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(54) Title: INFLUENZA TARGETS

(57) Abstract: The present invention relates to a pharmaceutical composition comprising an inhibitor of influenza virus replication. Yet another aspect is a screening method for identification of new targets for the prevention, alleviation or/and treatment of influenza.

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Influenza Targets

Description

The present invention relates to a pharmaceutical composition comprising an inhibitor of influenza virus replication. Yet another aspect is a screening method for identification of new targets for the prevention, alleviation or/and treatment of influenza.

In view of the threatening influenza pandemic, there is an acute need to develop and make available lastingly effective drugs. In Germany alone the annual occurrence of influenza causes between 5,000 and 20,000 deaths a year (source: Robert-Koch Institute). The recurring big influenza pandemics are especially feared. The first big pandemic, the so-called "Spanish Flu", cost about 40 million lives in the years 1918-1919 including a high percentage of healthy, middle-aged people. A similar pandemic could be caused by the H5N1 influenza virus, which at the moment replicates mainly in birds, if acquired mutations enable the virus to be transmitted from person to person. The probability of a human pandemic has recently grown more acute with the spreading of bird flu (H5N1) worldwide and the infection of domestic animals. It is only a question of time until a highly pathogenic human influenza-recombinant emerges. More recently, a novel influenza virus variant has emerged, i.e. the influenza A (H1N1) 'swine flu' strain, posing an unpredictable pandemic threat. The methods available at the moment for prophylaxis or therapy of an influenza infection, such as vaccination with viral surface proteins or the use of antiviral drugs (neuraminidase inhibitors or ion channel blockers), have various disadvantages. Already at this early stage resistance is appearing against one of our most effective preparations (Tamiflu), which may make it unsuitable to contain a pandemic. A central problem in the use of vaccines and drugs against influenza is the variability of the pathogen. Up to now the development of effective vaccines has required accurate prediction of the pathogen variant. Drugs directed against viral components can rapidly lose their effectiveness because of mutations of the pathogen.

An area of research which has received little attention up to now is the identification of critical target structures in the host cell. Viruses are dependent on certain cellular proteins to be able to replicate within the host. The knowledge of such cellular factors that are essential for viral replication but dispensable (at least temporarily) for humans could lead to the development of novel drugs. Rough estimates predict about 500 genes in the human genome which are essential for viral multiplication. Of these, 10% at least are probably dispensable temporarily or even permanently for the human organism. Inhibition of these genes and their products, which in contrast to the viral targets are constant in their structure, would enable the development of a new generation of antiviral drugs in the shortest time. Inhibition of such gene products could overcome the development of viral escape mutants that are not longer sensitive to antiviral drugs.

It is the object of the present invention to provide screenings methods for compounds suitable for the prevention, alleviation or/and treatment of an influenza virus infection.

In the context of the present invention, it was surprisingly found that modulation (activation or inhibition) of particular genes leads to reduction of influenza virus replication. Tables 1, 2, 3 and 4 describe targets for the prevention, alleviation or/and treatment of an influenza virus infection.

Examples of genes which upon downregulation increase the influenza virus replication are described in Tables 1, 2, 3 and 4. Thus, by increasing expression or/and activity of these genes or/and gene products, the influenza virus replication can be reduced.

Examples of genes which upon downregulation decrease the influenza virus replication are also described in Tables 1, 2, 3 and 4. Thus, by decreasing expression or/and activity of these genes or/and gene products, the influenza virus replication can be reduced.

Subject of the present invention is thus a screening method covering different aspects related to influenza virus infection, in particular influenza virus replication. A first aspect of the present invention is a screening method for identification of a compound suitable for the prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(a) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,
(b) contacting the cell or/and the organism of (a) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the gene of (a) or/and the gene product thereof,
(c) determining the amount of influenza virus produced by the cell or/and the organism, and
(d) selecting a compound which reduces the amount of the influenza virus produced by the cell or/and the organism.

The gene of (a) may be selected from from Table 1, Table 2, Table 3 and Table 4. Preferably, the gene of (a) is selected from Table 4.

The method of the present invention may comprise a cellular screening assay. A cellular screening assay includes the determination of the activity or/and expression of a gene of (a) or/and the gene product thereof. The screening assay may be performed in vivo or/and in vitro.

Another aspect of the present invention is a screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(i) providing a cell or/and a non-human organism capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,

(ii) contacting a compound with the cell or/and the organism of (i),

(iii) determining the amount or/and the activity of gene product of the gene of (i), and

(iv) selecting a compound which modulates the amount or/and the activity of the gene product of (i).

The gene of (i) may be selected from Table 1, Table 2, Table 3 and Table 4. Preferably, the gene of (i) is selected from Table 4.

The compound of (iv) may reduce the amount of the influenza virus produced by the cell or/and the organism.

"Modulation" in the context of the present invention may be "activation" or "inhibition". Modulation of the expression of a gene may be downregulation or upregulation, in particular of transcription or/and translation. It can easily be determined by a skilled person if a gene is upregulated or downregulated. In the context of the present invention, upregulation (activation) of gene expression may be an upregulation by a factor of at least 2, preferably at least 4. Downregulation (inhibition) in the context of the present invention may be a reduction of gene expression by a factor of at least 2, preferably at least 4. Most preferred is essentially complete inhibition of gene expression, e.g. by RNA interference.

Modulation of the activity of the gene may be decrease or increase of the activity. In the context of the present invention, “activity” of the gene or/and gene product includes transcription, translation, posttranslational modification, modulation of the activity of the gene or/and gene product. The activity may be modulated by ligand binding, which ligand may be an activator or inhibitor. “Inhibition of the activity” may be a decrease of activity of a gene or gene product by a factor of at least 2, preferably at least 4. “Inhibition of the activity” includes essentially complete inhibition of activity.

“Activation of the activity” may be an increase of activity of a gene or gene product by a factor of at least 2, preferably at least 4.

The activity may also be modulated by an miRNA molecule, an shRNA molecule, an siRNA molecule, an antisense nucleic acid, a decoy nucleic acid or/and any other nucleic acid, as described herein. Modulation may also be performed by a small molecule, an antibody, an aptamer, or/and a spiegelmer (mirror image aptamer).

An activator of a gene identified by the method of the present invention may be suitable of reducing the amount of the influenza virus produced by a cell or/and an organism. In Tables 1, 2, 3 and 4, genes are described which upon inhibition (e.g. by siRNA) increase virus replication. Therefore, upon activation of these genes, virus replication may be reduced. In the tables, such genes are characterized by positive z-scores or/and by negative values of normalized percent inhibition (NPI).

An inhibitor of a gene identified by the method of the present invention is suitable of reducing the amount of the influenza virus produced by a cell or/and an organism. In Tables 1, 2, 3 and 4, genes are described which upon inhibition (e.g. by siRNA) decrease virus replication. In the tables, such genes are characterized by negative z-scores or/and by positive values of normalized percent inhibition (NPI).

Modulation may be performed by a single nucleic acid species or by a combination of nucleic acids comprising 2, 3 4, 5, 6 or even more different nucleic acid species, which may be selected from sequences of Tables 1, 2, 3, and 4 and fragments thereof. Preferred combinations are described in Table 4. It is also preferred that the combination modulates one gene, for instance selected from Tables 1, 2, 3, and 4. A combination of two nucleic acid species is preferred.

Modulation may be a knock-down performed by RNA interference. The nucleic acid or the combination of nucleic acid species may be an siRNA, which may comprise a sequence selected from the sequences of Tables 1, 2, 3, and 4 and fragments thereof. It is preferred that the combination knocks down one gene, for instance selected from Tables 1, 2, 3, and 4. A combination of two siRNA species is preferred.

In the context of the present invention, a "target" includes a nucleotide sequence in a gene or/and a genome, a nucleic acid, or/and a polypeptide which is involved in regulation of influenza virus replication in a host cell. The target may be directly or indirectly involved in regulation of influenza virus replication. In particular, a target is suitable for reduction of influenza virus replication, either by activation of the target or by inhibition of the target.

Examples of targets are genes and partial sequence of genes, such as regulatory sequences. The term “target” also includes a gene product such as RNA, in particular mRNA, tRNA, rRNA, miRNA, piRNA. A target may also include a polypeptide or/and a protein encoded by the target gene. Preferred gene products of a target gene are selected from mRNA, miRNA, polypeptide(s) and protein(s) encoded by the target gene. The most preferred gene product is a polypeptide or protein encoded by the target gene. A target protein or a target polypeptide may be posttranslationally modified or not.

"Gene product" of a gene as used herein includes RNA (in particular mRNA, tRNA, rRNA, miRNA and piRNA), a polypeptide or/and a protein encoded by said gene.

The cell employed in step (a) may be any cell capable of being infected with an influenza virus. Cell lines suitable for the production of an influenza virus are known. Preferably the cell is a mammalian cell or an avian cell. Also preferred is a human cell. Also preferred is an epithelial cell, such as a lung epithelial cell. The cell may be a cell line. A suitable lung epithelial cell line is A594. Another suitable cell is the human embryonic kidney cell line 293T. In one embodiment of the present invention, the method of the present invention employs a cell as described herein.

The non-human organism employed in step (a) may be any organism capable of being infected with an influenza virus.

The influenza virus employed in the method of the present invention may be an influenza A virus. The influenza A virus may be selected from influenza A viruses isolated so far from avian and mammalian organisms. In particular, the influenza A virus may be selected from H1N1, H1N2, H1N3, H1N4, H1N5, H1N6, H1N7, H1N9, H2N1, H2N2, H2N3, H2N4, H2N5, H2N7, H2N8, H2N9, H3N1, H3N2, H3N3, H3N4, H3N5, H3N6, H3N8, H4N1, H4N2, H4N3, H4N4, H4N5, H4N6, H4N8, H4N9, H5N1, H5N2, H5N3, H5N6, H5N7, H5N8, H5N9, H6N1, H6N2, H6N3, H6N4, H6N5, H6N6, H6N7, H6N8, H6N9, H7N1, H7N2, H7N3, H7N4, H7N5, H7N7, H7N8, H7N9, H9N1, H9N2, H9N3, H9N5, H9N6, H9N7, H9N8, H10N1, H10N3, H10N4, H10N6, H10N7, H10N8, H10N9, H11N2, H11N3, H11N6, H11N9, H12N1, H12N4, H12N5, H12N9, H13N2, H13N6, H13N8, H13N9, H14N5, H15N2, H15N8, H15N9 and H16N3. More particularly, the influenza A virus is selected from H1N1, H3N2, H7N7, H5N1. Even more particularly, the influenza A virus is strain Puerto Rico/8/34, the avian influenza virus isolate H5N1, the avian influenza strain A/FPV/Bratislava/79 (H7N7), strain A/WSN/33 (H1N1), strain A/Panama/99 (H3N2), or a swine flu strain H1N1, such as A/HH/04/2009.

The influenza virus may be an influenza B virus. In particular, the influenza B virus may be selected from representatives of the Victoria line and representatives of the Yamagata line.

The at least modulator of influenza virus replication employed in the method of the present invention of the present invention may be selected from the group consisting of nucleic acids, nucleic acid analogues such as ribozymes, peptides, polypeptides, antibodies, aptamers, spiegelmers, small molecules and decoy nucleic acids.

The modulator of influenza virus replication may be a compound having a molecular weight smaller than 1000 Dalton or smaller than 500 Dalton. In the context of the present invention, "small molecule" refers to a compound having a molecular weight smaller than 1000 Dalton or smaller than 500 Dalton.

The nucleic acid employed in the present invention may be an antisense nucleic acid or a DNA encoding the antisense nucleic acid.

The nucleic acid or/and nucleic acid fragment employed in the present invention may have a length of at least 15, preferably at least 17, more preferably at least 19, most preferably at least 21 nucleotides. The nucleic acid or/and the nucleic acid fragment may have a length of at the maximum 29, preferably at the maximum 27, more preferably at the maximum 25, especially more preferably at the maximum 23, most preferably at the maximum 22 nucleotides.

The nucleic acid employed in the present invention may be a microRNA (miRNA), a precursor, a fragment, or a derivative thereof. The miRNA may have the length of the nucleic acid as described herein. The miRNA may in particular have a length of about 22 nucleotides, more preferably 22 nucleotides.

A further aspect of the present invention is a pharmaceutical composition comprising at least one inhibitor of influenza virus replication optionally together with a pharmaceutically acceptable carrier, adjuvant, diluent or/and additive, for the prevention, alleviation or/and treatment of an influenza virus infection.

In the pharmaceutical composition of the present invention, the at least one inhibitor may be selected from the group consisting of nucleic acids, nucleic acid analogues such as ribozymes, peptides, polypeptides, and antibodies, and compounds having a molecular weight below 1000 Dalton.

The influenza virus infection may be an influenza A virus infection or an influenza B virus infection, as described herein.

The at least one inhibitor in the pharmaceutical composition of the present invention may be capable of modulating gene expression or/and gene product activity. Modulation of the expression or/and gene product activity may be activation, as described herein. Modulation of the expression or/and gene product activity may be inhibition, as described herein.

The inhibitor may be a modulator as described herein.

The pharmaceutical composition may comprise a nucleic acid being RNA or DNA. Preferably, the nucleic acid in the pharmaceutical composition is selected from

(a) RNA, analogues and derivatives thereof,
(b) DNA, analogues and derivatives thereof, and
(c) combinations of (a) and (b).

In the pharmaceutical composition of the present invention, the at least one inhibitor may comprise

(a) a nucleic acid comprising a nucleotide sequence selected from sequences of Table 1, Table 2, Table 3 and Table 4,
(b) a fragment of the sequence of (a) having a length of at least 70%, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% of the sequence of (a),
(c) a nucleic acid comprising a sequence which is at least 70 %, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% identical to the sequence of (a) or/and (b), or/and
(d) a sequence complementary to the sequence of (a), (b) or/and (c).

In the pharmaceutical composition, the nucleic acid of (a) preferably comprises a nucleotide sequence selected from the sequences of Table 4 and fragments thereof.

Suitable inhibitors of influenza virus replication in the pharmaceutical composition of the present invention are RNA molecules capable of RNA interference. The nucleic acid in the pharmaceutical composition of the present invention may comprise

- (i) an RNA molecule capable of RNA interference, such as siRNA or/and shRNA,
- (ii) a miRNA,
- (iii) a precursor of the RNA molecule (i) or/and (ii),
- (iv) a fragment of the RNA molecule (i), (ii) or/and (iii),
- (v) a derivative of the RNA molecule of (i), (ii) (iii) or/and (iv), or/and
- (vi) a DNA molecule encoding the RNA molecule of (i), (ii) (iii) or/and (iv).

A preferred nucleic acid is

- (i) a miRNA,
- (ii) a precursor of the RNA molecule (i), or/and
- (iii) a DNA molecule encoding the RNA molecule (i) or/and the precursor (ii).

Yet another preferred nucleic acid is

- (i) an RNA molecule capable of RNA interference, such as siRNA or/and shRNA,
- (ii) a precursor of the RNA molecule (i), or/and
- (iii) a DNA molecule encoding the RNA molecule (i) or/and the precursor (ii).

RNA molecules capable of RNA interference are described in WO 02/44321 the disclosure of which is included herein by reference. MicroRNAs are described in Bartel D (Cell 136:215-233, 2009), the disclosure of which is included herein by reference.

The RNA molecule of the present invention may be a double-stranded RNA molecule, preferably a double-stranded siRNA molecule with or without a single-stranded overhang alone at one end or at both ends. The siRNA molecule may comprise at least one nucleotide analogue or/and deoxyribonucleotide.

The RNA molecule of the present invention may be an shRNA molecule. The shRNA molecule may comprise at least one nucleotide analogue or/and deoxyribonucleotide.

In the pharmaceutical composition of the present invention the nucleic acid may be an antisense nucleic acid or a DNA encoding the antisense nucleic acid.

In the pharmaceutical composition of the present invention, the nucleic acid may have a length of at least 15, preferably at least 17, more preferably at least 19, most preferably at least 21 nucleotides. In the pharmaceutical composition of the present invention the nucleic acid may have a length of at the maximum 29, preferably at the maximum 27, more preferably at the maximum 25, especially more preferably at the maximum 23, most preferably at the maximum 21 nucleotides.

The pharmaceutical composition of the present invention may comprise an antibody. Preferably the antibody is directed against a polypeptide comprising

(a) an amino acid sequence encoded by a nucleic acid or/and gene selected from sequences of Table 1, Table 2, Table 3, and Table 4 and complementary sequences thereof,

(b) a fragment of the sequence of (a) having a length of at least 70%, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% of the sequence of (a), or/and

(c) an amino acid sequence comprising a sequence which is at least 70

%, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% identical to the sequence of (a) or/and (b).

Preferably, the pharmaceutical composition comprises a polypeptide of (a) comprising an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 4.

The antibody of the present invention may be a monoclonal or polyclonal antibody, a chimeric antibody, a chimeric single chain antibody, a Fab fragment or a fragment produced by a Fab expression library.

Techniques of preparing antibodies of the present invention are known by a skilled person. Monoclonal antibodies may be prepared by the human B-cell hybridoma technique or by the EBV-hybridoma technique (Köhler et al., 1975, Nature 256:495-497, Kozbor et al., 1985, J. Immunol. Methods 81,31-42, Cote et al., PNAS, 80:2026-2030, Cole et al., 1984, Mol. Cell Biol. 62:109-120). Chimeric antibodies (mouse/human) may be prepared by carrying out the methods of Morrison et al. (1984, PNAS, 81:6851-6855), Neuberger et al. (1984, 312:604-608) and Takeda et al. (1985, Nature 314:452-454). Single chain antibodies may be prepared by techniques known by a person skilled in the art.

Recombinant immunoglobulin libraries (Orlandi et al, 1989, PNAS 86:3833-3837, Winter et al., 1991, Nature 349:293-299) may be screened to obtain an antibody of the present invention. A random combinatory immunoglobulin library (Burton, 1991, PNAS, 88:11120-11123) may be used to generate an antibody with a related specifity having a different idiotypic composition.

Another strategy for antibody production is the in vivo stimulation of the lymphocyte population.

Furthermore, antibody fragments (containing $F(ab')_2$ fragments) of the present invention can be prepared by protease digestion of an antibody, e.g.

by pepsin. Reducing the disulfide bonding of such F(ab')$_2$ fragments results in the Fab fragments. In another approach, the Fab fragment may be directly obtained from an Fab expression library (Huse et al., 1989, Science 254:1275-1281).

Polyclonal antibodies of the present invention may be prepared employing an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1, Table 2, Table 3 and Table 4 or immunogenic fragments thereof as antigen by standard immunization protocols of a host, e.g. a horse, a goat, a rabbit, a human, etc., which standard immunization protocols are known by a person skilled in the art.

The antibody may be an antibody specific for a gene product of a target gene, in particular an antibody specific for a polypeptide or protein encoded by a target gene.

Aptamers and spiegelmers share binding properties with antibodies. Aptamers and spiegelmers are designed for specifically binding a target molecule.

The nucleic acid or the present invention may be selected from (a) aptamers, (b) DNA molecules encoding an aptamer, and (c) spiegelmers.

The skilled person knows aptamers. In the present invention, an “aptamer” may be a nucleic acid that can bind to a target molecule. Aptamers can be identified in combinational nucleic acid libraries (e.g. comprising $>10^{15}$ different nucleic acid sequences) by binding to the immobilized target molecule and subsequent identification of the nucleic acid sequence. This selection procedure may be repeated one or more times in order to improve the specificity. The person skilled in the art knows suitable methods for producing an aptamer specifically binding a predetermined molecule. The aptamer may have a length of a nucleic acid as described herein. The aptamer may have a length of up to 300, up to 200, up to 100, or up to 50 nucleotides. The aptamer may have a length of at least 10, at least 15, or at least 20 nucleotides. The aptamer may be encoded by a DNA molecule. The aptamer may comprise at least one nucleotide analogue or/and at least one nucleotide derivatives, as described herein.

The skilled person knows spiegelmers. In the present invention, a “spiegelmer” may be a nucleic acid that can bind to a target molecule. The person skilled in the art knows suitable methods for production of a spiegelmer specifically binding a predetermined molecule. The spiegelmer comprises nucleotides capable of forming bindings which are nuclease resistant. Preferably the spiegelmer comprises L nucleotides. More preferably, the spiegelmer is an L-oligonucleotide. The spiegelmer may have a length of a nucleic acid as described herein. The spiegelmer may have a length of up to 300, up to 200, up to 100, or up to 50 nucleotides. The spiegelmer may have a length of at least 10, at least 15, or at least 20 nucleotides. The spiegelmer may comprise at least one nucleotide analogue or/and at least one nucleotide derivatives, as described herein.

The skilled person knows decoy nucleic acids. In the present invention, a “decoy” or “decoy nucleic acid” may be a nucleic acid capable of specifically binding a nucleic acid binding protein, such as a DNA binding protein. The decoy nucleic acid may be a DNA molecule, preferably a double stranded DNA molecule. The decoy nucleic acid comprises a sequence termed “recognition sequence” which can be recognized by a nucleic acid binding protein. The recognition sequence preferably has a length of at least 3, at least 5, or at least 10 nucleotides. The recognition sequence preferably has a length of up to 15, up to 20, or up to 25 nucleotides. Examples of nucleic acid binding proteins are transcription factors, which preferably bind double stranded DNA molecules. Transfection of a cell, an embryonated egg, or/and a non-human animal, as described herein, with a decoy nucleic acid may result in reduction of the activity of the nucleic acid binding protein to which the decoy nucleic acid binds. The decoy nucleic acid as described herein may have a length of nucleic acid molecules as described herein. The decoy nucleic acid molecule may have a length of up to 300, up to 200, up to 100, up to 50, up to 40, or up to 30 nucleotides. The decoy nucleic may have a length of at least 3, at least 5, at least 10, at least 15, or at least 20 nucleotides. The decoy nucleic acid may be encoded by a DNA molecule. The decoy nucleic acid may comprise at least one nucleotide analogue or/and at least one nucleotide derivatives, as described herein.

The pharmaceutical composition as described herein is preferably for use in human or veterinary medicine.

The pharmaceutical composition of any of the preceding claims further comprises an agent suitable of transportation of the at least inhibitor of influenza virus infection into a cell, in particular into a lung epithelial cell.

The carrier in the pharmaceutical composition may comprise a delivery system. The person skilled in the art knows delivery systems suitable for the pharmaceutical composition of the present invention. The pharmaceutical composition may be delivered in the form of a naked nucleic acid, in combination with viral vectors, non viral vectors including liposomes, nanoparticles or/and polymers. The pharmaceutical composition or/and the nucleic acid may be delivered by electroporation.

Naked nucleic acids include RNA, modified RNA, DNA, modified DNA, RNA-DNA-hybrids, aptamer fusions, plasmid DNA, minicircles, transposons.

Viral vectors include poxviruses, adenoviruses, adeno-associated viruses, vesicular stomatitis viruses, alphaviruses, measles viruses, polioviruses, hepatitis B viruses, retroviruses, and lentiviruses.

Liposomes include stable nucleic acid-lipid particles (SNALP), cationic liposomes, cationic cardiolipin analogue-based liposomes, neutral liposomes, liposome-polycation-DNA, cationic immunoliposomes, immunoliposomes, liposomes containing lipophilic derivatives of cholesterol, lauric acid and lithocholic acid. Examples of compounds suitable for liposome formation are 1,2-dilauroyl-sn-glycero-3-phosphoethanolamine (DLPE); 1,2-dioleoyl-sn-glycero-3-phospho-L-serine (DOPS); cholesterol (CHOL); 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC).

Nanoparticles include $CaCO_3$ nanoparticles, chitosan-coated nanoparticle, folated lipid nanoparticle, nanosized nucleic acid carriers.

Polymers include polyethylenimines (PEI), polyester amines (PEA), polyethyleneglycol(PEG)-oligoconjugates, PEG liposomes, polymeric nanospheres.

The pharmaceutical composition may be delivered in combination with atelocollagen, carbon nanotubes, cyclodextrin-containing polycations, fusion proteins (e.g. protamine-antibody conjugates).

An RNA or/and a DNA molecule as described herein may comprise at least one nucleotide analogue. As used herein, “nucleotide analogue” may refer to building blocks suitable for a modification in the backbone, at least one ribose, at least one base, the 3' end or/and the 5' end in the nucleic acid. Backbone modifications include phosphorothioate linkage (PTs); peptide nucleic acids (PNAs); morpholino nucleic acids; phosphoroamidate-linked DNAs (PAs), which contain backbone nitrogen. Ribose modifications include Locked nucleic acids (LNA) e.g. with methylene bridge joining the 2' oxygen of ribose with the 4' carbon; 2’-deoxy-2’-fluorouridine; 2’-fluoro (2’-F); 2’-O-alkyl-RNAs (2-O-RNAs), e.g. 2’-O-methyl (2’-O-Me), 2’-O-methoxyethyl (2'-O-MOE). A modified base may be 2’-fluoropyrimidine. 5’ modifications include 5'-TAMRA-hexyl linker, 5'-Phosphate, 5'-Amino, 5'-Amino-C6 linker, 5'-Biotin, 5'-Fluorescein, 5'-Tetrachloro-fluorescein, 5'-Pyrene, 5'-Thiol, 5'-Amino, (12 Carbon) linker, 5'-Dabcyl, 5'-Cholesterol, 5'-DY547 (Cy3™ alternate). 3’ end modifications include 3'-inverted deoxythymidine, 3'-puromycin, 3’-dideoxy-cytidine, 3'-cholesterol, 3'-amino modifier (6 atom), 3'-DY547 (Cy3™ alternate).

In particular, nucleotide analogues as described herein are suitable building blocks in siRNA, antisense RNA, and aptamers.

As used herein, “nucleic acid analogue” refers to nucleic acids comprising at least one nucleotide analogue as described herein. Further, a nucleic acid molecule as described herein may comprise at least one deoxyribonucleotide and at least one ribonucleotide.

An RNA molecule of the present invention may comprise at least one deoxyribonucleotide or/and at least one nucleotide analogue. A DNA molecule of the present invention may comprise at least one ribonucleotide or/and at least one nucleotide analogue.

Derivatives as described herein refers to chemically modified compounds. Derivatives of nucleic acid molecules as described herein refers to nucleic acid molecules which are chemically modified. A modification may be introduced into the nucleic acid molecule, or/and into at least one nucleic acid building block employed in the production of the nucleic acid.

In the present invention the term “fragment” refers to fragments of nucleic acids, polypeptides and proteins. “Fragment” also refers to partial sequences of nucleic acids, polypeptides and proteins.

Fragments of polypeptides or/and peptides as employed in the present invention, in particular fragments of an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 1, Table 2, Table 3 and Table 4 may have a length of at least 5 amino acid residues, at least 10, or at least 20 amino acid residues. The length of said fragments may be 200 amino acid residues at the maximum, 100 amino acid residues at the maximum, 60 amino acid residues at the maximum, or 40 amino acid residues at the maximum.

A fragment of an amino acid sequence as described herein may have a length of at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, at least 99% of the sequence.

A fragment of a nucleotide sequence as described herein may have a length of at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, at least 99% of the sequence.

A fragment of a nucleic acid molecule given in Tables 1, 2, 3, and 4 may have a length of up to 1000, up to 2000, or up to 3000 nucleotides. A nucleic acid fragment may have a length of an siRNA molecule, an miRNA molecule, an aptamer, a spiegelmer, or/and a decoy as described herein. A nucleic acid fragment may also have a length of up to 300, up to 200, up to 100, or up to 50 nucleotides. A nucleic acid fragment may also have a length of at least 3, at least 5, at least 10, at least 15, or at least 20 nucleotides.

In the present invention, specific embodiments refer to any individual gene, nucleic acid sequence or/and gene product described in the present application. In a specific embodiment, an individual gene is selected from the genes described in Table 1, Table 2, Table 3, and Table 4. In another specific embodiment, an individual gene product is selected from the gene products produced by the genes described in Table 1, Table 2, Table 3, and Table 4. In yet another specific embodiment, an individual nucleic acid sequence is selected from the nucleic acid molecules described in Table 1, 2, 3 and 4. Further specific embodiment refer to any combination of genes, gene products and nucleic acid molecules described in the Tables 1, 2, 3, and 4.

In the present invention, a reference to Table 4 is a reference to a target, gene or/and nucleotide sequence selected from ACTN1, ATP6AP2, ATP6V1B2, BNIP3L, BRUNOL6, CUEDC2, CYC1, FNTB, GCLC, GNRH2, GRIN2C, GRP, HARBI1, HSPD1, ICAM2, KCNJ12, KPNB1, LAMC2,

LOC440733, MKL1, MRPS12, MYEF2, NDUFV3, NECAP2, ODZ4, PIK3R6, PPARA, RAB4A, SCAF1, SCARB1, SERPINA6, SERPINB2, SERPINE2, SEZ6L2, TBL3, TRERF1, TRIM60, and TUBB4.

In the present invention, a reference to Table 4 may also be a reference to a target gene or/and nucleotide sequence selected from ACTN1, BNIP3L, BRUNOL6, CUEDC2, CYC1, GCLC, GNRH2, GRIN2C, GRP, HARBI1, HSPD1, ICAM2, KCNJ12, LAMC2, LOC440733, MKL1, MRPS12, MYEF2, NDUFV3, NECAP2, ODZ4, PIK3R6, PPARA, RAB4A, SCAF1, SCARB1, SERPINA6, SERPINB2, SERPINE2, SEZ6L2, TBL3, TRERF1, TRIM60, and TUBB4.

Yet another aspect of the present invention is the use of an inhibitor of influenza virus replication capable of inhibiting or activating the expression of a gene selected from Table 1, Table 2, Table 3 and Table 4, or/and of inhibiting or activating a gene product thereof, for the manufacture of a medicament or/and vaccine for the prevention, alleviation or/and treatment of an influenza virus infection. Preferably, the gene is selected from Table 4. Preferably, those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in decrease of virus production are activated, wherein those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in increase of virus production are inhibited.

In the context of the present invention, "manufacture of a medicament or/and vaccine" includes the production of influenza virus, wherein the amount of influenza virus is increased by activating or inhibiting a gene selected from Tables 1, 2, 3 and 4, preferably Table 4. Preferably, those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in decrease of virus production are activated, wherein those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in increase of virus production are inhibited in the production of the medicament or/and vaccine.

Yet another aspect of the present invention is method for production of an influenza virus, wherein the amount of influenza virus is increased by activating or inhibiting a gene selected from Tables 1, 2, 3 and 4, preferably Table 4. Preferably, those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in decrease of virus production are activated, wherein those genes which upon inhibition by e.g. siRNA, as disclosed herein, result in increase of virus production are inhibited in the production of the influenza virus. In the method for production of an influenza virus, at least one gene selected from Tables 1, 2, 3 and 4, preferably Table 4, may be overexpressed if activation leads to an increased virus production.

Suitable methods for the production of influenza viruses, for instance in embryonated eggs or/and cell culture, are known in the state of the art.

Yet another aspect of the present invention is a method of prevention, alleviation or/and treatment of an influenza virus infection, comprising administering to a subject in need thereof a therapeutically effective amount of an inhibitor of influenza virus replication, as described herein. In the method of prevention, alleviation or/and treatment of an influenza virus infection, delivery systems and delivery methods as described herein may be used.

Yet another aspect of the present invention is the use of a nucleic acid comprising a gene sequence or/and a nucleotide sequence selected from Table 1, Table 2, Table 3, and Table 4 and fragments thereof in a method for screening for compounds or/and targets suitable for the prevention, alleviation or/and treatment of an influenza virus infection. Preferably a combination of at least two nucleic acids is used. It is also preferred that the nucleic acid or the combination is selected from Table 4. The combination may inhibit expression or/and activity of a gene, preferably selected from Tables 1, 2, 3 and 4, more preferably selected from Table 4.

The invention is further illustrated by the following figures, tables and examples.

Figure and Table legends:

Figure 1 | Genome-wide RNAi screen reveals host factors required for the influenza infectious cycle. a, Outline of the screening procedures. b, Negative Log(p-values) of enriched terms according to the GO of the cellular compartments. Numbers of identified factors per ontology, numbers of genes associated with the GO term, and the enrichment factors are indicated. c, Interaction amongst hits associated with RNA splicing, as assessed using the STRING interaction database. Green circles, primary hit; white circle, non-hit. Members of ribosomal and spliceosomal multi-protein complexes are enclosed in larger circles. Thick grey border indicates hits identified in Reactome analysis (see Fig. 10).

Figure 2 | Host cell factors affect replication of a broad range of influenza virus variants. a, Four siRNAs per gene were individually transfected in A549 cells followed by infection with influenza A/WSN/33 or A/Hamburg/04/2009 viruses (both at MOI 0.001) in four independent experiments. Infectious viral particles (IVP) were quantified at 48 h p.i. using the replication assay and analysed by calculating the normalised percent of inhibition. **b**, Venn diagram of hits validated in **a**. **c**, siRNAs (as indicated) were transfected in A549 cells and then infected (48 h later) with the avian H5N1 strain (A/Vietnam/1203/2004, MOI 0.1). Plaque forming units (PFU) were quantified at 20 h p.i. using the replication assay. Data show mean + standard error of the mean (S.E.M) of duplicate samples.

Figure 3 | Dissection of infection processes affected by host cell factors. a, Transfected A549 cells were infected with influenza A/WSN/33 virus (MOI 5) for 3 h (upper panel) and 5 h (lower panel). Samples were stained for nuclei (blue) and NP (green). **b,** At 48 h p.t., A549 cells were infected with influenza A/WSN/33 virus (MOI 1). At 2 h p.i., vRNA and viral mRNA were quantified by qRT-PCR. RNA levels were normalised to the non-targeting (Allstars) siRNA control. **c,** Transfected A549 cells were infected with influenza A/WSN/33 virus (MOI 10) for 45 min. Samples were stained for influenza virus (green) and CD63 (red). Images are representative of three independent experiments in **a** and **c**.

Figure 4 | In-depth analysis of the impact of p27 and CLK1 on influenza A virus infection. a, Quantification of virus replication in primary NHBE cells after siRNA-mediated target knockdown using the replication assay. Cells were infected with influenza A/WSN/33 virus (MOI 0.1) 48 h p.t. **b**, A549 cells were pretreated with TG003 (50 µM) or DMSO for 24 h and subsequently infected with influenza A/WSN/33 virus (MOI 0.01). IVPs were quantified at 40 h p.i.. **c, d**, Ratio of spliced M2 to unspliced M1 after inhibition of CLK1 by TG003 at the RNA **(c)** or protein level **(d)**. A549 cells were pretreated for 2 h or 24 h with TG003 (50 µM) or DMSO, then infected with influenza A/WSN/33 virus (MOI 4) for 5 h. **e,** C57BL/6 wild-type or homozygous $p27^{-/-}$ mice (n=4) were intranasally infected with influenza A/Puerto Rico/8/34 virus (10× LD50) and at 48 h p.i. IVPs within the lungs were quantified. Student's *t-test* was used to determine p value, * $p = 0.041$. Data in **a,b** are mean + standard deviation (SD) of three independent experiments. Blots in **c,d** are representative of three independent experiments.

Figure 5 | Screening Controls. Depicted are representative images of the non-targeting (Allstars) and inhibitory (siNP) control samples, stained with an anti-NP antibody and analysed by automatic microscopy. **c,** Graph depicts light units exerted by the corresponding supernatants transferred onto 293T reporter cells.

Figure 6 | Relative frequency distribution of screening data. Shown are data gained from the luciferase reporter assay (left panel), percentage of infected cells (middle panel), and the number of infected cells (right panel) across all screening samples and controls. All data are normalised to the plate median.

Figure 7 | Histogram of Pearson's correlation coefficients calculated for all siRNA screening plates. Distribution of pairwise correlations for the normalised values of number of infected cells derived from all siRNA screening plates. Blue lines indicates all plates, red line indicates sets of replicates. Only values originating from sample wells were used for calculating the correlation coefficients. Control well values were excluded from this analysis.

Figure 8 | Workflow of RNAi screen data analysis. Data analysis procedures (left panel) and associated applied thresholds (right panel) are shown. Raw screening data from from all three read-out parameters was subjected to an analysis pipeline incorporating statistical thresholds at each stage. The data analysis workflow was done separately for all three read-outs and the final hit lists of each one were combined to provide a definitive primary hit list of 287 factors.

Figure 9 | Gene enrichment analysis. Negative Log10(p-values) of enriched terms according to the gene ontology of the molecular function, biological process, and cellular compartments. Values at bars indicate the number of identified factors per ontology, the number of genes associated with the term and the enrichment factor.

Figure 10 | Reactome analysis. The 287 'high-confidence' hits identified in the primary screen, were analyzed using the online web-resource Reactome http://www.reactome.org), a database of biological pathways in human cells. Each pathway is referred to as an event. The hits were uploaded as gene-identifiers using the 'sky-painter' tool, calculating a one-tailed Fisher's exact test for the probability of observing at least N genes from an event. 104 identifiers could be matched to 399 out of 4374 events. Several categories showed a significant overrepresentation such as Gene Expression (p=3.4e-07, 29/384), Transcription (p=1.1e-03, 14/198), Membrane Trafficking (2.5e-03, 6/50) or Influenza- (1.9e-04, 15/187) and HIV- infection (2.5e-01, 14/406). Single events are coloured according to the number of matching identifiers from blue (1 matching identifier) to red (12 matching identifiers). Prominent categories showing overrepresentation of hits were coloured and important events were marked using an arrow. Several events were further analysed using the STRING database. (Figure 11)

Figure 11 | Interaction networks of the identified hits. Interactions amongst hits associated with vacuolar ATPases, nuclear transport, coat complex formation and translation, as assessed using the STRING interaction database (http://string.embl.de). Green circles, primary hit; dark green circles, primary hit also identified by a *Drosophila*-based influenza screen (13). All hits included in one large circle: members of one multi-protein complex, e.g. 40S ribosomal subunit. Hits with a thick grey border are also included in the Reactome pathway analysis (Figure 10).

Figure 12 | Host cell viability determination by WST-1 assay. A549 cells were transfected with indicated siRNAs followed by adding the WST-1 reagent 48h later to analyse eventually toxic effects due to siRNA transfections. Background subtracted mean values from two replicates are illustrated as a heat map. An siRNA targeting PLK1 was used as positive control. Missing siRNAs (less than four per gene) are indicated by grey boxes.

Figure 13 | Host cell factors affect replication of a H1N1 influenza virus variants. A subset of siRNAs was again transfected in A549 cells that were infected (48 h later) with the A/WSN/33 (**a**) or A/Hamburg/04/2009 (**b**) virus strains. IVPs in the virus containing supernatants were determined using the replication assay. Infection rate is expressed as a percentage of the non-targeting (Allstars) transfected control. Data show mean + S.E.M of duplicate samples. Cells transfected with the non-targeting control (Allstars) exhibited ca. 1.8×10^6 IVP/ml in the supernatant of A/WSN/33 infected and $6.6. \times 10^3$ IVP/ml upon A/Hamburg/04/2009 (A/H/04/09) virus infection. The inhibitory NP siRNA reduced the amount of infectious particles to $2.6. \times 10^4$ IVP/ml (A/WSN/33) and $4.5. \times 10^2$ IVP/ml (A/Hamburg/04/2009), respectively.

Figure 14 | Relative frequency distributions of NP expression. Relative frequency distributions of mean values of nuclear NP 3 h p.i.. Shown are values gained from two separate wells of the Allstars (Allstars W1 and W2) and NP (siNP W1 and W2) control as well as two independent siRNAs for the indicated target genes. Results are representative profiles of three independent experiments.

Figure 15 | Relative frequency distributions of nuclear export of NP. Relative frequency distributions of the ratios of cytosolic to nuclear NP 5 h p.i. Shown are values gained from two separate wells of the Allstars (Allstars W1 and W2) and NP (siNP W1 and W2) control as well as two independent siRNAs for the indicated target genes. Results are representative profiles of three independent experiments.

Figure 16 | P-values of differences between relative frequency distributions. Negative Log10(p-values) of the samples shown in Figures 14 and 15 as assessed by the one-sided Kolmogorov-Smirnov test.

Figure 17 | Quantification of co-localised virus particles. SON knockdown and control cells were infected with influenza A virus (A/WSN/33) for 45 min at 37 °C after incubation on ice. Cells were fixed and stained for influenza A virus and CD63 as described. Confocal pictures were taken and co-localisation was determined as described in Methods. Total numbers of viral particles and co-localised particles were quantified using ImageJ "Analyse particle" function. In total 34 cells were quantified for each condition. Diagram shows mean numbers of particles for two independent experiments. Control, black bars; Son knockdown, hatched bars; ** < 0.005; standard error of the mean (S.E.) is depicted.

Figure 18 | Influence of the chemical CLK1 inhibitor TG003 on cell viability. A549 cells were incubated with TG003 (50 µM, dissolved in DMSO), with DMSO or left untreated. Cell viability was evaluated at the indicated time points using the WST-1 assay, according to the manufacturer's instructions. Shown are the mean values from three replicates. Error bars indicate the standard deviation.

Figure 19 | Influence of the chemical CLK1 inhibitor TG003 on VSV replication. A549 cells were pretreated with TG003 (50 µM, dissolved in DMSO) or DMSO (as a control), for 24 h and subsequently infected with VSV (MOI 0.01). After infection, the inhibitor or DMSO was added again at identical concentrations. The supernatants of treated or untreated cells were harvested at 24 h p.i. and infectious virus particles quantified by detecting plaques on MDCK cells.

Table 1 | Primary screening data and hit. Primary hit list and screening data. Shown are the Z-scores obtained from the CellHTS and the Genedata Screener® software analysis, and the RSA analysis for the classification of a particular siRNA as a hit. The mean cell number as an indicator for cell viability is shown. siRNAs leading to a mean cell number below 750 were defined as toxic. Gene expression fold changes upon infection, plus corresponding p-values and expression intensities as assessed by microarray analysis are also given.

Table 2 | Hit validation data. Shown are the siRNA IDs as provided by the supplier, the WST assay data, and the normalised percent inhibition data together with the number of validated siRNAs per gene for both tested viruses.

Tables 3 and 4 | Targets identified in the siRNA screen of the Example. Disclosed are oligonucleotide sequences employed in the siRNA screen of example 1. Up to four oligonucleotide sequences ("siRNA1 Target", "siRNA2 Target", "siRNA3 Target", "siRNA4 Target",) specific for a target gene were employed.

Example

Human host cell factors crucial for influenza virus replication identified by genome-wide RNAi screen

Summary

Influenza A virus, being responsible for seasonal epidemics and reoccurring pandemics, represents a global threat to public health (1). High mutation rates facilitate the generation of viral escape mutants rendering vaccines and drugs directed against virus-encoded targets potentially ineffective (2). In contrast, targeting host cell determinants temporarily dispensable for the host but crucial for virus replication could prevent viral escape.

In this example, the discovery of 287 human host cell genes influencing influenza A virus replication in a genome-wide RNAi screen is described. Using an independent assay we confirmed 168 hits (59%) inhibiting either the endemic H1N1 (119 hits) or the current pandemic swine-origin (121 hits) influenza A virus strains, with an overlap of 60%. Importantly, a subset of these common hits was also essential for replication of a highly pathogenic avian H5N1 strain. In-depth analyses of several factors provided insights into their infection stage relevance. Notably, SON DNA binding protein (SON) (3) was found to be important for normal trafficking of influenza virions to late endosomes early in infection. We also show that a small molecule inhibitor of CDC-like kinase 1 (CLK1) (4) reduces influenza virus replication by more than two orders of magnitude, an effect connected with impaired splicing of the viral M2 mRNA. Furthermore, influenza virus-infected p27$^{-/-}$ (cyclin-dependent kinase inhibitor 1B; Cdkn1b) mice accumulated significantly lower viral titers in the lung providing in vivo evidence for the importance of this gene. Thus, our results highlight the potency of genome-wide RNAi screening for the dissection of virus-host interactions and the identification of drug targets for a broad range of

influenza viruses.

Introduction

During the course of infection, the influenza virus encounters numerous bottle necks, constituted by host cell functions essential or inhibitory for viral propagation (5). Comprehensive knowledge of such critical host cell determinants could provide valuable insight into the molecular mechanisms of viral replication and facilitate the development of a novel generation of drugs that target host cell factors and are thus less prone to select for resistant viral mutants. To identify host cell factors involved in the viral infection cycle in human cells, we conducted a genome-wide RNAi screen using a two-step approach (Fig. 1a): First, A549 human lung epithelial cells, transfected with siRNAs 48 h prior to infection with influenza A H1N1 virus (A/WSN/33), were stained with a virus-specific antibody at 24 h post infection (p.i.) to monitor cell infection rates. Second, virus supernatants from these transfected A549 cells were transferred onto 293T human embryonic kidney reporter cells, containing an inducible influenza virus-specific luciferase construct (FlaA) (6). Assay reliability was confirmed with an siRNA directed against influenza virus nucleoprotein (NP) mRNA (7). Knockdown of NP effectively blocked viral replication, as assessed by immunofluorescence staining and the luciferase reporter assay (Fig. 5). Statistical analyses further confirmed the robustness of our assay controls (NP and the non-targeting Allstars siRNA) and reproducibility of results (Figs. 6 and 7). Using this bipartite assay, we screened a genome-wide siRNA library consisting of ca. 62,000 siRNAs targeting ca. 17,000 annotated genes and ca. 6,000 predicted genes.

For identification of primary hits, three parameters were included: luciferase expression, the percentage of infected cells, as determined by immunofluorescence microscopy, and the total number of infected cells. After excluding non-expressed genes and toxic siRNAs, primary screening data from all three parameters were separately subjected to an analyses pipeline with statistical checkpoints at each step, finally leading to hit selection based on Z-scores below -2 (Fig. 8 and Methods). Results from each of the three parameters were combined, and from a total of 22,843 human genes (annotated and predicted) 287 were designated primary hits (Table 1).

Among these high-confidence candidates we found several genes known to play a pivotal role in influenza virus replication, e.g. the nuclear export factors NXF1 (8) and XPO1 (9), as well as the vacuolar ATPase ATP6V0D1 (10,11). Gene ontology (GO) term enrichment analysis revealed our dataset was markedly enriched in gene categories associated with the proton-transporting two-sector ATPase complex, the spliceosome, the small ribosomal subunit, the eukaryotic translation initiation factor 3 (EIF3), the COPI coated vesicle transport and the nuclear pore complex (Fig. 1b and Fig. 9), which comprise functional categories already associated with viral replication. Further bioinformatic analysis using Reactome (12) corroborated the GO results (Fig. 10). In-depth analysis of selected enriched functional categories using the STRING database revealed numerous interactions between factors associated with the same GO term (Fig. 11). Interestingly, we found multiple factors connected with pre-mRNA splicing (Fig. 1c), which escaped detection in a previous RNAi screen using *Drosophila* cells (13). However, the small ribosomal subunit and EIF3 were enriched in the *Drosophila*-based influenza screen (13) but not in other viral RNAi screens (14, 15, 16, 17), indicating these factors could be influenza-specific (18).

Next, we independently ascertained the significance of all 287 primary hits for replication of the influenza A/WSN/33 (H1N1) and the current pandemic swine-origin influenza A/Hamburg/04/2009 (H1N1) viruses. The number of viruses released from siRNA transfected A549 cells was determined by titrating supernatants on Madin-Darby canine kidney (MDCK) cells. For each primary hit four different siRNAs were used individually to knockdown gene function. We found that 119 (A/WSN/33) and 121 (A/Hamburg/04/2009) of the 287 primary hits decreased virus number by more than fivefold in comparison to control samples, with a least two siRNAs (Fig 2a), without impairing cell viability (Fig. 12). In total, 168 primary hits were validated, comprising an overall validation rate of ~59%. Remarkably, of the factors inhibiting viral replication, 72 were common to both influenza virus strains, indicative of their broad inhibitory potential (Fig. 2b and Table 2).

Validation was extended to the highly pathogenic avian-origin influenza A virus of the H5N1 subtype (A/Vietnam/1203/2004) using a subset of the common siRNAs. The knockdown efficiencies shown in the following Table (percentages of knockdown ± standard deviation as obtained in three independent experiments):

siRNA	**Knockdown [%]**	**SD [%]**
ATP6V0D1_1	95%	2%
ATP6V0D1_2	98%	1%
COPG_1	89%	8%
COPG_2	63%	25%
EIF4A3_1	96%	2%
EIF4A3_2	95%	3%
NUP205_1	85%	12%
NUP205_2	83%	7%
NUP98_1	86%	10%
NUP98_2	83%	6%
NXF1_1	53%	39%
NXF1_2	79%	17%
SON_1	77%	19%
SON_2	81%	16%

Strikingly, H5N1 virus replication decreased by more than two orders of magnitude using these siRNAs (Fig. 2c). Likewise, knockdown of identical targets inhibited replication of influenza A/WSN/33 (H1N1) virus and the pandemic A/Hamburg/04/2009 (H1N1) strain (Fig. 13). The observation that a subset of common factors blocked replication of both swine and avian-origin virus variants corroborates that these proteins constitute crucial sub-type independent host-cell checkpoints.

The life-stage relevance of 18 targets, representing a variety of functional categories and affecting both H1N1 influenza viruses, was assessed by immunofluorescence staining for NP as a marker of viral ribonucleoprotein (vRNP) localisation (19). Typically, vRNP is confined to the nucleus early in infection, but enters the cytoplasm for packaging into progeny virions late in infection (19). Here, upon knockdown of all targets, NP gave a mainly nuclear signal at 3 h p.i. (Fig. 3a, upper panel), shifting towards cytoplasmic staining 2 h later (Fig. 3a, lower panel). In addition to the expected blockage of NP synthesis upon inhibition of NXF1 (8,20), knockdown of several identified hits such as COPG, SON, and ATP6V0C appeared to reduce NP expression levels (Fig. 3a, upper panel) and to delay export of NP from the nucleus (Fig. 3a, lower panel). Relative frequency distribution analysis of NP expression and cytosolic to nuclear NP ratios within single cells corroborated our microscopic observations (Figs. 14-16). In total, knock down of 11 genes significantly reduced NP expression and interfered with nuclear export of NP.

To analyse the impact of targets, shown to affect NP synthesis and localisation, on the synthesis of viral RNA, we infected siRNA-transfected cells with influenza virus and determined the levels of viral genomic RNA (vRNA) and viral mRNA at 2 h p.i. by qRT-PCR (7). Most of the analysed targets had no effect on virus cell entry, as indicated by robust vRNA detection (Fig. 3b). However, for many targets, including identified ATPases and SON, a protein known to repress Hepatitis B virion production (3), plus several factors involved in RNA biogenesis, e.g. NXF1, viral mRNA, synthesis was substantially reduced (Fig. 3b). This demonstrates virus propagation is affected at a stage between virus entry and mRNA synthesis. Knockdown of SON also reduced vRNA levels (Fig. 3b), indicating it functions in an infection step preceding viral mRNA synthesis. Accordingly, considerably less virus particles co-localised with CD63-labelled late endosomes upon SON knockdown (Fig. 3c; Fig. 17), suggesting this factor is important for trafficking of influenza virions early in the infection cycle. Intriguingly, knockdown of the nucleoporin 98kDa (NUP98) increased vRNA level (Fig. 3b), most likely due to accelerated de novo vRNA synthesis, but at the same time dramatically decreased viral progeny (Fig. 2a; Fig. 13). Consistent with its reported antiviral (8) and proviral functions (13), these seemingly contradictory results suggest NUP98 exerts an inhibitory effect early in the life cycle but is mandatory for completion of viral replication. Taken together, these data reveal that the 11 targets (identified as reducing NP expression levels) interfere with early events in virus replication. In contrast, knockdown of the remaining 7 factors analysed in this set of experiments, such as CLK1 or p27 (CDKN1B), probably exert their function during later infection stages.

To more closely mimic in vivo conditions, we tested the effect of target knockdown on influenza virus replication in primary normal human bronchial epithelial cells (NHBE). Most notably, knockdown of CLK1 and ATP6V0D1 strongly reduced viral growth in these cells (Fig. 4a). We independently assessed the function of CLK1 by treating A549 cells with TG003, a chemical inhibitor of CLK1 (4). Influenza virus propagation was inhibited by more than 93% (Fig. 4b) without exerting detectable toxic effects (Fig. 18). CLK1 regulates alternative splicing in mammalian cells by phosphorylating the splicing factor SF2/ASF (21, 22), therefore we hypothesized that inhibition of CLK1 would affect splicing of viral RNAs. In accordance, TG003 reduced levels of spliced M2 viral RNA, whereas unspliced M1 and NS1/NS2 were unaffected (Fig. 4c, data not shown). Immunoblot analysis corroborated our qRT-PCR results, revealing drastically reduced M2 protein levels following treatment with TG003, whereas M1 protein levels remained relatively constant (Fig. 4d). Since the SF2/ASF complex is important for splicing and the shuttling of spliced viral mRNAs to the cytoplasm (23), it is conceivable that reduction of M2 protein expression was at least partially caused by nuclear retention of its mRNA transcript. Our finding that CLK1 is involved in processing viral M2 mRNA is consistent with the essential role of the SF2/ASF splicing factor in viral M2 ion channel protein production (24). Interestingly, replication of vesicular stomatitis virus (VSV), which, unlike influenza, does not depend on splicing of its own viral RNA, was only slightly reduced in the presence of TG003 (Fig. 19).

During the primary screen and the hit validation, knockdown of the cell cycle regulator p27 led to a strong inhibition of influenza virus replication. To confirm the impact of p27 on viral replication under in vivo conditions, $p27^{-/-}$ mice were intranasally infected with influenza A/Puerto Rico/8/34 (H1N1) virus. At 2 d p.i., virus load within the lungs of $p27^{-/-}$ mice was significantly reduced (Fig 4e). The observation that a lack of p27 reduces influenza virus replication in vivo but does not affect mouse viability, indicates certain cellular proteins involved in influenza virus replication are dispensable for the host organism.

Thus, this first genome-wide RNAi screen in human cells for factors affecting influenza virus replication has provided new and comprehensive information on host cell determinants of replication, and uncovered potential targets for novel antiviral strategies. We provide in vitro and in vivo evidence for the role of CLK1 and the tumor suppressor p27, using a small molecule inhibitor and a homozygous knockout model, respectively. The majority of the hits analysed in-depth appear to function during early infection processes such as viral protein synthesis and nuclear export of viral RNA. Importantly, most of the validated hits are essential for a broad spectrum of influenza viruses, including the pandemic swine-origin H1N1 influenza virus and even a highly pathogenic avian H5N1 strain. This holds promise for the therapeutic potential of these targets against novel emerging influenza viruses with minimised likelihood of developing drug resistant variants. In conclusion, transient interference with distinct host cell functions during infection is likely to extend our current armament, consisting of vaccines and virus-targeted drugs, in the battle against the recurring threat of seasonal and pandemic influenza virus infections.

In the present screen, a range of cellular functions were identified which were associated with influenza virus propagation. Amongst the significantly enriched functional categories are the small ribosomal subunit and the translation initiation factor EIF3, splicing associated genes, vesicular (coat complex formation) and nuclear transport, as well as vacuolar ATPases. In contrast, in other viral RNAi-based screens, including an influenza virus screen in *Drosophila* cells, mostly single metabolic functions were enriched in the hit lists (13, 14, 15, 17). This general observation strengthens the impact of performing RNAi screens in homologous host cell models.

The small ribosomal subunits and the translation initiation factor EIF3 components comprised a major cellular function enriched in a recent *Drosophila*-based influenza virus screen (13) but not in other viral RNAi screens (14-17). Yet, only single components of the large ribosomal subunit were included in either the previous or our current influenza screens. Toxicity, as determined by our WST assay (c.f. Fig. 11) and viable cell counts (c.f. Table 1), did not have a major impact on the knockdown cells. Kittler *et al.* found knockdown of many of these genes impacted the cell cycle (arrest) and division, but toxicity was a confounding factor in a minimal number of cases. A *Drosophila* C virus screen identified small as well as large ribosomal subunit genes as enriched and this finding was linked to IRES-mediated translation initiation (18). Translation of influenza mRNAs is initiated in a Cap-dependent and 5'-UTR-mediated manner (Garfinkel et al., Kash et al.) and the initiation factor EIF4E within the EIF4F complex is substituted by the viral polymerase (Burgui et al.). On the other hand, EIF4GI, another member of the EIF4F complex, is targeted by NS1, enhancing preferential translation of late viral mRNAs in particular (Aragon et al.). The eukaryotic 5'-UTR targeting factor GRSF-1, which also enhances translation of influenza mRNAs, was not identified as a hit in our screen (Kash et al.). Besides these known factors, other host cell proteins may play an important role in initiating translation of viral mRNAs (Burgui et al.). The identification of defined translation machinery components in two influenza virus RNAi screens but not other viral screens, suggests these factors could be influenza virus A specific. We speculate that the small ribosomal subunit as well as EIF3 complete the pre-initiation complex that initiates virus-specific, selective translation and probably contribute to the inhibition of host cell gene translation.

Since pre-mRNA splicing is a major cellular function known to be important for gene expression in a variety of viral systems (reviewed by e.g. Engelhardt et al.), we expected this function to be identified in our screen. Yet, the *Drosophila* influenza virus screen does not show the same enrichment of splicing factors. This could be due to the experimental limitations of the *Drosophila* host cell system for influenza A virus infection and replication, therefore other processes might be important in this experimental system. This might also apply to other cellular processes we identified. König *et al.* (17) found many splicing factors in their HIV early stage replication screen. HIV mRNA splicing is a very complex and highly regulated process that ensures co-ordinated expression of the different viral proteins as well as production of unspliced genomic RNA (reviewed by e.g. Stoltzfus et al). Brass *et al.* (16) detected several splicing associated factors amongst the HIV-dependency factors (HDFs) included in their screen. Because the individual flavivirus proteins are derived by co- and post-translational cleavage from a polyprotein translated from an unspliced RNA (e.g. Beasley et al), splicing factors are virtually missing in the Dengue and West Nile virus hit lists (14, 15). Furthermore, vacuolar ATPases are enriched in our screen as well as the West Nile virus screen (14). Both viruses rely upon acidification of the phagosome to enter the cytoplasm (reviewed by e.g. Bouvier et al.). Single vacuolar ATPase subunits were also included in the *Drosophila*-based influenza virus screen (13).

The nuclear transport factors are required for export of the viral RNA into the cytoplasm to be translated and incorporated into new virus particles. The cyclin-dependent kinase inhibitor 1B (p27, also CDKN1B) involved in cell cycle regulation and other cellular processes (Borriello et al.), is associated with this network. Phosphorylation at certain amino acid residues regulates cellular localisation and thereby function and stability (Ishida et al., Connor et al.). p27 is exported into the cytoplasm by XPO1/RanGTP. p27 is a tumour suppressor in the nucleus, whereas is acts as an oncogene with pro-metastatic capability in the cytoplasm. This functional versatility (reviewed by e.g. Borriello et al.) makes is difficult to trace the step involved in influenza virus replication. To connect it to the cell-cycle arrest associated with knockdown of many ribosomal subunits (see above) is one promising route for future investigation.

Two different COP vesicles operate in the early secretory pathway (reviewed by Lee et al.). COPII vesicles mediate exit from the endoplasmatic reticulum (ER) and transport to the ER-Golgi-intermediate compartment (ERGIC), whereas COPI vesicles are involved in retrograde transport from the Golgi apparatus to the ER or between different Golgi cisternae and in anterograde transport. The influenza glycoproteins HA and NA are synthesised at the ER, transported to the Golgi apparatus and then trafficked to the plasma membrane (Bouvier et al.). Therefore, factors involved in early secretory pathway of the host cell are likely candidates affecting influenza propagation. In the present work, we have shown that knockdown of COPA, COPB1, COPB2, COPD, COPE or COPG reduced number of infectious viruses, demonstrating that these factors are important for the production of infectious influenza A viruses. Specifically, knockdown of COPG dramatically reduced levels of NP at 3 h p.i. (Fig. 3a and Figs.14-16), hinting at a role in early infection processes. These observations are in agreement with a previous RNAi screen that identified COPG as essential for influenza A virus replication in insect cells (13). The underlying mechanism of COPI function in influenza A virus replication is still unknown. Knockdown of COPI constituents could directly affect transport of viral glycoproteins to the plasma membrane. This hypothesis is supported by recent work demonstrating that anterograde transport of proteins in COPB1 knockdown cells is blocked or at least reduced (Styers et al., Rennolds et al.). Interestingly, only components of the COPI machinery have been identified in the present screen. The involvement of COPII vesicles in normal trafficking of membrane proteins from the ER to the plasma membrane could hint to other functions of COPI during influenza A virus infection including maintenance of the steady-state distribution of Golgi proteins or ER quality control mechanisms (Tu et al., Zerangue et al.). In this scenario, knockdown of COPI proteins would result in incorrect folding or incorrect glycosylation of viral proteins including HA and NA, which either reduce transport of these proteins to the plasma membrane or interfere with the normal function of these proteins. Detailed analysis is on the way to clarify the role of COPI proteins during influenza virus infection.

In summary, these findings highlight the significance of our screen. Many molecular functions of the host cell known, or expected, to play important roles in influenza virus replication were recovered in our analysis. As an extension to previous RNAi-based viral screens (13, 14, 16, 17), which report single functional categories, our findings reveal a range of different molecular networks.

Methods

Summary: siRNA screening

All siRNAs (4 µl/well, 200 nM) were arrayed in 384-well plates. To each well, 8 µl of RPMI medium (Invitrogen, Karlsruhe, Germany) containing 0.35 µl HiperFect (Qiagen) was added and plates were shaken for 1 min. After 10 min incubation at room temperature (RT), a cell suspension (28 µl) of 500 cells was added to give a final siRNA concentration of 20 nM. Cells were incubated at 37 °C and 5% CO_2 for 48 h before infection at MOI 0.12. At 24 hours post infection (p.i.), supernatants were transferred onto freshly seeded 293T reporter cells, incubated for 16 h at 37 °C and 5% CO_2 and then luciferase activities were measured. The A549 cells were fixed, stained for nuclei and NP, and analysed using the Acumen ^{e}X3 Cytometer (TTP Labtech, Royston, U.K.). All multiwell pipetting steps were performed using a Biomek® FX^{P} Laboratory Automation Workstation (Beckman Coulter, Krefeld, Germany). An siRNA library (Qiagen Hu_Genome 1.0 and Human

Druggable Genome siRNA Set V2.0;Qiagen, Hilden, Germany) containing four siRNAs per gene for the druggable genome (25) and two siRNAs per gene for non-druggable and predicted genes was screened three times independently. The following siRNAs with the indicated target sequence were included in all screening plates as controls: siNP (5'-AAGGAUCUUAUUUCUUCGGAG-3'), siPLK1 (5'-CACCATATGAATTGTACAGAA-3') and Allstars (Qiagen, Hilden, Germany).

Cells and viruses

The A549 human lung epithelial cell line (CCL-185, ATCC-LGC, Wesel, Germany) was grown in DMEM media (Invitrogen, Karlsruhe, Germany) supplemented with 4 mM L-glutamine, 4 mM sodium pyruvate, 100 U/ml penicillin/streptomycin and 10% fetal calf serum (FCS, Biochrome, Berlin, Germany) (DMEM complete medium), at 37 °C and 5% CO_2. The human embryonic kidney cell line 293T (CRL-11268, ATCC-LGC) and the Madin Darby Canine Kidney cells (MDCK, CCL-34, ATCC-LGC) were grown in DMEM supplemented with 4 mM L-glutamine, 100 U/ml penicillin/streptomycin and 10% FCS. Primary normal human bronchial epithelial cells (NHBE, CC-2541, Lonza, Cologne, Germany) were grown in Clonetics® BEGM® BulletKit® (CC-3170, Lonza) supplemented with the following growth supplements: BPE, Hydrocortisone, hEGF, Epinephrine, Transferrin, Insulin, Retinoic Acid, Triiodothyronine, GA-1000. Supplements added at 0.5 ml/500 ml medium, except BPE (2 ml/500 ml). Cells were regularly checked for mycoplasma contamination by PCR. The influenza virus strains A/WSN/33 (H1N1) and A/Puerto Rico/8/34 (H1N1) were grown in the allantoic cavities of 11-day-old embryonated chicken eggs. Production of recombinant highly pathogenic influenza A/Vietnam/1203/2004 virus (H5N1) by reverse genetics was done essentially as described previously (26). The pandemic H1N1 A/Hamburg/04/2009 strain was provided by S. Becker (Philipps University, Marburg, Germany) and was propagated in MDCK cells in DMEM supplemented with 1 μg trypsin/ml in the absence of FCS. Virus stocks were titrated by standard plaque assay on MDCK cells using an agar overlay medium (27).

siRNA screening

All siRNAs (4 µl/well; 200 nM) were arrayed in 384-well plates. To each well, 8 µl of RPMI medium (Invitrogen, Karlsruhe, Germany) containing 0.35 µl HiperFect (Qiagen) was added and plates were shaken for 1 min. After 10 min incubation at room temperature (RT), a cell suspension (28 µl) containing 500 cells was added to give a final siRNA concentration of 20 nM. Cells were incubated at 37 °C and 5% CO_2 for 48 h before infection at an MOI of 0.12 (see below). At 24 hours post infection (p.i.), supernatants were transferred onto freshly seeded 293T reporter cells, incubated for 16 h at 37 °C and 5% CO_2 and then luciferase activities were measured (see below). The A549 cells were fixed, stained for nuclei and NP, and analysed using the Acumen ^{e}X3 Cytometer (TTP Labtech, Royston, UK). The number of automatically counted nuclei was further used to estimate cytotoxic effects of specific siRNAs. The siRNA was classified as being toxic, if 750 or fewer nuclei were determined within one well of a 384-well plate. All multiwell pipetting steps were performed using a Biomek® FX^{P} Laboratory Automation Workstation (Beckman Coulter, Krefeld, Germany). An siRNA library (Qiagen Hu_Genome 1.0 and Human Druggable Genome siRNA Set V2.0; Qiagen, Hilden, Germany) containing four siRNAs per gene for the druggable genome (25) and two siRNAs per gene for non-druggable and predicted genes, was screened three times independently. The following siRNAs with the indicated target sequence were included in all screening plates as controls: siNP (5'-AAGGAUCUUAUUUCUUCGGAG-3'), siPLK1 (5'-CACCATATGAATTGTACAGAA-3') and Allstars (Qiagen, Hilden, Germany).

Luciferase reporter assay

To quantify infectious viruses in the supernatants of siRNA transfected A549 cells during the primary RNAi screen, we used a luciferase-based reporter system. 293T cells were transfected in batches with a FluA luc plasmid (6), one day later seeded into 384-well plates at concentrations of 1×10^{4}/well, and subsequently infected with 12.5 µl of virus containing supernatant. At 16 h p.i., Bright-Glo™ firefly luciferase substrate (Promega, Madison, WI, USA) was added and luciferase activities in cell lysates were measured using the Envision multilabel plate reader (PerkinElmer, Rodgau, Germany). Transfection of 239T cells with the influenza virus-specific luciferase construct (FlaA) induces expression of firefly luciferase transcripts flanked by the untranslated region of the influenza A/WSN/33 virus nucleoprotein (NP) segment. Luciferase expression is therefore only detectable in the presence of the viral polymerase, thus allowing quantification of infectious viruses.

siRNA transfection for validation experiments in 96- and 12-well plates

All siRNAs were purchased from Qiagen. For siRNA transfection of A549 cells in 96-well plates, 20 µl of a 100 nM siRNA dilution in DMEM w/o supplements was mixed with 1 µl HiperFect + 9 µl DMEM medium and incubated for 10 min at RT. Complex formation was stopped by addition of 25 µl DMEM complete medium. Next, 3000 A549 cells in 50 µl DMEM complete medium were seeded into each well and incubated at 37 °C and 5% CO_2 for the indicated time periods. For siRNA transfection of NHBE cells in 96-well plates, BEGM medium (with/without supplements) was used and 15,000 cells/well were seeded. For Western blot experiments, siRNA transfection was carried out in 12-well plates. For each well, 1 µl of a 20 µM siRNA solution was diluted in 99 µl RPMI (Invitrogen) supplemented with 25 mM HEPES (Invitrogen). The mix was incubated at RT for 5 min before addition of 5 µl HiperFect (Qiagen) and further 15 min incubation at RT. Each complex was added to 50,000 A549 cells in 900 µl DMEM complete medium, mixed carefully, and then transferred to 12-well plates. After 6 h incubation at 37 °C and 5% CO_2, the medium was exchanged for fresh DMEM complete medium and the cells were incubated for an additional 48 h using the same growth conditions.

Indirect immunofluorescence labeling

Cells were fixed with 3.7% formaldehyde and permeabilised with 0.3% Triton X-100, 10% FCS in PBS. Samples were sequentially incubated with a primary antibody against the viral nucleoprotein (NP, clone AA5H, AbD Serotec, UK) diluted 1:10000 in PBS with 10% FCS, 0.1% Tween 20 for 1 h at RT, followed by an incubation with the secondary Cy3 conjugated antibody directed against mouse IgG (1:100 in PBS with 10% FCS, 0.1% Tween 20 and 0.1% Hoechst dye used to stain cellular DNA). Numbers of infected versus non-infected cells were determined using automated microscopy (Olympus, Soft Imaging Solutions, München, Germany) or, for the primary siRNA screen, the Acumen eX3 microplate cytometer (TTP LabTech, Melbourn, UK).

Automated microscopy and image analysis

The numbers of influenza infected and host cells were determined using an automated microscope (Olympus Soft Imaging Solutions). Images were taken with DAPI and Cy3 filter sets (AHF-Analysetechnik, Tübingen, Germany). Scan^R Analysis Software (Olympus Soft Imaging Solutions) was used to automatically identify and quantify influenza nuclear protein (NP) and cell nuclei. For determination of NP localisation, mean and total intensities of NP were analysed. NP located within the same area as the Hoechst staining was defined as nuclear NP. NP located within a 5-pixel-wide ring around the nuclei was defined as cytosolic NP. The distance between the inner edge of the ring and the nuclei was set at 1 pixel. For each experiments identical camera setting were used.

Host cell viability determination by WST-1 assay

Determination of host cell viability upon siRNA tranfection was performed using cell proliferation assay WST-1 (Roche, Mannheim, Germany). WST-1 reagent was added to the cells 48 h after siRNA transfection and incubated at 37 °C for 1.5 h. Absorbance was measured at 460 nm and at the reference wavelength 590 nm. Non-targeting siRNA Allstars and siPLK1 were used as a positive and negative control, respectively.

Virus infection

Cells were washed with PBS and then infected with influenza at the indicated MOIs in infection buffer (PBS supplemented with 0.2% bovine serum albumin) for 60 min at RT. Cells were washed again (in infection buffer) and incubated for the indicated time periods at 37 °C in DMEM supplemented with 0.2% bovine serum albumin, 4 mM L-glutamine and antibiotics (A549) or BEGM with supplements (NHBE), unless otherwise stated. All infection experiments with A/WSN/33, A/Puerto Rico/8/34 and with A/Hamburg/04/2009 H1N1 viruses were performed under biosafety level (BSL) 2 conditions, whereas BSL 3 conditions were used for experiments with A/Vietnam/1203/2004 (HN51).

Replication assay

To quantify infectious virus particles in infected cell culture supernatants, 5,000 or 12,000 MDCK cells were seeded in 384- or 96-well plates, respectively. One day later the cells were washed twice, infected with a dilution series of cell culture supernatants and incubated at RT for 1 h. Infection buffer (as above) was added (40 µl or 100 µl/well) and plates were incubated at 37 °C, 5% CO_2 for 6 h, followed by fixation with 3.7% formaldehyde, antibody staining and automatic image processing, as described in 'Indirect immunofluorescence labeling'.

Gene enrichment and network analysis

For gene enrichment analysis, we modified the R-script available from the Gaggle web site (http://gaggle.systemsbiology.net/svn/gaggle/PIPE2.0/trunk/PIPEletResourceDir/ GOTableEnrichment/GOEnrichmentScript.R). This script applies the R-package GOstats developed by Falcon, S. and Gentleman, R. (28) and is available at the Bioconductor web site (http://www.bioconductor.org). Briefly, we defined a gene universe consisting of 22843 genes contained and annotated in the genome-wide library and processed the hit list against this universe with respect to molecular function (MF), cellular component (CC) and biological process (BP). Each Gene Ontology term is associated with X number of genes, providing a relative frequency A. In the hit list, the same term is connected to Y genes giving a relative frequency B. B divided by A is the enrichment factor.

The 287 'high-confidence' hits were also uploaded as gene-identifiers using the Sky-Painter tool of the Reactome website (www.reactome.org). Significant events calculated by the application's Fisher's exact test were identified and coloured accordingly. Network analysis was carried out using the STRING database (http://string.embl.de/).

Confocal microscopy

Fusion between influenza viruses and cellular endosomes was detected using confocal microscopy. A549 cells were plated onto cover slips in 12-well plates at a density of 5×10^4 cells/well and directly transfected in suspension with indicated siRNAs, followed by infection with influenza A/WSN/33 virus (MOI 10) 48 h post transfection. During the infection process, cells were kept on ice for 45 min, washed twice with cold infection buffer (see above) and subsequently incubated with pre-warmed infection media (DMEM supplemented with 0.2% bovine serum albumin, 4 mM L-glutamine and antibiotics). After 15, 45 and 90 min cells were fixed with 4% paraformaldehyde and permeabilised for 20 min with 0.2% BSA in PBS and 0.2% Triton X-100. Cells were then incubated for 1 h with antibodies targeting CD63 (Millipore) at a dilution of 1:70 and a polyclonal serum against influenza (1:1000), followed by incubation with a fluorescently labelled secondary antibody (dilution 1:100). Samples were mounted in MOWIOL. Images were taken with a Leica TCS-SP confocal microscope and processed using Adobe Photoshop 11.0.

Immunoblotting

For immunoblotting, cells were washed with PBS and lysed in 1x SDS sample buffer containing 75mM Tris HCl (pH 6.8), 25% glycerol, 0.6% SDS, 7.5% β-mercaptoethanol and 0.001% bromphenol blue. Protein lysates (20 µl) were loaded and separated on a 10% SDS-polyacrylamide gel. Separated proteins were transferred to a PVDF membrane and detected using mouse monoclonal antibodies against viral matrix protein (M1, AbD Serotec, UK), viral ion channel protein (M2,Santa Cruz) or β-actin (Sigma, Germany) at 1:100, 1:1000 or 1:2500 dilution, respectively, followed by incubation with a secondary sheep anti-mouse IgG Horseradish peroxidase (1:10000). Staining was performed with ECL Western Blotting Detection Reagent (Amersham, Piscataway, NJ, USA). β-actin was used as a loading control. Band intensities were determined using the Aida image analyzer (V.4.03) (2D/ Densitometry) and normalised to β-actin.

Quantitative RT-PCR

For the detection of viral RNA (vRNA) or viral mRNA, quantitative RT-PCR (qRT-PCR) was performed as previously described (7). Briefly, A549 cells infected with influenza A/WSN/33 virus (MOI 1) were lysed with RLT lysis buffer (Qiagen, Hilden, Germany). For reverse transcription of viral mRNA, an oligo(dT)18 primer was used: the negative stranded vRNA of the gene segment PA was converted to cDNA using a PA-specific oligonucleotide (5'-GCTTCTTATCGTTCAGGCTCTTAGG-3'). Resulting cDNAs were quantified by qRT-PCR with oligonucleotides specific for PA (5'-GCTTCTTATCGTTCAGGCTCTTAGG-3' and 5'-CCGAGAAGCATTAAGCAAAACCCAG-3'). GAPDH was amplified using the oligonucleotides, GAPDH for: 5'- GGTATCGTGGAAGGACTCATGAC-3'; GAPDH_rev: 5'- ATGCCAGTGAGCTTCCCGTTCAG-3'. Levels of GAPDH were used for normalisation. All experiments were done in triplicate.

To quantify the levels of spliced and unspliced mRNAs, infection of A549 cells with influenza A/WSN/33 virus was performed at an MOI of 4 for 5 h. RNA was then isolated using the RNeasy Mini Kit (Qiagen) and treated with DNase (Ambion) according to manufacturer's instructions. Reverse transcription of viral mRNA was performed using oligo(dT) primer and the synthesised cDNA was subjected to real-time PCR using primers specific for M1 (5'-GACCAATCCTGTCACCTC-3' and 5'-GATCTCCGTTCCCATTAAGAG-3') and M2 (5'-GAGGTCGAAACGCCTAT-3' and 5'-CTCCAGCTCTATGTTGACAAA-3'), as described previously (29). Levels of M1 and M2 mRNA were normalised to GAPDH.

Validation of RNAi by quantitative PCR

siRNA validation was performed as previously described (30). Briefly, one day before transfection 3,000 cells per well were seeded onto a 96-well plate. Transfection was performed with a final siRNA concentration of 56 nM with 0.25 µl HiPerFect(Qiagen). Knockdown measurements were performed independently three times. After 48 h, RNA was isolated using the RNeasy 96 BioRobot 8000 system (Qiagen). The relative amount of target mRNA was determined by quantitative PCR using the Quantitect SYBR Green RT–PCR kit following the manufacturer's instructions (Qiagen) and the following primers:

GAPDH forward 5'-GGTATCGTGGAAGGACTCATGAC-3',
GAPDH reverse 5'-ATGCCAGTGAGCTTCCCGTTCAG-3',
ATP6V0D1 forward 5'-TGTCGCAACATCGTGTGGAT-3',
ATP6V0D1 reverse 5'-GAGTGCAATTGAGAGCCTTGG-3',
COPG forward 5'-TCCGCTATGCTGCTGTTCGTA-3',
COPG reverse 5'-GCGGTTTGAATCTGTGACCAG-3',
EIF4A3 forward 5'-TGATCTTGGCTCCCACAAGAG-3',
EIF4A3 reverse 5'-ATTGGTGCCTCCAATGCAG-3',
NUP98 forward 5'-TTCCGGAATCCGATGTCAGA-3',
NUP98 reverse 5'-TGTAAAGCCTTTGGCCGGACT-3',
NUP205 forward 5'-ACCTTCGGAAGGATCTTCCAA -3';
NUP205 reverse 5'-GGAGTCCCAGAATCACCACAA-3';
NXF1 forward 5'-TGAGCAAACGATACGATGGC-3',
NXF1 reverse 5'-TCTGCGATTCAGGACAACGTC-3',
SON forward 5'-CAAGCCTTAGAGCTGGCATTG-3',
SON reverse 5'-GCTTGCGTGATTTGTGTTCAG-3'.

The relative expression levels of target mRNA were normalized against control transfected cells. GAPDH was used as an internal standard.

Chemical inhibitors

The chemical inhibitor TG003 (Sigma-Aldrich, Munich, Germany) directed against the kinase CLK1 was dissolved in DMSO to a concentration of 10 mM.

Animal experiments

Animals were housed and bred under pathogen free conditions, biosafety level 2 according to German Animal Protection Law (Tierschutzgesetz TierSchG). Animal testing was approved by the local authorities (Landesamt für Gesundheit und Soziales Berlin LAGeSo: Reference number G0217/08). C57BL/6/J and p27$^{-/-}$ mice (B6.129S4-*Cdkn1b*^{tm1Mlf}/J) were provided by Charles River (Sulzfeld, Germany) or bred in house, respectively. Mice aged between 7 and 15 weeks were intranasally infected with influenza A/Puerto Rico/8/34 virus (10× LD_{50}; in 50 µl PBS). Two days later, lungs of infected animals were isolated and homogenised, followed by centrifugation at 800 × g for 8 min at 4 °C. The amount of infectious viruses in the supernatant was quantified using the replication assay (see above). Proteins for use in immunoblotting experiments were obtained by adding TRIZOL Reagent (GIBCO BRL) to the remaining cell pellet, according to the manufacturer's instructions.

Data analysis

For identification of primary hits, three parameters were included: luciferase expression, the percentage of infected cells as determined by immunofluorescence microscopy, and the total number of infected cells. The latter parameter was informative because the number of viruses per well correlated with the number of infected cells, with minor influence of cells present. To maximize the robustness of the hit selection and to minimize false positives due to off-target effects, raw screening data from all three parameters were subjected separately to an analysis pipeline incorporating statistical checkpoints at each step (Fig. 8). First, we excluded non-expressed genes by determining constitutive or inducible expression via microarray profiling of non-infected and infected A549 samples (5814 genes were not expressed). Second, we excluded toxic siRNAs which reduced total cell numbers (<750 cells/well) upon transfection were also excluded (1520 siRNAs) using the microscopic assay applied throughout the primary screen. Third, non-toxic siRNAs targeting expressed genes were further analysed. For statistical analysis of luciferase assay data obtained from the genome-wide screen, the following plate-wise quality control criteria were used: (i) the average signal from the non-targeting control wells (Allstars) was greater than 10,000 counts, and (ii) the difference in signal strength between the non-targeting control (Allstars) and (iii) the inhibitory control (NP) was at least two orders of magnitude. Using Genedata's Screener® software (www.genedata.com), we excluded wells with phenotypes attributable to positional effects. The revised raw data were subjected to statistical analysis using cellHTS (31), an R-implemented software package for the analysis of cell-based high-throughput RNAi screen data. Raw data were normalised using the B-score method to further exclude positional effects (32). Next, a z-score transformation was applied to center and scale the plate-wise data. The z-scores were calculated using the following equation:

$$z = \frac{X - \mu}{\sigma}.$$

where X is a raw score to be standardized, σ is the standard deviation of the population, and μ is the mean of the population. The medians of the centered and scaled values of at least three independent replicates were used for redundant siRNA activity (RSA) analysis (33), which applies a rank-based hypergeometric distribution test to identify hits. Only genes for which two corresponding siRNAs were scored as hits were analysed further. Next, Genedata's Screener® package was used to select all genes with a robust z-score of less than -2.

For the analysis of the hit validation data, for each siRNA the normalised percent inhibition of infectious virus particles was calculated. Briefly, the difference of each sample value subtracted from the median of the non-targeting control (Allstars) values of the particular plate was divided by the difference of the medians of the non-targeting control and the inhibitory control (siNP). An 80% normalised inhibition threshold was applied. Genes were scored as validated hits if at least two siRNAs, which did not impair cell viability, fulfilled this criteria.

The ratios of cytosolic to nuclear NP at 5 h p.i. and levels of total NP at 3 h p.i. in samples tested were non-normally distributed. Therefore, to assess the significance of differences between distributions of the target knockdown samples and non-targeting control reference samples (Allstars), we applied the minimal distance estimation Kolmogorov-Smirnov test using the statistical software environment R (http://www.r-project.org/). The samples sizes are individually defined as the number of main objects per well detected by the automated image analysis package Scan^R.

Significant differences in the amount of infectious viruses gained from the lungs of $p27^{-/-}$ and control mice were tested using a one-tailed t-test assuming different standard deviations for the samples and the controls (Welch-test).

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Claims

1. Pharmaceutical composition comprising at least one inhibitor of influenza virus replication optionally together with a pharmaceutically acceptable carrier, adjuvant, diluent or/and additive, for the prevention, alleviation or/and treatment of an influenza virus infection.

2. The pharmaceutical composition of claim 1, wherein the at least one inhibitor is selected from the group consisting of nucleic acids, nucleic acid analogues such as ribozymes, peptides, polypeptides, and antibodies, and compounds having a molecular weight below 1000 Dalton.

3. The pharmaceutical composition of claim 1 or 2, wherein the influenza virus infection is an influenza A virus infection.

4. The pharmaceutical composition of any of the claims 1 to 3, wherein the at least one inhibitor is capable of modulating gene expression or/and gene product activity.

5. The pharmaceutical composition of claim 4, wherein modulation of the expression or/and gene product activity is activation.

6. The pharmaceutical composition of claim 4, wherein modulation of the expression or/and gene product activity is inhibition.

7. The pharmaceutical composition as claimed in any of the claims 2 to 6, wherein the nucleic acid is RNA or DNA.

8. The pharmaceutical composition as claimed in claim 7, wherein the at least one inhibitor comprises

(a) a nucleic acid comprising a nucleotide sequence selected from sequences of Table 1, Table 2, Table 3 and Table 4,
(b) a fragment of the sequence of (a) having a length of at least 70%, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% of the sequence of (a),
(c) a nucleic acid comprising a sequence which is at least 70 %, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% identical to the sequence of (a) or/and (b), or/and
(d) a sequence complementary to the sequence of (a), (b) or/and (c).

9. The pharmaceutical composition as claimed in claim 8, wherein the nucleic acid of (a) comprises a nucleotide sequence selected from the sequences of Table 4 and fragments thereof.

10. The pharmaceutical composition as claimed in any of the claims 7 to 9, wherein the nucleic acid comprises
(i) an RNA molecule capable of RNA interference, such as siRNA or/and shRNA,
(ii) a miRNA,
(iii) a precursor of the RNA molecule (i) or/and (ii),
(iv) a fragment of the RNA molecule (i), (ii) or/and (iii),
(v) a derivative of the RNA molecule of (i), (ii) (iii) or/and (iv), or/and
(vi) a DNA molecule encoding the RNA molecule of (i), (ii) (iii) or/and (iv).

11. The pharmaceutical composition as claimed in any of the claims 7 to 10, wherein the RNA molecule is a double-stranded RNA molecule, preferably a double-stranded siRNA molecule with or without a single-stranded overhang alone at one end or at both ends.

12. The pharmaceutical composition as claimed in any of the claims 7 to 11 wherein the RNA molecule comprises at least one nucleotide analogue or/and deoxyribonucleotide.

13. The pharmaceutical composition as claimed in any of the claims 7 to 9, wherein the nucleic acid is an antisense nucleic acid or a DNA encoding the antisense nucleic acid.

14. The pharmaceutical composition as claimed in any of the claims 7 to 13, wherein the nucleic acid has a length of at least 15, preferably at least 17, more preferably at least 19, most preferably at least 21 nucleotides.

15. The pharmaceutical composition as claimed in any of the claims 7 to 14, wherein the nucleic acid has a length of at the maximum 29, preferably at the maximum 27, more preferably at the maximum 25, especially more preferably at the maximum 23, most preferably at the maximum 21 nucleotides.

16. The pharmaceutical composition as claimed in any of the claims 1 to 6 comprising an antibody, wherein the antibody is preferably directed against a polypeptide comprising
    (a) an amino acid sequence encoded by a nucleic acid or/and gene selected from sequences of Table 1, Table 2, Table 3, and Table 4 and complementary sequences thereof,
    (b) a fragment of the sequence of (a) having a length of at least 70%, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% of the sequence of (a), or/and
    (c) an amino acid sequence comprising a sequence which is at least 70 %, at least 80 %, at least 90 %, at least 95 %, at least 98 %, or at least 99% identical to the sequence of (a) or/and (b).

17. The pharmaceutical composition as claimed in claim 16, wherein the polypeptide of (a) comprises an amino acid sequence encoded by a nucleic acid or/and gene selected from Table 4.

18. The pharmaceutical composition of any of the preceding claims further comprising an agent suitable of transportation of the at least inhibitor of

influenza virus infection into a cell, in particular into a lung epithelial cell.

19. The pharmaceutical composition of claim 18, wherein the further agent is chitosan, which preferably is formulated in nanoparticles.

20. A screening method for identification of a compound suitable for the prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps
    (a) providing a cell or/and a non-human organism capable of being infected with an influenza virus and capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,
    (b) contacting the cell or/and the organism of (a) with an influenza virus and with a compound known to be capable of modulating the expression or/and activity of the gene of (a) or/and the gene product thereof,
    (c) determining the amount of influenza virus produced by the cell or/and the organism, and
    (d) selecting a compound which reduces the amount of the influenza virus produced by the cell or/and the organism.

21. The method of claim 20, wherein the gene of (a) is selected from Table 1, Table 2, Table 3 and Table 4.

22. The method of claim 21, wherein the gene of (a) is selected from Table 4.

23. The method of any of the claims 20 to 22 comprising a cellular screening assay.

24. A screening method for identification of a compound suitable for prevention, alleviation or/and treatment of an influenza virus infection, comprising the steps

(i) providing a cell or/and a non-human organism capable of expressing a gene, wherein the gene or/and gene product thereof is capable of modulating an influenza virus replication,
(ii) contacting a compound with the cell or/and the organism of (i),
(iii) determining the amount or/and the activity of gene product of the gene of (i), and
(iv) selecting a compound which modulates the amount or/and the activity of the gene product of (i).

25. The method of claim 24, wherein the gene of (i) is selected from Table 1, Table 2, Table 3 and Table 4.

26. The method of claim 25, wherein the gene of (i) is selected from Table 4.

27. The method of any of the claims 24 to 26, wherein the compound of (iv) reduces the amount of the influenza virus produced by the cell or/and the organism.

28. The method of any of the claims 24 to 27, wherein modulation of the expression of a gene is downregulation or upregulation.

29. The method of any of the claims 24 to 27, wherein modulation of the activity of the gene is decrease or increase of the activity.

30. The screening method of any of the claims 24 to 29, wherein the influenza is selected from influenza A viruses.

31. The screening method of any of the claims 24 to 30, wherein the cell is a mammalian cell, in particular a human cell.

32. Use of an inhibitor of influenza virus replication capable of inhibiting or activating the expression of a gene selected from Table 1, Table 2, Table 3 and Table 4, or/and of inhibiting or activating a gene product thereof,

for the manufacture of a medicament or/and vaccine for the prevention, alleviation or/and treatment of an influenza virus infection.

33. Use of claim 32, wherein the gene is selected from Table 4.

34. Use of a nucleic acid comprising a gene sequence or/and a nucleotide sequence selected from Table 1, Table 2, Table 3, and Table 4 and fragments thereof in a method for screening for compounds or/and targets suitable for the prevention, alleviation or/and treatment of an influenza virus infection.

35. Use of claim 34, wherein a combination of at least two nucleic acids is used.

36. Use of claims 34 to 35, wherein the nucleic acid or the combination is selected from Table 4.

37. Use of claim 36, wherein the combination of nucleic acids inhibits expression or/and activity of a gene.

Figure 1

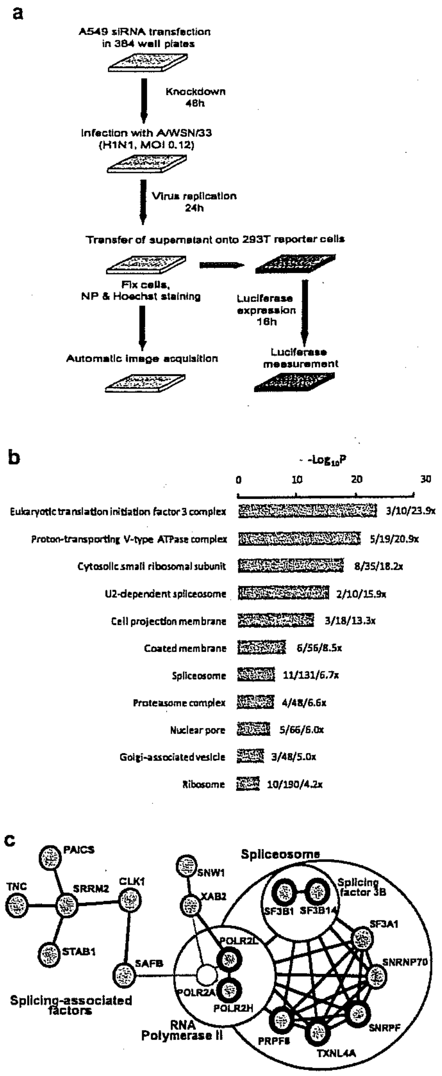

a
A549 siRNA transfection in 384 well plates
Knockdown 48h
Infection with A/WSN/33 (H1N1, MOI 0.12)
Virus replication 24h
Transfer of supernatant onto 293T reporter cells
Fix cells, NP & Hoechst staining
Automatic image acquisition
Luciferase expression 16h
Luciferase measurement
b
-Log10P
0
10
20
30
Eukaryotic translation initiation factor 3 complex
3/10/23.9x
Proton-transporting V-type ATPase complex
5/19/20.9x
Cytosolic small ribosomal subunit
8/35/18.2x
U2-dependent spliceosome
2/10/15.9x
Cell projection membrane
3/18/13.3x
Coated membrane
6/56/8.5x
Spliceosome
11/131/6.7x
Proteasome complex
4/48/6.6x
Nuclear pore
5/66/6.0x
Golgi-associated vesicle
3/48/5.0x
Ribosome
10/190/4.2x
c
PAICS
TNC
SRRM2
CLK1
STAB1
SAFB
Splicing-associated factors
SNW1
XAB2
Spliceosome
Splicing factor 3B
SF3B1
SF3B14
SF3A1
SNRNP70
POLR2L
POLR2A
POLR2H
RNA Polymerase II
PRPF8
TXNL4A
SNRPF

Figure 2

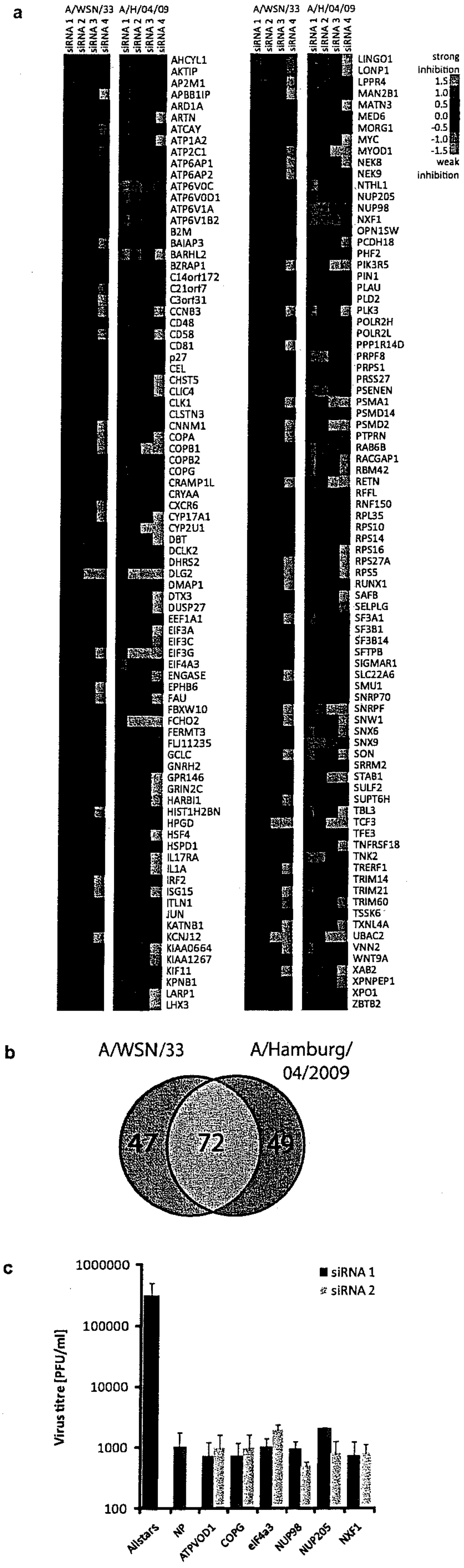

a
A/WSN/33
A/H/04/09
siRNA 1
siRNA 2
siRNA 3
siRNA 4
siRNA 1
siRNA 2
siRNA 3
siRNA 4
AHCYL1
AKTIP
AP2M1
APBB1IP
ARD1A
ARTN
ATCAY
ATP1A2
ATP2C1
ATP6AP1
ATP6AP2
ATP6V0C
ATP6V0D1
ATP6V1A
ATP6V1B2
B2M
BAIAP3
BARHL2
BZRAP1
C14orf172
C21orf7
C3orf31
CCNB3
CD48
CD58
CD81
p27
CEL
CHST5
CLIC4
CLK1
CLSTN3
CNNM1
COPA
COPB1
COPB2
COPG
CRAMP1L
CRYAA
CXCR6
CYP17A1
CYP2U1
DBT
DCLK2
DHRS2
DLG2
DMAP1
DTX3
DUSP27
EEF1A1
EIF3A
EIF3C
EIF3G
EIF4A3
ENGASE
EPHB6
FAU
FBXW10
FCHO2
FERMT3
FLJ11235
GCLC
GNRH2
GPR146
GRIN2C
HARBI1
HIST1H2BN
HPGD
HSF4
HSPD1
IL17RA
IL1A
IRF2
ISG15
ITLN1
JUN
KATNB1
KCNJ12
KIAA0664
KIAA1267
KIF11
KPNB1
LARP1
LHX3
A/WSN/33
A/H/04/09
siRNA 1
siRNA 2
siRNA 3
siRNA 4
siRNA 1
siRNA 2
siRNA 3
siRNA 4
LINGO1
LONP1
LPPR4
MAN2B1
MATN3
MED6
MORG1
MYC
MYOD1
NEK8
NEK9
NTHL1
NUP205
NUP98
NXF1
OPN1SW
PCDH18
PHF2
PIK3R5
PIN1
PLAU
PLD2
PLK3
POLR2H
POLR2L
PPP1R14D
PRPF8
PRPS1
PRSS27
PSENEN
PSMA1
PSMD14
PSMD2
PTPRN
RAB6B
RACGAP1
RBM42
RETN
RFFL
RNF150
RPL35
RPS10
RPS14
RPS16
RPS27A
RPS5
RUNX1
SAFB
SELPLG
SF3A1
SF3B1
SF3B14
SFTPB
SIGMAR1
SLC22A6
SMU1
SNRP70
SNRPF
SNW1
SNX6
SNX9
SON
SRRM2
STAB1
SULF2
SUPT6H
TBL3
TCF3
TFE3
TNFRSF18
TNK2
TRERF1
TRIM14
TRIM21
TRIM60
TSSK6
TXNL4A
UBAC2
VNN2
WNT9A
XAB2
XPNPEP1
XPO1
ZBTB2
strong inhibition
1.5
1.0
0.5
0.0
-0.5
-1.0
-1.5
weak inhibition
b
A/WSN/33
A/Hamburg/ 04/2009
47
72
49
c
1000000
100000
10000
1000
100
Virus titre [PFU/ml]
siRNA 1
siRNA 2
Allstars
NP
ATPV0D1
COPG
eIF4a3
NUP98
NUP205
NXF1

Figure 3

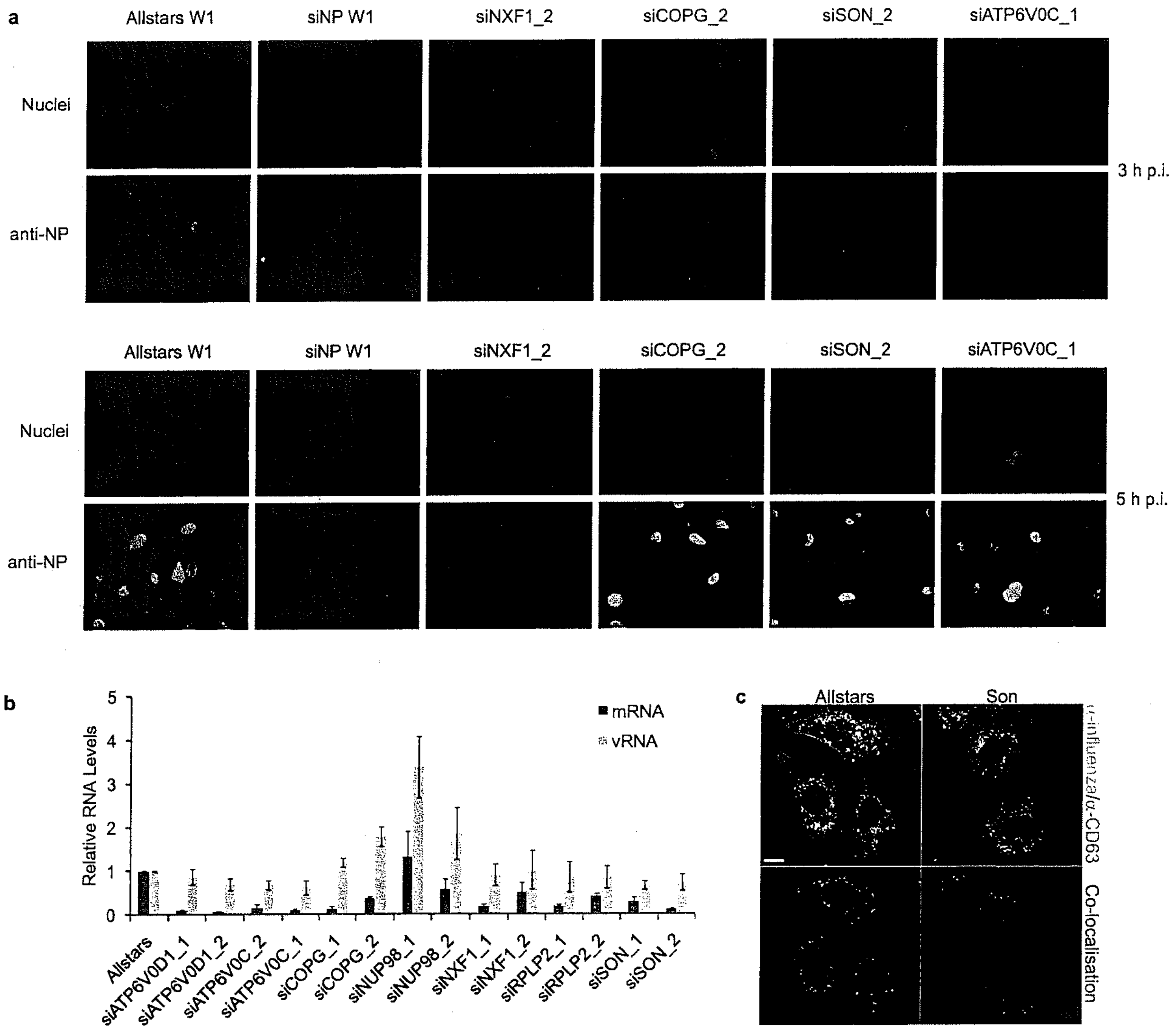

a
Allstars W1
siNP W1
siNXF1_2
siCOPG_2
siSON_2
siATP6V0C_1
Nuclei
anti-NP
3 h p.i.
Allstars W1
siNP W1
siNXF1_2
siCOPG_2
siSON_2
siATP6V0C_1
Nuclei
anti-NP
5 h p.i.
b
Relative RNA Levels
0
1
2
3
4
5
mRNA
vRNA
Allstars
siATP6V0D1_1
siATP6V0D1_2
siATP6V0C_2
siATP6V0C_1
siCOPG_1
siCOPG_2
siNUP98_1
siNUP98_2
siNXF1_1
siNXF1_2
siRPLP2_1
siRPLP2_2
siSON_1
siSON_2
c
Allstars
Son
α-influenza/α-CD63
Co-localisation

Figure 4

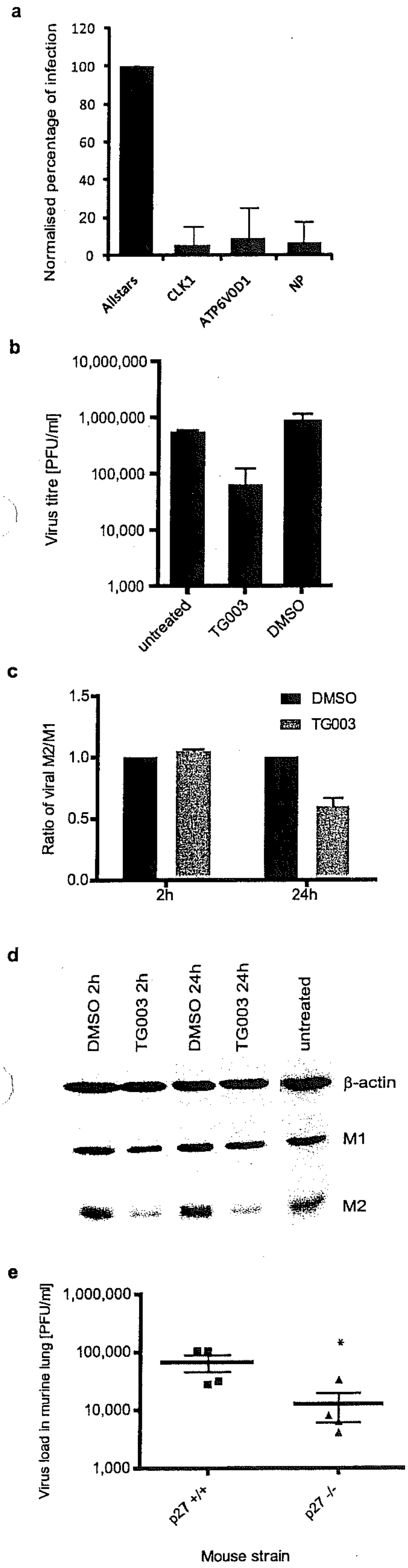

a
Normalised percentage of infection
120
100
80
60
40
20
0
Allstars
CLK1
ATP6V0D1
NP
b
Virus titre [PFU/ml]
10,000,000
1,000,000
100,000
10,000
1,000
untreated
TG003
DMSO
c
Ratio of viral M2/M1
1.5
1.0
0.5
0.0
DMSO
TG003
2h
24h
d
DMSO 2h
TG003 2h
DMSO 24h
TG003 24h
untreated
β-actin
M1
M2
e
Virus load in murine lung [PFU/ml]
1,000,000
100,000
10,000
1,000
*
p27 +/+
p27 -/-
Mouse strain

Figure 5

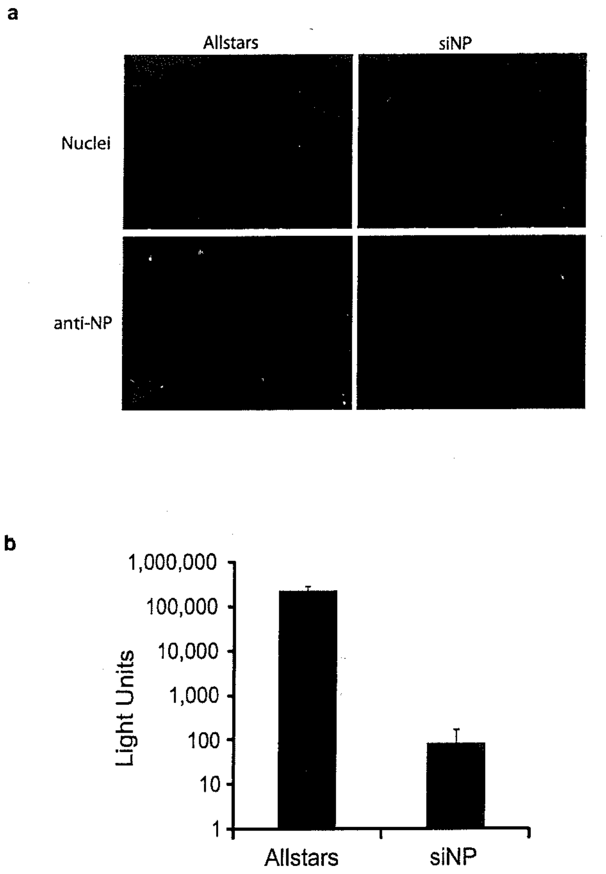

a
Allstars
siNP
Nuclei
anti-NP
b
Light Units
1,000,000
100,000
10,000
1,000
100
10
1
Allstars
siNP

Figure 6

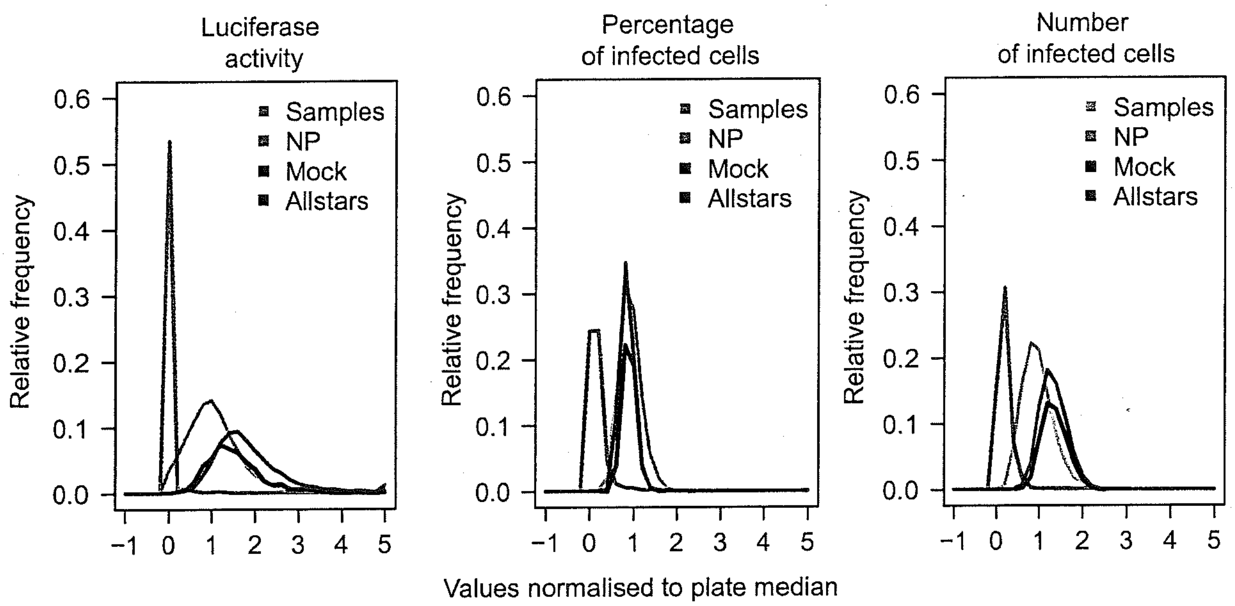

Luciferase activity
Percentage of infected cells
Number of infected cells
Samples
NP
Mock
Allstars
Relative frequency
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1
0
1
2
3
4
5
Values normalised to plate median

Figure 7

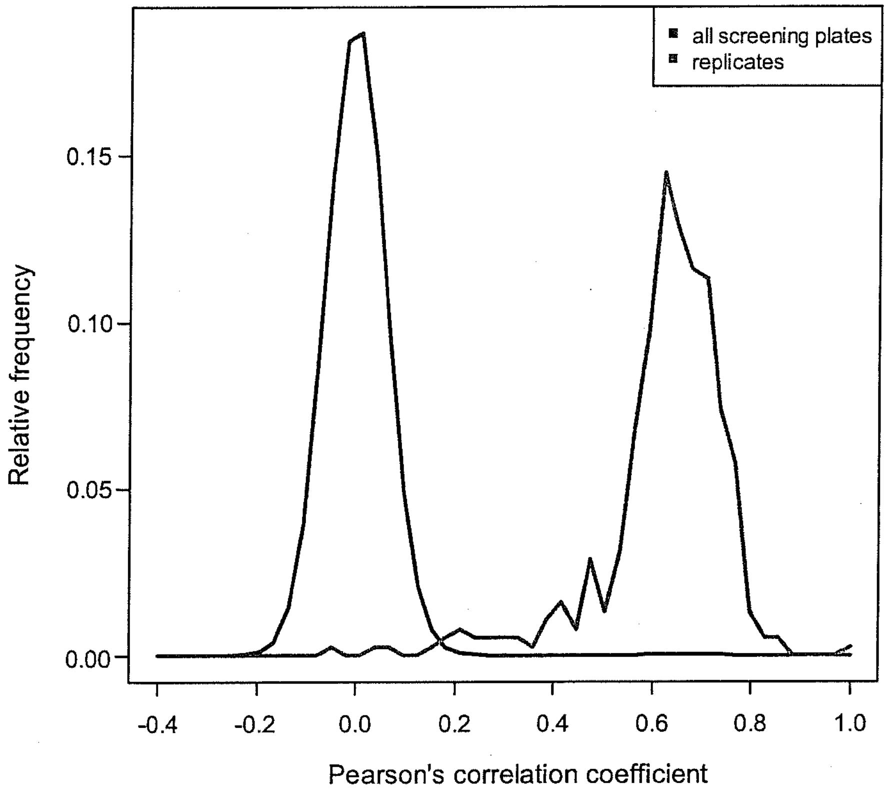

■ all screening plates
▪ replicates
Relative frequency
0.15
0.10
0.05
0.00
-0.4
-0.2
0.0
0.2
0.4
0.6
0.8
1.0
Pearson's correlation coefficient

Figure 8

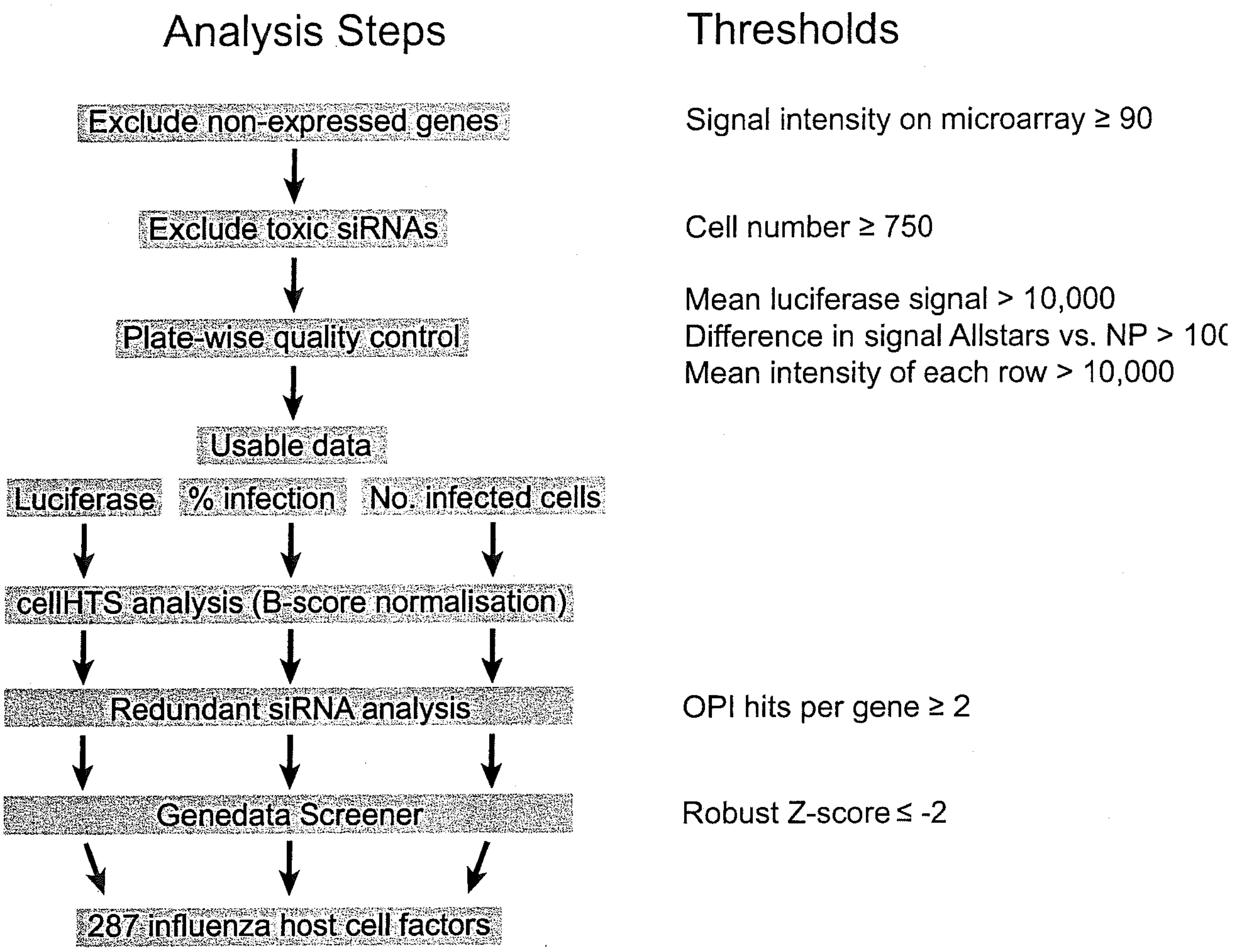
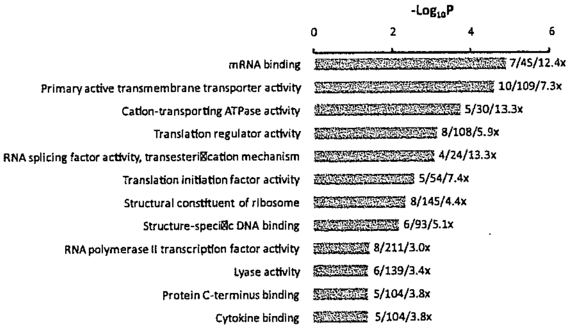

Analysis Steps
Thresholds
Exclude non-expressed genes
Signal intensity on microarray ≥ 90
Exclude toxic siRNAs
Cell number ≥ 750
Plate-wise quality control
Mean luciferase signal > 10,000
Difference in signal Allstars vs. NP > 10
Mean intensity of each row > 10,000
Usable data
Luciferase
% infection
No. infected cells
cellHTS analysis (B-score normalisation)
Redundant siRNA analysis
OPI hits per gene ≥ 2
Genedata Screener
Robust Z-score ≤ -2
287 influenza host cell factors

Figure 9

Molecular Function



Biological Process

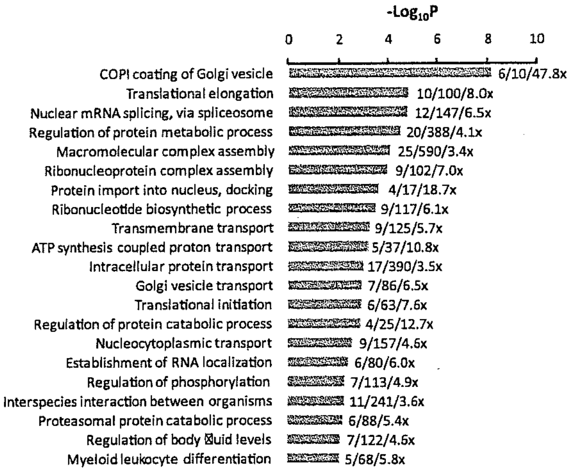
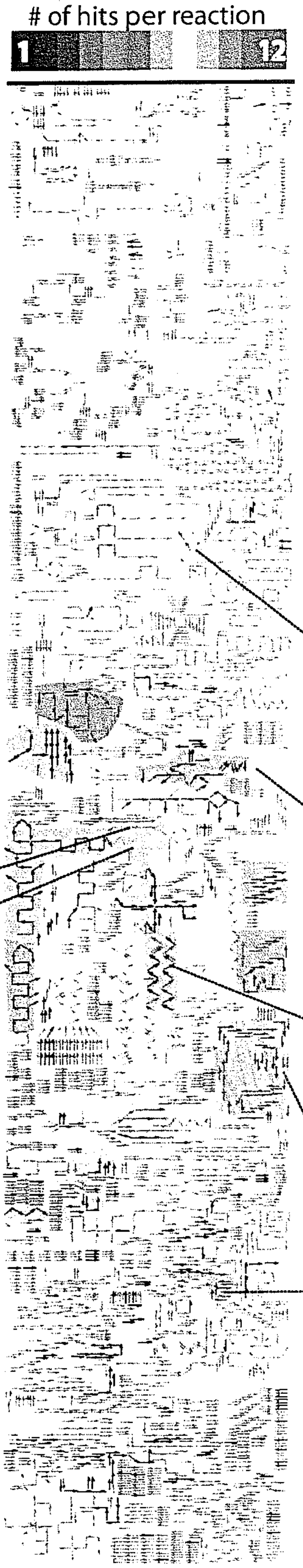


Figure 10



Translation
Matching identifiers: EEF1A1, RPL35, FAU, EIF3S5, EIF3S4, EIF3S10, RPS10, RPS14, RPS5, RPS16, RPS24, RPS3, RPS27A,EIF3S8

Gene Expression
Matching identifiers: NXF1, GTF2H3, SKIIP, RPL35, EIF3S5, SF3B14, SF3A1, POLR2L, RPS10, MED6, RPS14, RPS5, RPS16, CRSP2 SNRPF, EIF3S8, EEF1A1, EIF3S4, FAU, PRPF8, EIF3S10, SARS, POLR2H, SNRP70, SF3B1, RPS24, RPS3, RPS27A, TXNL4A

mRNA Splicing
(POLR2H, PRPF8, SNRPF, SF3B14, SF3B1, POLR2L, TXNL4A)

Formation of the Spliceosomal C complex
(POLR2H, PRPF8, SNRPF, SF3B14, SF3B1, SF3A1, POLR2L, TXNL4A)

Cell Cycle
Matching identifiers: PSMD14, PSMA1, CKS1B, PSMD2, NUP98 TK2, CDKN1B, E2F1, XPO1, PSMC6, RPS27A

Cell Cycle Checkpoints
Matching identifiers: PSMD14, PSMA1, PSMD2, MDM2, RPS27A, PSMC6, CDKN1B

Metabolism of amino acids
Matching identifiers: PSMD14, PSMA1, PSMD2, PAOX, DBT, PSMC6

FADH2 + NAD+ --> FAD + NADH + H+*(DBT)*
2-methyl-1-hydroxypropyl-TPP + lipoamide
--> S-(isobutyryl)-dihydrolipoamide + TPP *(DBT)*

HIV-Infection
Matching identifiers: PSMD14,PSMA1,GTF2H3,PSMD2, NUP98, POLR2L, POLR2H, XPO1, AP2M1, B2M, NUP205, RPS27A, PSMC6, KPNB1
Pol II elongation complex moves on the HIV-1 template as transcript elongates *(POLR2L,POLR2H)*

DNA Repair
Matching identifiers: POLR2H, NTHL1, GTF2H3, XAB2, POLR2L, RPS27A
Dual incision reaction in TC-NER*(POLR2H, GTF2H3, XAB2, POLR2L)*

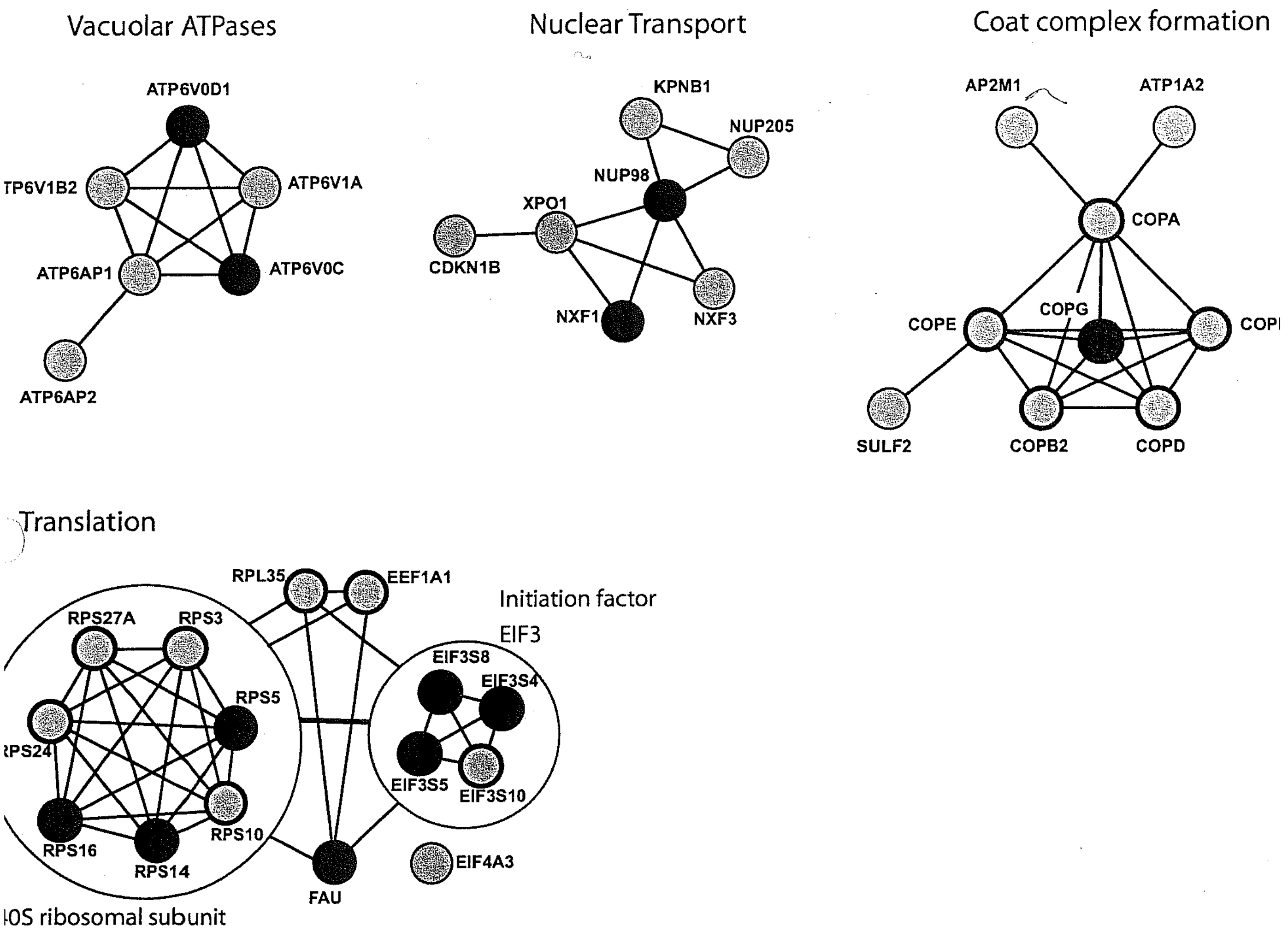
Influenza Infection
Matching identifiers: RPL35, FAU, POLR2L, RPS10, POLR2H, RPS14, SNRNP70, RPS5, RPS16, SNRPF, XPO1, RPS24, RPS3, RPS27A, KPNB1

Viral Protein Synthesis
(RPL35, FAU, RPS10, RPS14, RPS5, RPS16, RPS24, RPS27A, RPS3)

Membrane Trafficking
Matching identifiers: COPB1,COPB2,COPA,COPE,COPG,ARCN1

COPI Mediated Transport
(COPB1,COPB2,COPA,COPE,COPG,ARCN1)

Signaling in Immune System
Matching identifiers: CD58, CD48, JUN, PIK3CB, CHUK, CD47, SELPLG, B2M, CD81, RPS27A


Vacuolar ATPases

Nuclear Transport

Coat complex formation

Translation

Figure 12

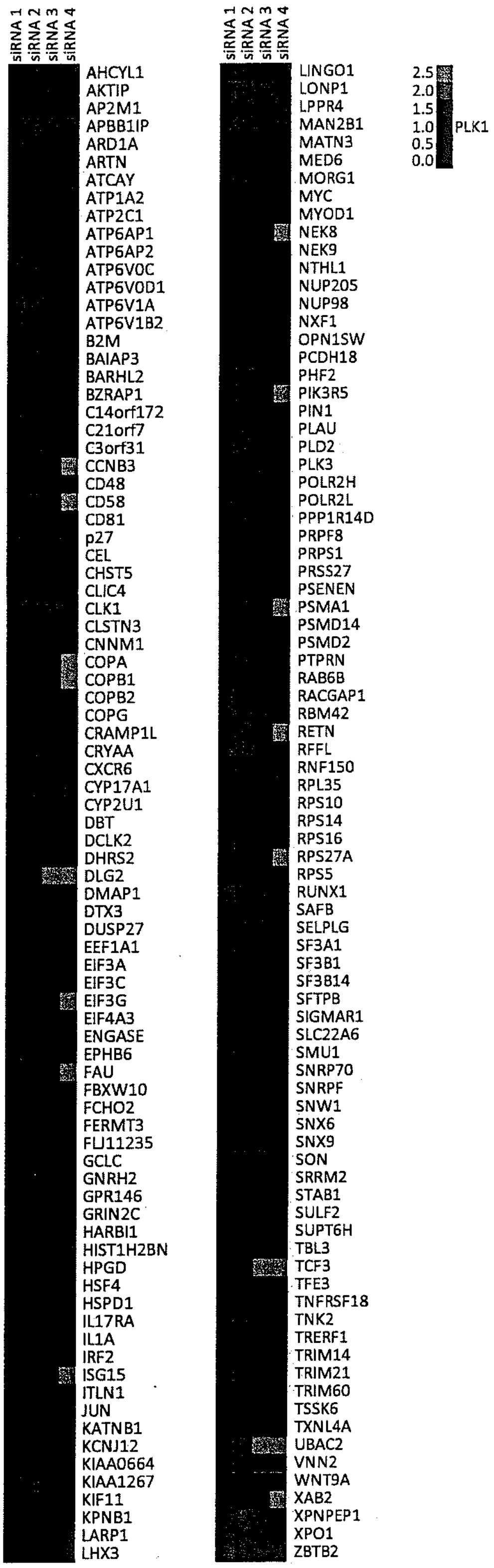
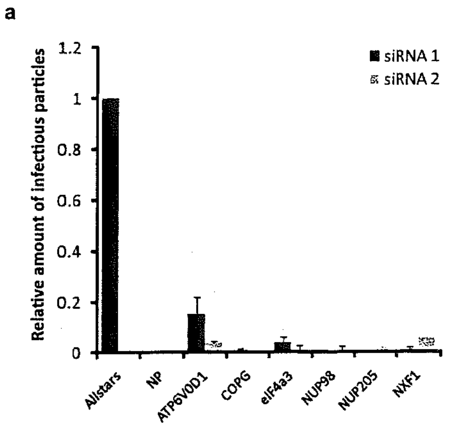

siRNA 1
siRNA 2
siRNA 3
siRNA 4
AHCYL1
AKTIP
AP2M1
APBB1IP
ARD1A
ARTN
ATCAY
ATP1A2
ATP2C1
ATP6AP1
ATP6AP2
ATP6V0C
ATP6V0D1
ATP6V1A
ATP6V1B2
B2M
BAIAP3
BARHL2
BZRAP1
C14orf172
C21orf7
C3orf31
CCNB3
CD48
CD58
CD81
p27
CEL
CHST5
CLIC4
CLK1
CLSTN3
CNNM1
COPA
COPB1
COPB2
COPG
CRAMP1L
CRYAA
CXCR6
CYP17A1
CYP2U1
DBT
DCLK2
DHRS2
DLG2
DMAP1
DTX3
DUSP27
EEF1A1
EIF3A
EIF3C
EIF3G
EIF4A3
ENGASE
EPHB6
FAU
FBXW10
FCHO2
FERMT3
FLJ11235
GCLC
GNRH2
GPR146
GRIN2C
HARBI1
HIST1H2BN
HPGD
HSF4
HSPD1
IL17RA
IL1A
IRF2
ISG15
ITLN1
JUN
KATNB1
KCNJ12
KIAA0664
KIAA1267
KIF11
KPNB1
LARP1
LHX3
siRNA 1
siRNA 2
siRNA 3
siRNA 4
LINGO1
LONP1
LPPR4
MAN2B1
MATN3
MED6
MORG1
MYC
MYOD1
NEK8
NEK9
NTHL1
NUP205
NUP98
NXF1
OPN1SW
PCDH18
PHF2
PIK3R5
PIN1
PLAU
PLD2
PLK3
POLR2H
POLR2L
PPP1R14D
PRPF8
PRPS1
PRSS27
PSENEN
PSMA1
PSMD14
PSMD2
PTPRN
RAB6B
RACGAP1
RBM42
RETN
RFFL
RNF150
RPL35
RPS10
RPS14
RPS16
RPS27A
RPS5
RUNX1
SAFB
SELPLG
SF3A1
SF3B1
SF3B14
SFTPB
SIGMAR1
SLC22A6
SMU1
SNRP70
SNRPF
SNW1
SNX6
SNX9
SON
SRRM2
STAB1
SULF2
SUPT6H
TBL3
TCF3
TFE3
TNFRSF18
TNK2
TRERF1
TRIM14
TRIM21
TRIM60
TSSK6
TXNL4A
UBAC2
VNN2
WNT9A
XAB2
XPNPEP1
XPO1
ZBTB2
2.5
2.0
1.5
1.0
0.5
0.0
PLK1

Figure 13


a
Relative amount of infectious particles
1.2
1
0.8
0.6
0.4
0.2
0
siRNA 1
siRNA 2
Allstars
NP
ATP6V0D1
COPG
eIF4a3
NUP98
NUP205
NXF1

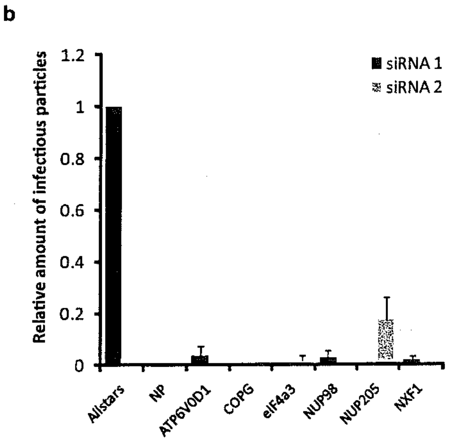

b
Relative amount of infectious particles
1.2
1
0.8
0.6
0.4
0.2
0
siRNA 1
siRNA 2
Allstars
NP
ATP6V0D1
COPG
eIF4a3
NUP98
NUP205
NXF1

Figure 14

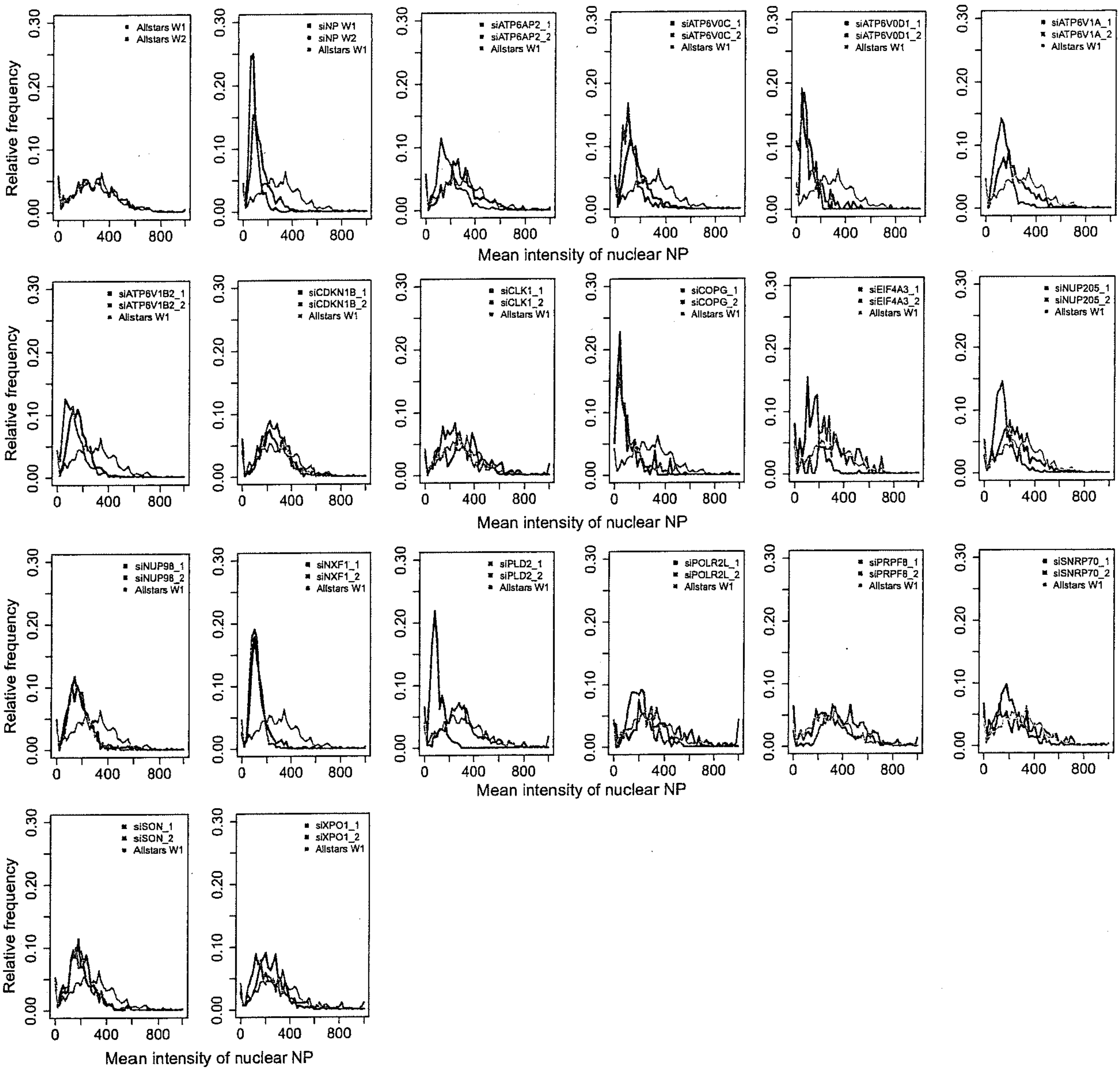

Allstars W1
Allstars W2
siNP W1
siNP W2
Allstars W1
siATP6AP2_1
siATP6AP2_2
Allstars W1
siATP6V0C_1
siATP6V0C_2
Allstars W1
siATP6V0D1_1
siATP6V0D1_2
Allstars W1
siATP6V1A_1
siATP6V1A_2
Allstars W1
siATP6V1B2_1
siATP6V1B2_2
Allstars W1
siCDKN1B_1
siCDKN1B_2
Allstars W1
siCLK1_1
siCLK1_2
Allstars W1
siCOPG_1
siCOPG_2
Allstars W1
siEIF4A3_1
siEIF4A3_2
Allstars W1
siNUP205_1
siNUP205_2
Allstars W1
siNUP98_1
siNUP98_2
Allstars W1
siNXF1_1
siNXF1_2
Allstars W1
siPLD2_1
siPLD2_2
Allstars W1
siPOLR2L_1
siPOLR2L_2
Allstars W1
siPRPF8_1
siPRPF8_2
Allstars W1
siSNRP70_1
siSNRP70_2
Allstars W1
siSON_1
siSON_2
Allstars W1
siXPO1_1
siXPO1_2
Allstars W1
Relative frequency
0.00
0.10
0.20
0.30
0
400
800
Mean intensity of nuclear NP

Figure 15

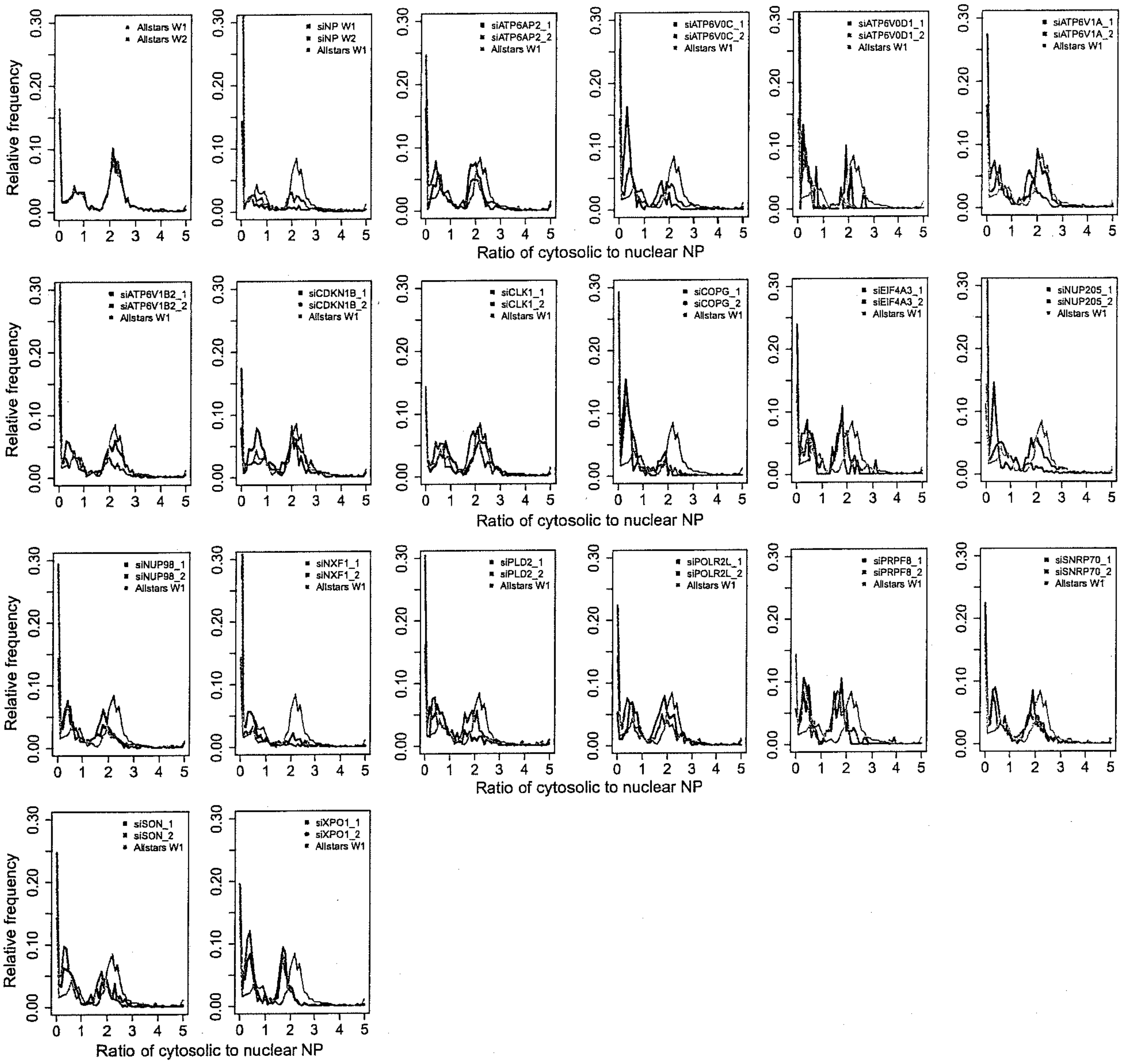

Allstars W1
Allstars W2
siNP W1
siNP W2
Allstars W1
siATP6AP2_1
siATP6AP2_2
Allstars W1
siATP6V0C_1
siATP6V0C_2
Allstars W1
siATP6V0D1_1
siATP6V0D1_2
Allstars W1
siATP6V1A_1
siATP6V1A_2
Allstars W1
siATP6V1B2_1
siATP6V1B2_2
Allstars W1
siCDKN1B_1
siCDKN1B_2
Allstars W1
siCLK1_1
siCLK1_2
Allstars W1
siCOPG_1
siCOPG_2
Allstars W1
siEIF4A3_1
siEIF4A3_2
Allstars W1
siNUP205_1
siNUP205_2
Allstars W1
siNUP98_1
siNUP98_2
Allstars W1
siNXF1_1
siNXF1_2
Allstars W1
siPLD2_1
siPLD2_2
Allstars W1
siPOLR2L_1
siPOLR2L_2
Allstars W1
siPRPF8_1
siPRPF8_2
Allstars W1
siSNRP70_1
siSNRP70_2
Allstars W1
siSON_1
siSON_2
Allstars W1
siXPO1_1
siXPO1_2
Allstars W1
Relative frequency
0.00
0.10
0.20
0.30
0
1
2
3
4
5
Ratio of cytosolic to nuclear NP

Figure 16

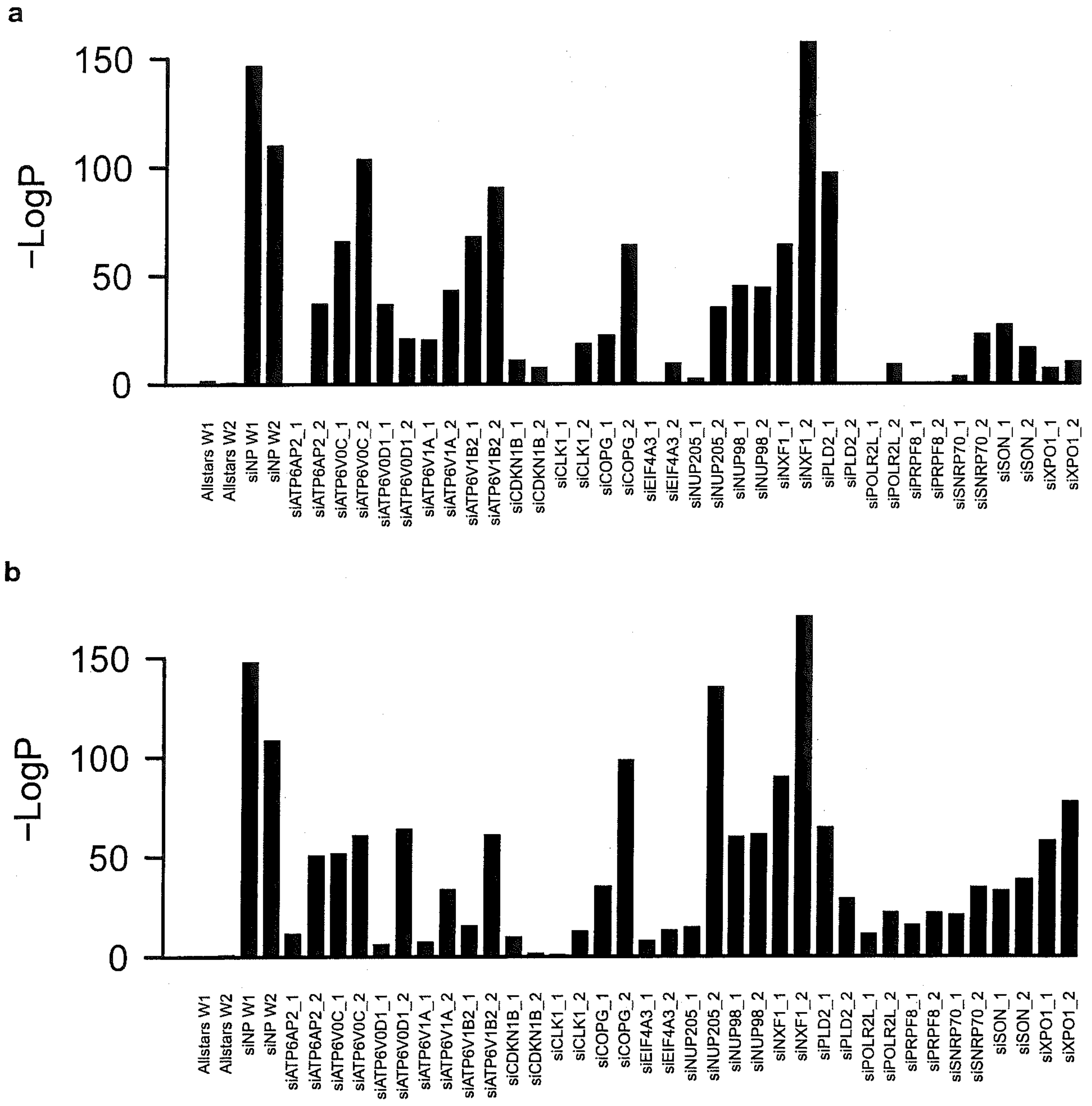

a
-LogP
150
100
50
0
Allstars W1
Allstars W2
siNP W1
siNP W2
siATP6AP2_1
siATP6AP2_2
siATP6V0C_1
siATP6V0C_2
siATP6V0D1_1
siATP6V0D1_2
siATP6V1A_1
siATP6V1A_2
siATP6V1B2_1
siATP6V1B2_2
siCDKN1B_1
siCDKN1B_2
siCLK1_1
siCLK1_2
siCOPG_1
siCOPG_2
siEIF4A3_1
siEIF4A3_2
siNUP205_1
siNUP205_2
siNUP98_1
siNUP98_2
siNXF1_1
siNXF1_2
siPLD2_1
siPLD2_2
siPOLR2L_1
siPOLR2L_2
siPRPF8_1
siPRPF8_2
siSNRP70_1
siSNRP70_2
siSON_1
siSON_2
siXPO1_1
siXPO1_2
b
-LogP
150
100
50
0
Allstars W1
Allstars W2
siNP W1
siNP W2
siATP6AP2_1
siATP6AP2_2
siATP6V0C_1
siATP6V0C_2
siATP6V0D1_1
siATP6V0D1_2
siATP6V1A_1
siATP6V1A_2
siATP6V1B2_1
siATP6V1B2_2
siCDKN1B_1
siCDKN1B_2
siCLK1_1
siCLK1_2
siCOPG_1
siCOPG_2
siEIF4A3_1
siEIF4A3_2
siNUP205_1
siNUP205_2
siNUP98_1
siNUP98_2
siNXF1_1
siNXF1_2
siPLD2_1
siPLD2_2
siPOLR2L_1
siPOLR2L_2
siPRPF8_1
siPRPF8_2
siSNRP70_1
siSNRP70_2
siSON_1
siSON_2
siXPO1_1
siXPO1_2

Figure 17

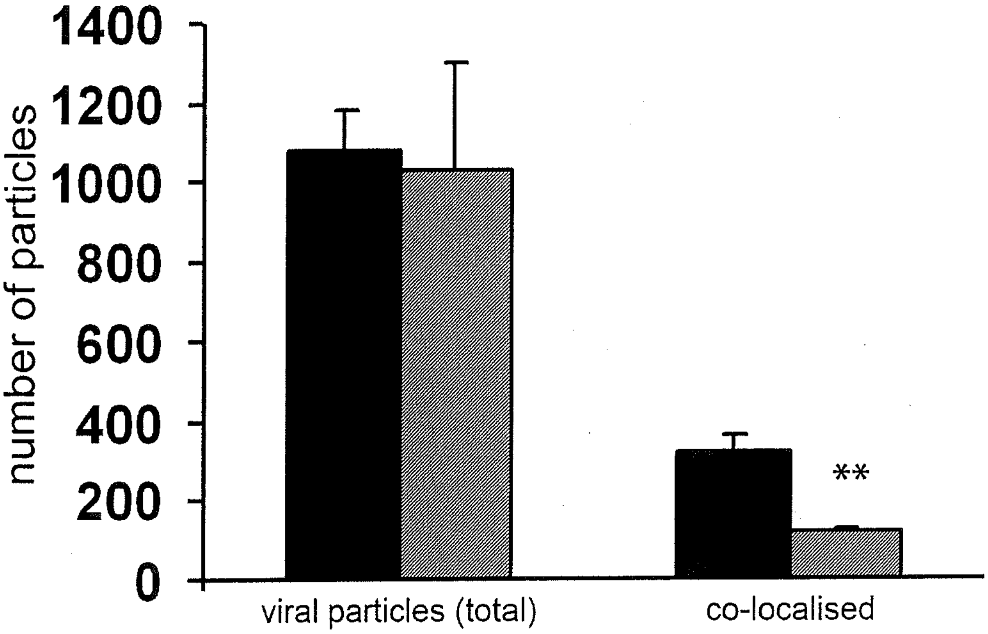

number of particles
1400
1200
1000
800
600
400
200
0
**
viral particles (total)
co-localised

Figure 18

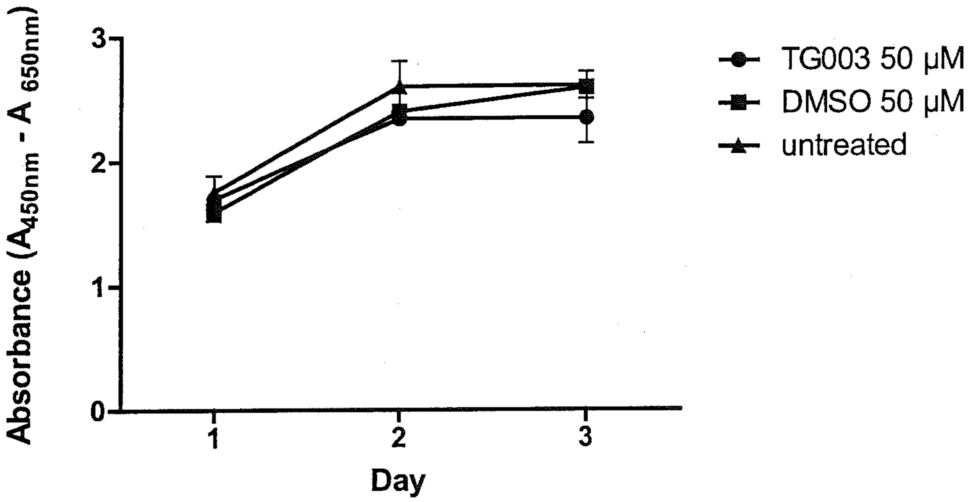
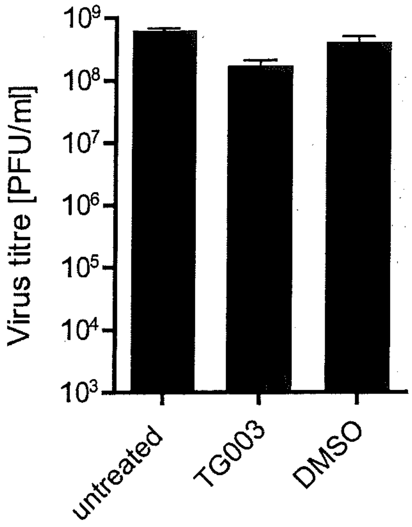

Absorbance (A_{450nm} - A_{650nm})
3
2
1
0
1
2
3
Day
TG003 50 µM
DMSO 50 µM
untreated

Figure 19


Virus titre [PFU/ml]
10^9
10^8
10^7
10^6
10^5
10^4
10^3
untreated
TG003
DMSO

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
23456	ABCB10	NM_012089	ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP), MEMBER 10	-2.07	-0.26	-0.6	-2.49	-2.02
23456	ABCB10	NM_012089	ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP), MEMBER 10	-0.28	0.99	-0.43	-2.49	-0.07
23456	ABCB10	NM_012089	ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP), MEMBER 10	-3.54	-1.38	-0.49	-2.49	-2.66
23456	ABCB10	NM_012089	ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP), MEMBER 10	-1.42	-1.57	-1.62	-2.49	-0.77
368	ABCC6	BC050733	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTR/MRP), MEMBER 6	-1.45	0.61	0.38	-8.06	-0.89
368	ABCC6	BC050733	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTR/MRP), MEMBER 6	-0.3	-0.48	-0.72	-8.06	-2.14
368	ABCC6	BC050733	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTR/MRP), MEMBER 6	-3.13	-0.39	-0.48	-8.06	-6.31
368	ABCC6	BC050733	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTR/MRP), MEMBER 6	-1.9	-0.28	-1.1	-8.06	-1.49
31	ACACA	NM_198839	ACETYL-COENZYME A CARBOXYLASE ALPHA	-1.57	-0.7	-0.67	-9.18	-1.57
31	ACACA	NM_198839	ACETYL-COENZYME A CARBOXYLASE ALPHA	-0.47	0.16	-0.05	-9.18	-1.05
31	ACACA	NM_198839	ACETYL-COENZYME A CARBOXYLASE ALPHA	-4.34	-1.92	-1.37	-9.18	-7.54
31	ACACA	NM_198839	ACETYL-COENZYME A CARBOXYLASE ALPHA	-0.97	-0.27	0.4	-9.18	-7.93
130399	ACVR1C	NM_145259	ACTIVIN A RECEPTOR, TYPE IC	-2.69	-0.11	0.09	-9.59	-8.7
130399	ACVR1C	NM_145259	ACTIVIN A RECEPTOR, TYPE IC	0.08	-0.0065	0.13	-9.59	-0.18
130399	ACVR1C	NM_145259	ACTIVIN A RECEPTOR, TYPE IC	0.44	-0.06	0.58	-9.59	0.09
130399	ACVR1C	NM_145259	ACTIVIN A RECEPTOR, TYPE IC	-2.23	-0.02	0.18	-9.59	-5.98
10768	AHCYL1	NM_006621	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	-0.79	-1.04	-0.6	-0.65	-1.01
10768	AHCYL1	NM_006621	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	-0.52	-0.25	1.05	-0.65	-0.36
10768	AHCYL1	NM_006621	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	-0.38	-1.42	-0.23	-0.65	-0.22
10768	AHCYL1	NM_006621	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	-2.01	-1.68	-1.25	-0.65	-2.02
51390	AIG1	NM_016108	ANDROGEN-INDUCED 1	-6.17	-0.93	-1.32	-9.36	-8.26
51390	AIG1	NM_016108	ANDROGEN-INDUCED 1	-3.15	-1.03	-0.31	-9.36	-3.33
81693	AMN	NM_030943	AMNIONLESS HOMOLOG (MOUSE)	0.59	2.94	2.05	-9.32	0.93
81693	AMN	NM_030943	AMNIONLESS HOMOLOG (MOUSE)	-1.93	-1.41	-1.82	-9.32	-8.17
81693	AMN	NM_030943	AMNIONLESS HOMOLOG (MOUSE)	-0.88	-0.001	0.16	-9.32	-0.38
81693	AMN	NM_030943	AMNIONLESS HOMOLOG (MOUSE)	-0.33	-1.02	-0.94	-9.32	-5.37
255239	ANKK1	NM_178510	ANKYRIN REPEAT AND KINASE DOMAIN CONTAINING 1	-0.15	0.39	0.23	-9.42	0.06
255239	ANKK1	NM_178510	ANKYRIN REPEAT AND KINASE DOMAIN CONTAINING 1	-7.04	-1.85	-1.37	-9.42	-8.37
255239	ANKK1	NM_178510	ANKYRIN REPEAT AND KINASE DOMAIN CONTAINING 1	-2.31	-1.23	-1.14	-9.42	-2.1
255239	ANKK1	NM_178510	ANKYRIN REPEAT AND KINASE DOMAIN CONTAINING 1	-0.34	0	0	-9.42	1.12
1173	AP2M1	BC013796	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	-4.96	0.32	-1.36	-3.03	-7.4
1173	AP2M1	BC013796	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	0.02	-0.31	-0.33	-3.03	-1.55
1173	AP2M1	BC013796	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	-0.44	-0.11	-0.01	-3.03	-1.51
1173	AP2M1	BC013796	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	-2.01	-0.45	-0.76	-3.03	-3.66
54518	APBB1IP	NM_019043	AMYLOID BETA (A4) PRECURSOR PROTEIN-BINDING, FAMILY B, MEMBER 1 INTERACTING PROTEIN	-3.96	-0.15	-0.48	-8.75	-7.25
54518	APBB1IP	NM_019043	AMYLOID BETA (A4) PRECURSOR PROTEIN-BINDING, FAMILY B, MEMBER 1 INTERACTING PROTEIN	-3.27	1.42	-0.58	-8.75	-1.57
8883	APPBP1	NM_003905	AMYLOID BETA PRECURSOR PROTEIN BINDING PROTEIN 1	0.96	0.83	0.93	-0.49	0.47
8883	APPBP1	NM_003905	AMYLOID BETA PRECURSOR PROTEIN BINDING PROTEIN 1	-0.03	0.35	1.25	-0.49	0.47
8883	APPBP1	NM_003905	AMYLOID BETA PRECURSOR PROTEIN BINDING PROTEIN 1	-0.84	-2.03	-0.99	-0.49	-1
8883	APPBP1	NM_003905	AMYLOID BETA PRECURSOR PROTEIN BINDING PROTEIN 1	-1.07	-1.66	-1.06	-0.49	-1
372	ARCN1	NM_001655	ARCHAIN 1	-5.73	-1.63	-1.4	-7.97	-5.69
372	ARCN1	NM_001655	ARCHAIN 1	-3.28	-2.26	-1.4	-7.97	-8.5
8260	ARD1	NM_003491	ARD1 HOMOLOG A, N-ACETYLTRANSFERASE (S. CEREVISIAE)	1.76	-0.34	-0.08	-8.4	1.49
8260	ARD1	NM_003491	ARD1 HOMOLOG A, N-ACETYLTRANSFERASE (S. CEREVISIAE)	0.08	0.35	0.5	-8.4	-1.05
8260	ARD1	NM_003491	ARD1 HOMOLOG A, N-ACETYLTRANSFERASE (S. CEREVISIAE)	-1.55	-0.08	-0.06	-8.4	-1.76
8260	ARD1	NM_003491	ARD1 HOMOLOG A, N-ACETYLTRANSFERASE (S. CEREVISIAE)	-2.99	-0.88	-0.89	-8.4	-6.77
9048	ARTN	NM_057160	ARTEMIN	-6.31	-0.66	-1.12	-8.17	-6.46
9048	ARTN	NM_057160	ARTEMIN	0.008	1.08	0.18	-8.17	0.4
9048	ARTN	NM_057160	ARTEMIN	-1.07	-1.8	-1.28	-8.17	-0.86
9048	ARTN	NM_057160	ARTEMIN	-0.81	-1.45	-1.34	-8.17	-1.39
443	ASPA	NM_000049	ASPARTOACYLASE (CANAVAN DISEASE)	-2.16	-1.13	-0.81	-8.53	-6.95
443	ASPA	NM_000049	ASPARTOACYLASE (CANAVAN DISEASE)	-1.47	-1.81	-0.87	-8.53	-1.95
443	ASPA	NM_000049	ASPARTOACYLASE (CANAVAN DISEASE)	-4.73	-0.2	-1.86	-8.53	-8.59
443	ASPA	NM_000049	ASPARTOACYLASE (CANAVAN DISEASE)	0.39	-0.04	-0.19	-8.53	-0.09
85300	ATCAY	NM_033064	ATAXIA, CEREBELLAR, CAYMAN TYPE (CAYTAXIN)	-2.08	-0.96	-0.98	-9.45	-8.54
85300	ATCAY	NM_033064	ATAXIA, CEREBELLAR, CAYMAN TYPE (CAYTAXIN)	-4.06	-1.28	-1.53	-9.45	-8.42

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
477	ATP1A2	NM_000702	ATPASE, NA+/K+ TRANSPORTING, ALPHA 2 (+) POLYPEPTIDE	0.65	-0.4	0.32	-9.43	1.46
477	ATP1A2	NM_000702	ATPASE, NA+/K+ TRANSPORTING, ALPHA 2 (+) POLYPEPTIDE	-11.36	-1.57	-1.16	-9.43	-8.39
477	ATP1A2	NM_000702	ATPASE, NA+/K+ TRANSPORTING, ALPHA 2 (+) POLYPEPTIDE	-1.55	-0.42	-1.38	-9.43	-2.2
477	ATP1A2	NM_000702	ATPASE, NA+/K+ TRANSPORTING, ALPHA 2 (+) POLYPEPTIDE	0.41	0.23	1.02	-9.43	0.72
27032	ATP2C1	NM_014382	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	-0.42	0.02	-0.9	-8.73	-0.14
27032	ATP2C1	NM_014382	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	0.3	-0.08	0.88	-8.73	-0.008
27032	ATP2C1	NM_014382	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	-2.11	-1.99	-2.42	-8.73	-1.64
27032	ATP2C1	NM_014382	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	-4.35	-0.43	-1.52	-8.73	-7.24
537	ATP6AP1	AK090462	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 1	-6.62	-0.94	-1.04	-9.56	-8.64
537	ATP6AP1	AK090462	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 1	-1.15	-1.37	-1.01	-9.56	-3.48
10159	ATP6AP2	NM_005765	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	-0.04	-0.06	-0.04	0.44	0.29
10159	ATP6AP2	NM_005765	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	-0.96	-1.44	-1.26	0.44	-0.72
10159	ATP6AP2	NM_005765	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	0.84	-0.67	-0.04	0.44	0.99
10159	ATP6AP2	NM_005765	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	-0.002	-1.67	-0.87	0.44	0.53
527	ATP6V0C	NM_001694	ATPASE, H+ TRANSPORTING, LYSOSOMAL 16KDA, V0 SUBUNIT C	-4.07	-1.76	-1.45	-9.55	-8.61
527	ATP6V0C	NM_001694	ATPASE, H+ TRANSPORTING, LYSOSOMAL 16KDA, V0 SUBUNIT C	-0.1	-1.96	-0.96	-9.55	0.71
9114	ATP6V0D1	NM_004691	ATPASE, H+ TRANSPORTING, LYSOSOMAL 38KDA, V0 SUBUNIT D1	-0.08	-2.23	-1.21	-9.25	-8.06
9114	ATP6V0D1	NM_004691	ATPASE, H+ TRANSPORTING, LYSOSOMAL 38KDA, V0 SUBUNIT D1	-3.18	-1.78	-2.3	-9.25	-3.94
523	ATP6V1A	NM_001690	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	0.86	-2.02	-0.03	-8.98	-0.1
523	ATP6V1A	NM_001690	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	-1.59	-1.17	-1.12	-8.98	-1.22
523	ATP6V1A	NM_001690	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	-4.17	-0.57	-0.8	-8.98	-7.61
523	ATP6V1A	NM_001690	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	1.07	-0.03	1.36	-8.98	1.32
526	ATP6V1B2	NM_001693	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	-0.78	-0.01	-0.15	-0.47	-1.63
526	ATP6V1B2	NM_001693	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	-0.88	-1.04	-0.54	-0.47	-1.05
526	ATP6V1B2	NM_001693	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	0.6	-0.69	-0.18	-0.47	0.92
526	ATP6V1B2	NM_001693	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	-0.06	-1.74	-1.82	-0.47	-0.32
8312	AXIN1	NM_003502	AXIN 1	-1.53	0.01	-0.27	-9.12	-1.34
8312	AXIN1	NM_003502	AXIN 1	-4.32	0.38	-1.14	-9.12	-8.43
8312	AXIN1	NM_003502	AXIN 1	-0.18	0.64	0.63	-9.12	0.51
8312	AXIN1	NM_003502	AXIN 1	-3.68	-1.2	-0.48	-9.12	-7.83
567	B2M	NM_004048	BETA-2-MICROGLOBULIN	-3.48	-0.33	-1.35	-7.89	-6.1
567	B2M	NM_004048	BETA-2-MICROGLOBULIN	0.78	1.11	0.73	-7.89	1.01
567	B2M	NM_004048	BETA-2-MICROGLOBULIN	0.8	-0.27	0.48	-7.89	0.49
567	B2M	NM_004048	BETA-2-MICROGLOBULIN	0	-0.54	-1.91	-7.89	-7.54
93010	B3GNT7	AK000770	UDP-GLCNAC:BETAGAL BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE 7	-2.1	-0.81	-1.65	-1.48	-1.76
93010	B3GNT7	AK000770	UDP-GLCNAC:BETAGAL BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE 7	-0.96	-1.24	-1.45	-1.48	-0.26
60468	BACH2	NM_021813	BTB AND CNC HOMOLOGY 1, BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR 2	-0.33	-0.36	-0.58	-8.54	-6.95
60468	BACH2	NM_021813	BTB AND CNC HOMOLOGY 1, BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR 2	0.004	-0.75	-1.28	-8.54	0.24
60468	BACH2	NM_021813	BTB AND CNC HOMOLOGY 1, BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR 2	-1.19	-0.005	-0.11	-8.54	-1.42
60468	BACH2	NM_021813	BTB AND CNC HOMOLOGY 1, BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR 2	0.23	-1.21	-1.18	-8.54	-5.09
10458	BAIAP2	NM_006340	BAI1-ASSOCIATED PROTEIN 2	-0.08	0.11	-0.78	-8.94	-0.009
10458	BAIAP2	NM_006340	BAI1-ASSOCIATED PROTEIN 2	-3.08	0.05	-0.7	-8.94	-7.54
10458	BAIAP2	NM_006340	BAI1-ASSOCIATED PROTEIN 2	-2.2	-0.44	-1.64	-8.94	-2.82
10458	BAIAP2	NM_006340	BAI1-ASSOCIATED PROTEIN 2	-1.44	-0.94	-0.001	-8.94	-5.74
8938	BAIAP3	NM_003933	BAI1-ASSOCIATED PROTEIN 3	0.5	-1.05	-0.92	0.05	-0.02
8938	BAIAP3	NM_003933	BAI1-ASSOCIATED PROTEIN 3	0.51	1.01	0.28	0.05	0.02
8938	BAIAP3	NM_003933	BAI1-ASSOCIATED PROTEIN 3	-1.2	-2.26	-1.29	0.05	-0.54
8938	BAIAP3	NM_003933	BAI1-ASSOCIATED PROTEIN 3	0.83	1.78	0.15	0.05	2.57
343472	BARHL2	NM_020063	BARH-LIKE 2 (DROSOPHILA)	-5.08	-0.23	-1.04	-9.38	-8.3
343472	BARHL2	NM_020063	BARH-LIKE 2 (DROSOPHILA)	-2.95	-1.12	-0.99	-9.38	-1.81
4671	BIRC1	NM_004536	BACULOVIRAL IAP REPEAT-CONTAINING 1	-0.002	-0.19	-1.03	-2.02	-0.42
4671	BIRC1	NM_004536	BACULOVIRAL IAP REPEAT-CONTAINING 1	-1.02	-0.43	-0.71	-2.02	-2.52
4671	BIRC1	NM_004536	BACULOVIRAL IAP REPEAT-CONTAINING 1	0.45	0.19	-0.47	-2.02	0.71
4671	BIRC1	NM_004536	BACULOVIRAL IAP REPEAT-CONTAINING 1	-3.04	-0.42	-1.39	-2.02	-2.65
7862	BRPF1	NM_004634	BROMODOMAIN AND PHD FINGER CONTAINING, 1	-1.56	-0.56	-1.55	-8.41	-1.61
7862	BRPF1	NM_004634	BROMODOMAIN AND PHD FINGER CONTAINING, 1	-7.33	-0.05	-0.67	-8.41	-6.78

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7862	BRPF1	NM_004634	BROMODOMAIN AND PHD FINGER CONTAINING, 1	0.78	0.007	0.42	-8.41	0.36
7862	BRPF1	NM_004634	BROMODOMAIN AND PHD FINGER CONTAINING, 1	-0.33	-0.42	-0.02	-8.41	-0.78
9256	BZRAP1	NM_004758	BENZODIAZAPINE RECEPTOR (PERIPHERAL) ASSOCIATED PROTEIN 1	-0.26	-0.16	-0.03	-8.62	-0.31
9256	BZRAP1	NM_004758	BENZODIAZAPINE RECEPTOR (PERIPHERAL) ASSOCIATED PROTEIN 1	-0.37	0.9	-0.83	-8.62	-1.16
9256	BZRAP1	NM_004758	BENZODIAZAPINE RECEPTOR (PERIPHERAL) ASSOCIATED PROTEIN 1	-5.44	-0.73	-0.86	-8.62	-7.07
9256	BZRAP1	NM_004758	BENZODIAZAPINE RECEPTOR (PERIPHERAL) ASSOCIATED PROTEIN 1	-1.8	-1.65	-0.69	-8.62	-7.66
80195	C10orf57	NM_025125	CHROMOSOME 10 OPEN READING FRAME 57	-5.13	-1.21	-1.58	-9.42	-8.37
80195	C10orf57	NM_025125	CHROMOSOME 10 OPEN READING FRAME 57	-0.25	0.02	0.67	-9.42	0.9
80195	C10orf57	NM_025125	CHROMOSOME 10 OPEN READING FRAME 57	-1.94	-0.22	-0.63	-9.42	-2.58
80195	C10orf57	NM_025125	CHROMOSOME 10 OPEN READING FRAME 57	-0.19	0.87	1.85	-9.42	-0.37
115708	C14orf172	NM_152307	CHROMOSOME 14 OPEN READING FRAME 172	-3.04	-0.49	-0.89	-9.01	-7.66
115708	C14orf172	NM_152307	CHROMOSOME 14 OPEN READING FRAME 172	0.53	3.03	0.31	-9.01	4.47
115708	C14orf172	NM_152307	CHROMOSOME 14 OPEN READING FRAME 172	-3.13	-0.33	-1.08	-9.01	-1.92
115708	C14orf172	NM_152307	CHROMOSOME 14 OPEN READING FRAME 172	-1.13	-0.74	-0.52	-9.01	-1.63
91978	C19orf20	BC009520	CHROMOSOME 19 OPEN READING FRAME 20	-1.52	-0.22	0.53	-7.98	-6.21
91978	C19orf20	BC009520	CHROMOSOME 19 OPEN READING FRAME 20	-2.87	-0.62	-1.25	-7.98	-1.55
150142	C21orf121	BC029588	CHROMOSOME 21 OPEN READING FRAME 121	-0.57	-1.17	0.1	-2.91	-1.95
150142	C21orf121	BC029588	CHROMOSOME 21 OPEN READING FRAME 121	-4.51	-1.41	-1.14	-2.91	-2.76
56911	C21orf7	NM_020152	CHROMOSOME 21 OPEN READING FRAME 7	-1.26	-1.13	-1.65	-7.83	-6.03
56911	C21orf7	NM_020152	CHROMOSOME 21 OPEN READING FRAME 7	-5.18	-1.75	-1.7	-7.83	-2.24
25927	C2orf32	NM_015463	CHROMOSOME 2 OPEN READING FRAME 32	-1.56	0.11	-0.54	-3.17	-2.13
25927	C2orf32	NM_015463	CHROMOSOME 2 OPEN READING FRAME 32	-1.66	-0.74	-1.2	-3.17	-1.61
85315	C6orf33	BC030664	PROGESTIN AND ADIPOQ RECEPTOR FAMILY MEMBER VIII	1.07	-1.1	-0.13	-7.48	-0.08
85315	C6orf33	BC030664	PROGESTIN AND ADIPOQ RECEPTOR FAMILY MEMBER VIII	-1.34	0	0.21	-7.48	-6.69
85315	C6orf33	BC030664	PROGESTIN AND ADIPOQ RECEPTOR FAMILY MEMBER VIII	-2.29	-0.69	-0.25	-7.48	-5.35
85315	C6orf33	BC030664	PROGESTIN AND ADIPOQ RECEPTOR FAMILY MEMBER VIII	-1.64	-0.54	-0.29	-7.48	-5.61
377677	CA13	AK095314	CARBONIC ANHYDRASE XIII	-2.31	-2.05	-1.08	-2.54	-5.87
377677	CA13	AK095314	CARBONIC ANHYDRASE XIII	-1.51	-0.63	-0.67	-2.54	-2.29
377677	CA13	AK095314	CARBONIC ANHYDRASE XIII	-0.03	-0.2	0.04	-2.54	0.16
377677	CA13	AK095314	CARBONIC ANHYDRASE XIII	-1.61	1.5	-0.02	-2.54	-1.71
85417	CCNB3	NM_033031	CYCLIN B3	-4.03	-0.34	-1.34	-8.75	-7.26
85417	CCNB3	NM_033031	CYCLIN B3	0.69	1.96	0.9	-8.75	-0.07
85417	CCNB3	NM_033031	CYCLIN B3	-0.36	-1.96	-1.8	-8.75	-0.72
85417	CCNB3	NM_033031	CYCLIN B3	1.1	-0.57	0.07	-8.75	0.38
961	CD47	NM_001777	CD47 ANTIGEN (RH-RELATED ANTIGEN, INTEGRIN-ASSOCIATED SIGNAL TRANSDUCER)	-4.72	-1.02	-2.4	-9.48	-8.68
961	CD47	NM_001777	CD47 ANTIGEN (RH-RELATED ANTIGEN, INTEGRIN-ASSOCIATED SIGNAL TRANSDUCER)	0.13	0.23	0.05	-9.48	-8.48
961	CD47	NM_001777	CD47 ANTIGEN (RH-RELATED ANTIGEN, INTEGRIN-ASSOCIATED SIGNAL TRANSDUCER)	0.58	0	0.66	-9.48	0.72
961	CD47	NM_001777	CD47 ANTIGEN (RH-RELATED ANTIGEN, INTEGRIN-ASSOCIATED SIGNAL TRANSDUCER)	-0.63	-0.94	-1.05	-9.48	-1.81
962	CD48	NM_001778	CD48 ANTIGEN (B-CELL MEMBRANE PROTEIN)	-0.27	-0.4	-0.97	-7.11	-0.41
962	CD48	NM_001778	CD48 ANTIGEN (B-CELL MEMBRANE PROTEIN)	-1.09	-1.59	-0.51	-7.11	-1.24
962	CD48	NM_001778	CD48 ANTIGEN (B-CELL MEMBRANE PROTEIN)	-1.86	-0.88	-0.98	-7.11	-1.84
962	CD48	NM_001778	CD48 ANTIGEN (B-CELL MEMBRANE PROTEIN)	-4.26	-1.5	-0.74	-7.11	-7.38
965	CD58	NM_001779	CD58 ANTIGEN, (LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3)	0.11	0.01	2.05	-0.05	-0.04
965	CD58	NM_001779	CD58 ANTIGEN, (LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3)	-1.53	-1.68	-0.86	-0.05	-9.58
965	CD58	NM_001779	CD58 ANTIGEN, (LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3)	-0.3	-1	-1.11	-0.05	-2.06
965	CD58	NM_001779	CD58 ANTIGEN, (LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3)	0.7	0.03	0.54	-0.05	0.99
975	CD81	NM_004356	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	-10.83	-1.46	-1.7	-8.25	-6.57
975	CD81	NM_004356	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	0.41	-1.25	-1.86	-8.25	1.18
975	CD81	NM_004356	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	0.05	-0.87	-0.001	-8.25	0.73
975	CD81	NM_004356	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	-1.25	0.01	-0.58	-8.25	-2.01
1027	CDKN1B	NM_004064	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	-1.93	-2.2	-0.72	-7.19	-2.04
1027	CDKN1B	NM_004064	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	-1.19	0.09	-0.33	-7.19	-1.01
1027	CDKN1B	NM_004064	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	-0.54	0.38	-0.09	-7.19	-0.5
1027	CDKN1B	NM_004064	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	-2.13	-0.96	-0.97	-7.19	-5.28
1056	CEL	NM_001807	CARBOXYL ESTER LIPASE (BILE SALT-STIMULATED LIPASE)	-5.88	-0.08	-0.7	-8.8	-7.33
1056	CEL	NM_001807	CARBOXYL ESTER LIPASE (BILE SALT-STIMULATED LIPASE)	-1.07	-0.21	-1.27	-8.8	-0.4

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1056	CEL	NM_001807	CARBOXYL ESTER LIPASE (BILE SALT-STIMULATED LIPASE)	-2.25	-0.11	-1.42	-8.8	-8.51
1056	CEL	NM_001807	CARBOXYL ESTER LIPASE (BILE SALT-STIMULATED LIPASE)	0.005	0.67	1.41	-8.8	-0.41
11033	CENTA1	NM_006869	CENTAURIN, ALPHA 1	-0.08	-1.34	-1.62	-9.31	-0.53
11033	CENTA1	NM_006869	CENTAURIN, ALPHA 1	-5	-2.03	-1.58	-9.31	-8.17
11033	CENTA1	NM_006869	CENTAURIN, ALPHA 1	-0.86	2.02	1.9	-9.31	-0.56
11033	CENTA1	NM_006869	CENTAURIN, ALPHA 1	-2.17	0.01	-0.2	-9.31	-1.65
1128	CHRM1	NM_000738	CHOLINERGIC RECEPTOR, MUSCARINIC 1	-6.96	-1.52	-2.1	-8.65	-7.11
1128	CHRM1	NM_000738	CHOLINERGIC RECEPTOR, MUSCARINIC 1	0.62	0.76	2.25	-8.65	1.13
1128	CHRM1	NM_000738	CHOLINERGIC RECEPTOR, MUSCARINIC 1	0.31	1.59	0.47	-8.65	-0.1
1128	CHRM1	NM_000738	CHOLINERGIC RECEPTOR, MUSCARINIC 1	-4.91	-0.43	-0.99	-8.65	-6.02
23563	CHST5	AK025820	CARBOHYDRATE (N-ACETYLGLUCOSAMINE 6-O) SULFOTRANSFERASE 5	-0.85	0.38	-1.08	-1.04	-0.4
23563	CHST5	AK025820	CARBOHYDRATE (N-ACETYLGLUCOSAMINE 6-O) SULFOTRANSFERASE 5	-2.93	-0.33	-1.45	-1.04	-2.88
1147	CHUK	AF009225	CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE	-1.59	-0.31	0.08	-9.32	-5.28
1147	CHUK	AF009225	CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE	-1.2	1.43	-0.44	-9.32	-8.18
1147	CHUK	AF009225	CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE	0.38	0.03	-0.57	-9.32	0.19
1147	CHUK	AF009225	CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE	-2.4	-0.6	-1.31	-9.32	-7.81
1163	CKS1B	NM_001826	CDC28 PROTEIN KINASE REGULATORY SUBUNIT 1B	-1.63	-0.98	-0.01	-9	-5.57
1163	CKS1B	NM_001826	CDC28 PROTEIN KINASE REGULATORY SUBUNIT 1B	0.44	0.32	0.59	-9	2.28
1163	CKS1B	NM_001826	CDC28 PROTEIN KINASE REGULATORY SUBUNIT 1B	0.65	-0.49	0.41	-9	-0.11
1163	CKS1B	NM_001826	CDC28 PROTEIN KINASE REGULATORY SUBUNIT 1B	-1.75	-0.52	-0.6	-9	-7.65
25932	CLIC4	NM_013943	CHLORIDE INTRACELLULAR CHANNEL 4	-4.89	-1.44	-0.32	-9.92	-9.58
25932	CLIC4	NM_013943	CHLORIDE INTRACELLULAR CHANNEL 4	1.05	-1.03	0.14	-9.92	1.03
25932	CLIC4	NM_013943	CHLORIDE INTRACELLULAR CHANNEL 4	-0.15	-0.47	-0.38	-9.92	-0.27
25932	CLIC4	NM_013943	CHLORIDE INTRACELLULAR CHANNEL 4	0.51	0.08	0.32	-9.92	1.17
1195	CLK1	NM_004071	CDC-LIKE KINASE 1	0.64	-0.14	0.04	-9.25	1.07
1195	CLK1	NM_004071	CDC-LIKE KINASE 1	-4.65	-0.24	-0.34	-9.25	-8.05
1195	CLK1	NM_004071	CDC-LIKE KINASE 1	-3	-0.29	-0.11	-9.25	-1.51
1195	CLK1	NM_004071	CDC-LIKE KINASE 1	0.4	0.03	0.13	-9.25	2.95
9746	CLSTN3	NM_014718	CALSYNTENIN 3	-2.61	-0.27	-0.66	-7.88	-6.09
9746	CLSTN3	NM_014718	CALSYNTENIN 3	-2.48	-0.86	-0.73	-7.88	-9.58
1258	CNGB1	NM_001297	CYCLIC NUCLEOTIDE GATED CHANNEL BETA 1	0.52	1.55	0.16	0.04	0.88
1258	CNGB1	NM_001297	CYCLIC NUCLEOTIDE GATED CHANNEL BETA 1	-2.53	-1.97	-0.83	0.04	-5.37
1258	CNGB1	NM_001297	CYCLIC NUCLEOTIDE GATED CHANNEL BETA 1	-2.17	-0.97	-1.37	0.04	-5.27
1258	CNGB1	NM_001297	CYCLIC NUCLEOTIDE GATED CHANNEL BETA 1	0.01	1.96	1.68	0.04	1.5
26507	CNNM1	NM_020348	CYCLIN M1	-0.93	-0.28	-1.04	-4.76	-1.82
26507	CNNM1	NM_020348	CYCLIN M1	-3.31	-0.96	-1.07	-4.76	-3.2
1314	COPA	NM_004371	COATOMER PROTEIN COMPLEX, SUBUNIT ALPHA	-9.84	-1.17	-0.99	-9.55	-8.65
1314	COPA	NM_004371	COATOMER PROTEIN COMPLEX, SUBUNIT ALPHA	-6.73	-1.5	-1.2	-9.55	-8.05
1315	COPB	NM_016451	COATOMER PROTEIN COMPLEX, SUBUNIT BETA	-4.65	-0.89	-1.21	-7.29	-5.39
1315	COPB	NM_016451	COATOMER PROTEIN COMPLEX, SUBUNIT BETA	-0.86	-0.96	-1.12	-7.29	-0.07
9276	COPB2	NM_004766	COATOMER PROTEIN COMPLEX, SUBUNIT BETA 2 (BETA PRIME)	-0.002	0.33	1.39	-9.4	0.08
9276	COPB2	NM_004766	COATOMER PROTEIN COMPLEX, SUBUNIT BETA 2 (BETA PRIME)	-6.26	-2.11	-2.15	-9.4	-8.33
9276	COPB2	NM_004766	COATOMER PROTEIN COMPLEX, SUBUNIT BETA 2 (BETA PRIME)	-9.06	0.6	-1.16	-9.4	-8.22
9276	COPB2	NM_004766	COATOMER PROTEIN COMPLEX, SUBUNIT BETA 2 (BETA PRIME)	-5.05	-1.62	-1.08	-9.4	-8.29
11316	COPE	NM_007263	COATOMER PROTEIN COMPLEX, SUBUNIT EPSILON	-3.22	-0.22	-1.03	-7.74	-4.08
11316	COPE	NM_007263	COATOMER PROTEIN COMPLEX, SUBUNIT EPSILON	-1.69	0.44	-0.75	-7.74	-5.93
22820	COPG	NM_016128	COATOMER PROTEIN COMPLEX, SUBUNIT GAMMA	-7.28	-0.7	-1.61	-9.34	-8.69
22820	COPG	NM_016128	COATOMER PROTEIN COMPLEX, SUBUNIT GAMMA	-1.52	-2.32	-0.83	-9.34	-8.22
22820	COPG	NM_016128	COATOMER PROTEIN COMPLEX, SUBUNIT GAMMA	-3.8	-1.26	-0.91	-9.34	-7.76
22820	COPG	NM_016128	COATOMER PROTEIN COMPLEX, SUBUNIT GAMMA	-1.59	-1.02	-0.08	-9.34	0.46
57585	CRAMP1L	AB037847	CRM, CRAMPED-LIKE (DROSOPHILA)	-0.49	-0.1	0.06	-3.65	-0.93
57585	CRAMP1L	AB037847	CRM, CRAMPED-LIKE (DROSOPHILA)	-0.12	0.23	0.45	-3.65	-1.42
57585	CRAMP1L	AB037847	CRM, CRAMPED-LIKE (DROSOPHILA)	-3.11	-0.001	-1.04	-3.65	-4.25
57585	CRAMP1L	AB037847	CRM, CRAMPED-LIKE (DROSOPHILA)	-1.6	-0.35	-0.46	-3.65	-2.66
9282	CRSP2	AF070563	COFACTOR REQUIRED FOR SP1 TRANSCRIPTIONAL ACTIVATION, SUBUNIT 2, 150KDA	0.01	2.14	0.09	-2.57	0.02
9282	CRSP2	AF070563	COFACTOR REQUIRED FOR SP1 TRANSCRIPTIONAL ACTIVATION, SUBUNIT 2, 150KDA	-1.85	0.03	-0.63	-2.57	-1.97

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9282	CRSP2	AF070563	COFACTOR REQUIRED FOR SP1 TRANSCRIPTIONAL ACTIVATION, SUBUNIT 2, 150KDA	-1.46	-0.05	-0.09	-2.57	-0.7
9282	CRSP2	AF070563	COFACTOR REQUIRED FOR SP1 TRANSCRIPTIONAL ACTIVATION, SUBUNIT 2, 150KDA	-1.58	-1.16	-0.9	-2.57	-5.16
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	0.57	1.49	0.13	-8.27	0.74
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	0.19	0.009	1.15	-8.27	0.74
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	-0.08	0.75	-0.08	-8.27	-6.6
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	-2.63	0.74	0.11	-8.27	-6.6
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	-0.32	0.009	-0.37	-8.27	-0.87
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	-0.001	1.09	0.25	-8.27	-0.87
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	-1.87	-0.3	-0.72	-8.27	-6.47
1408	Cry2	NM_021117	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	0.05	-0.16	-0.27	-8.27	-6.47
1409	CRYAA	NM_000394	CRYSTALLIN, ALPHA A	-7.83	-0.69	-1.68	-9.45	-8.42
1409	CRYAA	NM_000394	CRYSTALLIN, ALPHA A	-1.31	-0.28	-1.04	-9.45	-2.51
30818	CSEN	NM_013434	KV CHANNEL INTERACTING PROTEIN 3, CALSENILIN	0.17	-1.45	-1.75	-2.26	-1.52
30818	CSEN	NM_013434	KV CHANNEL INTERACTING PROTEIN 3, CALSENILIN	-2.48	-1.39	-1.31	-2.26	-2.65
30818	CSEN	NM_013434	KV CHANNEL INTERACTING PROTEIN 3, CALSENILIN	-0.35	-1.43	-1.18	-2.26	-0.36
30818	CSEN	NM_013434	KV CHANNEL INTERACTING PROTEIN 3, CALSENILIN	-1.42	-1.02	-1.6	-2.26	-7.93
119016	CTGLF1	NM_133446	CENTAURIN, GAMMA-LIKE FAMILY, MEMBER 1	-1.76	0.41	-0.2	-8.89	-7.46
119016	CTGLF1	NM_133446	CENTAURIN, GAMMA-LIKE FAMILY, MEMBER 1	-2.41	0.29	-1.18	-8.89	-6.5
1499	CTNNB1	NM_001904	CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1, 88KDA	0.003	3.55	3.02	-7.52	0.96
1499	CTNNB1	NM_001904	CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1, 88KDA	-0.81	-1.7	-0.34	-7.52	-5.66
1499	CTNNB1	NM_001904	CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1, 88KDA	0.32	-0.83	-0.33	-7.52	1.95
1499	CTNNB1	NM_001904	CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1, 88KDA	-0.76	-1.45	-0.12	-7.52	-1.74
10663	CXCR6	NM_006564	CHEMOKINE (C-X-C MOTIF) RECEPTOR 6	-4.01	-1.85	-1.65	-8.06	-6.33
10663	CXCR6	NM_006564	CHEMOKINE (C-X-C MOTIF) RECEPTOR 6	-0.17	1.19	2.37	-8.06	-0.27
10663	CXCR6	NM_006564	CHEMOKINE (C-X-C MOTIF) RECEPTOR 6	-0.06	-1.49	-0.02	-8.06	-0.64
10663	CXCR6	NM_006564	CHEMOKINE (C-X-C MOTIF) RECEPTOR 6	-0.25	-0.62	-0.83	-8.06	-0.55
1586	CYP17A1	NM_000102	CYTOCHROME P450, FAMILY 17, SUBFAMILY A, POLYPEPTIDE 1	-0.77	0.005	-0.22	-9.48	-0.79
1586	CYP17A1	NM_000102	CYTOCHROME P450, FAMILY 17, SUBFAMILY A, POLYPEPTIDE 1	0.08	-0.58	-0.26	-9.48	-0.02
1586	CYP17A1	NM_000102	CYTOCHROME P450, FAMILY 17, SUBFAMILY A, POLYPEPTIDE 1	-1.88	-1.02	-0.006	-9.48	-3.91
1586	CYP17A1	NM_000102	CYTOCHROME P450, FAMILY 17, SUBFAMILY A, POLYPEPTIDE 1	-6.58	-0.19	-0.77	-9.48	-8.48
113612	CYP2U1	NM_183075	CYTOCHROME P450, FAMILY 2, SUBFAMILY U, POLYPEPTIDE 1	0.1	-0.52	-0.92	-8.5	0.59
113612	CYP2U1	NM_183075	CYTOCHROME P450, FAMILY 2, SUBFAMILY U, POLYPEPTIDE 1	-2.76	0.36	0.04	-8.5	-6.9
113612	CYP2U1	NM_183075	CYTOCHROME P450, FAMILY 2, SUBFAMILY U, POLYPEPTIDE 1	0.48	-0.32	-0.81	-8.5	0.23
113612	CYP2U1	NM_183075	CYTOCHROME P450, FAMILY 2, SUBFAMILY U, POLYPEPTIDE 1	-2.4	-0.009	-0.55	-8.5	-1.85
7818	DAP3	NM_033657	DEATH ASSOCIATED PROTEIN 3	0.08	1.2	0.86	-1.53	0.89
7818	DAP3	NM_033657	DEATH ASSOCIATED PROTEIN 3	0.006	0.94	-0.58	-1.53	0.04
7818	DAP3	NM_033657	DEATH ASSOCIATED PROTEIN 3	-2.65	-1.75	-1.41	-1.53	-1.47
7818	DAP3	NM_033657	DEATH ASSOCIATED PROTEIN 3	-2.36	-1.04	-1.69	-1.53	-2.17
1629	DBT	NM_001918	DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	1.34	0.2	1.97	-7.71	0.52
1629	DBT	NM_001918	DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	0.01	-1.61	-1.02	-7.71	-0.01
1629	DBT	NM_001918	DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	1.02	-0.87	-0.15	-7.71	-5.89
1629	DBT	NM_001918	DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	-2.68	-1.66	-1.2	-7.71	-5.3
166614	DCAMKL2	NM_152619	DOUBLECORTIN AND CAM KINASE-LIKE 2	-0.004	0.62	0.4	-9.56	-0.75
166614	DCAMKL2	NM_152619	DOUBLECORTIN AND CAM KINASE-LIKE 2	-0.15	0.25	0.18	-9.56	-0.15
166614	DCAMKL2	NM_152619	DOUBLECORTIN AND CAM KINASE-LIKE 2	-1.75	-0.71	-0.31	-9.56	-8.64
166614	DCAMKL2	NM_152619	DOUBLECORTIN AND CAM KINASE-LIKE 2	-2.46	-1.7	-0.67	-9.56	-9.58
9775	DDX48	NM_014740	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 48	-0.35	-1.03	-1.11	-2.29	-1.83
9775	DDX48	NM_014740	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 48	-0.03	0.04	-0.9	-2.29	0.26
9775	DDX48	NM_014740	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 48	-2.36	-0.93	-1.39	-2.29	-2.16
9775	DDX48	NM_014740	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 48	-3.96	-0.06	-0.69	-2.29	-5.68
91319	DERL3	AL389876	DER1-LIKE DOMAIN FAMILY, MEMBER 3	-3.34	-0.17	-0.47	-8.31	-6.64
91319	DERL3	AL389876	DER1-LIKE DOMAIN FAMILY, MEMBER 3	-3.56	-1.57	-1.58	-8.31	-8.58
10202	DHRS2	AK000345	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 2	-1.1	-1.23	-1.26	-8.64	-8.05
10202	DHRS2	AK000345	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 2	-2.22	-1.67	-0.74	-8.64	-7.1
10202	DHRS2	AK000345	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 2	0.67	-0.41	0.01	-8.64	1.08
10202	DHRS2	AK000345	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 2	-1.65	-2.16	-2.17	-8.64	-1.98

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1740	DLG2	NM_001364	DISCS, LARGE HOMOLOG 2, CHAPSYN-110 (DROSOPHILA)	-3.65	-0.84	-2	-7.77	-5.8
1740	DLG2	NM_001364	DISCS, LARGE HOMOLOG 2, CHAPSYN-110 (DROSOPHILA)	1.06	0.26	0.09	-7.77	1.07
1740	DLG2	NM_001364	DISCS, LARGE HOMOLOG 2, CHAPSYN-110 (DROSOPHILA)	-0.29	1.16	0.62	-7.77	-0.17
1740	DLG2	NM_001364	DISCS, LARGE HOMOLOG 2, CHAPSYN-110 (DROSOPHILA)	-4.96	-0.53	-1.15	-7.77	-7.72
55929	DMAP1	NM_019100	DNA METHYLTRANSFERASE 1 ASSOCIATED PROTEIN 1	-2.7	-0.58	-0.44	-8.22	-6.53
55929	DMAP1	NM_019100	DNA METHYLTRANSFERASE 1 ASSOCIATED PROTEIN 1	-3.38	0.01	-0.64	-8.22	-2.32
196403	DTX3	NM_178502	DELTEX 3 HOMOLOG (DROSOPHILA)	-0.76	0.9	0.01	-9.92	-1.25
196403	DTX3	NM_178502	DELTEX 3 HOMOLOG (DROSOPHILA)	0.59	0.67	0.97	-9.92	2.49
196403	DTX3	NM_178502	DELTEX 3 HOMOLOG (DROSOPHILA)	-3.81	-0.21	-0.61	-9.92	-9.58
196403	DTX3	NM_178502	DELTEX 3 HOMOLOG (DROSOPHILA)	-2.17	-0.19	-0.004	-9.92	-2.19
1869	E2F1	NM_005225	E2F TRANSCRIPTION FACTOR 1	0	0.68	0.38	-2.19	0.24
1869	E2F1	NM_005225	E2F TRANSCRIPTION FACTOR 1	-2.91	-2.29	-2.26	-2.19	-7.81
1869	E2F1	NM_005225	E2F TRANSCRIPTION FACTOR 1	-0.67	-0.08	-0.19	-2.19	-0.24
1869	E2F1	NM_005225	E2F TRANSCRIPTION FACTOR 1	-1.69	-1.47	-1.67	-2.19	-1.88
1915	EEF1A1	NM_001402	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-2.97	-0.43	-0.88	-9.32	-1.96
1915	EEF1A1	NM_001402	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-3.24	-1.3	-1.24	-9.32	-8.27
1915	EEF1A1	NM_001402	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-1.81	-2.08	-1.59	-9.32	-8.17
1915	EEF1A1	NM_001402	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1	-2.95	-1.68	-1.57	-9.32	-2.77
8661	EIF3S10	NM_003750	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 10 THETA, 150/170KDA	-5.62	-0.79	-1.62	-9	-7.64
8661	EIF3S10	NM_003750	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 10 THETA, 150/170KDA	-1.87	-0.35	-0.47	-9	-8.36
8666	EIF3S4	NM_003755	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 4 DELTA, 44KDA	-3.07	-1.09	-1.45	-4.64	-3.23
8666	EIF3S4	NM_003755	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 4 DELTA, 44KDA	-2.16	-1.39	-0.76	-4.64	-2.47
8665	EIF3S5	NM_003754	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA	1.3	-0.12	-0.22	-9.4	0.59
8665	EIF3S5	NM_003754	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA	-1.67	0.36	-0.48	-9.4	-1.99
8665	EIF3S5	NM_003754	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA	-1.61	-0.34	-0.5	-9.4	-2.55
8665	EIF3S5	NM_003754	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA	-2.75	0.01	-0.8	-9.4	-8.32
8663	EIF3S8	NM_003752	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-3.04	-0.15	-0.82	-7.65	1.17
8663	EIF3S8	NM_003752	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-4.31	-1.16	-0.79	-7.65	-5.82
8663	EIF3S8	NM_003752	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-2.53	-0.05	0.11	-7.65	-4.28
8663	EIF3S8	NM_003752	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-0.01	0.04	0.16	-7.65	-7.44
2051	EPHB6	NM_004445	EPH RECEPTOR B6	-0.16	-0.36	-1.26	-0.47	-0.27
2051	EPHB6	NM_004445	EPH RECEPTOR B6	-2.85	-1.38	-0.7	-0.47	-1.96
2051	EPHB6	NM_004445	EPH RECEPTOR B6	-0.05	1.56	1.37	-0.47	-0.05
2051	EPHB6	NM_004445	EPH RECEPTOR B6	-0.55	-1.09	-1.48	-0.47	-1.76
2197	FAU	NM_001997	FINKEL-BISKIS-REILLY MURINE SARCOMA VIRUS (FBR-MUSV) UBIQUITOUSLY EXPRESSED (FOX DERIVED); RIBOSOMAL PROTEIN S30	0.12	1.1	0.05	-8.66	0.14
2197	FAU	NM_001997	FINKEL-BISKIS-REILLY MURINE SARCOMA VIRUS (FBR-MUSV) UBIQUITOUSLY EXPRESSED (FOX DERIVED); RIBOSOMAL PROTEIN S30	-2.51	1.11	-1.02	-8.66	-2.49
2197	FAU	NM_001997	FINKEL-BISKIS-REILLY MURINE SARCOMA VIRUS (FBR-MUSV) UBIQUITOUSLY EXPRESSED (FOX DERIVED); RIBOSOMAL PROTEIN S30	-0.81	0.36	-0.72	-8.66	-0.44
2197	FAU	NM_001997	FINKEL-BISKIS-REILLY MURINE SARCOMA VIRUS (FBR-MUSV) UBIQUITOUSLY EXPRESSED (FOX DERIVED); RIBOSOMAL PROTEIN S30	-5.26	-1.2	-1.87	-8.66	-8.24
10517	FBXW10	NM_031456	F-BOX AND WD-40 DOMAIN PROTEIN 10	-4.87	-1.03	-0.78	-8.02	-6.27
10517	FBXW10	NM_031456	F-BOX AND WD-40 DOMAIN PROTEIN 10	-1.87	-0.74	-0.21	-8.02	-5.9
26190	FBXW2	NM_012164	F-BOX AND WD-40 DOMAIN PROTEIN 2	0.14	0.57	1.88	-0.18	0.24
26190	FBXW2	NM_012164	F-BOX AND WD-40 DOMAIN PROTEIN 2	0.38	2.14	1.9	-0.18	0.74
26190	FBXW2	NM_012164	F-BOX AND WD-40 DOMAIN PROTEIN 2	-4.93	-1.01	-1.38	-0.18	-7.45
26190	FBXW2	NM_012164	F-BOX AND WD-40 DOMAIN PROTEIN 2	-1.25	-0.41	-1.13	-0.18	-0.16
115548	FCHO2	AL832928	FCH DOMAIN ONLY 2	-1.06	-1.01	-1.57	-8.75	-1.9
115548	FCHO2	AL832928	FCH DOMAIN ONLY 2	-3.68	-0.24	-1.35	-8.75	-7.26
9965	FGF19	NM_005117	FIBROBLAST GROWTH FACTOR 19	-2.2	1.44	-1.15	-2.55	-1.9
9965	FGF19	NM_005117	FIBROBLAST GROWTH FACTOR 19	0.06	0.5	0.6	-2.55	1.3
9965	FGF19	NM_005117	FIBROBLAST GROWTH FACTOR 19	-2.84	-0.22	-0.56	-2.55	-2.04
9965	FGF19	NM_005117	FIBROBLAST GROWTH FACTOR 19	-1.66	-0.54	-1.09	-2.55	-1.72
29109	FHOD1	NM_013241	FORMIN HOMOLOGY 2 DOMAIN CONTAINING 1	-2.37	-1.19	-1.68	-2.31	-5.3
29109	FHOD1	NM_013241	FORMIN HOMOLOGY 2 DOMAIN CONTAINING 1	-3.02	-0.68	-1.47	-2.31	-1.55
23770	FKBP8	NM_012181	FK506 BINDING PROTEIN 8, 38KDA	0.01	0.35	0.15	-1.63	-0.34
23770	FKBP8	NM_012181	FK506 BINDING PROTEIN 8, 38KDA	-2.96	-2.53	-1.98	-1.63	-5.16
23770	FKBP8	NM_012181	FK506 BINDING PROTEIN 8, 38KDA	-0.58	-1.95	-0.94	-1.63	-0.49
23770	FKBP8	NM_012181	FK506 BINDING PROTEIN 8, 38KDA	-2.18	-1.73	-1.12	-1.63	-1.16

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11328	FKBP9	NM_007270	FK506 BINDING PROTEIN 9, 63 KDA	0.92	0.41	0.57	-7.88	1.18
11328	FKBP9	NM_007270	FK506 BINDING PROTEIN 9, 63 KDA	-2.88	-1.58	-1.17	-7.88	-6.21
11328	FKBP9	NM_007270	FK506 BINDING PROTEIN 9, 63 KDA	-2.4	-0.21	-1.13	-7.88	-6.09
11328	FKBP9	NM_007270	FK506 BINDING PROTEIN 9, 63 KDA	0.73	0.62	0.3	-7.88	3.15
54475	FLJ10458	NM_018096	NOTCHLESS HOMOLOG 1 (DROSOPHILA)	-0.03	1.71	1.18	-9.5	0.16
54475	FLJ10458	NM_018096	NOTCHLESS HOMOLOG 1 (DROSOPHILA)	-0.85	-1.1	-0.02	-9.5	-8.62
54475	FLJ10458	NM_018096	NOTCHLESS HOMOLOG 1 (DROSOPHILA)	0.96	0.5	0.21	-9.5	0.77
54475	FLJ10458	NM_018096	NOTCHLESS HOMOLOG 1 (DROSOPHILA)	-0.33	-1.41	-0.63	-9.5	-8.53
54508	FLJ11235	AK002097	HYPOTHETICAL PROTEIN FLJ11235	-1.24	0.97	-1.28	-9.52	-1.62
54508	FLJ11235	AK002097	HYPOTHETICAL PROTEIN FLJ11235	-1.39	-1.5	-2.33	-9.52	-8.57
79714	FLJ12436	NM_024661	COILED-COIL DOMAIN CONTAINING 51	0.01	-1.28	-0.44	-7.44	-0.3
79714	FLJ12436	NM_024661	COILED-COIL DOMAIN CONTAINING 51	-5.72	-1.62	-2.78	-7.44	-5.56
54962	FLJ20516	NM_017858	TIMELESS-INTERACTING PROTEIN	-2.12	-1.24	-2.08	-9.3	-5.39
54962	FLJ20516	NM_017858	TIMELESS-INTERACTING PROTEIN	0.32	-0.12	-0.03	-9.3	1.88
54962	FLJ20516	NM_017858	TIMELESS-INTERACTING PROTEIN	-1.05	0.29	-0.08	-9.3	-0.36
54962	FLJ20516	NM_017858	TIMELESS-INTERACTING PROTEIN	-2.09	-0.6	-0.4	-9.3	-8.14
64772	FLJ21865	NM_022759	ENDO-BETA-N-ACETYLGLUCOSAMINIDASE	-2.38	-0.38	-0.47	-9.52	-2.69
64772	FLJ21865	NM_022759	ENDO-BETA-N-ACETYLGLUCOSAMINIDASE	-5.95	-0.92	0.06	-9.52	-8.56
79864	FLJ23554	NM_024806	HYPOTHETICAL PROTEIN FLJ23554	-2.51	-0.84	-1.22	-8.82	-7
79864	FLJ23554	NM_024806	HYPOTHETICAL PROTEIN FLJ23554	-13.96	-1.46	-1.3	-8.82	-7.36
497049	FLJ25758	BC033035	HYPOTHETICAL LOCUS FLJ25758	-1.75	-0.53	-0.54	-4.1	-2.75
497049	FLJ25758	BC033035	HYPOTHETICAL LOCUS FLJ25758	-1.53	1.3	0.36	-4.1	-3.27
64400	FTS	NM_022476	FUSED TOES HOMOLOG (MOUSE)	-1.83	-0.87	-1.15	-9.06	-7.74
64400	FTS	NM_022476	FUSED TOES HOMOLOG (MOUSE)	-1.7	-0.16	-0.3	-9.06	-7.74
64400	FTS	NM_022476	FUSED TOES HOMOLOG (MOUSE)	0.003	2.54	-0.62	-9.06	0.3
64400	FTS	NM_022476	FUSED TOES HOMOLOG (MOUSE)	0.83	3.14	0.2	-9.06	0.3
9636	G1P2	NM_005101	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-15K)	-0.25	-1.01	-0.36	0.2	-0.46
9636	G1P2	NM_005101	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-15K)	-0.27	-0.56	-0.87	0.2	-5.65
9636	G1P2	NM_005101	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-15K)	-0.004	-0.23	-1.06	0.2	0.13
9636	G1P2	NM_005101	INTERFERON, ALPHA-INDUCIBLE PROTEIN (CLONE IFI-15K)	-1.69	-1.27	-1.28	0.2	-1.49
2729	GCLC	M90656	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	0.68	0.03	-0.05	1.06	0.66
2729	GCLC	M90656	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	0.43	-1.21	-0.33	1.06	0.72
2729	GCLC	M90656	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	0.79	-1.1	-0.96	1.06	1.46
2729	GCLC	M90656	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	-0.88	-1.29	-0.93	1.06	-1.11
2662	GDF10	BC028237	GROWTH DIFFERENTIATION FACTOR 10	-2.71	-0.1	-0.63	-8.44	-2.19
2662	GDF10	BC028237	GROWTH DIFFERENTIATION FACTOR 10	-2.43	-1.38	0.008	-8.44	-1.81
2662	GDF10	BC028237	GROWTH DIFFERENTIATION FACTOR 10	-2.75	-0.52	-1.23	-8.44	-6.82
2662	GDF10	BC028237	GROWTH DIFFERENTIATION FACTOR 10	0.26	0.48	0.52	-8.44	1.9
91227	GGTL4	NM_080839	GAMMA-GLUTAMYLTRANSFERASE-LIKE 4	-1.14	-1.04	-1.12	-9.57	-0.49
91227	GGTL4	NM_080839	GAMMA-GLUTAMYLTRANSFERASE-LIKE 4	-1.57	-0.81	-1.52	-9.57	-8.66
2797	GNRH2	NM_001501	GONADOTROPIN-RELEASING HORMONE 2	-0.93	0.05	-0.29	-1.61	-1.08
2797	GNRH2	NM_001501	GONADOTROPIN-RELEASING HORMONE 2	-0.2	-0.12	-1.73	-1.61	-0.009
2797	GNRH2	NM_001501	GONADOTROPIN-RELEASING HORMONE 2	-0.75	-1.08	-1.13	-1.61	-1.59
2797	GNRH2	NM_001501	GONADOTROPIN-RELEASING HORMONE 2	0.61	0	-0.01	-1.61	0.39
115330	GPR146	NM_138445	G PROTEIN-COUPLED RECEPTOR 146	-0.07	-0.29	0.008	-8.7	1.39
115330	GPR146	NM_138445	G PROTEIN-COUPLED RECEPTOR 146	-0.15	0.59	-0.3	-8.7	-0.91
115330	GPR146	NM_138445	G PROTEIN-COUPLED RECEPTOR 146	-2.87	-2.04	-1.97	-8.7	-2.28
115330	GPR146	NM_138445	G PROTEIN-COUPLED RECEPTOR 146	-2.14	-0.08	-0.67	-8.7	-7.19
2905	GRIN2C	NM_000835	GLUTAMATE RECEPTOR, IONOTROPIC, N-METHYL D-ASPARTATE 2C	-2.37	-0.03	-0.61	-9.14	-7.86
2905	GRIN2C	NM_000835	GLUTAMATE RECEPTOR, IONOTROPIC, N-METHYL D-ASPARTATE 2C	0.13	1.46	2	-9.14	-0.32
2905	GRIN2C	NM_000835	GLUTAMATE RECEPTOR, IONOTROPIC, N-METHYL D-ASPARTATE 2C	-1.79	-0.25	-1.14	-9.14	-2.19
2905	GRIN2C	NM_000835	GLUTAMATE RECEPTOR, IONOTROPIC, N-METHYL D-ASPARTATE 2C	-0.002	0.3	0	-9.14	0.11
2948	GSTM4	NM_147148	GLUTATHIONE S-TRANSFERASE M4	-1.36	-0.82	-1.62	-2.27	-1.96
2948	GSTM4	NM_147148	GLUTATHIONE S-TRANSFERASE M4	-0.68	0.53	-1.15	-2.27	-1.39
2967	GTF2H3	NM_001516	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 3, 34KDA	-1.62	1.8	0.91	-8.63	-5.65
2967	GTF2H3	NM_001516	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 3, 34KDA	0.0025	1.67	1.52	-8.63	0.24

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2967	GTF2H3	NM_001516	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 3, 34KDA	-0.01	-0.004	-1.17	-8.63	-0.18
2967	GTF2H3	NM_001516	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 3, 34KDA	-1.94	-2.09	-1.4	-8.63	-7.09
57493	HEG	BC004539	HEG HOMOLOG 1 (ZEBRAFISH)	-1.19	-1.5	-1.28	0.69	0.5
57493	HEG	BC004539	HEG HOMOLOG 1 (ZEBRAFISH)	0.88	-1	-0.14	0.69	1.1
57493	HEG	BC004539	HEG HOMOLOG 1 (ZEBRAFISH)	0.77	0.1	0.26	0.69	2.42
57493	HEG	BC004539	HEG HOMOLOG 1 (ZEBRAFISH)	-1.32	-2.11	-1.53	0.69	-1.58
26091	HERC4	AB046813	HECT DOMAIN AND RLD 4	0.28	0.24	-1.18	-9.92	0.77
26091	HERC4	AB046813	HECT DOMAIN AND RLD 4	-0.05	0.2	-0.55	-9.92	1.14
26091	HERC4	AB046813	HECT DOMAIN AND RLD 4	-0.78	-0.72	-1.2	-9.92	-1.69
26091	HERC4	AB046813	HECT DOMAIN AND RLD 4	-2.2	-1.63	-0.92	-9.92	-9.58
8341	HIST1H2BN	NM_003520	HISTONE 1, H2BN	-2.89	-0.24	-0.98	-7.5	-5.63
8341	HIST1H2BN	NM_003520	HISTONE 1, H2BN	-1.69	0.24	-1.27	-7.5	-1.63
3248	HPGD	NM_000860	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	0.26	3.14	1.82	-8.03	0.95
3248	HPGD	NM_000860	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	-2.79	-0.84	-0.5	-8.03	-8.25
3248	HPGD	NM_000860	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	0.007	-1.26	-0.64	-8.03	-0.64
3248	HPGD	NM_000860	HYDROXYPROSTAGLANDIN DEHYDROGENASE 15-(NAD)	-2.76	-2.04	-1.43	-8.03	-5.55
3299	HSF4	NM_001538	HEAT SHOCK TRANSCRIPTION FACTOR 4	-3.23	-0.3	-0.67	-8.63	-8.49
3299	HSF4	NM_001538	HEAT SHOCK TRANSCRIPTION FACTOR 4	-2.04	0.23	-0.68	-8.63	-7.08
3299	HSF4	NM_001538	HEAT SHOCK TRANSCRIPTION FACTOR 4	-0.001	0.54	1.04	-8.63	-1.22
3299	HSF4	NM_001538	HEAT SHOCK TRANSCRIPTION FACTOR 4	-0.66	0.002	-0.04	-8.63	-2.2
3329	HSPD1	NM_002156	HEAT SHOCK 60KDA PROTEIN 1 (CHAPERONIN)	-0.36	-1.45	-1.5	-0.16	-2.13
3329	HSPD1	NM_002156	HEAT SHOCK 60KDA PROTEIN 1 (CHAPERONIN)	0.02	-0.07	0.16	-0.16	0.41
3329	HSPD1	NM_002156	HEAT SHOCK 60KDA PROTEIN 1 (CHAPERONIN)	0.7	-1.03	-0.05	-0.16	-0.01
3329	HSPD1	NM_002156	HEAT SHOCK 60KDA PROTEIN 1 (CHAPERONIN)	0.001	-0.42	0.004	-0.16	-0.11
3444	IFNA7	NM_021057	INTERFERON, ALPHA 7	0.67	-0.28	0.009	-2.34	1.47
3444	IFNA7	NM_021057	INTERFERON, ALPHA 7	-2.73	-0.19	-0.43	-2.34	-2.29
3444	IFNA7	NM_021057	INTERFERON, ALPHA 7	-4.15	-1.68	-1.07	-2.34	-6.05
3444	IFNA7	NM_021057	INTERFERON, ALPHA 7	0.02	-0.16	-0.89	-2.34	1.26
3455	IFNAR2	NM_000874	INTERFERON (ALPHA, BETA AND OMEGA) RECEPTOR 2	-1.1	-0.88	-1.29	-9.05	-2.3
3455	IFNAR2	NM_000874	INTERFERON (ALPHA, BETA AND OMEGA) RECEPTOR 2	0.6	-0.06	0.61	-9.05	1.78
3455	IFNAR2	NM_000874	INTERFERON (ALPHA, BETA AND OMEGA) RECEPTOR 2	0.08	0.61	-0.003	-9.05	0.002
3455	IFNAR2	NM_000874	INTERFERON (ALPHA, BETA AND OMEGA) RECEPTOR 2	-6.03	-2.22	-1.51	-9.05	-7.72
3460	IFNGR2	NM_005534	INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA TRANSDUCER 1)	-0.03	-0.88	-0.16	-2.03	-0.28
3460	IFNGR2	NM_005534	INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA TRANSDUCER 1)	-0.08	-0.25	-1.03	-2.03	0.18
3460	IFNGR2	NM_005534	INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA TRANSDUCER 1)	-2.68	-0.36	-1	-2.03	-1.74
3460	IFNGR2	NM_005534	INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA TRANSDUCER 1)	-1.25	-0.85	-0.23	-2.03	-2.46
3547	IGSF1	NM_001555	IMMUNOGLOBULIN SUPERFAMILY, MEMBER 1	-0.87	-2.23	-1.14	-3.58	-1.63
3547	IGSF1	NM_001555	IMMUNOGLOBULIN SUPERFAMILY, MEMBER 1	-4.43	-0.37	-1.12	-3.58	-3.44
3550	IK	AY007094	IK CYTOKINE, DOWN-REGULATOR OF HLA II	-1.4	-0.66	-0.78	-8.77	-5.24
3550	IK	AY007094	IK CYTOKINE, DOWN-REGULATOR OF HLA II	-3.25	-0.88	-0.79	-8.77	-2.25
3550	IK	AY007094	IK CYTOKINE, DOWN-REGULATOR OF HLA II	-3.72	-0.1	-0.71	-8.77	-6.99
3550	IK	AY007094	IK CYTOKINE, DOWN-REGULATOR OF HLA II	-3.29	-1.94	-1.07	-8.77	-8.18
23765	IL17R	NM_014339	INTERLEUKIN 17 RECEPTOR	-9.65	-1.41	-1.65	-9.46	-8.45
23765	IL17R	NM_014339	INTERLEUKIN 17 RECEPTOR	-1.08	-1.01	-1.55	-9.46	-0.26
23765	IL17R	NM_014339	INTERLEUKIN 17 RECEPTOR	-0.77	-0.002	-0.98	-9.46	-0.13
23765	IL17R	NM_014339	INTERLEUKIN 17 RECEPTOR	0.89	0.35	-0.6	-9.46	0.47
3552	IL1A	NM_000575	INTERLEUKIN 1, ALPHA	0.05	0.35	0.78	-8.24	0.68
3552	IL1A	NM_000575	INTERLEUKIN 1, ALPHA	0.59	0.03	0.24	-8.24	0.25
3552	IL1A	NM_000575	INTERLEUKIN 1, ALPHA	-3.72	-1.36	-0.74	-8.24	-8.4
3552	IL1A	NM_000575	INTERLEUKIN 1, ALPHA	-1.32	-1.23	-0.54	-8.24	-2.6
3660	IRF2	NM_002199	INTERFERON REGULATORY FACTOR 2	-1.92	-0.39	0.45	-8.37	-5.82
3660	IRF2	NM_002199	INTERFERON REGULATORY FACTOR 2	-5.65	-0.29	-0.72	-8.37	-6.72
3660	IRF2	NM_002199	INTERFERON REGULATORY FACTOR 2	0.65	0.75	0.38	-8.37	0.88
3660	IRF2	NM_002199	INTERFERON REGULATORY FACTOR 2	-0.87	0	-0.78	-8.37	-2.22
55600	ITLN1	NM_017625	INTELECTIN 1 (GALACTOFURANOSE BINDING)	-0.78	-0.35	-0.71	-8.99	-5.51
55600	ITLN1	NM_017625	INTELECTIN 1 (GALACTOFURANOSE BINDING)	-0.93	-1.1	-0.22	-8.99	-7.63

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55600	ITLN1	NM_017625	INTELECTIN 1 (GALACTOFURANOSE BINDING)	1.22	0.16	0.38	-8.99	0.8
55600	ITLN1	NM_017625	INTELECTIN 1 (GALACTOFURANOSE BINDING)	-0.66	-1.75	-1.26	-8.99	-1.08
3725	JUN	BC002646	V-JUN SARCOMA VIRUS 17 ONCOGENE HOMOLOG (AVIAN)	-0.9	-1.18	-1.72	-3.11	-1.82
3725	JUN	BC002646	V-JUN SARCOMA VIRUS 17 ONCOGENE HOMOLOG (AVIAN)	0.009	-0.99	-0.02	-3.11	-1.17
3725	JUN	BC002646	V-JUN SARCOMA VIRUS 17 ONCOGENE HOMOLOG (AVIAN)	-2.58	-0.59	-0.83	-3.11	-5.29
3725	JUN	BC002646	V-JUN SARCOMA VIRUS 17 ONCOGENE HOMOLOG (AVIAN)	-1.59	-0.35	-1.6	-3.11	-2.81
10300	KATNB1	NM_005886	KATANIN P80 (WD REPEAT CONTAINING) SUBUNIT B 1	-3.95	-0.53	-1.65	-9.54	-7.68
10300	KATNB1	NM_005886	KATANIN P80 (WD REPEAT CONTAINING) SUBUNIT B 1	-8.35	-1.16	-0.72	-9.54	-8.68
3768	KCNJ12	AK024229	POTASSIUM INWARDLY-RECTIFYING CHANNEL, SUBFAMILY J, MEMBER 12	0.25	-1.3	-0.49	-0.19	1.38
3768	KCNJ12	AK024229	POTASSIUM INWARDLY-RECTIFYING CHANNEL, SUBFAMILY J, MEMBER 12	-1.38	-0.29	-1.3	-0.19	-1.46
3768	KCNJ12	AK024229	POTASSIUM INWARDLY-RECTIFYING CHANNEL, SUBFAMILY J, MEMBER 12	0.16	-1.54	-1.08	-0.19	-0.13
3768	KCNJ12	AK024229	POTASSIUM INWARDLY-RECTIFYING CHANNEL, SUBFAMILY J, MEMBER 12	0	1.42	1.58	-0.19	0.18
89822	KCNK17	NM_031460	POTASSIUM CHANNEL TASK-4; POTASSIUM CHANNEL TALK-2	0.4	-0.4	-0.17	-8.59	0.82
89822	KCNK17	NM_031460	POTASSIUM CHANNEL TASK-4; POTASSIUM CHANNEL TALK-2	-0.0025	0.69	0.02	-8.59	0.5
89822	KCNK17	NM_031460	POTASSIUM CHANNEL TASK-4; POTASSIUM CHANNEL TALK-2	-5.73	-0.76	-1.24	-8.59	-7.02
89822	KCNK17	NM_031460	POTASSIUM CHANNEL TASK-4; POTASSIUM CHANNEL TALK-2	-4.34	-0.89	-0.27	-8.59	-9.58
9776	KIAA0652	NM_014741	KIAA0652	0.84	-1.24	-1.39	0.65	0.74
9776	KIAA0652	NM_014741	KIAA0652	-0.94	-1.22	-1.42	0.65	-2.08
23277	KIAA0664	NM_015229	KIAA0664	-4.77	-0.38	-1.13	-9.34	-8.52
23277	KIAA0664	NM_015229	KIAA0664	-3.1	0.82	1.89	-9.34	-8.22
23277	KIAA0664	NM_015229	KIAA0664	-0.95	0.1	-0.85	-9.34	-0.38
23277	KIAA0664	NM_015229	KIAA0664	-0.01	1.26	0.33	-9.34	-0.43
57579	KIAA1411	AK002067	KIAA1411	-3.17	-1.1	-1.02	-3.44	-3.07
57579	KIAA1411	AK002067	KIAA1411	-1.83	-1.67	-0.42	-3.44	-1.55
3832	KIF11	NM_004523	KINESIN FAMILY MEMBER 11	-2.99	0.1	-1.71	-8.45	-6.83
3832	KIF11	NM_004523	KINESIN FAMILY MEMBER 11	-1.65	1.21	-2.2	-8.45	-1.3
3832	KIF11	NM_004523	KINESIN FAMILY MEMBER 11	-4.75	-0.26	-2.34	-8.45	-2.34
3832	KIF11	NM_004523	KINESIN FAMILY MEMBER 11	-2.12	-0.14	-2	-8.45	-8.57
3827	KNG1	NM_000893	KININOGEN 1	-1.16	1.11	0.23	-2.21	-2.08
3827	KNG1	NM_000893	KININOGEN 1	-3.22	0.05	-0.65	-2.21	-3.05
3827	KNG1	NM_000893	KININOGEN 1	0.01	-1.1	-0.45	-2.21	0.03
3827	KNG1	NM_000893	KININOGEN 1	-1.97	-0.96	-1.91	-2.21	-1.49
3837	KPNB1	NM_002265	KARYOPHERIN (IMPORTIN) BETA 1	-0.08	-1.63	-0.85	-0.38	0.28
3837	KPNB1	NM_002265	KARYOPHERIN (IMPORTIN) BETA 1	0.35	-1.29	-0.76	-0.38	-0.26
3837	KPNB1	NM_002265	KARYOPHERIN (IMPORTIN) BETA 1	-1.51	-2.29	-1.83	-0.38	-0.96
3837	KPNB1	NM_002265	KARYOPHERIN (IMPORTIN) BETA 1	0.04	1.3	-0.23	-0.38	0.32
9215	LARGE	NM_004737	LIKE-GLYCOSYLTRANSFERASE	-1.71	0.35	0.2	-9.2	-0.96
9215	LARGE	NM_004737	LIKE-GLYCOSYLTRANSFERASE	-0.99	-1.55	-0.58	-9.2	-8.4
9215	LARGE	NM_004737	LIKE-GLYCOSYLTRANSFERASE	0.28	1.44	0.42	-9.2	0.49
9215	LARGE	NM_004737	LIKE-GLYCOSYLTRANSFERASE	-3.14	-2	-0.47	-9.2	-7.97
23367	LARP	NM_015315	LA RIBONUCLEOPROTEIN DOMAIN FAMILY, MEMBER 1	-1.3	0.52	-1.06	-7.84	-0.73
23367	LARP	NM_015315	LA RIBONUCLEOPROTEIN DOMAIN FAMILY, MEMBER 1	-1.78	1.21	-0.5	-7.84	-0.73
23367	LARP	NM_015315	LA RIBONUCLEOPROTEIN DOMAIN FAMILY, MEMBER 1	-2.52	-0.38	-1.12	-7.84	-6.04
23367	LARP	NM_015315	LA RIBONUCLEOPROTEIN DOMAIN FAMILY, MEMBER 1	-4.59	-0.64	-1.42	-7.84	-6.04
79603	LASS4	NM_024552	LAG1 LONGEVITY ASSURANCE HOMOLOG 4 (S. CEREVISIAE)	-2.71	0.0085	-1.23	-9.92	-9.58
79603	LASS4	NM_024552	LAG1 LONGEVITY ASSURANCE HOMOLOG 4 (S. CEREVISIAE)	-5.64	-2.36	-2.36	-9.92	-3.35
3957	LGALS2	NM_006498	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 2 (GALECTIN 2)	-2.63	-1.88	-1.75	-7.99	-6.23
3957	LGALS2	NM_006498	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 2 (GALECTIN 2)	-0.64	-1.19	-0.64	-7.99	-1.79
8022	LHX3	NM_014564	LIM HOMEOBOX 3	0.31	-0.06	0.81	-2.17	0.89
8022	LHX3	NM_014564	LIM HOMEOBOX 3	-1.4	0.71	-1.27	-2.17	-2.14
8022	LHX3	NM_014564	LIM HOMEOBOX 3	-4.39	-0.11	-1.03	-2.17	-4.31
8022	LHX3	NM_014564	LIM HOMEOBOX 3	0.11	1.58	0.85	-2.17	0.52
283377	LOC283377	AF289571	SPRY DOMAIN CONTAINING 4	-5.26	-1.82	-1.93	-8.51	-7.01
283377	LOC283377	AF289571	SPRY DOMAIN CONTAINING 4	0.49	-0.18	0.69	-8.51	1.6
283377	LOC283377	AF289571	SPRY DOMAIN CONTAINING 4	-0.35	0.15	0.71	-8.51	-0.81
283377	LOC283377	AF289571	SPRY DOMAIN CONTAINING 4	-2.66	-1.56	-0.96	-8.51	-1.66

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284058	LOC284058	NM_015443	DKFZP727C091 PROTEIN	-3.99	-0.75	-1.54	-9.34	-8.22
284058	LOC284058	NM_015443	DKFZP727C091 PROTEIN	0.77	1.76	-1.28	-9.34	0.41
401431	LOC401431	BC028735	HYPOTHETICAL GENE LOC401431	-1.62	-1.74	-1.48	-8.78	-1.53
401431	LOC401431	BC028735	HYPOTHETICAL GENE LOC401431	-3.85	-1.94	-2.21	-8.78	-7.3
92235	LOC92235	AF119045	DUAL SPECIFICITY PHOSPHATASE 27 (PUTATIVE)	-1.7	-1.12	-1.31	-7.46	-5.59
92235	LOC92235	AF119045	DUAL SPECIFICITY PHOSPHATASE 27 (PUTATIVE)	-0.1	0.11	-0.93	-7.46	0.76
92235	LOC92235	AF119045	DUAL SPECIFICITY PHOSPHATASE 27 (PUTATIVE)	0.66	1.71	0.74	-7.46	2.03
92235	LOC92235	AF119045	DUAL SPECIFICITY PHOSPHATASE 27 (PUTATIVE)	-5.57	-1.63	-1.73	-7.46	-8.42
92312	LOC92312	AK095491	HYPOTHETICAL PROTEIN LOC92312	-1.34	-1.67	-0.82	-2.62	-1.1
92312	LOC92312	AK095491	HYPOTHETICAL PROTEIN LOC92312	-3.24	-0.16	-0.2	-2.62	-5.71
92312	LOC92312	AK095491	HYPOTHETICAL PROTEIN LOC92312	-3.57	-0.84	-1.4	-2.62	-3.25
92312	LOC92312	AK095491	HYPOTHETICAL PROTEIN LOC92312	-0.37	0.24	0.87	-2.62	0.16
9890	LPPR4	NM_014839	PLASTICITY RELATED GENE 1	-2.5	-0.2	-0.66	-8.19	-2.61
9890	LPPR4	NM_014839	PLASTICITY RELATED GENE 1	-1.93	-0.57	0.25	-8.19	-6.49
84918	LRP11	NM_032832	LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 11	0.14	-1.28	-0.64	-1.38	-0.16
84918	LRP11	NM_032832	LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 11	-3.43	-1.51	-1.38	-1.38	-2.72
53353	LRP1B	NM_018557	LOW DENSITY LIPOPROTEIN-RELATED PROTEIN 1B (DELETED IN TUMORS)	-1.22	0.23	0.35	-2.28	-1.87
53353	LRP1B	NM_018557	LOW DENSITY LIPOPROTEIN-RELATED PROTEIN 1B (DELETED IN TUMORS)	1.3	1.09	1.33	-2.28	2.68
53353	LRP1B	NM_018557	LOW DENSITY LIPOPROTEIN-RELATED PROTEIN 1B (DELETED IN TUMORS)	-5.2	-1.59	-1.87	-2.28	-2.62
53353	LRP1B	NM_018557	LOW DENSITY LIPOPROTEIN-RELATED PROTEIN 1B (DELETED IN TUMORS)	-1.75	-1.32	-1.1	-2.28	-7.04
84894	LRRN6A	AK027500	LEUCINE RICH REPEAT NEURONAL 6A	0.88	1.17	1.88	-0.87	1.63
84894	LRRN6A	AK027500	LEUCINE RICH REPEAT NEURONAL 6A	-2.89	-1.84	-1.26	-0.87	-5.11
84894	LRRN6A	AK027500	LEUCINE RICH REPEAT NEURONAL 6A	-3.59	-0.85	-0.5	-0.87	-2.89
84894	LRRN6A	AK027500	LEUCINE RICH REPEAT NEURONAL 6A	0.63	0.62	0.54	-0.87	1.1
80740	LY6G6C	NM_025261	LYMPHOCYTE ANTIGEN 6 COMPLEX, LOCUS G6C	-2.25	-0.5	-0.63	-7.48	-5.61
80740	LY6G6C	NM_025261	LYMPHOCYTE ANTIGEN 6 COMPLEX, LOCUS G6C	-2.67	-0.31	-0.96	-7.48	-3.04
4125	MAN2B1	NM_000528	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	-4.17	-1.79	-2.03	-9.47	-8.46
4125	MAN2B1	NM_000528	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	0.23	-0.64	-0.1	-9.47	-0.74
4125	MAN2B1	NM_000528	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	-2.16	-1.46	-0.12	-9.47	-8.65
4125	MAN2B1	NM_000528	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	0.21	-0.94	-0.43	-9.47	0.25
5606	MAP2K3	BC032478	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3	0.29	-0.63	-0.67	-7.92	-0.15
5606	MAP2K3	BC032478	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3	-3.57	-1.07	-1.72	-7.92	-6.14
5606	MAP2K3	BC032478	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3	-2.23	0	-0.92	-7.92	-1.96
5606	MAP2K3	BC032478	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3	-0.62	0.07	-0.39	-7.92	-5.48
4148	MATN3	NM_002381	MATRILIN 3	-1.14	0	0.41	-8.85	-1.31
4148	MATN3	NM_002381	MATRILIN 3	-1.04	1.64	0.02	-8.85	-1.55
4148	MATN3	NM_002381	MATRILIN 3	-4.2	-0.1	-0.38	-8.85	-3.92
4148	MATN3	NM_002381	MATRILIN 3	-2.03	1.54	0.03	-8.85	-7.41
4193	MDM2	BC067077	MDM2, TRANSFORMED 3T3 CELL DOUBLE MINUTE 2, P53 BINDING PROTEIN (MOUSE)	-2.7	-1.76	-1.92	-7.33	-5.08
4193	MDM2	BC067077	MDM2, TRANSFORMED 3T3 CELL DOUBLE MINUTE 2, P53 BINDING PROTEIN (MOUSE)	-1.98	0.04	-0.58	-7.33	-7.18
4193	MDM2	BC067077	MDM2, TRANSFORMED 3T3 CELL DOUBLE MINUTE 2, P53 BINDING PROTEIN (MOUSE)	-0.06	0.4	-0.33	-7.33	-0.46
4193	MDM2	BC067077	MDM2, TRANSFORMED 3T3 CELL DOUBLE MINUTE 2, P53 BINDING PROTEIN (MOUSE)	-0.44	0.67	-0.3	-7.33	-5.44
10001	MED6	BC004106	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION, SUBUNIT 6 HOMOLOG (YEAST)	-2.2	1.92	-0.2	-2.36	-1.74
10001	MED6	BC004106	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION, SUBUNIT 6 HOMOLOG (YEAST)	-0.94	0.71	-0.06	-2.36	-1.13
10001	MED6	BC004106	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION, SUBUNIT 6 HOMOLOG (YEAST)	-2.78	-0.44	-0.58	-2.36	-3.08
10001	MED6	BC004106	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION, SUBUNIT 6 HOMOLOG (YEAST)	-1.07	-0.37	-0.39	-2.36	-1.1
79171	MGC10433	NM_024321	HYPOTHETICAL PROTEIN MGC10433	-2.52	0.93	0.93	-8.68	-2.37
79171	MGC10433	NM_024321	HYPOTHETICAL PROTEIN MGC10433	-4.1	-1.51	-0.63	-8.68	-7.16
132001	MGC16471	NM_138807	CHROMOSOME 3 OPEN READING FRAME 31	-1.52	0.38	0.001	-2.7	-5.14
132001	MGC16471	NM_138807	CHROMOSOME 3 OPEN READING FRAME 31	-2.33	0.14	-0.53	-2.7	-1.82
124044	MGC26885	NM_152339	HYPOTHETICAL PROTEIN MGC26885	-1.07	-1.99	-1.63	-1.13	-0.51
124044	MGC26885	NM_152339	HYPOTHETICAL PROTEIN MGC26885	-2.53	-0.95	-1.63	-1.13	-1.91
84292	MGC4238	NM_032332	MITOGEN-ACTIVATED PROTEIN KINASE ORGANIZER 1	-3.22	-0.77	-1.5	-5.07	-3.45
84292	MGC4238	NM_032332	MITOGEN-ACTIVATED PROTEIN KINASE ORGANIZER 1	-4.78	0.07	-1	-5.07	-3.4
339512	MGC48998	NM_178550	CHROMOSOME 1 OPEN READING FRAME 110	-1.51	0.29	-0.7	-9.56	-1.78
339512	MGC48998	NM_178550	CHROMOSOME 1 OPEN READING FRAME 110	-4.43	0.003	-1.3	-9.56	-8.64

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
23417	MLYCD	NM_012213	MALONYL-COA DECARBOXYLASE	0.38	-0.06	0.35	-8.41	0.95
23417	MLYCD	NM_012213	MALONYL-COA DECARBOXYLASE	0.33	1.32	2.36	-8.41	1.87
23417	MLYCD	NM_012213	MALONYL-COA DECARBOXYLASE	-3.06	-0.54	-0.46	-8.41	-1.91
23417	MLYCD	NM_012213	MALONYL-COA DECARBOXYLASE	-2.93	-0.51	-1.16	-8.41	-6.78
83886	MPN	NM_031948	PROTEASE, SERINE 27	-5.71	-2.19	-0.59	-9.5	-8.52
83886	MPN	NM_031948	PROTEASE, SERINE 27	0.64	-0.3	0.7	-9.5	1.28
83886	MPN	NM_031948	PROTEASE, SERINE 27	-0.02	0.91	0.5	-9.5	-0.22
83886	MPN	NM_031948	PROTEASE, SERINE 27	-1.77	-1.49	-1.13	-9.5	-2.59
4482	MSRA	NM_012331	METHIONINE SULFOXIDE REDUCTASE A	-2.2	-0.91	-1.15	-7.66	-5.82
4482	MSRA	NM_012331	METHIONINE SULFOXIDE REDUCTASE A	-3.49	-0.007	-1.18	-7.66	-4.02
4486	MST1R	NM_002447	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)	-2.48	-0.92	-1.7	-8.97	-7.59
4486	MST1R	NM_002447	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)	-1.67	-0.64	-0.65	-8.97	-1.89
4486	MST1R	NM_002447	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)	-2.36	-0.42	-0.21	-8.97	-8.57
4486	MST1R	NM_002447	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)	-0.33	0.001	-0.39	-8.97	-5.93
4609	MYC	NM_002467	V-MYC MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG (AVIAN)	-0.05	-1.87	-0.59	0.25	-0.14
4609	MYC	NM_002467	V-MYC MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG (AVIAN)	0.65	-0.79	0.008	0.25	1.05
4609	MYC	NM_002467	V-MYC MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG (AVIAN)	-2.07	-1.41	-0.28	0.25	-2.18
4609	MYC	NM_002467	V-MYC MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG (AVIAN)	0.23	-0.48	0.27	0.25	1.09
4654	MYOD1	NM_002478	MYOGENIC DIFFERENTIATION 1	-0.28	-0.16	0.01	-7.72	0.27
4654	MYOD1	NM_002478	MYOGENIC DIFFERENTIATION 1	-2	-2.12	-0.32	-7.72	-5.9
4654	MYOD1	NM_002478	MYOGENIC DIFFERENTIATION 1	0.47	0.91	1.15	-7.72	-0.01
4654	MYOD1	NM_002478	MYOGENIC DIFFERENTIATION 1	-2.81	-1.98	-1.26	-7.72	-8.55
23040	MYT1L	AF036943	MYELIN TRANSCRIPTION FACTOR 1-LIKE	-2.24	-0.93	-1.28	-7.19	-5.2
23040	MYT1L	AF036943	MYELIN TRANSCRIPTION FACTOR 1-LIKE	-3	-1.51	-0.97	-7.19	-7.62
8440	NCK2	NM_003581	NCK ADAPTOR PROTEIN 2	-3.35	0.1	-0.24	-2.07	-2.09
8440	NCK2	NM_003581	NCK ADAPTOR PROTEIN 2	0.4	-0.15	0.5	-2.07	1.46
8440	NCK2	NM_003581	NCK ADAPTOR PROTEIN 2	-4.63	-1.11	-1.65	-2.07	-2.64
8440	NCK2	NM_003581	NCK ADAPTOR PROTEIN 2	0.17	0.14	0.95	-2.07	0.83
284086	NEK8	NM_178170	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 8	-2.68	-0.8	-1.24	-9.06	-7.73
284086	NEK8	NM_178170	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 8	0.07	-0.92	-0.9	-9.06	-0.71
284086	NEK8	NM_178170	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 8	-0.95	0.84	0.63	-9.06	-1.98
284086	NEK8	NM_178170	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 8	-1.98	-0.58	-0.51	-9.06	-8.45
91754	NEK9	AB082526	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 9	0.59	1.09	1.03	-9.44	0.63
91754	NEK9	AB082526	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 9	0.31	0.67	-0.43	-9.44	0.05
91754	NEK9	AB082526	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 9	-4.28	-0.8	-2.2	-9.44	-5.42
91754	NEK9	AB082526	NIMA (NEVER IN MITOSIS GENE A)- RELATED KINASE 9	-4.82	-1.43	-0.76	-9.44	-8.41
4861	NPAS1	NM_002517	NEURONAL PAS DOMAIN PROTEIN 1	-0.05	0.24	-0.55	-7.5	-0.22
4861	NPAS1	NM_002517	NEURONAL PAS DOMAIN PROTEIN 1	-0.51	-0.5	-0.44	-7.5	-2.65
4861	NPAS1	NM_002517	NEURONAL PAS DOMAIN PROTEIN 1	-4.92	-1.88	-1.71	-7.5	-5.8
4861	NPAS1	NM_002517	NEURONAL PAS DOMAIN PROTEIN 1	-1.84	-0.53	-0.7	-7.5	-5.63
4913	NTHL1	NM_002528	NTH ENDONUCLEASE III-LIKE 1 (E. COLI)	-1.04	0.87	0.15	-2.49	-1.39
4913	NTHL1	NM_002528	NTH ENDONUCLEASE III-LIKE 1 (E. COLI)	0.52	1.87	2.47	-2.49	-0.18
4913	NTHL1	NM_002528	NTH ENDONUCLEASE III-LIKE 1 (E. COLI)	-2.89	-0.73	0.57	-2.49	-2.05
4913	NTHL1	NM_002528	NTH ENDONUCLEASE III-LIKE 1 (E. COLI)	-2.78	0.95	-1.7	-2.49	-7.46
11163	NUDT4	NM_019094	NUDIX (NUCLEOSIDE DIPHOSPHATE LINKED MOIETY X)-TYPE MOTIF 4	-0.79	0.09	0.3	-7.23	-0.06
11163	NUDT4	NM_019094	NUDIX (NUCLEOSIDE DIPHOSPHATE LINKED MOIETY X)-TYPE MOTIF 4	0.35	-0.44	0.56	-7.23	0.92
11163	NUDT4	NM_019094	NUDIX (NUCLEOSIDE DIPHOSPHATE LINKED MOIETY X)-TYPE MOTIF 4	-6.03	-0.2	-0.89	-7.23	-8.06
11163	NUDT4	NM_019094	NUDIX (NUCLEOSIDE DIPHOSPHATE LINKED MOIETY X)-TYPE MOTIF 4	-2.42	-1.28	-1.63	-7.23	-5.32
23165	NUP205	D86978	NUCLEOPORIN 205KDA	-4.01	-1.89	-2.6	-9.53	-8.61
23165	NUP205	D86978	NUCLEOPORIN 205KDA	-4.16	-0.76	-0.5	-9.53	-6.92
4928	NUP98	NM_139131	NUCLEOPORIN 98KDA	-2.39	-1.33	-1.21	-7.89	-2.89
4928	NUP98	NM_139131	NUCLEOPORIN 98KDA	-3.07	-2.34	-2	-7.89	-6.05
4928	NUP98	NM_139131	NUCLEOPORIN 98KDA	-2.68	-1.65	-0.96	-7.89	-6.11
4928	NUP98	NM_139131	NUCLEOPORIN 98KDA	0.66	-0.004	0.02	-7.89	1.28
10482	NXF1	NM_006362	NUCLEAR RNA EXPORT FACTOR 1	-7.53	-3.69	-2.92	-9.47	-8.74
10482	NXF1	NM_006362	NUCLEAR RNA EXPORT FACTOR 1	-4.06	-2.02	-1.46	-9.47	-6.82

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56000	NXF3	NM_022052	NUCLEAR RNA EXPORT FACTOR 3	-2.13	-1.21	-0.78	-8.61	-2.07
56000	NXF3	NM_022052	NUCLEAR RNA EXPORT FACTOR 3	-9.1	-2.39	-2.43	-8.61	-7.06
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	-3.67	-1.27	-0.84	-8.16	-6.44
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	0.45	0.79	-0.18	-8.16	-6.44
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	-0.003	0.02	-0.34	-8.16	-6.4
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	-4.01	-0.68	-0.76	-8.16	-6.4
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	0.32	0.47	0.32	-8.16	-0.46
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	-3.14	-0.31	-0.06	-8.16	-0.46
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	0.01	0.42	0.94	-8.16	-0.89
89882	NYD-SP25	NM_033516	TUMOR PROTEIN D52-LIKE 3	-0.85	-0.16	-0.09	-8.16	-0.89
611	OPN1SW	NM_001708	OPSIN 1 (CONE PIGMENTS), SHORT-WAVE-SENSITIVE (COLOR BLINDNESS, TRITAN)	-3.11	-1.19	-1.31	-8.12	-3.11
611	OPN1SW	NM_001708	OPSIN 1 (CONE PIGMENTS), SHORT-WAVE-SENSITIVE (COLOR BLINDNESS, TRITAN)	-2.62	0.3	0.13	-8.12	-7.04
611	OPN1SW	NM_001708	OPSIN 1 (CONE PIGMENTS), SHORT-WAVE-SENSITIVE (COLOR BLINDNESS, TRITAN)	0.02	0.004	-0.6	-8.12	1.52
611	OPN1SW	NM_001708	OPSIN 1 (CONE PIGMENTS), SHORT-WAVE-SENSITIVE (COLOR BLINDNESS, TRITAN)	-0.15	0.14	-0.04	-8.12	0.71
10280	OPRS1	NM_005866	OPIOID RECEPTOR, SIGMA 1	-0.12	-0.59	-0.09	-1.52	-0.57
10280	OPRS1	NM_005866	OPIOID RECEPTOR, SIGMA 1	-1.05	-1.87	-0.97	-1.52	-3.05
10280	OPRS1	NM_005866	OPIOID RECEPTOR, SIGMA 1	-2.73	-1.5	-1.9	-1.52	-2.43
10280	OPRS1	NM_005866	OPIOID RECEPTOR, SIGMA 1	0.02	0.78	0.002	-1.52	1.36
64805	P2RY12	NM_022788	PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED, 12	0	0.008	-0.58	-9.41	0.85
64805	P2RY12	NM_022788	PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED, 12	0.008	-1.12	-1.21	-9.41	0.98
64805	P2RY12	NM_022788	PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED, 12	-0.009	-0.05	-0.74	-9.41	-0.25
64805	P2RY12	NM_022788	PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED, 12	-7.95	-1.95	-2.11	-9.41	-8.47
10606	PAICS	NM_006452	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE, PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE	-1.73	0	0.06	-9.59	-2.53
10606	PAICS	NM_006452	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE, PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE	-1.1	-0.11	-0.06	-9.59	-9.58
10606	PAICS	NM_006452	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE, PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE	-5.55	-0.38	-1.87	-9.59	-8.7
10606	PAICS	NM_006452	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE, PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE	0.41	0.86	2.11	-9.59	0.29
196743	PAOX	NM_152911	POLYAMINE OXIDASE (EXO-N4-AMINO)	0.72	-1.38	-1.27	-0.5	0.54
196743	PAOX	NM_152911	POLYAMINE OXIDASE (EXO-N4-AMINO)	-1.07	-2.1	-1.43	-0.5	-8.58
196743	PAOX	NM_152911	POLYAMINE OXIDASE (EXO-N4-AMINO)	-0.51	2.79	0.3	-0.5	-0.34
196743	PAOX	NM_152911	POLYAMINE OXIDASE (EXO-N4-AMINO)	-0.002	-0.51	-0.6	-0.5	-0.36
25859	PART1	NM_016590	PROSTATE ANDROGEN-REGULATED TRANSCRIPT 1	-1.59	-1.11	-0.85	-3.28	-2.07
25859	PART1	NM_016590	PROSTATE ANDROGEN-REGULATED TRANSCRIPT 1	-2.69	-0.81	-1.07	-3.28	-2.69
139135	PASD1	NM_173493	PAS DOMAIN CONTAINING 1	-2.57	-0.48	-0.02	-8.74	-7.24
139135	PASD1	NM_173493	PAS DOMAIN CONTAINING 1	-2.39	0	-0.89	-8.74	-1.84
54510	PCDH18	NM_019035	PROTOCADHERIN 18	-0.05	-0.35	-0.45	-1.91	-1.28
54510	PCDH18	NM_019035	PROTOCADHERIN 18	0.12	0.3	0.06	-1.91	0.54
54510	PCDH18	NM_019035	PROTOCADHERIN 18	-1.59	-0.61	-1.23	-1.91	-1.26
54510	PCDH18	NM_019035	PROTOCADHERIN 18	-2.11	-1.08	-1.32	-1.91	-3.09
5157	PDGFRL	NM_006207	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE	-1.23	0.45	-0.32	-2.17	-1.85
5157	PDGFRL	NM_006207	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE	-1.16	-1.13	-1.48	-2.17	-7.22
5157	PDGFRL	NM_006207	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE	-0.18	0.67	-0.001	-2.17	-0.2
5157	PDGFRL	NM_006207	PLATELET-DERIVED GROWTH FACTOR RECEPTOR-LIKE	-0.42	-1.28	-0.02	-2.17	-0.06
55851	PEN2	NM_019104	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	-0.94	0.09	-0.7	-8.22	-1.11
55851	PEN2	NM_019104	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	-1.24	-0.91	-0.63	-8.22	-5.12
55851	PEN2	NM_019104	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	-3.13	0.31	-1.35	-8.22	-6.53
55851	PEN2	NM_019104	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	-5.25	-1.57	-1.59	-8.22	-8.51
5184	PEPD	BC004305	PEPTIDASE D	-3	0.06	-0.54	-9.49	-5.69
5184	PEPD	BC004305	PEPTIDASE D	0.57	0.76	0.002	-9.49	2.51
5184	PEPD	BC004305	PEPTIDASE D	-0.02	-0.82	-1.02	-9.49	-0.79
5184	PEPD	BC004305	PEPTIDASE D	-10.19	-2.73	-1.19	-9.49	-8.49
5253	PHF2	NM_005392	PHD FINGER PROTEIN 2	-0.35	-0.58	-1.62	-8.77	-6.78
5253	PHF2	NM_005392	PHD FINGER PROTEIN 2	-9.28	-0.81	-1.09	-8.77	-7.3
337867	PHGDHL1	NM_177967	PHOSPHOGLYCERATE DEHYDROGENASE LIKE 1	-0.92	-0.7	-1.11	-2.42	-1.17
337867	PHGDHL1	NM_177967	PHOSPHOGLYCERATE DEHYDROGENASE LIKE 1	-1.49	-0.26	-1.29	-2.42	-7.18
337867	PHGDHL1	NM_177967	PHOSPHOGLYCERATE DEHYDROGENASE LIKE 1	-1.55	-0.39	-0.44	-2.42	-1.7
337867	PHGDHL1	NM_177967	PHOSPHOGLYCERATE DEHYDROGENASE LIKE 1	0.002	-0.09	0	-2.42	-0.12

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5288	PIK3C2G	NM_004570	PHOSPHOINOSITIDE-3-KINASE, CLASS 2, GAMMA POLYPEPTIDE	0	1.33	1.74	-0.46	0.4
5288	PIK3C2G	NM_004570	PHOSPHOINOSITIDE-3-KINASE, CLASS 2, GAMMA POLYPEPTIDE	-3.19	-1.02	-1.8	-0.46	-2.87
5288	PIK3C2G	NM_004570	PHOSPHOINOSITIDE-3-KINASE, CLASS 2, GAMMA POLYPEPTIDE	-0.28	-0.84	-0.9	-0.46	-0.01
5288	PIK3C2G	NM_004570	PHOSPHOINOSITIDE-3-KINASE, CLASS 2, GAMMA POLYPEPTIDE	-1.9	-2.09	-1.17	-0.46	-5.85
5291	PIK3CB	NM_006219	PHOSPHOINOSITIDE-3-KINASE, CATALYTIC, BETA POLYPEPTIDE	0.59	0.41	0.81	0.12	1.37
5291	PIK3CB	NM_006219	PHOSPHOINOSITIDE-3-KINASE, CATALYTIC, BETA POLYPEPTIDE	0.17	-1.16	-0.4	0.12	1.21
5291	PIK3CB	NM_006219	PHOSPHOINOSITIDE-3-KINASE, CATALYTIC, BETA POLYPEPTIDE	0.14	-0.79	-0.54	0.12	0.09
5291	PIK3CB	NM_006219	PHOSPHOINOSITIDE-3-KINASE, CATALYTIC, BETA POLYPEPTIDE	-1.15	-1.33	-1.31	0.12	-1.28
23533	PIK3R5	NM_014308	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 5, P101	-1.36	-1.28	-1.27	-2.28	-1.87
23533	PIK3R5	NM_014308	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 5, P101	-0.001	0.92	1.36	-2.28	0.2
23533	PIK3R5	NM_014308	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 5, P101	-4.44	-0.81	-1.01	-2.28	-3.08
23533	PIK3R5	NM_014308	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 5, P101	0.005	-0.08	-0.57	-2.28	-0.83
5300	PIN1	NM_006221	PROTEIN (PEPTIDYLPROLYL CIS/TRANS ISOMERASE) NIMA-INTERACTING 1	0.61	-0.0015	-0.12	-9.28	1.02
5300	PIN1	NM_006221	PROTEIN (PEPTIDYLPROLYL CIS/TRANS ISOMERASE) NIMA-INTERACTING 1	-0.74	-0.35	-1.06	-9.28	-8.11
5300	PIN1	NM_006221	PROTEIN (PEPTIDYLPROLYL CIS/TRANS ISOMERASE) NIMA-INTERACTING 1	-5.29	-1.84	-1.48	-9.28	-8.37
5300	PIN1	NM_006221	PROTEIN (PEPTIDYLPROLYL CIS/TRANS ISOMERASE) NIMA-INTERACTING 1	0.42	0.49	0.74	-9.28	-0.63
5328	PLAU	NM_002658	PLASMINOGEN ACTIVATOR, UROKINASE	-5.17	-1.91	-1.56	-9.5	-8.53
5328	PLAU	NM_002658	PLASMINOGEN ACTIVATOR, UROKINASE	-0.95	0.06	0.002	-9.5	-1.05
5328	PLAU	NM_002658	PLASMINOGEN ACTIVATOR, UROKINASE	-3	-2.03	-0.91	-9.5	-2.38
5328	PLAU	NM_002658	PLASMINOGEN ACTIVATOR, UROKINASE	0.7	-0.48	-0.1	-9.5	2.13
5338	PLD2	AF035483	PHOSPHOLIPASE D2	0.46	0.55	0.81	-9.4	0.64
5338	PLD2	AF035483	PHOSPHOLIPASE D2	-2.09	-1.25	-0.9	-9.4	-5.68
5338	PLD2	AF035483	PHOSPHOLIPASE D2	-7.28	-2.68	-2.42	-9.4	-8.32
5338	PLD2	AF035483	PHOSPHOLIPASE D2	-0.54	-0.74	-0.31	-9.4	-1.41
1263	PLK3	NM_004073	POLO-LIKE KINASE 3 (DROSOPHILA)	0.03	-1.33	-1.56	-9.44	-3.08
1263	PLK3	NM_004073	POLO-LIKE KINASE 3 (DROSOPHILA)	-3.03	-1.85	-1.5	-9.44	-8.4
1263	PLK3	NM_004073	POLO-LIKE KINASE 3 (DROSOPHILA)	-2.04	-0.94	-0.91	-9.44	-8.63
1263	PLK3	NM_004073	POLO-LIKE KINASE 3 (DROSOPHILA)	-0.004	-0.43	0.07	-9.44	1.59
5437	POLR2H	NM_006232	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE H	-2.31	-0.55	-0.4	-7.63	-3.65
5437	POLR2H	NM_006232	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE H	-2.6	-0.61	-0.66	-7.63	-5.79
5441	POLR2L	NM_021128	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE L, 7.6KDA	-2.07	-0.94	-1.47	-9.48	-8.48
5441	POLR2L	NM_021128	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE L, 7.6KDA	-3.71	-0.86	-1.21	-9.48	-5.05
54866	PPP1R14D	NM_017726	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14D	-0.06	-0.01	-0.04	-4.87	-3.37
54866	PPP1R14D	NM_017726	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14D	-0.45	-1.3	-0.39	-4.87	-6.64
54866	PPP1R14D	NM_017726	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14D	-2.46	-1.66	-1.9	-4.87	-3.02
54866	PPP1R14D	NM_017726	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14D	-0.65	-0.99	-0.53	-4.87	-3.17
10594	PRPF8	NM_006445	PRP8 PRE-MRNA PROCESSING FACTOR 8 HOMOLOG (YEAST)	-1.65	-1.05	-1.2	-9.32	-1.32
10594	PRPF8	NM_006445	PRP8 PRE-MRNA PROCESSING FACTOR 8 HOMOLOG (YEAST)	-5.05	-0.6	-1.26	-9.32	-8.18
10594	PRPF8	NM_006445	PRP8 PRE-MRNA PROCESSING FACTOR 8 HOMOLOG (YEAST)	-0.8	0.2	0.61	-9.32	-0.57
10594	PRPF8	NM_006445	PRP8 PRE-MRNA PROCESSING FACTOR 8 HOMOLOG (YEAST)	-2.96	-0.77	-0.7	-9.32	-6.58
5631	PRPS1	NM_002764	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1	-0.004	0.36	0.54	-7.74	0.64
5631	PRPS1	NM_002764	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1	-2.83	-0.64	-0.88	-7.74	-5.93
5631	PRPS1	NM_002764	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1	-2.63	-0.04	-1.48	-7.74	-2.51
5631	PRPS1	NM_002764	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1	0.24	0.25	0.88	-7.74	0.05
9361	PRSS15	NM_004793	PROTEASE, SERINE, 15	0.25	-0.47	-0.4	-9.16	0.8
9361	PRSS15	NM_004793	PROTEASE, SERINE, 15	-0.79	-0.008	-0.04	-9.16	-8.25
9361	PRSS15	NM_004793	PROTEASE, SERINE, 15	-2.51	-0.49	-1.07	-9.16	-2.44
9361	PRSS15	NM_004793	PROTEASE, SERINE, 15	-3.04	-0.81	-0.98	-9.16	-7.9
5660	PSAP	NM_002778	PROSAPOSIN (VARIANT GAUCHER DISEASE AND VARIANT METACHROMATIC LEUKODYSTROPHY)	-0.01	0.74	-0.42	-8.1	0.58
5660	PSAP	NM_002778	PROSAPOSIN (VARIANT GAUCHER DISEASE AND VARIANT METACHROMATIC LEUKODYSTROPHY)	-2.95	-1.78	-2.06	-8.1	-6.36
5660	PSAP	NM_002778	PROSAPOSIN (VARIANT GAUCHER DISEASE AND VARIANT METACHROMATIC LEUKODYSTROPHY)	-1.82	-0.02	-1.65	-8.1	-2.63
5660	PSAP	NM_002778	PROSAPOSIN (VARIANT GAUCHER DISEASE AND VARIANT METACHROMATIC LEUKODYSTROPHY)	-0.42	-0.02	0.02	-8.1	-0.12
5682	PSMA1	NM_148976	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, ALPHA TYPE, 1	-0.94	-2.24	-0.99	-3.02	0.99
5682	PSMA1	NM_148976	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, ALPHA TYPE, 1	0.51	0.98	0.3	-3.02	-0.5
5682	PSMA1	NM_148976	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, ALPHA TYPE, 1	-2.04	-0.79	-0.29	-3.02	-2.26
5682	PSMA1	NM_148976	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, ALPHA TYPE, 1	-1.96	-1.06	-0.68	-3.02	-2.19

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5706	PSMC6	NM_002806	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, ATPASE, 6	-2.26	0.36	-0.38	-8.98	-9.58
5706	PSMC6	NM_002806	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, ATPASE, 6	-3	0.44	-0.49	-8.98	-7.62
10213	PSMD14	NM_005805	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 14	0.09	0.76	0.62	-8.71	0.03
10213	PSMD14	NM_005805	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 14	-0.99	0.08	-0.16	-8.71	-7.2
10213	PSMD14	NM_005805	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 14	-5.17	-0.26	-1.01	-8.71	-6.79
10213	PSMD14	NM_005805	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 14	-1.85	2.64	0.21	-8.71	-7.27
5708	PSMD2	AL162014	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 2	-0.49	-0.01	-0.38	-2.02	-0.55
5708	PSMD2	AL162014	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 2	-3.66	-0.54	-0.5	-2.02	-8.37
5708	PSMD2	AL162014	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 2	-0.18	0.91	0.7	-2.02	-0.03
5708	PSMD2	AL162014	PROTEASOME (PROSOME, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 2	-2.4	0.6	-0.43	-2.02	-3.81
5798	PTPRN	NM_002846	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, N	0.05	-1.21	-0.88	-7.62	0.88
5798	PTPRN	NM_002846	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, N	-0.24	-0.27	0.005	-7.62	-5.77
5798	PTPRN	NM_002846	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, N	-2.06	-0.52	-0.88	-7.62	-3.78
5798	PTPRN	NM_002846	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, N	-3.48	-1.75	-0.75	-7.62	-7.77
51560	RAB6B	NM_016577	RAB6B, MEMBER RAS ONCOGENE FAMILY	0.78	0.59	0.01	-8.77	0.71
51560	RAB6B	NM_016577	RAB6B, MEMBER RAS ONCOGENE FAMILY	-5.59	-1.81	-1.35	-8.77	-7.28
51560	RAB6B	NM_016577	RAB6B, MEMBER RAS ONCOGENE FAMILY	-3.83	0.13	0.004	-8.77	-3.16
51560	RAB6B	NM_016577	RAB6B, MEMBER RAS ONCOGENE FAMILY	-1.37	-0.002	-0.02	-8.77	-2.06
29127	RACGAP1	NM_013277	RAC GTPASE ACTIVATING PROTEIN 1	-3.27	-2.85	-2.56	-8.52	-6.93
29127	RACGAP1	NM_013277	RAC GTPASE ACTIVATING PROTEIN 1	0.44	2.48	0.01	-8.52	2.56
29127	RACGAP1	NM_013277	RAC GTPASE ACTIVATING PROTEIN 1	0.44	0.65	0.13	-8.52	0.11
29127	RACGAP1	NM_013277	RAC GTPASE ACTIVATING PROTEIN 1	-0.9	-1.39	-0.38	-8.52	-0.8
10048	RANBP9	AF306510	RAN BINDING PROTEIN 9	-0.67	0.94	-0.09	-2.41	-1.38
10048	RANBP9	AF306510	RAN BINDING PROTEIN 9	-0.25	-0.71	-1.08	-2.41	-1.99
10048	RANBP9	AF306510	RAN BINDING PROTEIN 9	-3.32	-1.78	-1.27	-2.41	-2.15
10048	RANBP9	AF306510	RAN BINDING PROTEIN 9	0.49	-0.04	-0.002	-2.41	-0.3
5935	RBM3	NM_006743	RNA BINDING MOTIF (RNP1, RRM) PROTEIN 3	-2.18	-2.11	-1.9	-0.34	-6.5
5935	RBM3	NM_006743	RNA BINDING MOTIF (RNP1, RRM) PROTEIN 3	-2.02	-1.9	-1.94	-0.34	-6.5
5935	RBM3	NM_006743	RNA BINDING MOTIF (RNP1, RRM) PROTEIN 3	0.81	-0.63	0.51	-0.34	0.71
5935	RBM3	NM_006743	RNA BINDING MOTIF (RNP1, RRM) PROTEIN 3	0.3	-0.01	0.56	-0.34	0.71
56729	RETN	NM_020415	RESISTIN	-4.8	-1.79	-1.14	-7.88	-6.1
56729	RETN	NM_020415	RESISTIN	-0.62	-1.08	-0.47	-7.88	-2.62
56729	RETN	NM_020415	RESISTIN	-0.46	-1.26	-0.63	-7.88	-0.81
56729	RETN	NM_020415	RESISTIN	0.31	0.74	-0.29	-7.88	0.04
117584	RFFL	BC028424	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	-0.28	-0.14	0.12	-8.79	-0.04
117584	RFFL	BC028424	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	1.18	4.18	1.04	-8.79	1.76
117584	RFFL	BC028424	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	-3.59	-1.84	-1.17	-8.79	-2.96
117584	RFFL	BC028424	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	-6.51	-1.55	-1.24	-8.79	-8.45
57484	RNF150	AB033040	RING FINGER PROTEIN 150	-4.53	-2.26	-2.29	-9.54	-8.59
57484	RNF150	AB033040	RING FINGER PROTEIN 150	-1.13	-1.5	-1.57	-9.54	-8.56
57484	RNF150	AB033040	RING FINGER PROTEIN 150	-0.05	-0.15	-1.45	-9.54	-0.53
57484	RNF150	AB033040	RING FINGER PROTEIN 150	0.35	1.24	1.46	-9.54	1.48
11224	RPL35	NM_007209	RIBOSOMAL PROTEIN L35	-1.72	-0.39	-1.43	-8.23	-3.31
11224	RPL35	NM_007209	RIBOSOMAL PROTEIN L35	-1.87	0.04	-1.17	-8.23	-1.99
11224	RPL35	NM_007209	RIBOSOMAL PROTEIN L35	-1.69	-0.9	-1.54	-8.23	-1.1
11224	RPL35	NM_007209	RIBOSOMAL PROTEIN L35	-3.53	-0.61	-1.27	-8.23	-6.54
6204	RPS10	NM_001014	RIBOSOMAL PROTEIN S10	-2.7	-0.002	-0.3	-7.85	-8.45
6204	RPS10	NM_001014	RIBOSOMAL PROTEIN S10	-5.38	-0.77	-0.9	-7.85	-6.06
6208	RPS14	AF116710	RIBOSOMAL PROTEIN S14	-1.79	0.02	-1.47	-9.32	-1.92
6208	RPS14	AF116710	RIBOSOMAL PROTEIN S14	-3.86	-0.79	-0.05	-9.32	-8.17
6217	RPS16	NM_001020	RIBOSOMAL PROTEIN S16	-0.61	-0.94	-1.34	-4	-2.69
6217	RPS16	NM_001020	RIBOSOMAL PROTEIN S16	-3.37	-0.06	-1.16	-4	-3.76
6229	RPS24	NM_001026	RIBOSOMAL PROTEIN S24	-2.65	-0.53	-0.96	-7.76	-5.94
6229	RPS24	NM_001026	RIBOSOMAL PROTEIN S24	-2.36	-0.41	-1.1	-7.76	-2.81
6233	RPS27A	NM_002954	RIBOSOMAL PROTEIN S27A	-0.47	0.41	0.03	-9.41	-2.59
6233	RPS27A	NM_002954	RIBOSOMAL PROTEIN S27A	-1.69	-0.2	-0.11	-9.41	-5.72

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6233	RPS27A	NM_002954	RIBOSOMAL PROTEIN S27A	-3.26	-0.85	-0.36	-9.41	-8.35
6233	RPS27A	NM_002954	RIBOSOMAL PROTEIN S27A	-0.21	-0.44	-0.37	-9.41	-1.29
6188	RPS3	NM_001005	RIBOSOMAL PROTEIN S3	-1.64	-0.43	-0.7	-2.28	-2.09
6188	RPS3	NM_001005	RIBOSOMAL PROTEIN S3	-2.14	-0.009	-1.43	-2.28	-1.53
6193	RPS5	NM_001009	RIBOSOMAL PROTEIN S5	-2.69	-1.26	-1	-9.5	-2.91
6193	RPS5	NM_001009	RIBOSOMAL PROTEIN S5	-0.45	-1.14	-0.39	-9.5	-8.53
861	RUNX1	NM_001754	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE)	0.22	-2.09	-0.19	-0.44	-0.3
861	RUNX1	NM_001754	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE)	0.07	0.75	1.69	-0.44	1.44
861	RUNX1	NM_001754	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE)	-1.63	-1.68	-0.72	-0.44	-1.87
861	RUNX1	NM_001754	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE)	0.12	-1.19	-0.5	-0.44	0.82
6294	SAFB	NM_002967	SCAFFOLD ATTACHMENT FACTOR B	-1.55	-0.03	-0.24	-8.4	-6.61
6294	SAFB	NM_002967	SCAFFOLD ATTACHMENT FACTOR B	-0.02	-0.01	-0.25	-8.4	-0.32
6294	SAFB	NM_002967	SCAFFOLD ATTACHMENT FACTOR B	0.2	-0.74	0.8	-8.4	0.71
6294	SAFB	NM_002967	SCAFFOLD ATTACHMENT FACTOR B	-4.73	-0.13	-0.04	-8.4	-6.77
6301	SARS	NM_006513	SERYL-TRNA SYNTHETASE	-2.3	-0.41	-0.6	-8.02	-6.27
6301	SARS	NM_006513	SERYL-TRNA SYNTHETASE	-1.58	-0.52	-0.4	-8.02	-1.64
6339	SCNN1D	NM_002978	SODIUM CHANNEL, NONVOLTAGE-GATED 1, DELTA	0.24	0.01	-0.04	-9.92	1.32
6339	SCNN1D	NM_002978	SODIUM CHANNEL, NONVOLTAGE-GATED 1, DELTA	0.52	-1.25	-0.24	-9.92	1.49
6339	SCNN1D	NM_002978	SODIUM CHANNEL, NONVOLTAGE-GATED 1, DELTA	-0.65	-0.68	-0.46	-9.92	-5.67
6339	SCNN1D	NM_002978	SODIUM CHANNEL, NONVOLTAGE-GATED 1, DELTA	-2.64	-1.73	-0.65	-9.92	-9.58
6404	SELPLG	NM_003006	SELECTIN P LIGAND	-1.86	-0.43	-1.29	-8.3	-6.63
6404	SELPLG	NM_003006	SELECTIN P LIGAND	-2.93	0.03	-1.21	-8.3	-3.26
6404	SELPLG	NM_003006	SELECTIN P LIGAND	0.25	0.1	-0.17	-8.3	0.47
6404	SELPLG	NM_003006	SELECTIN P LIGAND	0.07	-0.39	-0.01	-8.3	0.001
5265	SERPINA1	AF113676	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 1	0.25	0.48	0.64	-2.35	0.32
5265	SERPINA1	AF113676	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 1	-0.21	-0.08	0.66	-2.35	-0.45
5265	SERPINA1	AF113676	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 1	-2.57	-0.56	-0.34	-2.35	-3.09
5265	SERPINA1	AF113676	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 1	-1.96	-0.03	-0.6	-2.35	-3.06
5055	SERPINB2	BC012609	SERPIN PEPTIDASE INHIBITOR, CLADE B (OVALBUMIN), MEMBER 2	-0.96	-1.59	-1.95	-0.14	-0.91
5055	SERPINB2	BC012609	SERPIN PEPTIDASE INHIBITOR, CLADE B (OVALBUMIN), MEMBER 2	1.49	0.26	0.05	-0.14	1.03
5055	SERPINB2	BC012609	SERPIN PEPTIDASE INHIBITOR, CLADE B (OVALBUMIN), MEMBER 2	-1.76	-2.06	-2.51	-0.14	-0.72
5055	SERPINB2	BC012609	SERPIN PEPTIDASE INHIBITOR, CLADE B (OVALBUMIN), MEMBER 2	-0.1	2.15	4.1	-0.14	-0.1
10291	SF3A1	NM_005877	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA	0.01	-0.98	0.06	-9.45	0.16
10291	SF3A1	NM_005877	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA	-5.68	-1.39	-1.07	-9.45	-7.7
10291	SF3A1	NM_005877	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA	-2.61	-1.64	-1.41	-9.45	-6.27
10291	SF3A1	NM_005877	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA	-2.05	0.21	0.4	-9.45	-8.42
23451	SF3B1	NM_012433	SPLICING FACTOR 3B, SUBUNIT 1, 155KDA	-3.15	0	-0.71	-9.05	-5.35
23451	SF3B1	NM_012433	SPLICING FACTOR 3B, SUBUNIT 1, 155KDA	-7.58	-0.28	-1.05	-9.05	-7.73
51639	SF3B14	NM_016047	SPLICING FACTOR 3B, 14 KDA SUBUNIT	-1.81	-0.28	-0.6	-3.92	-2.59
51639	SF3B14	NM_016047	SPLICING FACTOR 3B, 14 KDA SUBUNIT	-3.63	-1.07	-0.8	-3.92	-2.66
6439	SFTPB	NM_000542	SURFACTANT, PULMONARY-ASSOCIATED PROTEIN B	-1.37	-1.61	-0.27	-9.17	-1.01
6439	SFTPB	NM_000542	SURFACTANT, PULMONARY-ASSOCIATED PROTEIN B	-4.06	-1.67	-1.17	-9.17	-7.91
6439	SFTPB	NM_000542	SURFACTANT, PULMONARY-ASSOCIATED PROTEIN B	-0.07	0.06	-0.44	-9.17	-9.58
6439	SFTPB	NM_000542	SURFACTANT, PULMONARY-ASSOCIATED PROTEIN B	-0.02	-0.35	0.99	-9.17	-0.93
8778	SIGLEC5	NM_003830	SIALIC ACID BINDING IG-LIKE LECTIN 5	-0.5	1.16	0.68	-9.49	-0.13
8778	SIGLEC5	NM_003830	SIALIC ACID BINDING IG-LIKE LECTIN 5	1.02	-0.13	-0.76	-9.49	1.21
8778	SIGLEC5	NM_003830	SIALIC ACID BINDING IG-LIKE LECTIN 5	-1.99	-1.87	-1.5	-9.49	-1.85
8778	SIGLEC5	NM_003830	SIALIC ACID BINDING IG-LIKE LECTIN 5	-9.03	-1.16	-1.4	-9.49	-8.51
22938	SKIIP	NM_012245	SNW DOMAIN CONTAINING 1	-3.06	-0.1	-0.54	-2.33	-2.69
22938	SKIIP	NM_012245	SNW DOMAIN CONTAINING 1	-0.22	-0.03	-0.83	-2.33	0.01
22938	SKIIP	NM_012245	SNW DOMAIN CONTAINING 1	-1.9	1.57	1.05	-2.33	-2.06
22938	SKIIP	NM_012245	SNW DOMAIN CONTAINING 1	-0.65	0.54	0.35	-2.33	-0.95
6560	SLC12A4	NM_005072	SOLUTE CARRIER FAMILY 12 (POTASSIUM/CHLORIDE TRANSPORTERS), MEMBER 4	-1.63	-0.32	-0.94	-8.21	-9.58
6560	SLC12A4	NM_005072	SOLUTE CARRIER FAMILY 12 (POTASSIUM/CHLORIDE TRANSPORTERS), MEMBER 4	-3.6	-1.02	-0.18	-8.21	-6.51
9356	SLC22A6	NM_004790	SOLUTE CARRIER FAMILY 22 (ORGANIC ANION TRANSPORTER), MEMBER 6	-2.69	-2.54	-1.13	-9.03	-2.68
9356	SLC22A6	NM_004790	SOLUTE CARRIER FAMILY 22 (ORGANIC ANION TRANSPORTER), MEMBER 6	0.26	-1.01	1	-9.03	-7.69

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
9368	SLC9A3R1	NM_004252	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), MEMBER 3 REGULATOR 1	0.19	-0.16	0.01	-7.87	0.3
9368	SLC9A3R1	NM_004252	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), MEMBER 3 REGULATOR 1	-2.37	0.79	-0.42	-7.87	-6.08
9368	SLC9A3R1	NM_004252	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), MEMBER 3 REGULATOR 1	0.67	0.95	1.08	-7.87	0.95
9368	SLC9A3R1	NM_004252	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), MEMBER 3 REGULATOR 1	-1.6	-0.59	-0.86	-7.87	-6.64
55234	SMU1	NM_018225	SMU-1 SUPPRESSOR OF MEC-8 AND UNC-52 HOMOLOG (C. ELEGANS)	-3.34	-0.37	-1.27	-8.06	-6.32
55234	SMU1	NM_018225	SMU-1 SUPPRESSOR OF MEC-8 AND UNC-52 HOMOLOG (C. ELEGANS)	-6.62	0.18	0.8	-8.06	-7.01
6625	SNRP70	NM_003089	SMALL NUCLEAR RIBONUCLEOPROTEIN 70KDA POLYPEPTIDE (RNP ANTIGEN)	0.0045	-0.08	-0.07	-9.02	-0.21
6625	SNRP70	NM_003089	SMALL NUCLEAR RIBONUCLEOPROTEIN 70KDA POLYPEPTIDE (RNP ANTIGEN)	-4.05	-1.27	-0.91	-9.02	-9.58
6625	SNRP70	NM_003089	SMALL NUCLEAR RIBONUCLEOPROTEIN 70KDA POLYPEPTIDE (RNP ANTIGEN)	-1.83	-0.8	-0.27	-9.02	-7.67
6625	SNRP70	NM_003089	SMALL NUCLEAR RIBONUCLEOPROTEIN 70KDA POLYPEPTIDE (RNP ANTIGEN)	-0.05	-0.14	1.82	-9.02	-0.85
6636	SNRPF	NM_003095	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE F	-1.98	0.19	-0.66	-9.53	-2.74
6636	SNRPF	NM_003095	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE F	-3.69	0.11	-0.15	-9.53	-8.58
58533	SNX6	NM_021249	SORTING NEXIN 6	-1.29	0.01	0.14	-2.53	-1.7
58533	SNX6	NM_021249	SORTING NEXIN 6	-0.44	-0.96	-0.99	-2.53	-5.88
58533	SNX6	NM_021249	SORTING NEXIN 6	-3.22	-1.11	-1.5	-2.53	-2.77
58533	SNX6	NM_021249	SORTING NEXIN 6	-1.36	-1.23	-0.94	-2.53	-0.55
51429	SNX9	NM_016224	SORTING NEXIN 9	0.03	-0.92	-0.52	-9	-0.62
51429	SNX9	NM_016224	SORTING NEXIN 9	-3.18	-0.69	-1.05	-9	-7.09
51429	SNX9	NM_016224	SORTING NEXIN 9	-0.36	-0.58	-0.57	-9	0.006
51429	SNX9	NM_016224	SORTING NEXIN 9	-4.34	-0.68	-0.77	-9	-8.47
6651	SON	NM_138927	SON DNA BINDING PROTEIN	-5.13	-0.48	-1.67	-9.42	-7.9
6651	SON	NM_138927	SON DNA BINDING PROTEIN	-9.46	-0.99	-1.36	-9.42	-8.36
23524	SRRM2	NM_016333	SERINE/ARGININE REPETITIVE MATRIX 2	-1.81	-1.04	-1.61	-7.37	-5.48
23524	SRRM2	NM_016333	SERINE/ARGININE REPETITIVE MATRIX 2	-4.31	-0.93	-1.55	-7.37	-5.35
83983	SSTK	NM_032037	TESTIS-SPECIFIC SERINE KINASE 6	0.56	0.89	1.36	-7.55	0.88
83983	SSTK	NM_032037	TESTIS-SPECIFIC SERINE KINASE 6	-1.4	-0.78	-0.49	-7.55	-2.58
83983	SSTK	NM_032037	TESTIS-SPECIFIC SERINE KINASE 6	-2.73	-0.89	-0.01	-7.55	-2.38
83983	SSTK	NM_032037	TESTIS-SPECIFIC SERINE KINASE 6	-3.1	-0.95	-0.89	-7.55	-5.69
6755	SSTR5	NM_001053	SOMATOSTATIN RECEPTOR 5	-1.95	-0.73	-0.69	-9.26	-8.08
6755	SSTR5	NM_001053	SOMATOSTATIN RECEPTOR 5	-0.15	-0.04	-1.08	-9.26	0.31
6755	SSTR5	NM_001053	SOMATOSTATIN RECEPTOR 5	-2.18	-0.69	-0.59	-9.26	-2.89
6755	SSTR5	NM_001053	SOMATOSTATIN RECEPTOR 5	-0.51	-0.23	-0.89	-9.26	-8.42
23166	STAB1	AB052957	STABILIN 1	-2.17	-0.84	-0.6	-2.99	-5.72
23166	STAB1	AB052957	STABILIN 1	0.03	0.002	0.24	-2.99	0.54
23166	STAB1	AB052957	STABILIN 1	-3.12	-0.06	-1.19	-2.99	-2.09
23166	STAB1	AB052957	STABILIN 1	-0.58	0.07	0.06	-2.99	-0.44
252983	STXBP4	AK122865	SYNTAXIN BINDING PROTEIN 4	-1.15	-0.48	-2.51	-9.61	-2.06
252983	STXBP4	AK122865	SYNTAXIN BINDING PROTEIN 4	0.01	1.22	-1.22	-9.61	-8.75
55959	SULF2	NM_018837	SULFATASE 2	0.18	0.26	0.0065	-1.21	2.4
55959	SULF2	NM_018837	SULFATASE 2	1.33	2.3	1.59	-1.21	2.77
55959	SULF2	NM_018837	SULFATASE 2	-2.62	-1.69	-1.52	-1.21	-1.85
55959	SULF2	NM_018837	SULFATASE 2	-1.25	-1.47	-1.46	-1.21	-2.11
6830	SUPT6H	D79984	SUPPRESSOR OF TY 6 HOMOLOG (S. CEREVISIAE)	-2.53	0.63	-0.33	-9.5	-8.52
6830	SUPT6H	D79984	SUPPRESSOR OF TY 6 HOMOLOG (S. CEREVISIAE)	-3.15	0	-0.81	-9.5	-8.57
10607	TBL3	BC033227	TRANSDUCIN (BETA)-LIKE 3	0.59	1.29	-0.52	-8.98	0.8
10607	TBL3	BC033227	TRANSDUCIN (BETA)-LIKE 3	-1.09	-0.33	-1.55	-8.98	-0.85
10607	TBL3	BC033227	TRANSDUCIN (BETA)-LIKE 3	-0.1	-1.46	-1.76	-8.98	-7.61
10607	TBL3	BC033227	TRANSDUCIN (BETA)-LIKE 3	0.33	0.88	-0.36	-8.98	-8.53
30009	TBX21	NM_013351	TRANSCRIPTION FACTOR TBLYM	-0.02	1.26	0.34	-8.24	-0.39
30009	TBX21	NM_013351	TRANSCRIPTION FACTOR TBLYM	0.34	0.92	0.82	-8.24	0.96
30009	TBX21	NM_013351	TRANSCRIPTION FACTOR TBLYM	-0.32	-1.23	-1.09	-8.24	-5.19
30009	TBX21	NM_013351	TRANSCRIPTION FACTOR TBLYM	-1.27	-1.26	-0.15	-8.24	-6.55
6929	TCF3	NM_003200	TRANSCRIPTION FACTOR 3 (E2A IMMUNOGLOBULIN ENHANCER BINDING FACTORS E12/E47)	-0.62	-1.27	-1.04	-8.52	-1.32
6929	TCF3	NM_003200	TRANSCRIPTION FACTOR 3 (E2A IMMUNOGLOBULIN ENHANCER BINDING FACTORS E12/E47)	-0.29	0.53	1.12	-8.52	-9.58
6929	TCF3	NM_003200	TRANSCRIPTION FACTOR 3 (E2A IMMUNOGLOBULIN ENHANCER BINDING FACTORS E12/E47)	-2.32	-0.31	-1.07	-8.52	-6.93
6929	TCF3	NM_003200	TRANSCRIPTION FACTOR 3 (E2A IMMUNOGLOBULIN ENHANCER BINDING FACTORS E12/E47)	1.5	0.04	-0.99	-8.52	1.41

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
7030	TFE3	NM_006521	TRANSCRIPTION FACTOR BINDING TO IGHM ENHANCER 3	-1.38	0.11	-1.24	-8.49	-6.89
7030	TFE3	NM_006521	TRANSCRIPTION FACTOR BINDING TO IGHM ENHANCER 3	0.37	-0.02	0.61	-8.49	0.78
7030	TFE3	NM_006521	TRANSCRIPTION FACTOR BINDING TO IGHM ENHANCER 3	-3.58	-1.3	-1.3	-8.49	-8.13
7030	TFE3	NM_006521	TRANSCRIPTION FACTOR BINDING TO IGHM ENHANCER 3	-0.0065	0.22	1.25	-8.49	0.51
10469	TIMM44	NM_006351	TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 44 HOMOLOG (YEAST)	-4	-0.68	-1.96	-9.19	-7.96
10469	TIMM44	NM_006351	TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 44 HOMOLOG (YEAST)	-1.17	0.01	-1.11	-9.19	-1.69
7084	TK2	NM_004614	THYMIDINE KINASE 2, MITOCHONDRIAL	-3.82	-1.27	-1.15	-8.24	-6.55
7084	TK2	NM_004614	THYMIDINE KINASE 2, MITOCHONDRIAL	-2.58	-0.03	-0.46	-8.24	-8.57
7084	TK2	NM_004614	THYMIDINE KINASE 2, MITOCHONDRIAL	-0.89	-0.32	-0.34	-8.24	0.27
7084	TK2	NM_004614	THYMIDINE KINASE 2, MITOCHONDRIAL	0.56	0.48	0.09	-8.24	1.86
3371	TNC	NM_002160	TENASCIN C (HEXABRACHION)	-0.55	-1.17	-0.93	-2.05	-1.89
3371	TNC	NM_002160	TENASCIN C (HEXABRACHION)	-1.93	-0.28	-0.51	-2.05	-1.38
3371	TNC	NM_002160	TENASCIN C (HEXABRACHION)	-1.94	-0.29	-0.85	-2.05	-3.14
3371	TNC	NM_002160	TENASCIN C (HEXABRACHION)	-0.04	1.76	0.23	-2.05	-0.51
8784	TNFRSF18	NM_148901	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 18	-0.31	0.33	0.33	-9.12	-0.06
8784	TNFRSF18	NM_148901	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 18	-1.17	0.87	0.21	-9.12	-1.13
8784	TNFRSF18	NM_148901	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 18	-3.36	-1.36	-1.68	-9.12	-5.09
8784	TNFRSF18	NM_148901	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 18	-1.51	-0.37	-2.06	-9.12	-7.84
10188	TNK2	NM_005781	TYROSINE KINASE, NON-RECEPTOR, 2	-2.57	-0.22	-1	-7.67	-1.94
10188	TNK2	NM_005781	TYROSINE KINASE, NON-RECEPTOR, 2	-2.1	-1.14	-0.05	-7.67	-5.84
10188	TNK2	NM_005781	TYROSINE KINASE, NON-RECEPTOR, 2	-6.9	-0.12	-0.74	-7.67	-8.6
10188	TNK2	NM_005781	TYROSINE KINASE, NON-RECEPTOR, 2	-0.36	-1.1	-0.28	-7.67	-0.22
23471	TRAM1	NM_014294	TRANSLOCATION ASSOCIATED MEMBRANE PROTEIN 1	-1.06	-0.04	-1.36	-7.63	-8.6
23471	TRAM1	NM_014294	TRANSLOCATION ASSOCIATED MEMBRANE PROTEIN 1	0.59	-1.38	-0.05	-7.63	0.26
23471	TRAM1	NM_014294	TRANSLOCATION ASSOCIATED MEMBRANE PROTEIN 1	-4.15	-1.06	-1.18	-7.63	-5.79
23471	TRAM1	NM_014294	TRANSLOCATION ASSOCIATED MEMBRANE PROTEIN 1	-1.1	-1.17	-1.89	-7.63	-0.66
10131	TRAP1	NM_016292	TNF RECEPTOR-ASSOCIATED PROTEIN 1	-0.9	-0.88	-1.07	-8.1	-1.63
10131	TRAP1	NM_016292	TNF RECEPTOR-ASSOCIATED PROTEIN 1	-0.27	-1.73	-1.38	-8.1	-0.4
10131	TRAP1	NM_016292	TNF RECEPTOR-ASSOCIATED PROTEIN 1	-6.23	0.5	-0.83	-8.1	-6.37
10131	TRAP1	NM_016292	TNF RECEPTOR-ASSOCIATED PROTEIN 1	0.12	1.21	-0.09	-8.1	1.3
55809	TRERF1	NM_033502	TRANSCRIPTIONAL REGULATING FACTOR 1	0.06	1.26	0.33	-0.21	1.21
55809	TRERF1	NM_033502	TRANSCRIPTIONAL REGULATING FACTOR 1	0.11	0.34	-0.58	-0.21	0.27
55809	TRERF1	NM_033502	TRANSCRIPTIONAL REGULATING FACTOR 1	-0.33	-1.23	-1.17	-0.21	-0.49
55809	TRERF1	NM_033502	TRANSCRIPTIONAL REGULATING FACTOR 1	-0.18	-0.31	-1.16	-0.21	-4.01
28951	TRIB2	BC002637	TRIBBLES HOMOLOG 2 (DROSOPHILA)	-2.02	0.37	-0.7	-2.08	-1.55
28951	TRIB2	BC002637	TRIBBLES HOMOLOG 2 (DROSOPHILA)	-0.06	-0.4	0.41	-2.08	0.98
28951	TRIB2	BC002637	TRIBBLES HOMOLOG 2 (DROSOPHILA)	0.19	0.37	0.02	-2.08	0.67
28951	TRIB2	BC002637	TRIBBLES HOMOLOG 2 (DROSOPHILA)	-1.55	-0.07	-1.38	-2.08	-1.76
9830	TRIM14	NM_033219	TRIPARTITE MOTIF-CONTAINING 14	1.56	-0.06	0.44	-8.77	1.13
9830	TRIM14	NM_033219	TRIPARTITE MOTIF-CONTAINING 14	-3.19	-0.54	-0.33	-8.77	-8.51
9830	TRIM14	NM_033219	TRIPARTITE MOTIF-CONTAINING 14	-1.45	0.06	-0.24	-8.77	-7.29
9830	TRIM14	NM_033219	TRIPARTITE MOTIF-CONTAINING 14	-3.59	2.33	0.54	-8.77	-8.43
6737	TRIM21	NM_003141	TRIPARTITE MOTIF-CONTAINING 21	-4.33	-1.32	-0.97	-9.12	-5.01
6737	TRIM21	NM_003141	TRIPARTITE MOTIF-CONTAINING 21	-2.08	-1.26	-1.53	-9.12	-7.84
6737	TRIM21	NM_003141	TRIPARTITE MOTIF-CONTAINING 21	-0.35	1.77	1.29	-9.12	-0.33
6737	TRIM21	NM_003141	TRIPARTITE MOTIF-CONTAINING 21	-9.72	-2.72	-2.42	-9.12	-8.52
166655	TRIM60	NM_152620	TRIPARTITE MOTIF-CONTAINING 60	-2.21	-1.5	-1.51	0.29	-6.02
166655	TRIM60	NM_152620	TRIPARTITE MOTIF-CONTAINING 60	0.84	-1.05	0.001	0.29	0.26
166655	TRIM60	NM_152620	TRIPARTITE MOTIF-CONTAINING 60	0.5	-1.36	-0.28	0.29	0.39
166655	TRIM60	NM_152620	TRIPARTITE MOTIF-CONTAINING 60	-0.45	0.4	0.49	0.29	-0.69
10907	TXNL4A	NM_006701	THIOREDOXIN-LIKE 4A	0.7	-1.36	0.32	-2.67	1.08
10907	TXNL4A	NM_006701	THIOREDOXIN-LIKE 4A	-1.96	0.35	-0.27	-2.67	-1.8
10907	TXNL4A	NM_006701	THIOREDOXIN-LIKE 4A	-1.53	-1.86	-0.63	-2.67	-1.79
10907	TXNL4A	NM_006701	THIOREDOXIN-LIKE 4A	-2.48	-0.27	0.004	-2.67	-7.84
83706	URP2	NM_031471	UNC-112 RELATED PROTEIN 2	-2.64	-1.38	-0.8	-3.64	-3.51
83706	URP2	NM_031471	UNC-112 RELATED PROTEIN 2	-1.14	-1.15	-1.03	-3.64	-2.07

GeneID	Gene symbol	Genbank accession	Official full name	cellHTS, luciferase activity, Z-score	cellHTS, percentage of infected cells, Z-score	cellHTS, number of infected cells, Z-score	Genedata, luciferase activity, Z-score, gene-wise	Genedata, luciferase activity, Z-score, siRNA-wise
84833	USMG5	NM_032747	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5 HOMOLOG (MOUSE)	-1.6	-0.14	-1.22	-3.04	-2.05
84833	USMG5	NM_032747	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5 HOMOLOG (MOUSE)	-1.96	0.01	-0.34	-3.04	-2.82
84132	USP42	AK022759	UBIQUITIN SPECIFIC PEPTIDASE 42	-2.53	-0.7	-1.81	-2.69	-3.04
84132	USP42	AK022759	UBIQUITIN SPECIFIC PEPTIDASE 42	-0.53	1.15	-0.97	-2.69	-0.85
84132	USP42	AK022759	UBIQUITIN SPECIFIC PEPTIDASE 42	0.25	-0.004	-0.01	-2.69	0.38
84132	USP42	AK022759	UBIQUITIN SPECIFIC PEPTIDASE 42	-1.64	0.09	-1.53	-2.69	-2.69
8875	VNN2	NM_004665	VANIN 2	-1.98	-0.79	-1.7	0.36	-1.55
8875	VNN2	NM_004665	VANIN 2	1.31	-0.02	-0.04	0.36	-0.21
8875	VNN2	NM_004665	VANIN 2	0.28	0.12	-0.07	0.36	0.7
8875	VNN2	NM_004665	VANIN 2	-0.17	-0.19	-1.19	0.36	0.56
7483	WNT9A	NM_003395	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 9A	-1.2	-0.43	-1.17	-8.01	-5.42
7483	WNT9A	NM_003395	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 9A	-0.63	-0.29	-1.17	-8.01	-6.25
56949	XAB2	NM_020196	XPA BINDING PROTEIN 2	-0.27	0.97	0.18	-8.18	-1.57
56949	XAB2	NM_020196	XPA BINDING PROTEIN 2	-0.05	1.37	0.53	-8.18	0.12
56949	XAB2	NM_020196	XPA BINDING PROTEIN 2	-4.48	-0.18	-0.25	-8.18	-6.48
56949	XAB2	NM_020196	XPA BINDING PROTEIN 2	-1.52	-0.91	-0.27	-8.18	-3.07
7511	XPNPEP1	NM_020383	X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE	-5.15	-0.87	-1.48	-8.7	-7.19
7511	XPNPEP1	NM_020383	X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE	-1.8	-1.2	-0.53	-8.7	-9.58
7511	XPNPEP1	NM_020383	X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE	-0.39	0.91	-0.02	-8.7	-0.29
7511	XPNPEP1	NM_020383	X-PROLYL AMINOPEPTIDASE (AMINOPEPTIDASE P) 1, SOLUBLE	-0.01	-0.43	-0.01	-8.7	0.48
7514	XPO1	NM_003400	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-0.91	0.14	-0.41	-9.45	-1.53
7514	XPO1	NM_003400	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-6.47	-1.14	-0.64	-9.45	-8.42
7514	XPO1	NM_003400	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-1.08	-0.2	-0.49	-9.45	-1.13
7514	XPO1	NM_003400	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-4.92	-1.07	-1.06	-9.45	-8.56
57621	ZBTB2	NM_020861	ZINC FINGER AND BTB DOMAIN CONTAINING 2	-1.73	-0.07	0.23	-3.13	-2.1
57621	ZBTB2	NM_020861	ZINC FINGER AND BTB DOMAIN CONTAINING 2	-3.63	-0.01	-0.76	-3.13	-4.73
256112	ZNF37B	AK026980	ZINC FINGER PROTEIN 37B (KOX 21)	-3.64	-0.53	-0.63	-7.48	-5.62
256112	ZNF37B	AK026980	ZINC FINGER PROTEIN 37B (KOX 21)	-5.56	-0.08	-0.97	-7.48	-8.54
84450	ZNF512	NM_032434	ZINC FINGER PROTEIN 512	-2.91	0.4	-1.15	-3.46	-2.33
84450	ZNF512	NM_032434	ZINC FINGER PROTEIN 512	-3.41	-0.26	-0.54	-3.46	-2.67

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
23456	ABCB10	-1.28	-0.98	-0.23	-0.29	Yes	No	No	1268	-1.42	0.00905	301.25	195.22
23456	ABCB10	-1.28	1	-0.23	0.39	No	No	No	999	-1.42	0.00905	301.25	195.22
23456	ABCB10	-1.28	-1.62	-0.23	-0.13	Yes	No	Yes	2033	-1.42	0.00905	301.25	195.22
23456	ABCB10	-1.28	-1.06	-0.23	-1.24	No	Yes	Yes	1673	-1.42	0.00905	301.25	195.22
368	ABCC6	-0.69	0.33	-1.54	0.12	No	No	No	868	1.33	0.13	372.07	487.69
368	ABCC6	-0.69	-1.4	-1.54	-1.93	No	No	No	1017	1.33	0.13	372.07	487.69
368	ABCC6	-0.69	-0.89	-1.54	-1.03	Yes	No	No	1031	1.33	0.13	372.07	487.69
368	ABCC6	-0.69	-0.57	-1.54	-1.35	Yes	Yes	No	1009	1.33	0.13	372.07	487.69
31	ACACA	-0.84	-0.5	-0.75	-0.36	Yes	No	No	1702	-1.18	0.36	180.07	160.16
31	ACACA	-0.84	-0.43	-0.75	0.04	No	No	No	1893	-1.18	0.36	180.07	160.16
31	ACACA	-0.84	-0.73	-0.75	-1.54	Yes	Yes	Yes	1318	-1.18	0.36	180.07	160.16
31	ACACA	-0.84	-1.03	-0.75	-0.48	No	No	No	2622	-1.18	0.36	180.07	160.16
130399	ACVR1C	0.69	-0.1	0.53	0.24	Yes	No	No	1350	2.75	0.03	39.11	148.37
130399	ACVR1C	0.69	1.17	0.53	0.48	No	No	No	1280	2.75	0.03	39.11	148.37
130399	ACVR1C	0.69	0.41	0.53	0.09	No	No	No	1316	2.75	0.03	39.11	148.37
130399	ACVR1C	0.69	-1.58	0.53	-1.57	Yes	No	No	1364	2.75	0.03	39.11	148.37
10768	AHCYL1	-2.42	-1.51	-0.91	-0.2	No	No	Yes	1887	-2.25	1.33E-17	4217.41	1814.1
10768	AHCYL1	-2.42	-0.45	-0.91	-0.27	No	No	No	2157	-2.25	1.33E-17	4217.41	1814.1
10768	AHCYL1	-2.42	-1.91	-0.91	-1.62	No	No	Yes	2171	-2.25	1.33E-17	4217.41	1814.1
10768	AHCYL1	-2.42	-2.23	-0.91	-0.39	Yes	Yes	Yes	2101	-2.25	1.33E-17	4217.41	1814.1
51390	AIG1	-2.56	-2.05	-2.73	-2.33	Yes	Yes	No	1208	-1.52	0.02	1228.53	812.44
51390	AIG1	-2.56	-1.61	-2.73	-0.76	Yes	No	Yes	2034	-1.52	0.02	1228.53	812.44
81693	AMN	-1.01	1.67	-0.29	3.03	No	No	No	1436	4.31	8.63E-43	381.42	1674.12
81693	AMN	-1.01	-1.49	-0.29	-0.77	Yes	Yes	Yes	1101	4.31	8.63E-43	381.42	1674.12
81693	AMN	-1.01	-0.04	-0.29	-0.1	No	No	No	2368	4.31	8.63E-43	381.42	1674.12
81693	AMN	-1.01	-0.99	-0.29	-1.19	No	No	Yes	1076	4.31	8.63E-43	381.42	1674.12
255239	ANKK1	-1.46	-0.3	-0.28	0.04	No	No	No	1329	4.72	6.42E-13	127150.7	629734.75
255239	ANKK1	-1.46	-3.41	-0.28	-3.03	Yes	Yes	Yes	935	4.72	6.42E-13	127150.7	629734.75
255239	ANKK1	-1.46	-1.21	-0.28	-0.21	No	Yes	Yes	1452	4.72	6.42E-13	127150.7	629734.75
255239	ANKK1	-1.46	0.61	-0.28	0.52	No	No	No	1285	4.72	6.42E-13	127150.7	629734.75
1173	AP2M1	-0.32	0.65	-1.03	-1.6	Yes	Yes	No	602	-1.06	0.69	1064.44	1000.78
1173	AP2M1	-0.32	-0.45	-1.03	0.22	No	No	No	1159	-1.06	0.69	1064.44	1000.78
1173	AP2M1	-0.32	-0.35	-1.03	0.4	No	No	No	1040	-1.06	0.69	1064.44	1000.78
1173	AP2M1	-0.32	-0.37	-1.03	-0.55	Yes	No	No	1126	-1.06	0.69	1064.44	1000.78
54518	APBB1IP	1.43	0.43	-0.33	-0.38	Yes	No	No	1204	-1.69	0.00671	205.93	128.27
54518	APBB1IP	1.43	1.13	-0.33	0.23	Yes	No	No	1506	-1.69	0.00671	205.93	128.27
8883	APPBP1	-2.17	0.82	-0.78	0.6	No	No	No	1496	-2.29	1.32E-11	3973.02	1726.99
8883	APPBP1	-2.17	0.82	-0.78	0.6	No	No	No	1657	-2.29	1.32E-11	3973.02	1726.99
8883	APPBP1	-2.17	-2.1	-0.78	-1.1	No	No	Yes	2091	-2.29	1.32E-11	3973.02	1726.99
8883	APPBP1	-2.17	-2.1	-0.78	-1.1	No	Yes	Yes	2653	-2.29	1.32E-11	3973.02	1726.99
372	ARCN1	-2.39	-1.88	-2.37	-1.18	Yes	Yes	Yes	931	1.82	6.06E-06	612.71	1127.46
372	ARCN1	-2.39	-2.85	-2.37	-2.2	Yes	Yes	Yes	1218	1.82	6.06E-06	612.71	1127.46
8260	ARD1	-0.24	-0.51	-0.45	0.24	No	No	No	1671	1.09	0.39	1295.46	1421.86
8260	ARD1	-0.24	0.006	-0.45	-0.32	No	No	No	1335	1.09	0.39	1295.46	1421.86
8260	ARD1	-0.24	0.17	-0.45	0.04	Yes	No	No	1271	1.09	0.39	1295.46	1421.86
8260	ARD1	-0.24	-1.8	-0.45	-2.55	Yes	No	No	941	1.09	0.39	1295.46	1421.86
9048	ARTN	-2.41	-2.29	-1.36	-1.28	Yes	Yes	No	1119	10.4	4.51E-22	171.32	1963.18
9048	ARTN	-2.41	1	-1.36	0.55	No	No	No	1227	10.4	4.51E-22	171.32	1963.18
9048	ARTN	-2.41	-1.96	-1.36	-1.41	No	Yes	Yes	1162	10.4	4.51E-22	171.32	1963.18
9048	ARTN	-2.41	-0.54	-1.36	-0.13	No	Yes	Yes	1598	10.4	4.51E-22	171.32	1963.18
443	ASPA	-0.22	-0.93	-1.22	-0.86	Yes	No	Yes	1168	1	1	39.09	91.57
443	ASPA	-0.22	-1.71	-1.22	-0.56	No	No	Yes	1753	1	1	39.09	91.57
443	ASPA	-0.22	0.3	-1.22	-1.78	Yes	Yes	No	661	1	1	39.09	91.57
443	ASPA	-0.22	0.38	-1.22	-1.41	No	No	No	1098	1	1	39.09	91.57
85300	ATCAY	-1.4	0.52	-2.11	-0.57	Yes	No	No	1455	6.87	0	402.71	2811.98
85300	ATCAY	-1.4	-2.11	-2.11	-2.09	Yes	Yes	Yes	1771	6.87	0	402.71	2811.98

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
477	ATP1A2	-1.34	-0.69	-1.75	-0.52	No	No	No	1619	1	1	40.07	100.05
477	ATP1A2	-1.34	-1.29	-1.75	-2.23	Yes	Yes	Yes	871	1	1	40.07	100.05
477	ATP1A2	-1.34	0.2	-1.75	-1.38	No	Yes	No	973	1	1	40.07	100.05
477	ATP1A2	-1.34	1.39	-1.75	1.92	No	No	No	2042	1	1	40.07	100.05
27032	ATP2C1	-1.62	0.05	-2.38	-0.33	No	No	No	1098	-2.83	2.16E-10	2290.89	810.65
27032	ATP2C1	-1.62	-0.34	-2.38	0.5	No	No	No	1657	-2.83	2.16E-10	2290.89	810.65
27032	ATP2C1	-1.62	-2.22	-2.38	-1.87	Yes	Yes	Yes	1272	-2.83	2.16E-10	2290.89	810.65
27032	ATP2C1	-1.62	-1.64	-2.38	-2.96	Yes	Yes	No	876	-2.83	2.16E-10	2290.89	810.65
537	ATP6AP1	-3.01	-2.34	-2.65	-2.37	Yes	Yes	No	815	-1.16	0.06	4135.06	3517.71
537	ATP6AP1	-3.01	-2.35	-2.65	-2.07	No	Yes	Yes	1310	-1.16	0.06	4135.06	3517.71
10159	ATP6AP2	-2.25	-0.19	-0.96	0.35	No	No	No	1208	-1.16	0.2	4311.51	3752.7
10159	ATP6AP2	-2.25	-1.7	-0.96	-1.53	No	Yes	Yes	1025	-1.16	0.2	4311.51	3752.7
10159	ATP6AP2	-2.25	-1.78	-0.96	-0.24	No	No	No	2058	-1.16	0.2	4311.51	3752.7
10159	ATP6AP2	-2.25	-2.38	-0.96	-1.46	No	No	Yes	1812	-1.16	0.2	4311.51	3752.7
527	ATP6V0C	-2.95	-2.17	-1.61	-1.3	Yes	Yes	Yes	1159	-1.11	0.12	4627.82	4439.99
527	ATP6V0C	-2.95	-2.45	-1.61	-0.73	No	No	Yes	1536	-1.11	0.12	4627.82	4439.99
9114	ATP6V0D1	-3.83	-2.96	-2.69	-1.87	No	No	Yes	1448	1.07	0.37	1392.27	1514.22
9114	ATP6V0D1	-3.83	-2.89	-2.69	-2.25	Yes	Yes	Yes	1245	1.07	0.37	1392.27	1514.22
523	ATP6V1A	-2.12	-1.98	-2.06	-0.59	No	No	Yes	1575	2.27	4.24E-08	3658.96	8598.16
523	ATP6V1A	-2.12	-2.01	-2.06	-2.1	Yes	Yes	Yes	1223	2.27	4.24E-08	3658.96	8598.16
523	ATP6V1A	-2.12	-1.25	-2.06	-1.59	Yes	No	No	871	2.27	4.24E-08	3658.96	8598.16
523	ATP6V1A	-2.12	0.23	-2.06	0.24	No	No	No	2064	2.27	4.24E-08	3658.96	8598.16
526	ATP6V1B2	-2.93	-0.76	-1.88	-1.5	No	No	No	1535	1.05	0.69	1403.07	1513.38
526	ATP6V1B2	-2.93	-2.71	-1.88	-2.02	No	No	Yes	1675	1.05	0.69	1403.07	1513.38
526	ATP6V1B2	-2.93	-2.02	-1.88	-0.83	No	No	No	1831	1.05	0.69	1403.07	1513.38
526	ATP6V1B2	-2.93	-1.59	-1.88	-1.46	No	Yes	Yes	1925	1.05	0.69	1403.07	1513.38
8312	AXIN1	-2.25	-1.94	-1.53	-2.13	No	No	No	1606	-1.05	0.78	227.2	204.08
8312	AXIN1	-2.25	-0.51	-1.53	-1.5	Yes	Yes	No	1396	-1.05	0.78	227.2	204.08
8312	AXIN1	-2.25	1.35	-1.53	0.22	No	No	No	2128	-1.05	0.78	227.2	204.08
8312	AXIN1	-2.25	-1.86	-1.53	-1.24	Yes	No	Yes	2177	-1.05	0.78	227.2	204.08
567	B2M	0.69	-0.09	-0.47	-1.47	Yes	Yes	No	1141	6.47	0	4879.25	31752.99
567	B2M	0.69	1.18	-0.47	0.71	No	No	No	1717	6.47	0	4879.25	31752.99
567	B2M	0.69	0.32	-0.47	1.04	No	No	No	1871	6.47	0	4879.25	31752.99
567	B2M	0.69	0.85	-0.47	-1.14	No	Yes	No	1106	6.47	0	4879.25	31752.99
93010	B3GNT7	-2.1	-1.67	-2.77	-2.16	Yes	Yes	No	1070	1.11	0.52	97.88	119.09
93010	B3GNT7	-2.1	-0.81	-2.77	-2.05	No	Yes	Yes	1427	1.11	0.52	97.88	119.09
60468	BACH2	1.03	0.66	-0.19	0.87	No	No	No	1135	1	1	35.88	90.63
60468	BACH2	1.03	-1.44	-0.19	-1.74	No	Yes	No	653	1	1	35.88	90.63
60468	BACH2	1.03	0.6	-0.19	0.37	No	No	No	1463	1	1	35.88	90.63
60468	BACH2	1.03	-1.35	-0.19	-0.96	No	Yes	Yes	929	1	1	35.88	90.63
10458	BAIAP2	0.22	0.18	-0.81	-0.37	No	No	No	1231	1.77	0.02	163	279.32
10458	BAIAP2	0.22	0.7	-0.81	-0.72	Yes	No	No	1116	1.77	0.02	163	279.32
10458	BAIAP2	0.22	-1.34	-0.81	-1.72	Yes	Yes	No	1208	1.77	0.02	163	279.32
10458	BAIAP2	0.22	-0.51	-0.81	-0.03	No	No	No	1848	1.77	0.02	163	279.32
8938	BAIAP3	-2.5	-2	-0.98	-1.51	No	No	No	2417	1	1	41.72	98.49
8938	BAIAP3	-2.5	0.2	-0.98	-0.33	No	No	No	1853	1	1	41.72	98.49
8938	BAIAP3	-2.5	-2.07	-0.98	-1.06	No	Yes	Yes	2225	1	1	41.72	98.49
8938	BAIAP3	-2.5	0.82	-0.98	0.32	No	No	No	1212	1	1	41.72	98.49
343472	BARHL2	-0.73	0.19	-1.56	-0.52	Yes	Yes	No	1560	1	1	46.59	101.23
343472	BARHL2	-0.73	-1.27	-1.56	-1.31	Yes	No	Yes	1591	1	1	46.59	101.23
4671	BIRC1	-1.04	-0.97	-1.01	-1.09	No	Yes	No	1364	-1.05	0.74	143.98	148.4
4671	BIRC1	-1.04	-1.2	-1.01	-0.47	No	No	No	1192	-1.05	0.74	143.98	148.4
4671	BIRC1	-1.04	-0.23	-1.01	-0.63	No	No	No	1280	-1.05	0.74	143.98	148.4
4671	BIRC1	-1.04	-0.73	-1.01	-0.86	Yes	Yes	No	1186	-1.05	0.74	143.98	148.4
7862	BRPF1	-0.32	-1.46	-1.68	-2.5	No	Yes	No	1031	1.17	0.47	122.6	152.96
7862	BRPF1	-0.32	-0.7	-1.68	-1.89	Yes	No	No	1370	1.17	0.47	122.6	152.96

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
7862	BRPF1	-0.32	0.34	-1.68	1.11	No	No	No	2372	1.17	0.47	122.6	152.96
7862	BRPF1	-0.32	0.25	-1.68	0.23	No	No	No	2207	1.17	0.47	122.6	152.96
9256	BZRAP1	-0.98	-0.72	-1.59	-0.93	No	No	No	1707	3.16	8.75E-13	72.12	226.06
9256	BZRAP1	-0.98	0.08	-1.59	-1.63	No	No	No	1143	3.16	8.75E-13	72.12	226.06
9256	BZRAP1	-0.98	-1.03	-1.59	-1.29	Yes	No	No	1201	3.16	8.75E-13	72.12	226.06
9256	BZRAP1	-0.98	-1.41	-1.59	-0.98	No	No	Yes	1650	3.16	8.75E-13	72.12	226.06
80195	C10orf57	-0.85	-2.04	-1.44	-2.25	Yes	Yes	Yes	1100	-1.32	0.13	579.65	455.15
80195	C10orf57	-0.85	0.46	-1.44	1.38	No	No	No	1851	-1.32	0.13	579.65	455.15
80195	C10orf57	-0.85	-0.38	-1.44	-1.18	Yes	No	No	1480	-1.32	0.13	579.65	455.15
80195	C10orf57	-0.85	0.52	-1.44	0.74	No	No	No	2110	-1.32	0.13	579.65	455.15
115708	C14orf172	-1.37	-1.21	-0.98	-1.04	Yes	No	No	1178	-2.16	7.20E-06	265.5	126.91
115708	C14orf172	-1.37	3.02	-0.98	1.51	No	No	No	592	-2.16	7.20E-06	265.5	126.91
115708	C14orf172	-1.37	-0.23	-0.98	-1.03	Yes	Yes	No	1002	-2.16	7.20E-06	265.5	126.91
115708	C14orf172	-1.37	-1.64	-0.98	-0.47	No	No	No	1997	-2.16	7.20E-06	265.5	126.91
91978	C19orf20	-0.9	-0.78	-1.04	0.11	Yes	No	No	2817	1	1	56.4	101
91978	C19orf20	-0.9	-0.23	-1.04	-0.88	Yes	Yes	No	2845	1	1	56.4	101
150142	C21orf121	-1.94	-1.55	-1.64	0.21	No	No	Yes	2090	1	1	41.88	97.98
150142	C21orf121	-1.94	-1.47	-1.64	-1.35	Yes	Yes	Yes	1947	1	1	41.88	97.98
56911	C21orf7	-2.47	-1.16	-2.05	-0.96	No	Yes	Yes	1558	1	1	63.4	108.42
56911	C21orf7	-2.47	-1.94	-2.05	-1.85	Yes	Yes	Yes	2204	1	1	63.4	108.42
25927	C2orf32	0.39	0.5	-0.42	-0.43	Yes	No	No	949	1	1	83.56	118.33
25927	C2orf32	0.39	-0.81	-0.42	-0.6	Yes	Yes	No	2189	1	1	83.56	118.33
85315	C6orf33	-1.44	0.32	-0.53	-0.84	No	No	Yes	1346	1	1	83.77	112.99
85315	C6orf33	-1.44	0.004	-0.53	-0.5	No	No	No	1008	1	1	83.77	112.99
85315	C6orf33	-1.44	-1.67	-0.53	-1.07	Yes	No	No	1532	1	1	83.77	112.99
85315	C6orf33	-1.44	-1.18	-0.53	-0.42	Yes	No	No	996	1	1	83.77	112.99
377677	CA13	-1.55	-2.18	-0.13	-0.21	Yes	Yes	Yes	1648	1	1	118.03	122.82
377677	CA13	-1.55	0.21	-0.13	-0.87	Yes	No	No	1103	1	1	118.03	122.82
377677	CA13	-1.55	-1.01	-0.13	0.2	No	No	No	2230	1	1	118.03	122.82
377677	CA13	-1.55	1.45	-0.13	0.8	Yes	No	No	987	1	1	118.03	122.82
85417	CCNB3	-1.23	-1.02	-2.09	-2.17	Yes	Yes	No	706	1	1	79.27	110.18
85417	CCNB3	-1.23	1.95	-2.09	1.4	No	No	No	996	1	1	79.27	110.18
85417	CCNB3	-1.23	-1.9	-2.09	-1.41	No	Yes	Yes	1375	1	1	79.27	110.18
85417	CCNB3	-1.23	-1.96	-2.09	-0.93	No	No	No	2137	1	1	79.27	110.18
961	CD47	0.5	-0.81	-1.22	-2.11	Yes	Yes	Yes	812	2.08	8.82E-12	1486.47	3127.11
961	CD47	0.5	0.85	-1.22	0.69	No	No	No	2245	2.08	8.82E-12	1486.47	3127.11
961	CD47	0.5	0.66	-1.22	2.56	No	No	No	1908	2.08	8.82E-12	1486.47	3127.11
961	CD47	0.5	-1.03	-1.22	-1.37	No	No	No	1069	2.08	8.82E-12	1486.47	3127.11
962	CD48	-1.85	-1.01	-1.75	0.37	No	No	No	1370	1	1	37.76	94.05
962	CD48	-1.85	-2.72	-1.75	-1.71	No	No	Yes	1583	1	1	37.76	94.05
962	CD48	-1.85	-0.79	-1.75	-0.97	Yes	No	No	1215	1	1	37.76	94.05
962	CD48	-1.85	-1.65	-1.75	-1.77	Yes	No	Yes	1084	1	1	37.76	94.05
965	CD58	-2.19	-0.62	-1.55	0.63	No	No	No	2372	-1.29	0.04	381.41	301.97
965	CD58	-2.19	-2.06	-1.55	-1.44	Yes	No	Yes	2001	-1.29	0.04	381.41	301.97
965	CD58	-2.19	-2.16	-1.55	-1.64	No	Yes	Yes	1028	-1.29	0.04	381.41	301.97
965	CD58	-2.19	0.36	-1.55	0.63	No	No	No	1646	-1.29	0.04	381.41	301.97
975	CD81	-1.08	-2.41	-1.37	-2.84	Yes	Yes	Yes	1125	-1.4	0.00726	2021.48	1412.12
975	CD81	-1.08	-0.91	-1.37	-1.13	No	Yes	Yes	1433	-1.4	0.00726	2021.48	1412.12
975	CD81	-1.08	-0.7	-1.37	0.45	No	No	No	1828	-1.4	0.00726	2021.48	1412.12
975	CD81	-1.08	0.18	-1.37	-0.78	No	No	No	1115	-1.4	0.00726	2021.48	1412.12
1027	CDKN1B	-1.39	-2.08	-2.15	-2.22	Yes	No	Yes	1759	-1.68	0.00052	939.57	577.9
1027	CDKN1B	-1.39	0.13	-2.15	-1.02	No	No	No	1482	-1.68	0.00052	939.57	577.9
1027	CDKN1B	-1.39	1.53	-2.15	-0.96	No	No	No	1681	-1.68	0.00052	939.57	577.9
1027	CDKN1B	-1.39	-1.14	-2.15	-1.83	Yes	No	No	1145	-1.68	0.00052	939.57	577.9
1056	CEL	0.7	0.007	-1.8	-1.64	Yes	No	No	1007	1.5	0.16	71.19	137.23
1056	CEL	0.7	-0.46	-1.8	-1.25	No	Yes	No	1651	1.5	0.16	71.19	137.23

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1056	CEL	0.7	0.69	-1.8	-2.08	Yes	Yes	No	776	1.5	0.16	71.19	137.23
1056	CEL	0.7	2.22	-1.8	1.39	No	No	No	1902	1.5	0.16	71.19	137.23
11033	CENTA1	-1.45	-1.18	-0.23	-0.83	No	Yes	Yes	1128	1	1	54.47	98.55
11033	CENTA1	-1.45	-2.26	-0.23	-0.81	Yes	Yes	Yes	1083	1	1	54.47	98.55
11033	CENTA1	-1.45	2.05	-0.23	2.79	No	No	No	2083	1	1	54.47	98.55
11033	CENTA1	-1.45	-0.48	-0.23	0.13	Yes	No	No	1888	1	1	54.47	98.55
1128	CHRM1	-1.46	-1.64	-1.09	-1.89	Yes	Yes	Yes	966	1.71	0.04	91.26	186.66
1128	CHRM1	-1.46	0.47	-1.09	2.93	No	No	No	2101	1.71	0.04	91.26	186.66
1128	CHRM1	-1.46	1.77	-1.09	1.23	No	No	No	1616	1.71	0.04	91.26	186.66
1128	CHRM1	-1.46	-1.19	-1.09	-0.51	Yes	No	No	939	1.71	0.04	91.26	186.66
23563	CHST5	-0.87	0.1	-2.13	-1.68	No	Yes	No	963	-1.69	0.00572	190.21	117.77
23563	CHST5	-0.87	-0.76	-2.13	-1.68	Yes	Yes	No	850	-1.69	0.00572	190.21	117.77
1147	CHUK	1.31	0.8	-0.84	0.61	Yes	No	No	2026	-2.16	1.36E-14	378.76	175.46
1147	CHUK	1.31	-0.13	-0.84	-0.74	No	No	No	707	-2.16	1.36E-14	378.76	175.46
1147	CHUK	1.31	0.95	-0.84	-0.63	No	No	No	1412	-2.16	1.36E-14	378.76	175.46
1147	CHUK	1.31	-0.64	-0.84	-1.48	Yes	Yes	No	783	-2.16	1.36E-14	378.76	175.46
1163	CKS1B	-1.39	-0.52	-0.4	-0.41	Yes	No	No	1186	1.09	0.21	23650.84	25819.03
1163	CKS1B	-1.39	0.28	-0.4	-0.41	No	No	No	1344	1.09	0.21	23650.84	25819.03
1163	CKS1B	-1.39	-1.11	-0.4	1.52	No	No	No	1854	1.09	0.21	23650.84	25819.03
1163	CKS1B	-1.39	-1.46	-0.4	-1.69	Yes	No	No	914	1.09	0.21	23650.84	25819.03
25932	CLIC4	-2.1	-2.19	-0.83	-1.57	Yes	No	Yes	1208	-1.62	0.00144	1309.75	803.11
25932	CLIC4	-2.1	-2.08	-0.83	-0.98	No	No	Yes	1508	-1.62	0.00144	1309.75	803.11
25932	CLIC4	-2.1	-0.38	-0.83	-0.73	No	No	No	996	-1.62	0.00144	1309.75	803.11
25932	CLIC4	-2.1	-0.25	-0.83	1.49	No	No	No	1580	-1.62	0.00144	1309.75	803.11
1195	CLK1	-0.92	-0.43	-0.42	0	No	No	No	1652	-1.16	0.31	1680.17	1462.24
1195	CLK1	-0.92	-1.19	-0.42	-0.92	Yes	No	No	1297	-1.16	0.31	1680.17	1462.24
1195	CLK1	-0.92	-0.93	-0.42	-1.27	Yes	No	No	1613	-1.16	0.31	1680.17	1462.24
1195	CLK1	-0.92	-0.68	-0.42	0.51	No	No	No	1605	-1.16	0.31	1680.17	1462.24
9746	CLSTN3	-1.29	-0.53	-1.6	-1.29	Yes	No	No	1343	1.94	0.12	38.8	109.05
9746	CLSTN3	-1.29	-1.57	-1.6	-1.22	Yes	No	No	1645	1.94	0.12	38.8	109.05
1258	CNGB1	-1.51	2.82	-2.5	0.23	No	No	No	968	1.43	0.14	88.98	141.47
1258	CNGB1	-1.51	-1.23	-2.5	-1.96	Yes	No	Yes	1530	1.43	0.14	88.98	141.47
1258	CNGB1	-1.51	-2	-2.5	-2.26	Yes	Yes	No	847	1.43	0.14	88.98	141.47
1258	CNGB1	-1.51	2.22	-2.5	2.78	No	No	No	1686	1.43	0.14	88.98	141.47
26507	CNNM1	-1.74	-0.44	-2.24	-0.9	No	Yes	No	942	1	1	71.27	100.82
26507	CNNM1	-1.74	-1.53	-2.24	-2.03	Yes	Yes	No	1053	1	1	71.27	100.82
1314	COPA	-3	-2.43	-2.78	-2.06	Yes	No	Yes	992	-1.7	0.07	327.93	174.98
1314	COPA	-3	-2.34	-2.78	-2.24	Yes	Yes	Yes	1083	-1.7	0.07	327.93	174.98
1315	COPB	-2.35	-1.68	-1.93	-1.54	Yes	Yes	No	968	-4.55	1.49E-11	2103.08	452.72
1315	COPB	-2.35	-1.86	-1.93	-1.28	No	Yes	No	1198	-4.55	1.49E-11	2103.08	452.72
9276	COPB2	-2.45	0.94	-3.05	2.12	No	No	No	1811	-3.1	8.48E-26	4109.65	1311.4
9276	COPB2	-2.45	-2.38	-3.05	-2.88	Yes	Yes	Yes	812	-3.1	8.48E-26	4109.65	1311.4
9276	COPB2	-2.45	1.98	-3.05	-2.41	Yes	Yes	No	385	-3.1	8.48E-26	4109.65	1311.4
9276	COPB2	-2.45	-1.51	-3.05	-2.11	Yes	Yes	Yes	958	-3.1	8.48E-26	4109.65	1311.4
11316	COPE	0.56	0.28	-1.45	0.34	Yes	Yes	No	755	1.34	0.00026	763.9	1030.83
11316	COPE	0.56	0.38	-1.45	-1.19	Yes	No	No	1089	1.34	0.00026	763.9	1030.83
22820	COPG	-2.77	0.25	-2.18	-1.77	Yes	Yes	No	831	-2.58	3.09E-09	383.34	152.7
22820	COPG	-2.77	-3.1	-2.18	-2	Yes	No	Yes	1402	-2.58	3.09E-09	383.34	152.7
22820	COPG	-2.77	-1.62	-2.18	-1.73	Yes	No	Yes	1091	-2.58	3.09E-09	383.34	152.7
22820	COPG	-2.77	-1.35	-2.18	-1.1	Yes	No	Yes	1491	-2.58	3.09E-09	383.34	152.7
57585	CRAMP1L	-0.46	-0.45	-1.44	-0.62	No	No	No	1709	1.06	0.64	692.63	802.42
57585	CRAMP1L	-0.46	0.11	-1.44	0.82	No	No	No	1801	1.06	0.64	692.63	802.42
57585	CRAMP1L	-0.46	-0.45	-1.44	-1.66	Yes	Yes	No	802	1.06	0.64	692.63	802.42
57585	CRAMP1L	-0.46	-0.65	-1.44	-1.3	Yes	No	No	1180	1.06	0.64	692.63	802.42
9282	CRSP2	-0.28	2.59	-0.48	0.84	No	No	No	1088	-1.47	0.07	324.97	234.04
9282	CRSP2	-0.28	-0.31	-0.48	-1	Yes	No	No	1412	-1.47	0.07	324.97	234.04

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9282	CRSP2	-0.28	-0.42	-0.48	-0.21	No	No	No	1732	-1.47	0.07	324.97	234.04
9282	CRSP2	-0.28	-1	-0.48	-1.36	Yes	No	Yes	1339	-1.47	0.07	324.97	234.04
1408	Cry2	0.87	-0.02	-0.08	0.03	No	No	No	1355	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	-0.02	-0.08	0.03	No	No	No	2001	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	0.5	-0.08	-0.29	No	No	No	1165	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	0.5	-0.08	-0.29	Yes	No	No	1265	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	0.6	-0.08	-0.05	No	No	No	1114	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	0.6	-0.08	-0.05	No	No	No	849	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	-0.63	-0.08	-0.6	Yes	No	No	1417	-1.99	0.00027	208.86	122.12
1408	Cry2	0.87	-0.63	-0.08	-0.6	No	No	No	1527	-1.99	0.00027	208.86	122.12
1409	CRYAA	-0.24	-1.64	-1.55	-1.26	Yes	Yes	No	940	1.71	0.00548	129.04	233.29
1409	CRYAA	-0.24	-0.1	-1.55	-1.21	No	Yes	No	1103	1.71	0.00548	129.04	233.29
30818	CSEN	-1.92	-1.48	-1.79	-0.86	No	Yes	Yes	2030	1	1	73.56	108.46
30818	CSEN	-1.92	-0.93	-1.79	-1.69	Yes	Yes	Yes	878	1	1	73.56	108.46
30818	CSEN	-1.92	-1.45	-1.79	-0.63	No	Yes	Yes	2097	1	1	73.56	108.46
30818	CSEN	-1.92	-1.51	-1.79	-1.44	No	Yes	Yes	1247	1	1	73.56	108.46
119016	CTGLF1	0.81	0.46	-1.07	-1.26	Yes	No	No	892	-1.29	0.04	349.76	260.94
119016	CTGLF1	0.81	0.44	-1.07	-0.69	Yes	Yes	No	937	-1.29	0.04	349.76	260.94
1499	CTNNB1	-1.21	1.09	-0.5	1.26	No	No	No	1624	-1.19	0.25	2823.94	2100.44
1499	CTNNB1	-1.21	-2.42	-0.5	-0.69	No	No	Yes	2111	-1.19	0.25	2823.94	2100.44
1499	CTNNB1	-1.21	-0.8	-0.5	-0.19	No	No	No	1144	-1.19	0.25	2823.94	2100.44
1499	CTNNB1	-1.21	-0.69	-0.5	-0.69	No	No	Yes	1192	-1.19	0.25	2823.94	2100.44
10663	CXCR6	-2.13	-2.35	-1.9	-2.33	Yes	Yes	Yes	1608	1	1	40.1	95.93
10663	CXCR6	-2.13	1.28	-1.9	2.64	No	No	No	1613	1	1	40.1	95.93
10663	CXCR6	-2.13	-2.11	-1.9	-0.87	No	No	Yes	2881	1	1	40.1	95.93
10663	CXCR6	-2.13	-0.65	-1.9	-0.87	No	No	No	1161	1	1	40.1	95.93
1586	CYP17A1	-0.8	-0.31	-0.41	-0.61	No	No	No	970	2.06	0.05	94.07	206.43
1586	CYP17A1	-0.8	-0.75	-0.41	0.06	No	No	No	1720	2.06	0.05	94.07	206.43
1586	CYP17A1	-0.8	-0.91	-0.41	-0.35	No	No	Yes	1408	2.06	0.05	94.07	206.43
1586	CYP17A1	-0.8	-0.43	-0.41	-0.73	Yes	No	No	936	2.06	0.05	94.07	206.43
113612	CYP2U1	-0.58	-0.54	-1	-0.9	No	No	No	1429	1.17	0.18	177.62	240.02
113612	CYP2U1	-0.58	-0.45	-1	1.36	Yes	No	No	1318	1.17	0.18	177.62	240.02
113612	CYP2U1	-0.58	-0.65	-1	0.23	No	No	No	1677	1.17	0.18	177.62	240.02
113612	CYP2U1	-0.58	-1.12	-1	-2.1	Yes	No	No	905	1.17	0.18	177.62	240.02
7818	DAP3	-2.31	1.13	-1.66	-0.59	No	No	No	1804	-1.37	0.00075	11333.47	8221
7818	DAP3	-2.31	0.51	-1.66	0.31	No	No	No	1533	-1.37	0.00075	11333.47	8221
7818	DAP3	-2.31	-2.52	-1.66	-1.63	Yes	Yes	Yes	2436	-1.37	0.00075	11333.47	8221
7818	DAP3	-2.31	-1.81	-1.66	-1.8	Yes	Yes	Yes	1269	-1.37	0.00075	11333.47	8221
1629	DBT	-0.96	1.9	-0.37	2.93	No	No	No	1729	-1.14	0.41	126.46	113.93
1629	DBT	-0.96	-0.66	-0.37	-0.35	No	Yes	Yes	2663	-1.14	0.41	126.46	113.93
1629	DBT	-0.96	-1.32	-0.37	0.42	No	No	No	2374	-1.14	0.41	126.46	113.93
1629	DBT	-0.96	-2.42	-0.37	-2.41	Yes	Yes	Yes	1044	-1.14	0.41	126.46	113.93
166614	DCAMKL2	0.24	1.52	0.28	0.99	No	No	No	1249	1	1	72.22	107.38
166614	DCAMKL2	0.24	0.07	0.28	-0.75	No	No	No	1137	1	1	72.22	107.38
166614	DCAMKL2	0.24	-0.95	0.28	0.44	Yes	No	No	2003	1	1	72.22	107.38
166614	DCAMKL2	0.24	-0.91	0.28	-1.64	Yes	No	Yes	933	1	1	72.22	107.38
9775	DDX48	-0.33	-0.35	-1.31	-0.63	No	Yes	Yes	1566	-2.58	1.11E-17	18868.28	7242.39
9775	DDX48	-0.33	0.39	-1.31	-0.59	No	No	No	1003	-2.58	1.11E-17	18868.28	7242.39
9775	DDX48	-0.33	-0.77	-1.31	-1.08	Yes	Yes	No	1131	-2.58	1.11E-17	18868.28	7242.39
9775	DDX48	-0.33	0.09	-1.31	-1.11	Yes	No	No	819	-2.58	1.11E-17	18868.28	7242.39
91319	DERL3	0.15	0.11	-2.97	-0.75	Yes	No	No	951	1.46	0.06	90.38	136.45
91319	DERL3	0.15	-1.63	-2.97	-2.78	Yes	Yes	Yes	1075	1.46	0.06	90.38	136.45
10202	DHRS2	-1.69	-0.92	-1.34	-1.16	No	No	Yes	861	-1.5	0.00081	264.64	173.67
10202	DHRS2	-1.69	-1.63	-1.34	-1.54	Yes	No	Yes	1303	-1.5	0.00081	264.64	173.67
10202	DHRS2	-1.69	-0.14	-1.34	0.2	No	No	No	1938	-1.5	0.00081	264.64	173.67
10202	DHRS2	-1.69	-0.22	-1.34	-0.87	Yes	Yes	Yes	911	-1.5	0.00081	264.64	173.67

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
1740	DLG2	0.99	0.28	-0.29	-1.9	Yes	Yes	No	1024	1	1	38.48	93.54
1740	DLG2	0.99	0.58	-0.29	-0.03	No	No	No	2049	1	1	38.48	93.54
1740	DLG2	0.99	1.27	-0.29	1.1	No	No	No	2050	1	1	38.48	93.54
1740	DLG2	0.99	-1.45	-0.29	-2.09	Yes	No	No	1090	1	1	38.48	93.54
55929	DMAP1	-0.25	-0.48	-0.3	-0.34	Yes	No	No	1862	-1.88	5.73E-06	505.71	251.37
55929	DMAP1	-0.25	0.91	-0.3	0.2	Yes	No	No	1395	-1.88	5.73E-06	505.71	251.37
196403	DTX3	0.02	0.65	0.1	-0.01	No	No	No	1213	2.05	1.39E-32	653.44	1402.85
196403	DTX3	0.02	0.09	0.1	-0.04	No	No	No	1227	2.05	1.39E-32	653.44	1402.85
196403	DTX3	0.02	-0.31	0.1	-0.37	Yes	No	No	906	2.05	1.39E-32	653.44	1402.85
196403	DTX3	0.02	-0.86	0.1	0.19	Yes	No	No	1335	2.05	1.39E-32	653.44	1402.85
1869	E2F1	-2.18	-0.16	-2.37	-0.04	No	No	No	1387	1.65	4.54E-16	650.09	1076.32
1869	E2F1	-2.18	-2.47	-2.37	-2.53	Yes	Yes	Yes	1185	1.65	4.54E-16	650.09	1076.32
1869	E2F1	-2.18	-0.81	-2.37	-1.33	No	No	No	1147	1.65	4.54E-16	650.09	1076.32
1869	E2F1	-2.18	-1.73	-2.37	-1.86	Yes	Yes	Yes	859	1.65	4.54E-16	650.09	1076.32
1915	EEF1A1	-2.12	-1.12	-1.98	-1.74	Yes	No	No	1345	-2.46	4.16E-17	231930.21	76831.32
1915	EEF1A1	-2.12	-1.46	-1.98	-1.57	Yes	Yes	Yes	1310	-2.46	4.16E-17	231930.21	76831.32
1915	EEF1A1	-2.12	-2.54	-1.98	-1.52	Yes	Yes	Yes	1721	-2.46	4.16E-17	231930.21	76831.32
1915	EEF1A1	-2.12	-1.9	-1.98	-1.14	Yes	Yes	Yes	1371	-2.46	4.16E-17	231930.21	76831.32
8661	EIF3S10	-1.26	-1.04	-1.96	-1.28	Yes	Yes	No	945	-2.33	3.73E-38	21956.4	9404.2
8661	EIF3S10	-1.26	-0.94	-1.96	-1.56	Yes	No	No	1055	-2.33	3.73E-38	21956.4	9404.2
8666	EIF3S4	-1.26	-0.88	-1.45	-1.14	Yes	Yes	Yes	845	1.38	1.61E-06	3665.27	5061.95
8666	EIF3S4	-1.26	-1.58	-1.45	-2.08	Yes	No	Yes	1055	1.38	1.61E-06	3665.27	5061.95
8665	EIF3S5	0.81	0.59	-1.41	-1.41	No	No	No	1602	1.48	2.00E-04	3599.15	5496.24
8665	EIF3S5	0.81	0.91	-1.41	-1.16	Yes	No	No	1246	1.48	2.00E-04	3599.15	5496.24
8665	EIF3S5	0.81	-0.72	-1.41	-0.58	Yes	No	No	1198	1.48	2.00E-04	3599.15	5496.24
8665	EIF3S5	0.81	-0.2	-1.41	-1.24	Yes	No	No	1202	1.48	2.00E-04	3599.15	5496.24
8663	EIF3S8	-0.55	1.11	-1.46	-0.94	Yes	No	No	961	-1.84	1.51E-15	12712.56	7143.37
8663	EIF3S8	-0.55	-0.88	-1.46	-1.66	Yes	No	Yes	1152	-1.84	1.51E-15	12712.56	7143.37
8663	EIF3S8	-0.55	-0.47	-1.46	-1.19	Yes	No	No	1272	-1.84	1.51E-15	12712.56	7143.37
8663	EIF3S8	-0.55	-0.33	-1.46	-0.61	No	No	No	1495	-1.84	1.51E-15	12712.56	7143.37
2051	EPHB6	-2.33	-0.75	-1.69	-1.36	No	Yes	No	1342	2.28	0.01	69.53	188.63
2051	EPHB6	-2.33	-2.71	-1.69	-1.85	Yes	No	Yes	1702	2.28	0.01	69.53	188.63
2051	EPHB6	-2.33	0.78	-1.69	1.39	No	No	No	2364	2.28	0.01	69.53	188.63
2051	EPHB6	-2.33	-1.86	-1.69	-1.46	No	Yes	Yes	1107	2.28	0.01	69.53	188.63
2197	FAU	0.18	0.48	-1	-0.48	No	No	No	1129	1.12	0.17	62444.47	62227.25
2197	FAU	0.18	0.92	-1	-0.79	Yes	No	No	756	1.12	0.17	62444.47	62227.25
2197	FAU	0.18	-0.29	-1	-0.62	No	No	No	1237	1.12	0.17	62444.47	62227.25
2197	FAU	0.18	-2.63	-1	-2.44	Yes	Yes	Yes	1128	1.12	0.17	62444.47	62227.25
10517	FBXW10	-0.91	-1.11	-1.2	-1	Yes	No	Yes	967	7.05	1.12E-24	780.13	5653.5
10517	FBXW10	-0.91	-0.77	-1.2	-1	Yes	No	No	1311	7.05	1.12E-24	780.13	5653.5
26190	FBXW2	-1.02	0.98	-2.19	2.21	No	No	No	1860	-2.94	9.18E-09	415.16	145.77
26190	FBXW2	-1.02	1.16	-2.19	1.89	No	No	No	1547	-2.94	9.18E-09	415.16	145.77
26190	FBXW2	-1.02	-1.92	-2.19	-1.86	Yes	Yes	Yes	1609	-2.94	9.18E-09	415.16	145.77
26190	FBXW2	-1.02	-0.86	-2.19	-2.22	No	Yes	No	1531	-2.94	9.18E-09	415.16	145.77
115548	FCHO2	-1.21	-1.01	-1.86	-1.29	No	Yes	Yes	1170	-3.16	2.45E-08	447.84	146.63
115548	FCHO2	-1.21	-0.62	-1.86	-1.49	Yes	Yes	No	1576	-3.16	2.45E-08	447.84	146.63
9965	FGF19	-0.44	0.85	-0.52	-1.2	Yes	Yes	No	843	1.04	0.78	47.58	99.89
9965	FGF19	-0.44	0.2	-0.52	0.69	No	No	No	1650	1.04	0.78	47.58	99.89
9965	FGF19	-0.44	-0.81	-0.52	-0.5	Yes	No	No	1595	1.04	0.78	47.58	99.89
9965	FGF19	-0.44	-0.61	-0.52	-0.5	Yes	Yes	No	1500	1.04	0.78	47.58	99.89
29109	FHOD1	-1.26	-1.53	-1.81	-1.83	Yes	Yes	Yes	1008	-1.33	0.00153	652.74	488.16
29109	FHOD1	-1.26	-0.39	-1.81	-0.95	Yes	Yes	No	1371	-1.33	0.00153	652.74	488.16
23770	FKBP8	-2	-0.14	-2.49	0.43	No	No	No	1233	1.16	0.45	66.83	97.55
23770	FKBP8	-2	-2.36	-2.49	-2.54	Yes	Yes	Yes	828	1.16	0.45	66.83	97.55
23770	FKBP8	-2	-1.6	-2.49	-0.63	No	No	Yes	1336	1.16	0.45	66.83	97.55
23770	FKBP8	-2	-2.06	-2.49	-2.24	Yes	No	Yes	1046	1.16	0.45	66.83	97.55

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
11328	FKBP9	-0.93	0.08	-0.35	1.06	No	No	No	1970	1.05	0.43	5248.74	5484.83
11328	FKBP9	-0.93	-1.26	-0.35	-2.08	Yes	Yes	Yes	838	1.05	0.43	5248.74	5484.83
11328	FKBP9	-0.93	0.03	-0.35	-0.38	Yes	Yes	No	1788	1.05	0.43	5248.74	5484.83
11328	FKBP9	-0.93	0.52	-0.35	0.31	No	No	No	1516	1.05	0.43	5248.74	5484.83
54475	FLJ10458	-1.6	2.34	0.21	1.95	No	No	No	1906	-1.18	0.02	954.23	804.23
54475	FLJ10458	-1.6	-1.35	0.21	0.03	No	No	Yes	1543	-1.18	0.02	954.23	804.23
54475	FLJ10458	-1.6	0.19	0.21	-0.39	No	No	No	2042	-1.18	0.02	954.23	804.23
54475	FLJ10458	-1.6	-1.18	0.21	-1.31	No	No	Yes	1426	-1.18	0.02	954.23	804.23
54508	FLJ11235	-2.16	-1.02	-2.36	-1.88	No	Yes	No	885	2.91	1.80E-10	237.47	888.71
54508	FLJ11235	-2.16	-1.87	-2.36	-1.37	No	Yes	Yes	2358	2.91	1.80E-10	237.47	888.71
79714	FLJ12436	-2.57	-1.79	-3.4	-1.07	No	No	Yes	1883	-1.31	0.00489	1024.19	779.92
79714	FLJ12436	-2.57	-2.27	-3.4	-2.79	Yes	Yes	Yes	1226	-1.31	0.00489	1024.19	779.92
54962	FLJ20516	-0.8	-1.1	-1.07	-1.32	Yes	Yes	Yes	1218	-1.14	0.08	973.71	844.33
54962	FLJ20516	-0.8	-0.41	-1.07	-0.06	No	No	No	1616	-1.14	0.08	973.71	844.33
54962	FLJ20516	-0.8	0.9	-1.07	-0.19	No	No	No	1310	-1.14	0.08	973.71	844.33
54962	FLJ20516	-0.8	-1.6	-1.07	-1.57	Yes	No	No	1148	-1.14	0.08	973.71	844.33
64772	FLJ21865	-1.05	-0.81	-2.11	-1.2	Yes	No	No	992	-1.59	0.00274	464.47	285.45
64772	FLJ21865	-1.05	-0.95	-2.11	-1.67	Yes	No	No	1179	-1.59	0.00274	464.47	285.45
79864	FLJ23554	-2.09	-1.05	-2.4	-0.53	No	Yes	No	1128	-1.23	0.39	156.05	138.99
79864	FLJ23554	-2.09	-2.2	-2.4	-3.13	Yes	Yes	Yes	883	-1.23	0.39	156.05	138.99
497049	FLJ25758	0.29	-0.8	-0.71	-0.64	Yes	No	No	1112	1	1	39.07	90.67
497049	FLJ25758	0.29	0.72	-0.71	-0.24	Yes	No	No	871	1	1	39.07	90.67
64400	FTS	-0.71	-0.84	-0.73	-1.35	Yes	Yes	No	1132	-2.24	2.71E-18	344.6	155.35
64400	FTS	-0.71	-0.84	-0.73	-1.35	Yes	No	No	1100	-2.24	2.71E-18	344.6	155.35
64400	FTS	-0.71	2.84	-0.73	-0.62	No	No	No	929	-2.24	2.71E-18	344.6	155.35
64400	FTS	-0.71	2.84	-0.73	-0.62	No	No	No	613	-2.24	2.71E-18	344.6	155.35
9636	G1P2	-2.09	-2.19	-1.13	-1.08	No	No	Yes	2075	70.46	0	567.03	39674.31
9636	G1P2	-2.09	-0.47	-1.13	-0.48	No	No	No	1439	70.46	0	567.03	39674.31
9636	G1P2	-2.09	-0.65	-1.13	-0.95	No	Yes	No	1366	70.46	0	567.03	39674.31
9636	G1P2	-2.09	-1.66	-1.13	-0.91	Yes	Yes	Yes	1694	70.46	0	567.03	39674.31
2729	GCLC	-2.12	-0.35	-0.94	-0.29	No	No	No	1271	-7.16	0	3726.22	519.06
2729	GCLC	-2.12	-1.76	-0.94	-1.18	No	No	Yes	2354	-7.16	0	3726.22	519.06
2729	GCLC	-2.12	-1.68	-0.94	-1.12	No	No	Yes	1779	-7.16	0	3726.22	519.06
2729	GCLC	-2.12	-1.45	-0.94	-0.39	No	No	Yes	2160	-7.16	0	3726.22	519.06
2662	GDF10	-0.82	-0.8	-0.46	-0.45	Yes	No	No	1376	1	1	45.02	97.94
2662	GDF10	-0.82	-1.19	-0.46	0.01	Yes	No	Yes	2025	1	1	45.02	97.94
2662	GDF10	-0.82	-0.72	-0.46	-0.86	Yes	Yes	No	1403	1	1	45.02	97.94
2662	GDF10	-0.82	0.16	-0.46	0.99	No	No	No	1816	1	1	45.02	97.94
91227	GGTL4	-1.73	-1.4	-2.26	-1.78	No	Yes	Yes	1080	1.6	0.00043	575.17	1278.4
91227	GGTL4	-1.73	-1.75	-2.26	-2.73	Yes	Yes	No	1455	1.6	0.00043	575.17	1278.4
2797	GNRH2	-0.89	0.007	-2.08	0.37	No	No	No	1361	2.18	3.29E-16	332.21	727.54
2797	GNRH2	-0.89	-0.65	-2.08	-1.65	No	Yes	No	829	2.18	3.29E-16	332.21	727.54
2797	GNRH2	-0.89	-1.49	-2.08	-1.87	No	Yes	Yes	1385	2.18	3.29E-16	332.21	727.54
2797	GNRH2	-0.89	-0.33	-2.08	-0.17	No	No	No	2069	2.18	3.29E-16	332.21	727.54
115330	GPR146	-1.27	-1.63	-1.97	-0.4	No	No	No	1643	1.39	0.32	60.16	117.35
115330	GPR146	-1.27	0.22	-1.97	-0.18	No	No	No	781	1.39	0.32	60.16	117.35
115330	GPR146	-1.27	-1.85	-1.97	-2.26	Yes	Yes	Yes	1156	1.39	0.32	60.16	117.35
115330	GPR146	-1.27	-0.17	-1.97	-1.57	Yes	No	No	765	1.39	0.32	60.16	117.35
2905	GRIN2C	-0.97	-0.84	-1	-0.86	Yes	No	No	1218	2.43	0.02	126.2	315.78
2905	GRIN2C	-0.97	1.12	-1	1.7	No	No	No	2073	2.43	0.02	126.2	315.78
2905	GRIN2C	-0.97	-1.02	-1	-2	Yes	Yes	No	1146	2.43	0.02	126.2	315.78
2905	GRIN2C	-0.97	0.15	-1	-0.06	No	No	No	1797	2.43	0.02	126.2	315.78
2948	GSTM4	-1.62	-1.31	-2.43	-1.81	No	Yes	No	1117	1	1	56.62	99.36
2948	GSTM4	-1.62	0.45	-2.43	-1.91	No	Yes	No	999	1	1	56.62	99.36
2967	GTF2H3	0.66	1.39	-0.12	-0.21	Yes	No	No	1197	1	1	85.5	110.48
2967	GTF2H3	0.66	0.84	-0.12	1.05	No	No	No	1729	1	1	85.5	110.48

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
2967	GTF2H3	0.66	0.07	-0.12	0.84	No	Yes	No	1699	1	1	85.5	110.48
2967	GTF2H3	0.66	-1.86	-0.12	-1.69	Yes	Yes	Yes	1737	1	1	85.5	110.48
57493	HEG	-2.02	-1.61	-0.17	-0.16	No	Yes	Yes	1840	1	1	40.05	94.26
57493	HEG	-2.02	-0.82	-0.17	-0.25	No	No	Yes	1885	1	1	40.05	94.26
57493	HEG	-2.02	0.04	-0.17	1.9	No	No	No	2161	1	1	40.05	94.26
57493	HEG	-2.02	-2.5	-0.17	-2	No	Yes	Yes	1850	1	1	40.05	94.26
26091	HERC4	-0.29	-0.16	-1.36	-1.13	No	Yes	No	1015	-3.37	1.88E-28	1552.7	460.38
26091	HERC4	-0.29	-0.005	-1.36	-0.9	No	No	No	1028	-3.37	1.88E-28	1552.7	460.38
26091	HERC4	-0.29	-0.4	-1.36	-1.12	No	Yes	No	1415	-3.37	1.88E-28	1552.7	460.38
26091	HERC4	-0.29	-2.06	-1.36	-1.29	Yes	No	Yes	2237	-3.37	1.88E-28	1552.7	460.38
8341	HIST1H2BN	-0.11	-0.83	-1.22	-1.02	Yes	No	No	1411	1.73	2.56E-08	417.97	716.03
8341	HIST1H2BN	-0.11	1.07	-1.22	-1.17	Yes	Yes	No	995	1.73	2.56E-08	417.97	716.03
3248	HPGD	-1.21	2.73	-1.57	2.1	No	No	No	1074	-2.4	9.66E-42	1428.06	593.22
3248	HPGD	-1.21	-1.01	-1.57	-1.44	Yes	No	No	1443	-2.4	9.66E-42	1428.06	593.22
3248	HPGD	-1.21	-0.4	-1.57	0.34	No	No	Yes	1991	-2.4	9.66E-42	1428.06	593.22
3248	HPGD	-1.21	-2.74	-1.57	-1.71	Yes	Yes	Yes	1661	-2.4	9.66E-42	1428.06	593.22
3299	HSF4	-0.51	-0.49	-0.91	-0.56	Yes	No	No	962	2.23	0.00041	178.59	389.97
3299	HSF4	-0.51	-0.76	-0.91	-0.93	Yes	No	No	1088	2.23	0.00041	178.59	389.97
3299	HSF4	-0.51	0.11	-0.91	1.43	No	No	No	2099	2.23	0.00041	178.59	389.97
3299	HSF4	-0.51	-0.67	-0.91	-1.06	No	No	No	1538	2.23	0.00041	178.59	389.97
3329	HSPD1	-2.07	-1.65	-0.61	-1.28	No	Yes	Yes	1223	-1.42	0.03	62308.62	21324.16
3329	HSPD1	-2.07	-0.03	-0.61	0.91	No	No	No	2066	-1.42	0.03	62308.62	21324.16
3329	HSPD1	-2.07	-1.69	-0.61	-0.26	No	No	Yes	2439	-1.42	0.03	62308.62	21324.16
3329	HSPD1	-2.07	-0.61	-0.61	-0.82	No	No	No	2488	-1.42	0.03	62308.62	21324.16
3444	IFNA7	-0.93	0.29	-1.33	0.57	No	No	No	1365	13.16	0	200.24	2677.03
3444	IFNA7	-0.93	-0.17	-1.33	-0.5	Yes	No	No	1217	13.16	0	200.24	2677.03
3444	IFNA7	-0.93	-1.28	-1.33	-1.76	Yes	Yes	Yes	1435	13.16	0	200.24	2677.03
3444	IFNA7	-0.93	0.07	-1.33	-1.09	No	No	No	1255	13.16	0	200.24	2677.03
3455	IFNAR2	-1.38	-1.14	-1.8	-1.45	No	Yes	No	1228	1	1	38.69	94.84
3455	IFNAR2	-1.38	-0.17	-1.8	-0.48	No	No	No	1797	1	1	38.69	94.84
3455	IFNAR2	-1.38	1.46	-1.8	0.57	No	No	No	1673	1	1	38.69	94.84
3455	IFNAR2	-1.38	-3.17	-1.8	-2.94	Yes	Yes	Yes	1690	1	1	38.69	94.84
3460	IFNGR2	-1.23	-1.18	-1.08	-0.42	No	No	No	1461	-2.69	2.00E-05	491.3	184.99
3460	IFNGR2	-1.23	-0.15	-1.08	-1.07	No	Yes	No	1003	-2.69	2.00E-05	491.3	184.99
3460	IFNGR2	-1.23	-1.02	-1.08	-1.72	Yes	Yes	No	1481	-2.69	2.00E-05	491.3	184.99
3460	IFNGR2	-1.23	-0.64	-1.08	-0.78	No	No	No	1898	-2.69	2.00E-05	491.3	184.99
3547	IGSF1	-2.68	-2.56	-1.38	-1.59	No	Yes	Yes	1867	1	1	40.48	93.45
3547	IGSF1	-2.68	0.97	-1.38	-1.06	Yes	Yes	No	1606	1	1	40.48	93.45
3550	IK	-1.49	0.12	-2.03	-0.83	No	No	No	1183	-1.86	1.01E-11	12376.58	6608.89
3550	IK	-1.49	-1.1	-2.03	-0.76	Yes	No	No	1528	-1.86	1.01E-11	12376.58	6608.89
3550	IK	-1.49	-0.43	-2.03	-0.88	Yes	No	No	1028	-1.86	1.01E-11	12376.58	6608.89
3550	IK	-1.49	-2.04	-2.03	-2.57	Yes	Yes	Yes	1382	-1.86	1.01E-11	12376.58	6608.89
23765	IL17R	-1.28	-1.54	-1.57	-1.74	Yes	Yes	Yes	820	-1.09	0.49	195.19	181.66
23765	IL17R	-1.28	-1.37	-1.57	-1.71	No	Yes	Yes	1400	-1.09	0.49	195.19	181.66
23765	IL17R	-1.28	0.03	-1.57	-0.81	No	No	No	1443	-1.09	0.49	195.19	181.66
23765	IL17R	-1.28	1.04	-1.57	-0.59	No	No	No	1816	-1.09	0.49	195.19	181.66
3552	IL1A	-0.86	0.97	-1.38	1.9	No	No	No	1481	1	1	39.5	91.51
3552	IL1A	-0.86	-0.16	-1.38	0.5	No	No	No	1954	1	1	39.5	91.51
3552	IL1A	-0.86	-0.75	-1.38	-1.43	Yes	No	Yes	1108	1	1	39.5	91.51
3552	IL1A	-0.86	-1.31	-1.38	-1.68	No	No	Yes	1319	1	1	39.5	91.51
3660	IRF2	-0.58	-0.87	-1.93	1.28	No	No	No	1433	-1.11	0.48	258.97	253.11
3660	IRF2	-0.58	-0.54	-1.93	-1.77	Yes	No	No	879	-1.11	0.48	258.97	253.11
3660	IRF2	-0.58	0.93	-1.93	0.31	No	No	No	1428	-1.11	0.48	258.97	253.11
3660	IRF2	-0.58	-0.97	-1.93	-1.67	No	No	No	1043	-1.11	0.48	258.97	253.11
55600	ITLN1	-2.39	-0.33	-0.87	-0.79	No	No	No	1377	1	1	37.47	91.41
55600	ITLN1	-2.39	-0.95	-0.87	-0.74	No	No	Yes	1460	1	1	37.47	91.41

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
55600	ITLN1	-2.39	0.76	-0.87	1.46	No	No	No	1447	1	1	37.47	91.41
55600	ITLN1	-2.39	-2.04	-0.87	-1.1	No	Yes	Yes	2039	1	1	37.47	91.41
3725	JUN	-0.91	-1.64	-1.58	-1.8	No	Yes	Yes	1543	12.52	0	246.87	3217
3725	JUN	-0.91	-0.78	-1.58	-0.24	No	No	No	2184	12.52	0	246.87	3217
3725	JUN	-0.91	-1.59	-1.58	-0.94	Yes	No	No	1200	12.52	0	246.87	3217
3725	JUN	-0.91	0.1	-1.58	-1.28	Yes	Yes	No	1188	12.52	0	246.87	3217
10300	KATNB1	-2.39	-1.1	-2.21	-2.2	Yes	Yes	No	1169	1.7	0.07	83.27	152.12
10300	KATNB1	-2.39	-1.88	-2.21	-1.22	Yes	No	Yes	1537	1.7	0.07	83.27	152.12
3768	KCNJ12	-2.12	-1.69	-0.27	0.002	No	No	Yes	1925	1	1	72.22	105.95
3768	KCNJ12	-2.12	0.12	-0.27	-1.01	No	Yes	No	1386	1	1	72.22	105.95
3768	KCNJ12	-2.12	-2.38	-0.27	-1.54	No	Yes	Yes	1254	1	1	72.22	105.95
3768	KCNJ12	-2.12	2.16	-0.27	2.94	No	No	No	1676	1	1	72.22	105.95
89822	KCNK17	-0.71	-0.95	-0.88	0.7	No	No	No	1690	1	1	40.54	99.94
89822	KCNK17	-0.71	-0.34	-0.88	0.95	No	No	No	1580	1	1	40.54	99.94
89822	KCNK17	-0.71	-0.44	-0.88	-1.93	Yes	Yes	No	830	1	1	40.54	99.94
89822	KCNK17	-0.71	-1.11	-0.88	-1.74	Yes	No	No	1066	1	1	40.54	99.94
9776	KIAA0652	-2.11	-1.68	-1.07	-1.16	No	Yes	Yes	1751	-1.52	0.00501	239.69	161.84
9776	KIAA0652	-2.11	-1.55	-1.07	-0.9	No	Yes	Yes	1802	-1.52	0.00501	239.69	161.84
23277	KIAA0664	0.54	-0.71	-0.12	-0.72	Yes	Yes	No	806	1.81	1.11E-06	2379.49	5386.8
23277	KIAA0664	0.54	0.9	-0.12	3.22	Yes	No	No	1796	1.81	1.11E-06	2379.49	5386.8
23277	KIAA0664	0.54	-0.38	-0.12	-0.54	No	No	No	1524	1.81	1.11E-06	2379.49	5386.8
23277	KIAA0664	0.54	2.08	-0.12	0.39	No	No	No	2004	1.81	1.11E-06	2379.49	5386.8
57579	KIAA1411	-1.17	-0.85	-1.58	-1.01	Yes	Yes	Yes	1534	-1.83	0.00067	211.25	125.66
57579	KIAA1411	-1.17	-2.04	-1.58	-1.28	Yes	No	Yes	2677	-1.83	0.00067	211.25	125.66
3832	KIF11	1	0.42	-2.47	-1.71	Yes	Yes	No	753	-1.89	1.22E-19	957.4	504.81
3832	KIF11	1	0.85	-2.47	-2.25	Yes	Yes	No	490	-1.89	1.22E-19	957.4	504.81
3832	KIF11	1	0.07	-2.47	-1.93	Yes	Yes	No	717	-1.89	1.22E-19	957.4	504.81
3832	KIF11	1	-0.27	-2.47	-1.94	Yes	Yes	No	935	-1.89	1.22E-19	957.4	504.81
3827	KNG1	-1.2	1.64	-1.78	1.32	No	No	No	1684	1.09	0.67	39.77	107.02
3827	KNG1	-1.2	-0.02	-1.78	-0.38	Yes	No	No	1126	1.09	0.67	39.77	107.02
3827	KNG1	-1.2	-1.31	-1.78	0.31	No	No	Yes	1978	1.09	0.67	39.77	107.02
3827	KNG1	-1.2	-1.08	-1.78	-2.23	Yes	Yes	No	822	1.09	0.67	39.77	107.02
3837	KPNB1	-2.48	-1.88	-1.51	-1.03	No	No	Yes	2407	-1.89	3.88E-08	43798.17	22890.76
3837	KPNB1	-2.48	-1.25	-1.51	-0.55	No	No	Yes	1581	-1.89	3.88E-08	43798.17	22890.76
3837	KPNB1	-2.48	-2.16	-1.51	-1.38	Yes	Yes	Yes	1887	-1.89	3.88E-08	43798.17	22890.76
3837	KPNB1	-2.48	1.33	-1.51	-1.54	No	No	No	1053	-1.89	3.88E-08	43798.17	22890.76
9215	LARGE	-1.2	0.71	-0.56	0.04	Yes	No	No	1268	-3.09	7.01E-25	672.29	216.24
9215	LARGE	-1.2	-1.46	-0.56	-0.53	No	No	Yes	1448	-3.09	7.01E-25	672.29	216.24
9215	LARGE	-1.2	1.67	-0.56	1.05	No	No	No	1346	-3.09	7.01E-25	672.29	216.24
9215	LARGE	-1.2	-1.37	-0.56	-1.01	Yes	No	Yes	1280	-3.09	7.01E-25	672.29	216.24
23367	LARP	-0.04	0.75	-1.72	-1.56	No	Yes	No	691	1	0.98	216.78	228.14
23367	LARP	-0.04	0.75	-1.72	-1.56	Yes	No	No	888	1	0.98	216.78	228.14
23367	LARP	-0.04	-0.99	-1.72	-1.39	Yes	Yes	No	1442	1	0.98	216.78	228.14
23367	LARP	-0.04	-0.99	-1.72	-1.39	Yes	Yes	No	1231	1	0.98	216.78	228.14
79603	LASS4	-2.74	-0.36	-2.3	-1.77	Yes	No	No	970	1.19	0.35	89.29	129.65
79603	LASS4	-2.74	-2.81	-2.3	-2.29	Yes	Yes	Yes	1933	1.19	0.35	89.29	129.65
3957	LGALS2	-2.33	-1.84	-1.81	-1.18	Yes	Yes	Yes	1465	-2.38	0.00046	455.72	200.08
3957	LGALS2	-2.33	-1.34	-1.81	-1.45	No	No	Yes	1306	-2.38	0.00046	455.72	200.08
8022	LHX3	0.88	-0.46	-1.94	1.14	No	No	No	2711	1	1	39.37	93.31
8022	LHX3	0.88	0.92	-1.94	-1.55	No	Yes	No	931	1	1	39.37	93.31
8022	LHX3	0.88	-1.26	-1.94	-2.38	Yes	Yes	No	1185	1	1	39.37	93.31
8022	LHX3	0.88	2.43	-1.94	1.7	No	No	No	1912	1	1	39.37	93.31
283377	LOC283377	-1.5	-2.46	-0.38	-3.02	Yes	Yes	Yes	1219	-1.27	0.1	365.61	296.64
283377	LOC283377	-1.5	-1.25	-0.38	-0.4	No	No	No	1806	-1.27	0.1	365.61	296.64
283377	LOC283377	-1.5	-0.21	-0.38	0.56	No	No	No	1664	-1.27	0.1	365.61	296.64
283377	LOC283377	-1.5	-1.12	-0.38	-0.32	Yes	No	Yes	1630	-1.27	0.1	365.61	296.64

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284058	LOC284058	-1.48	-1.21	-2.42	-1.9	Yes	Yes	No	1019	-1.95	0.00019	1198.56	607.95
284058	LOC284058	-1.48	-1.88	-2.42	-3.19	No	Yes	No	1218	-1.95	0.00019	1198.56	607.95
401431	LOC401431	-2.78	-1.4	-1.96	-1.35	Yes	Yes	Yes	1454	-1.86	1.00E-05	222	121.8
401431	LOC401431	-2.78	-2.68	-1.96	-2.27	Yes	Yes	Yes	2130	-1.86	1.00E-05	222	121.8
92235	LOC92235	-1.97	-1.57	-1.64	-0.93	No	Yes	Yes	1380	1	1	39.75	102.14
92235	LOC92235	-1.97	-0.74	-1.64	-1.32	No	No	No	1274	1	1	39.75	102.14
92235	LOC92235	-1.97	1.58	-1.64	1.64	No	No	No	1703	1	1	39.75	102.14
92235	LOC92235	-1.97	-2.39	-1.64	-3.09	Yes	Yes	Yes	798	1	1	39.75	102.14
92312	LOC92312	-1.73	-1.69	-1.58	-0.99	No	No	Yes	1853	1.04	0.8	286.84	319.36
92312	LOC92312	-1.73	-0.91	-1.58	-1.8	Yes	No	No	820	1.04	0.8	286.84	319.36
92312	LOC92312	-1.73	-1.33	-1.58	-1.54	Yes	Yes	No	1376	1.04	0.8	286.84	319.36
92312	LOC92312	-1.73	0.8	-1.58	3.04	No	No	No	2478	1.04	0.8	286.84	319.36
9890	LPPR4	-0.98	-0.57	-0.4	-0.42	Yes	No	No	1191	1	1	39.94	93.06
9890	LPPR4	-0.98	-0.84	-0.4	0.08	Yes	No	No	1099	1	1	39.94	93.06
84918	LRP11	-2.36	-1.59	-1.96	-0.74	No	No	Yes	1600	-2.92	2.00E-05	647.07	222.25
84918	LRP11	-2.36	-1.86	-1.96	-1.67	Yes	Yes	Yes	1254	-2.92	2.00E-05	647.07	222.25
53353	LRP1B	-0.98	-0.18	-1.95	0.11	No	No	No	2011	1	1	37.1	92.5
53353	LRP1B	-0.98	0.03	-1.95	1	No	No	No	1335	1	1	37.1	92.5
53353	LRP1B	-0.98	-1.81	-1.95	-1.56	Yes	Yes	Yes	1514	1	1	37.1	92.5
53353	LRP1B	-0.98	-0.64	-1.95	-1.98	No	No	Yes	966	1	1	37.1	92.5
84894	LRRN6A	-2	0.44	0.78	0.83	No	No	No	1603	-1.23	0.00043	3353.17	2725.38
84894	LRRN6A	-2	-2.69	0.78	-2.54	Yes	Yes	Yes	1092	-1.23	0.00043	3353.17	2725.38
84894	LRRN6A	-2	-1.6	0.78	-1.01	Yes	No	No	1187	-1.23	0.00043	3353.17	2725.38
84894	LRRN6A	-2	0.36	0.78	1.49	No	No	No	1587	-1.23	0.00043	3353.17	2725.38
80740	LY6G6C	0.18	0.51	-1.1	-0.88	Yes	No	No	1475	1.94	0.00567	189.2	359.88
80740	LY6G6C	0.18	0.03	-1.1	-0.93	Yes	No	No	1744	1.94	0.00567	189.2	359.88
4125	MAN2B1	-1.07	-1.21	-2.06	-2.3	Yes	Yes	Yes	1011	1.35	3.81E-06	3634.69	4942.01
4125	MAN2B1	-1.07	-0.08	-2.06	-0.73	No	No	No	1334	1.35	3.81E-06	3634.69	4942.01
4125	MAN2B1	-1.07	-1.19	-2.06	-1.63	Yes	No	Yes	1011	1.35	3.81E-06	3634.69	4942.01
4125	MAN2B1	-1.07	-0.9	-2.06	-0.26	No	No	No	1305	1.35	3.81E-06	3634.69	4942.01
5606	MAP2K3	-1.96	-1.05	-1.49	-0.85	No	No	No	2204	1.83	1.00E-04	4047.62	7560.94
5606	MAP2K3	-1.96	-2.01	-1.49	-2.46	Yes	Yes	Yes	1260	1.83	1.00E-04	4047.62	7560.94
5606	MAP2K3	-1.96	-0.97	-1.49	-0.55	Yes	No	No	1844	1.83	1.00E-04	4047.62	7560.94
5606	MAP2K3	-1.96	-1.57	-1.49	-1.71	No	No	No	1486	1.83	1.00E-04	4047.62	7560.94
4148	MATN3	1.33	0.44	0.19	1.39	No	No	No	2316	-1.19	0.17	132.24	112.06
4148	MATN3	1.33	1.17	0.19	-0.08	No	No	No	814	-1.19	0.17	132.24	112.06
4148	MATN3	1.33	-0.1	0.19	-1.28	Yes	No	No	938	-1.19	0.17	132.24	112.06
4148	MATN3	1.33	1.23	0.19	0.3	Yes	No	No	1070	-1.19	0.17	132.24	112.06
4193	MDM2	0.77	-1.89	-1.44	-1.6	Yes	Yes	Yes	1275	1	1	66.69	99.8
4193	MDM2	0.77	0.68	-1.44	-0.72	Yes	No	No	774	1	1	66.69	99.8
4193	MDM2	0.77	0.43	-1.44	-1.37	No	No	No	909	1	1	66.69	99.8
4193	MDM2	0.77	1.9	-1.44	0.54	No	No	No	941	1	1	66.69	99.8
10001	MED6	0.01	1.86	-0.32	-0.006	Yes	No	No	903	-1.96	0.00042	240.74	128.76
10001	MED6	0.01	1.1	-0.32	-1.06	No	No	No	736	-1.96	0.00042	240.74	128.76
10001	MED6	0.01	-1.46	-0.32	-0.48	Yes	No	No	1546	-1.96	0.00042	240.74	128.76
10001	MED6	0.01	-0.09	-0.32	-0.17	No	No	No	1297	-1.96	0.00042	240.74	128.76
79171	MGC10433	-1.49	2.27	-0.18	0.75	Yes	No	No	1509	-1.37	0.00053	1489.26	1081.6
79171	MGC10433	-1.49	-2.52	-0.18	-1.9	Yes	No	Yes	1855	-1.37	0.00053	1489.26	1081.6
132001	MGC16471	0.85	-0.51	-0.76	-0.67	Yes	No	No	1708	-2.62	7.71E-18	1123.31	430.66
132001	MGC16471	0.85	0.9	-0.76	-0.53	Yes	No	No	2246	-2.62	7.71E-18	1123.31	430.66
124044	MGC26885	-1.67	-1.24	-2.29	-2.27	No	Yes	Yes	1267	3.72	0	3630.52	13551
124044	MGC26885	-1.67	-1.35	-2.29	-1.64	Yes	Yes	No	1825	3.72	0	3630.52	13551
84292	MGC4238	-2.15	-1.71	-2.38	-1.93	Yes	Yes	No	1247	-2.06	2.23E-07	431.26	205.14
84292	MGC4238	-2.15	-0.02	-2.38	-1.04	Yes	Yes	No	2194	-2.06	2.23E-07	431.26	205.14
339512	MGC48998	-0.12	-0.17	-1.87	-0.31	Yes	No	No	1091	1	1	39.32	96.12
339512	MGC48998	-0.12	-0.34	-1.87	-1.54	Yes	Yes	No	759	1	1	39.32	96.12

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
23417	MLYCD	-0.86	-0.6	0.46	1.17	No	No	No	1779	-2.03	7.00E-05	625.08	258.47
23417	MLYCD	-0.86	1.53	0.46	3.44	No	No	No	1673	-2.03	7.00E-05	625.08	258.47
23417	MLYCD	-0.86	-0.96	0.46	-0.29	Yes	No	No	1602	-2.03	7.00E-05	625.08	258.47
23417	MLYCD	-0.86	-1.25	0.46	-0.64	Yes	Yes	No	1565	-2.03	7.00E-05	625.08	258.47
83886	MPN	-2.25	-3.52	-1.76	-2.86	Yes	No	Yes	1600	1	1	38.75	94.72
83886	MPN	-2.25	-1.71	-1.76	0.1	No	No	No	1302	1	1	38.75	94.72
83886	MPN	-2.25	0.77	-1.76	1.81	No	No	No	1395	1	1	38.75	94.72
83886	MPN	-2.25	-0.52	-1.76	-1.42	No	Yes	Yes	860	1	1	38.75	94.72
4482	MSRA	-0.85	-1.9	-1.27	-0.56	Yes	Yes	No	1544	1.4	0.01	1338.01	1895.06
4482	MSRA	-0.85	0.14	-1.27	-1.05	Yes	Yes	No	1282	1.4	0.01	1338.01	1895.06
4486	MST1R	0.09	-0.85	-1.34	-1.1	Yes	Yes	No	970	-1.02	0.88	272.82	278.77
4486	MST1R	0.09	-1.43	-1.34	-1.84	Yes	No	No	797	-1.02	0.88	272.82	278.77
4486	MST1R	0.09	-0.03	-1.34	-0.51	Yes	No	No	959	-1.02	0.88	272.82	278.77
4486	MST1R	0.09	1.05	-1.34	-0.13	No	No	No	878	-1.02	0.88	272.82	278.77
4609	MYC	-2.18	-2.01	-1.22	-1.53	No	No	Yes	1812	-2.24	8.27E-06	4343.41	1886.53
4609	MYC	-2.18	-1.01	-1.22	1.17	No	No	No	1586	-2.24	8.27E-06	4343.41	1886.53
4609	MYC	-2.18	-1.91	-1.22	-1.02	Yes	No	Yes	1576	-2.24	8.27E-06	4343.41	1886.53
4609	MYC	-2.18	-0.85	-1.22	-0.13	No	No	No	1896	-2.24	8.27E-06	4343.41	1886.53
4654	MYOD1	-0.33	1.24	0.67	1.6	No	No	No	1812	3.03	3.59E-24	199.21	602.99
4654	MYOD1	-0.33	-0.35	0.67	0.54	Yes	No	Yes	1792	3.03	3.59E-24	199.21	602.99
4654	MYOD1	-0.33	1.38	0.67	-0.05	No	No	No	1788	3.03	3.59E-24	199.21	602.99
4654	MYOD1	-0.33	-1.86	0.67	-0.65	Yes	Yes	Yes	1981	3.03	3.59E-24	199.21	602.99
23040	MYT1L	-1.55	-1	-1.37	-0.89	Yes	Yes	No	1044	1	1	39.89	97.17
23040	MYT1L	-1.55	-1.64	-1.37	-1.69	Yes	No	Yes	2143	1	1	39.89	97.17
8440	NCK2	-1.53	-1.78	0.07	-1.47	Yes	No	No	1622	1.26	0.28	80.17	119.71
8440	NCK2	-1.53	-0.08	0.07	1.05	No	No	No	2396	1.26	0.28	80.17	119.71
8440	NCK2	-1.53	-2	0.07	-1.45	Yes	Yes	Yes	1523	1.26	0.28	80.17	119.71
8440	NCK2	-1.53	1.44	0.07	1.65	No	No	No	2342	1.26	0.28	80.17	119.71
284086	NEK8	-1.08	-0.91	-0.85	-0.63	Yes	Yes	No	1265	4.47	2.99E-09	89.82	674.95
284086	NEK8	-1.08	-1.62	-0.85	-2.25	No	No	No	909	4.47	2.99E-09	89.82	674.95
284086	NEK8	-1.08	0.47	-0.85	1.12	No	No	No	2461	4.47	2.99E-09	89.82	674.95
284086	NEK8	-1.08	-0.44	-0.85	-0.75	Yes	No	No	1227	4.47	2.99E-09	89.82	674.95
91754	NEK9	-0.78	1.06	-1.01	0.03	No	No	No	1502	-2.89	2.59E-24	4905.29	1694.92
91754	NEK9	-0.78	0.19	-1.01	-0.89	No	No	No	1103	-2.89	2.59E-24	4905.29	1694.92
91754	NEK9	-0.78	-1.4	-1.01	-1.83	Yes	Yes	No	921	-2.89	2.59E-24	4905.29	1694.92
91754	NEK9	-0.78	-1.27	-1.01	-0.81	Yes	No	Yes	1293	-2.89	2.59E-24	4905.29	1694.92
4861	NPAS1	-0.68	-0.19	-1.74	-1.22	No	No	No	1170	1	1	82.78	112.64
4861	NPAS1	-0.68	-0.53	-1.74	-0.02	No	No	No	1500	1	1	82.78	112.64
4861	NPAS1	-0.68	-2.25	-1.74	-2.16	Yes	Yes	Yes	1324	1	1	82.78	112.64
4861	NPAS1	-0.68	0.51	-1.74	-1.1	Yes	No	No	978	1	1	82.78	112.64
4913	NTHL1	1.34	0.82	-0.48	-0.47	No	No	No	1422	-1.98	6.06E-06	1666.1	826.37
4913	NTHL1	1.34	2.22	-0.48	4.05	No	No	No	1867	-1.98	6.06E-06	1666.1	826.37
4913	NTHL1	1.34	-0.65	-0.48	-0.21	Yes	No	No	2360	-1.98	6.06E-06	1666.1	826.37
4913	NTHL1	1.34	0.67	-0.48	-1.52	Yes	Yes	No	832	-1.98	6.06E-06	1666.1	826.37
11163	NUDT4	-1.11	-0.82	-0.99	-0.12	No	No	No	1593	-1.13	0.33	2347.7	2065.29
11163	NUDT4	-1.11	-0.07	-0.99	2.65	No	No	No	2042	-1.13	0.33	2347.7	2065.29
11163	NUDT4	-1.11	-1.14	-0.99	-0.85	Yes	No	No	1228	-1.13	0.33	2347.7	2065.29
11163	NUDT4	-1.11	-1.3	-0.99	-1.9	Yes	Yes	Yes	1136	-1.13	0.33	2347.7	2065.29
23165	NUP205	-2.53	-2.22	-1.43	-1.57	Yes	Yes	Yes	1277	-2.35	1.97E-07	2087.16	866.14
23165	NUP205	-2.53	-1.78	-1.43	-1.06	Yes	No	No	2615	-2.35	1.97E-07	2087.16	866.14
4928	NUP98	-1.81	-1.4	-0.7	-0.68	Yes	No	Yes	1883	-1.49	0.00079	1444.77	960.27
4928	NUP98	-1.81	-1.45	-0.7	-1.58	Yes	Yes	Yes	1288	-1.49	0.00079	1444.77	960.27
4928	NUP98	-1.81	-1.49	-0.7	-0.4	Yes	No	Yes	2531	-1.49	0.00079	1444.77	960.27
4928	NUP98	-1.81	0.41	-0.7	0.67	No	No	No	1750	-1.49	0.00079	1444.77	960.27
10482	NXF1	-3.4	-2.61	-2.71	-2.86	Yes	Yes	Yes	760	1.77	5.00E-05	417.78	763.52
10482	NXF1	-3.4	-2.64	-2.71	-2	Yes	No	Yes	1746	1.77	5.00E-05	417.78	763.52

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56000	NXF3	-3.49	-1.29	-3.35	-1.21	No	No	No	1834	2.16	0.00127	181.59	388.83
56000	NXF3	-3.49	-3.04	-3.35	-2.75	Yes	Yes	Yes	1284	2.16	0.00127	181.59	388.83
89882	NYD-SP25	-1.14	-0.35	-0.37	-0.29	Yes	No	Yes	950	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-0.35	-0.37	-0.29	No	No	No	966	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-1.39	-0.37	-0.49	No	No	No	1137	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-1.39	-0.37	-0.49	Yes	No	No	1626	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-1.35	-0.37	-1.15	No	No	No	1227	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-1.35	-0.37	-1.15	Yes	No	No	1124	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-0.32	-0.37	0.91	No	No	No	1157	1.05	0.77	38.91	94.66
89882	NYD-SP25	-1.14	-0.32	-0.37	0.91	No	No	No	1141	1.05	0.77	38.91	94.66
611	OPN1SW	-1.44	-1.73	-1.23	-1.07	Yes	Yes	Yes	933	2.07	0.01	103.26	239.6
611	OPN1SW	-1.44	-0.26	-1.23	0.3	Yes	No	No	931	2.07	0.01	103.26	239.6
611	OPN1SW	-1.44	0.005	-1.23	-0.5	No	No	No	839	2.07	0.01	103.26	239.6
611	OPN1SW	-1.44	0.69	-1.23	0.07	No	No	No	642	2.07	0.01	103.26	239.6
10280	OPRS1	-2.32	-1.17	-1.78	-0.41	No	No	No	1708	-1.65	0.00107	1099.24	674.02
10280	OPRS1	-2.32	-1.84	-1.78	-1.38	No	No	Yes	1541	-1.65	0.00107	1099.24	674.02
10280	OPRS1	-2.32	-2.1	-1.78	-2.31	Yes	Yes	Yes	1114	-1.65	0.00107	1099.24	674.02
10280	OPRS1	-2.32	1.08	-1.78	-0.34	No	No	No	1276	-1.65	0.00107	1099.24	674.02
64805	P2RY12	-2.08	0.68	-1.47	-0.26	No	No	No	1293	1	1	39.33	96.84
64805	P2RY12	-2.08	-1.69	-1.47	-1.2	No	No	Yes	857	1	1	39.33	96.84
64805	P2RY12	-2.08	-0.42	-1.47	-1.16	No	No	No	1412	1	1	39.33	96.84
64805	P2RY12	-2.08	-2.9	-1.47	-2.86	Yes	Yes	Yes	894	1	1	39.33	96.84
10606	PAICS	-1.18	-1.23	-1.03	0.02	No	No	No	2160	1.04	0.79	6477.21	6843.76
10606	PAICS	-1.18	-1.05	-1.03	-0.97	No	No	No	2118	1.04	0.79	6477.21	6843.76
10606	PAICS	-1.18	-0.79	-1.03	-1.9	Yes	Yes	No	1207	1.04	0.79	6477.21	6843.76
10606	PAICS	-1.18	0.1	-1.03	1.22	No	No	No	2436	1.04	0.79	6477.21	6843.76
196743	PAOX	-2.21	-1.52	-1.45	-1.09	No	Yes	Yes	1923	-1.15	0.43	582.42	503.75
196743	PAOX	-2.21	-2.21	-1.45	-1.79	No	Yes	Yes	1233	-1.15	0.43	582.42	503.75
196743	PAOX	-2.21	2.27	-1.45	0.37	No	No	No	1173	-1.15	0.43	582.42	503.75
196743	PAOX	-2.21	-1.75	-1.45	-1.11	No	No	No	1856	-1.15	0.43	582.42	503.75
25859	PART1	-1.69	-1.62	-1.54	-1.26	Yes	No	Yes	1046	1	1	40.45	97.03
25859	PART1	-1.69	-0.15	-1.54	-1.08	Yes	Yes	No	1410	1	1	40.45	97.03
139135	PASD1	-0.4	-0.66	-1.92	-0.46	Yes	No	No	1668	1	1	40.47	98.53
139135	PASD1	-0.4	-0.18	-1.92	-1.78	Yes	No	No	1724	1	1	40.47	98.53
54510	PCDH18	-0.79	-1.36	-2.15	-1.76	No	No	No	1098	1	1	39.3	98.81
54510	PCDH18	-0.79	0.72	-2.15	0.63	No	No	No	1107	1	1	39.3	98.81
54510	PCDH18	-0.79	-0.54	-2.15	-1.7	Yes	Yes	No	996	1	1	39.3	98.81
54510	PCDH18	-0.79	-1.23	-2.15	-1.27	Yes	Yes	Yes	764	1	1	39.3	98.81
5157	PDGFRL	-0.94	1.21	-0.98	-0.13	No	No	No	1059	1.45	1.52E-09	2446.3	3553.16
5157	PDGFRL	-0.94	-1.15	-0.98	-1.64	No	Yes	Yes	876	1.45	1.52E-09	2446.3	3553.16
5157	PDGFRL	-0.94	0.46	-0.98	-0.62	No	No	No	1078	1.45	1.52E-09	2446.3	3553.16
5157	PDGFRL	-0.94	-1.06	-0.98	-0.78	No	No	Yes	1558	1.45	1.52E-09	2446.3	3553.16
55851	PEN2	-1.3	0.61	-2.81	-0.58	No	No	No	1235	1.14	0.4	720.93	831.45
55851	PEN2	-1.3	-0.75	-2.81	-0.03	No	No	No	1639	1.14	0.4	720.93	831.45
55851	PEN2	-1.3	-0.91	-2.81	-2.56	Yes	Yes	No	736	1.14	0.4	720.93	831.45
55851	PEN2	-1.3	-2.62	-2.81	-2.18	Yes	Yes	Yes	1512	1.14	0.4	720.93	831.45
5184	PEPD	-1.26	-0.48	-1.79	-0.93	No	No	No	1005	-1.16	0.01	5636.8	4850.01
5184	PEPD	-1.26	0.27	-1.79	-0.49	No	No	No	1100	-1.16	0.01	5636.8	4850.01
5184	PEPD	-1.26	-0.25	-1.79	-1.43	No	Yes	No	1187	-1.16	0.01	5636.8	4850.01
5184	PEPD	-1.26	-2	-1.79	-2.26	Yes	Yes	Yes	767	-1.16	0.01	5636.8	4850.01
5253	PHF2	-1.68	-0.66	-2.62	-1.48	No	Yes	No	1101	-1.27	0.00616	837.72	720.01
5253	PHF2	-1.68	-1.36	-2.62	-2.23	Yes	Yes	No	1076	-1.27	0.00616	837.72	720.01
337867	PHGDHL1	-0.74	-2.08	-1.11	-2.67	No	Yes	No	1611	-1.03	0.87	710.51	702.6
337867	PHGDHL1	-0.74	-0.32	-1.11	-0.85	No	Yes	No	829	-1.03	0.87	710.51	702.6
337867	PHGDHL1	-0.74	-0.66	-1.11	-0.93	Yes	No	No	1314	-1.03	0.87	710.51	702.6
337867	PHGDHL1	-0.74	0.78	-1.11	-0.41	No	No	No	1308	-1.03	0.87	710.51	702.6

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5288	PIK3C2G	-2.28	0.76	-1.9	1.04	No	No	No	1693	1	1	37.55	91.62
5288	PIK3C2G	-2.28	-2.37	-1.9	-2.83	Yes	Yes	No	1025	1	1	37.55	91.62
5288	PIK3C2G	-2.28	0.33	-1.9	-1.33	No	No	No	1208	1	1	37.55	91.62
5288	PIK3C2G	-2.28	-2.19	-1.9	-2	Yes	Yes	Yes	1031	1	1	37.55	91.62
5291	PIK3CB	-2.02	0.81	-1.47	0.34	No	No	No	2024	-2.85	1.00E-05	394.31	144.9
5291	PIK3CB	-2.02	-1.61	-1.47	-0.05	No	No	Yes	2106	-2.85	1.00E-05	394.31	144.9
5291	PIK3CB	-2.02	-1.09	-1.47	-1.3	No	No	No	2476	-2.85	1.00E-05	394.31	144.9
5291	PIK3CB	-2.02	-2.39	-1.47	-1.52	No	Yes	Yes	1552	-2.85	1.00E-05	394.31	144.9
23533	PIK3R5	-0.24	-1.06	-0.71	-1.13	No	Yes	Yes	1465	4.37	1.60E-06	80.39	361.88
23533	PIK3R5	-0.24	2.06	-0.71	2.17	No	No	No	1421	4.37	1.60E-06	80.39	361.88
23533	PIK3R5	-0.24	-0.27	-0.71	-0.41	Yes	Yes	No	1263	4.37	1.60E-06	80.39	361.88
23533	PIK3R5	-0.24	0.29	-0.71	-0.64	No	No	No	452	4.37	1.60E-06	80.39	361.88
5300	PIN1	-0.42	0.08	-0.55	-0.31	No	No	No	1610	1.31	0.00198	865.09	1135.52
5300	PIN1	-0.42	0.45	-0.55	-0.77	No	Yes	No	1101	1.31	0.00198	865.09	1135.52
5300	PIN1	-0.42	-1.53	-0.55	-1.51	Yes	Yes	Yes	1769	1.31	0.00198	865.09	1135.52
5300	PIN1	-0.42	-0.42	-0.55	0.03	No	No	No	1982	1.31	0.00198	865.09	1135.52
5328	PLAU	-2.6	-2.04	-2.12	-1.86	Yes	Yes	Yes	1353	2.04	1.64E-08	4782.46	9919.05
5328	PLAU	-2.6	0.31	-2.12	-1.36	No	No	No	789	2.04	1.64E-08	4782.46	9919.05
5328	PLAU	-2.6	-2.19	-2.12	-1.71	Yes	No	Yes	1663	2.04	1.64E-08	4782.46	9919.05
5328	PLAU	-2.6	-0.8	-2.12	0.58	No	No	No	1176	2.04	1.64E-08	4782.46	9919.05
5338	PLD2	-2.05	-0.27	-0.63	0.25	No	No	No	1856	1	1	68.81	106.84
5338	PLD2	-2.05	-1.63	-0.63	-0.38	No	No	No	1739	1	1	68.81	106.84
5338	PLD2	-2.05	-2.99	-0.63	-2.39	Yes	Yes	Yes	1317	1	1	68.81	106.84
5338	PLD2	-2.05	-0.79	-0.63	-0.58	No	No	No	1501	1	1	68.81	106.84
1263	PLK3	-1.55	-1.22	-2.23	-1.79	No	Yes	Yes	910	-1.24	0.27	609.77	500.2
1263	PLK3	-1.55	-2.42	-2.23	-1.19	Yes	Yes	Yes	1673	-1.24	0.27	609.77	500.2
1263	PLK3	-1.55	-1.26	-2.23	-1.89	Yes	No	No	1333	-1.24	0.27	609.77	500.2
1263	PLK3	-1.55	-0.61	-2.23	-0.2	No	No	No	1727	-1.24	0.27	609.77	500.2
5437	POLR2H	-1.13	-0.64	-0.24	-0.29	Yes	No	No	1099	-1.54	0.02	1729.93	1139.32
5437	POLR2H	-1.13	-1.15	-0.24	0.07	Yes	No	No	1188	-1.54	0.02	1729.93	1139.32
5441	POLR2L	-1.07	-1.36	-0.79	-0.7	Yes	Yes	No	1104	-1.08	0.49	32701.42	22885.54
5441	POLR2L	-1.07	-0.76	-0.79	-0.65	Yes	Yes	No	992	-1.08	0.49	32701.42	22885.54
54866	PPP1R14D	-2.63	-1.69	-2.04	-1.42	No	No	No	1699	1	1	39.61	91.97
54866	PPP1R14D	-2.63	-0.87	-2.04	-1.39	No	No	Yes	1119	1	1	39.61	91.97
54866	PPP1R14D	-2.63	-2.53	-2.04	-1.85	Yes	Yes	Yes	1747	1	1	39.61	91.97
54866	PPP1R14D	-2.63	-2.07	-2.04	-1.22	No	No	No	1603	1	1	39.61	91.97
10594	PRPF8	-1.53	-1.46	-2.07	-1.44	Yes	Yes	Yes	1257	-2.03	3.68E-14	2436.77	1276.65
10594	PRPF8	-1.53	-1.25	-2.07	-2.02	Yes	Yes	No	1060	-2.03	3.68E-14	2436.77	1276.65
10594	PRPF8	-1.53	1.55	-2.07	0.92	No	No	No	1989	-2.03	3.68E-14	2436.77	1276.65
10594	PRPF8	-1.53	-2.08	-2.07	-2.17	Yes	No	No	1361	-2.03	3.68E-14	2436.77	1276.65
5631	PRPS1	-0.26	0.67	-0.23	1.59	No	No	No	1884	-1.19	0.00256	4155.8	3491.36
5631	PRPS1	-0.26	-0.83	-0.23	-0.83	Yes	No	No	834	-1.19	0.00256	4155.8	3491.36
5631	PRPS1	-0.26	0.14	-0.23	-0.85	Yes	Yes	No	1152	-1.19	0.00256	4155.8	3491.36
5631	PRPS1	-0.26	-0.52	-0.23	0.58	No	No	No	1647	-1.19	0.00256	4155.8	3491.36
9361	PRSS15	-0.61	-0.22	-1.03	-0.35	No	No	No	1248	-2.08	1.82E-27	3108.72	1489.59
9361	PRSS15	-0.61	-0.32	-1.03	-0.23	No	No	No	1672	-2.08	1.82E-27	3108.72	1489.59
9361	PRSS15	-0.61	-0.31	-1.03	-1.85	Yes	Yes	No	1289	-2.08	1.82E-27	3108.72	1489.59
9361	PRSS15	-0.61	-1.34	-1.03	-0.67	Yes	No	No	1631	-2.08	1.82E-27	3108.72	1489.59
5660	PSAP	-0.25	0.46	-0.88	-0.73	No	No	No	1056	-1.09	0.28	6195.42	5627.6
5660	PSAP	-0.25	-1.8	-0.88	-1.66	Yes	Yes	Yes	1016	-1.09	0.28	6195.42	5627.6
5660	PSAP	-0.25	0.15	-0.88	-0.77	Yes	Yes	No	1256	-1.09	0.28	6195.42	5627.6
5660	PSAP	-0.25	-0.3	-0.88	0.21	No	No	No	2040	-1.09	0.28	6195.42	5627.6
5682	PSMA1	-1.08	-1.46	-0.78	-1.37	No	No	Yes	1183	-1.49	4.55E-12	8129.01	5426.65
5682	PSMA1	-1.08	1.23	-0.78	1.12	No	No	No	1073	-1.49	4.55E-12	8129.01	5426.65
5682	PSMA1	-1.08	-1.51	-0.78	-1.14	Yes	No	No	1083	-1.49	4.55E-12	8129.01	5426.65
5682	PSMA1	-1.08	-0.45	-0.78	-0.69	Yes	No	No	1196	-1.49	4.55E-12	8129.01	5426.65

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
5706	PSMC6	0.43	-0.31	-0.24	-0.37	Yes	No	No	881	-1.99	1.51E-37	5190.44	2612.87
5706	PSMC6	0.43	1.52	-0.24	0.12	Yes	No	No	819	-1.99	1.51E-37	5190.44	2612.87
10213	PSMD14	1.65	1.61	-0.15	1.36	No	No	No	1578	-1.87	2.27E-09	8150.88	4324.8
10213	PSMD14	1.65	-0.76	-0.15	-0.7	No	No	No	1449	-1.87	2.27E-09	8150.88	4324.8
10213	PSMD14	1.65	0.55	-0.15	-1.52	Yes	Yes	No	1310	-1.87	2.27E-09	8150.88	4324.8
10213	PSMD14	1.65	4.63	-0.15	-0.19	Yes	No	No	1210	-1.87	2.27E-09	8150.88	4324.8
5708	PSMD2	0.94	0.23	-0.77	-0.58	No	No	No	1389	1.24	0.02	1860.27	2317.37
5708	PSMD2	0.94	-0.71	-0.77	-1.75	Yes	No	No	1260	1.24	0.02	1860.27	2317.37
5708	PSMD2	0.94	2.18	-0.77	-0.57	No	No	No	1630	1.24	0.02	1860.27	2317.37
5708	PSMD2	0.94	0.27	-0.77	-0.67	Yes	No	No	1046	1.24	0.02	1860.27	2317.37
5798	PTPRN	-1.25	0.21	-1.47	0.81	No	No	Yes	1688	1	1	52.04	99.3
5798	PTPRN	-1.25	1.69	-1.47	-1	No	No	No	1854	1	1	52.04	99.3
5798	PTPRN	-1.25	-1.04	-1.47	-1.2	Yes	No	No	1232	1	1	52.04	99.3
5798	PTPRN	-1.25	-1.18	-1.47	-1.27	Yes	No	Yes	1558	1	1	52.04	99.3
51560	RAB6B	-1.42	0.5	-0.84	-0.57	No	No	No	1385	1	1	97.82	116.73
51560	RAB6B	-1.42	-1.43	-0.84	-2.3	Yes	Yes	Yes	738	1	1	97.82	116.73
51560	RAB6B	-1.42	0.79	-0.84	-0.24	Yes	No	No	1163	1	1	97.82	116.73
51560	RAB6B	-1.42	-1.25	-0.84	0.28	No	No	No	1347	1	1	97.82	116.73
29127	RACGAP1	-2.54	-2.98	-1.83	-2.67	Yes	Yes	Yes	1105	-3.63	5.51E-35	2438.91	668.9
29127	RACGAP1	-2.54	2.18	-1.83	-0.1	No	No	No	769	-3.63	5.51E-35	2438.91	668.9
29127	RACGAP1	-2.54	1.48	-1.83	0.19	No	No	No	1126	-3.63	5.51E-35	2438.91	668.9
29127	RACGAP1	-2.54	-1.91	-1.83	-1.13	No	No	No	1890	-3.63	5.51E-35	2438.91	668.9
10048	RANBP9	-1.14	1.19	-1.36	0.003	No	No	No	1116	-1.58	1.34E-15	2193.08	1381.03
10048	RANBP9	-1.14	-0.89	-1.36	-1.21	No	Yes	No	1066	-1.58	1.34E-15	2193.08	1381.03
10048	RANBP9	-1.14	-2.14	-1.36	-1.62	Yes	Yes	Yes	1543	-1.58	1.34E-15	2193.08	1381.03
10048	RANBP9	-1.14	-0.3	-1.36	-0.58	No	No	No	1333	-1.58	1.34E-15	2193.08	1381.03
5935	RBM3	-1.94	-1.89	-2.41	-1.95	Yes	Yes	Yes	868	1.75	2.00E-05	5962.13	10622.76
5935	RBM3	-1.94	-1.89	-2.41	-1.95	Yes	Yes	Yes	801	1.75	2.00E-05	5962.13	10622.76
5935	RBM3	-1.94	-0.85	-2.41	0.78	No	No	No	2220	1.75	2.00E-05	5962.13	10622.76
5935	RBM3	-1.94	-0.85	-2.41	0.78	No	No	No	2507	1.75	2.00E-05	5962.13	10622.76
56729	RETN	-1.77	-1.43	-1.08	-0.98	Yes	Yes	Yes	1217	1.84	0.12	39.73	109.88
56729	RETN	-1.77	-0.12	-1.08	0.95	No	No	Yes	1353	1.84	0.12	39.73	109.88
56729	RETN	-1.77	-1.96	-1.08	-1.46	No	No	Yes	1163	1.84	0.12	39.73	109.88
56729	RETN	-1.77	1.71	-1.08	0.29	No	No	No	833	1.84	0.12	39.73	109.88
117584	RFFL	-2.4	0.31	-2.52	0.56	No	No	No	1525	-4.56	0	1643.89	360.25
117584	RFFL	-2.4	3.39	-2.52	0.72	No	No	No	909	-4.56	0	1643.89	360.25
117584	RFFL	-2.4	-2.01	-2.52	-1.97	Yes	Yes	Yes	1254	-4.56	0	1643.89	360.25
117584	RFFL	-2.4	-2.17	-2.52	-2.42	Yes	Yes	Yes	876	-4.56	0	1643.89	360.25
57484	RNF150	-0.43	-0.89	-1.1	-1.69	Yes	Yes	Yes	827	3.4	0.03	37.79	163.26
57484	RNF150	-0.43	-0.96	-1.1	-1.15	No	Yes	Yes	1062	3.4	0.03	37.79	163.26
57484	RNF150	-0.43	-0.26	-1.1	-0.42	No	Yes	No	998	3.4	0.03	37.79	163.26
57484	RNF150	-0.43	2.37	-1.1	4.11	No	No	No	1571	3.4	0.03	37.79	163.26
11224	RPL35	-0.66	-1.82	-2.82	-2.4	Yes	Yes	No	839	1.21	0.01	105532.56	113877.17
11224	RPL35	-0.66	-0.39	-2.82	-1.76	Yes	Yes	No	777	1.21	0.01	105532.56	113877.17
11224	RPL35	-0.66	-0.6	-2.82	-1.44	Yes	Yes	No	869	1.21	0.01	105532.56	113877.17
11224	RPL35	-0.66	-0.52	-2.82	-2.2	Yes	Yes	No	661	1.21	0.01	105532.56	113877.17
6204	RPS10	-0.81	-0.71	-2.58	-0.94	Yes	No	No	927	1.37	6.11E-07	66601.67	76685.34
6204	RPS10	-0.81	-0.67	-2.58	-2.12	Yes	No	No	990	1.37	6.11E-07	66601.67	76685.34
6208	RPS14	0	0.46	-1.06	-0.04	Yes	Yes	No	891	-1.27	0.00042	233151.65	183762.34
6208	RPS14	0	-1.18	-1.06	-1.6	Yes	No	No	919	-1.27	0.00042	233151.65	183762.34
6217	RPS16	-1.48	-1.21	-2.07	-1.6	No	Yes	No	1045	-1.29	1.00E-05	165211.18	127826.35
6217	RPS16	-1.48	-0.75	-2.07	-1.76	Yes	Yes	No	1119	-1.29	1.00E-05	165211.18	127826.35
6229	RPS24	0.09	0.05	-2.13	-1.69	Yes	No	No	879	1.16	0.02	69312.98	80456.53
6229	RPS24	0.09	-0.03	-2.13	-1.51	Yes	Yes	No	757	1.16	0.02	69312.98	80456.53
6233	RPS27A	-1.19	0.77	-2.66	-1.05	No	No	No	663	1.09	0.48	129877.59	141113.9
6233	RPS27A	-1.19	-0.81	-2.66	-1.89	Yes	No	No	731	1.09	0.48	129877.59	141113.9

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
6233	RPS27A	-1.19	-1.34	-2.66	-2.3	Yes	No	No	785	1.09	0.48	129877.59	141113.9
6233	RPS27A	-1.19	-1.47	-2.66	-2.19	No	No	No	951	1.09	0.48	129877.59	141113.9
6188	RPS3	-1.41	-0.45	-2.63	-1.12	Yes	No	No	941	1.07	0.43	71825.01	66249.89
6188	RPS3	-1.41	-1.16	-2.63	-2.13	Yes	Yes	No	1002	1.07	0.43	71825.01	66249.89
6193	RPS5	-1.82	-1.63	-1.92	-1.43	Yes	Yes	Yes	759	1.23	0.00332	49108.73	55882.59
6193	RPS5	-1.82	-1.06	-1.92	-1.85	No	No	Yes	1009	1.23	0.00332	49108.73	55882.59
861	RUNX1	-2.08	-2.72	0.3	1.73	No	No	Yes	2938	-1.42	5.00E-04	232.05	162.49
861	RUNX1	-2.08	0.03	0.3	0.19	No	No	No	2800	-1.42	5.00E-04	232.05	162.49
861	RUNX1	-2.08	-1.66	0.3	-1.39	Yes	No	Yes	1365	-1.42	5.00E-04	232.05	162.49
861	RUNX1	-2.08	-1.68	0.3	-0.03	No	No	Yes	2240	-1.42	5.00E-04	232.05	162.49
6294	SAFB	-0.37	0.26	-0.39	-0.42	No	No	No	1269	-1.5	9.00E-05	1625.65	1075.23
6294	SAFB	-0.37	-1.39	-0.39	-0.52	No	No	No	1575	-1.5	9.00E-05	1625.65	1075.23
6294	SAFB	-0.37	-0.65	-0.39	1.12	No	No	No	2801	-1.5	9.00E-05	1625.65	1075.23
6294	SAFB	-0.37	-0.3	-0.39	-0.69	Yes	No	No	946	-1.5	9.00E-05	1625.65	1075.23
6301	SARS	-1.01	-0.71	-1.17	-1.03	Yes	No	No	1057	-1.7	2.00E-05	1717.11	997.81
6301	SARS	-1.01	-1.17	-1.17	-0.96	Yes	No	No	1394	-1.7	2.00E-05	1717.11	997.81
6339	SCNN1D	-0.82	0.53	0.19	0.47	No	No	No	1260	10.61	1.55E-30	178.34	2013.79
6339	SCNN1D	-0.82	-0.71	0.19	-0.11	No	No	Yes	1492	10.61	1.55E-30	178.34	2013.79
6339	SCNN1D	-0.82	-0.35	0.19	0.02	No	No	No	1133	10.61	1.55E-30	178.34	2013.79
6339	SCNN1D	-0.82	-2.14	0.19	-1.05	Yes	No	Yes	1396	10.61	1.55E-30	178.34	2013.79
6404	SELPLG	-0.3	-1.02	-0.13	-1.23	Yes	Yes	No	1166	4.16	3.67E-06	130.48	583.36
6404	SELPLG	-0.3	0.92	-0.13	-0.28	Yes	Yes	No	983	4.16	3.67E-06	130.48	583.36
6404	SELPLG	-0.3	-1.11	-0.13	0.72	No	No	No	1517	4.16	3.67E-06	130.48	583.36
6404	SELPLG	-0.3	-0.88	-0.13	0.22	No	No	No	1826	4.16	3.67E-06	130.48	583.36
5265	SERPINA1	-1.33	-0.001	-1.2	0.15	No	No	No	1584	2.27	1.07E-06	129.91	303.6
5265	SERPINA1	-1.33	-0.22	-1.2	0.5	No	No	No	1545	2.27	1.07E-06	129.91	303.6
5265	SERPINA1	-1.33	-1.59	-1.2	-1.17	Yes	No	No	1602	2.27	1.07E-06	129.91	303.6
5265	SERPINA1	-1.33	-0.06	-1.2	-1.01	Yes	No	No	1057	2.27	1.07E-06	129.91	303.6
5055	SERPINB2	-2.39	-2.05	-1.05	-1.75	No	Yes	Yes	1454	1.98	9.00E-05	130.15	254.44
5055	SERPINB2	-2.39	0.01	-1.05	-0.78	No	No	No	1486	1.98	9.00E-05	130.15	254.44
5055	SERPINB2	-2.39	-1.89	-1.05	-0.23	Yes	Yes	Yes	1626	1.98	9.00E-05	130.15	254.44
5055	SERPINB2	-2.39	2.81	-1.05	4.34	No	No	No	2694	1.98	9.00E-05	130.15	254.44
10291	SF3A1	-2.1	-1.74	-0.97	-0.83	No	No	No	1920	1.03	0.82	686.93	698.77
10291	SF3A1	-2.1	-1.79	-0.97	-0.98	Yes	Yes	Yes	1671	1.03	0.82	686.93	698.77
10291	SF3A1	-2.1	-1.46	-0.97	-1.21	Yes	Yes	Yes	1527	1.03	0.82	686.93	698.77
10291	SF3A1	-2.1	0.12	-0.97	0.38	Yes	No	No	1600	1.03	0.82	686.93	698.77
23451	SF3B1	-0.09	-0.15	-1.04	-0.73	Yes	No	No	927	-2.54	1.67E-21	5304.78	2096.32
23451	SF3B1	-0.09	-0.18	-1.04	-0.88	Yes	Yes	No	1686	-2.54	1.67E-21	5304.78	2096.32
51639	SF3B14	-1.43	-1.17	-0.92	-0.63	Yes	No	No	1495	1.28	0.00182	7891.3	10156.27
51639	SF3B14	-1.43	-1.17	-0.92	-1.17	Yes	No	Yes	1758	1.28	0.00182	7891.3	10156.27
6439	SFTPB	-1.05	-1.15	-0.79	-0.7	No	No	Yes	1374	1	1	39.95	101.19
6439	SFTPB	-1.05	-0.96	-0.79	-1.22	Yes	Yes	Yes	1000	1	1	39.95	101.19
6439	SFTPB	-1.05	0.16	-0.79	-0.51	No	No	No	998	1	1	39.95	101.19
6439	SFTPB	-1.05	-0.05	-0.79	1.01	No	No	No	1908	1	1	39.95	101.19
8778	SIGLEC5	-2.55	1.32	-1.7	-0.22	No	No	No	1885	1.08	0.71	48.02	162.87
8778	SIGLEC5	-2.55	0.06	-1.7	-0.6	No	No	No	1295	1.08	0.71	48.02	162.87
8778	SIGLEC5	-2.55	-2.63	-1.7	-1.38	No	Yes	Yes	1827	1.08	0.71	48.02	162.87
8778	SIGLEC5	-2.55	-1.49	-1.7	-1.97	Yes	Yes	Yes	1274	1.08	0.71	48.02	162.87
22938	SKIIP	0.17	0.02	-0.47	-0.46	Yes	No	No	1481	-1.16	0.02	4265.29	3652.4
22938	SKIIP	0.17	-0.12	-0.47	-0.75	No	No	No	1147	-1.16	0.02	4265.29	3652.4
22938	SKIIP	0.17	2.72	-0.47	1.51	Yes	No	No	1776	-1.16	0.02	4265.29	3652.4
22938	SKIIP	0.17	0.86	-0.47	-0.46	No	No	No	1651	-1.16	0.02	4265.29	3652.4
6560	SLC12A4	-0.83	-0.73	-0.65	-0.81	Yes	No	No	1062	-1.81	0.0072	224.35	131.75
6560	SLC12A4	-0.83	-0.41	-0.65	0.76	Yes	No	Yes	1562	-1.81	0.0072	224.35	131.75
9356	SLC22A6	-1.94	-2.31	-1.56	-1.26	Yes	Yes	Yes	1144	1	1	40.51	94.72
9356	SLC22A6	-1.94	-0.73	-1.56	0.85	No	No	No	1500	1	1	40.51	94.72

GeneID	Gene symbol	Genedata, percentage of infected cells, Z-score, gene-wise	Genedata, percentage of infected cells, Z-score, siRNA-wise	Genedata, number of infected cells, Z-score, gene-wise	Genedata, number of infected cells, Z-score, siRNA-wise	RSA, luciferase activity, OPI Hit	RSA, number of infected cells, OPI Hit	RSA, percentage of infected cells, OPI Hit	Mean cell number	Expression fold change, non-infected/ infected	Expression fold change, p-value	Expression, intensity non-infected cells	Expression, intensity infected cells
9368	SLC9A3R1	-0.18	-0.24	-0.27	0.11	No	No	No	1832	-1.97	0.00022	2553.64	1307.25
9368	SLC9A3R1	-0.18	-0.57	-0.27	-0.79	Yes	No	No	1425	-1.97	0.00022	2553.64	1307.25
9368	SLC9A3R1	-0.18	0.62	-0.27	1.58	No	No	No	1915	-1.97	0.00022	2553.64	1307.25
9368	SLC9A3R1	-0.18	-0.89	-0.27	-1.16	Yes	No	No	1177	-1.97	0.00022	2553.64	1307.25
55234	SMU1	-0.3	-0.33	-1.35	-1.11	Yes	Yes	No	1124	-3.17	3.85E-09	848.41	288.37
55234	SMU1	-0.3	0.84	-1.35	1.69	Yes	No	No	2016	-3.17	3.85E-09	848.41	288.37
6625	SNRP70	-0.9	-0.61	-0.3	-0.34	No	No	No	1458	-1.23	0.09	305.83	251.7
6625	SNRP70	-0.9	-0.17	-0.3	-1.11	Yes	No	Yes	1536	-1.23	0.09	305.83	251.7
6625	SNRP70	-0.9	-2.22	-0.3	-0.76	Yes	No	No	1937	-1.23	0.09	305.83	251.7
6625	SNRP70	-0.9	-0.64	-0.3	0.88	No	No	No	2535	-1.23	0.09	305.83	251.7
6636	SNRPF	-0.09	-0.18	-0.13	0.15	Yes	No	No	943	-1.13	0.01	13350.67	11655.33
6636	SNRPF	-0.09	0.34	-0.13	-1.14	Yes	No	No	837	-1.13	0.01	13350.67	11655.33
58533	SNX6	-1.4	-0.32	-1.54	0.04	No	No	No	1766	-2.02	0.00047	1239.95	612.05
58533	SNX6	-1.4	-0.15	-1.54	-1.39	No	No	No	1216	-2.02	0.00047	1239.95	612.05
58533	SNX6	-1.4	-1.15	-1.54	-1.25	Yes	Yes	Yes	1481	-2.02	0.00047	1239.95	612.05
58533	SNX6	-1.4	-1.76	-1.54	-1.27	No	No	Yes	2309	-2.02	0.00047	1239.95	612.05
51429	SNX9	-2.28	-1.53	-1.96	-0.92	No	No	No	1543	-2.13	0.00168	1155.07	538.85
51429	SNX9	-2.28	-2.12	-1.96	-1.62	Yes	Yes	No	944	-2.13	0.00168	1155.07	538.85
51429	SNX9	-2.28	-0.91	-1.96	0.2	No	No	No	1784	-2.13	0.00168	1155.07	538.85
51429	SNX9	-2.28	-2.33	-1.96	-1.75	Yes	No	No	1253	-2.13	0.00168	1155.07	538.85
6651	SON	-2.2	-1.12	-1.68	-1.35	Yes	Yes	No	1205	-1.55	7.00E-11	2987.14	1923.06
6651	SON	-2.2	-1.74	-1.68	-1.3	Yes	Yes	No	1686	-1.55	7.00E-11	2987.14	1923.06
23524	SRRM2	-2.66	-2.08	-2.48	-2.03	Yes	Yes	Yes	1364	-1.03	0.82	21031.83	20376.87
23524	SRRM2	-2.66	-1.66	-2.48	-1.95	Yes	Yes	No	1463	-1.03	0.82	21031.83	20376.87
83983	SSTK	-1.07	1.01	0.28	0.25	No	No	No	1745	1	1	42.85	98.84
83983	SSTK	-1.07	-0.97	0.28	-1.04	No	No	No	1809	1	1	42.85	98.84
83983	SSTK	-1.07	-0.18	0.28	1.1	Yes	No	No	1655	1	1	42.85	98.84
83983	SSTK	-1.07	-1.36	0.28	-1.24	Yes	No	No	1463	1	1	42.85	98.84
6755	SSTR5	-0.65	-0.99	-1.55	-1.04	Yes	No	No	1203	1.45	0.19	51.11	107.11
6755	SSTR5	-0.65	-0.08	-1.55	-1.38	No	Yes	No	657	1.45	0.19	51.11	107.11
6755	SSTR5	-0.65	-1.34	-1.55	-1.58	Yes	No	No	932	1.45	0.19	51.11	107.11
6755	SSTR5	-0.65	-0.59	-1.55	-1.26	No	No	No	719	1.45	0.19	51.11	107.11
23166	STAB1	-0.35	-1.67	-1.12	-1.91	Yes	No	No	1147	1.22	0.37	61.54	102.22
23166	STAB1	-0.35	0.76	-1.12	0.43	No	No	No	1474	1.22	0.37	61.54	102.22
23166	STAB1	-0.35	0.24	-1.12	-0.94	Yes	Yes	No	1107	1.22	0.37	61.54	102.22
23166	STAB1	-0.35	-0.01	-1.12	0.13	No	No	No	2039	1.22	0.37	61.54	102.22
252983	STXBP4	-0.8	-0.7	-2.6	-2.03	No	Yes	No	944	-2.48	1.61E-06	364.36	152.79
252983	STXBP4	-0.8	0.94	-2.6	-0.97	No	No	No	1982	-2.48	1.61E-06	364.36	152.79
55959	SULF2	-2	0.04	-0.94	-0.6	No	No	No	1239	-1.74	2.14E-07	2444.14	1395.28
55959	SULF2	-2	1.06	-0.94	0.73	No	No	No	1422	-1.74	2.14E-07	2444.14	1395.28
55959	SULF2	-2	-1.59	-0.94	-1.65	Yes	Yes	Yes	1361	-1.74	2.14E-07	2444.14	1395.28
55959	SULF2	-2	-1.77	-0.94	-1.03	No	Yes	Yes	1238	-1.74	2.14E-07	2444.14	1395.28
6830	SUPT6H	0.68	0.37	-0.55	-0.28	Yes	No	No	821	-1.18	0.04	1402.94	1175.64
6830	SUPT6H	0.68	-0.27	-0.55	-0.53	Yes	No	No	1558	-1.18	0.04	1402.94	1175.64
10607	TBL3	1.13	1.85	-1.52	-0.19	No	No	No	1390	1	1	41.68	100.45
10607	TBL3	1.13	-0.27	-1.52	-1.69	No	Yes	No	1031	1	1	41.68	100.45
10607	TBL3	1.13	-1.5	-1.52	-1.82	No	Yes	Yes	2156	1	1	41.68	100.45
10607	TBL3	1.13	1.34	-1.52	-0.77	No	No	No	1219	1	1	41.68	100.45
30009	TBX21	0.39	1.87	0.83	0.91	No	No	No	1907	4.18	1.94E-07	56.71	227.43
30009	TBX21	0.39	1.29	0.83	2.16	No	No	No	1395	4.18	1.94E-07	56.71	227.43
30009	TBX21	0.39	-1.25	0.83	-1.34	No	Yes	Yes	1491	4.18	1.94E-07	56.71	227.43
30009	TBX21	0.39	-1.22	0.83	-0.82	No	No	Yes	1751	4.18	1.94E-07	56.71	227.43
6929	TCF3	-0.03	-1.22	-0.06	-0.17	No	Yes	Yes	1597	-1.16	0.08	2438.08	2089.82
6929	TCF3	-0.03	0.5	-0.06	0.81	No	No	No	1738	-1.16	0.08	2438.08	2089.82
6929	TCF3	-0.03	-1.11	-0.06	-1.13	Yes	Yes	No	1074	-1.16	0.08	2438.08	2089.82
6929	TCF3	-0.03	-0.13	-0.06	-0.56	No	No	No	1407	-1.16	0.08	2438.08	2089.82

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7030	TFE3	-0.14	-0.3	-1.19	-1.01	No	Yes	No	947	1.48	0.01	600.43	910.95
7030	TFE3	-0.14	0.01	-1.19	0.13	No	No	No	2249	1.48	0.01	600.43	910.95
7030	TFE3	-0.14	-1.77	-1.19	-2.15	Yes	Yes	Yes	1414	1.48	0.01	600.43	910.95
7030	TFE3	-0.14	0.19	-1.19	0.61	No	No	No	2837	1.48	0.01	600.43	910.95
10469	TIMM44	0.73	-0.28	-1.46	-0.88	Yes	Yes	No	935	-1.08	0.66	391.48	376.04
10469	TIMM44	0.73	0.48	-1.46	-1.26	No	Yes	No	1285	-1.08	0.66	391.48	376.04
7084	TK2	-1.38	-1.21	-1.59	-1.77	Yes	Yes	Yes	772	-1.95	3.00E-05	274.48	144.05
7084	TK2	-1.38	-0.85	-1.59	-1.7	Yes	No	No	1225	-1.95	3.00E-05	274.48	144.05
7084	TK2	-1.38	0.54	-1.59	0.33	No	No	No	1387	-1.95	3.00E-05	274.48	144.05
7084	TK2	-1.38	-0.17	-1.59	-0.36	No	No	No	1323	-1.95	3.00E-05	274.48	144.05
3371	TNC	-0.72	-1.46	-1.78	-1.66	No	No	Yes	1084	1.51	0.14	79.33	140.38
3371	TNC	-0.72	-1.06	-1.78	-1.25	Yes	No	No	1445	1.51	0.14	79.33	140.38
3371	TNC	-0.72	-0.64	-1.78	-1.52	Yes	No	No	977	1.51	0.14	79.33	140.38
3371	TNC	-0.72	0.28	-1.78	0.65	No	No	No	1768	1.51	0.14	79.33	140.38
8784	TNFRSF18	-1.19	0.67	-1.52	0.81	No	No	No	2147	1.97	0.04	79.34	180.59
8784	TNFRSF18	-1.19	0.9	-1.52	0.19	No	No	No	1465	1.97	0.04	79.34	180.59
8784	TNFRSF18	-1.19	-1.14	-1.52	-1.24	Yes	Yes	Yes	1287	1.97	0.04	79.34	180.59
8784	TNFRSF18	-1.19	-1.22	-1.52	-1.49	Yes	Yes	No	1203	1.97	0.04	79.34	180.59
10188	TNK2	-1.05	-0.67	-1.08	-0.9	Yes	Yes	No	1151	4.43	0	332.71	1523.38
10188	TNK2	-1.05	-1.12	-1.08	-0.08	Yes	No	Yes	2098	4.43	0	332.71	1523.38
10188	TNK2	-1.05	-0.76	-1.08	-1.69	Yes	No	No	1046	4.43	0	332.71	1523.38
10188	TNK2	-1.05	-1.08	-1.08	-0.86	No	No	Yes	1599	4.43	0	332.71	1523.38
23471	TRAM1	-1.78	-0.4	-1.72	-1.39	No	Yes	No	824	-1.5	0.00165	10737.57	7140.24
23471	TRAM1	-1.78	-1.43	-1.72	-0.22	No	No	Yes	1735	-1.5	0.00165	10737.57	7140.24
23471	TRAM1	-1.78	-1.88	-1.72	-1.55	Yes	Yes	Yes	1483	-1.5	0.00165	10737.57	7140.24
23471	TRAM1	-1.78	-1.47	-1.72	-1.56	No	Yes	Yes	1278	-1.5	0.00165	10737.57	7140.24
10131	TRAP1	-1.1	-0.99	-1.72	-1.28	No	Yes	No	1405	-1.54	0.05	531.41	355.78
10131	TRAP1	-1.1	-1.26	-1.72	-1.39	No	Yes	Yes	1487	-1.54	0.05	531.41	355.78
10131	TRAP1	-1.1	0.24	-1.72	-1.43	Yes	No	No	927	-1.54	0.05	531.41	355.78
10131	TRAP1	-1.1	1.16	-1.72	-1.02	No	No	No	911	-1.54	0.05	531.41	355.78
55809	TRERF1	-2.15	0.04	-1.48	1.59	No	No	No	1385	-2.3	2.00E-05	314.84	141.91
55809	TRERF1	-2.15	0.97	-1.48	-0.84	No	No	No	1025	-2.3	2.00E-05	314.84	141.91
55809	TRERF1	-2.15	-2.02	-1.48	-1.23	No	Yes	Yes	1850	-2.3	2.00E-05	314.84	141.91
55809	TRERF1	-2.15	-1.71	-1.48	-1.25	No	Yes	No	1141	-2.3	2.00E-05	314.84	141.91
28951	TRIB2	0.44	0.2	-0.32	-0.35	Yes	No	No	1021	2.37	0.01	64.03	184.12
28951	TRIB2	0.44	-1.33	-0.32	-0.09	No	No	No	1750	2.37	0.01	64.03	184.12
28951	TRIB2	0.44	0.88	-0.32	0.74	No	No	No	1732	2.37	0.01	64.03	184.12
28951	TRIB2	0.44	-1.03	-0.32	-2.23	Yes	Yes	No	990	2.37	0.01	64.03	184.12
9830	TRIM14	0.11	-0.15	0.02	0.86	No	No	No	1553	3.06	2.96E-13	272.13	1063.67
9830	TRIM14	0.11	-0.54	0.02	-0.46	Yes	No	No	1182	3.06	2.96E-13	272.13	1063.67
9830	TRIM14	0.11	0.37	0.02	-0.52	No	No	No	834	3.06	2.96E-13	272.13	1063.67
9830	TRIM14	0.11	3.38	0.02	1.02	Yes	No	No	779	3.06	2.96E-13	272.13	1063.67
6737	TRIM21	-2.89	-2.26	-2.02	-1.12	Yes	No	Yes	1730	1.78	1.00E-05	105.01	186.24
6737	TRIM21	-2.89	-1.53	-2.02	-1.95	Yes	Yes	Yes	1912	1.78	1.00E-05	105.01	186.24
6737	TRIM21	-2.89	0.98	-2.02	1.07	No	No	No	1679	1.78	1.00E-05	105.01	186.24
6737	TRIM21	-2.89	-2.92	-2.02	-2.68	Yes	Yes	Yes	1834	1.78	1.00E-05	105.01	186.24
166655	TRIM60	-2.09	-2.4	-0.65	-1.91	Yes	Yes	Yes	1430	1	1	39.26	96.75
166655	TRIM60	-2.09	-2.04	-0.65	-1.53	No	No	Yes	1314	1	1	39.26	96.75
166655	TRIM60	-2.09	-0.99	-0.65	0.09	No	No	Yes	2110	1	1	39.26	96.75
166655	TRIM60	-2.09	1.55	-0.65	0.99	No	No	No	1435	1	1	39.26	96.75
10907	TXNL4A	-0.12	0.73	0.17	0.73	No	No	Yes	1990	1.25	3.68E-07	7109.4	8569.69
10907	TXNL4A	-0.12	0.71	0.17	-0.16	Yes	No	No	1368	1.25	3.68E-07	7109.4	8569.69
10907	TXNL4A	-0.12	-1.1	0.17	-1.02	Yes	No	Yes	1751	1.25	3.68E-07	7109.4	8569.69
10907	TXNL4A	-0.12	-0.28	0.17	0.5	Yes	No	No	1523	1.25	3.68E-07	7109.4	8569.69
83706	URP2	-2.36	-1.87	-0.9	-0.61	Yes	No	Yes	1407	2.18	0.00115	73.38	170
83706	URP2	-2.36	-0.83	-0.9	-1.02	No	Yes	Yes	1581	2.18	0.00115	73.38	170

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84833	USMG5	-0.15	-0.22	-1.35	-1.11	Yes	Yes	No	1256	1.84	1.21E-15	7022.34	12961.08
84833	USMG5	-0.15	-0.47	-1.35	-1.37	Yes	No	No	1654	1.84	1.21E-15	7022.34	12961.08
84132	USP42	0.003	-0.42	-1.42	-1.81	Yes	Yes	No	835	1.52	0.00201	876.1	1363.96
84132	USP42	0.003	2	-1.42	-0.84	No	No	No	491	1.52	0.00201	876.1	1363.96
84132	USP42	0.003	-0.52	-1.42	-0.75	No	No	No	1708	1.52	0.00201	876.1	1363.96
84132	USP42	0.003	0.28	-1.42	-0.63	Yes	Yes	No	767	1.52	0.00201	876.1	1363.96
8875	VNN2	-0.84	-1.85	-2.07	-2.51	Yes	Yes	No	1285	4.25	2.13E-09	73.12	301.55
8875	VNN2	-0.84	-0.34	-2.07	-0.12	No	No	No	1975	4.25	2.13E-09	73.12	301.55
8875	VNN2	-0.84	0.67	-2.07	1.35	No	No	No	1520	4.25	2.13E-09	73.12	301.55
8875	VNN2	-0.84	-1.46	-2.07	-1.96	No	Yes	No	1111	4.25	2.13E-09	73.12	301.55
7483	WNT9A	0.03	0.13	-1	-0.57	No	Yes	No	1129	1	1	41.07	96.2
7483	WNT9A	0.03	-0.63	-1	-0.85	No	Yes	No	1452	1	1	41.07	96.2
56949	XAB2	0.32	0.45	-0.87	-0.76	No	No	No	753	1.1	0.61	51.13	114.19
56949	XAB2	0.32	0.12	-0.87	0.43	No	No	No	865	1.1	0.61	51.13	114.19
56949	XAB2	0.32	-0.03	-0.87	-0.96	Yes	No	No	650	1.1	0.61	51.13	114.19
56949	XAB2	0.32	-0.86	-0.87	-0.85	No	No	No	976	1.1	0.61	51.13	114.19
7511	XPNPEP1	-0.93	-1.26	-1.23	-2.03	Yes	Yes	No	891	-1.54	1.00E-04	251.14	172.24
7511	XPNPEP1	-0.93	-1.42	-1.23	-0.86	No	No	Yes	1625	-1.54	1.00E-04	251.14	172.24
7511	XPNPEP1	-0.93	0.35	-1.23	-1.1	No	No	No	962	-1.54	1.00E-04	251.14	172.24
7511	XPNPEP1	-0.93	-0.8	-1.23	-0.29	No	No	No	2013	-1.54	1.00E-04	251.14	172.24
7514	XPO1	-1.12	0.44	-1.81	-1.12	No	No	No	1118	-2.96	5.00E-06	1900.77	619.57
7514	XPO1	-1.12	-1.3	-1.81	-1.33	Yes	No	Yes	1354	-2.96	5.00E-06	1900.77	619.57
7514	XPO1	-1.12	-0.39	-1.81	-1.45	No	No	No	1200	-2.96	5.00E-06	1900.77	619.57
7514	XPO1	-1.12	-0.94	-1.81	-1.61	Yes	Yes	Yes	1644	-2.96	5.00E-06	1900.77	619.57
57621	ZBTB2	-1.05	-0.54	-1.29	-0.07	Yes	No	No	1951	-1.52	5.89E-07	207.72	136.89
57621	ZBTB2	-1.05	-1.41	-1.29	-1.33	Yes	No	No	1970	-1.52	5.89E-07	207.72	136.89
256112	ZNF37B	-1.31	-1.09	-2.05	-1.63	Yes	No	No	859	1	1	68.64	104.31
256112	ZNF37B	-1.31	0.005	-2.05	-1.47	Yes	No	No	1048	1	1	68.64	104.31
84450	ZNF512	0.75	0.7	-1.68	-1.36	Yes	Yes	No	808	-2.74	2.49E-13	396.8	146.72
84450	ZNF512	0.75	-0.33	-1.68	-1.35	Yes	No	No	1386	-2.74	2.49E-13	396.8	146.72

Target Gene Information			siRNA				Viability Assay			
Gene symbol	GeneID	Official full name	siRNA1 ID	siRNA2 ID	siRNA3 ID	siRNA4 ID	siRNA1	siRNA2	siRNA3	siRNA4
AHCYL1	10768	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	Hs_AHCYL1_4	Hs_AHCYL1_2	Hs_AHCYL1_3	Hs_AHCYL1_1	1.36	1.47	1.55	1.71
AKTIP	64400	AKT interacting protein	Hs_FTS_1	Hs_FTS_2	Hs_FTS_3	Hs_FTS_4	1.62	1.68	1.81	1.76
AP2M1	1173	adaptor-related protein complex 2, mu 1 subunit	Hs_AP2M1_7	Hs_AP2M1_3	Hs_AP2M1_5	Hs_AP2M1_6	1.61	1.51	1.57	1.59
APBB1IP	54518	AMYLOID BETA (A4) PRECURSOR PROTEIN-BINDING, FAMILY B, MEMBER 1 INTERACTING PROTEIN	Hs_APBB1IP_3	Hs_APBB1IP_8	Hs_APBB1IP_7	Hs_APBB1IP_6	1.82	1.86	1.91	1.9
ARD1A	8260	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	Hs_ARD1_1	Hs_ARD1_3	Hs_ARD1_5	Hs_ARD1A_1	1.81	1.83	1.72	1.88
ARTN	9048	ARTEMIN	Hs_ARTN_8	Hs_ARTN_7	Hs_ARTN_9	Hs_ARTN_1	1.57	1.38	1.63	1.68
ATCAY	85300	ATAXIA, CEREBELLAR, CAYMAN TYPE (CAYTAXIN)	Hs_ATCAY_2	Hs_ATCAY_3	Hs_ATCAY_4	Hs_ATCAY_5	1.82	1.81	1.9	1.83
ATP1A2	477	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	Hs_ATP1A2_2	Hs_ATP1A2_3	Hs_ATP1A2_4	Hs_ATP1A2_5	1.65	1.67	1.64	1.61
ATP2C1	27032	ATPASE, CA++ TRANSPORTING, TYPE 2C, MEMBER 1	Hs_ATP2C1_2	Hs_ATP2C1_7	Hs_ATP2C1_6	Hs_ATP2C1_5	1.82	1.7	1.79	1.85
ATP6AP1	537	ATPase, H+ transporting, lysosomal accessory protein 1	Hs_ATP6AP1_5	Hs_ATP6AP1_6	Hs_ATP6AP1_7	Hs_ATP6AP1_8	1.62	1.63	1.69	1.7
ATP6AP2	10159	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	Hs_ATP6AP2_7	Hs_ATP6AP2_8	Hs_ATP6AP2_6	Hs_ATP6AP2_4	1.84	1.87	1.93	1.84
ATP6V0C	527	ATPASE, H+ TRANSPORTING, LYSOSOMAL 16KDA, V0 SUBUNIT C	Hs_ATP6V0C_7	Hs_ATP6V0C_8	Hs_ATP6V0C_6	Hs_ATP6V0C_5	1.83	1.91	1.88	1.85
ATP6V0D1	9114	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	Hs_ATP6V0D1_1	Hs_ATP6V0D1_2	Hs_ATP6V0D1_3	Hs_ATP6V0D1_4	1.66	1.46	1.84	1.78
ATP6V1A	523	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	Hs_ATP6V1A_1	Hs_ATP6V1A_3	Hs_ATP6V1A_2	Hs_ATP6V1A_4	1.9	1.93	1.91	1.86
ATP6V1B2	526	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	Hs_ATP6V1B2_2	Hs_ATP6V1B2_4	Hs_ATP6V1B2_5	Hs_ATP6V1B2_6	1.55	1.55	1.8	1.89
B2M	567	beta-2-microglobulin	Hs_B2M_3	Hs_B2M_4	Hs_B2M_5	Hs_B2M_6	1.34	1.35	1.57	1.59
BAIAP3	8938	BAI1-associated protein 3	Hs_BAIAP3_1	Hs_BAIAP3_2	Hs_BAIAP3_5	Hs_BAIAP3_6	1.71	1.78	1.77	1.84
BARHL2	343472	BARH-LIKE 2 (DROSOPHILA)	Hs_BARHL2_3	Hs_BARHL2_7	Hs_BARHL2_6	Hs_BARHL2_4	1.77	1.9	1.88	1.82
BZRAP1	9256	benzodiazapine receptor (peripheral) associated protein 1	Hs_BZRAP1_1	Hs_BZRAP1_2	Hs_BZRAP1_4	Hs_BZRAP1_5	1.8	1.63	1.55	1.86
C14orf172	115708	CHROMOSOME 14 OPEN READING FRAME 172	Hs_C14orf172_1	Hs_C14orf172_4	Hs_C14orf172_3	Hs_C14orf172_2	1.77	1.8	1.91	1.79
C21orf7	56911	chromosome 21 open reading frame 7	Hs_C21orf7_1	Hs_C21orf7_2	Hs_C21orf7_3	Hs_C21orf7_4	1.63	1.57	1.62	1.58
C3orf31	132001	chromosome 3 open reading frame 31	Hs_C3orf31_1	Hs_C3orf31_2	Hs_C3orf31_3	Hs_C3orf31_4	1.7	1.63	1.72	1.73
CCNB3	85417	cyclin B3	Hs_CCNB3_7	Hs_CCNB3_6	Hs_CCNB3_8	NA	1.5	1.52	1.49	NA
CD48	962	CD48 molecule	Hs_CD48_1	Hs_CD48_2	Hs_CD48_3	Hs_CD48_4	1.46	1.48	1.37	1.64
CD58	965	CD58 molecule	Hs_CD58_2	Hs_CD58_5	Hs_CD58_6	NA	1.88	1.86	1.84	NA
CD81	975	CD81 molecule	Hs_CD81_10	Hs_CD81_11	Hs_CD81_8	Hs_CD81_9	1.55	1.36	1.53	1.64
CDKN1B	1027	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	Hs_CDKN1B_6	Hs_CDKN1B_3	Hs_CDKN1B_8	Hs_CDKN1B_7	1.86	1.89	1.86	1.84
CEL	1056	carboxyl ester lipase (bile salt-stimulated lipase)	Hs_CEL_1	Hs_CEL_3	Hs_CEL_5	Hs_CEL_6	1.58	1.72	1.56	1.52
CHST5	23563	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	Hs_CHST5_2	Hs_CHST5_5	Hs_CHST5_7	Hs_CHST5_8	1.47	1.45	1.48	1.44
CLIC4	25932	chloride intracellular channel 4	Hs_CLIC4_5	Hs_CLIC4_2	Hs_CLIC4_3	Hs_CLIC4_4	1.77	1.77	1.68	1.62
CLK1	1195	CDC-LIKE KINASE 1	Hs_CLK1_1	Hs_CLK1_11	Hs_CLK1_2	Hs_CLK1_6	1.89	1.92	1.89	1.85
CLSTN3	9746	calsyntenin 3	Hs_CLSTN3_1	Hs_CLSTN3_2	Hs_CLSTN3_4	Hs_CLSTN3_5	1.7	1.76	1.87	1.84
CNNM1	26507	cyclin M1	Hs_CNNM1_3	Hs_CNNM1_5	Hs_CNNM1_6	Hs_CNNM1_7	1.72	1.76	1.71	1.39
COPA	1314	coatomer protein complex, subunit alpha	Hs_COPA_5	Hs_COPA_6	Hs_COPA_7	NA	1.73	1.75	1.8	NA
COPB1	1315	coatomer protein complex, subunit beta 1	Hs_COPB_5	Hs_COPB1_4	Hs_COPB1_5	NA	1.69	1.65	1.74	NA
COPB2	9276	coatomer protein complex, subunit beta 2 (beta prime)	Hs_COPB2_6	Hs_COPB2_7	Hs_COPB2_1	Hs_COPB2_3	1.56	1.48	1.43	1.63
COPG	22820	coatomer protein complex, subunit gamma	Hs_COPG_1	Hs_COPG_5	Hs_COPG_6	Hs_COPG_7	1.6	1.3	1.66	1.67
CRAMP1L	57585	Crm, cramped-like (Drosophila)	Hs_CRAMP1L_1	Hs_CRAMP1L_2	Hs_CRAMP1L_7	Hs_CRAMP1L_8	1.64	1.5	1.85	1.81
CRYAA	1409	crystallin, alpha A	Hs_CRYAA_1	Hs_CRYAA_2	Hs_CRYAA_3	Hs_CRYAA_4	1.8	1.7	1.76	1.77
CXCR6	10663	chemokine (C-X-C motif) receptor 6	Hs_CXCR6_1	Hs_CXCR6_2	Hs_CXCR6_3	Hs_CXCR6_4	1.83	1.79	1.8	1.83
CYP17A1	1586	cytochrome P450, family 17, subfamily A, polypeptide 1	Hs_CYP17A1_1	Hs_CYP17A1_2	Hs_CYP17A1_3	Hs_CYP17A1_5	1.85	1.87	1.84	1.82
CYP2U1	113612	cytochrome P450, family 2, subfamily U, polypeptide 1	Hs_CYP2U1_1	Hs_CYP2U1_2	Hs_CYP2U1_3	Hs_CYP2U1_5	1.44	1.58	1.46	1.49
DBT	1629	dihydrolipoamide branched chain transacylase E2	Hs_DBT_2	Hs_DBT_4	Hs_DBT_5	Hs_DBT_6	1.7	1.36	1.63	1.67
DCLK2	166614	doublecortin-like kinase 2	Hs_DCAMKL2_2	Hs_DCAMKL2_3	Hs_DCAMKL2_5	Hs_DCAMKL2_6	1.57	1.58	1.68	1.65
DHRS2	10202	dehydrogenase/reductase (SDR family) member 2	Hs_DHRS2_8	Hs_DHRS2_9	Hs_DHRS2_3	Hs_DHRS2_5	1.65	1.78	1.77	1.64
DLG2	1740	discs, large homolog 2 (Drosophila)	Hs_DLG2_2	Hs_DLG2_5	NA	NA	1.8	1.79	NA	NA
DMAP1	55929	DNA METHYLTRANSFERASE 1 ASSOCIATED PROTEIN 1	Hs_DMAP1_6	Hs_DMAP1_5	Hs_DMAP1_4	Hs_DMAP1_3	1.83	1.87	1.91	1.82
DTX3	196403	deltex homolog 3 (Drosophila)	Hs_DTX3_4	Hs_DTX3_5	Hs_DTX3_6	Hs_DTX3_7	1.67	1.75	1.67	1.67
DUSP27	92235	dual specificity phosphatase 27 (putative)	Hs_DUSP27_1	Hs_DUSP27_2	Hs_DUSP27_3	Hs_DUSP27_4	1.85	1.81	1.7	1.54
EEF1A1	1915	eukaryotic translation elongation factor 1 alpha 1	Hs_EEF1A1_10	Hs_EEF1A1_11	Hs_EEF1A1_12	Hs_EEF1A1_9	1.76	1.75	1.87	1.64
EIF3A	8661	eukaryotic translation initiation factor 3, subunit A	Hs_EIF3S10_6	Hs_EIF3S10_2	Hs_EIF3S10_7	Hs_EIF3S10_8	1.69	1.72	1.75	1.69
EIF3C	8663	eukaryotic translation initiation factor 3, subunit C	Hs_EIF3S8_5	Hs_EIF3S8_6	Hs_EIF3C_1	Hs_EIF3C_2	1.62	1.52	1.36	1.44
EIF3G	8666	eukaryotic translation initiation factor 3, subunit G	Hs_EIF3S4_1	Hs_EIF3S4_10	Hs_EIF3S4_2	NA	1.71	1.47	1.63	NA
EIF4A3	9775	eukaryotic translation initiation factor 4A, isoform 3	Hs_DDX48_3	Hs_DDX48_4	Hs_DDX48_5	Hs_DDX48_6	1.65	1.77	1.71	1.77
ENGASE	64772	endo-beta-N-acetylglucosaminidase	Hs_FLJ21865_1	Hs_FLJ21865_5	Hs_FLJ21865_6	Hs_FLJ21865_7	1.6	1.53	1.47	1.64
EPHB6	2051	EPH RECEPTOR B6	Hs_EPHB6_3	Hs_EPHB6_4	Hs_EPHB6_6	Hs_EPHB6_10	1.86	1.77	1.94	1.85
FAU	2197	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	Hs_FAU_2	Hs_FAU_4	Hs_FAU_5	NA	1.6	1.45	1.49	NA
FBXW10	10517	F-box and WD repeat domain containing 10	Hs_FBXW10_11	Hs_FBXW10_3	Hs_FBXW10_6	Hs_FBXW10_7	1.56	1.45	1.48	1.66
FCHO2	115548	FCH DOMAIN ONLY 2	Hs_FCHO2_3	Hs_FCHO2_8	Hs_FCHO2_7	Hs_FCHO2_4	1.61	1.43	1.69	1.82

Target Gene Information			siRNA				Viability Assay			
Gene symbol	GeneID	Official full name	siRNA1 ID	siRNA2 ID	siRNA3 ID	siRNA4 ID	siRNA1	siRNA2	siRNA3	siRNA4
FERMT3	83706	fermitin family homolog 3 (Drosophila)	Hs_URP2_4	Hs_URP2_5	Hs_URP2_6	Hs_URP2_7	1.74	1.73	1.73	1.75
FLJ11235	54508	hypothetical FLJ11235	Hs_FLJ11235_1	Hs_FLJ11235_2	Hs_FLJ11235_3	Hs_FLJ11235_4	1.8	1.85	1.85	1.82
GCLC	2729	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	Hs_GCLC_4	Hs_GCLC_7	Hs_GCLC_10	Hs_GCLC_11	1.78	1.78	1.83	1.83
GNRH2	2797	GONADOTROPIN-RELEASING HORMONE 2	Hs_GNRH2_8	Hs_GNRH2_7	Hs_GNRH2_6	Hs_GNRH2_5	1.83	1.64	1.85	1.9
GPR146	115330	G protein-coupled receptor 146	Hs_GPR146_1	Hs_GPR146_3	Hs_GPR146_4	Hs_GPR146_5	1.65	1.55	1.61	1.7
GRIN2C	2905	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	Hs_GRIN2C_1	Hs_GRIN2C_2	Hs_GRIN2C_3	Hs_GRIN2C_5	1.75	1.75	1.79	1.83
HARBI1	9776	KIAA0652	Hs_KIAA0652_7	Hs_KIAA0652_3	Hs_KIAA0652_4	Hs_KIAA0652_5	1.51	1.46	1.77	1.74
HIST1H2BN	8341	histone cluster 1, H2bn	Hs_HIST1H2BN_10	Hs_HIST1H2BN_2	Hs_HIST1H2BN_4	Hs_HIST1H2BN_9	1.76	1.69	1.64	1.67
HPGD	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)	Hs_HPGD_1	Hs_HPGD_2	Hs_HPGD_3	Hs_HPGD_4	1.73	1.77	1.83	1.83
HSF4	3299	heat shock transcription factor 4	Hs_HSF4_1	Hs_HSF4_2	Hs_HSF4_3	Hs_HSF4_4	1.82	1.86	1.72	1.81
HSPD1	3329	heat shock 60kDa protein 1 (chaperonin)	Hs_HSPD1_5	Hs_HSPD1_7	Hs_HSPD1_8	Hs_HSPD1_1	1.63	1.53	1.71	1.67
IL17RA	23765	interleukin 17 receptor A	Hs_IL17R_1	Hs_IL17R_2	Hs_IL17RA_1	Hs_IL17RA_2	1.77	1.81	1.8	1.78
IL1A	3552	interleukin 1, alpha	Hs_IL1A_1	Hs_IL1A_2	Hs_IL1A_3	Hs_IL1A_4	1.59	1.58	1.67	1.43
IRF2	3660	INTERFERON REGULATORY FACTOR 2	Hs_IRF2_2	Hs_IRF2_3	Hs_IRF2_1	Hs_IRF2_4	1.68	1.6	1.59	1.88
ISG15	9636	ISG15 ubiquitin-like modifier	Hs_G1P2_1	Hs_ISG15_1	Hs_ISG15_3	NA	1.69	1.82	1.79	NA
ITLN1	55600	intelectin 1 (galactofuranose binding)	Hs_ITLN1_1	Hs_ITLN1_3	Hs_ITLN1_4	Hs_ITLN1_5	1.79	1.74	1.77	1.72
JUN	3725	jun oncogene	Hs_JUN_5	Hs_JUN_1	Hs_JUN_2	Hs_JUN_3	1.46	1.47	1.57	1.52
KATNB1	10300	katanin p80 (WD repeat containing) subunit B 1	Hs_KATNB1_1	Hs_KATNB1_2	Hs_KATNB1_3	Hs_KATNB1_4	1.46	1.38	1.38	1.55
KCNJ12	3768	potassium inwardly-rectifying channel, subfamily J, member 12	Hs_KCNJ12_2	Hs_KCNJ12_4	Hs_KCNJ12_5	Hs_KCNJ12_6	1.64	1.65	1.34	1.49
KIAA0664	23277	KIAA0664	Hs_KIAA0664_2	Hs_KIAA0664_3	Hs_KIAA0664_4	Hs_KIAA0664_5	1.59	1.71	1.7	1.75
KIAA1267	284058	DKFZP727C091 PROTEIN	Hs_LOC284058_3	Hs_KIAA1267_2	Hs_LOC284058_4	Hs_KIAA1267_1	1.7	1.88	1.9	1.74
KIF11	3832	kinesin family member 11	Hs_KIF11_6	Hs_KIF11_7	Hs_KIF11_8	Hs_KIF11_14	1.37	1.42	1.46	1.76
KPNB1	3837	KARYOPHERIN (IMPORTIN) BETA 1	Hs_KPNB1_2	Hs_KPNB1_3	Hs_KPNB1_6	Hs_KPNB1_4	1.73	1.71	1.84	1.68
LARP1	23367	La ribonucleoprotein domain family, member 1	Hs_LARP_4	Hs_LARP1_1	Hs_LARP1_2	Hs_LARP1_3	1.67	1.54	1.7	1.66
LHX3	8022	LIM homeobox 3	Hs_LHX3_2	Hs_LHX3_3	Hs_LHX3_4	Hs_LHX3_5	1.64	1.71	1.72	1.5
LINGO1	84894	leucine rich repeat and Ig domain containing 1	Hs_LRRN6A_1	Hs_LRRN6A_4	Hs_LRRN6A_5	Hs_LRRN6A_6	1.47	1.68	1.72	1.62
LONP1	9361	lon peptidase 1, mitochondrial	Hs_PRSS15_1	Hs_PRSS15_2	Hs_PRSS15_4	Hs_PRSS15_5	1.68	1.85	1.9	1.85
LPPR4	9890	plasticity related gene 1	Hs_LPPR4_6	Hs_LPPR4_7	Hs_LPPR4_8	Hs_LPPR4_9	1.81	1.86	1.78	1.78
MAN2B1	4125	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	Hs_MAN2B1_4	Hs_MAN2B1_2	Hs_MAN2B1_3	Hs_MAN2B1_5	1.86	1.81	1.92	1.81
MATN3	4148	matrilin 3	Hs_MATN3_1	Hs_MATN3_2	Hs_MATN3_3	Hs_MATN3_5	1.77	1.75	1.82	1.75
MED6	10001	mediator complex subunit 6	Hs_MED6_1	Hs_MED6_2	Hs_MED6_6	Hs_MED6_7	1.67	1.54	1.53	1.71
MORG1	84292	MITOGEN-ACTIVATED PROTEIN KINASE ORGANIZER 1	Hs_MGC4238_3	Hs_MORG1_3	Hs_MORG1_2	Hs_MGC4238_4	1.82	1.64	1.85	1.81
MYC	4609	v-myc myelocytomatosis viral oncogene homolog (avian)	Hs_MYC_5	Hs_MYC_7	Hs_LOC731404_4	Hs_MYC_1	1.69	1.72	1.76	1.63
MYOD1	4654	myogenic differentiation 1	Hs_MYOD1_1	Hs_MYOD1_3	Hs_MYOD1_4	Hs_MYOD1_5	1.69	1.67	1.69	1.7
NEK8	284086	NIMA (never in mitosis gene a)- related kinase 8	Hs_NEK8_5	Hs_NEK8_6	Hs_NEK8_10	NA	1.66	1.7	1.57	NA
NEK9	91754	NIMA (never in mitosis gene a)- related kinase 9	Hs_NEK9_7	Hs_NEK9_10	Hs_NEK9_11	Hs_NEK9_2	1.81	1.77	1.84	1.79
NTHL1	4913	nth endonuclease III-like 1 (E. coli)	Hs_NTHL1_3	Hs_NTHL1_4	Hs_NTHL1_5	Hs_NTHL1_6	1.85	1.84	1.83	1.71
NUP205	23165	nucleoporin 205kDa	Hs_NUP205_3	Hs_NUP205_4	Hs_NUP205_8	Hs_NUP205_9	1.72	1.57	1.79	1.79
NUP98	4928	nucleoporin 98kDa	Hs_NUP98_3	Hs_NUP98_5	Hs_NUP98_7	Hs_NUP98_8	1.79	1.83	1.87	1.8
NXF1	10482	nuclear RNA export factor 1	Hs_NXF1_1	Hs_NXF1_2	Hs_NXF1_3	Hs_NXF1_4	1.66	1.57	1.55	1.64
OPN1SW	611	opsin 1 (cone pigments), short-wave-sensitive	Hs_OPN1SW_1	Hs_OPN1SW_2	Hs_OPN1SW_3	Hs_OPN1SW_4	1.76	1.84	1.79	1.87
PCDH18	54510	protocadherin 18	Hs_PCDH18_1	Hs_PCDH18_2	Hs_PCDH18_3	Hs_PCDH18_4	1.6	1.66	1.68	1.65
PHF2	5253	PHD FINGER PROTEIN 2	Hs_PHF2_3	Hs_PHF2_4	Hs_PHF2_5	Hs_PHF2_6	1.72	1.82	1.89	1.68
PIK3R5	23533	phosphoinositide-3-kinase, regulatory subunit 5	Hs_PIK3R5_2	Hs_PIK3R5_3	Hs_PIK3R5_4	NA	1.83	1.84	1.88	NA
PIN1	5300	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	Hs_PIN1_5	Hs_PIN1_6	Hs_PIN1_3	Hs_PIN1_4	1.66	1.65	1.72	1.51
PLAU	5328	PLASMINOGEN ACTIVATOR, UROKINASE	Hs_PLAU_2	Hs_PLAU_10	Hs_PLAU_11	Hs_PLAU_4	1.76	1.78	1.84	1.69
PLD2	5338	phospholipase D2	Hs_PLD2_2	Hs_PLD2_3	Hs_PLD2_5	Hs_PLD2_6	1.78	1.83	1.9	1.83
PLK3	1263	polo-like kinase 3 (Drosophila)	Hs_PLK3_5	Hs_PLK3_6	Hs_PLK3_7	Hs_PLK3_8	1.6	1.82	1.76	1.81
POLR2H	5437	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE H	Hs_POLR2H_2	Hs_POLR2H_3	Hs_POLR2H_4	Hs_POLR2H_5	1.39	1.43	1.79	1.65
POLR2L	5441	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	Hs_POLR2L_1	Hs_POLR2L_2	Hs_POLR2L_3	Hs_POLR2L_4	1.68	1.59	1.76	1.72
PPP1R14D	54866	protein phosphatase 1, regulatory (inhibitor) subunit 14D	Hs_PPP1R14D_1	Hs_PPP1R14D_2	Hs_PPP1R14D_5	Hs_PPP1R14D_6	1.72	1.82	1.76	1.85
PRPF8	10594	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	Hs_PRPF8_2	Hs_PRPF8_3	Hs_PRPF8_4	Hs_PRPF8_5	1.46	1.6	1.67	1.74
PRPS1	5631	phosphoribosyl pyrophosphate synthetase 1	Hs_PRPS1_1	Hs_PRPS1_3	Hs_PRPS1_4	Hs_PRPS1_5	1.7	1.79	1.67	1.76
PRSS27	83886	protease, serine 27	Hs_MPN_1	Hs_MPN_2	Hs_PRSS27_1	Hs_PRSS27_2	1.82	1.88	1.78	1.78
PSENEN	55851	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	Hs_PEN2_1	Hs_PEN2_6	Hs_PSENEN_1	Hs_PEN2_3	1.72	1.62	1.74	1.87
PSMA1	5682	proteasome (prosome, macropain) subunit, alpha type, 1	Hs_PSMA1_1	Hs_PSMA1_12	Hs_PSMA1_3	NA	1.72	1.86	1.79	NA
PSMD14	10213	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Hs_PSMD14_1	Hs_PSMD14_3	Hs_PSMD14_4	Hs_PSMD14_5	1.68	1.53	1.65	1.67
PSMD2	5708	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Hs_PSMD2_5	Hs_PSMD2_6	Hs_PSMD2_2	Hs_PSMD2_4	1.53	1.34	1.47	1.27
PTPRN	5798	protein tyrosine phosphatase, receptor type, N	Hs_PTPRN_3	Hs_PTPRN_4	Hs_PTPRN_5	Hs_PTPRN_6	1.65	1.76	1.86	1.82

Target Gene Information			siRNA				Viability Assay			
Gene symbol	GeneID	Official full name	siRNA1 ID	siRNA2 ID	siRNA3 ID	siRNA4 ID	siRNA1	siRNA2	siRNA3	siRNA4
RAB6B	51560	RAB6B, member RAS oncogene family	Hs_RAB6B_2	Hs_RAB6B_3	Hs_RAB6B_4	Hs_RAB6B_6	1.59	1.58	1.59	1.8
RACGAP1	29127	RAC GTPASE ACTIVATING PROTEIN 1	Hs_RACGAP1_1	Hs_RACGAP1_5	Hs_RACGAP1_3	Hs_RACGAP1_4	1.56	1.64	1.54	1.88
RBM42	79171	RNA binding motif protein 42	Hs_MGC10433_1	Hs_MGC10433_2	Hs_MGC10433_4	Hs_MGC10433_5	1.63	1.78	1.89	1.83
RETN	56729	RESISTIN	Hs_RETN_3	Hs_RETN_2	Hs_RETN_5	NA	1.77	1.83	1.8	NA
RFFL	117584	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	Hs_RFFL_4	Hs_RFFL_1	Hs_RFFL_3	Hs_RFFL_5	1.75	1.68	1.92	1.88
RNF150	57484	ring finger protein 150	Hs_RNF150_3	Hs_RNF150_5	Hs_RNF150_6	Hs_RNF150_7	1.76	1.7	1.82	1.68
RPL35	11224	ribosomal protein L35	Hs_RPL35_5	Hs_RPL35_6	Hs_RPL35_3	Hs_RPL35_4	1.53	1.61	1.48	1.31
RPS10	6204	ribosomal protein S10	Hs_RPS10_2	Hs_RPS10_5	Hs_RPS10_7	Hs_RPS10_8	1.69	1.59	1.55	1.67
RPS14	6208	ribosomal protein S14	Hs_RPS14_4	Hs_RPS14_6	Hs_RPS14_8	Hs_RPS14_9	1.57	1.65	1.73	1.55
RPS16	6217	RIBOSOMAL PROTEIN S16	Hs_RPS16_5	Hs_RPS16_8	Hs_RPS16_7	Hs_RPS16_6	1.49	1.51	1.76	1.49
RPS27A	6233	ribosomal protein S27a	Hs_RPS27A_2	Hs_RPS27A_3	Hs_RPS27A_7	NA	1.46	1.39	1.42	NA
RPS5	6193	ribosomal protein S5	Hs_RPS5_2	Hs_RPS5_5	Hs_RPS5_6	Hs_RPS5_7	1.33	1.31	1.3	1.2
RUNX1	861	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE;	Hs_RUNX1_5	Hs_RUNX1_4	Hs_RUNX1_6	Hs_RUNX1_2	1.82	1.86	1.92	1.84
SAFB	6294	scaffold attachment factor B	Hs_SAFB_1	Hs_SAFB_3	Hs_SAFB_4	Hs_SAFB_5	1.79	1.78	1.73	1.83
SELPLG	6404	selectin P ligand	Hs_SELPLG_2	Hs_SELPLG_3	Hs_SELPLG_4	Hs_SELPLG_5	1.88	1.85	1.86	1.84
SF3A1	10291	splicing factor 3a, subunit 1, 120kDa	Hs_SF3A1_1	Hs_SF3A1_2	Hs_SF3A1_3	Hs_SF3A1_5	1.63	1.8	1.88	1.69
SF3B1	23451	splicing factor 3b, subunit 1, 155kDa	Hs_SF3B1_4	Hs_SF3B1_5	Hs_SF3B1_6	Hs_SF3B1_7	1.65	1.6	1.46	1.41
SF3B14	51639	splicing factor 3B, 14 kDa subunit	Hs_SF3B14_2	Hs_SF3B14_5	Hs_SF3B14_6	Hs_SF3B14_7	1.8	1.72	1.72	1.83
SFTPB	6439	surfactant protein B	Hs_SFTPB_15	Hs_SFTPB_16	Hs_SFTPB_17	Hs_SFTPB_4	1.76	1.82	1.84	1.5
SIGMAR1	10280	sigma non-opioid intracellular receptor 1	Hs_OPRS1_1	Hs_OPRS1_3	Hs_OPRS1_4	Hs_OPRS1_5	1.45	1.54	1.58	1.49
SLC22A6	9356	solute carrier family 22 (organic anion transporter), member 6	Hs_SLC22A6_3	Hs_SLC22A6_6	Hs_SLC22A6_7	Hs_SLC22A6_8	1.87	1.75	1.87	1.85
SMU1	55234	SMU-1 SUPPRESSOR OF MEC-8 AND UNC-52 HOMOLOG (C. ELEGANS)	Hs_SMU1_7	Hs_LOC728623_1	Hs_LOC728623_2	Hs_SMU1_6	1.82	1.84	1.86	1.83
SNRP70	6625	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	Hs_SNRP70_2	Hs_SNRP70_3	Hs_SNRP70_4	Hs_SNRP70_5	1.59	1.54	1.65	1.71
SNRPF	6636	small nuclear ribonucleoprotein polypeptide F	Hs_SNRPF_6	Hs_SNRPF_7	Hs_SNRPF_8	Hs_SNRPF_9	1.43	1.6	1.49	1.59
SNW1	22938	SNW domain containing 1	Hs_SKIIP_5	Hs_SKIIP_6	Hs_SKIIP_7	Hs_SNW1_2	1.29	1.43	1.63	1.71
SNX6	58533	SORTING NEXIN 6	Hs_SNX6_10	Hs_SNX6_11	Hs_SNX6_4	Hs_SNX6_3	1.83	1.88	1.85	1.81
SNX9	51429	sorting nexin 9	Hs_SNX9_1	Hs_SNX9_2	Hs_SNX9_3	Hs_SNX9_4	1.54	1.83	1.89	1.83
SON	6651	SON DNA binding protein	Hs_SON_2	Hs_SON_4	Hs_SON_5	Hs_SON_6	1.31	1.31	1.32	1.21
SRRM2	23524	SERINE/ARGININE REPETITIVE MATRIX 2	Hs_SRRM2_4	Hs_SRRM2_7	Hs_SRRM2_5	Hs_SRRM2_3	1.85	1.62	1.76	1.89
STAB1	23166	stabilin 1	Hs_STAB1_1	Hs_STAB1_2	Hs_STAB1_3	Hs_STAB1_4	1.48	1.47	1.55	1.47
SULF2	55959	sulfatase 2	Hs_SULF2_10	Hs_SULF2_5	Hs_SULF2_6	Hs_SULF2_9	1.67	1.79	1.87	1.85
SUPT6H	6830	suppressor of Ty 6 homolog (S. cerevisiae)	Hs_SUPT6H_5	Hs_SUPT6H_6	Hs_SUPT6H_7	Hs_SUPT6H_8	1.51	1.58	1.62	1.64
TBL3	10607	TRANSDUCIN (BETA)-LIKE 3	Hs_TBL3_4	Hs_TBL3_3	Hs_TBL3_5	Hs_TBL3_6	1.75	1.83	1.87	1.78
TCF3	6929	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47;	Hs_TCF3_1	Hs_TCF3_5	NA	NA	1.71	1.72	NA	NA
TFE3	7030	transcription factor binding to IGHM enhancer 3	Hs_TFE3_1	Hs_TFE3_2	Hs_TFE3_3	Hs_TFE3_4	1.82	1.74	1.7	1.68
TNFRSF18	8784	tumor necrosis factor receptor superfamily, member 18	Hs_TNFRSF18_2	Hs_TNFRSF18_4	Hs_TNFRSF18_5	Hs_TNFRSF18_6	1.58	1.58	1.74	1.75
TNK2	10188	tyrosine kinase, non-receptor, 2	Hs_TNK2_4	Hs_TNK2_5	Hs_TNK2_6	Hs_TNK2_8	1.74	1.87	1.9	1.81
TRERF1	55809	transcriptional regulating factor 1	Hs_TRERF1_3	Hs_TRERF1_6	Hs_TRERF1_7	Hs_TRERF1_8	1.81	1.8	1.57	1.78
TRIM14	9830	tripartite motif-containing 14	Hs_TRIM14_1	Hs_TRIM14_5	Hs_TRIM14_6	Hs_TRIM14_7	1.52	1.53	1.49	1.57
TRIM21	6737	tripartite motif-containing 21	Hs_TRIM21_11	Hs_TRIM21_6	Hs_TRIM21_7	Hs_TRIM21_8	1.69	1.83	1.89	1.84
TRIM60	166655	tripartite motif-containing 60	Hs_TRIM60_3	Hs_TRIM60_6	Hs_TRIM60_7	Hs_TRIM60_8	1.78	1.83	1.82	1.83
TSSK6	83983	testis-specific serine kinase 6	Hs_SSTK_2	Hs_SSTK_3	Hs_SSTK_4	Hs_TSSK6_1	1.56	1.48	1.57	1.72
TXNL4A	10907	thioredoxin-like 4A	Hs_TXNL4A_1	Hs_TXNL4A_3	Hs_TXNL4A_5	Hs_TXNL4A_6	1.62	1.43	1.64	1.74
UBAC2	337867	UBA domain containing 2	Hs_PHGDHL1_5	Hs_PHGDHL1_6	NA	NA	1.89	1.85	NA	NA
VNN2	8875	VANIN 2	Hs_VNN2_1	Hs_VNN2_4	Hs_VNN2_2	Hs_VNN2_9	1.83	1.82	1.88	1.82
WNT9A	7483	wingless-type MMTV integration site family, member 9A	Hs_WNT9A_1	Hs_WNT9A_2	Hs_WNT9A_3	Hs_WNT9A_4	1.4	1.53	1.62	1.45
XAB2	56949	XPA binding protein 2	Hs_XAB2_5	Hs_XAB2_6	Hs_XAB2_4	NA	1.65	1.68	1.78	NA
XPNPEP1	7511	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Hs_XPNPEP1_1	Hs_XPNPEP1_2	Hs_XPNPEP1_3	Hs_XPNPEP1_4	1.74	1.84	1.82	1.82
XPO1	7514	exportin 1 (CRM1 homolog, yeast)	Hs_XPO1_1	Hs_XPO1_2	Hs_XPO1_5	Hs_XPO1_6	1.64	1.83	1.84	1.8
ZBTB2	57621	zinc finger and BTB domain containing 2	Hs_ZBTB2_1	Hs_ZBTB2_2	Hs_ZBTB2_3	Hs_ZBTB2_4	1.8	1.89	1.84	1.83

		A/WSN/33 Validation Data						A/Hamburg/04/09 Validation Data				
Gene symbol	GeneID	siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene		siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene
AHCYL1	10768	0.69	0.8	-0.16	0.28	0		0.81	0.82	0.17	0.32	2
AKTIP	64400	0.97	0.87	0.38	0.28	2		0.98	0.6	0.29	1.06	2
AP2M1	1173	0.86	0.92	0.81	0.62	3		0.89	0.26	0.45	0.94	2
APBB1IP	54518	0.42	-1.76	0.24	-0.1	0		1.12	0.62	-0.19	0.9	2
ARD1A	8260	1	0.99	0.87	0.86	4		1	1.05	0.92	1	4
ARTN	9048	0.49	1	-0.37	0.97	2		0.59	1.11	0.17	-2.23	1
ATCAY	85300	0.92	0.85	-0.64	-0.8	2		-0.44	1.13	0.44	1.04	2
ATP1A2	477	-0.04	1	0.76	0.87	2		0.35	0.83	0.64	-239.08	1
ATP2C1	27032	0.61	-0.33	-0.78	0.74	0		0.94	0.12	0.04	1.04	2
ATP6AP1	537	1	0.78	0.98	0.92	3		1.02	0.53	0.31	0.95	2
ATP6AP2	10159	0.8	0.61	0.9	0.69	2		1.01	0.74	0.98	0.93	3
ATP6V0C	527	0.88	0.92	0.95	0.99	4		1.33	1.22	1.11	1.03	4
ATP6V0D1	9114	0.84	0.75	0.89	0.46	2		0.6	1.14	1.23	1.1	3
ATP6V1A	523	0.89	0.16	0.83	0.79	2		1.11	0.46	0.41	0.98	2
ATP6V1B2	526	0.86	0.8	0.45	0.89	2		1.25	1.13	-0.26	1.02	3
B2M	567	1	0.05	0.09	0.99	2		0.85	0.88	-0.38	1.02	3
BAIAP3	8938	0.56	0.43	-0.07	-1.03	0		0.66	0.81	0.87	0.85	3
BARHL2	343472	0.83	0.32	0.84	0.82	3		0.12	-21.94	1.35	1.21	2
BZRAP1	9256	0.8	0.99	0.99	0.96	4		0.96	1	1.04	-0.45	3
C14orf172	115708	0.61	0.86	0.56	0.89	2		0.82	0.43	0.85	-0.18	2
C21orf7	56911	0.22	0.44	-0.87	0.48	0		0.91	0.79	-0.22	0.84	2
C3orf31	132001	0.65	0.89	-0.59	-3.54	1		1.01	0.99	0.7	0.47	2
CCNB3	85417	1	0.82	-0.67	NA	2		0.73	0.85	-0.7	NA	1
CD48	962	-0.14	0.74	0.78	0.88	1		0.11	0.7	0.85	1.08	2
CD58	965	0.8	0.09	0.98	NA	2		0.87	0.77	0.97	NA	2
CD81	975	0.41	-0.36	0.41	0.8	1		0.85	0.66	0.42	1.09	2
CDKN1B	1027	0.22	0.84	0.93	0.62	2		0.88	0.77	0.91	1.03	3
CEL	1056	0.66	0.72	0.7	0.06	0		0.17	1.01	0.99	-0.54	2
CHST5	23563	0.99	0.59	0.04	1	2		0.5	1.02	0.94	-1.5	2
CLIC4	25932	-0.41	0.66	-0.28	-0.29	0		-1.85	0.94	0.05	1	2
CLK1	1195	0.84	0.58	0.88	0.51	2		0.9	0.82	0.89	0.87	4
CLSTN3	9746	0.85	0.86	0.71	0.09	2		0.69	0.64	0.77	0.15	0
CNNM1	26507	0.88	0.17	0.28	-1.88	1		0.86	1	-0.58	0.43	2
COPA	1314	1	1	1	NA	3		1.01	1.05	1.05	NA	3
COPB1	1315	0.97	1	0.99	NA	3		0.65	1	-2.35	NA	1
COPB2	9276	1	1	1	1	4		0.16	1.01	0.96	1	3
COPG	22820	1.01	0.97	0.97	1.01	4		-0.08	0.94	0.22	1.16	2
CRAMP1L	57585	0.6	0.69	0.7	0.57	0		0.82	0.93	0.75	1	3
CRYAA	1409	0.95	0.92	0.59	0.49	2		0.73	-0.26	0.48	0.9	1
CXCR6	10663	-1.15	1	1	0.9	3		0.42	0.47	0.15	0.21	0
CYP17A1	1586	-1.63	0.92	0.18	0.88	2		-1.89	1.04	-0.27	0.82	2
CYP2U1	113612	-0.12	0.47	0.91	0.6	1		-2.14	1	1	-2.33	2
DBT	1629	0.77	1	1	0.93	3		1.02	0.92	-2	1	3
DCLK2	166614	0.95	0.95	-0.01	0.95	3		1.02	-0.51	0.66	-0.16	1
DHRS2	10202	0.8	0.11	0.93	0.68	2		0.33	0.18	0.43	-0.23	0
DLG2	1740	0.91	1	NA	NA	2		-2.41	0.98	NA	NA	1
DMAP1	55929	1	-0.11	0.41	0.78	1		0.82	0.11	0.82	0.9	3
DTX3	196403	0.84	0.68	0.91	0.98	3		0.6	-17.71	0.84	1.01	2
DUSP27	92235	0.63	-0.48	-0.58	0.97	1		0.6	0.8	-17.12	0.89	2
EEF1A1	1915	0.93	0.77	0.29	0.78	1		0.59	0.94	0.79	0.88	2
EIF3A	8661	1	1	0.98	0.93	4		1	1	1.05	-6.63	3
EIF3C	8663	0.88	0.96	0.99	0.98	4		0.82	-0.94	0.58	0.53	1
EIF3G	8666	-0.71	0.95	0.99	NA	2		-9.14	-1.61	0.99	NA	1
EIF4A3	9775	0.99	0.42	0.98	0.97	3		0.98	0.23	1.19	0.98	3
ENGASE	64772	0.86	0.93	-0.05	0.17	2		-0.62	-0.24	0.73	-0.98	0
EPHB6	2051	0.83	0.96	-7.86	0.86	3		0.32	-0.03	0.59	-0.12	0
FAU	2197	1	1	1	NA	3		0.28	1.02	0.64	NA	1
FBXW10	10517	-0.21	0.17	0.28	0.91	1		0.8	0.94	0.9	0.47	2
FCHO2	115548	0.93	0.94	0.45	0.59	2		-6.59	-2.94	-0.4	-5.58	0

		A/WSN/33 Validation Data						A/Hamburg/04/09 Validation Data				
Gene symbol	GeneID	siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene		siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene
FERMT3	83706	0.51	-0.36	0.86	-0.25	1		-0.35	-0.71	0.89	0.86	2
FLJ11235	54508	0.95	1	0.76	0.77	2		1	0.28	0.93	0.95	3
GCLC	2729	0.93	-0.21	0.82	0.53	2		1.02	0.6	0.99	0.89	3
GNRH2	2797	0.24	0.71	0.73	0.99	1		0.61	0.73	0.84	0.94	2
GPR146	115330	-0.06	0.57	0.09	-0.25	0		1.02	-3.24	0.96	-0.35	2
GRIN2C	2905	0.85	0.86	0.39	0.28	2		0.33	-47.73	0.64	0.92	1
HARBI1	9776	0.19	0.99	0.12	0.83	2		0.54	0.9	-1.17	0.36	1
HIST1H2BN	8341	0.89	0.99	-1.17	-0.04	2		1	1	0.64	-0.01	2
HPGD	3248	0.47	0.55	0.96	0.46	1		0.74	0.21	0.9	0.94	2
HSF4	3299	0.99	0.91	0.84	0.86	4		0.81	1	-8.36	1.01	3
HSPD1	3329	0.93	0.97	-0.21	0.59	2		1.02	0.3	0.98	0.95	3
IL17RA	23765	1	0.03	-0.09	-0.05	1		1.04	0.48	1.01	-1.44	2
IL1A	3552	0.7	0.97	0.35	0.66	1		1	1	0.95	-4.12	3
IRF2	3660	-0.48	0.96	-3.5	0.94	2		0.97	0.68	0.41	0.61	1
ISG15	9636	0.85	0.49	0.97	NA	2		1	0.85	0.21	NA	2
ITLN1	55600	0.91	0.99	0.89	0.59	3		0.59	0.86	1.02	0.71	2
JUN	3725	0.61	1	0.57	0.97	2		0.75	0.99	1.01	0.65	2
KATNB1	10300	0.72	0.96	-0.3	0.7	1		0.89	0.97	0.35	0.31	2
KCNJ12	3768	-1.52	0.55	0.74	-0.41	0		0.97	1.01	1	0.73	3
KIAA0664	23277	0.97	-0.14	0.83	0.16	2		-0.15	-0.29	0.86	-10.73	1
KIAA1267	284058	0.9	0.92	0.7	0.47	2		0.88	0.94	0.62	-1.06	2
KIF11	3832	1	0.88	0.96	-0.35	3		-0.21	0.32	1	0.64	1
KPNB1	3837	0.96	0.98	0.99	0.97	4		0.85	1.11	0.91	1.05	4
LARP1	23367	0.97	1	0.98	0.79	3		-2.57	1	0.98	0.83	3
LHX3	8022	1	1	0.84	0.99	4		1	-3.65	0.58	0.96	2
LINGO1	84894	0.68	0.99	-0.72	0.64	1		0.42	1	0.88	-1.74	2
LONP1	9361	0.47	-0.11	0.91	-0.72	1		0.82	-1.21	0.9	0.12	2
LPPR4	9890	0.93	1	-1.09	0.85	3		0.69	1	0.71	0.92	2
MAN2B1	4125	0.95	0.99	0.89	-1.68	3		-0.23	0.5	0.84	-0.01	1
MATN3	4148	0.38	0.78	0.62	0.64	0		-2.05	0.87	0.87	0.31	2
MED6	10001	1	0.98	1	0.96	4		0.62	0.92	1	1	3
MORG1	84292	0.02	0.94	0.89	0.03	2		-0.32	1.01	0.38	0.81	2
MYC	4609	0.96	0.66	1	0.83	3		0.85	0.99	1	-2.51	3
MYOD1	4654	-0.89	0.86	0.87	0.67	2		-0.12	0.08	-9.36	-15.75	0
NEK8	284086	0.93	0	-0.02	NA	1		1	0.84	0.88	NA	3
NEK9	91754	0.66	-1.3	0.83	0.94	2		0.61	0.46	0.99	0.46	1
NTHL1	4913	0.64	0.88	0.13	0.67	1		1.27	0	1.02	0.69	2
NUP205	23165	0.93	0.99	-0.57	0.93	3		1.13	0.92	0.69	0.96	3
NUP98	4928	1	0.99	0.98	1	4		1.28	1.11	1.13	1.24	4
NXF1	10482	0.97	0.99	1	1	4		1.21	1.01	1.17	1.25	4
OPN1SW	611	0.86	0.95	0.18	-0.71	2		0.96	1.01	0.74	0.7	2
PCDH18	54510	0.16	0.68	0.97	0.91	2		-1.01	0.2	1.01	0.25	1
PHF2	5253	0.42	0.98	0.83	0.95	3		-0.23	1.05	0.07	0.03	1
PIK3R5	23533	0.98	-0.7	0.83	NA	2		0.99	-3.35	0.1	NA	1
PIN1	5300	0.95	0.9	1	0.61	3		-0.59	1	0.77	-0.46	1
PLAU	5328	0.98	-0.49	0.64	0.82	2		0.67	0.33	1.01	0.34	1
PLD2	5338	0.32	0.99	0.87	0.05	2		1.01	1.09	-0.06	-0.27	2
PLK3	1263	0.79	0.7	0.54	-1.4	0		1.23	1.07	0.97	-2.93	3
POLR2H	5437	0.74	0.73	0.75	0.88	1		1.02	1.05	0.56	0.61	2
POLR2L	5441	0.7	0.99	-0.13	0.46	1		0.87	0.92	0.51	0.4	2
PPP1R14D	54866	0.93	0.99	-0.5	-3.07	2		1	0.58	0.02	0.87	2
PRPF8	10594	0.94	0.74	0.99	0.9	3		1.29	0.29	1.29	1.08	3
PRPS1	5631	0.91	0.99	0.9	1	4		0.98	0.37	0.99	0.94	3
PRSS27	83886	0.06	1	0.79	0.92	2		0.99	0.9	0.93	0.5	3
PSENEN	55851	0.89	0.95	0.25	0.53	2		1.18	1.07	0.07	1.24	3
PSMA1	5682	0.94	0.71	0.97	NA	2		0.77	1.03	-1.2	NA	1
PSMD14	10213	0.91	0.88	0.84	0.5	3		0.58	0.47	0.46	0.89	1
PSMD2	5708	0.98	0.94	0.99	NA	3		-5.45	-0.07	1.02	NA	1
PTPRN	5798	0.99	0.73	0.94	-1.48	2		1.01	1.07	-0.37	-0.75	2

		A/WSN/33 Validation Data						A/Hamburg/04/09 Validation Data				
Gene symbol	GeneID	siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene		siRNA1 NPI	siRNA2 NPI	siRNA3 NPI	siRNA4 NPI	Hits per gene
RAB6B	51560	0.87	0.3	0.6	-0.06	1		1.24	0.43	1.13	1.13	3
RACGAP1	29127	0.29	0.75	0.84	-0.62	1		1.24	0.5	0.97	-1.13	2
RBM42	79171	0.9	0.77	-0.06	0.44	1		1.11	0.99	-0.98	1.19	3
RETN	56729	0.92	0.98	0.84	NA	3		0.9	-1.57	0.99	NA	2
RFFL	117584	0.87	0.98	0.36	0.66	2		0.69	0.87	-0.6	0.77	1
RNF150	57484	0.37	0.49	-0.47	0.59	0		0.9	0.99	-0.32	0.95	3
RPL35	11224	0.96	0.98	0.98	0.96	4		1	0.1	0.5	0.55	1
RPS10	6204	1	0.88	0.95	0.98	4		0.65	-0.26	0.8	-0.43	1
RPS14	6208	1	0.96	-0.06	1	3		0.97	-0.29	0.49	0.82	2
RPS16	6217	0.98	0.91	-0.25	0.99	3		0.82	-13.05	0.42	0.57	1
RPS27A	6233	1	1	0.87	NA	3		0.74	0.96	0.47	NA	1
RPS5	6193	0.85	1	0.93	NA	3		0.96	1	0.17	NA	2
RUNX1	861	0.85	-0.13	0.76	-6.71	1		0.91	0.87	0.73	-0.24	2
SAFB	6294	0.5	0.48	1	0.91	2		-5.89	1	0.82	0.82	3
SELPLG	6404	0.08	0.94	-0.74	0.53	1		-0.96	0.98	0.86	0.76	2
SF3A1	10291	1	1	-3.47	0.95	3		1.16	0.24	0.65	0.76	1
SF3B1	23451	-0.03	0.99	1	1	3		0.13	1	0.98	0.46	2
SF3B14	51639	1	1	1	1	4		1.04	0.96	1	1.06	4
SFTPB	6439	0.29	0.97	0.87	0.99	3		0.59	0.7	0.16	0.45	0
SIGMAR1	10280	0.97	-0.75	0.56	0.36	1		1	1	0.8	0.7	2
SLC22A6	9356	-1.56	0.78	-0.6	0.91	1		0.87	0.09	0.61	0.91	2
SMU1	55234	0.96	0.34	-0.47	0.39	1		0.96	0.79	0.19	0.93	2
SNRP70	6625	0.03	0.9	0.63	0.91	2		-0.59	1.02	-0.22	0.92	2
SNRPF	6636	0.95	-2.32	0.99	0.81	3		-3.57	0.75	-2.57	-0.79	0
SNW1	22938	NA	0.96	0.75	0.9	2		NA	0.11	-0.39	0.58	0
SNX6	58533	0.35	0.85	0.61	0.44	1		-0.56	1.18	-0.93	0.91	2
SNX9	51429	1	0.36	0.31	0.73	1		1.28	1.13	0.24	1.22	3
SON	6651	1	0.99	0.99	NA	3		0.87	1.2	0.93	NA	3
SRRM2	23524	0.75	0.13	0.28	0.88	1		-0.04	0.97	0.99	0.56	2
STAB1	23166	0.98	1	0.95	0.92	4		1	-1.21	-2.27	0.36	1
SULF2	55959	0.81	0.67	0.99	0.91	3		0.87	0.67	0.6	0.33	1
SUPT6H	6830	-1.15	1	0.98	0.99	3		0.77	0.64	0.57	0.99	1
TBL3	10607	0.97	0.72	0.87	0.8	3		1.17	0.48	0.86	-5.43	2
TCF3	6929	0.88	0.51	NA	NA	1		1.02	1	NA	NA	2
TFE3	7030	0.93	0.83	0.98	0.49	3		0.95	0.96	-0.21	0.38	2
TNFRSF18	8784	0.48	0.91	0.7	0.89	2		0	-1.29	0.55	0.51	0
TNK2	10188	0.59	0.94	0.99	-0.51	2		1.27	1.25	0.7	0.07	2
TRERF1	55809	1	-1.72	1	0.96	3		1	0.75	1.02	0.82	3
TRIM14	9830	-0.2	0.49	0.07	0.89	1		0.63	0.91	0.76	1	2
TRIM21	6737	-2.49	0.81	0.38	-0.61	1		0.43	0.84	-0.62	1.16	2
TRIM60	166655	-0.89	0.83	0.51	0.82	2		0.98	0.79	0.93	-1.02	2
TSSK6	83983	-0.44	0.99	0.74	1	2		0.92	0.4	0.6	1	2
TXNL4A	10907	-1.67	0.98	0.1	0.97	2		0.14	1.04	-1.25	0.87	2
UBAC2	337867	1	0.86	NA	NA	2		0.9	0.95	NA	NA	2
VNN2	8875	-1.44	0.5	0.5	1	1		0.48	0.11	1.02	1.16	2
WNT9A	7483	1	0.55	0.01	1	2		1.02	-0.3	1	1	3
XAB2	56949	0.95	1	0.92	NA	3		0.67	1.06	1.05	NA	2
XPNPEP1	7511	-0.14	0.97	0.42	0.92	2		0.8	0.99	-1.13	0.06	1
XPO1	7514	0.86	0.96	0.78	-0.51	2		0.87	0.8	0.48	0.79	2
ZBTB2	57621	0.81	-0.02	0.83	0.26	2		0.29	0.67	0.73	0.2	0

Table 3

GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
AAMP	14	angio-associated, migratory cell protein	Hs_AAMP_1	Hs_AAMP_3	Hs_AAMP_4
ACTN1	87	ACTININ, ALPHA 1	Hs_ACTN1_13	Hs_ACTN1_8	Hs_ACTN1_7
AHCYL1	10768	S-ADENOSYLHOMOCYSTEINE HYDROLASE-LIKE 1	Hs_AHCYL1_4	Hs_AHCYL1_2	Hs_AHCYL1_3
AIG1	51390	ANDROGEN-INDUCED 1	Hs_AIG1_5	Hs_AIG1_6	Hs_AIG1_4
AKR1C4	1109	ALDO-KETO REDUCTASE FAMILY 1, MEMBER C4 (CHLORDECONE REDUCTASE; 3-ALPHA HYDROXYSTEROID DEHYDROGENASE, TYPE I; DIHYDRODIOL DEHYDROGENASE 4)	Hs_AKR1C4_3	Hs_AKR1C4_2	Hs_AKR1C4_1
AKTIP	64400	AKT interacting protein	Hs_FTS_1	Hs_FTS_2	Hs_FTS_3
ALDH7A1	501	ALDEHYDE DEHYDROGENASE 7 FAMILY, MEMBER A1	Hs_ALDH7A1_1	Hs_ALDH7A1_4	Hs_ALDH7A1_2
ALX4	60529	ARISTALESS-LIKE HOMEOBOX 4	Hs_ALX4_3	Hs_ALX4_2	Hs_ALX4_1
AP2M1	1173	adaptor-related protein complex 2, mu 1 subunit	Hs_AP2M1_7	Hs_AP2M1_3	Hs_AP2M1_5
APBB1IP	54518	AMYLOID BETA (A4) PRECURSOR PROTEIN-BINDING, FAMILY B, MEMBER 1 INTERACTING PROTEIN	Hs_APBB1IP_3	Hs_APBB1IP_8	Hs_APBB1IP_7
ARD1A	8260	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	Hs_ARD1_1	Hs_ARD1_3	Hs_ARD1_5
ARTN	9048	ARTEMIN	Hs_ARTN_8	Hs_ARTN_7	Hs_ARTN_9
ASAH3L	340485	N-acylsphingosine amidohydrolase 3-like	Hs_ASAH3L_1	Hs_ASAH3L_2	Hs_ASAH3L_3
ATCAY	85300	ATAXIA, CEREBELLAR, CAYMAN TYPE (CAYTAXIN)	Hs_ATCAY_2	Hs_ATCAY_3	Hs_ATCAY_4
ATP1A2	477	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	Hs_ATP1A2_2	Hs_ATP1A2_3	Hs_ATP1A2_4
ATP6AP1	537	ATPase, H+ transporting, lysosomal accessory protein 1	Hs_ATP6AP1_5	Hs_ATP6AP1_6	Hs_ATP6AP1_7
ATP6AP2	10159	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	Hs_ATP6AP2_7	Hs_ATP6AP2_8	Hs_ATP6AP2_6
ATP6V0C	527	ATPASE, H+ TRANSPORTING, LYSOSOMAL 16KDA, V0 SUBUNIT C	Hs_ATP6V0C_7	Hs_ATP6V0C_8	Hs_ATP6V0C_6
ATP6V0D1	9114	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	Hs_ATP6V0D1_1	Hs_ATP6V0D1_2	Hs_ATP6V0D1_3
ATP6V1A	523	ATPASE, H+ TRANSPORTING, LYSOSOMAL 70KDA, V1 SUBUNIT A	Hs_ATP6V1A_1	Hs_ATP6V1A_3	Hs_ATP6V1A_2
ATP6V1B2	526	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	Hs_ATP6V1B2_2	Hs_ATP6V1B2_4	Hs_ATP6V1B2_5
AZIN1	51582	ANTIZYME INHIBITOR 1	Hs_OAZIN_4	Hs_OAZIN_2	Hs_OAZIN_1
B2M	567	beta-2-microglobulin	Hs_B2M_3	Hs_B2M_4	Hs_B2M_5
B3GNT1	11041	UDP-GLCNAC:BETAGAL BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE 6	Hs_B3GNT1_5	Hs_B3GNT1_7	Hs_B3GNT1_8
BAIAP3	8938	BAI1-associated protein 3	Hs_BAIAP3_1	Hs_BAIAP3_2	Hs_BAIAP3_5
BARHL2	343472	BARH-LIKE 2 (DROSOPHILA)	Hs_BARHL2_3	Hs_BARHL2_7	Hs_BARHL2_6
BNIP3L	665	BCL2/ADENOVIRUS E1B 19KDA INTERACTING PROTEIN 3-LIKE	Hs_BNIP3L_7	Hs_BNIP3L_12	Hs_BNIP3L_10
BRUNOL6	60677	BRUNO-LIKE 6, RNA BINDING PROTEIN (DROSOPHILA)	Hs_BRUNOL6_8	Hs_BRUNOL6_7	Hs_BRUNOL6_5
BZRAP1	9256	benzodiazapine receptor (peripheral) associated protein 1	Hs_BZRAP1_1	Hs_BZRAP1_2	Hs_BZRAP1_4
C14orf172	115708	CHROMOSOME 14 OPEN READING FRAME 172	Hs_C14orf172_1	Hs_C14orf172_4	Hs_C14orf172_3
C19orf47	126526	HYPOTHETICAL PROTEIN FLJ36888	Hs_FLJ36888_5	Hs_FLJ36888_4	Hs_C19orf47_1
C21orf7	56911	chromosome 21 open reading frame 7	Hs_C21orf7_1	Hs_C21orf7_2	Hs_C21orf7_3
C3orf31	132001	chromosome 3 open reading frame 31	Hs_C3orf31_1	Hs_C3orf31_2	Hs_C3orf31_3
C4orf29	80167	HYPOTHETICAL PROTEIN FLJ21106	Hs_C4orf29_3	Hs_C4orf29_2	Hs_C4orf29_1

Table 3

2

GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
CARD9	64170	caspase recruitment domain family, member 9	Hs_CARD9_1	Hs_CARD9_2	Hs_CARD9_3
CASP8AP2	9994	CASP8 ASSOCIATED PROTEIN 2	Hs_CASP8AP2_5	Hs_CASP8AP2_3	Hs_CASP8AP2_6
CCNB3	85417	cyclin B3	Hs_CCNB3_7	Hs_CCNB3_6	Hs_CCNB3_8
CD48	962	CD48 molecule	Hs_CD48_1	Hs_CD48_2	Hs_CD48_3
CD58	965	CD58 molecule	Hs_CD58_2	Hs_CD58_5	Hs_CD58_6
CD6	923	CD6 ANTIGEN	Hs_CD6_1	Hs_CD6_2	Hs_CD6_3
CD63	967	CD63 molecule	Hs_CD63_10	Hs_CD63_7	Hs_CD63_8
CD81	975	CD81 molecule	Hs_CD81_10	Hs_CD81_11	Hs_CD81_8
CDC23	8697	CDC23 (CELL DIVISION CYCLE 23, YEAST, HOMOLOG)	Hs_CDC23_5	Hs_CDC23_4	Hs_CDC23_7
CDK4	1019	CYCLIN-DEPENDENT KINASE 4	Hs_CDK4_9	Hs_CDK4_6	Hs_CDK4_4
CDKN1B	1027	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (P27, KIP1)	Hs_CDKN1B_6	Hs_CDKN1B_3	Hs_CDKN1B_8
CEL	1056	carboxyl ester lipase (bile salt-stimulated lipase)	Hs_CEL_1	Hs_CEL_3	Hs_CEL_5
CHST5	23563	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	Hs_CHST5_2	Hs_CHST5_5	Hs_CHST5_7
CIB3	117286	CALCIUM AND INTEGRIN BINDING FAMILY MEMBER 3	Hs_CIB3_3	Hs_CIB3_6	Hs_CIB3_8
CLIC4	25932	chloride intracellular channel 4	Hs_CLIC4_5	Hs_CLIC4_2	Hs_CLIC4_3
CLK1	1195	CDC-LIKE KINASE 1	Hs_CLK1_1	Hs_CLK1_11	Hs_CLK1_2
CNNM1	26507	cyclin M1	Hs_CNNM1_3	Hs_CNNM1_5	Hs_CNNM1_6
COPA	1314	coatomer protein complex, subunit alpha	Hs_COPA_5	Hs_COPA_6	Hs_COPA_7
COPB1	1315	coatomer protein complex, subunit beta 1	Hs_COPB_5	Hs_COPB1_4	Hs_COPB1_5
COPB2	9276	coatomer protein complex, subunit beta 2 (beta prime)	Hs_COPB2_6	Hs_COPB2_7	Hs_COPB2_1
COPG	22820	coatomer protein complex, subunit gamma	Hs_COPG_1	Hs_COPG_5	Hs_COPG_6
CRAMP1L	57585	Crm, cramped-like (Drosophila)	Hs_CRAMP1L_1	Hs_CRAMP1L_2	Hs_CRAMP1L_7
CRYAA	1409	crystallin, alpha A	Hs_CRYAA_1	Hs_CRYAA_2	Hs_CRYAA_3
CTA-216E10.6	79640	HYPOTHETICAL PROTEIN FLJ23584	Hs_CTA-216E10.6_1	Hs_CTA-216E10.6_3	Hs_CTA-216E10.6_2
CUEDC2	79004	CUE DOMAIN CONTAINING 2	Hs_CUEDC2_5	Hs_CUEDC2_6	Hs_CUEDC2_4
CXCR6	10663	chemokine (C-X-C motif) receptor 6	Hs_CXCR6_1	Hs_CXCR6_2	Hs_CXCR6_3
CYC1	1537	CYTOCHROME C-1	Hs_CYC1_1	Hs_CYC1_2	Hs_CYC1_3
CYP17A1	1586	cytochrome P450, family 17, subfamily A, polypeptide 1	Hs_CYP17A1_1	Hs_CYP17A1_2	Hs_CYP17A1_3
CYP2U1	113612	cytochrome P450, family 2, subfamily U, polypeptide 1	Hs_CYP2U1_1	Hs_CYP2U1_2	Hs_CYP2U1_3
DBT	1629	dihydrolipoamide branched chain transacylase E2	Hs_DBT_2	Hs_DBT_4	Hs_DBT_5
DCLK2	166614	doublecortin-like kinase 2	Hs_DCAMKL2_2	Hs_DCAMKL2_3	Hs_DCAMKL2_5
DGKH	160851	diacylglycerol kinase, eta	Hs_DGKH_1	Hs_DGKH_4	Hs_DGKH_5
DGUOK	1716	DEOXYGUANOSINE KINASE	Hs_DGUOK_7	Hs_DGUOK_6	Hs_DGUOK_1
DHRS2	10202	dehydrogenase/reductase (SDR family) member 2	Hs_DHRS2_8	Hs_DHRS2_9	Hs_DHRS2_3
DLG2	1740	discs, large homolog 2 (Drosophila)	Hs_DLG2_2	Hs_DLG2_5	NA
DMAP1	55929	DNA METHYLTRANSFERASE 1 ASSOCIATED PROTEIN 1	Hs_DMAP1_6	Hs_DMAP1_5	Hs_DMAP1_4
DMRT1	1761	DOUBLESEX AND MAB-3 RELATED TRANSCRIPTION FACTOR 1	Hs_DMRT1_3	Hs_DMRT1_7	Hs_DMRT1_8
DTX3	196403	deltex homolog 3 (Drosophila)	Hs_DTX3_4	Hs_DTX3_5	Hs_DTX3_6
DUSP27	92235	dual specificity phosphatase 27 (putative)	Hs_DUSP27_1	Hs_DUSP27_2	Hs_DUSP27_3
E2F1	1869	E2F TRANSCRIPTION FACTOR 1	Hs_E2F1_3	Hs_E2F1_4	Hs_E2F1_7

Table 3

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GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
EEF1A1	1915	eukaryotic translation elongation factor 1 alpha 1	Hs_EEF1A1_10	Hs_EEF1A1_11	Hs_EEF1A1_12
EIF3A	8661	eukaryotic translation initiation factor 3, subunit A	Hs_EIF3S10_6	Hs_EIF3S10_2	Hs_EIF3S10_7
EIF3C	8663	eukaryotic translation initiation factor 3, subunit C	Hs_EIF3S8_5	Hs_EIF3S8_6	Hs_EIF3C_1
EIF3G	8666	eukaryotic translation initiation factor 3, subunit G	Hs_EIF3S4_1	Hs_EIF3S4_10	Hs_EIF3S4_2
EIF4A3	9775	eukaryotic translation initiation factor 4A, isoform 3	Hs_DDX48_3	Hs_DDX48_4	Hs_DDX48_5
ENGASE	64772	endo-beta-N-acetylglucosaminidase	Hs_FLJ21865_1	Hs_FLJ21865_5	Hs_FLJ21865_6
EPB49	2039	erythrocyte membrane protein band 4.9 (dematin)	Hs_EPB49_1	Hs_EPB49_2	Hs_EPB49_3
EPHB6	2051	EPH RECEPTOR B6	Hs_EPHB6_3	Hs_EPHB6_4	Hs_EPHB6_6
ERN2	10595	ENDOPLASMIC RETICULUM TO NUCLEUS SIGNALLING 2	Hs_ERN2_10	Hs_ERN2_4	Hs_ERN2_3
FAU	2197	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	Hs_FAU_2	Hs_FAU_4	Hs_FAU_5
FBXW10	10517	F-box and WD repeat domain containing 10	Hs_FBXW10_11	Hs_FBXW10_3	Hs_FBXW10_6
FCHO2	115548	FCH DOMAIN ONLY 2	Hs_FCHO2_3	Hs_FCHO2_8	Hs_FCHO2_7
FCRL6	343413	Fc receptor-like 6	Hs_LOC343413_3	Hs_LOC343413_4	Hs_FCRL6_1
FERMT3	83706	fermitin family homolog 3 (Drosophila)	Hs_URP2_4	Hs_URP2_5	Hs_URP2_6
FGF3	2248	FIBROBLAST GROWTH FACTOR 3 (MURINE MAMMARY TUMOR VIRUS INTEGRATION SITE (V-INT-2) ONCOGENE HOMOLOG)	Hs_FGF3_3	Hs_FGF3_4	Hs_FGF3_6
FLJ11235	54508	hypothetical FLJ11235	Hs_FLJ11235_1	Hs_FLJ11235_2	Hs_FLJ11235_3
FLJ20489	55652	HYPOTHETICAL PROTEIN FLJ20489	Hs_FLJ20489_3	Hs_FLJ20489_4	Hs_FLJ20489_5
FLJ34077	404033	weakly similar to zinc finger protein 195	Hs_FLJ34077_1	Hs_FLJ34077_2	Hs_FLJ34077_3
FNTB	2342	FARNESYLTRANSFERASE, CAAX BOX, BETA	Hs_FNTB_7	Hs_FNTB_1	Hs_FNTB_10
G6PC	2538	GLUCOSE-6-PHOSPHATASE, CATALYTIC (GLYCOGEN STORAGE DISEASE TYPE I, VON GIERKE DISEASE)	Hs_G6PC_3	Hs_G6PC_1	Hs_G6PC_6
GCLC	2729	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	Hs_GCLC_4	Hs_GCLC_7	Hs_GCLC_10
GNMT	27232	glycine N-methyltransferase	Hs_GNMT_2	Hs_GNMT_3	Hs_GNMT_4
GNRH2	2797	GONADOTROPIN-RELEASING HORMONE 2	Hs_GNRH2_8	Hs_GNRH2_7	Hs_GNRH2_6
GPR146	115330	G protein-coupled receptor 146	Hs_GPR146_1	Hs_GPR146_3	Hs_GPR146_4
GRID2	2895	GLUTAMATE RECEPTOR, IONOTROPIC, DELTA 2	Hs_GRID2_3	Hs_GRID2_2	Hs_GRID2_4
GRIN2C	2905	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	Hs_GRIN2C_1	Hs_GRIN2C_2	Hs_GRIN2C_3
GRP	2922	GASTRIN-RELEASING PEPTIDE	Hs_GRP_6	Hs_GRP_9	Hs_GRP_8
GSK3A	2931	GLYCOGEN SYNTHASE KINASE 3 ALPHA	Hs_GSK3A_6	Hs_GSK3A_12	Hs_GSK3A_11
HARBI1	9776	KIAA0652	Hs_KIAA0652_7	Hs_KIAA0652_3	Hs_KIAA0652_4
HIBCH	26275	3-hydroxyisobutyryl-Coenzyme A hydrolase	Hs_HIBCH_1	Hs_HIBCH_2	Hs_HIBCH_3
HIST1H2BN	8341	histone cluster 1, H2bn	Hs_HIST1H2BN_10	Hs_HIST1H2BN_2	Hs_HIST1H2BN_4
HPGD	3248	hydroxyprostaglandin dehydrogenase 15-(NAD)	Hs_HPGD_1	Hs_HPGD_2	Hs_HPGD_3
HSF4	3299	heat shock transcription factor 4	Hs_HSF4_1	Hs_HSF4_2	Hs_HSF4_3
HSPD1	3329	heat shock 60kDa protein 1 (chaperonin)	Hs_HSPD1_5	Hs_HSPD1_7	Hs_HSPD1_8
ICAM2	3384	INTERCELLULAR ADHESION MOLECULE 2	Hs_ICAM2_4	Hs_ICAM2_5	Hs_ICAM2_7
ICEBERG	59082	ICEBERG caspase-1 inhibitor	Hs_ICEBERG_1	Hs_ICEBERG_2	Hs_ICEBERG_4
IL17RA	23765	interleukin 17 receptor A	Hs_IL17R_1	Hs_IL17R_2	Hs_IL17RA_1
IL1A	3552	interleukin 1, alpha	Hs_IL1A_1	Hs_IL1A_2	Hs_IL1A_3

Table 3

GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
IQCF2	389123	IQ motif containing F2	Hs_IQCF2_1	Hs_IQCF2_2	Hs_IQCF2_3
IRF2	3660	INTERFERON REGULATORY FACTOR 2	Hs_IRF2_2	Hs_IRF2_3	Hs_IRF2_1
ISG15	9636	ISG15 ubiquitin-like modifier	Hs_G1P2_1	Hs_ISG15_1	Hs_ISG15_3
ITLN1	55600	intelectin 1 (galactofuranose binding)	Hs_ITLN1_1	Hs_ITLN1_3	Hs_ITLN1_4
JARID1D	8284	jumonji, AT rich interactive domain 1D	Hs_SMCY_1	Hs_SMCY_2	Hs_SMCY_3
JUN	3725	jun oncogene	Hs_JUN_5	Hs_JUN_1	Hs_JUN_2
KATNB1	10300	katanin p80 (WD repeat containing) subunit B 1	Hs_KATNB1_1	Hs_KATNB1_2	Hs_KATNB1_3
KCNAB3	9196	POTASSIUM VOLTAGE-GATED CHANNEL, SHAKER-RELATED SUBFAMILY, BETA MEMBER 3	Hs_KCNAB3_4	Hs_KCNAB3_1	Hs_KCNAB3_3
KCNJ12	3768	potassium inwardly-rectifying channel, subfamily J, member 12	Hs_KCNJ12_2	Hs_KCNJ12_4	Hs_KCNJ12_5
KIAA0664	23277	KIAA0664	Hs_KIAA0664_2	Hs_KIAA0664_3	Hs_KIAA0664_4
KIAA0947	23379	KIAA0947 PROTEIN	Hs_KIAA0947_2	Hs_KIAA0947_5	Hs_KIAA0947_4
KIAA1128	54462	KIAA1128	Hs_KIAA1128_4	Hs_KIAA1128_3	Hs_KIAA1128_5
KIAA1267	284058	DKFZP727C091 PROTEIN	Hs_LOC284058_3	Hs_KIAA1267_2	Hs_LOC284058_4
KIF11	3832	kinesin family member 11	Hs_KIF11_6	Hs_KIF11_7	Hs_KIF11_8
KIF23	9493	KINESIN FAMILY MEMBER 23	Hs_KIF23_11	Hs_KIF23_5	Hs_KIF23_2
KIF3A	11127	kinesin family member 3A	Hs_KIF3A_10	Hs_KIF3A_4	Hs_KIF3A_5
KPNB1	3837	KARYOPHERIN (IMPORTIN) BETA 1	Hs_KPNB1_2	Hs_KPNB1_3	Hs_KPNB1_6
LAMC2	3918	LAMININ, GAMMA 2	Hs_LAMC2_1	Hs_LAMC2_4	Hs_LAMC2_2
LARP1	23367	La ribonucleoprotein domain family, member 1	Hs_LARP_4	Hs_LARP1_1	Hs_LARP1_2
LHX3	8022	LIM homeobox 3	Hs_LHX3_2	Hs_LHX3_3	Hs_LHX3_4
LINGO1	84894	leucine rich repeat and Ig domain containing 1	Hs_LRRN6A_1	Hs_LRRN6A_4	Hs_LRRN6A_5
LOC162993	162993	hypothetical protein LOC162993	Hs_LOC162993_1	Hs_LOC162993_2	Hs_LOC162993_3
LOC399940	399940	similar to Tripartite motif protein 49 (RING finger protein 18) (Testis-specific ring-finger protein)	Hs_LOC399940_5	Hs_LOC399940_6	Hs_LOC399940_7
LOC401431	401431	hypothetical gene LOC401431	Hs_LOC401431_1	Hs_LOC401431_2	Hs_LOC401431_3
LOC440733	440733	similar to 40S ribosomal protein S15 (RIG protein)	Hs_LOC440733_11	Hs_LOC440733_12	Hs_LOC440733_13
LPPR4	9890	plasticity related gene 1	Hs_LPPR4_6	Hs_LPPR4_7	Hs_LPPR4_8
MAN2B1	4125	MANNOSIDASE, ALPHA, CLASS 2B, MEMBER 1	Hs_MAN2B1_4	Hs_MAN2B1_2	Hs_MAN2B1_3
MAP2K3	5606	mitogen-activated protein kinase kinase 3	Hs_MAP2K3_5	Hs_MAP2K3_6	Hs_MAP2K3_7
MATN3	4148	matrilin 3	Hs_MATN3_1	Hs_MATN3_2	Hs_MATN3_3
MED6	10001	mediator complex subunit 6	Hs_MED6_1	Hs_MED6_2	Hs_MED6_6
MKL1	57591	MEGAKARYOBLASTIC LEUKEMIA (TRANSLOCATION) 1	Hs_MKL1_1	Hs_MKL1_8	Hs_MKL1_6
MRPS12	6183	MITOCHONDRIAL RIBOSOMAL PROTEIN S12	Hs_MRPS12_7	Hs_MRPS12_1	Hs_MRPS12_3
MYC	4609	v-myc myelocytomatosis viral oncogene homolog (avian)	Hs_MYC_5	Hs_MYC_7	Hs_LOC731404_4
MYEF2	50804	MYELIN EXPRESSION FACTOR 2	Hs_MYEF2_4	Hs_MYEF2_5	Hs_MYEF2_8
MYOD1	4654	myogenic differentiation 1	Hs_MYOD1_1	Hs_MYOD1_3	Hs_MYOD1_4
NAE1	8883	AMYLOID BETA PRECURSOR PROTEIN BINDING PROTEIN 1	Hs_APPBP1_5	Hs_APPBP1_7	Hs_APPBP1_8

Table 3

GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
NDUFV3	4731	NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN 3, 10KDA	Hs_NDUFV3_3	Hs_NDUFV3_4	Hs_NDUFV3_5
NECAP2	55707	NECAP ENDOCYTOSIS ASSOCIATED 2	Hs_FLJ10420_3	Hs_NECAP2_1	Hs_NECAP2_3
NEK8	284086	NIMA (never in mitosis gene a)- related kinase 8	Hs_NEK8_5	Hs_NEK8_6	Hs_NEK8_10
NEK9	91754	NIMA (never in mitosis gene a)- related kinase 9	Hs_NEK9_7	Hs_NEK9_10	Hs_NEK9_11
NSF	4905	N-ETHYLMALEIMIDE-SENSITIVE FACTOR	Hs_NSF_12	Hs_NSF_11	Hs_NSF_10
NTHL1	4913	nth endonuclease III-like 1 (E. coli)	Hs_NTHL1_3	Hs_NTHL1_4	Hs_NTHL1_5
NUP205	23165	nucleoporin 205kDa	Hs_NUP205_3	Hs_NUP205_4	Hs_NUP205_8
NUP98	4928	nucleoporin 98kDa	Hs_NUP98_3	Hs_NUP98_5	Hs_NUP98_7
NXF1	10482	nuclear RNA export factor 1	Hs_NXF1_1	Hs_NXF1_2	Hs_NXF1_3
ODZ4	26011	odz, odd Oz/ten-m homolog 4 (Drosophila)	Hs_ODZ4_2	Hs_ODZ4_3	Hs_ODZ4_4
OPN1SW	611	opsin 1 (cone pigments), short-wave-sensitive	Hs_OPN1SW_1	Hs_OPN1SW_2	Hs_OPN1SW_3
P76	196463	mannose-6-phosphate protein p76	Hs_LOC196463_1	Hs_LOC196463_2	Hs_LOC196463_3
PCDH18	54510	protocadherin 18	Hs_PCDH18_1	Hs_PCDH18_2	Hs_PCDH18_3
PHF2	5253	PHD FINGER PROTEIN 2	Hs_PHF2_3	Hs_PHF2_4	Hs_PHF2_5
PIK3R5	23533	phosphoinositide-3-kinase, regulatory subunit 5	Hs_PIK3R5_2	Hs_PIK3R5_3	Hs_PIK3R5_4
PIK3R6	146850	CHROMOSOME 17 OPEN READING FRAME 38	Hs_C17orf38_3	Hs_C17orf38_4	Hs_C17orf38_5
PIN1	5300	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	Hs_PIN1_5	Hs_PIN1_6	Hs_PIN1_3
PKHD1	5314	polycystic kidney and hepatic disease 1 (autosomal recessive)	Hs_PKHD1_1	Hs_PKHD1_3	Hs_PKHD1_5
PKN1	5585	PROTEIN KINASE N1	Hs_PKN1_6	Hs_PKN1_3	Hs_PKN1_7
PLAU	5328	PLASMINOGEN ACTIVATOR, UROKINASE	Hs_PLAU_2	Hs_PLAU_10	Hs_PLAU_11
PLD2	5338	phospholipase D2	Hs_PLD2_2	Hs_PLD2_3	Hs_PLD2_5
PLK3	1263	polo-like kinase 3 (Drosophila)	Hs_PLK3_5	Hs_PLK3_6	Hs_PLK3_7
POLK	51426	POLYMERASE (DNA DIRECTED) KAPPA	Hs_POLK_4	Hs_POLK_1	Hs_POLK_2
POLR2H	5437	POLYMERASE (RNA) II (DNA DIRECTED) POLYPEPTIDE H	Hs_POLR2H_2	Hs_POLR2H_3	Hs_POLR2H_4
POLR2L	5441	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	Hs_POLR2L_1	Hs_POLR2L_2	Hs_POLR2L_3
PPARA	5465	PEROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, ALPHA	Hs_PPARA_8	Hs_PPARA_7	Hs_PPARA_6
PPP1R14D	54866	protein phosphatase 1, regulatory (inhibitor) subunit 14D	Hs_PPP1R14D_1	Hs_PPP1R14D_2	Hs_PPP1R14D_5
PRDX5	25824	PEROXIREDOXIN 5	Hs_PRDX5_1	Hs_PRDX5_3	Hs_PRDX5_4
PRPF8	10594	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	Hs_PRPF8_2	Hs_PRPF8_3	Hs_PRPF8_4
PRPS1	5631	phosphoribosyl pyrophosphate synthetase 1	Hs_PRPS1_1	Hs_PRPS1_3	Hs_PRPS1_4
PRSS27	83886	protease, serine 27	Hs_MPN_1	Hs_MPN_2	Hs_PRSS27_1
PRX	57716	PERIAXIN	Hs_PRX_3	Hs_PRX_6	Hs_PRX_7
PSENEN	55851	PRESENILIN ENHANCER 2 HOMOLOG (C. ELEGANS)	Hs_PEN2_1	Hs_PEN2_6	Hs_PSENEN_1
PSMA1	5682	proteasome (prosome, macropain) subunit, alpha type, 1	Hs_PSMA1_1	Hs_PSMA1_12	Hs_PSMA1_3
PSMD2	5708	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Hs_PSMD2_5	Hs_PSMD2_6	Hs_PSMD2_2
PTPLA	9200	PROTEIN TYROSINE PHOSPHATASE-LIKE (PROLINE INSTEAD OF CATALYTIC ARGININE), MEMBER A	Hs_PTPLA_8	Hs_PTPLA_3	Hs_PTPLA_1

Table 3

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GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID
PTPRN	5798	protein tyrosine phosphatase, receptor type, N	Hs_PTPRN_3	Hs_PTPRN_4	Hs_PTPRN_5
RAB4A	5867	RAB4A, MEMBER RAS ONCOGENE FAMILY	Hs_RAB4A_5	Hs_RAB4A_11	Hs_RAB4A_10
RAB6B	51560	RAB6B, member RAS oncogene family	Hs_RAB6B_2	Hs_RAB6B_3	Hs_RAB6B_4
RACGAP1	29127	RAC GTPASE ACTIVATING PROTEIN 1	Hs_RACGAP1_1	Hs_RACGAP1_5	Hs_RACGAP1_3
RAX	30062	retina and anterior neural fold homeobox	Hs_RAX_2	Hs_RAX_3	Hs_RAX_5
RBM42	79171	RNA binding motif protein 42	Hs_MGC10433_1	Hs_MGC10433_2	Hs_MGC10433_4
RETN	56729	RESISTIN	Hs_RETN_3	Hs_RETN_2	Hs_RETN_5
RFFL	117584	RING FINGER AND FYVE-LIKE DOMAIN CONTAINING 1	Hs_RFFL_4	Hs_RFFL_1	Hs_RFFL_3
RNF150	57484	ring finger protein 150	Hs_RNF150_3	Hs_RNF150_5	Hs_RNF150_6
RPL35	11224	ribosomal protein L35	Hs_RPL35_5	Hs_RPL35_6	Hs_RPL35_3
RPLP2	6181	ribosomal protein, large, P2	Hs_RPLP2_1	Hs_RPLP2_2	Hs_RPLP2_3
RPS10	6204	ribosomal protein S10	Hs_RPS10_2	Hs_RPS10_5	Hs_RPS10_7
RPS14	6208	ribosomal protein S14	Hs_RPS14_4	Hs_RPS14_6	Hs_RPS14_8
RPS16	6217	RIBOSOMAL PROTEIN S16	Hs_RPS16_5	Hs_RPS16_8	Hs_RPS16_7
RPS27A	6233	ribosomal protein S27a	Hs_RPS27A_2	Hs_RPS27A_3	Hs_RPS27A_7
RPS5	6193	ribosomal protein S5	Hs_RPS5_2	Hs_RPS5_5	Hs_RPS5_6
RPS6KA6	27330	ribosomal protein S6 kinase, 90kDa, polypeptide 6	Hs_RPS6KA6_10	Hs_RPS6KA6_3	Hs_RPS6KA6_6
RUNX1	861	RUNT-RELATED TRANSCRIPTION FACTOR 1 (ACUTE MYELOID LEUKEMIA 1; AML1 ONCOGENE)	Hs_RUNX1_5	Hs_RUNX1_4	Hs_RUNX1_6
SAFB	6294	scaffold attachment factor B	Hs_SAFB_1	Hs_SAFB_3	Hs_SAFB_4
SCAF1	58506	SERINE ARGININE-RICH PRE-MRNA SPLICING FACTOR SR-A1	Hs_SR-A1_2	Hs_SR-A1_3	Hs_SR-A1_4
SCAMP4	113178	SECRETORY CARRIER MEMBRANE PROTEIN 4	Hs_SCAMP4_7	Hs_SCAMP4_3	Hs_SCAMP4_4
SCARB1	949	scavenger receptor class B, member 1	Hs_SCARB1_6	Hs_SCARB1_7	Hs_SCARB1_8
SDC1	6382	SYNDECAN 1	Hs_SDC1_3	Hs_SDC1_1	Hs_SDC1_6
SELPLG	6404	selectin P ligand	Hs_SELPLG_2	Hs_SELPLG_3	Hs_SELPLG_4
SERPINA6	866	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 6	Hs_SERPINA6_4	Hs_SERPINA6_3	Hs_SERPINA6_1
SERPINB2	5055	serpin peptidase inhibitor, clade B (ovalbumin), member 2	Hs_SERPINB2_2	Hs_SERPINB2_5	Hs_SERPINB2_6
SERPINE2	5270	SERPIN PEPTIDASE INHIBITOR, CLADE E (NEXIN, PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1), MEMBER 2	Hs_SERPINE2_6	Hs_SERPINE2_1	Hs_SERPINE2_7
SEZ6L2	26470	seizure related 6 homolog (mouse)-like 2	Hs_SEZ6L2_10	Hs_SEZ6L2_7	Hs_SEZ6L2_8
SF3A1	10291	splicing factor 3a, subunit 1, 120kDa	Hs_SF3A1_1	Hs_SF3A1_2	Hs_SF3A1_3
SF3B1	23451	splicing factor 3b, subunit 1, 155kDa	Hs_SF3B1_4	Hs_SF3B1_5	Hs_SF3B1_6
SF3B14	51639	splicing factor 3B, 14 kDa subunit	Hs_SF3B14_2	Hs_SF3B14_5	Hs_SF3B14_6
SFTPB	6439	surfactant protein B	Hs_SFTPB_15	Hs_SFTPB_16	Hs_SFTPB_17
SIGMAR1	10280	sigma non-opioid intracellular receptor 1	Hs_OPRS1_1	Hs_OPRS1_3	Hs_OPRS1_4
SLC12A4	6560	SOLUTE CARRIER FAMILY 12 (POTASSIUM/CHLORIDE TRANSPORTERS), MEMBER 4	Hs_SLC12A4_4	Hs_SLC12A4_5	Hs_SLC12A4_6
SLC22A6	9356	solute carrier family 22 (organic anion transporter), member 6	Hs_SLC22A6_3	Hs_SLC22A6_6	Hs_SLC22A6_7
SLC25A19	60386	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Hs_SLC25A19_1	Hs_SLC25A19_3	Hs_SLC25A19_5

Table 3

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GeneSymbol	LocusID	Gene Description	siRNA1_ID	siRNA2_ID	siRNA3_ID
SLC4A8	9498	solute carrier family 4, sodium bicarbonate cotransporter, member 8	Hs_SLC4A8_1	Hs_SLC4A8_2	Hs_SLC4A8_3
SLC7A1	6541	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	Hs_SLC7A1_1	Hs_SLC7A1_2	Hs_SLC7A1_3
SMU1	55234	SMU-1 SUPPRESSOR OF MEC-8 AND UNC-52 HOMOLOG (C. ELEGANS)	Hs_SMU1_7	Hs_LOC728623_1	Hs_LOC728623_2
SNRP70	6625	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	Hs_SNRP70_2	Hs_SNRP70_3	Hs_SNRP70_4
SNRPF	6636	small nuclear ribonucleoprotein polypeptide F	Hs_SNRPF_6	Hs_SNRPF_7	Hs_SNRPF_8
SNX6	58533	SORTING NEXIN 6	Hs_SNX6_10	Hs_SNX6_11	Hs_SNX6_4
SNX9	51429	sorting nexin 9	Hs_SNX9_1	Hs_SNX9_2	Hs_SNX9_3
SON	6651	SON DNA binding protein	Hs_SON_2	Hs_SON_4	Hs_SON_5
SRRM2	23524	SERINE/ARGININE REPETITIVE MATRIX 2	Hs_SRRM2_4	Hs_SRRM2_7	Hs_SRRM2_5
STAB1	23166	stabilin 1	Hs_STAB1_1	Hs_STAB1_2	Hs_STAB1_3
SULF2	55959	sulfatase 2	Hs_SULF2_10	Hs_SULF2_5	Hs_SULF2_6
SUPT6H	6830	suppressor of Ty 6 homolog (S. cerevisiae)	Hs_SUPT6H_5	Hs_SUPT6H_6	Hs_SUPT6H_7
TBL3	10607	TRANSDUCIN (BETA)-LIKE 3	Hs_TBL3_4	Hs_TBL3_3	Hs_TBL3_5
TCF3	6929	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	Hs_TCF3_1	Hs_TCF3_5	NA
TFE3	7030	transcription factor binding to IGHM enhancer 3	Hs_TFE3_1	Hs_TFE3_2	Hs_TFE3_3
TMEM50B	757	transmembrane protein 50B	Hs_C21orf4_3	Hs_C21orf4_5	Hs_C21orf4_7
TNFRSF18	8784	tumor necrosis factor receptor superfamily, member 18	Hs_TNFRSF18_2	Hs_TNFRSF18_4	Hs_TNFRSF18_5
TNK2	10188	tyrosine kinase, non-receptor, 2	Hs_TNK2_4	Hs_TNK2_5	Hs_TNK2_6
TRERF1	55809	transcriptional regulating factor 1	Hs_TRERF1_3	Hs_TRERF1_6	Hs_TRERF1_7
TRIM14	9830	tripartite motif-containing 14	Hs_TRIM14_1	Hs_TRIM14_5	Hs_TRIM14_6
TRIM21	6737	tripartite motif-containing 21	Hs_TRIM21_11	Hs_TRIM21_6	Hs_TRIM21_7
TRIM60	166655	tripartite motif-containing 60	Hs_TRIM60_3	Hs_TRIM60_6	Hs_TRIM60_7
TSSK6	83983	testis-specific serine kinase 6	Hs_SSTK_2	Hs_SSTK_3	Hs_SSTK_4
TUBB4	10382	TUBULIN, BETA 4	Hs_TUBB4_2	Hs_TUBB4_3	Hs_TUBB4_6
TXNL4A	10907	thioredoxin-like 4A	Hs_TXNL4A_1	Hs_TXNL4A_3	Hs_TXNL4A_5
UBAC2	337867	UBA domain containing 2	Hs_PHGDHL1_5	Hs_PHGDHL1_6	NA
UBE2N	7334	UBIQUITIN-CONJUGATING ENZYME E2N (UBC13 HOMOLOG, YEAST)	Hs_UBE2N_5	Hs_UBE2N_6	Hs_UBE2N_7
VNN2	8875	VANIN 2	Hs_VNN2_1	Hs_VNN2_4	Hs_VNN2_2
WNT3A	89780	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 3A	Hs_WNT3A_4	Hs_WNT3A_2	Hs_WNT3A_1
WNT9A	7483	wingless-type MMTV integration site family, member 9A	Hs_WNT9A_1	Hs_WNT9A_2	Hs_WNT9A_3
XAB2	56949	XPA binding protein 2	Hs_XAB2_5	Hs_XAB2_6	Hs_XAB2_4
XPNPEP1	7511	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Hs_XPNPEP1_1	Hs_XPNPEP1_2	Hs_XPNPEP1_3
XPO1	7514	exportin 1 (CRM1 homolog, yeast)	Hs_XPO1_1	Hs_XPO1_2	Hs_XPO1_5
XRCC6	2547	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)	Hs_XRCC6_2	Hs_XRCC6_3	Hs_XRCC6_4

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
AAMP	14	Hs_AAMP_5	GAGGAAGAGATACTAGTTAAA	CTGGATGTGGAAAGTCCCGAA	CTGGACTTTGCCCTCAGCAAA	CCGCATGGAGTCCGAATCGGA	1,71
ACTN1	87	Hs_ACTN1_4	AACACCATGCATGCCATGCAA	CCGGCCCGAGCTGATTGACTA	AAGGATGATCCACTCACAAAT	AACGATTACATGCAGCCAGAA	1,74
AHCYL1	10768	Hs_AHCYL1_1	CCCACTTGGATTTATAGTATA	AAACAGTTGTATCGTATGCAA	CTGATAGAACTCTATAATGCA	CAGGGTGGTAAAGCTAAATGA	1,36
AIG1	51390	Hs_AIG1_3	CACGACGGTTCTGCCCTTTAT	AAAGCCTAAATTGGAATGAGA	ATGCAAATGCTGACTAATAAA	GAGAAATATGTTAAAGTCAAA	1,85
AKR1C4	1109	Hs_AKR1C4_5	ATGGACCATCCTGATTATCCA	GAGGGTGTTGCACGACATCTA	CTGGGAACCCAACGACATAAA	CAGGTGAGACGCCACTACCAA	1,63
AKTIP	64400	Hs_FTS_4	AAGGTGAAGAGAAGACATTAA	CTGCACTGTCTTACTGATTTA	TCAGCACTACTTAATAGTTTA	TTGCATTCATTTAAACTAATA	1,62
ALDH7A1	501	Hs_ALDH7A1_3	AAGGTCTACTTGTACTATCAA	AAGGATGATTGGAGGACCTAT	TCCGATTCTCTATGTCTTTAA	CGGGAGAAGATCCAAGTACTA	1,77
ALX4	60529	Hs_ALX4_5	CAGCAGCTACCTGAGTGTCAA	CCGGACCACCTTCACCAGCTA	CAGGTTCCCTGCTACGCTAAA	CCCGTCCTGGCTCGGCAACAA	1,62
AP2M1	1173	Hs_AP2M1_6	TGCCATCGTGTGGAAGATCAA	ACGTGTGACTTCGTCCAGTTA	TGGAGGCTTATTCATCTATAA	TTGGAGGCTTATTCATCTATA	1,61
APBB1IP	54518	Hs_APBB1IP_6	CAGAATATCTGCCCAAATGTA	CACTGGTATCAGCCAATATGA	AACCATTAACCCAGTAGAGTT	CCAGAGCTGAATTTAACTACA	1,82
ARD1A	8260	Hs_ARD1A_1	AACTTTCAGATCAGTGAAGTG	CACAGAGAGCACAGATGTCAA	CCGGGCCGCCCTGCACCTCTA	ATCAGTGAAGTGGAGCCCAAA	1,81
ARTN	9048	Hs_ARTN_1	ACCCTGCGGATCCCAGCCTAA	CCGGAAAGGTGCCTAGAAGAA	CAGGCCCTGTAGGGACAGCAT	CTGCAAAGCACCTAACACATA	1,57
ASAH3L	340485	Hs_ASAH3L_4	CAACAAGAAATCATCAGTCAA	TTGGGTCAGATGCTTGATGAA	CACGATCAGCAATGTCTTATT	CAGAAGGTATCTACCAAAGAT	1,67
ATCAY	85300	Hs_ATCAY_5	CTCGCCTTTGTTTGCCAGTAA	TCCCAACACGCTAAATTTCAA	ACGAGTTTCCCTCTAATCCTA	ATGATCCGGCCTTACATGAAA	1,82
ATP1A2	477	Hs_ATP1A2_5	CCGATTAATTGGAGATTACTA	AACAATCAGATTAGACACTAT	ACCCATAGCAATGGAGATTGA	CAAGGAGATCCCGCTCGACAA	1,65
ATP6AP1	537	Hs_ATP6AP1_8	CTGGTGATGTTGTGCTAACAA	TCCGAAGATGTCCCATACACA	CAGCAATGGCTCCGTCGCCTA	AAACTTCTCTGTGGCGTACAA	1,62
ATP6AP2	10159	Hs_ATP6AP2_4	GGGAACGAGTTTAGTATATTA	ATGTGCTTATATAATCGCTTA	AACATGGATCCTGGATATGAT	TCCCTATAACCTTGCATATAA	1,84
ATP6V0C	527	Hs_ATP6V0C_5	TGCGCGGAGCTGTGTCCAATA	GCGGATGATTTAGAATTGTCA	CACAAAGTAGACCCTCTCCGA	CCCACCAGCCACAGAATATTA	1,83
ATP6V0D1	9114	Hs_ATP6V0D1_4	CACTTTCATGTTCCTCCCTAA	CCGCGCCTTCATCATCACCAT	AAGGCTCTCAATTGCACTCTT	CAACTACATCCCTATCTTCTA	1,66
ATP6V1A	523	Hs_ATP6V1A_4	ATGGAGGTTGATGGTAAGGTA	GAGCTTGAATTTGAAGGTGTA	ACCCAAATTGTGATAGCATAA	TAAGGTAGAGTCAATTATGAA	1,9
ATP6V1B2	526	Hs_ATP6V1B2_6	CAGGCTGGTTTGGTAAAGAAA	ACCATGTTACCCTGTAATTAA	GAGGATATGCTTGGTCGGGTA	CAGGGTAATCTTTGTGGCACA	1,55
AZIN1	51582	Hs_AZIN1_1	CGGATTTGCTTGTTCCAGTAA	CAGGTTAAGCTTGTCTGGTCA	CCGGATTTGCTTGTTCCAGTA	ACACTCGCAGTTAATATCATA	1,7
B2M	567	Hs_B2M_6	AAGTGGGATCGAGACATGTAA	CTGGGTTTCATCCATCCGACA	AACATCTTGGTCAGATTTGAA	AAGATAGTTAAGCGTGCATAA	1,34
B3GNT1	11041	Hs_B3GNT1_6	CAGCACAATAAGATCCTATAT	CTGGGTCAACCTGCCGGAAGA	ATGCGTGTTCACACCCACAAA	ACGGTCCGTGGACCAGGTCAA	1,4
BAIAP3	8938	Hs_BAIAP3_6	TGGGATCATGACGACGATGTA	GTCGACCTTGCTGGACATTAA	CTCGCCTGACTCCATCCAGAA	CCCGCTCATGAAGTACCTGGA	1,71
BARHL2	343472	Hs_BARHL2_4	CAGCAAGACCAAACTCGACAA	TCGCCTTATTTCTATCACCCA	CAGAGTGCAACCAGTAAGTGA	TCCGACCACCAGCTCAATCAA	1,77
BNIP3L	665	Hs_BNIP3L_1	TAGCATTTGATGTCTAAATAA	AAACGAGATCAGGTTAGCAAA	CTGGGTGGAGCTACCCATGAA	AAGAAAAGTGCGGACTGGGTA	1,63
BRUNOL6	60677	Hs_BRUNOL6_9	CCCACCTGTAAAGTAGATTCA	TACCTTCTGTCTCTTAGTCTA	AAGCTGATCAATGGTGGTGAA	CTGAAGGCCTCTGATCTGATA	1,87
BZRAP1	9256	Hs_BZRAP1_5	CACAGTGAGTATGTAACTTGA	CCGCCGTCTGGTGGTCCTCAA	CAGAGCTAAATGGCTCCTTAA	CTGGAAGACATGCCTGGATTA	1,8
C14orf172	115708	Hs_C14orf172_2	CCAAGTGTGAGTGATGAGCAA	CACGGTGGAGTTCCACCAGCA	CCGCAGCGGCACGCCCATGAA	CACCATGAGCTTCGTGGCATA	1,77
C19orf47	126526	Hs_FLJ36888_3	TCGAGCCTGTTGAGACTGTTA	TGCCGTGATGTTTGTGGATAA	CACCGTCAGGACATGTGCAAA	CTCGGTCACTGTGTCCAACAA	1,6
C21orf7	56911	Hs_C21orf7_4	CTGAGAATTGTTGTAAAGTAA	AAGGTGTGGAATAACCCTTAA	TTCAAATATGCTCAAATTTAA	AAGGAGCTCATTGCCAAGTTA	1,63
C3orf31	132001	Hs_C3orf31_4	AGCCCTCGATAGAAATCTGAA	ACCCTGTCGCATGGCATTCAA	CACGTCCATCCAGAATAACTA	CTCGTGGGTGACCTTCCGCAA	1,7
C4orf29	80167	Hs_FLJ21106_4	AAGCGCTTCAATCAAACACTT	TGGGTGTGAGCAAGTTAGATA	GCCCGTCCTATGATTAAAGAA	TACCACCTACTTAGTAAAGAA	1,72

Table 3

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GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
CARD9	64170	Hs_CARD9_5	CCGCGTCTTCTCCATGATCAT	CAGCGACAACACCGACACTGA	CTGGTCATCCGCAAACGGAAA	ACGTAAGGACTCCAAGATGTA	1,73
CASP8AP2	9994	Hs_CASP8AP2_1	CAGTCTGATCTCAATAAGGAA	CAGCTGATGTGCGGAAGTCAA	CACATACGTAGATCTAACGAA	AAGACTGATCACAGAGCTAAA	1,78
CCNB3	85417	NA	AAGGCTGTGTATTACAAGTAT	AGGGCTAAGCATGCATGTTAA	AAGCTGGTGGATCTCTACCTA	NA	1,5
CD48	962	Hs_CD48_4	CAGAAGCATGCTGCTGAATTA	CACCCTTATGCCACATAATTA	CTGCAAGTGCTTGACCCTGTA	CTGGCGAGTCTGTAAACTACA	1,46
CD58	965	NA	TAGCAGTAATTACAACATGTA	AAGCATTGAAGTCCAATGCAT	CAGTGTACTCTTAGCAATCCA	NA	1,88
CD6	923	Hs_CD6_5	CCGGCAGGATGTACTACTCAT	CTGGCGGTTCAACAACTCCAA	CAGCACTACTGCGGCCACAAA	AAGGAAACGTTATACCTTGTA	1,65
CD63	967	Hs_CD63_9	GCGGTGGAAGGAGGAATGAAA	ATGGTCTGAGTTTGTCTTAGA	ATGTGTGAAGTTCTTGCTCTA	TAGAGATAAGGTGATGTCAGA	1,69
CD81	975	Hs_CD81_9	CACCTCAGTGCTCAAGAACAA	CTGACTCCGTCATTTAATAAA	CGCTGTGATCATGATCTTCGA	CTGCACCAAGTGCATCAAGTA	1,55
CDC23	8697	Hs_CDC23_8	TACGAGAAACTCAATCAACTA	CTGCAATAGCAAGAAAGCCTA	ACAGCAGGAGGTAATATGCTA	AAGGACGATGAAACAGTTGAT	1,7
CDK4	1019	Hs_CDK4_13	TGCCTATGGGACAGTGTACAA	AAGGTAACCCTGGTGTTTGAG	AAGCCTCTCTTCTGTGGAAAC	AAGGATCTGATGCGCCAGTTT	1,79
CDKN1B	1027	Hs_CDKN1B_7	ACCGACGATTCTTCTACTCAA	CTGTAAGTAACTTCACATTAA	CAACAACACAATAACACTAAA	CCAATTATTGTTACACATTAA	1,86
CEL	1056	Hs_CEL_6	AGCCCTGACGCTGGCCTATAA	CCCGTTATGATCTGGATCTAT	TGGGTTCGTGGAAGGCGTCAA	CATCGTGGTCACCTTCAACTA	1,58
CHST5	23563	Hs_CHST5_8	CAGGGAGTAAGTTACTGCTAA	CCACGCGTTGCCCTTCACTAA	CACGGGTAAAGTGATCCGTCA	CAGCAAGCAGGACGTATGCAA	1,47
CIB3	117286	Hs_CIB3_7	CTGGAGCAGACGGTGACCAAA	TGGCAGCATGCCCGAGCTGAA	CCGCGACCTCAAGGCTTACTA	CCAGAGGATTGCCCAGGTATT	1,57
CLIC4	25932	Hs_CLIC4_4	TAGCAGTACAATGATTAGTAA	CAGGGAAGTTAGTCAAATGAA	CACGAACATGCAGTTATTGAA	CTGGATATGTACTAACGAATA	1,77
CLK1	1195	Hs_CLK1_6	CACGATAGTAAGGAGCATTTA	CAGGACGATGAGACACTCAAA	AACGTGATGAACGCACCTTAA	GAGAAAGATTATCATAGTCGA	1,89
CNNM1	26507	Hs_CNNM1_7	CTGGGTTATCTGCATCTCAAA	CTCACTGAACTCATTGATCGA	TGGCGCGTGATTGACATTACA	CACGCTGGAGGATATCATAGA	1,72
COPA	1314	NA	CACACGGGTGAAGGGCAACAA	AGAGATGTTAACCAAATTCGA	TCCGATGATCAGACCATCCGA	NA	1,73
COPB1	1315	NA	AACTCCAGATGGGAGACTTTT	CACGTTAATTAACGTGCCAAT	AAGATTTACCGAGGAGCATTA	NA	1,69
COPB2	9276	Hs_COPB2_3	ACGATTCTTCAGAGTATGCAA	CAGGTTTCAAGGGTAGTGAAA	CAGTACGTATTTGGCATTCAA	AGGCGTGAATTGCATTGATTA	1,56
COPG	22820	Hs_COPG_7	CCGAGCCACCTTCTACCTAAA	CACCGACTCCACTATGTTGAA	AGGCCCGTGTATTTAATGAAA	TCCGTCGGATGTGCTACTTGA	1,6
CRAMP1L	57585	Hs_CRAMP1L_8	CCCGACAACCTTGCCACCCAA	CTGCATAATGATCCCATTTCA	AGGGCGGAACCTGCGGATCAA	CTGGTGTGCATGATGAACGAA	1,64
CRYAA	1409	Hs_CRYAA_4	CCGGGACAAGTTCGTCATCTT	CCCGGAGGACCTCACCGTGAA	CAGCCCGCGGCAATCAATAAA	ACCGCACCTCACACTCCTTTA	1,8
CTA-216E10.6	79640	Hs_FLJ23584_3	GAGGTGCGAAACTGTCTTCAA	CAGGGTGGAGGTGGGAATGAT	TTCAGGAACTAGGGAATAGAA	AAGGTGGAAGTAAGAAAGCTA	1,65
CUEDC2	79004	Hs_CUEDC2_3	CCCGACGGAGCAGAAGAGAGA	CGGCCCGAAATGCTCAAAGAA	TTGCTCCATAGTGTTAACCTA	ATGCTGGTAGAGGGAAAGGAA	1,72
CXCR6	10663	Hs_CXCR6_4	TCGTTTCATTGTAGTGGTTAA	CAGGTCATGTGCAAGAGCCTA	CTGCTATTCAGTCATAATCAA	CACCAGCATGTTCCAGTTATA	1,83
CYC1	1537	Hs_CYC1_4	CCCATCATGGGAATAAATTAA	CAGCATGGACTTCGTGGCCTA	TACCATGTCCCAGATAGCCAA	GCGGGAAGGTCTCTACTTCAA	1,8
CYP17A1	1586	Hs_CYP17A1_5	CAGGCTGAGGGTAGCACCTAA	CCGGAGTGACTCTATCACCAA	TGAGTTGAATGTCATACAGAA	CAGACACGGCCATATGCATAA	1,85
CYP2U1	113612	Hs_CYP2U1_5	CAAGGGTATACCATTCCTAAA	CCGGAGGATTTCTACCCTAAT	CAGCGCTTTGATTACACTAAT	CTGGGACTGATACCACAACTA	1,44
DBT	1629	Hs_DBT_6	TAGCCATATACAGACAGTATA	ATGACTGTTCCTATACTAGTA	CAGGGTTTGATTGTCCCTAAT	CTGGTTAAGCTCCGAGAAGAA	1,7
DCLK2	166614	Hs_DCAMKL2_6	CCGCACTATCTACACCATCGA	CTGAGCTTGACCGTTGCATAA	ACCATTTCGTAAAGTCGATTA	CTCGGTGTACCGCGGGACAAA	1,57
DGKH	160851	Hs_DGKH_6	CCGGATCTAGATTCCGTAGAT	CTCCTAGTGCTTAGTGGTCAA	CAGGTGGAGTATAATGACATA	TGGGAGTTCGATTATCAACAA	1,47
DGUOK	1716	Hs_DGUOK_5	CTGTAGCAACATGGCAGAATA	CAGCTGCATGGCCAACACGAA	ACCCTTCAGTTCCATGGCCAA	CCGGATCACATTACATGGCTT	1,77
DHRS2	10202	Hs_DHRS2_5	CTCTCTGTAATTTGTGCTTTA	TAGATTTGGCTGATCCAATTA	CTGGAAGAACTTCAAGGAACA	CAGGAAGGGCGTCCTGGCTAA	1,65
DLG2	1740	NA	TACGCTCGATTTGAGGCCAAA	CAGAGCCATGTTCGACTACGA	NA	NA	1,8
DMAP1	55929	Hs_DMAP1_3	ACAGACCTTAAGATACCAGTA	CCCAAGGACACCATCATTGAT	CAGGTTCAATAAGACTGTGCA	CCGGCTGTTCCTGAGACTGCA	1,83
DMRT1	1761	Hs_DMRT1_6	CTGCATGATTTAAGTGCTTTA	CACCTACTACAGCAGCTTCTA	CCAGTACAGGATGCATTCTTA	AAGAGAGAACAATGGCAGTAA	1,59
DTX3	196403	Hs_DTX3_7	TCAGATACAGTTCTCCCTTAA	TGGGCGGATGCTGGTCTCTAA	AAGGGTATCACAGATGACTGA	TGGCGAGACTTCTGACATCTA	1,67
DUSP27	92235	Hs_DUSP27_4	AAGCTTTGGTGTTTCACTTAA	CAGAAAGTCTATCCTATGGCA	CTACCTGATGATCTTCCACAA	TACATCCAGAAAGGCCATGAA	1,85
E2F1	1869	Hs_E2F1_5	CAGATGGTTATGGTGATCAAA	CTCACTGAATCTGACCACCAA	CAGATCTCCCTTAAGAGCAAA	AACTCCTCGCAGATCGTCATC	1,88

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
EEF1A1	1915	Hs_EEF1A1_9	AAGTGAATCTTTGGAAACAAA	CACCTGTAAGATTTACCAGTA	CAAGTCTGTAATGAAGTGTTA	AAGGAATATCATTTAAAGCTA	1,76
EIF3A	8661	Hs_EIF3S10_8	GAGGATCTAGATAATATTCAA	CAGGATCGTACTGACAGATTA	ATGGCTAAACAGGTTGAACAA	CAGCGTCGCCTTGCAACACTA	1,69
EIF3C	8663	Hs_EIF3C_2	CCGCCGACGCATGATCAGCAA	AACGAATGGATGAAGAATTTA	CTGACCTAGAGGACTATCTTA	CCCGAGCAGTCTGCGGATGAA	1,62
EIF3G	8666	NA	AAGAGGACCTGAACTGCCAGG	CTCCCGCATCTACCTGGCTAA	CAAGGAGGTCATCAACGGAAA	NA	1,71
EIF4A3	9775	Hs_DDX48_6	CCGGAAGGGTGTGGCCATTAA	CCCATAAACTCTATACTTCTA	CCGCATCTTGGTGAAACGTGA	ATGATTCGTCGCAGAAGCCTA	1,65
ENGASE	64772	Hs_FLJ21865_7	CAGGCAATTAATTAGGAGTAA	CTGCGACGGCTTCTTCACTAA	CACGGACGTCACAGTTGCTTT	CGGCCGGGAAGGAGCATCAAA	1,6
EPB49	2039	Hs_EPB49_4	CCGCCCAGATTCCAACATCTA	CAGAAGATCTATCCCTATGAA	GTGGATATAATGATATCTATA	CTGGCTGTTGTGGAGACAGAA	1,79
EPHB6	2051	Hs_EPHB6_10	CTGGAGCTTTGGGATACTCAT	CGCCAATCTCTAGATCAACAA	CTCCTGGATTACATCTACTTA	CGGGAAGTCGATCCTGCTTAT	1,86
ERN2	10595	Hs_ERN2_2	CACCTGCACTCTTTACACATA	AGGGATGATCCCGTCATCGAA	CTGGTTCGGCGGGAAGTTCAA	ACCAATGTACGTCACAGAAAT	1,61
FAU	2197	NA	CCGCCGTTCAGTCGCCAATAT	GGCCGCATGCTTGGAGGTAAA	AAGTGAGAGGTCAGACTCCTA	NA	1,6
FBXW10	10517	Hs_FBXW10_7	CAGGATCAATGACATATCACA	AAGGCGAATTATACTCTCTTA	CCCGTTGAATTCCGAGGCCAT	GAGAACGAAGAATGAGTACAA	1,56
FCHO2	115548	Hs_FCHO2_4	AAACATGTAATATATAATTTA	ATCGGATAGAAATTAAGCCTA	TAGTGTAATATCAGGCCTAAA	AAACCACTAATTGTTCCGTTA	1,61
FCRL6	343413	Hs_FCRL6_2	CTGTGGTGCATAGAACCTCAA	CAGGGATGGAAGAATACACCA	CTGATGGTTATTGCTGCTGCA	TCCGATCCTGTATTCCTTCTA	1,81
FERMT3	83706	Hs_URP2_7	CTGGCTGCGCTTCAAGTACTA	CTGCCGAATTGTACACGAGTA	AAGTTCTGCATTAAACTCCTA	CCCGTTTCCAGCGAAAGTTCA	1,74
FGF3	2248	Hs_FGF3_5	TTGTGTCATCACAACATTAAA	CGGGCGGTACCTGGCCATGAA	CCGCGTCTGGGTTCTCAGCTA	CAGCGCCGAGAGACTGTGGTA	1,83
FLJ11235	54508	Hs_FLJ11235_4	CAGGATCAGCATAACCGCCAA	CCGTAGCACAGTAGAAATGAA	ACCTAGGACGTTAGCCCTTAA	CTCATAGTGATTTGCCACAAA	1,8
FLJ20489	55652	Hs_FLJ20489_6	ACGCACGTGATGTACATGCAA	CTGGACCTATGCTGCAGGCAA	CAGCCTCTATGCCCACCGCTA	CAGGACGAGTGTGGTCTCCCA	1,8
FLJ34077	404033	Hs_FLJ34077_4	CAGCCTGATGATGCAGTAGAA	AAGGGAAACAAGAGCATAAAT	TTGGAACTGGGTGTTGAAATA	CAGAGTGGATTCATCCTGTAT	1,73
FNTB	2342	Hs_FNTB_3	CACGTCCATAGAACAGGCAAA	ACCCACATATGCAGCAGTCAA	CTCCGTAGCCTCGCTGACCAA	TCCGCTCGCCGTAGCGCTTTA	1,67
G6PC	2538	Hs_G6PC_5	TGGGATCCAGTCAACACATTA	TAGCAGAGCAATCACCACCAA	CCAAGTCGAGCTGGTCTTCTA	AGGGATTGAGGAGGACTACTA	1,57
GCLC	2729	Hs_GCLC_11	CCGGATCATATTTACATGGAT	CATCGACTTGACGATAGATAA	CACCCTCGCTTCAGTACCTTA	ATCAGGCTCTTTGCACAATAA	1,78
GNMT	27232	Hs_GNMT_5	AGGGAAGAACATCTACTATAA	AACATCAGTGCTGATAGTGAA	CAGACGGAAGGGTAAACAATA	CAGCCGCACCGCCGAGTACAA	1,56
GNRH2	2797	Hs_GNRH2_5	CCCGCCATCCTCCAATAAAGT	CTGAAGGAGCCATCTCATCCA	TGGCTGGTACCCTGGAGGAAA	CAGACTGCCCATGGCCTCCCA	1,83
GPR146	115330	Hs_GPR146_5	CAGGGTTCTGAGAACATTTCA	CTGGTGTTAAATGGAGCTATT	CAGCATTCAGTTTGTCAATGA	CAGTATGAACCTGTCCTAAAT	1,65
GRID2	2895	Hs_GRID2_5	AACGATGTGGACGTACAGGAA	CACGATTACAAATGGGATCAA	AAGCAATGGATCGGAGAACAA	CACCGGATCACAAATACGGAA	1,87
GRIN2C	2905	Hs_GRIN2C_5	CTGGACGAGATCAGCAGGGTA	CCCAGCTTTCACTATCGGCAA	CACCCACATGGTCAAGTTCAA	GTCGATGTGCTTGCCGATCTA	1,75
GRP	2922	Hs_GRP_7	ATCAGTTCTACGGATCATCAA	CCAGCTGAACCAGCAATGATA	CAGAGGATAGCAGCAACTTCA	CGGAGGGACCGTGCTGACCAA	1,75
GSK3A	2931	Hs_GSK3A_7	AAGCTTTAACTGAGACTCCGA	AAGAAAGACGAGCTTTACCTA	ACCACAGTCGTAGCCACTCTA	CAAAGGTGTTCAAATCTCGAA	1,78
HARBI1	9776	Hs_KIAA0652_5	CTGGGCGTATGATTGACTTAA	CAGGAAGTCCTGGGTGCTAAA	CAGGTATTGTTACTTGAATAA	AAGGCGGGAGTGACCGCTTAA	1,51
HIBCH	26275	Hs_HIBCH_4	CACGGGAGTCATAACACTAAA	CAACTTAGGTATACAATATAA	TAGCCTTGAAATCTCCTTCAA	TCGAGGTTTAATGCATTCAAA	1,36
HIST1H2BN	8341	Hs_HIST1H2BN_9	CTCCTTCGTCAATGACATCTT	CAAGGCCATGGGCATCATGAA	CACCAAGTACACCAGTTCCAA	CCGCCTGGCGCATTACAACAA	1,76
HPGD	3248	Hs_HPGD_4	CTGGCAGTGACTAATCAGTAA	CAAGAGCTTCTTAGAGTAGTA	CAGCCGGTTTATTGTGCTTCA	CAAGACTATGATACAACTCCA	1,73
HSF4	3299	Hs_HSF4_4	CCGACTATCCCTGCACATAAA	CAGAGCCGTTTCGCCAAGGAA	CCGGGTCATTGGCAAGCTGAT	AAGGGCGAGAATGGACCCTGA	1,82
HSPD1	3329	Hs_HSPD1_1	AAGGCTTCGAGAAGATTAGCA	CACCACCAGATGAGAAGTTAA	CAGGGTTTGGTGACAATAGAA	CGGGCTTATGCCAAAGATGTA	1,63
ICAM2	3384	Hs_ICAM2_3	CGGGAAGCAGGAGTCAATGAA	TCCCATGACACGGTCCTCCAA	CACGGTGGTCACTGGAACTCA	AACATCTTTCACAAACACTCA	1,81
ICEBERG	59082	Hs_ICEBERG_5	CAGTGGGTGCAGGCACAATAA	AGCCAGGAAGACATGAACAAA	CCAAGTCTTGCTGCAAATTTA	AACCTGATTAATTTCATCAAT	1,51
IL17RA	23765	Hs_IL17RA_2	CAGCGGTCTGGTTATCGTCTA	CGGCACCTACGTAGTCTGCTA	CAGCTGGATTCACCCTCGAAA	TCCCGACTGGTTCGAATGTGA	1,77
IL1A	3552	Hs_IL1A_4	AAGGCAAAGCACGAAATGTTA	CACGCCTACTTAAGACAATTA	TCGAGTTGAATGAACATAGAA	CTGAGGTGATTTATGCCTTAA	1,59

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
IQCF2	389123	Hs_IQCF2_4	CAGGGCTAATGAACCATCTAA	AAGCATTGAATGGAAGACATT	TCGAGGGTGCTGGAGAAGAAA	CAGCTCTGATCGCCTACGCAA	1,76
IRF2	3660	Hs_IRF2_4	CACCTTATCTTAAAGCACTTA	CGGTCCTGACTTCAACTATAA	ACGGTGAACATCATAGTTGTA	CCCTATCAGAACGGCCTTCTA	1,68
ISG15	9636	NA	CCGGAAATAAAGGCTGTTGTA	AAGATGCTGGCGGGCAACGAA	CTCATCTTTGCCAGTACAGGA	NA	1,69
ITLN1	55600	Hs_ITLN1_5	CTGCGGGATTTGTTCAGTTCA	ACCCAGTAGCTAGAATGTTAA	CCCGGTGATCCCTGTGGTCTA	TGGAGTGGATATGGAACTCAT	1,79
JARID1D	8284	Hs_SMCY_4	CCCAGAGACGTTGGATCTCAA	CAGGGTAGAAACGTTGAGAAT	CTGACGATTGCTTAGCATTAA	CGCGTCCAAAGGCTAAATGAA	1,81
JUN	3725	Hs_JUN_3	AAGAACGTGACAGATGAGCAG	AAGAAGTGTCCGAGAACTAAA	TTCGTTAACATTGACCAAGAA	CGCGCGCGAGTCGACAAGTAA	1,46
KATNB1	10300	Hs_KATNB1_4	CTGCTGTAATTTATAAGGCAA	CAGGGAGGAGAGGCTGCATAA	CTGAACATCGTCAACCAGAAA	CAGCCTGGATTTCCACCCGTA	1,46
KCNAB3	9196	Hs_KCNAB3_5	AGGGAACATCCTCAAGAGCAA	CCGAGCGAGGTTTAAGCCGAA	AACCCTAGGGAACATCCTCAA	AACCTGTTTGACACCGCCGAA	1,62
KCNJ12	3768	Hs_KCNJ12_6	TTGGGTGAGACTGTTTACAAA	TGCGAAGGATCTGGTAGAGAA	CAGCTCCTACCTGGCCAATGA	CTCGCACTTCCACAAGACCTA	1,64
KIAA0664	23277	Hs_KIAA0664_5	CTCGGCCAAGCACATCTTCAA	AAGGGCCATATTCAAGGTGCA	CAGCCCGACCTTCAAGAAGAA	CGCCTTCGACATTCGCTTCAA	1,59
KIAA0947	23379	Hs_KIAA0947_3	CTGGCAGTTTATTGCTCTTAA	TCGGTGTTGCCTAATCAAGTA	CAGGTAGGATTTCTACACCTA	ATGGATTAGTTCTCAAATCTA	1,82
KIAA1128	54462	Hs_KIAA1128_6	ACCGTATATTTATGAAGCATA	GAGCATAATTATCTCAGGTAA	AAGAGCCTAACAATACTCAAA	TACGGTCAAGTATGCTAACAA	1,83
KIAA1267	284058	Hs_KIAA1267_1	CAGCCTAGATTTCCGAAATAA	TCGCGTAGAGAAACTGCAATA	CACCATATCCCTATGCATAAA	GAGACGCAGGTCAGAATGGAA	1,7
KIF11	3832	Hs_KIF11_14	ACGGAGGAGATAGAACGTTTA	GCCGATAAGATAGAAGATCAA	CTCGGGAAGCTGGAAATATAA	AACTGGATCGTAAGAAGGCAG	1,37
KIF23	9493	Hs_KIF23_3	CACGCACAACCCAAGCGCAAA	AACGACATAACTTACGACAAA	TAGGAATAGTATGGATATACA	CCATAGCGTGTTCAACATTAA	1,82
KIF3A	11127	Hs_KIF3A_6	CAAGAACGCTTGGATATTGAA	GCCGATCAATAAATCAGAGAA	AAGACCTGATGTGGGAGTTTA	CTGGTTCAGAAAGACAGGCAA	1,46
KPNB1	3837	Hs_KPNB1_4	CAAGAACTCTTTGACATCTAA	AAGGGCGGAGATCGAAGACTA	CTGGAATCGTCCAGGGATTAA	CTGGTACAACCCAGAGTAGAA	1,73
LAMC2	3918	Hs_LAMC2_3	CAGGCATATGGATGAGTTCAA	CCCAATTGGTTTCTACAACGA	CCGGACGGTGCTGTGGTGCAA	TACTTTGAGTATCGAAGGTTA	1,64
LARP1	23367	Hs_LARP1_3	CACCTAATCCACAGAAAGTAA	CAAGCGCCAGATTGAATACTA	TCCATGACTCTTGACATCCTA	CAGAGGAGGTCAGCAACCTAA	1,67
LHX3	8022	Hs_LHX3_5	CAGCTCTTTCCAAGACTTCAA	CTGGCCTGTGTGTAAGTCAAA	CCCACAGATGTCTGTTGCCAA	CTCCATCAGATCCTTTGGGAA	1,64
LINGO1	84894	Hs_LRRN6A_6	AAGGACTTCCCTGATGTGCTA	CCGCTGGCGGCTCAACTTCAA	CTAGGCAAGAACCGCATCAAA	CTGGCCCTACTTGGACACCAT	1,47
LOC162993	162993	Hs_LOC162993_4	CAGGTATTCCACATACCTTAA	CAGCACTTGCTAAACATCTAA	CAGGACTTAAATTACACATCA	TCGGGCCTTAGTACCCATTTA	1,53
LOC399940	399940	Hs_LOC399940_8	TTGATCAAAGTTCCCTGATAT	ATGGGACAAATAAGTTACATT	CTCAGTGGATTCAGAGTTGAT	TGCAGCCTGAAAGAACCAATA	1,71
LOC401431	401431	Hs_LOC401431_4	CAGGGAATTATTCACATGGCA	ATGACTTTGATTTCTGCATAA	CCCGAGGATGTGGAGCCGCAA	AAGCCTCATCTGGGCCCACAA	1,56
LOC440733	440733	Hs_LOC440733_14	ATCATGATGGTTAGCCATTTA	CAGCTGAAACTTTCTTGATCA	AAAGAGCATTATCTAAGTAAT	AACAACCTTTAGATATGCAAA	1,64
LPPR4	9890	Hs_LPPR4_9	CTGCTCGGGCCAAGTGGTTAA	AAGCTAGATTGTCTACCATCA	CCCATTCGGTTCTACATTATT	CCGGAGTCTTAGCATGCCGTA	1,81
MAN2B1	4125	Hs_MAN2B1_5	CGCCAAGGAGCTGGTCGATTA	TCGACCCACCTGGAAACTGAA	GCGCCTTGATTATCAAGATAA	TCGGCCGGCCCTCAAACGCTA	1,86
MAP2K3	5606	Hs_MAP2K3_8	ACGGATATCCTGCATGTCCAA	CCGGGCCACCGTGAACTCACA	ACCATTGGAGACAGAAACTTT	TCGACTGTTTCTACACTGTCA	1,72
MATN3	4148	Hs_MATN3_5	CACCTTGAATGCCGACAAGAA	CACCACTGTGAGTGTAGCCAA	AAGGTCAGCTCGTATCTTCAA	TATGGACAAATACATCGTTAA	1,77
MED6	10001	Hs_MED6_7	AAGGGTATTGGTGGCACTTCA	TCCCACTAGCTGATTACTATA	CACCCAAATTTGTGCAGCTAA	AAGCCTGTTCCAGTGGATCAA	1,67
MKL1	57591	Hs_MKL1_7	TAGTGTCTTGGTGTAGTGTAA	AGCAAGATTGCCATCACGAAA	AAGGGCCTGGATGCAAGGTTA	ATCACGTGTGATTGACATGTA	1,67
MRPS12	6183	Hs_MRPS12_8	TTCCATCAGGACCACTATTAA	CACGTTTACCCGCAAGCCGAA	CCCACTCAGAGCGAGGCTAAA	ACCCTGGCGCTTGTGATGTAA	1,61
MYC	4609	Hs_MYC_1	GATCCCGGAGTTGGAAAACAA	CTCGGTGCAGCCGTATTTCTA	ATCCACGAAACTTTGCCCATA	CCCAAGGTAGTTATCCTTAAA	1,69
MYEF2	50804	Hs_MYEF2_3	CAGAATAATGAATGGCATAAA	ATCGATATGGATCGAGGATTT	CTCGTAGGGCATTGCAGCGAA	TCCTTTAATGTTGTAATTGAA	1,87
MYOD1	4654	Hs_MYOD1_5	TACAGGGAATTTGTACGTTTA	CTGCACGTCGAGCAATCCAAA	CACGTGGGCGCGCTCCTGAAA	CTCCGACGGCATGATGGACTA	1,69
NAE1	8883	Hs_APPBP1_6	ATGGACTAGTTGGTTATATGA	AAAGATGATTATGTCCACGAA	TCGATCCTTAGCTGAAGAATA	GTGGGTAATCATGTTGCCAAA	1,69

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
NDUFV3	4731	Hs_NDUFV3_6	ACACTGATTATCCAACATATA	ATCCATATAATTAGAGAATTT	CCCGCTGTGCATAATCGGTTT	CTGAGCCGTTTGACAACACTA	1,44
NECAP2	55707	Hs_NECAP2_2	AAGGAGCTCAGTAAACTAGAA	CAGGTACTTCGTGATCCGCAT	CAACATCGCAAACATGAAGAA	CTGCAGCTTGAGCTACAATCA	1,8
NEK8	284086	NA	ACGGACAGTTGGGCACCAATA	CCAGAAGCTGGTGATCATCAA	TAGAGTTAGAAGGCAGACCTA	NA	1,66
NEK9	91754	Hs_NEK9_2	CAGGTGTCATGTGGTGATGAT	TGCCTTCGGATCAGATTATTA	CAGAGCTCTGTCAAGGAGTAA	TACACTTGGGTGAACATGCAA	1,81
NSF	4905	Hs_NSF_9	AGGCAGACTTTCTACATGCAA	GTGGGTCAATTCCTTAGTATA	ATCCAACTTCCCGTTCATCAA	TTGGCCCTCTTAAGAGAAGAA	1,64
NTHL1	4913	Hs_NTHL1_6	GAGCAAGGTGAAATACATCAA	CAGGCTGAGGTGGACCAAGAA	ACCGTCTGTGAAGTGGCTTTA	GTGGACCAAGAAGGCAACCAA	1,85
NUP205	23165	Hs_NUP205_9	CAGCACTTCCTGGAATATTAA	CAAGATGTGCATGATAAGATA	GAGAGTCAACTGGCTCTAATA	AGGGTGCATTAGAGCTGCTAA	1,72
NUP98	4928	Hs_NUP98_8	CTGGAGTTAGCACTAACATAA	CAGTGTATTACTGCTATGAAA	AACCCTATTGCCAAACCTATT	CTCACTAAGGTTGGTTACTAT	1,79
NXF1	10482	Hs_NXF1_4	CAGAACAAGTAGAACAGCTAA	AACGCGTTAATTTCCCTCAAA	CCGAAGGATATCTATCATCAT	CGCGAACGATTTCCCAAGTTA	1,66
ODZ4	26011	Hs_ODZ4_5	CCGGCCGGCCTTTAACCTCAA	CCGCAGGGTGATATACAAGTA	TCGGTTTATCCGGAAGAACAA	CTGCGGGTTCACAACCGAAAT	1,81
OPN1SW	611	Hs_OPN1SW_4	CAAGAGTGCTTGCATCTACAA	CGCCATGTACATGGTCAACAA	GCGCTACATTGTCATCTGTAA	TTGGCCTGTTTGCAACAGCTA	1,76
P76	196463	Hs_LOC196463_4	CTGGATGAACACGGTGGTGAA	CAGGCTGATGAGGTACAATGA	GTGGATGATCGTGGACTACAA	CTGGAAGTTCGCGCCTGTCAA	1,48
PCDH18	54510	Hs_PCDH18_4	CTGAGTATAGTTTGACTGTAA	CCCGAAGCAACTGGTAAGCAA	CTGCGCCATAGTAGCAGGTAA	CCGGAGAATATTTCTCTCACA	1,6
PHF2	5253	Hs_PHF2_6	TTGAACATTTATATAATCTAA	TCGCCTCTAGCTGGAAACAAA	AGGACCGCTTATTCCACTTTA	CCGCATCGTCTCCAAACAACA	1,72
PIK3R5	23533	NA	ATCGCAGATCAAAGTGGACAA	TAGGATCCTTTCTAGAAGGAA	CAGGATCTATAAACTCTTCAA	NA	1,83
PIK3R6	146850	Hs_C17orf38_6	TCGCTGGACAAGGACGATCAA	CACCTTCAGGACGAACAATAT	CAGGGATGTGGTCAGATTCGA	TCGCCGCACCCTGGAGCACTA	1,7
PIN1	5300	Hs_PIN1_4	GACCGCCAGATTCTCCCTTAA	CAGTATTTATTGTTCCCACAA	CAGGCCGAGTGTACTACTTCA	CGGCTACATCCAGAAGATCAA	1,66
PKHD1	5314	Hs_PKHD1_7	CACCGGCATATTGGAAGTGTA	CACGAGATAGCTGTACTTTCA	CTGATGAGTATTGAAGTACTA	CAAGATTACTGAGATACGGAA	1,66
PKN1	5585	Hs_PKN1_8	CCGCAAGGAGCTGAAGCTGAA	CCGGAGCAGCCTCAAAGCAGA	CACGGGTGACATATCGGTGGA	CTCGGACAGCTCACCTCAGAA	1,64
PLAU	5328	Hs_PLAU_4	CTGCCTGCCCTCGATGTATAA	CAGGGCTCTGATATTCCATGA	TCGCTCAAGGCTTAACTCCAA	AAGGCTTAACTCCAACACGCA	1,76
PLD2	5338	Hs_PLD2_6	CCGGCCTTTCGAAGATTTCAT	CAGCCTGCTGACAGACACTAA	TGGGCGGACGGTTCTGAACAA	CAGCAAGGTGCTCATCGCAGA	1,78
PLK3	1263	Hs_PLK3_8	CAGAAAGACTGTGCACTACAA	CTGCATCAAGCAGGTTCACTA	CCCGCAGAGCCGCGTCGCCAA	CAGCGCGAGAAGATCCTAAAT	1,6
POLK	51426	Hs_POLK_5	CAAGGATTTACCCATTAGAAA	TAGGATGGGACTTAATGATAA	AAGGATAAACCCATTGCTGTA	TGGAATTAGAACAAAGCCGAA	1,85
POLR2H	5437	Hs_POLR2H_5	ATGGATCTAATCTTAGATGTA	CAGGTCATGGGCATTGTTCAA	AACATTCAAATTTACCCTGTA	TTGAGTATGTAATGTATGGAA	1,39
POLR2L	5441	Hs_POLR2L_4	AAGGTCTTTCAGAACCACTAA	CTGGAAGGAACCATCCAGTAA	CTGGGAGGTTGCCACTGCAAA	CGGCAACAAGTGGGAGGCTTA	1,68
PPARA	5465	Hs_PPARA_5	TCGGCGAACGATTCGACTCAA	CAGTGGAGCATTGAACATCGA	CAAGAGAATCTACGAGGCCTA	AAGCTTTGGCTTTACGGAATA	1,71
PPP1R14D	54866	Hs_PPP1R14D_6	CCGCCTGACAGTGAAGTATGA	CAGGAGCTCTTCCAGGATCAA	AGGGACATTTGCATACTCCTA	CACCCGGACTCCTCCAAGATA	1,72
PRDX5	25824	Hs_PRDX5_5	CAGCCAGGAGGCGGAGTGGAA	CTGAGTGTTAATGATGCCTTT	ATGGTGGTACAGGATGGCATA	TGGGAAGGAGACAGACTTATT	1,87
PRPF8	10594	Hs_PRPF8_5	ACGGGCATGTATCGATACAAA	ATGGCTTGTCATCCTGAATAA	CAACGTCGTCATCAACTATAA	CTCATCGTGGACCACAACATA	1,46
PRPS1	5631	Hs_PRPS1_5	AACATGCTTCCTGCTATGTAA	CCCAAGGTCTATGCTAAATTA	CACCATCTGCTTGACTATGTA	CCGGGCGCCAATCTCAGCCAA	1,7
PRSS27	83886	Hs_PRSS27_2	CCCACCAGACTCATTTGTAAA	ACCAGTGCCCTTCACCAATTA	AATAATAATAATAATGAATGA	CACCTCTGAGACGTCCCTGTA	1,82
PRX	57716	Hs_PRX_5	CAGGCTACTTCGAACCAGGAA	CCGAGTGTTCTTCGAGAACTT	GGCGGAGTTGGTGGAAATTAT	CCCGCGGGCCAAGGTGGCCAA	1,87
PSENEN	55851	Hs_PEN2_3	CTCGCCCAAAGAAGACTACAA	CTCCCAGGACAGGCTCCTTAA	CGCGCAAACGTCCATAACTGA	CAGAGCCAAATCAAAGGCTAT	1,72
PSMA1	5682	NA	CTGCCTGTGTCTCGTCTTGTA	CAGGGCAGGATTCATCAAATT	CACAGTTGGTCTGAAATCAAA	NA	1,72
PSMD2	5708	Hs_PSMD2_4	TGGGTGTGTTCCGAAAGTTTA	CTCCGGAGGGCTGTACCTTTA	CAGGGTTCCAGACGCATACAA	TAGCGAACACTTTGACTCCAA	1,53
PTPLA	9200	Hs_PTPLA_2	CACTGTTTAATTGGAATTGTA	AAGTGAGTTCAAGAATCTTTA	TTGAGATAGTTCACTGTTTAA	AAGTATTCAGAAGACACTTAA	1,66

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
PTPRN	5798	Hs_PTPRN_6	CTGGTGAAGTCTGAACTGGAA	CAGGAAGGTGAACAAGTGCTA	CACGATGACCTCACCCAGTAT	CCCTATGACCATGCCCGCATA	1,65
RAB4A	5867	Hs_RAB4A_9	AATGCAGGAACTGGCAAATCT	CACACTTGAAATACTAGATCA	AAGATGACTCAAATCATACAA	CAGGTCCGTGACGAGAAGTTA	1,73
RAB6B	51560	Hs_RAB6B_6	ATCCATGTTCTTAGAGCCTCA	ATGGCCAGAGTGGGTCGTCAA	AACAATTAACTGAGCAAATTA	CAGGGATCACATCACTCTTAA	1,59
RACGAP1	29127	Hs_RACGAP1_4	CACCACAGACACCAGATATTA	CTGGTAGATAGAAGAGCTAAA	CAGGTGGATGTAGAGATCAAA	AGGATGAGTCATGGAATTTAA	1,56
RAX	30062	Hs_RAX_6	CAGGCTGAAGCTCCTAAACTT	CCGCGAGGAGCTGGCCGGCAA	ACCGGCGAAGCGAAACTGTCA	CACGACTTTCACCACGTACCA	1,76
RBM42	79171	Hs_MGC10433_5	CCGCCCAATTATCGCGACCAA	CCGCTTCCCATCCTTCCTTAA	CTCCAGTACCTGGAATCCCAA	GAGCATGTGGAAGGACCGGAA	1,63
RETN	56729	NA	CAGGAGGTCGCCGGCTCCCTA	CTCCATGGAAGAAGCCATCAA	TCCCTAATATTTAGGGCAATA	NA	1,77
RFFL	117584	Hs_RFFL_5	CCGGCTATACAAGGATCAGAA	ATCGGTTTCTTCAGTGCCTTA	TCGCAACTTTGTCAACTACAA	CTCCATGACATCTCTACCGAA	1,75
RNF150	57484	Hs_RNF150_7	AACCCGGAACTTGCAGAAATA	AGACGTCATCTTTACTACTAA	ATGGCAATGTCTCTCATCCAA	CGCCTTCGTGAACATCACCTA	1,76
RPL35	11224	Hs_RPL35_4	CCGTGTTCTCACAGTTATTAA	TGCAGCAATGGCCAAGATCAA	CAGGAAATTCTACAAGGGCAA	CGAGGAGAACCTGAAGACCAA	1,53
RPLP2	6181	Hs_RPLP2_4	CAAGGTTATCAGTGAGCTGAA	AAGGAGGAGTCTGAAGAGTCA	CAGCGCCAAGGACATCAAGAA	CAGCGTGGGTATCGAGGCGGA	1,38
RPS10	6204	Hs_RPS10_8	ACCGCGCATGCTCCTTCCTTT	AACCGGATTGCCATTTATGAA	GACATTTCTACTGGTACCTTA	ACCAATGAGGGTATCCAGTAT	1,69
RPS14	6208	Hs_RPS14_9	CCATATCTTTGCATCCTTCAA	TCGGGCGGATTGAGGATGTCA	ATCACCGCCCTACACATCAAA	TGGGATGAAGGTAAAGGCAGA	1,57
RPS16	6217	Hs_RPS16_6	ATGATTGAGCCGCGCACGCTA	ACGCGGCAATGGTCTCATCAA	TCGGACGCAAGAAGACAGCGA	CCCGCGCTCGCTACCAGAAAT	1,49
RPS27A	6233	NA	CTGACTTACTGTTTCAACAAA	CTGGCTGTCCTGAAATATTAT	TCGAGGTTGAACCCTCGGATA	NA	1,46
RPS5	6193	Hs_RPS5_7	CTCGAACTCCTATGCCATTAA	CGCGTGGTCTACGCCGAGTGA	TTCCCAGCTGCTGCCCAATAA	CAGGCTGTGTTCTCAGGATGA	1,33
RPS6KA6	27330	Hs_RPS6KA6_9	CAGGTCCACAATATTCATACT	TTGGATCATCTGCACCAATTA	GGCGAGGTAAATGGTCTTAAA	TTCATCGTGATCTTAAACCTA	1,82
RUNX1	861	Hs_RUNX1_2	CTCCCTTTCATGTTAATCAAA	CAGGTCGTTCTTATCTAGAGA	CAGGATACAAGGCAGATCCAA	CCGCACCTTATCAATTGCAAA	1,82
SAFB	6294	Hs_SAFB_5	ACGGACTGTAGTAATGGATAA	CTGCCATATTGTAGCTCAATA	CCGAAGATGACTCGGATACAA	AGGGTGCGTGAACGCAGTGAA	1,79
SCAF1	58506	Hs_SR-A1_5	CTGGGCTCCATTGGCGTCAAA	CTGGACGTATTTATGGCTCCA	CACGGTGGGCCGGCTTGACAA	CACGGCTACTGTGTTGGACAT	1,64
SCAMP4	113178	Hs_SCAMP4_5	ACCCGTGTTCATCTCATCCGA	CAGGATGCTGTTGCTGTAGGA	CAGCCTGCGCTGGTTGGTGAA	CCCGTCAAATCTGTGCCTTAT	1,88
SCARB1	949	Hs_SCARB1_9	CCGATCCATGAAGCTAATGTA	TAGGGAGAGGCTCGTCAACAA	CACCGTGTCCTTCCTCGAGTA	CAGCGAGATCCTGAAGGGCGA	1,41
SDC1	6382	Hs_SDC1_2	CAGGGCCTCCTGGACAGGAAA	TCCGACTGCTTTGGACCTAAA	CAGGTGCTTTGCAAGATATCA	CCGCAAATTGTGGCTACTAAT	1,75
SELPLG	6404	Hs_SELPLG_5	CAGCAATTTGTCCGTCAACTA	ATGGAGATACAGACCACTCAA	TCCATGGAACCTACTACCAAA	CCGGAGACAGGCCACCGAATA	1,88
SERPINA6	866	Hs_SERPINA6_5	CAGCAGACAGATCAACAGCTA	CAACAGCTATGTCAAGAATAA	CACCAGCTTAGAAATGACTAT	AGGGTTATGAACCCAGTGTAA	1,75
SERPINB2	5055	Hs_SERPINB2_7	CAGAAGGGTAGTTATCCTGAT	AACCTATGACAAACTCAACAA	CTGGAAAGTGAAATAACCTAT	TGCGAGCTTCCGGGAAGAATA	1,73
SERPINE2	5270	Hs_SERPINE2_10	CTGGGAGGTATTGGAGGGAAA	AACGCCGTGTTTGTTAAGAAT	CGGCGTAAATGGAGTTGGTAA	AACTCCTGTCTTGCTAGACAA	1,45
SEZ6L2	26470	Hs_SEZ6L2_9	TCCATGCTTGGAGAAGGACAA	CAGGATCCACTATCAGGCCTA	CCGGCTGCTTCTGCACTTCCA	CTCGCTGGATGAGGACAATGA	1,4
SF3A1	10291	Hs_SF3A1_5	CAGGATAAGACGGAATGGAAA	CGCAAGGATTATGATCCCAAA	CAGCATGTAGGTAGCGTCCTA	CTCATTCAGGAGCGCTATGAA	1,63
SF3B1	23451	Hs_SF3B1_7	ACGATGACTATTCATCATCTA	GACCGGGAAGATGAATACAAA	AAGCATAGGCGGACCATGATA	TACGAGTTTGCTTGGTCAGAA	1,65
SF3B14	51639	Hs_SF3B14_7	AACATTCGACTTCCACCTGAA	AACAGCTTATGTGGTCTATGA	AAGAATGCATGTGATCACCTA	AAATATGGACCTATTCGTCAA	1,8
SFTPB	6439	Hs_SFTPB_4	CACGATGAGGAAGTTCCTGGA	CCGACCTTTGATGAGAACTCA	GCCCTGAGTTCTGGTGCCAAA	CAGGATCTCTCCGAGCAGCAA	1,76
SIGMAR1	10280	Hs_OPRS1_5	CCGGCTTGAGCTCACCACCTA	AGGGATATCCATGCTTATGTA	CAGCGTCTTCCATTCCAGAAA	TCCATCTGTCTGTTTCTATTA	1,45
SLC12A4	6560	Hs_SLC12A4_7	CAAGAACATGATGGAAATTGA	TCCCGTGTTTCCGGTATGCAT	CACGTCGAATGCCACTTTGAA	CGCCGGCATGATCTACAAATA	1,44
SLC22A6	9356	Hs_SLC22A6_8	CACCTTGATTGGCTATGTCTA	CACCGATGGCTGGATCTATGA	CAGGACCAGTCCATTGTCCGA	TGCCACTAGCTTTGCATACTA	1,87
SLC25A19	60386	Hs_SLC25A19_6	CTCCCTGTGATCAGTTACCAA	CTCGTATGAATTCTTCTGTAA	CAGGGTGAGCCCAAGGTCTAT	TCCGCTGGACCTCTTCAAGAA	1,58

Table 3

GeneSymbol	LocusID	siRNA4 ID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST
SLC4A8	9498	Hs_SLC4A8_5	AGCCGTCATTATTAACAGGAA	GACGGCTATCTTAAAGTTTAT	TGGGACCAGTACAATTCTCAA	ATGATCGCGGATGGATTATTA	1,81
SLC7A1	6541	Hs_SLC7A1_4	GAGGGTTGGTTTATTATCAAA	ACGGATCTGGATATACACTAT	ACGCTTATGACTCCTAATGTA	CAGCACCCAATAGACTATTTA	1,79
SMU1	55234	Hs_SMU1_6	TTGCACGAAGCTCGCATTGAA	TAGGAGCCGTTAAGTATATAT	AACAGTAAAGTGCTTCATATT	TACGATGTTACGCAACCACTA	1,82
SNRP70	6625	Hs_SNRP70_5	AAGATTGAGCGGCGACAGCAA	CTCCGGAGAATGGGTATTTGA	CCGGAGAGAGTTTGAGGTGTA	CTCCTCCAACTCGTGCTGAAA	1,59
SNRPF	6636	Hs_SNRPF_9	AAGGGCTATCTGGTATCTGTA	TTGGCGGCCATTTCTCTTGAA	GCCGTGGTTACGATGAGTTTA	AAAGATTACTCACTGAACTAA	1,43
SNX6	58533	Hs_SNX6_3	AAGGTCTAGGTCACTAGTGGA	CAGGCCGAAACTTCCCAACAA	TAGACTAAACCAAGTATTGTA	ACCGCGGACTTAAAGCAATAA	1,83
SNX9	51429	Hs_SNX9_4	CAGCCGCTTTCCAGTGATGTA	ACAGATCTCAATGATGCAATA	TCCAGTGGCTATCAAGGTGAA	ATGGAATGTAATCACGAGTAT	1,54
SON	6651	Hs_SON_6	ATGATGTTGATTTATCTTTAA	AAAGATATTCATCTTGATTTA	CAGCGCTGGAATCCTATAATA	TAGGTCTTTCGTGGTCAGTAA	1,31
SRRM2	23524	Hs_SRRM2_3	CGCCACCTAAACAGAAATCTA	CCCGCCGTCGTTCAAGGTCTA	CTCGATCATCTCCGGAGCTAA	CAGGGATGTCTTCAAATCAGA	1,85
STAB1	23166	Hs_STAB1_4	CACGAAATACTCCTACAAGTA	CACGCCAACTGTAGCCAGGTA	CACCTCGTGCGCGGCCATCAA	TAGGAACAATGGTCACTTGTA	1,48
SULF2	55959	Hs_SULF2_9	AGGGATGTCCTCAACCAGCTA	ATGACAGATTCTGGAGGATAA	TCGAAAGTGGCCAGAAATGAA	CACATCGACCACGAGATTGAA	1,67
SUPT6H	6830	Hs_SUPT6H_8	TCAGTGTATGCTAGGCAACAA	CTGCCGCATCATGAAGATTGA	CAGGGTGATGTGATTATCCGA	CTGCAAGGAACTGCCCGGCAA	1,51
TBL3	10607	Hs_TBL3_6	CCGTATCTGGAGAATGAACAA	CTGCGTCACGTGGAACACCAA	CCACGTTGTCGTGGCCTCCAA	CTGGGACATCGTGCGGCACTA	1,75
TCF3	6929	NA	CCCGGATCACTCAAGCAATAA	GAGCGGAACCTGAATCCCAAA	NA	NA	1,71
TFE3	7030	Hs_TFE3_4	TCGCAGGCGATTCAACATTAA	TCCGGGATTGTTGCTGACATA	CAGCTCCGAATTCAGGAACTA	AAGGAGATTGATGATGTCATT	1,82
TMEM50B	757	Hs_TMEM50B_2	AATGGAGTAGATTGTACATTA	ATGGAGTAGATTGTACATTAA	AAGGGATAATACATGATCAAA	TTGGTGCATATGTTACCCAAA	1,77
TNFRSF18	8784	Hs_TNFRSF18_6	CAGGAGGGAGAGAGAGACACA	CAGCAGAAGTGGGTGCAGGAA	CTGCATGTGTGTCCAGCCTGA	TGGGTCGGGATTCTCAGGTCA	1,58
TNK2	10188	Hs_TNK2_8	CAAGCTGCACATCCAGATGAA	ACGCAAGTCGTGGATGAGTAA	CGGCAGTCAGATCCTGCATAA	TACCTGCTTCTTCCAGAGAAA	1,74
TRERF1	55809	Hs_TRERF1_8	CCGCAACAAATTCGCCCATCA	AGAGTGGGTACTGTTCGGTAA	CAGCGTATCTCCATGCAAGAA	CTGCGGAAGCCTGTCAGGTTA	1,81
TRIM14	9830	Hs_TRIM14_7	CACCGAGAAGCTCAAGGCTAA	CACGTGCAGAAACTCAGCCAA	CTCAGATTACTACTTGACGAA	GGCCAAGAAATTCATTGATAA	1,52
TRIM21	6737	Hs_TRIM21_8	CAGCAGCACGCTTGACAATGA	CAGAGCATACCTGGAAATGAA	CACGCAGAGTTTGTGCAGCAA	CTGGATATTACCTCTCCAGAA	1,69
TRIM60	166655	Hs_TRIM60_8	GAGCCCTTGAGGAATAATATA	TTGCGTCAGGTCCTAAGACAA	AAGGATCTAGATGATACCTTT	AGCTCCGTAATTTGACTGAAA	1,78
TSSK6	83983	Hs_TSSK6_1	CCGGTTGGAACCTGCAATAAA	CAAGGGTACCGTGGCCATCAA	CGCAGTCACTTCACAAGGCAA	GAAGGTGGCCACATCCAAGAA	1,56
TUBB4	10382	Hs_TUBB4_5	CTGCCTCACCCTCAATAAATA	TGAGCCCTAATTTATCTTTAA	CTCTGGAAACCGCACCTTTAA	CTCGAGGCTTCTGACCTTTGA	1,77
TXNL4A	10907	Hs_TXNL4A_6	AAGGTTTACTCTGGTTATAAA	CAGCATCGCCGAGAAGGTTAA	ATGCCGCGAGCTGGGCTTTAA	CAAGGACTACTCCACCAAGTA	1,62
UBAC2	337867	NA	CCGGCAGCTGATGTTCTCTCA	TACATCTGGATTGTAGCCATA	NA	NA	1,89
UBE2N	7334	Hs_UBE2N_8	AAGATAGTACTGAATGGAGTA	CTGGCCCTGAGCATGCATAAA	TCCCAATTTGACAATCGTATT	AGCAGTTGTGACTGACATGTA	1,78
VNN2	8875	Hs_VNN2_9	AACACACATCATGTCAGCCTA	CAGCAATTCAGCAATAACTTA	CTGAAGTGCTACTTACCGAAA	CAGGATTACATGGCCGAAGGA	1,83
WNT3A	89780	Hs_WNT3A_3	ACCGCCATCCTCTGCCTCAAA	GCCGCGCTACACCTACTTCAA	CCCGACTGTGCTGCTCGCGAA	CAGGAACTACGTGGAGATCAT	1,85
WNT9A	7483	Hs_WNT9A_4	CCGGCTGAAGCTGGAGCGGAA	CCGTGTGGACTTCCACAACAA	CAAGTATGAGACGGCACTCAA	CAGCAGCAAGTTCGTCAAGGA	1,4
XAB2	56949	NA	CACGTACAACACGCAGGTCAA	CCGCGTGTACAAGTCACTGAA	CCGGACCTTGTCTTCGAGGAA	NA	1,65
XPNPEP1	7511	Hs_XPNPEP1_4	AAGGAGAACCTCGTTGACAAA	CCCGACTTCTTTGGCCAGTGA	ATGAGATTGCGTGGCTATTTA	CCCGACTGGAACCAAAGGTCA	1,74
XPO1	7514	Hs_XPO1_6	CCCATTGTAAAGCGACTTCAA	TACATGTTACTCCCTAATCAA	TTCTCAGAATATGAATACGAA	ATGGTTAGTCGAATGGCTAAA	1,64
XRCC6	2547	Hs_G22P1_3	TTTGTACTATATACTGTTAAA	AAGCTCTATCGGGAAACAAAT	ACCGAGGGCGATGAAGAAGCA	GAGGATCATGCTGTTCACCAA	1,42

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
AAMP	14	1,71	1,83	1,72	0,69	0,06	-0,33	0,02	0	0,87	0,07	0,4	0,97	2
ACTN1	87	1,64	1,68	1,9	-1,68	0,63	-0,42	0,13	0	1,03	0,97	0,26	-0,4	2
AHCYL1	10768	1,47	1,55	1,71	0,72	0,87	-0,15	0,73	1	0,8	0,82	0,17	0,32	2
AIG1	51390	1,87	1,87	1,78	0,97	0,74	0,83	0,81	3	-1,56	0,4	0,83	0,93	2
AKR1C4	1109	1,63	1,83	1,78	0,82	0,53	0,78	0,9	2	0,68	0,11	0,52	0,83	1
AKTIP	64400	1,68	1,81	1,76	0,96	0,58	0,38	0,17	1	0,98	0,6	0,29	1,06	2
ALDH7A1	501	1,61	1,9	1,87	0,88	1,01	0,74	0,84	3	0,83	0,9	-0,08	0,87	3
ALX4	60529	1,67	1,6	1,71	0,91	0,85	0,62	0,95	3	1,38	0,9	0,99	-0,85	3
AP2M1	1173	1,51	1,57	1,59	0,86	0,92	0,81	0,62	3	0,89	0,26	0,45	0,94	2
APBB1IP	54518	1,86	1,91	1,9	0,49	-0,5	0,47	0,28	0	0,98	0,62	-0,21	0,9	2
ARD1A	8260	1,83	1,72	1,88	1	0,99	0,87	0,86	4	1	1,05	0,92	1	4
ARTN	9048	1,38	1,63	1,68	0,8	0,96	-0,15	0,97	2	0,59	1,11	-0,45	-2,59	1
ASAH3L	340485	1,79	1,85	1,72	0,86	0,96	-0,08	0,6	2	0,9	0,85	0,51	0,81	3
ATCAY	85300	1,81	1,9	1,83	0,91	0,84	0,42	-1,46	2	0,08	1,13	0,44	1,04	2
ATP1A2	477	1,67	1,64	1,61	-0,04	1	0,76	0,87	2	0,35	0,83	0,64	-239,08	1
ATP6AP1	537	1,63	1,69	1,7	1	0,78	0,98	0,92	3	1,02	0,53	0,31	0,95	2
ATP6AP2	10159	1,87	1,93	1,84	0,8	0,67	0,83	0,49	2	1,01	0,74	0,98	0,93	3
ATP6V0C	527	1,91	1,88	1,85	0,75	0,91	0,96	0,96	3	1,33	1,22	1,11	1,03	4
ATP6V0D1	9114	1,46	1,84	1,78	0,84	0,75	0,89	0,46	2	0,6	1,14	1,23	1,1	3
ATP6V1A	523	1,93	1,91	1,86	0,89	-0,71	0,83	0,93	3	1,11	0,5	0,3	0,98	2
ATP6V1B2	526	1,55	1,8	1,89	0,88	0,8	0,46	0,99	2	1,25	1,13	-0,26	1,02	3
AZIN1	51582	1,82	1,87	1,69	0,53	0,94	0,92	0,47	2	0,31	1,32	0,8	0,7	1
B2M	567	1,35	1,57	1,59	1	0,05	0,09	0,99	2	0,85	0,88	-0,38	1,02	3
B3GNT1	11041	1,53	1,56	1,7	0,87	0,91	-2,1	0,81	3	0,38	-1,6	-1,1	0,98	1
BAIAP3	8938	1,78	1,77	1,84	0,56	0,43	-0,07	-1,03	0	0,66	0,81	0,87	0,85	3
BARHL2	343472	1,9	1,88	1,82	-0,19	0,32	0,81	0,64	1	0,12	-6,6	1,25	1,17	2
BNIP3L	665	1,65	1,8	1,87	0,87	-0,67	0,72	0,92	2	0,72	0,95	0,66	0,98	2
BRUNOL6	60677	1,88	1,88	1,77	0,12	-0,66	0,87	0,83	2	-0,01	-4,07	1,38	1,32	2
BZRAP1	9256	1,63	1,55	1,86	0,8	0,99	0,99	0,96	4	0,96	1	1,04	-0,45	3
C14orf172	115708	1,8	1,91	1,79	0,83	0,86	0,56	0,87	3	0,82	0,43	0,85	-0,18	2
C19orf47	126526	1,57	1,58	1,73	-0,47	0,85	0,86	0,98	3	0,44	0,9	-0,36	0,93	2
C21orf7	56911	1,57	1,62	1,58	0,51	0,44	-0,51	0,38	0	0,91	0,85	-0,22	0,94	3
C3orf31	132001	1,63	1,72	1,73	0,65	0,89	-0,59	-3,54	1	1,01	0,99	0,7	0,47	2
C4orf29	80167	1,53	1,68	1,64	0,67	0,78	0,09	0,98	1	-1,47	1,04	-1,21	1,01	2

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
CARD9	64170	1,81	1,87	1,61	0,71	0,49	-1,44	0,49	0	0,86	-2,13	1,23	0,44	2
CASP8AP2	9994	1,86	1,9	1,83	0,8	0,96	0,53	0,82	2	0,55	0,84	0,81	-0,75	2
CCNB3	85417	1,52	1,49	NA	1	0,82	-0,67	NA	2	0,73	0,85	-0,7	NA	1
CD48	962	1,48	1,37	1,64	-0,14	0,63	0,62	-0,72	0	0,18	0,7	0,85	1,08	2
CD58	965	1,86	1,84	NA	0,8	0,09	0,98	NA	2	0,87	0,77	0,97	NA	2
CD6	923	1,83	1,83	1,8	0,93	0,81	0,48	0,92	3	1,01	0,6	0,95	0,89	3
CD63	967	1,79	1,86	1,81	0,81	-0,38	-0,13	-0,73	1	-0,11	0,1	1,21	0,85	2
CD81	975	1,36	1,53	1,64	-0,57	-0,15	0,35	0,73	0	0,85	0,66	0,38	1,09	2
CDC23	8697	1,59	1,65	1,52	0,78	0,99	-0,25	1	2	0,64	0,38	-0,04	0,74	0
CDK4	1019	1,62	1,88	1,87	0,76	0,96	0,23	1	2	0,53	-0,27	0,86	0,99	2
CDKN1B	1027	1,89	1,86	1,84	0,75	0,84	0,74	0,62	1	0,64	0,7	0,91	1,08	2
CEL	1056	1,72	1,56	1,52	0,66	0,72	0,7	0,06	0	0,17	1,01	0,99	-0,54	2
CHST5	23563	1,45	1,48	1,44	0,99	0,59	0,04	1	2	0,5	1,02	0,94	-1,5	2
CIB3	117286	1,52	1,61	1,84	0,85	0,88	0,68	0,61	2	-1,57	0,82	1,1	0,21	2
CLIC4	25932	1,77	1,68	1,62	-0,41	0,66	-0,28	-0,29	0	-1,85	0,94	0,05	1	2
CLK1	1195	1,92	1,89	1,85	0,84	0,58	0,88	0,51	2	0,9	0,82	0,89	0,87	4
CNNM1	26507	1,76	1,71	1,39	0,88	0,17	0,28	-1,88	1	0,86	1	-0,58	0,43	2
COPA	1314	1,75	1,8	NA	1	1	1	NA	3	1,01	1,05	1,05	NA	3
COPB1	1315	1,65	1,74	NA	0,97	1	0,99	NA	3	0,65	1	-2,35	NA	1
COPB2	9276	1,48	1,43	1,63	1	1	1	1	4	0,16	1,01	0,96	1	3
COPG	22820	1,3	1,66	1,67	0,91	0,97	0,22	1	3	0,9	0,94	0,22	1,16	3
CRAMP1L	57585	1,5	1,85	1,81	0,6	0,69	0,7	0,57	0	0,82	0,93	0,75	1	3
CRYAA	1409	1,7	1,76	1,77	0,95	0,92	0,59	0,49	2	0,73	-0,26	0,48	0,9	1
CTA-216E10.6	79640	1,51	1,71	1,74	0,51	0,99	0,19	1,01	2	0,25	1,04	0,29	-0,35	1
CUEDC2	79004	1,5	1,33	1,5	0,78	1	0,82	0,89	3	1,16	0,48	1,08	-0,29	2
CXCR6	10663	1,79	1,8	1,83	-1,15	1	1	0,9	3	0,42	0,47	0,15	0,21	0
CYC1	1537	1,47	1,7	1,84	-0,93	0,39	0,85	0,93	2	0,18	0,5	1,1	0,36	1
CYP17A1	1586	1,87	1,84	1,82	-1,63	0,92	0,18	0,88	2	-1,89	1,04	-0,27	0,82	2
CYP2U1	113612	1,58	1,46	1,49	-0,12	0,47	0,91	0,6	1	-2,14	1	1	-2,33	2
DBT	1629	1,36	1,63	1,67	0,77	1	1	0,93	3	1,02	0,92	-2	1	3
DCLK2	166614	1,58	1,68	1,65	0,95	0,95	-0,01	0,95	3	1,02	-0,51	0,66	-0,16	1
DGKH	160851	1,37	1,53	1,63	-0,51	-0,23	0,63	0,92	1	-0,44	0,96	-4,95	1,02	2
DGUOK	1716	1,61	1,7	1,76	0,56	0,72	0,86	0,98	2	0,04	-1,76	0,7	0,37	0
DHRS2	10202	1,78	1,77	1,64	0,8	0,11	0,93	0,68	2	0,33	0,18	0,43	-0,23	0
DLG2	1740	1,79	NA	NA	0,91	1	NA	NA	2	-2,41	0,98	NA	NA	1
DMAP1	55929	1,87	1,91	1,82	1,01	0,48	-0,69	0,68	1	0,82	0,11	0,82	0,9	3
DMRT1	1761	1,93	1,92	1,71	0,91	0,94	0,94	0,6	3	0,98	0,73	-1,2	0,73	1
DTX3	196403	1,75	1,67	1,67	0,84	0,68	0,91	0,98	3	0,6	-17,71	0,84	1,01	2
DUSP27	92235	1,81	1,7	1,54	0,63	-0,48	-0,58	0,97	1	0,6	0,8	-17,12	0,89	2
E2F1	1869	1,76	1,9	1,74	0,87	0,75	0,81	0,79	2	0,29	0,03	1,01	-4,6	1

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
EEF1A1	1915	1,75	1,87	1,64	0,93	0,65	0,29	0,77	1	0,6	0,94	0,79	0,9	2
EIF3A	8661	1,72	1,75	1,69	1	1	0,98	0,93	4	1	1	1,05	-6,63	3
EIF3C	8663	1,52	1,36	1,44	0,88	0,96	0,99	0,98	4	0,82	-0,94	0,58	0,53	1
EIF3G	8666	1,47	1,63	NA	-0,71	0,95	0,99	NA	2	-9,14	-1,61	0,99	NA	1
EIF4A3	9775	1,77	1,71	1,77	0,98	0,63	0,91	0,61	2	0,98	0,23	1,19	0,98	3
ENGASE	64772	1,53	1,47	1,64	0,86	0,93	-0,05	0,17	2	-0,62	-0,24	0,73	-0,98	0
EPB49	2039	1,72	1,86	1,79	0,9	0,63	0,18	-0,84	1	0,98	0,94	0,77	0,28	2
EPHB6	2051	1,77	1,94	1,85	0,97	0,98	0,39	0,89	3	0,32	-0,66	0,59	-0,12	0
ERN2	10595	1,42	1,75	1,86	-0,04	0,61	0,95	0,49	1	0,57	0,81	1,02	0,95	3
FAU	2197	1,45	1,49	NA	1	1	1	NA	3	0,28	1,02	0,64	NA	1
FBXW10	10517	1,45	1,48	1,66	-1,32	0,17	-2,43	0,88	1	0,83	0,94	0,9	0,38	3
FCHO2	115548	1,43	1,69	1,82	0,94	0,94	0,45	0,59	2	-1,75	-0,56	-0,06	-1,94	0
FCRL6	343413	1,65	1,86	1,75	0,78	0,95	0,32	0,32	1	1,02	1,1	1,08	0,86	4
FERMT3	83706	1,73	1,73	1,75	0,51	-0,36	0,86	-0,25	1	-0,35	-0,71	0,89	0,86	2
FGF3	2248	1,57	1,79	1,81	0,22	0,98	0,96	0,88	3	0,87	0,64	0,99	0,04	2
FLJ11235	54508	1,85	1,85	1,82	0,95	1	0,76	0,77	2	1	0,28	0,93	0,95	3
FLJ20489	55652	1,65	1,74	1,86	-1,1	0,76	0,75	-1,8	0	0,82	0,8	0,93	1,15	3
FLJ34077	404033	1,74	1,81	1,6	0,61	0,44	0,42	0,94	1	0,23	-0,1	1,06	1,35	2
FNTB	2342	1,82	1,92	1,81	0,94	0,9	0,77	0,35	2	0,6	-1,3	0,98	0,08	1
G6PC	2538	1,57	1,85	1,85	0,85	0,95	0,73	0,98	3	0,2	0,5	0,02	0,67	0
GCLC	2729	1,78	1,83	1,83	1	0,36	0,77	0,39	1	1,02	0,6	0,99	0,89	3
GNMT	27232	1,78	1,8	1,74	0,96	0,03	0,87	0,01	2	1,02	-5,16	0,99	1,19	3
GNRH2	2797	1,64	1,85	1,9	0,71	0,93	0,73	0,99	2	0,86	1	0,7	0,94	3
GPR146	115330	1,55	1,61	1,7	-0,06	0,57	0,09	-0,25	0	1,02	-3,24	0,96	-0,35	2
GRID2	2895	1,8	1,81	1,85	0,96	0,11	0,59	-0,3	1	1,3	0,71	1,02	0,57	2
GRIN2C	2905	1,75	1,79	1,83	0,85	0,86	0,39	0,28	2	0,33	-47,73	0,64	0,92	1
GRP	2922	1,61	1,79	1,75	0,82	0,57	0,86	0,83	3	-0,33	0,73	0,09	0,56	0
GSK3A	2931	1,71	1,85	1,87	0,62	0,96	0,37	0,71	1	0,93	0,64	0,94	-0,69	2
HARBI1	9776	1,46	1,77	1,74	0,31	0,88	0,74	0,83	2	0,54	0,9	-1,17	0,48	1
HIBCH	26275	1,49	1,53	1,73	0,2	0,36	-0,29	0,11	0	1,06	0,8	-0,46	0,98	3
HIST1H2BN	8341	1,69	1,64	1,67	0,89	0,99	-1,17	-0,04	2	1	1	0,64	-0,01	2
HPGD	3248	1,77	1,83	1,83	0,47	0,38	0,93	0,19	1	1,02	0,28	0,9	0,94	3
HSF4	3299	1,86	1,72	1,81	0,99	0,91	0,84	0,86	4	0,81	1	-8,36	1,01	3
HSPD1	3329	1,53	1,71	1,67	0,93	0,97	-0,21	0,59	2	1,02	0,3	0,98	0,95	3
ICAM2	3384	1,89	1,9	1,85	0,98	0,94	0,46	0,21	2	0,95	-1,1	0,82	1,11	3
ICEBERG	59082	1,48	1,44	1,74	0,55	0,53	-6,7	0,39	0	1,02	0,94	-0,54	0,94	3
IL17RA	23765	1,81	1,8	1,78	1	0,03	-0,09	-0,05	1	1,04	0,48	1,01	-1,44	2
IL1A	3552	1,58	1,67	1,43	0,7	0,97	0,35	0,66	1	1	1	0,95	-4,12	3

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
IQCF2	389123	1,79	1,89	1,8	0,85	-0,26	0,57	-0,86	1	1,15	-0,37	1,19	0,35	2
IRF2	3660	1,6	1,59	1,88	0,12	0,95	-0,66	0,95	2	0,97	0,68	0,41	0,61	1
ISG15	9636	1,82	1,79	NA	0,85	0,49	0,97	NA	2	1	0,85	0,21	NA	2
ITLN1	55600	1,74	1,77	1,72	0,91	0,99	0,89	0,59	3	0,59	0,86	1,02	0,71	2
JARID1D	8284	1,85	1,89	1,75	0,02	-0,43	0,6	0,56	0	0,29	0,1	0,83	1,28	2
JUN	3725	1,47	1,57	1,52	0,61	1	0,57	0,97	2	0,75	0,99	1,01	0,65	2
KATNB1	10300	1,38	1,38	1,55	0,73	0,96	-0,26	0,7	1	0,9	0,97	0,35	0,31	2
KCNAB3	9196	1,81	1,87	1,71	0,91	0,79	0,99	0,18	2	0,53	0,13	-0,12	0,86	1
KCNJ12	3768	1,65	1,34	1,49	-1,52	0,55	0,74	-0,41	0	0,97	1,01	1	0,73	3
KIAA0664	23277	1,71	1,7	1,75	0,97	-0,14	0,83	0,16	2	-0,15	-0,29	0,86	-10,73	1
KIAA0947	23379	1,83	1,9	1,67	0,73	0,99	0,49	0,1	1	1,02	1,01	-1	0,94	3
KIAA1128	54462	1,87	1,91	1,83	0,46	0,65	0,68	0,53	0	0,48	0,82	0,1	1,32	2
KIAA1267	284058	1,88	1,9	1,74	0,86	0,41	0,89	0,4	2	0,88	0,94	0,62	-0,06	2
KIF11	3832	1,42	1,46	1,76	1	0,88	0,96	-0,35	3	-0,21	0,32	1	0,64	1
KIF23	9493	1,9	1,91	1,72	0,98	0,86	-0,13	0,93	3	0,91	0,42	0,52	0,7	1
KIF3A	11127	1,43	1,54	1,46	-0,08	0,82	0,34	1	2	0,44	1,02	0,54	1,35	2
KPNB1	3837	1,71	1,84	1,68	0,9	0,98	0,98	0,91	4	0,85	1,11	0,91	1,05	4
LAMC2	3918	1,62	1,59	1,89	0,76	0,9	0,72	0,77	1	1	0,7	0,99	0,85	3
LARP1	23367	1,54	1,7	1,66	0,97	1	0,98	0,79	3	-2,57	1	0,98	0,83	3
LHX3	8022	1,71	1,72	1,5	1	1	0,84	0,99	4	1	-3,65	0,58	0,96	2
LINGO1	84894	1,68	1,72	1,62	0,68	0,99	-0,72	0,64	1	0,42	1	0,88	-1,74	2
LOC162993	162993	1,79	1,81	1,75	0,76	0,32	-0,21	-0,57	0	1,19	0,98	-2,52	0,94	3
LOC399940	399940	1,32	1,56	1,73	0,66	-1,57	0,37	0,38	0	0,31	0,98	-0,23	1,07	2
LOC401431	401431	1,65	1,36	1,7	-1,91	1	-0,33	0,45	1	-0,21	0,97	0,56	1,04	2
LOC440733	440733	1,64	1,58	1,71	-0,67	0,84	-0,12	0,46	1	0,73	0,94	0,78	0,8	2
LPPR4	9890	1,86	1,78	1,78	0,93	1	-1,09	0,85	3	0,69	1	0,71	0,92	2
MAN2B1	4125	1,81	1,92	1,81	0,94	1	0,88	-1,68	3	-0,23	0,5	0,84	-0,41	1
MAP2K3	5606	1,65	1,8	1,87	0,87	0,83	0,28	0,83	3	0,51	0,4	-1,89	-0,65	0
MATN3	4148	1,75	1,82	1,75	0,38	0,78	0,62	0,64	0	-2,05	0,87	0,87	0,31	2
MED6	10001	1,54	1,53	1,71	1	0,98	1	0,96	4	0,62	0,92	1	1	3
MKL1	57591	1,58	1,73	1,87	0,86	0,7	0,64	0,71	1	0,37	0,68	0,89	0,96	2
MRPS12	6183	1,82	1,88	1,78	0,85	0,8	0,98	0,3	3	0,19	-0,13	0,23	-0,66	0
MYC	4609	1,72	1,76	1,63	0,96	0,66	1	0,83	3	0,85	0,99	1	-2,51	3
MYEF2	50804	1,86	1,9	1,85	0,9	0,87	-0,05	0,59	2	-3,19	-0,05	-5,79	0,75	0
MYOD1	4654	1,67	1,69	1,7	-0,89	0,86	0,87	0,67	2	-0,12	0,08	-9,36	-15,75	0
NAE1	8883	1,82	1,85	1,72	0,86	0,88	0,83	0,97	4	-1,3	- 155,63	0,8	0,44	1

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
NDUFV3	4731	1,51	1,6	1,68	0,48	0,9	0,37	0,88	2	-1,67	1,02	0,56	-0,49	1
NECAP2	55707	1,88	1,81	1,85	0,96	-0,91	0,89	-0,27	2	1,1	0,18	1,29	0,6	2
NEK8	284086	1,7	1,57	NA	0,93	0	-0,02	NA	1	1	0,84	0,88	NA	3
NEK9	91754	1,77	1,84	1,79	0,66	-1,3	0,83	0,94	2	0,61	0,46	0,99	0,46	1
NSF	4905	1,94	1,9	1,74	0,48	0,55	0,48	0,83	1	0,82	0,26	0,9	0,53	2
NTHL1	4913	1,84	1,83	1,71	0,48	0,86	-0,11	0,67	1	1,2	0	1,02	0,69	2
NUP205	23165	1,57	1,79	1,79	0,53	0,98	-2,15	0,88	2	1,13	0,92	0,8	0,96	4
NUP98	4928	1,83	1,87	1,8	0,98	0,93	0,91	0,99	4	1,28	1,11	1,14	1,24	4
NXF1	10482	1,57	1,55	1,64	0,92	0,94	1	1	4	1,21	1,01	1,17	1,25	4
ODZ4	26011	1,85	1,89	1,84	0,38	0,74	0,73	0,36	0	0,53	1,25	1,2	0,02	2
OPN1SW	611	1,84	1,79	1,87	0,86	0,95	0,18	-0,71	2	0,96	1,01	0,74	0,7	2
P76	196463	1,44	1,4	1,66	0,13	0,89	-0,36	-1,36	1	1,15	0,98	0,81	0,42	3
PCDH18	54510	1,66	1,68	1,65	0,16	0,68	0,97	0,91	2	-1,01	0,2	1,01	0,25	1
PHF2	5253	1,82	1,89	1,68	0,87	0,97	0,75	0,99	3	-0,23	1,05	0,07	-0,4	1
PIK3R5	23533	1,84	1,88	NA	0,98	-0,7	0,83	NA	2	0,99	-3,35	0,1	NA	1
PIK3R6	146850	1,65	1,73	1,68	-0,11	0,99	0,63	0,96	2	-0,63	1,1	0,26	0,42	1
PIN1	5300	1,65	1,72	1,51	0,95	0,9	1	0,61	3	-0,59	1	0,77	-0,46	1
PKHD1	5314	1,48	1,76	1,83	-1,01	0,8	-1,25	-0,14	0	0,7	1,13	0,89	-1,49	2
PKN1	5585	1,53	1,69	1,82	0,9	0,97	0,59	1	3	0,7	0,5	-1,9	0,78	0
PLAU	5328	1,78	1,84	1,69	0,98	0,92	0,51	0,83	3	0,67	0,33	1,24	-0,3	1
PLD2	5338	1,83	1,9	1,83	0,32	0,97	0,64	0,52	1	1,01	1,09	-0,06	-0,27	2
PLK3	1263	1,82	1,76	1,81	0,79	0,01	0,45	-0,67	0	1,2	1,07	0,97	-1,89	3
POLK	51426	1,69	1,68	1,81	0,78	0,55	0,96	0,78	1	1,18	0,36	0,87	0,7	2
POLR2H	5437	1,43	1,79	1,65	0,96	0,82	0,65	0,94	3	1,02	1,05	0,56	0,61	2
POLR2L	5441	1,59	1,76	1,72	0,65	0,94	-0,15	0,58	1	0,8	0,92	0,51	0,46	2
PPARA	5465	1,85	1,9	1,84	0,54	0,38	0,68	0,75	0	-6,98	0,57	0,81	0,91	2
PPP1R14D	54866	1,82	1,76	1,85	0,93	0,84	0,56	0,74	2	0,77	0,58	0,02	0,87	1
PRDX5	25824	1,62	1,74	1,87	-0,3	0,62	0,12	0,1	0	1,01	0,99	0,21	0,12	2
PRPF8	10594	1,6	1,67	1,74	0,66	0,65	0,96	0,83	2	1,09	0,29	1,29	1,08	3
PRPS1	5631	1,79	1,67	1,76	0,91	0,99	0,9	1	4	0,98	0,37	0,99	0,94	3
PRSS27	83886	1,88	1,78	1,78	0,06	1	0,79	0,92	2	0,99	0,9	0,93	0,5	3
PRX	57716	1,85	1,88	1,86	1,01	0,67	0,85	-1,64	2	1,21	-0,35	0,97	-1,56	2
PSENEN	55851	1,62	1,74	1,87	0,93	1	0,28	0,36	2	1,04	1,07	0,07	1,24	3
PSMA1	5682	1,86	1,79	NA	0,94	0,71	0,97	NA	2	0,77	1,03	-1,2	NA	1
PSMD2	5708	1,34	1,47	1,27	0,98	0,94	0,99	NA	3	-5,45	-0,07	1,02	NA	1
PTPLA	9200	1,52	1,82	1,75	0,92	0,82	0,41	0,87	3	0,62	1,01	0,6	0,66	1

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
PTPRN	5798	1,76	1,86	1,82	0,98	0,87	0,34	-1,48	2	1,26	0,86	-0,37	-0,75	2
RAB4A	5867	1,89	1,84	1,78	0,81	0,85	0,72	0,88	3	-1,57	0,44	-0,3	0,33	0
RAB6B	51560	1,58	1,59	1,8	0,75	0,94	0,41	-0,07	1	1,24	0,43	1,13	1,13	3
RACGAP1	29127	1,64	1,54	1,88	0,33	-0,25	0,69	-0,48	0	1,24	0,5	0,97	-0,21	2
RAX	30062	1,66	1,9	1,82	0,96	0,81	0,57	0,14	2	1,25	0,57	1,08	0,51	2
RBM42	79171	1,78	1,89	1,83	0,73	0,4	-0,23	0,05	0	1,11	0,99	-0,75	1,1	3
RETN	56729	1,83	1,8	NA	0,87	0,83	0,86	NA	3	0,9	-1,57	0,99	NA	2
RFFL	117584	1,68	1,92	1,88	0,91	0,97	0,42	-0,18	2	0,69	0,87	-0,6	0,77	1
RNF150	57484	1,7	1,82	1,68	0,37	0,49	-0,47	0,59	0	0,9	0,99	-0,32	0,95	3
RPL35	11224	1,61	1,48	1,31	0,96	0,98	0,98	0,96	4	1	0,1	0,5	0,55	1
RPLP2	6181	1,31	1,33	1,49	0,86	0,97	0,87	0,99	4	1,26	1,08	1,2	1,04	4
RPS10	6204	1,59	1,55	1,67	1	0,88	0,95	0,98	4	0,65	-0,26	0,8	-0,43	1
RPS14	6208	1,65	1,73	1,55	1	0,96	-0,06	1	3	0,97	-0,29	0,49	0,82	2
RPS16	6217	1,51	1,76	1,49	0,96	0,96	0,02	0,99	3	0,82	0,9	0,42	0,7	2
RPS27A	6233	1,39	1,42	NA	1	1	0,87	NA	3	0,74	0,96	0,47	NA	1
RPS5	6193	1,31	1,3	1,2	0,85	1	0,93	NA	3	0,96	1	0,17	NA	2
RPS6KA6	27330	1,75	1,9	1,69	0,17	0,92	0,96	0,1	2	-1,28	0,95	0,4	0,69	1
RUNX1	861	1,86	1,92	1,84	0,84	-0,15	0,76	0,16	1	0,91	0,87	0,95	-0,29	3
SAFB	6294	1,78	1,73	1,83	0,5	0,48	1	0,91	2	-5,89	1	0,82	0,82	3
SCAF1	58506	1,64	1,65	1,79	0,92	0,5	0,93	-0,02	2	1,01	0,62	-0,13	-0,63	1
SCAMP4	113178	1,82	1,87	1,37	0,68	0,96	0,97	0,66	2	0,1	0,57	1,35	1,02	2
SCARB1	949	1,32	1,52	1,77	0,94	0,99	0,27	0,71	2	0,17	-2,22	0,82	-0,2	1
SDC1	6382	1,64	1,62	1,63	-0,67	0,72	0,86	0,91	2	0,4	-0,06	0,91	0,36	1
SELPLG	6404	1,85	1,86	1,84	0,08	0,94	-0,74	0,53	1	-0,96	0,98	0,86	0,76	2
SERPINA6	866	1,63	1,83	1,88	0,67	0,95	0,95	0,78	2	0,28	0,34	-2,4	-0,75	0
SERPINB2	5055	1,73	1,83	1,76	0,84	-0,25	0,83	-0,36	2	0,34	0	0,12	0,15	0
SERPINE2	5270	1,45	1,54	1,83	0,75	0,89	0,41	0,85	2	1,2	0,8	0,3	0,4	1
SEZ6L2	26470	1,3	1,75	1,58	0,03	0,95	-0,43	0,93	2	0,6	-0,16	-1,49	1,08	1
SF3A1	10291	1,8	1,88	1,69	0,94	0,91	-0,65	0,84	3	1,16	0,24	0,65	0,8	2
SF3B1	23451	1,6	1,46	1,41	-0,03	0,99	1	1	3	0,13	1	0,98	0,46	2
SF3B14	51639	1,72	1,72	1,83	1	1	1	1	4	1,04	0,96	1	1,06	4
SFTPB	6439	1,82	1,84	1,5	0,29	0,97	0,87	0,99	3	0,59	0,7	0,16	0,45	0
SIGMAR1	10280	1,54	1,58	1,49	0,97	-0,75	0,56	0,36	1	1	1	0,8	0,7	2
SLC12A4	6560	1,69	1,66	1,8	0,44	0,68	0,82	0,98	2	-0,8	-0,15	0,35	0,74	0
SLC22A6	9356	1,75	1,87	1,85	-1,56	0,78	-0,6	0,91	1	0,87	0,09	0,61	0,91	2
SLC25A19	60386	1,48	1,72	1,63	0,95	0,44	-0,83	0,89	2	0,48	0,29	-0,57	-3,18	0

Table 3

GeneSymbol	LocusID	siRNA2 WST	siRNA3 WST	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
SLC4A8	9498	1,67	1,5	1,65	0,71	-0,02	0,27	-0,69	0	-0,24	0,9	0,83	0,6	2
SLC7A1	6541	1,73	1,84	1,83	0,16	0,74	-0,79	0,18	0	0,57	0,95	0,96	-0,8	2
SMU1	55234	1,84	1,86	1,83	0,89	0,8	-0,42	-0,21	2	0,96	0,79	-0,02	0,93	2
SNRP70	6625	1,54	1,65	1,71	0,23	0,88	-0,01	0,91	2	0,41	1,03	-0,22	0,91	2
SNRPF	6636	1,6	1,49	1,59	0,95	-2,32	0,99	0,81	3	-3,57	0,75	-2,57	-0,79	0
SNX6	58533	1,88	1,85	1,81	0,81	0,91	0,8	0,82	3	0,33	1,18	-0,93	0,91	2
SNX9	51429	1,83	1,89	1,83	0,89	0,36	0,3	0,55	1	1,27	1,13	0,24	1,2	3
SON	6651	1,31	1,32	1,21	0,94	0,94	0,89	NA	3	0,87	1,28	0,93	NA	3
SRRM2	23524	1,62	1,76	1,89	0,59	0,22	0,29	0,88	1	-0,04	0,97	1,13	0,87	3
STAB1	23166	1,47	1,55	1,47	0,98	1	0,95	0,92	4	1	-1,21	-2,27	0,36	1
SULF2	55959	1,79	1,87	1,85	0,61	0,67	0,93	0,95	2	0,87	0,67	0,7	0,51	1
SUPT6H	6830	1,58	1,62	1,64	-1,15	1	0,98	0,99	3	0,77	0,64	0,57	0,99	1
TBL3	10607	1,83	1,87	1,78	0,96	0,89	0,73	0,8	2	1,17	0,48	0,86	-11,7	2
TCF3	6929	1,72	NA	NA	0,88	0,51	NA	NA	1	1,02	1	NA	NA	2
TFE3	7030	1,74	1,7	1,68	0,93	0,83	0,98	0,49	3	0,95	0,96	-0,21	0,38	2
TMEM50B	757	1,77	1,84	1,79	0,01	0,63	0,28	-0,44	0	0,25	0,91	1	0,95	3
TNFRSF18	8784	1,58	1,74	1,75	0,36	0,89	0,7	0,89	2	0,47	-0,05	0,55	0,51	0
TNK2	10188	1,87	1,9	1,81	0,56	0,96	0,91	0,13	2	1,06	1,25	0,7	0,06	2
TRERF1	55809	1,8	1,57	1,78	1	-1,72	1	0,96	3	1	0,75	1,02	0,82	3
TRIM14	9830	1,53	1,49	1,57	-0,2	0,49	0,07	0,89	1	0,63	0,91	0,76	1	2
TRIM21	6737	1,83	1,89	1,84	-1,27	0	0,38	0,64	0	0,43	0,84	-0,62	1,16	2
TRIM60	166655	1,83	1,82	1,83	-0,89	0,83	0,51	0,82	2	0,98	0,79	0,93	-1,02	2
TSSK6	83983	1,48	1,57	1,72	-0,44	0,66	-0,05	0,99	1	0,92	0,4	0,63	1,01	2
TUBB4	10382	1,84	1,87	1,81	0,9	0,94	0,88	0,78	3	0,94	-0,79	0,97	0,2	2
TXNL4A	10907	1,43	1,64	1,74	-0,72	0,95	-0,28	0,97	2	0,14	1,04	-1,09	0,87	2
UBAC2	337867	1,85	NA	NA	1	0,86	NA	NA	2	0,9	0,95	NA	NA	2
UBE2N	7334	1,86	1,91	1,8	0,88	0,25	0,47	0,88	2	0,52	0,49	0,7	1,05	1
VNN2	8875	1,82	1,88	1,82	0,26	0,4	0,51	1	1	0,48	0,11	1,02	1,1	2
WNT3A	89780	1,91	1,87	1,77	0,36	-0,16	0,64	0,81	1	0,53	0,4	0,91	1,1	2
WNT9A	7483	1,53	1,62	1,45	1	0,55	0,01	1	2	1,02	-0,3	1	1	3
XAB2	56949	1,68	1,78	NA	0,95	1	0,92	NA	3	0,67	1,06	1,05	NA	2
XPNPEP1	7511	1,84	1,82	1,82	-0,14	0,97	0,42	0,92	2	0,8	0,99	-1,13	0,06	1
XPO1	7514	1,83	1,84	1,8	0,91	0,96	-0,37	0,28	2	0,87	0,86	0,48	0,79	2
XRCC6	2547	1,63	1,61	1,69	0,47	-0,45	0	-0,32	0	-0,27	1,13	0,84	-0,22	2

Table 4

1

GeneSymbol	LocusID	Gene Description	siRNA1_ID	siRNA2_ID	siRNA3_ID	siRNA4_ID
ACTN1	87	ACTININ, ALPHA 1	Hs_ACTN1_13	Hs_ACTN1_8	Hs_ACTN1_7	Hs_ACTN1_4
ATP6AP2	10159	ATPASE, H+ TRANSPORTING, LYSOSOMAL ACCESSORY PROTEIN 2	Hs_ATP6AP2_7	Hs_ATP6AP2_8	Hs_ATP6AP2_6	Hs_ATP6AP2_4
ATP6V1B2	526	ATPASE, H+ TRANSPORTING, LYSOSOMAL 56/58KDA, V1 SUBUNIT B2	Hs_ATP6V1B2_2	Hs_ATP6V1B2_4	Hs_ATP6V1B2_5	Hs_ATP6V1B2_6
BNIP3L	665	BCL2/ADENOVIRUS E1B 19KDA INTERACTING PROTEIN 3-LIKE	Hs_BNIP3L_7	Hs_BNIP3L_12	Hs_BNIP3L_10	Hs_BNIP3L_1
BRUNOL6	60677	BRUNO-LIKE 6, RNA BINDING PROTEIN (DROSOPHILA)	Hs_BRUNOL6_8	Hs_BRUNOL6_7	Hs_BRUNOL6_5	Hs_BRUNOL6_9
CUEDC2	79004	CUE DOMAIN CONTAINING 2	Hs_CUEDC2_5	Hs_CUEDC2_6	Hs_CUEDC2_4	Hs_CUEDC2_3
CYC1	1537	CYTOCHROME C-1	Hs_CYC1_1	Hs_CYC1_2	Hs_CYC1_3	Hs_CYC1_4
FNTB	2342	FARNESYLTRANSFERASE, CAAX BOX, BETA	Hs_FNTB_7	Hs_FNTB_1	Hs_FNTB_10	Hs_FNTB_3
GCLC	2729	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	Hs_GCLC_4	Hs_GCLC_7	Hs_GCLC_10	Hs_GCLC_11
GNRH2	2797	GONADOTROPIN-RELEASING HORMONE 2	Hs_GNRH2_8	Hs_GNRH2_7	Hs_GNRH2_6	Hs_GNRH2_5
GRIN2C	2905	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	Hs_GRIN2C_1	Hs_GRIN2C_2	Hs_GRIN2C_3	Hs_GRIN2C_5
GRP	2922	GASTRIN-RELEASING PEPTIDE	Hs_GRP_6	Hs_GRP_9	Hs_GRP_8	Hs_GRP_7
HARBI1	9776	KIAA0652	Hs_KIAA0652_7	Hs_KIAA0652_3	Hs_KIAA0652_4	Hs_KIAA0652_5
HSPD1	3329	heat shock 60kDa protein 1 (chaperonin)	Hs_HSPD1_5	Hs_HSPD1_7	Hs_HSPD1_8	Hs_HSPD1_1
ICAM2	3384	INTERCELLULAR ADHESION MOLECULE 2	Hs_ICAM2_4	Hs_ICAM2_5	Hs_ICAM2_7	Hs_ICAM2_3
KCNJ12	3768	potassium inwardly-rectifying channel, subfamily J, member 12	Hs_KCNJ12_2	Hs_KCNJ12_4	Hs_KCNJ12_5	Hs_KCNJ12_6
KPNB1	3837	KARYOPHERIN (IMPORTIN) BETA 1	Hs_KPNB1_2	Hs_KPNB1_3	Hs_KPNB1_6	Hs_KPNB1_4
LAMC2	3918	LAMININ, GAMMA 2	Hs_LAMC2_1	Hs_LAMC2_4	Hs_LAMC2_2	Hs_LAMC2_3
LOC440733	440733	similar to 40S ribosomal protein S15 (RIG protein)	Hs_LOC440733_11	Hs_LOC440733_12	Hs_LOC440733_13	Hs_LOC440733_14
MKL1	57591	MEGAKARYOBLASTIC LEUKEMIA (TRANSLOCATION) 1	Hs_MKL1_1	Hs_MKL1_8	Hs_MKL1_6	Hs_MKL1_7
MRPS12	6183	MITOCHONDRIAL RIBOSOMAL PROTEIN S12	Hs_MRPS12_7	Hs_MRPS12_1	Hs_MRPS12_3	Hs_MRPS12_8
MYEF2	50804	MYELIN EXPRESSION FACTOR 2	Hs_MYEF2_4	Hs_MYEF2_5	Hs_MYEF2_8	Hs_MYEF2_3
NDUFV3	4731	NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN 3, 10KDA	Hs_NDUFV3_3	Hs_NDUFV3_4	Hs_NDUFV3_5	Hs_NDUFV3_6
NECAP2	55707	NECAP ENDOCYTOSIS ASSOCIATED 2	Hs_FLJ10420_3	Hs_NECAP2_1	Hs_NECAP2_3	Hs_NECAP2_2
ODZ4	26011	odz, odd Oz/ten-m homolog 4 (Drosophila)	Hs_ODZ4_2	Hs_ODZ4_3	Hs_ODZ4_4	Hs_ODZ4_5
PIK3R6	146850	CHROMOSOME 17 OPEN READING FRAME 38	Hs_C17orf38_3	Hs_C17orf38_4	Hs_C17orf38_5	Hs_C17orf38_6

Table 4

2

GeneSymbol	LocusID	Gene Description	siRNA1 ID	siRNA2 ID	siRNA3 ID	siRNA4 ID
PPARA	5465	PEROXISOME PROLIFERATIVE ACTIVATED RECEPTOR, ALPHA	Hs_PPARA_8	Hs_PPARA_7	Hs_PPARA_6	Hs_PPARA_5
RAB4A	5867	RAB4A, MEMBER RAS ONCOGENE FAMILY	Hs_RAB4A_5	Hs_RAB4A_11	Hs_RAB4A_10	Hs_RAB4A_9
SCAF1	58506	SERINE ARGININE-RICH PRE-MRNA SPLICING FACTOR SR-A1	Hs_SR-A1_2	Hs_SR-A1_3	Hs_SR-A1_4	Hs_SR-A1_5
SCARB1	949	scavenger receptor class B, member 1	Hs_SCARB1_6	Hs_SCARB1_7	Hs_SCARB1_8	Hs_SCARB1_9
SERPINA6	866	SERPIN PEPTIDASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 6	Hs_SERPINA6_4	Hs_SERPINA6_3	Hs_SERPINA6_1	Hs_SERPINA6_5
SERPINB2	5055	serpin peptidase inhibitor, clade B (ovalbumin), member 2	Hs_SERPINB2_2	Hs_SERPINB2_5	Hs_SERPINB2_6	Hs_SERPINB2_7
SERPINE2	5270	SERPIN PEPTIDASE INHIBITOR, CLADE E (NEXIN, PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1), MEMBER 2	Hs_SERPINE2_6	Hs_SERPINE2_1	Hs_SERPINE2_7	Hs_SERPINE2_10
SEZ6L2	26470	seizure related 6 homolog (mouse)-like 2	Hs_SEZ6L2_10	Hs_SEZ6L2_7	Hs_SEZ6L2_8	Hs_SEZ6L2_9
TBL3	10607	TRANSDUCIN (BETA)-LIKE 3	Hs_TBL3_4	Hs_TBL3_3	Hs_TBL3_5	Hs_TBL3_6
TRERF1	55809	transcriptional regulating factor 1	Hs_TRERF1_3	Hs_TRERF1_6	Hs_TRERF1_7	Hs_TRERF1_8
TRIM60	166655	tripartite motif-containing 60	Hs_TRIM60_3	Hs_TRIM60_6	Hs_TRIM60_7	Hs_TRIM60_8
TUBB4	10382	TUBULIN, BETA 4	Hs_TUBB4_2	Hs_TUBB4_3	Hs_TUBB4_6	Hs_TUBB4_5

Table 4

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GeneSymbol	LocusID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST	siRNA2 WST	siRNA3 WST
ACTN1	87	AACACCATGCATGCCATGCAA	CCGGCCCGAGCTGATTGACTA	AAGGATGATCCACTCACAAAT	AACGATTACATGCAGCCAGAA	1,74	1,64	1,68
ATP6AP2	10159	GGGAACGAGTTTAGTATATTA	ATGTGCTTATATAATCGCTTA	AACATGGATCCTGGATATGAT	TCCCTATAACCTTGCATATAA	1,84	1,87	1,93
ATP6V1B2	526	CAGGCTGGTTTGGTAAAGAAA	ACCATGTTACCCTGTAATTAA	GAGGATATGCTTGGTCGGGTA	CAGGGTAATCTTTGTGGCACA	1,55	1,55	1,8
BNIP3L	665	TAGCATTTGATGTCTAAATAA	AAACGAGATCAGGTTAGCAAA	CTGGGTGGAGCTACCCATGAA	AAGAAAAGTGCGGACTGGGTA	1,63	1,65	1,8
BRUNOL6	60677	CCCACCTGTAAAGTAGATTCA	TACCTTCTGTCTCTTAGTCTA	AAGCTGATCAATGGTGGTGAA	CTGAAGGCCTCTGATCTGATA	1,87	1,88	1,88
CUEDC2	79004	CCCGACGGAGCAGAAGAGAGA	CGGCCCGAAATGCTCAAAGAA	TTGCTCCATAGTGTTAACCTA	ATGCTGGTAGAGGGAAAGGAA	1,72	1,5	1,33
CYC1	1537	CCCATCATGGGAATAAATTAA	CAGCATGGACTTCGTGGCCTA	TACCATGTCCCAGATAGCCAA	GCGGGAAGGTCTCTACTTCAA	1,8	1,47	1,7
FNTB	2342	CACGTCCATAGAACAGGCAAA	ACCCACATATGCAGCAGTCAA	CTCCGTAGCCTCGCTGACCAA	TCCGCTCGCCGTAGCGCTTTA	1,67	1,82	1,92
GCLC	2729	CCGGATCATATTTACATGGAT	CATCGACTTGACGATAGATAA	CACCCTCGCTTCAGTACCTTA	ATCAGGCTCTTTGCACAATAA	1,78	1,78	1,83
GNRH2	2797	CCCGCCATCCTCCAATAAAGT	CTGAAGGAGCCATCTCATCCA	TGGCTGGTACCCTGGAGGAAA	CAGACTGCCCATGGCCTCCCA	1,83	1,64	1,85
GRIN2C	2905	CTGGACGAGATCAGCAGGGTA	CCCAGCTTTCACTATCGGCAA	CACCCACATGGTCAAGTTCAA	GTCGATGTGCTTGCCGATCTA	1,75	1,75	1,79
GRP	2922	ATCAGTTCTACGGATCATCAA	CCAGCTGAACCAGCAATGATA	CAGAGGATAGCAGCAACTTCA	CGGAGGGACCGTGCTGACCAA	1,75	1,61	1,79
HARBI1	9776	CTGGGCGTATGATTGACTTAA	CAGGAAGTCCTGGGTGCTAAA	CAGGTATTGTTACTTGAATAA	AAGGCGGGAGTGACCGCTTAA	1,51	1,46	1,77
HSPD1	3329	AAGGCTTCGAGAAGATTAGCA	CACCACCAGATGAGAAGTTAA	CAGGGTTTGGTGACAATAGAA	CGGGCTTATGCCAAAGATGTA	1,63	1,53	1,71
ICAM2	3384	CGGGAAGCAGGAGTCAATGAA	TCCCATGACACGGTCCTCCAA	CACGGTGGTCACTGGAACTCA	AACATCTTTCACAAACACTCA	1,81	1,89	1,9
KCNJ12	3768	TTGGGTGAGACTGTTTACAAA	TGCGAAGGATCTGGTAGAGAA	CAGCTCCTACCTGGCCAATGA	CTCGCACTTCCACAAGACCTA	1,64	1,65	1,34
KPNB1	3837	CAAGAACTCTTTGACATCTAA	AAGGGCGGAGATCGAAGACTA	CTGGAATCGTCCAGGGATTAA	CTGGTACAACCCAGAGTAGAA	1,73	1,71	1,84
LAMC2	3918	CAGGCATATGGATGAGTTCAA	CCCAATTGGTTTCTACAACGA	CCGGACGGTGCTGTGGTGCAA	TACTTTGAGTATCGAAGGTTA	1,64	1,62	1,59
LOC440733	440733	ATCATGATGGTTAGCCATTTA	CAGCTGAAACTTTCTTGATCA	AAAGAGCATTATCTAAGTAAT	AACAACCTTTAGATATGCAAA	1,64	1,64	1,58
MKL1	57591	TAGTGTCTTGGTGTAGTGTAA	AGCAAGATTGCCATCACGAAA	AAGGGCCTGGATGCAAGGTTA	ATCACGTGTGATTGACATGTA	1,67	1,58	1,73
MRPS12	6183	TTCCATCAGGACCACTATTAA	CACGTTTACCCGCAAGCCGAA	CCCACTCAGAGCGAGGCTAAA	ACCCTGGCGCTTGTGATGTAA	1,61	1,82	1,88
MYEF2	50804	CAGAATAATGAATGGCATAAA	ATCGATATGGATCGAGGATTT	CTCGTAGGGCATTGCAGCGAA	TCCTTTAATGTTGTAATTGAA	1,87	1,86	1,9
NDUFV3	4731	ACACTGATTATCCAACATATA	ATCCATATAATTAGAGAATTT	CCCGCTGTGCATAATCGGTTT	CTGAGCCGTTTGACAACACTA	1,44	1,51	1,6
NECAP2	55707	AAGGAGCTCAGTAAACTAGAA	CAGGTACTTCGTGATCCGCAT	CAACATCGCAAACATGAAGAA	CTGCAGCTTGAGCTACAATCA	1,8	1,88	1,81
ODZ4	26011	CCGGCCGGCCTTTAACCTCAA	CCGCAGGGTGATATACAAGTA	TCGGTTTATCCGGAAGAACAA	CTGCGGGTTCACAACCGAAAT	1,81	1,85	1,89
PIK3R6	146850	TCGCTGGACAAGGACGATCAA	CACCTTCAGGACGAACAATAT	CAGGGATGTGGTCAGATTCGA	TCGCCGCACCCTGGAGCACTA	1,7	1,65	1,73

Table 4

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GeneSymbol	LocusID	siRNA1 Target	siRNA2 Target	siRNA3 Target	siRNA4 Target	siRNA1 WST	siRNA2 WST	siRNA3 WST
PPARA	5465	TCGGCGAACGATTCGACTCAA	CAGTGGAGCATTGAACATCGA	CAAGAGAATCTACGAGGCCTA	AAGCTTTGGCTTTACGGAATA	1,71	1,85	1,9
RAB4A	5867	AATGCAGGAACTGGCAAATCT	CACACTTGAAATACTAGATCA	AAGATGACTCAAATCATACAA	CAGGTCCGTGACGAGAAGTTA	1,73	1,89	1,84
SCAF1	58506	CTGGGCTCCATTGGCGTCAAA	CTGGACGTATTTATGGCTCCA	CACGGTGGGCCGGCTTGACAA	CACGGCTACTGTGTTGGACAT	1,64	1,64	1,65
SCARB1	949	CCGATCCATGAAGCTAATGTA	TAGGGAGAGGCTCGTCAACAA	CACCGTGTCCTTCCTCGAGTA	CAGCGAGATCCTGAAGGGCGA	1,41	1,32	1,52
SERPINA6	866	CAGCAGACAGATCAACAGCTA	CAACAGCTATGTCAAGAATAA	CACCAGCTTAGAAATGACTAT	AGGGTTATGAACCCAGTGTAA	1,75	1,63	1,83
SERPINB2	5055	CAGAAGGGTAGTTATCCTGAT	AACCTATGACAAACTCAACAA	CTGGAAAGTGAAATAACCTAT	TGCGAGCTTCCGGGAAGAATA	1,73	1,73	1,83
SERPINE2	5270	CTGGGAGGTATTGGAGGGAAA	AACGCCGTGTTTGTTAAGAAT	CGGCGTAAATGGAGTTGGTAA	AACTCCTGTCTTGCTAGACAA	1,45	1,45	1,54
SEZ6L2	26470	TCCATGCTTGGAGAAGGACAA	CAGGATCCACTATCAGGCCTA	CCGGCTGCTTCTGCACTTCCA	CTCGCTGGATGAGGACAATGA	1,4	1,3	1,75
TBL3	10607	CCGTATCTGGAGAATGAACAA	CTGCGTCACGTGGAACACCAA	CCACGTTGTCGTGGCCTCCAA	CTGGGACATCGTGCGGCACTA	1,75	1,83	1,87
TRERF1	55809	CCGCAACAAATTCGCCCATCA	AGAGTGGGTACTGTTCGGTAA	CAGCGTATCTCCATGCAAGAA	CTGCGGAAGCCTGTCAGGTTA	1,81	1,8	1,57
TRIM60	166655	GAGCCCTTGAGGAATAATATA	TTGCGTCAGGTCCTAAGACAA	AAGGATCTAGATGATACCTTT	AGCTCCGTAATTTGACTGAAA	1,78	1,83	1,82
TUBB4	10382	CTGCCTCACCCTCAATAAATA	TGAGCCCTAATTTATCTTTAA	CTCTGGAAACCGCACCTTTAA	CTCGAGGCTTCTGACCTTTGA	1,77	1,84	1,87

Table 4

GeneSymbol	LocusID	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
ACTN1	87	1,9	-1,68	0,63	-0,42	0,13	0	1,03	0,97	0,26	-0,4	2
ATP6AP2	10159	1,84	0,8	0,67	0,83	0,49	2	1,01	0,74	0,98	0,93	3
ATP6V1B2	526	1,89	0,88	0,8	0,46	0,99	2	1,25	1,13	-0,26	1,02	3
BNIP3L	665	1,87	0,87	-0,67	0,72	0,92	2	0,72	0,95	0,66	0,98	2
BRUNOL6	60677	1,77	0,12	-0,66	0,87	0,83	2	-0,01	-4,07	1,38	1,32	2
CUEDC2	79004	1,5	0,78	1	0,82	0,89	3	1,16	0,48	1,08	-0,29	2
CYC1	1537	1,84	-0,93	0,39	0,85	0,93	2	0,18	0,5	1,1	0,36	1
FNTB	2342	1,81	0,94	0,9	0,77	0,35	2	0,6	-1,3	0,98	0,08	1
GCLC	2729	1,83	1	0,36	0,77	0,39	1	1,02	0,6	0,99	0,89	3
GNRH2	2797	1,9	0,71	0,93	0,73	0,99	2	0,86	1	0,7	0,94	3
GRIN2C	2905	1,83	0,85	0,86	0,39	0,28	2	0,33	-47,73	0,64	0,92	1
GRP	2922	1,75	0,82	0,57	0,86	0,83	3	-0,33	0,73	0,09	0,56	0
HARBI1	9776	1,74	0,31	0,88	0,74	0,83	2	0,54	0,9	-1,17	0,48	1
HSPD1	3329	1,67	0,93	0,97	-0,21	0,59	2	1,02	0,3	0,98	0,95	3
ICAM2	3384	1,85	0,98	0,94	0,46	0,21	2	0,95	-1,1	0,82	1,11	3
KCNJ12	3768	1,49	-1,52	0,55	0,74	-0,41	0	0,97	1,01	1	0,73	3
KPNB1	3837	1,68	0,9	0,98	0,98	0,91	4	0,85	1,11	0,91	1,05	4
LAMC2	3918	1,89	0,76	0,9	0,72	0,77	1	1	0,7	0,99	0,85	3
LOC440733	440733	1,71	-0,67	0,84	-0,12	0,46	1	0,73	0,94	0,78	0,8	2
MKL1	57591	1,87	0,86	0,7	0,64	0,71	1	0,37	0,68	0,89	0,96	2
MRPS12	6183	1,78	0,85	0,8	0,98	0,3	3	0,19	-0,13	0,23	-0,66	0
MYEF2	50804	1,85	0,9	0,87	-0,05	0,59	2	-3,19	-0,05	-5,79	0,75	0
NDUFV3	4731	1,68	0,48	0,9	0,37	0,88	2	-1,67	1,02	0,56	-0,49	1
NECAP2	55707	1,85	0,96	-0,91	0,89	-0,27	2	1,1	0,18	1,29	0,6	2
ODZ4	26011	1,84	0,38	0,74	0,73	0,36	0	0,53	1,25	1,2	0,02	2
PIK3R6	146850	1,68	-0,11	0,99	0,63	0,96	2	-0,63	1,1	0,26	0,42	1

Table 4

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GeneSymbol	LocusID	siRNA4 WST	siRNA1 NPI WSN	siRNA2 NPI WSN	siRNA3 NPI WSN	siRNA4 NPI WSN	Hits per gene WSN	siRNA1 NPI HH	siRNA2 NPI HH	siRNA3 NPI HH	siRNA4 NPI HH	Hits per gene HH
PPARA	5465	1,84	0,54	0,38	0,68	0,75	0	-6,98	0,57	0,81	0,91	2
RAB4A	5867	1,78	0,81	0,85	0,72	0,88	3	-1,57	0,44	-0,3	0,33	0
SCAF1	58506	1,79	0,92	0,5	0,93	-0,02	2	1,01	0,62	-0,13	-0,63	1
SCARB1	949	1,77	0,94	0,99	0,27	0,71	2	0,17	-2,22	0,82	-0,2	1
SERPINA6	866	1,88	0,67	0,95	0,95	0,78	2	0,28	0,34	-2,4	-0,75	0
SERPINB2	5055	1,76	0,84	-0,25	0,83	-0,36	2	0,34	0	0,12	0,15	0
SERPINE2	5270	1,83	0,75	0,89	0,41	0,85	2	1,2	0,8	0,3	0,4	1
SEZ6L2	26470	1,58	0,03	0,95	-0,43	0,93	2	0,6	-0,16	-1,49	1,08	1
TBL3	10607	1,78	0,96	0,89	0,73	0,8	2	1,17	0,48	0,86	-11,7	2
TRERF1	55809	1,78	1	-1,72	1	0,96	3	1	0,75	1,02	0,82	3
TRIM60	166655	1,83	-0,89	0,83	0,51	0,82	2	0,98	0,79	0,93	-1,02	2
TUBB4	10382	1,81	0,9	0,94	0,88	0,78	3	0,94	-0,79	0,97	0,2	2

International application No.

PCT/EP2010/070548

INTERNATIONAL SEARCH REPORT

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   ☒ on paper

   ☒ in electronic form

   b. (time)

   ☐ in the international application as filed

   ☐ together with the international application in electronic form

   ☒ subsequently to this Authority for the purpose of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2010/070548

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N15/113 A61P31/16 A61K31/713
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N A61K

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

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

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

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2008/043561 A2 (MAX PLANCK GESELLSCHAFT [DE]; MEYER THOMAS F [DE]; KARLAS ALEXANDER [D) 17 April 2008 (2008-04-17) the whole document -----	1-37
X	HAO, L. ET AL.: "Drosophila RNAi screen identifies host genes important for influenza virus replication", NATURE, vol. 454, 20 August 2001 (2001-08-20), pages 890-893, XP002629478, cited in the application the whole document ----- -/--	1-8, 10-16, 18-21, 23-25, 27,28, 30-32

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

☒ See patent family annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
23 March 2011	01/04/2011

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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/172489 A1 (LUDWIG STEFAN [DE] ET AL) 26 July 2007 (2007-07-26)	1-7, 10-15, 18,19
A	the whole document	8,9,16, 17,20-37
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