAB34, member RAS oncogene family

Entry Factors	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral (HCV & VSV)	RAB5A	5868	NM_004162	RAB5A, member RAS oncogene family
Proviral (HCV & VSV)	RAC1	5879	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
Proviral (HCV & VSV)	RBP4	5950	NM_006744	retinol binding protein 4, plasma
Proviral (HCV & VSV)	SUV420H1	51111	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)
Antiviral (HCV & VSV)	IKBKB	3551	NM_001556	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
Antiviral (HCV & VSV)	NFKB2	4791	NM_002502	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)

E. Identification of host factors affecting HCV replication

The effect of various host factors on HCV replication was measured using a HCV subgenomic replicon assay. Huh 7.5.1 cells were transfected with siRNA using the protocol described in part A. After 48 hours, SGR-Luc-JFH-1 subgenomic replicon RNA, which contains the luciferase gene, was transiently transfected into the Huh7.5.1 cells. After 72 hours, cells were lysed directly in 96-well plates and Renilla luciferase reporter activities were measured using Renilla Luciferase assay system (Promega) to determine levels of HCV RNA replication. siRNA pools were classified as proviral or antiviral hits if the average normalized HCV subgenomic replicon activities were decreased or increased for more than 1.5-fold comparing with non-targeting control siRNA and the P value was less than 0.05. 52 human genes were identified to be important for HCV RNA replication. These genes are listed in Table 9. As shown in Table 13, 17 genes restrict HCV infection at the RNA replication level.

Table 9. Host Factors Affecting Replication

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
ABCB6	0.58	0.16	0.006	Proviral
ABCE1	0.78	0.22	0.040	
ACBD3	1.00	0.12	0.500	
ADFP	0.70	0.18	0.096	
AKT2	0.68	0.18	0.014	
AP1GBP1	1.11	0.27	0.249	
AP3B1	0.92	0.32	0.337	
APC2	1.47	0.44	0.042	
APOBEC2	0.48	0.07	0.001	Proviral
APOBEC3B	1.13	0.16	0.111	
APOE	0.78	0.07	0.206	
ARHGAP22	1.18	0.33	0.193	
ARHGEF7	0.88	0.10	0.137	
ARL10A	0.86	0.20	0.197	
ARRDC2	1.03	0.14	0.349	
ART5	1.33	0.47	0.085	
BAIAP2	0.84	0.25	0.135	
BCL7A	0.91	0.06	0.156	
BCL9L	0.56	0.09	0.000	Proviral
C1QA	0.79	0.21	0.036	
C1QB	0.75	0.16	0.009	
CABP1	1.00	0.32	0.486	
CCDC8	0.98	0.24	0.436	
CCL26	0.96	0.24	0.391	
CCL3L1	0.73	0.06	0.003	
CCND1	0.58	0.16	0.003	Proviral
CD3E	0.27	0.05	0.001	Proviral
CD81	0.54	0.04	0.004	Proviral
CDC42EP3	0.62	0.11	0.047	Proviral
CDCA3	0.72	0.09	0.094	
CDH1	1.32	0.22	0.037	

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
CDKL5	1.09	0.40	0.326	
CEBPD	0.42	0.06	0.004	Proviral
CHKA	0.47	0.10	0.012	Proviral
CHUK	1.12	0.22	0.252	
CLSTN1	0.78	0.11	0.013	Proviral
CNOT1 (KIAA1007)	0.45	0.06	0.009	Proviral
CNOT2	0.87	0.06	0.031	
CNOT3	0.72	0.23	0.084	
CNOT6L	0.81	0.16	0.112	
CPD	0.95	0.34	0.412	
CRLF2	0.25	0.02	0.001	Proviral
CRLF3	0.55	0.11	0.003	Proviral
CSF3R	0.97	0.07	0.306	
CSNK1A1L	0.99	0.22	0.474	
CTGF	0.85	0.29	0.247	
CTNNAL1	1.03	0.36	0.436	
CTNNB1	0.81	0.19	0.080	
CTSF	0.66	0.17	0.005	Proviral
CX3CL1	1.35	0.12	0.001	
CXCL12	3.01	0.42	0.000	Antiviral
CYBA	1.06	0.13	0.256	
CYLD	0.64	0.11	0.002	Proviral
DAF (CD55)	0.97	0.14	0.383	
DDOST	0.78	0.18	0.050	
DDX21	0.69	0.20	0.018	Proviral
DDX26	0.38	0.03	0.003	Proviral
DDX3X	0.43	0.14	0.000	Proviral
DDX6	0.45	0.06	0.014	Proviral
DEFB126	0.83	0.25	0.136	
DGAT1	0.59	0.10	0.000	Proviral
DICER1	1.43	0.13	0.013	Antiviral
DNMT1	0.55	0.10	0.022	Proviral

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
DOCK3	1.21	0.21	0.060	
E2F1	1.36	0.18	0.006	
ECT2	0.65	0.15	0.054	Proviral
EIF3S6	0.29	0.04	0.003	Proviral
ERBB2	1.91	0.19	0.000	Antiviral
FBLN5	0.54	0.10	0.024	Proviral
FBXO38	0.99	0.21	0.477	
FKBP1	0.72	0.22	0.032	Proviral
FLT4	0.41	0.21	0.002	Proviral
FOXA2	0.96	0.21	0.387	
FOXP3	0.70	0.10	0.007	
FXYD6	1.45	0.19	0.001	Antiviral
GCAT	0.60	0.11	0.000	Proviral
GLG1	1.06	0.17	0.243	
GNAZ	2.33	0.82	0.004	Antiviral
GNB2L1	0.48	0.03	0.000	Proviral
GNG8	0.89	0.25	0.265	
GPR145 (MCHR2)	0.60	0.18	0.001	Proviral
GPR153	0.61	0.08	0.005	Proviral
GPR62	1.22	0.30	0.171	
GPSN2	0.48	0.20	0.001	Proviral
GSPT1	0.63	0.11	0.001	Proviral
GTF3A	0.49	0.10	0.016	Proviral
HAS1	0.36	0.02	0.002	Proviral
HEXA	0.56	0.13	0.030	Proviral
HIPK3	1.02	0.25	0.435	
HNRPK	1.22	0.37	0.125	
HPX	1.03	0.36	0.443	
HSPCA	0.89	0.21	0.200	
IDE	1.28	0.35	0.097	
IFITM2	1.73	0.26	0.001	Antiviral
IFITM3	1.58	0.28	0.005	Antiviral

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
IFIX (PYHIN1)	0.94	0.16	0.354	
IGFBP6	0.26	0.03	0.001	Proviral
IGSF11	0.83	0.28	0.146	
IGSF4D (CADM2)	0.74	0.24	0.030	
IKBKB	0.84	0.13	0.099	
IKBKE	1.33	0.20	0.012	
IL10RB	1.21	0.28	0.133	
IL17RB	1.08	0.14	0.222	
IL1B	0.67	0.09	0.000	
IMP4	0.55	0.14	0.003	Proviral
IMPDH1	0.95	0.62	0.428	
IREB2	1.10	0.23	0.231	
IRF3	1.37	0.39	0.055	
ITGA7	0.41	0.05	0.003	Proviral
ITGB1BP2	0.68	0.11	0.005	
KIAA1904 (LRRC62)	0.57	0.11	0.001	Proviral
LCK	0.72	0.12	0.002	Proviral
LOC56902 (PNO1)	1.06	0.31	0.358	
LTB	0.88	0.24	0.283	
MAP3K6	0.61	0.05	0.005	Proviral
MAP4	1.16	0.09	0.045	
MAPK1	0.55	0.07	0.000	Proviral
MARK3	0.55	0.08	0.003	Proviral
MAVS	1.10	0.29	0.249	
MGC11061 (YIPF4)	1.01	0.24	0.461	
MGC15476 (DACT3)	0.75	0.12	0.034	
MMP11	1.06	0.10	0.253	
MMP9	1.40	0.47	0.054	
MVD	0.39	0.03	0.003	Proviral
MYO3A	1.19	0.34	0.137	

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
NCOR2	0.70	0.15	0.014	
NDRG1	0.71	0.10	0.030	
NDUFB4	0.90	0.16	0.182	
NEK4	0.65	0.09	0.009	Proviral
NEMO	1.21	0.10	0.052	
NFKB1	2.45	0.93	0.005	Antiviral
NFKB2	1.05	0.19	0.322	
NIK	0.98	0.24	0.451	
NOL6	0.50	0.09	0.017	Proviral
OSBP	0.58	0.10	0.001	Proviral
OTUB1	1.84	1.94	0.182	Antiviral
PACE-1 (SCYL3)	1.21	0.29	0.094	
PARP11	1.18	0.36	0.176	
PDAP1	1.83	0.24	0.000	Antiviral
PIAS1	0.49	0.09	0.000	Proviral
PIK4CA	0.13	0.02	0.001	Proviral
PLB1	1.04	0.21	0.376	
PLEK2	1.70	0.51	0.010	Antiviral
PPIA	0.73	0.20	0.041	
PPP2R1A	0.69	0.15	0.010	
PPP2R2A	1.09	0.25	0.250	
PRG2	0.99	0.09	0.444	
PRKRIP1	0.55	0.13	0.007	Proviral
PROX1	1.01	0.25	0.491	
PTHR1	1.19	0.36	0.165	
PTK2B	0.61	0.10	0.000	Proviral
PTK9 (TWF1)	2.86	0.60	0.000	Antiviral
PTPRH	0.59	0.11	0.020	Proviral
RAB10	0.95	0.09	0.239	
RAB11A	1.03	0.10	0.330	
RAB34	0.76	0.09	0.031	
RAB5A	0.89	0.16	0.142	

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
RAB9P40 (RABEPK)	0.68	0.13	0.058	
RAC1	0.92	0.29	0.298	
RAF1	0.77	0.22	0.050	
RBM9	1.17	0.14	0.062	
RBP4	0.66	0.14	0.006	Proviral
RELA	1.16	0.29	0.142	
RELB	1.90	0.49	0.002	Antiviral
RFWD3	1.20	0.22	0.066	
RGPD5	0.57	0.12	0.004	Proviral
RGR	0.94	0.17	0.317	
RIPK2	1.79	0.38	0.001	Antiviral
RIT1	0.96	0.19	0.371	
RNF207	1.06	0.31	0.343	
RNF31	1.09	0.39	0.309	
ROBO1	0.93	0.27	0.356	
ROCK2	1.15	0.24	0.138	
RPS6KL1	0.94	0.16	0.295	
RSAD2	0.95	0.16	0.150	
RYK	1.13	0.19	0.209	
SH3TC1	0.92	0.29	0.287	
SIK2 (SNF1LK2)	1.24	0.27	0.060	
SMAD5	0.89	0.19	0.290	
SMAD6	0.31	0.06	0.001	Proviral
SMARCD3	0.70	0.23	0.046	
SMURF1	0.85	0.20	0.111	
SMURF2	0.79	0.20	0.142	
SNARK (NUAK2)	0.80	0.31	0.183	
SNRPD1	0.44	0.07	0.008	Proviral
SPCS1	1.24	0.56	0.183	
SPCS2	1.31	0.29	0.032	
SPCS3	0.93	0.16	0.242	
SREBP1	1.41	0.27	0.006	

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
SRI	1.28	0.20	0.025	
SRRM2	0.93	0.09	0.207	
STAT1	1.56	0.17	0.000	Antiviral
STAT3	0.82	0.33	0.197	
STK22C	0.96	0.28	0.397	
SUV420H1	1.04	0.30	0.415	
TANK (TRAF2)	0.84	0.24	0.171	
TAZ	0.47	0.11	0.012	Proviral
TBK1	1.10	0.11	0.213	
TFAP2A	0.51	0.07	0.015	Proviral
TGFBR1	2.47	1.08	0.009	Antiviral
TLK2	1.02	0.12	0.440	
TM6SF2	1.34	0.21	0.014	
TNFRSF10C	0.36	0.08	0.000	Proviral
TNFRSF10D	0.90	0.20	0.267	
TNFRSF18	1.03	0.28	0.408	
TNRC11 (MED12)	0.62	0.16	0.003	Proviral
TNS	1.06	0.28	0.337	
TP53	1.23	0.50	0.224	
TRAPPC5	1.08	0.27	0.323	
TRIM42	0.92	0.19	0.291	
TRIM46	0.99	0.08	0.450	
TRIM62	0.70	0.09	0.203	
TRRAP	0.96	0.37	0.407	
TUBB4 (TUBB3)	0.73	0.12	0.006	
TWIST1	0.41	0.09	0.004	Proviral
UBE1L	1.46	0.30	0.008	
UBE2E3	1.40	0.49	0.072	
UBE2J1	0.43	0.13	0.003	Proviral
UBE2J2	1.21	0.41	0.159	
UBE2M	0.88	0.20	0.144	
UBE2S	0.55	0.10	0.022	Proviral

Entrez Gene Symbol	HCV Subgenomic Replicon Assays			HCV RNA Replication Hits
	Average Normalized HCV Subgenomic Replicon Activity	SD	P Value	
USP11	0.89	0.12	0.275	
USP16	1.53	0.32	0.006	Antiviral
USP51	1.04	0.24	0.413	
UTP14A	0.45	0.12	0.000	Proviral
VAMP1	1.02	0.18	0.428	
VTN	1.08	0.32	0.302	
WIF1	0.66	0.16	0.006	Proviral
WNT10B	0.72	0.08	0.023	
XBP1	0.72	0.09	0.004	
XPNPEP1	0.80	0.31	0.161	
ZNF337	1.79	0.29	0.001	Antiviral

Table 13. Host Factors Modulating HCV RNA Replication

RNA Replication	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral	APOBEC2	10930	NM_006789	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2
Proviral	BCL9L	283149	NM_182557	B-cell CLL/lymphoma 9-like
Proviral	CD3E	916	NM_000733	CD3e molecule, epsilon
Proviral	CEBPD	1052	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta
Proviral	CHKA	1119	NM_001277	choline kinase alpha
Proviral	CLSTN1	22883	NM_014944	calsyntenin 1
Proviral	CNOT1 (KIAA1007)	23019	NM_016284	CCR4-NOT transcription complex, subunit 1
Proviral	CTSF	8722	NM_003793	cathepsin F
Proviral	CYLD	1540	NM_015247	cylindromatosis (turban tumor syndrome)
Proviral	DDX21	9188	NM_004728	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
Proviral	DDX26	26512	NM_001039938	integrator complex subunit 6
Proviral	DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
Proviral	DDX6	1656	NM_004397	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6

RNA Replication	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral	DGAT1	8694	NM_012079	diacylglycerol O-acyltransferase homolog 1 (mouse)
Proviral	DNMT1	1786	NM_001379	DNA (cytosine-5-)-methyltransferase 1
Proviral	EIF3S6	3646	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa
Proviral	FBLN5	10516	NM_006329	fibulin 5
Proviral	FKBP1	63943	NM_022110	FK506 binding protein like
Proviral	FLT4	2324	NM_002020	fms-related tyrosine kinase 4
Proviral	GNB2L1	10399	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
Proviral	GPR153	38750 ₉	XM_291419	G protein-coupled receptor 153
Proviral	GPSN2	9524	NM_004868	glycoprotein, synaptic 2
Proviral	GSPT1	2935	NM_002094	G1 to S phase transition 1
Proviral	GTF3A	2971	NM_002097	general transcription factor IIIA
Proviral	HAS1	3036	NM_001523	hyaluronan synthase 1
Proviral	HEXA	3073	NM_000520	hexosaminidase A (alpha polypeptide)
Proviral	IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6
Proviral	IMP4	92856	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
Proviral	ITGA7	3679	NM_002206	integrin, alpha 7
Proviral	LRRC62 (KIAA1904)	11479 ₄	XM_056282	leucine rich repeat containing 62
Proviral	LCK	3932	NM_005356, NM_001042771	lymphocyte-specific protein tyrosine kinase
Proviral	MAP3K6	9064	NM_004672	mitogen-activated protein kinase kinase kinase 6
Proviral	MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1
Proviral	MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3
Proviral	MVD	4597	NM_002461	mevalonate (diphospho) decarboxylase
Proviral	NEK4	6787	NM_003157	NIMA (never in mitosis gene a)-related kinase 4
Proviral	NOL6	65083	NM_022917	nucleolar protein family 6 (RNA-associated)
Proviral	OSBP	5007	NM_002556	oxysterol binding protein
Proviral	PIAS1	8554	NM_016166	protein inhibitor of activated STAT, 1

RNA Replication	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral	PI4KA	5297	NM_002650	phosphatidylinositol 4-kinase, catalytic, alpha
Proviral	PRKRIP1	79706	NM_024653	PRKR interacting protein 1 (IL11 inducible)
Proviral	PTK2B	2185	NM_004103	PTK2B protein tyrosine kinase 2 beta
Proviral	RBP4	5950	NM_006744	retinol binding protein 4, plasma
Proviral	RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5
Proviral	SMAD6	4091	NM_005585	SMAD family member 6
Proviral	TFAP2A	7020	NM_003220	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
Proviral	TNRC11 (MED12)	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
Proviral	TWIST1	7291	NM_000474	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)
Proviral	UBE2J1	51465	NM_016021	ubiquitin-conjugating enzyme E2, J1
Proviral	UBE2S	27338	NM_014501	ubiquitin-conjugating enzyme E2S
Proviral	UTP14A	10813	NM_006649	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
Proviral	WIF1	11197	NM_007191	WNT inhibitory factor 1
Antiviral	CXCL12	6387	NM_000609	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
Antiviral	DICER1	23405	NM_030621, NM_177438	dicer 1, ribonuclease type III
Antiviral	ERBB2	2064	NM_004448	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
Antiviral	FXRD6	53826	NM_022003	FXRD domain containing ion transport regulator 6
Antiviral	GNAZ	2781	NM_002073	guanine nucleotide binding protein (G protein), alpha z polypeptide
Antiviral	IFITM2	10581	NM_006435	interferon induced transmembrane protein 2 (1-8D)
Antiviral	IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)

RNA Replication	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Antiviral	NEMO	8517	NM_003639	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma
Antiviral	NFKB1	4790	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
Antiviral	OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1
Antiviral	PLEK2	26499	NM_016445	pleckstrin 2
Antiviral	RELA	5970	NM_021975	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
Antiviral	RELB	5971	NM_006509	v-rel reticuloendotheliosis viral oncogene homolog B
Antiviral	RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2
Antiviral	STAT1	6772	NM_007315, NM_139266	signal transducer and activator of transcription 1, 91kDa
Antiviral	TGFBR1	7046	NM_004612	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
Antiviral	TP53	7157	NM_000546	tumor protein p53

F. Identification of host factors affecting IRES-mediated translation

An HCV IRES-luciferase assay was used to identify host factors associated with HCV IRES-mediated translation. Briefly, Huh7.5.1 cells were transfected with siRNA as described in part A. After 48 hours, the transfected cells were transiently transfected with pHCV-CLX-CMV WT RNA. Cell lysate was prepared at 24 h following HCV RNA transfection, and assayed for firefly luciferase reporter activities using Luciferase assay system (Promega). siRNA pools were classified as proviral or antiviral hits if the average normalized firefly luciferase activities were decreased or increased for more than 1.5-fold comparing with non-targeting control siRNA and the P value was less than 0.05. These results are shown in Table 10.

Table 10. Host Factors Modulating HCV Translation

Entrez Gene Symbol	Average Normalized IRES-Luciferase Activity	SD	P values	IRES-Mediated Translation Hits
ABCB6	1.34	0.15	0.002	
APOBEC2	0.93	0.22	0.274	
BCL9L	1.40	0.30	0.009	
CCND1	0.97	0.06	0.299	
CD3E	0.80	0.10	0.009	
CD81	1.01	0.17	0.449	
CDC42EP3	0.71	0.09	0.000	
CEBPD	0.84	0.11	0.028	
CHUK	0.91	0.04	0.039	
CLSTN1	0.99	0.31	0.475	
CRLF2 OTP	0.69	0.09	0.001	
CRLF2 SIG	1.13	0.06	0.006	
CRLF3	0.57	0.09	0.000	Proviral
CTSF	0.85	0.10	0.025	
CYLD	0.88	0.30	0.215	
DDX21	0.76	0.21	0.026	
DDX26	0.87	0.18	0.092	
DDX3X	0.56	0.02	0.000	Proviral
DDX6	0.77	0.13	0.003	
DGAT1	1.03	0.32	0.426	
DICER1	1.13	0.27	0.172	
DNMT1	0.88	0.13	0.048	
EIF3S6	1.44	0.21	0.002	
ERBB2	1.15	0.04	0.002	
FBLN5	0.59	0.07	0.000	Proviral
FKBP1	0.62	0.11	0.000	Proviral
FLT4	0.66	0.10	0.000	Proviral
FOXP3	1.05	0.20	0.279	
FXYD6	1.68	0.21	0.000	Antiviral
GCAT	1.06	0.26	0.312	
GLG1	1.22	0.51	0.187	
GNB2L1	0.76	0.14	0.048	
GPR145	0.93	0.28	0.346	

GPR153	1.70	0.51	0.008	Antiviral
GPSN2	1.27	0.26	0.046	
GSPT1	1.08	0.30	0.303	
GTF3A	0.79	0.10	0.023	
HAS1	1.48	0.24	0.003	
HEXA	1.09	0.17	0.163	
IFITM2	2.35	0.32	0.000	Antiviral
IFITM3	1.49	0.13	0.000	Antiviral
IGFBP6	0.45	0.10	0.000	Proviral
IMP4	0.98	0.10	0.414	
ITGA7	0.97	0.07	0.254	
KIAA1007	1.09	0.05	0.147	
KIAA1904	1.46	0.12	0.000	
LCK	0.83	0.08	0.016	
MAP3K6	1.20	0.16	0.030	
MAPK1	0.56	0.05	0.000	Proviral
MARK3	0.46	0.06	0.000	Proviral
MVD	1.44	0.07	0.000	
NEK4	0.99	0.20	0.455	
NFKB1	1.00	0.12	0.492	
NOL6	0.33	0.10	0.000	Proviral
OSBP	1.12	0.04	0.018	
OTUB1	1.77	0.21	0.000	Antiviral
PIAS1	0.39	0.03	0.000	Proviral
PIK4CA	0.78	0.08	0.001	
PLEK2	2.26	0.23	0.000	Antiviral
PRKRIP1	0.87	0.04	0.015	
PTK2B	1.07	0.28	0.317	
RAB34	0.85	0.10	0.022	
RAB5A	1.04	0.09	0.277	
RBP4	1.16	0.07	0.005	
RELB	1.16	0.23	0.098	
RGPD5	0.64	0.06	0.000	Proviral
RIPK2	1.55	0.30	0.003	Antiviral
SMAD6	0.42	0.04	0.000	Proviral
SNRPD1	0.73	0.04	0.000	
STAT1	1.78	0.16	0.000	Antiviral
TFAP2A	1.36	0.13	0.011	
TGFBR1	1.32	0.20	0.027	

TNFRSF10C	0.86	0.08	0.126	
TNRC11	1.82	0.12	0.000	Antiviral
TRIM62	1.45	0.23	0.009	
TWIST1	1.14	0.10	0.025	
UBE2J1	0.90	0.02	0.206	
UBE2S	1.40	0.17	0.009	
UTP14A	1.12	0.29	0.208	
WIF1	0.88	0.13	0.078	

Twelve of these host factors are specifically involved in HCV IRES-mediated translation, and nine host factors are antiviral by inhibiting HCV IRES-mediated translation (Table 12).

5 Table 12. Host Factors Modulating HCV Translation

IRES-Mediated Translation	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral	CRLF3	51379	NM_015986	cytokine receptor-like factor 3
Proviral	DDX3X	1654	NM_001356	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
Proviral	FBLN5	10516	NM_006329	fibulin 5
Proviral	FKBP1	63943	NM_022110	FK506 binding protein like
Proviral	FLT4	2324	NM_002020	fms-related tyrosine kinase 4
Proviral	IGFBP6	3489	NM_002178	insulin-like growth factor binding protein 6
Proviral	MAPK1	5594	NM_138957, NM_002745	mitogen-activated protein kinase 1
Proviral	MARK3	4140	NM_002376	MAP/microtubule affinity-regulating kinase 3
Proviral	NOL6	65083	NM_022917	nucleolar protein family 6 (RNA-associated)
Proviral	PIAS1	8554	NM_016166	protein inhibitor of activated STAT, 1
Proviral	RGPD5	84220	NM_005054	RANBP2-like and GRIP domain containing 5
Proviral	SMAD6	4091	NM_005585	SMAD family member 6
Antiviral	FXRD6	53826	NM_022003	FXRD domain containing ion transport regulator 6
Antiviral	GPR153	387509	XM_291419	G protein-coupled receptor 153
Antiviral	IFITM2	10581	NM_006435	interferon induced transmembrane protein 2 (1-8D)

Antiviral	IFITM3	10410	NM_021034	interferon induced transmembrane protein 3 (1-8U)
Antiviral	OTUB1	55611	NM_017670	OTU domain, ubiquitin aldehyde binding 1
Antiviral	PLEK2	26499	NM_016445	pleckstrin 2
Antiviral	RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2
Antiviral	STAT1	6772	NM_007315, NM_139266	signal transducer and activator of transcription 1, 91kDa
Antiviral	TNRC11 (MED12)	9968	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (<i>S. cerevisiae</i>)

G. Identification of Host Factors Modulating HCV Trafficking, Assembly, and Release

A conjugative analysis of virological assays with HCV cell culture system (HCVcc), including intracytoplasmic HCV RNA quantification, infectious viral production assays, and confocal microscopic imaging of viral and cellular factors, validated that 77 host proteins are required for HCV endocytic trafficking, virion assembly, and particle release. These host factors are listed in Table 14.

Table 14. Host Factors Modulating Trafficking, Assembly and release

Trafficking, Assembly, Release	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
Proviral	ABCB6	10058	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6
Proviral	ADFP	123	NM_001122	adipose differentiation-related protein
Proviral	AP1GBP1	11276	NM_007247	AP1 gamma subunit binding protein 1
Proviral	AP3B1	8546	NM_003664	adaptor-related protein complex 3, beta 1 subunit
Proviral	APOE	348	NM_000041	apolipoprotein E
Proviral	ARHGAP22	58504	NM_021226	Rho GTPase activating protein 22
Proviral	C1QA	712	NM_015991	complement component 1, q subcomponent, A chain
Proviral	C1QB	713	NM_000491	complement component 1, q subcomponent, B chain
Proviral	CCDC8	83987	NM_032040	coiled-coil domain containing 8
Proviral	CCL26	10344	NM_006072	chemokine (C-C motif) ligand 26
Proviral	CDCA3	83461	NM_031299	cell division cycle associated 3

Proviral	CHUK	1147	NM_001278	conserved helix-loop-helix ubiquitous kinase
Proviral	CPD	1362	NM_001304	carboxypeptidase D
Proviral	CSNK1A1L	122011	NM_145203	casein kinase 1, alpha 1-like
Proviral	CTGF	1490	NM_001901	connective tissue growth factor
Proviral	CTNNAL1	8727	NM_003798	catenin (cadherin-associated protein), alpha-like 1
Proviral	CX3CL1	6376	NM_002996	chemokine (C-X3-C motif) ligand 1
Proviral	CD55 (DAF)	1604	NM_000574	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
Proviral	DEFB126	81623	NM_030931	defensin, beta 126
Proviral	FOXA2	3170	NM_021784	forkhead box A2
Proviral	GCAT	23464	NM_014291	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
Proviral	GLG1	2734	NM_012201	golgi glycoprotein 1
Proviral	GNG8	94235	NM_033258	guanine nucleotide binding protein (G protein), gamma 8
Proviral	HIPK3	10114	NM_005734	homeodomain interacting protein kinase 3
Proviral	IDE	3416	NM_004969	insulin-degrading enzyme
Proviral	IKBKE	9641	NM_014002	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
Proviral	IL17RB	55540	NM_018725	interleukin 17 receptor B
Proviral	IRF3	3661	NM_001571	interferon regulatory factor 3
Proviral	PNO1 (LOC56902)	56902	NM_020143	partner of NOB1 homolog (S. cerevisiae)
Proviral	LTB	4050	NM_002341, NM_009588	lymphotoxin beta (TNF superfamily, member 3)
Proviral	MAVS	57506	NM_020746	mitochondrial antiviral signaling protein
Proviral	MYO3A	53904	NM_017433	myosin IIIA
Proviral	NIK	9020	NM_003954	mitogen-activated protein kinase kinase kinase 14
Proviral	SCYL3 (PACE-1)	57147	NM_020423	SCY1-like 3 (S. cerevisiae)
Proviral	PARP11	57097	NM_020367	poly (ADP-ribose) polymerase family, member 11
Proviral	PLB1	151056	NM_153021	phospholipase B1
Proviral	PLEK2	26499	NM_016445	pleckstrin 2
Proviral	PPIA	5478	NM_021130	peptidylprolyl isomerase A (cyclophilin A)
Proviral	PPP2R1A	5518	NM_014225	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha

				isoform
Proviral	PPP2R2A	5520	NM_002717	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
Proviral	PRG2	5553	NM_002728	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)
Proviral	PROX1	5629	NM_002763	prospero-related homeobox 1
Proviral	PTHR1	5745	NM_000316	parathyroid hormone receptor 1
Proviral	RAB10	10890	NM_016131	RAB10, member RAS oncogene family
Proviral	RAB9P40 (RABEPK)	10244	NM_005833	Rab9 effector protein with kelch motifs
Proviral	RAF1	5894	NM_002880	v-raf-1 murine leukemia viral oncogene homolog 1
Proviral	RBM9	23543	NM_014309	RNA binding motif protein 9
Proviral	Rgr	266747	NM_153615	Ral-GDS related protein Rgr
Proviral	RIPK2	8767	NM_003821	receptor-interacting serine-threonine kinase 2
Proviral	RNF207	388591	NM_207396	ring finger protein 207
Proviral	ROCK2	9475	NM_004850	Rho-associated, coiled-coil containing protein kinase 2
Proviral	RPS6KL1	83694	NM_031464	ribosomal protein S6 kinase-like 1
Proviral	RYK	6259	NM_002958	RYK receptor-like tyrosine kinase
Proviral	SH3TC1	54436	NM_018986	SH3 domain and tetratricopeptide repeats 1
Proviral	SIK2 (SNF1LK2)	23235	NM_015191	SNF1-like kinase 2
Proviral	SMAD5	4090	NM_005903	SMAD family member 5
Proviral	SMARCD3	6604	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
Proviral	SMURF1	57154	NM_020429	SMAD specific E3 ubiquitin protein ligase 1
Proviral	SNARK (NUAK2)	81788	NM_030952	NUAK family, SNF1-like kinase, 2
Proviral	SPCS1	28972	NM_014041	signal peptidase complex subunit 1 homolog (S. cerevisiae)
Proviral	SPCS2	9789	NM_014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)
Proviral	SPCS3	60559	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)
Proviral	SREBP1	6720	NM_004176	sterol regulatory element binding transcription factor 1

Proviral	SRI	6717	NM_003130	sorcin
Proviral	SRRM2	23524	NM_016333	serine/arginine repetitive matrix 2
Proviral	STAT3	6774	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)
Proviral	TM6SF2	53345	NM_001001524	transmembrane 6 superfamily member 2
Proviral	TRAPPC5	126003	XM_058961	trafficking protein particle complex 5
Proviral	TRIM42	287015	NM_152616	tripartite motif-containing 42
Proviral	TRIM46	80128	NM_025058	tripartite motif-containing 46
Proviral	TRRAP	8295	NM_003496	transformation/transcription domain-associated protein
Proviral	UBE1L	7318	NM_003335	ubiquitin-activating enzyme E1-like
Proviral	UBE2M	9040	NM_003969	ubiquitin-conjugating enzyme E2M
Proviral	UBE2S	27338	NM_014501	ubiquitin-conjugating enzyme E2S
Proviral	USP11	8237	NM_004651	ubiquitin specific peptidase 11
Proviral	USP51	158880	NM_201286	ubiquitin specific peptidase 51
Proviral	XPNPEP1	7511	NM_020383	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
Antiviral	ECT2	1894	NM_018098	epithelial cell transforming sequence 2 oncogene
Antiviral	HNRPK	3190	NM_002140	heterogeneous nuclear ribonucleoprotein K
Antiviral	IL10RB	3588	NM_000628	interleukin 10 receptor, beta
Antiviral	IMPDH1	3614	NM_000883	IMP (inosine monophosphate) dehydrogenase 1
Antiviral	NDRG1	10397	NM_006096	N-myc downstream regulated gene 1
Antiviral	PTPRH	5794	NM_002842	protein tyrosine phosphatase, receptor type, H
Antiviral	RSAD2	91543	NM_080657	radical S-adenosyl methionine domain containing 2
Antiviral	TNS1	7145	NM_022648	tensin 1

With stringent criteria for selection, 62 genes selected for this study were shown to have an undetectable affect (i.e., no detectable activity) on HCV infection. These genes are listed in Table 15.

Table 15. Host Factors Having no Effect on the HCV Life-Cycle

No Effect on HCV Life Cycle	Entrez Gene Symbol	Entrez Gene ID	Genbank Acc. No.	Gene Name
X	ABCE1	6059	NM_002940	ATP-binding cassette, sub-family E (OABP), member 1
X	ACBD3	64746	NM_022735	acyl-Coenzyme A binding domain containing 3
X	AKT2	208	NM_001626	v-akt murine thymoma viral oncogene homolog 2
X	APC2	10297	NM_005883	adenomatosis polyposis coli 2
X	APOBEC3B	9582	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
X	ARL10	285598	NM_173664	ADP-ribosylation factor-like 10
X	ART5	116969	NM_053017	ADP-ribosyltransferase 5
X	BAIAP2	10458	NM_006340	BAI1-associated protein 2
X	BCL7A	605	NM_020993	B-cell CLL/lymphoma 7A
X	CABP1	9478	NM_004276	calcium binding protein 1
X	CCL3L1	6349	NM_021006	chemokine (C-C motif) ligand 3-like 1
X	CCND1	595	NM_053056	cyclin D1
X	CDKL5	6792	NM_003159	cyclin-dependent kinase-like 5
X	CNOT6L	246175	NM_144571	CCR4-NOT transcription complex, subunit 6-like
X	CRLF2	64109	NM_022148	cytokine receptor-like factor 2
X	CRLF3	51379	NM_015986	cytokine receptor-like factor 3
X	CSF3R	1441	NM_000760	colony stimulating factor 3 receptor (granulocyte)
X	CTNNB1	1499	NM_001904	catenin (cadherin-associated protein), beta 1, 88kDa
X	DDOST	1650	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
X	DOCK3	1795	NM_004947	dedicator of cytokinesis 3
X	E2F1	1869	NM_005225	E2F transcription factor 1
X	FBXO38	81545	NM_030793	F-box protein 38
X	FOXP3	50943	NM_014009	forkhead box P3
X	HPX	3263	NM_000613	hemopexin
X	HSPCA	3320	NM_005348, NM_001017963	heat shock protein 90kDa alpha (cytosolic), class A member 1
X	IFIX (PYHIN1)	149628	NM_152501	pyrin and HIN domain family, member 1
X	IGSF11	152404	NM_152538	immunoglobulin superfamily, member 11
X	IGSF4D (CADM2)	253559	NM_153184	cell adhesion molecule 2
X	IL1B	3553	NM_000576	interleukin 1, beta

X	IREB2	3658	NM_004136	iron-responsive element binding protein 2
X	ITGB1BP2	26548	NM_012278	integrin beta 1 binding protein (melusin) 2
X	YIPF4 (MGC11061)	84272	NM_032312	Yip1 domain family, member 4
X	DACT3 (MGC15476)	147906	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)
X	MMP11	4320	NM_005940	matrix metalloproteinase 11 (stromelysin 3)
X	MMP9	4318	NM_004994	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
X	NCOR2	9612	NM_006312	nuclear receptor co-repressor 2
X	NDUFB4	4710	NM_004547	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
X	PDAP1	11333	NM_014891	PDGFA associated protein 1
X	TWF1 (PTK9)	5756	NM_002822	twinfilin, actin-binding protein, homolog 1 (Drosophila)
X	RAB11A	8766	NM_004663	RAB11A, member RAS oncogene family
X	RFWD3	55159	NM_018124	ring finger and WD repeat domain 3
X	RIT1	6016	NM_006912	Ras-like without CAAX 1
X	RNF31	55072	NM_017999	ring finger protein 31
X	ROBO1	6091	NM_002941	roundabout, axon guidance receptor, homolog 1 (Drosophila)
X	SMURF2	64750	NM_022739	SMAD specific E3 ubiquitin protein ligase 2
X	SNRPD1	6632	NM_006938	small nuclear ribonucleoprotein D1 polypeptide 16kDa
X	STK22C (TSSK3)	81629	NM_052841	testis-specific serine kinase 3
X	TANK (TRAF2)	10010	NM_004180, NM_133484	TRAF family member-associated NFKB activator
X	WWTR1	25937	NM_015472	WW domain containing transcription regulator 1
X	TBK1	29110	NM_013254	TANK-binding kinase 1
X	TLK2	11011	NM_006852	tousled-like kinase 2
X	TNFRSF10C	8794	NM_003841	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
X	TNFRSF10D	8793	NM_003840	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
X	TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18
X	TUBB4 (TUBB3)	10381	NM_006086	tubulin, beta 3
X	UBE2E3	10477	NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
X	UBE2J2	118424	NM_058167	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
X	USP16	10600	NM_006447	ubiquitin specific peptidase 16

X	VAMP1	6843	NM_014231	vesicle-associated membrane protein 1 (synaptobrevin 1)
X	VTN	7448	NM_000638	vitronectin
X	WNT10B	7480	NM_003394	wingless-type MMTV integration site family, member 10B
X	ZNF337	26152	NM_015655	zinc finger protein 337

A major concern of RNAi-based mammalian genetics is false negatives, stemming in part from inefficient targeting or nonspecific toxicity. To preserve new connections and minimize bias, we have performed bioinformatics meta-analyses after the selection of our validated gene set, which integrated several HCV host factor data sets and disclosed statistically enriched complexes and pathways. By performing hypothesis-driven follow-up studies of these highlighted pathways, we were able to identify 22 additional host factors that were not previously identified by our primary screen. These host factors are listed in Table 16.

Table 16. False-Negative Host Factors

Entrez Gene Symbol	Entrez Gene ID	GenBank Acc. No.	Gene Name	Primary Screen Hit	Entry	IRES-Mediated Translation	RNA Replication	Trafficking, Assembly, Release
CYLD	1540	NM_015247	cylindromatosis (turban tumor syndrome)	No			Proviral	
DDX26	26512	NM_001039938	integrator complex subunit 6	No			Proviral	
DICER1	23405	NM_030621, NM_177438	dicer 1, ribonuclease type III	No			Antiviral	
GLG1	2734	NM_012201	golgi glycoprotein 1	No				Proviral
IKBKB	3551	NM_001556	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	No	Antiviral (HCV & VSV)			
IKBKE	9641	NM_014002	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	No				Proviral
IL10RB	3588	NM_000628	interleukin 10 receptor, beta	No				Antiviral
LTB	4050	NM_002341, NM_009588	lymphotoxin beta (TNF superfamily, member 3)	No				Proviral
MAVS	57506	NM_020746	mitochondrial antiviral signaling protein	No				Proviral
NEMO	8517	NM_003639	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	No			Antiviral	
NFKB1	4790	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	No			Antiviral	
NFKB2	4791	NM_002502	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	No	Antiviral (HCV & VSV)			
NIK	9020	NM_003954	mitogen-activated protein kinase kinase kinase 14	No				Proviral

PIAS1	8554	NM_016166	protein inhibitor of activated STAT, 1	No				
RAB34	83871	NM_031934	RAB34, member RAS oncogene family	No	Proviral (HCV & VSV)			
RAB5A	5868	NM_004162	RAB5A, member RAS oncogene family	No	Proviral (HCV & VSV)			
RELA	5970	NM_021975	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	No			Antiviral	
RELB	5971	NM_006509	v-rel reticuloendotheliosis viral oncogene homolog B	No			Antiviral	
RSAD2	91543	NM_080657	radical S-adenosyl methionine domain containing 2	No				Antiviral
SREBP1	6720	NM_004176	sterol regulatory element binding transcription factor 1	No				Proviral
STAT1	6772	NM_007315, NM_139266	signal transducer and activator of transcription 1, 91kDa	No		Antiviral	Antiviral	
TP53	7157	NM_000546	tumor protein p53	No			Antiviral	

Example 3.

Among the host factors identified in the primary screen described in Example 1, IKK α was a strongly positive hit as a proviral factor. IKK α is an I κ B kinase that plays a predominant role in non-canonical NF κ B activation pathway. Innate immunity mediated by activation of NF- κ B is a fundamental early signaling step of host antiviral defense. This Example demonstrates an NF- κ B-independent function of IKK α in hepatitis C virus infection and propagation.

A. To demonstrate the effect of Ikk α on the HCV life-cycle, an siRNA screen was performed as described in Example 1. Briefly, siRNA's for the IKK α gene were transiently transfected into Huh 7.5.1 cells and after 72 hours, the cells infected with hepatitis C virus. AT 48 hours post-infection, 80 ml of media were removed and used for "late-stage" experiments. After removal of the media, the infected cells were fixed and stained with anti-HCV core 6G7 monoclonal antibody, as described in Example 1. The results of this experiment are shown in Figure 5(A). The data show that siRNA silencing of IKK α production resulted in a marked decrease of HCV production in Huh7.5 cells.

The 80 ml of medium removed from the infected cells were replica plated onto a new 96-well plate, which contained 10,000 Huh 7.5.1 cells per well plated out 24 h before viral supernatant addition. At 48 h post-infection, the cells were fixed, stained, and imaged using the staining and imaging protocol described in Example 1. The results of these "late stage: experiments are shown in Figure 5(B).

B. To study the functional effects of various NF- κ B pathway host factors on HCV infection, Huh7.5.1 cells were transfected with siRNA's targeting these specific factors, and then infected with HCV, as described in Example 1. Intracellular and extracellular HCV RNA levels were then determined at 48 hours post-infection, using the protocol described in Example 1. The results of this experiment, which are shown in Figure 6, demonstrate that siRNA silencing of IKK α , and two IKK α upstream activators, NF- κ B inducing kinase (NIK) and lymphotoxin- β (LTB), resulted in a marked decrease of HCV RNA production in Huh 7.5. cells. Likewise, overexpression of the dominant negative IKK α mutant (kinase-defective) suppressed HCV infection (Figure 7). In contrast, as shown in Figure 6, siRNA knocking-down of two other key I κ B kinases, IKK β and IKK α /NEMO, and components of NF- κ B transcription factors, enhanced HCV

replication, confirming the role of NF- κ B in innate antiviral defense. Using various virologic assays including HCVcc, HCVpp and HCV replicon, silencing of IKK α specifically blocked HCV assembly. Confocal microscopy showed a marked diminution of core-associated lipid droplets, presumably site of viral assembly, in IKK α -silenced cells infected with HCV. We further showed by confocal microscopy and co-immunoprecipitation that NS5B but not other HCV proteins interacts specifically with and activates IKK α . The activated IKK α translocates to the nucleus and induces a CREB-binding protein (CBP)-mediated transcriptional program that includes SREBP1, a critical transcriptional factor controlling lipid metabolism and biogenesis of lipid droplets. SREBP1 was identified as a proviral factor in the genome-wide siRNA screen and siRNA knock-down of SREBP1 displayed the same phenotype as IKK α silencing in HCV infection. Our study demonstrates that HCV has evolved a mechanism to exploit the host innate defense for its own advantage.

C. Effect of IKK α silencing on HCV RNA levels.

To measure the effect of silencing of IKK α expression on HCV RNA levels, Huh7.5.1 cells were transiently transfected with a pool of siRNAs, or individual siRNAs, against IKK α , and then infected with HCV. At 48 hours post-infection, the levels of intracellular and extracellular HCV RNA were measured using quantitative PCR, as described in Example 2(C). CD81, a major receptor of HCV, was used as a positive control for the early stage of the HCV lifecycle. ApoE, which is required for infectious viral particle formation, was the positive control for the late stage. The results are shown in Figure 8.

D. Effect of IKK α silencing on viral entry and RNA replication

HCV pseudovirus and replicon assays, described in Example 2, parts D and E, respectively, were used to measure the effect of IKK α silencing on viral entry and replication. Positive siRNA controls of CD81 and PIK4CA were used for the HCVpp and HCV replicon assays, respectively. These assays, the results of which are shown in Figure 9, demonstrate that IKK α is not involved in HCV entry (panel A) or HCV replication (panel B).

Example 4

This Example demonstrates the ability of certain compounds to inhibit HCV entry.

Several proviral host factors identified in the initial siRNA screen suggest that a special process of HCV entry involves macropinocytosis. Thus, we tested various compounds that have been shown to target various host factors associated with macropinocytosis of viral entry. Huh7.5.1 cells were infected with HCVpp in increasing concentrations of compounds as indicated, and assayed for luciferase activities 48 h later. The results, which are shown in Figure 10, show that HCV entry was inhibited by these compounds, i.e., rotterlin, colchicines, EIPA, wormannin, cytochalasin, and U0126.

To further confirm the HCVpp data, Huh7.5.1 cells were infected with HCVcc in the presence of varying concentrations of the Rottlerin and EIPA. After 4 h of infection, the culture medium was removed, the cells washed to remove the inoculating virus, fresh medium added and the cells incubated for 48 hours. At the end of the incubation period, HCV RNA levels in the culture supernatant were determined as described in Example 2(C). The results, which are shown in Figure 11, indicate that both drugs inhibited HCV infection.

HCV replication involves formation of membranous webs, which are sites of RNA replication. The present work identified several ADP-ribosylation factors and related proteins as proviral factors. Brefeldin A and golgicide A are compounds that have been shown to interfere with the functions of these factors in membrane-associated mechanisms of secretory and endocytic pathways. To test the effects of these drugs on HCV infection, Huh7.5.1 cells were infected with HCVcc in the presence of increasing concentrations of the compounds for 4 h and the culture supernatant was then removed with washing to remove the inoculating virus. Infected cells were treated with the same concentrations of the compounds for an additional 48 h and the culture supernatant was harvested for HCV RNA determination. The results, which are shown in Figure 12, indicate that both drugs inhibit HCV infection.

The present work enabled the reconstruction of an in-depth network map of cellular pathways and machineries that are associated with the complete life cycle of HCV (summarized in Table 1). A comprehensive investigation of HCV-host interactions

yields critical insights into HCV pathogenesis and valuable targets for prophylactic and therapeutic interventions.

While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various
5 changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims.

10

CLAIMS

1. A method to inhibit viral infection, said method comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection.
2. A method to inhibit viral infection, said method comprising contacting a cell with an inhibitory compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection.
3. A method to protect a patient from hepatitis C virus infection comprising administering an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1.
4. A method to protect a patient from hepatitis C virus infection comprising administering an inhibitory compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1.
5. A method to enhance viral infection, said method comprising contacting a cell with an enhancing compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection.
6. A method to enhance viral infection, said method comprising contacting a cell with an enhancing compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection.
7. The method of any of Claims 3-4 wherein said protection is prophylactic.
8. The method of any of Claims 3-4 wherein said protection is therapeutic.
9. The method of any of Claims 1-6, wherein said host factor is encoded by a nucleic acid molecule listed in Table 2.

10. The method of any of Claims 1, 2, 5 or 6, wherein said virus is a Flavivirus.
11. The method of any of Claims 1, 2, 5 or 6, wherein said virus is hepatitis C virus.
12. The method of any of Claims 1-2, wherein said method comprises contacting a patient with said inhibitory compound.
- 5 13. The method of Claim 12, wherein said patient is infected with said virus.
14. The method of any of Claims 1-4, wherein said inhibitory compound is selected from one or more of the compounds listed in Table 3.
15. The method of any of Claims 1-4, wherein said inhibitory compound is selected from colchicine, cytochalasin, EIPA, rottlerin, UO126, wortmannin or a mixture of two or
10 more of said compounds.
16. The method of any of Claims 1-4, wherein said inhibitory compound is selected from brefeldin A, golgicide A or a mixture thereof.
17. The method of any of Claims 1-4, wherein said inhibitory compound comprises a small interfering RNA (siRNA).
- 15 18. The method of Claim 17, wherein said siRNA is selected from one or more of the siRNAs listed in Table 4.
19. The method of any of Claims 1-6, wherein said host factor is encoded by a nucleic acid molecule listed in Table 11.
20. The method of any of Claims 1-6, wherein said host factor is encoded by a nucleic
20 acid molecule listed in Table 12.
21. The method of any of Claims 1-6, wherein said host factor is encoded by a nucleic acid molecule listed in Table 13
22. The method of any of Claims 1-6, wherein said host factor is encoded by a nucleic acid molecule listed in Table 14.
- 25 23. The method of any of Claims 1-4, wherein said host factor is encoded by a nucleic acid molecule comprising SEQ ID NO:79.

24. The method of any of Claims 1-4, wherein said host factor comprises amino acid sequence SEQ ID NO:80.
25. An inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule
5 having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection.
26. An inhibitory compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby inhibiting viral infection.
27. An enhancing compound that interacts with a host factor encoded by a nucleic
10 acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection.
28. An enhancing compound that modulates a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, thereby enhancing viral infection.
- 15 29. The compound of any of Claims 25-28, wherein said host factor is encoded by a nucleic acid molecule listed in Table 2.
30. The compound of any of Claims 25-28, wherein said host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14.
31. The inhibitory compound of any of Claims 25-26, wherein said host factor is
20 encoded by a nucleic acid molecule comprising SEQ ID NO:79.
32. The inhibitory compound of any of Claims 25-26, wherein said host factor comprises amino acid sequence SEQ ID NO:80.
33. The compound of any of Claims 25-28, wherein said virus is hepatitis C virus.
34. A method to identify a compound that inhibits viral infection, said method
25 comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to inhibit said infection, wherein said host factor is encoded by a nucleic acid molecule listed in Table 5 or is encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1.

35. A method to identify a compound that inhibits viral infection, said method comprising:

(a) combining a candidate compound with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for said candidate compound to interact with said host factor;

(b) assaying for the presence of said interaction; and

(c) determining if said interaction results in a decrease in the amount of virus obtained upon infection of a cell with said virus;

10 wherein a decrease in the amount of virus indicates that said compound inhibits viral infection.

36. A method to identify a compound that inhibits viral infection, said method comprising assaying a candidate compound for the ability to modulate a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, wherein the ability to modulate said pathway identifies a compound that inhibits viral infection.

37. A method to identify a compound that enhances viral infection, said method comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to enhance said infection, wherein said host factor is encoded by a nucleic acid molecule listed in Table 5 or is encoded by a nucleic acid molecule having a SEQ ID NO. listed in Table 1.

38. A method to identify a compound that enhances viral infection, said method comprising:

25 (a) combining a candidate compound with a host factor encoded by a nucleic acid molecule listed in Table 5 or with a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1 under conditions suitable for said candidate compound to interact with said host factor;

(b) assaying for the presence of said interaction; and

(c) determining if said interaction results in an increase in the amount of virus obtained upon infection of a cell with said virus;

wherein an increase in the amount of virus indicates that said compound enhances viral infection.

5 39. A method to identify a compound that enhances viral infection, said method comprising assaying a candidate compound for the ability to modulate a pathway comprising a host factor encoded by a nucleic acid molecule listed in Table 5 or a host factor encoded by a nucleic acid molecule having a SEQ ID NO: listed in Table 1, wherein the ability to modulate said pathway identifies a compound that enhances viral
10 infection.

40. The method of any of Claims 34-39, wherein said host factor is encoded by a nucleic acid molecule listed in Table 2.

41. The method of any of Claims 34-39, wherein said virus is a Flavivirus.

42. The method of any of Claims 34-39, wherein said virus is hepatitis C virus.

15 43. The method of Claim 34, wherein said assay comprises:

(a) contacting said candidate compound with said host factor under conditions suitable for formation of a complex between said compound and said host factor; and

(b) detecting the presence of a complex, if present;

wherein detection of a complex indicates that the candidate compound inhibits viral
20 infection.

44. The method of Claim 34, wherein said assay comprises:

(a) contacting said candidate compound with said host factor under conditions suitable for allowing an interaction between said compound and said host factor; and

(b) determining if said interaction results in modification of said host factor;

25 wherein modification of said host factor indicates that the candidate compound inhibits viral infection.

45. The method of Claim 35 or Claim 38, wherein said interaction is selected from the group consisting of (a) formation of a complex between said candidate compound and said host factor and (b) modification of said host factor.

46. The method of Claim 37, wherein said assay comprises:

- 5 (a) contacting said candidate compound with said host factor under conditions suitable for formation of a complex between said compound and said host factor; and
- (b) detecting the presence of a complex, if present;

wherein detection of a complex indicates that the candidate compound enhances viral infection.

10 47. The method of Claim 37, wherein said assay comprises:

- (a) contacting said candidate compound with said host factor under conditions suitable for allowing an interaction between said compound and said host factor and said host factor; and
- (b) determining if said interaction results in modification of said host factor;

15 wherein modification of said host factor indicates that the candidate compound enhances viral infection.

48. The method of any of Claims 34-39, wherein said host factor is encoded by a nucleic acid molecule listed in Table 11, Table 12, Table 13 or Table 14.

49. An inhibitory compound identified by the method of any of Claims 34-36.

20 50. An enhancing compound identified by the method of any of Claims 37-39.

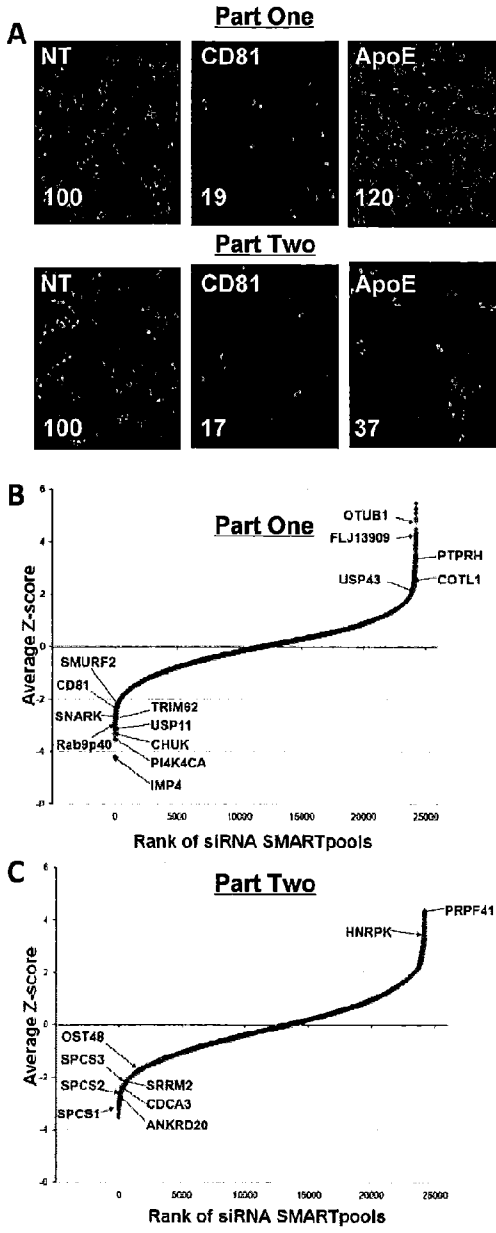
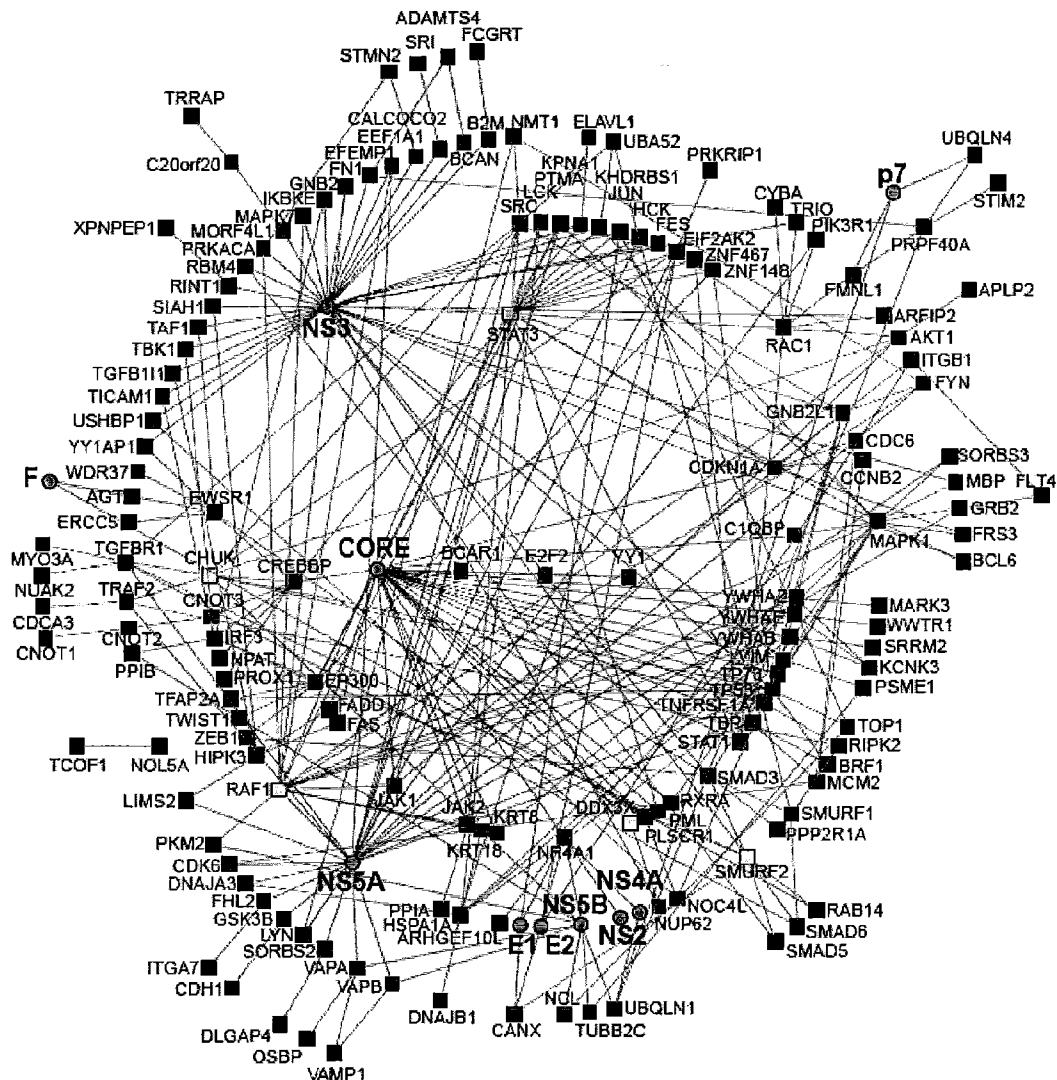


Figure 1



-  HCV-encoded proteins
 HCV-interacting proteins (human)
 siRNA screen hits
 HCV-interacting proteins that are also siRNA screen hits
-  Interactions between HCV-encoded proteins and HCV-interacting proteins
 Interactions between siRNA screen hits and HCV-interacting proteins

Figure 2

Interactions between siRNA screen hits and:

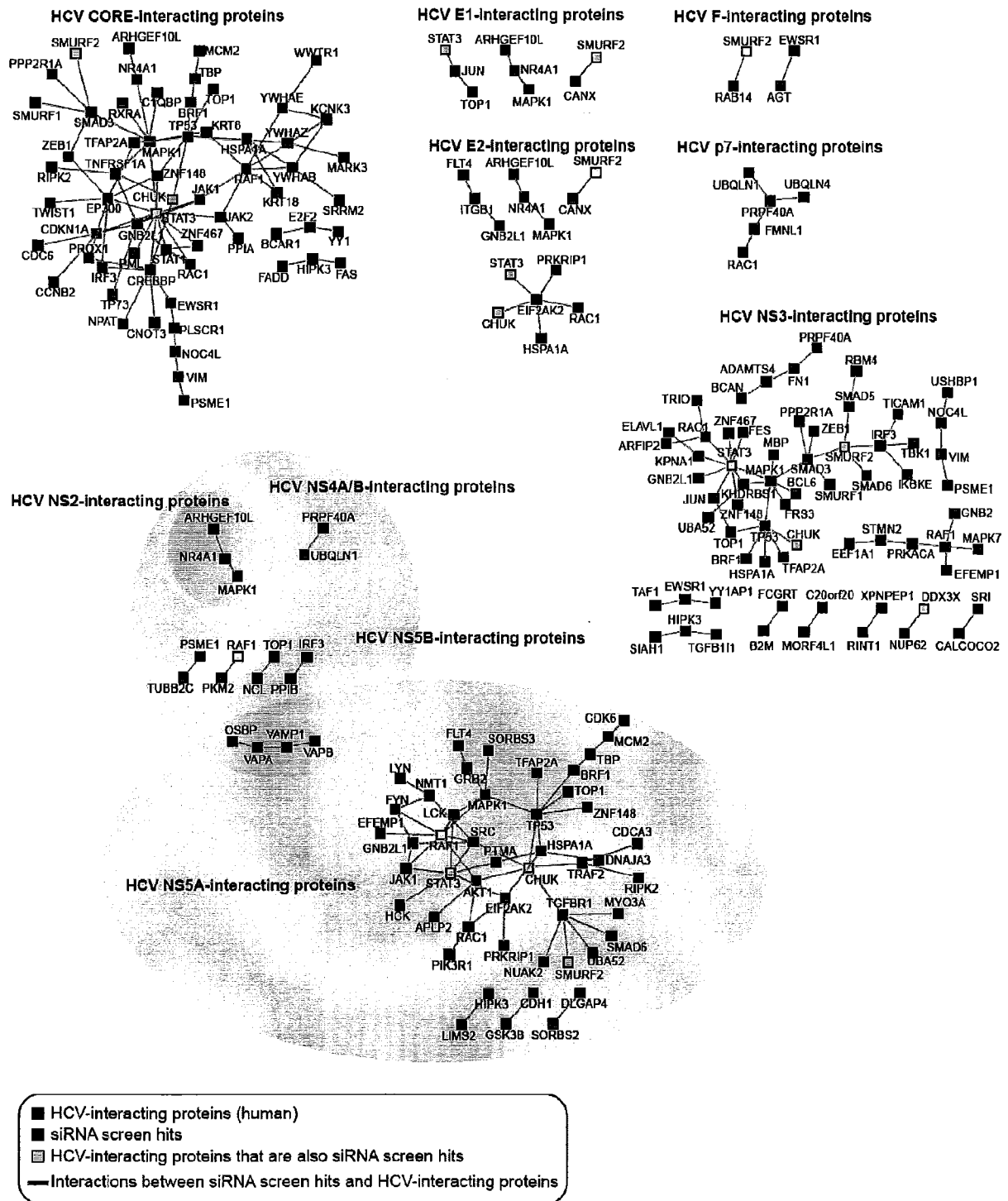


Figure 3

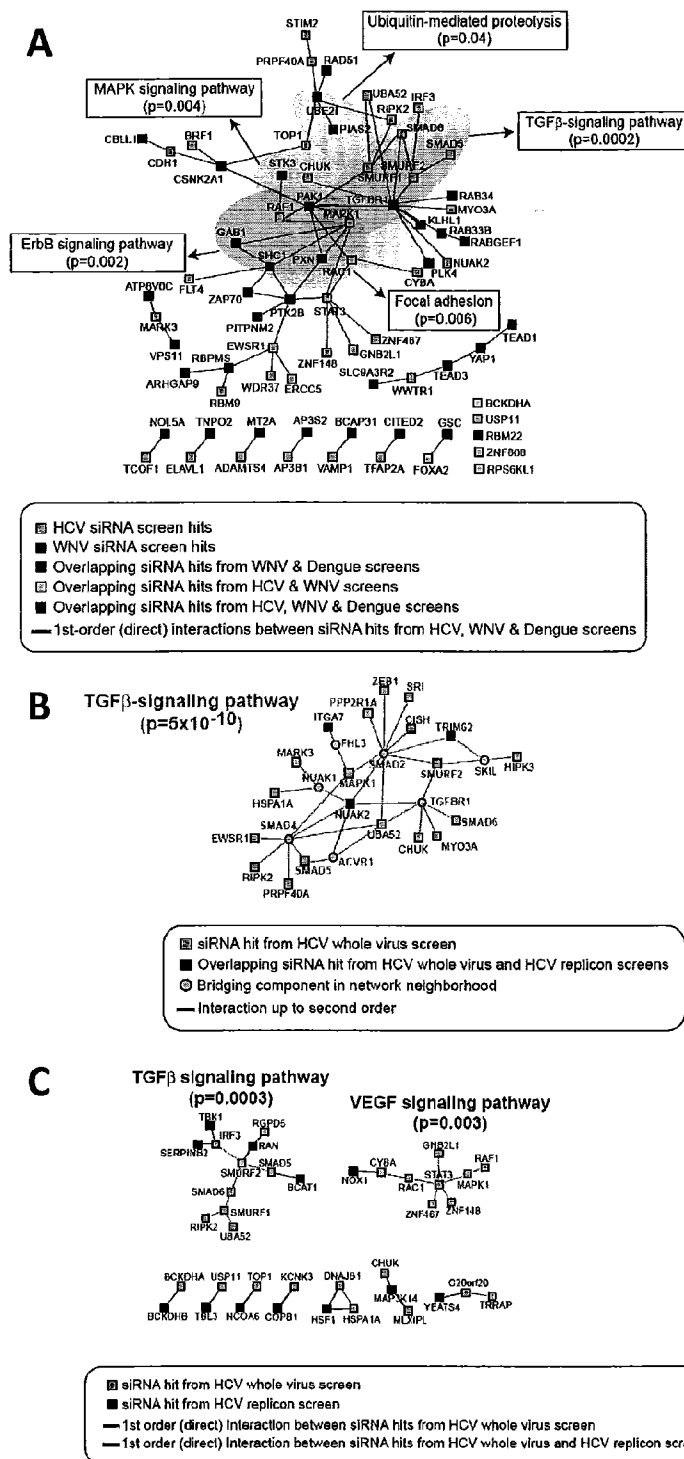


Figure 4

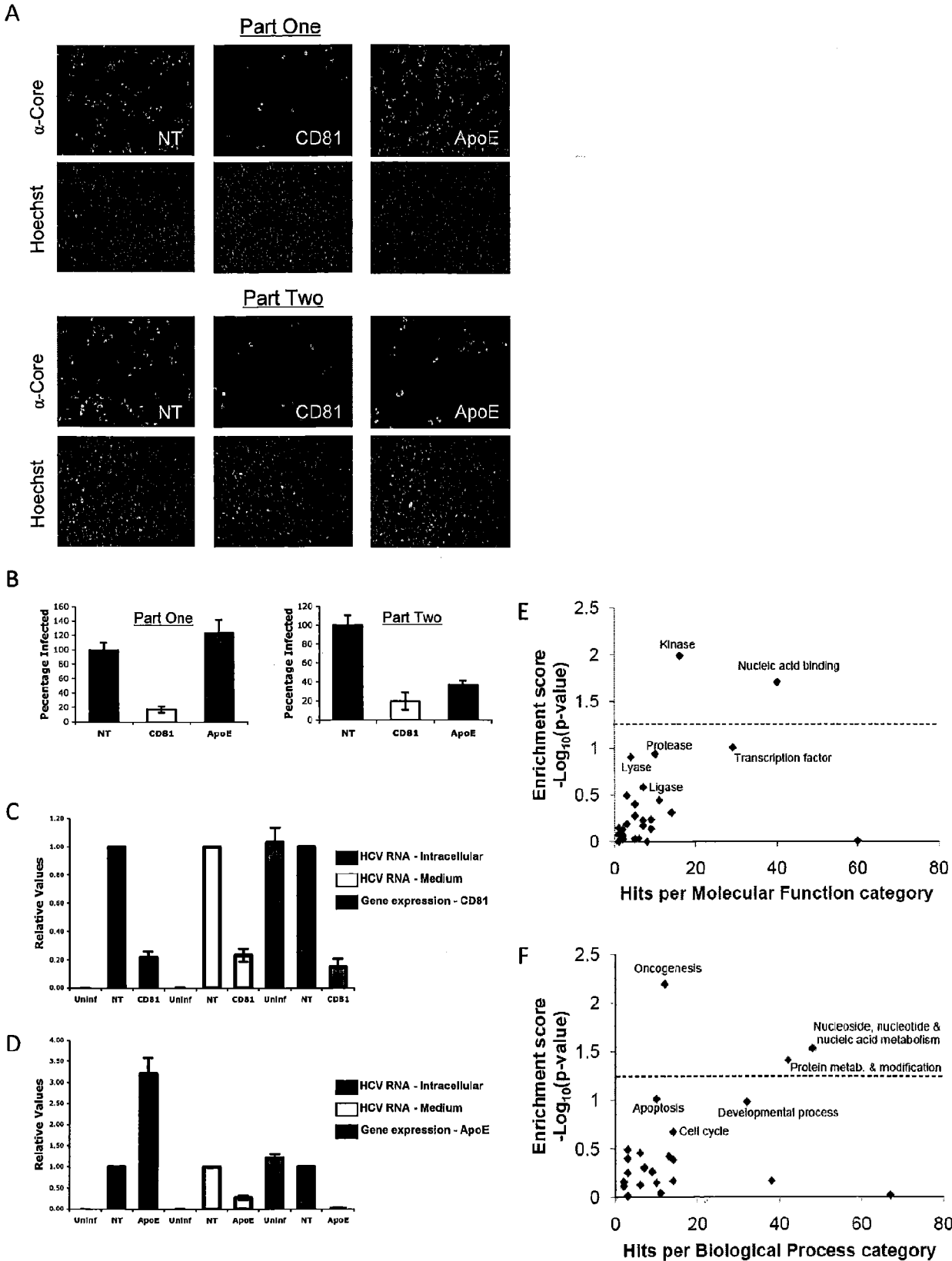
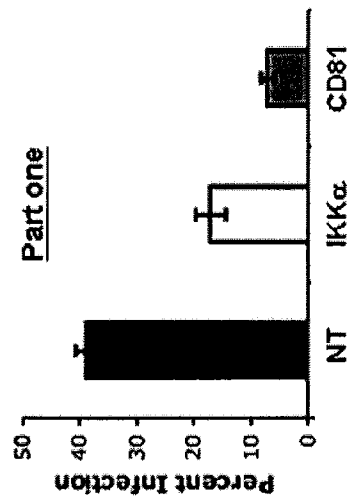


Figure S1

A



B.

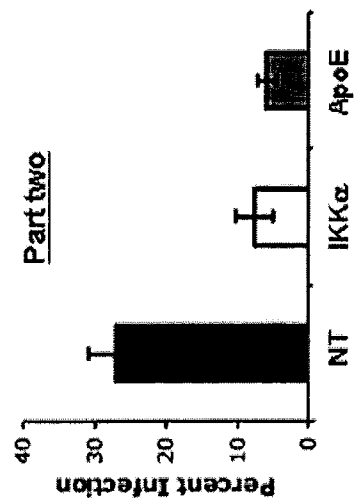


Figure 5

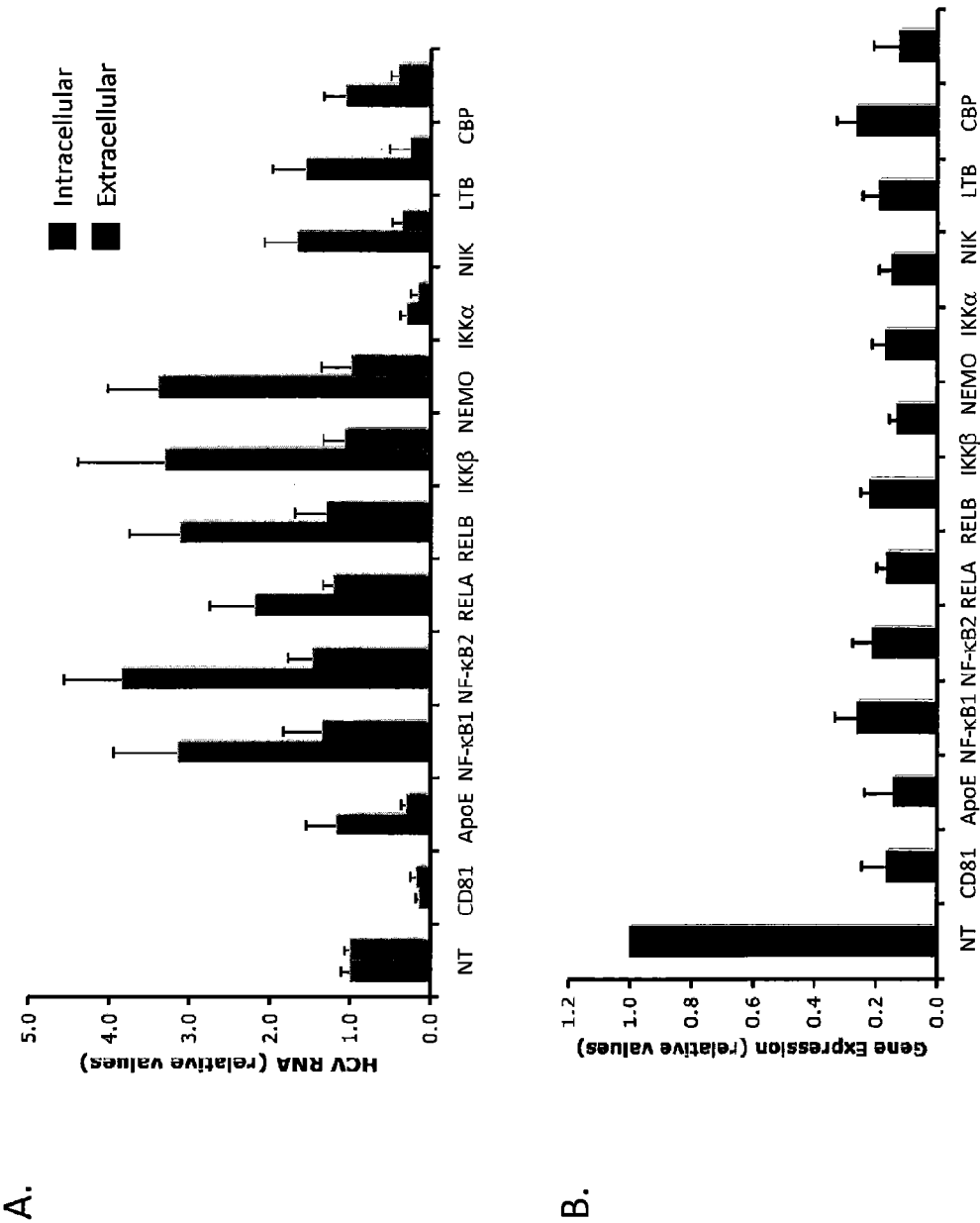


Figure 6

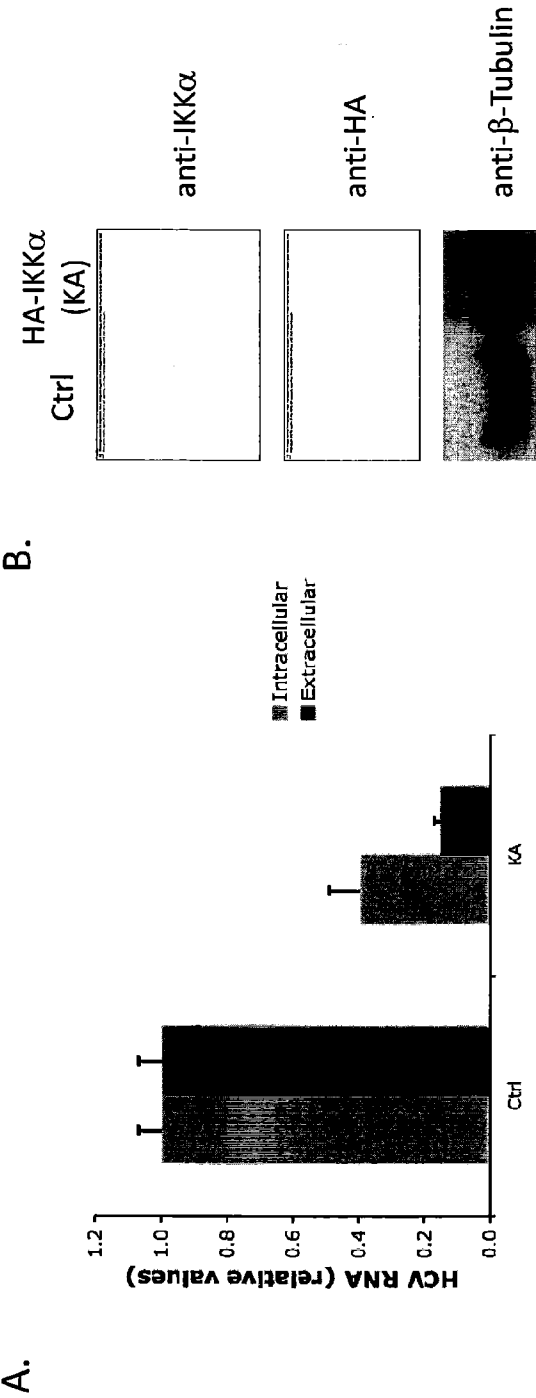


Figure 7

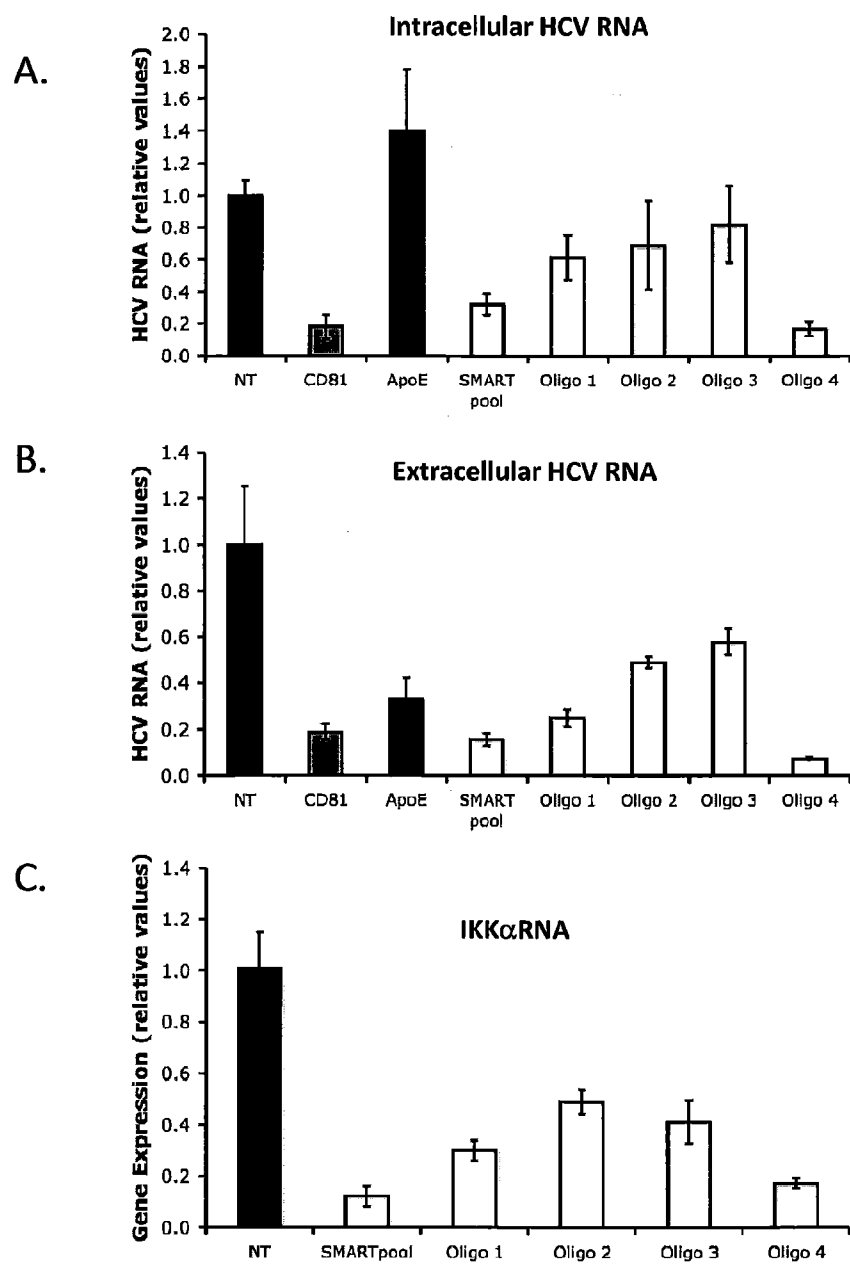


Figure 8

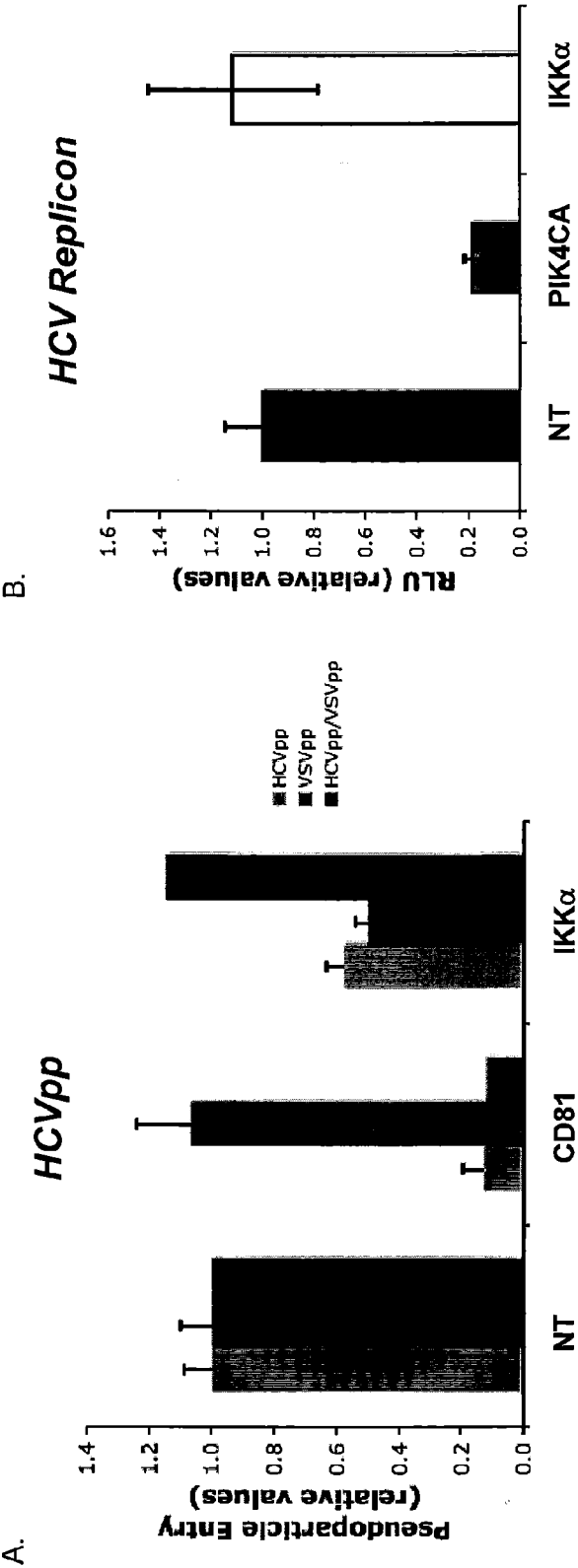


Figure 9

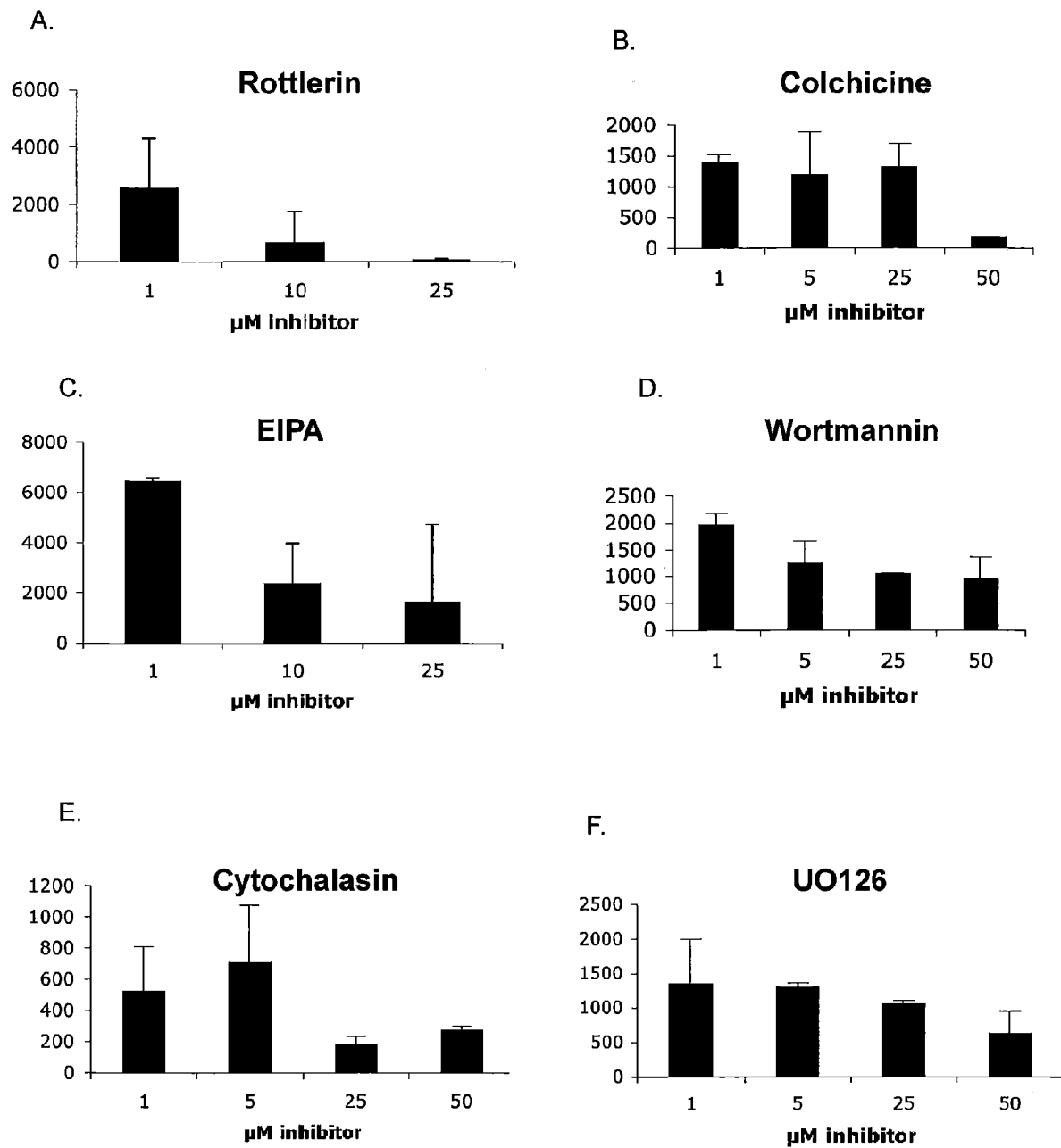


Figure 10

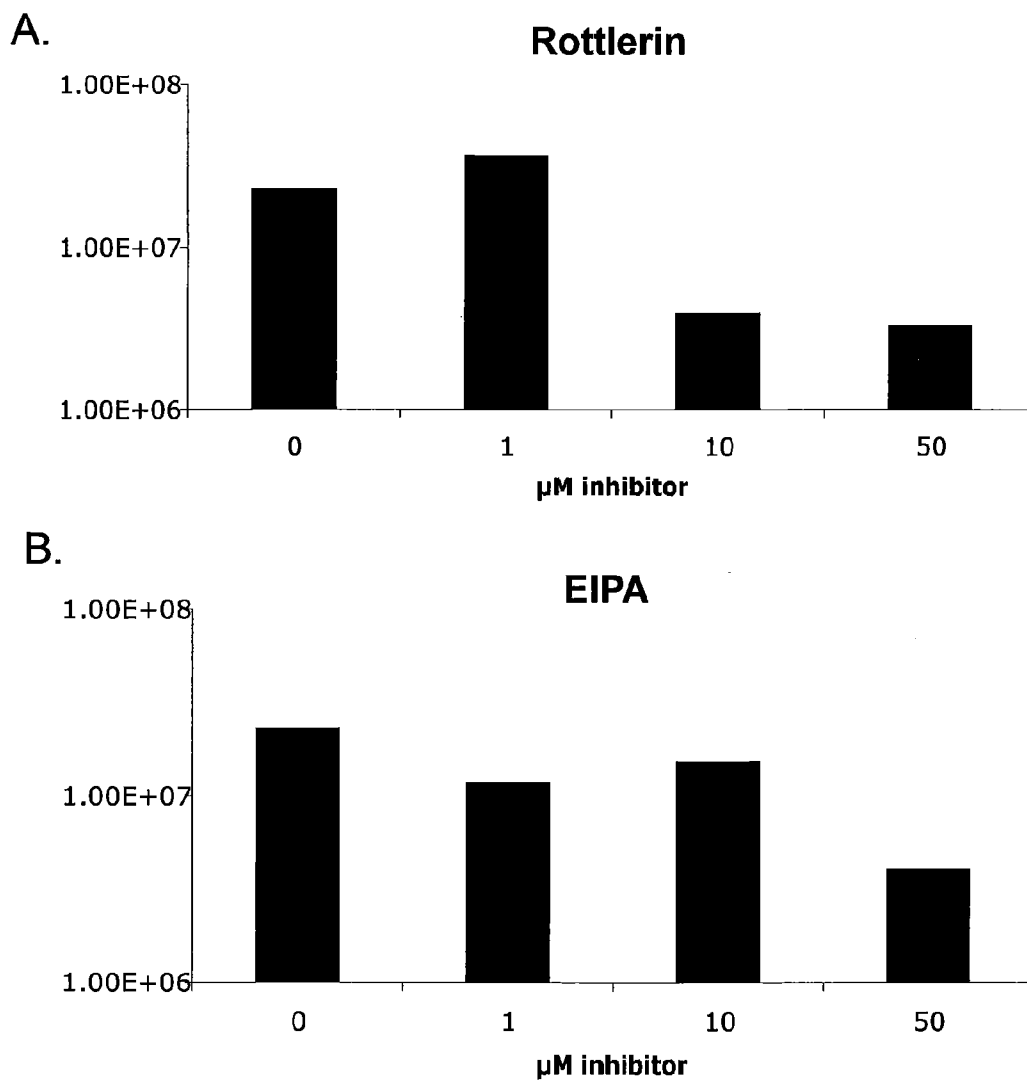


Figure 11

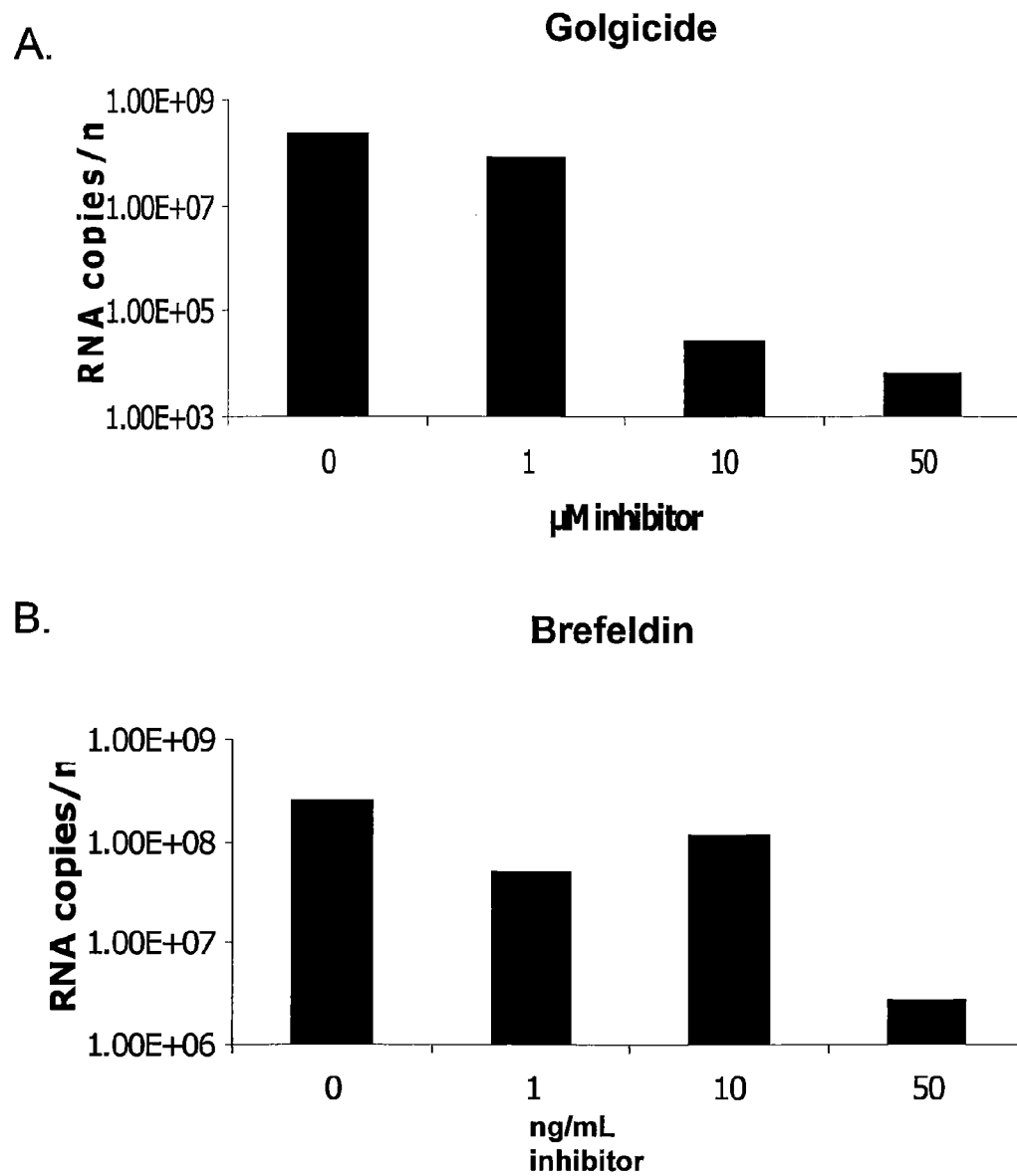


Figure 12

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 10/40918

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 31/04, 31/12, 39/395 (2010.01)

USPC - 514/740, 676, 2

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)

IPC(8): A61K 31/04, 31/12, 39/395 (2010.01)

USPC: 514/740, 676, 2

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

USPC - 514/740, 514/676, 514/2

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

PubWest, DialogPRO--Chemical Engineering and Biotechnology Abstracts, INSPEC, NTIS (National Technical Information Service), PASCAL, Current Contents Search, MEDLINE Search terms: Viral inhibition, hepatitis C, CHUK, IKK, modulate pathway, infection, therapeutic, prophylactic, inhibitory compound, colchicine

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	US 2008/0044413 A1 (Hammond, et al.) 21 February 2008 (21.02.2008), para [0021], [0032], [0033], [0086], [0202], [0274], [0275], [0298]	1-4, 7, 8, 10-15, 17, 22, 25, 26, 30, 33 ----- 16
Y	US 2008/0161324 A1 (JOHANSEN et al.) 03 July 2008 (03.07.2008) abstract, Table 4, para [0030]; [0042]	16
A	US 2005/0107386 A1 (Narla, et al.) 19 May 2005 (19.05.2005)	1-4, 7, 8, 10-17, 22, 25, 26, 30, 33

☐ Further documents are listed in the continuation of Box C.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

14 November 2010 (14.11.2010)

Date of mailing of the international search report

24 NOV 2010

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents
P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-3201

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PCT Helpdesk: 571-272-4300

PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 10/40918

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:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I: Claims 1-4, 7, 8, 10-17, 22, 25, 26, 30, and 33, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or Table 1; limited to the first factor listed in Table 5, CHUK (IKK-a).

Group II: claims 5, 6, 10, 11, 22, 27, 28, 30, and 33, directed to a method to enhance viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 5 or Table 1; limited to the first factor listed in Table 5, CHUK (IKK-a).

- Please see extra sheet for continuation -

1. ☐ 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 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.:
4. ☒ 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.:
1-4, 7, 8, 10-17, 22, 25, 26, 30, and 33, limited to the first factor in Table 5, CHUK (IKK-a).

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.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 10/40918

Continuation of Box III: Lack of Unity of Invention

Group III: claims 1, 9, and 29 directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 2; limited to the first factor listed in Table 2, ABCB6.

Group IV: claims 1, 17 and 18, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor, wherein the inhibitor comprises a small interfering RNA (siRNA) listed in Table 4; limited to the first siRNA listed in Table 4: SEQ ID NO: 790.

Group V: claims 1 and 19, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 11; limited to the first factor listed in Table 11, CD81.

Group VI: claims 1 and 20, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 12; limited to the first factor listed in Table 12, CRLF3.

Group VII: claims 1 and 21, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule listed in Table 13; limited to the first factor listed in Table 13, APOBEC2.

Group VIII: claims 1, 23, and 31, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule comprising SEQ ID NO: 79.

Group IX: claims 1, 24, and 32, directed to a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule comprising SEQ ID NO: 80.

Group X: claims 34-36, 41-45, 48, and 49, directed to a method to identify a compound that inhibits viral infection, comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to inhibit said infection, wherein said host factor is encoded by a nucleic acid molecule listed in Table 5 or Table 1; limited to the first factor listed in Table 5: CHUK (IKK-a).

Group XI: claims 37-39, 46, 47, and 50, directed to a method to identify a compound that enhances viral infection, comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to enhance said infection, wherein said host factor is encoded by a nucleic acid molecule listed in Table 5 or Table 1; limited to the first factor listed in Table 5: CHUK (IKK-a).

Group XII: claims 34 and 40, directed to a method to identify a compound that inhibits viral infection, comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to inhibit said infection, wherein said host factor is encoded by a nucleic acid molecule listed in Table 2; limited to the first factor listed in Table 2: ABCB6.

The inventions listed as Groups I - XII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The special technical feature of the claims of Groups I and III-IX is a method of inhibiting or protecting a patient from a viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule, wherein each Group is directed to a different host factor. The special technical feature of the Group II claims is a method to enhance viral infection, comprising contacting a cell with an inhibitory compound that interacts with a host factor encoded by a nucleic acid molecule. The special technical features of the claims of Groups X and XII is a method to identify a compound that inhibits viral infection, comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to inhibit said infection, wherein said host factor is encoded by a nucleic acid molecule, wherein each Group is directed to a different host factor. Additionally, the special technical feature of the Group XI claims is a method to identify a compound that enhances viral infection, comprising assaying a candidate compound for the ability to interact with a host factor in such a manner as to enhance said infection.

The only common technical element shared by the above groups is that they are related to cellular factors that modulate viral infection. Groups I and III-IX share a further common technical element of being related to administration of a compound that inhibits viral infection by modulating the activity of a pathway involving a cellular factor. These common technical elements do not represent an improvement over the prior art of US 2005/0107386 A1 to Naria et al. (see abstract, para [0113], [0117]). The cellular factors of Group II share a common technical element of being related to administration of a compound that enhances viral infection by modulating the activity of a pathway involving a cellular factor. This common technical element does not improve upon the prior art of US 2004/0126385 A1 to Biswas et al. (see para [0034], [0036], [0037]). Additionally, the claims of Groups X-XII share the common technical element of being related to methods of identifying compounds that inhibit or enhance infection by interacting with cellular factors. These common technical elements do not improve upon the prior art of Naria et al. (see para [0247]-[0256]) and Biswas (see para [0066] [0067]). Therefore, the inventions of Groups I - XII lack unity of invention under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Note: Applicants may elect for additional factors or sequences to be searched by identifying the factor and sequences specifically associated with said factor, and paying an additional invention search fee for each invention.